



ishp  b
2021

PROGRAM

In partnership with and hosted virtually by

Cold Spring Harbor Laboratory

July 13, 14, 15, 19 & 20

CSHL Historical Images:

Cover: Students at the harbor, with Jones Laboratory on the right, circa 1897.

Page 3: George Shull's field of hybrid corn, next to the Carnegie Laboratory, built 1905. (See: "The Composition of a Field of Maize," *Journal of Heredity*, Volume 05-4, Issue 1 (January 1908): 296–301.)

Page 7: The propagating house. (Director Charles Davenport noted in 1906: "During the year, three greenhouses... have been completed. One of the houses is used during the winter, for the cultivation of lettuce and grasses required as food by the canaries and young poultry.")

Page 13: Students at CSHL, circa 1890-1895.

Page 17: Overview of the CSHL grounds. Around 1910, scientists at the Station for Experimental Evolution studied hereditary traits such as twin inheritance, extra nipples and double horns in sheep and goats, among other Mendelian characters. (These studies led Alexander Graham Bell to donate a black ram with 6 nipples and a 4-horned, 3-nippled sheep.)

Back cover: Research laboratories at CSHL, ranging from the historic Jones Laboratory of 1893, the oldest laboratory in continuous use, to the newly built Hillside campus. (Photo circa 2015.)

Program Directory

[Welcome from President](#)

[Welcome from Program Chairs](#)

[Officers and Committee Chairs 2019-21](#)

[Template for the start times of talks and breaks](#)

[Instructions to attendees, chairs, and presenters](#)

[Twitter style guide](#)

[Social media and recording etiquette guide](#)

[Timetable](#)

[Schedule](#)

[Abstracts](#)

[Index](#)

[Sponsors](#)



Welcome from the President

Hello! If there were an ISHPSSB Presidential sash, I'd gladly put it on, to welcome you in ceremonial splendor. But all I've got along those lines are some old conference goodies: a T-shirt from Oslo (2019); a bag from São Paulo (2017); a folder from Salt Lake City (2011); and a bag from Exeter (2007). Here's the result:



For this 2021 edition of the conference, hosted virtually by Cold Spring Harbor Laboratory, there are no bags etc., alas. But there are sessions galore, spanning the usual, invigoratingly interdisciplinary range, and running in parallel over the course of five days. There are timely plenaries, on Darwin's *Descent of Man* (150 years old this year), on the open data movement (25 years after the Bermuda Principles), and on “viral vulnerabilities” (all too current). There are meetings for the membership as a whole, to discuss Society business and celebrate the recipients of our 2021 prizes. And there are all manner of informal opportunities for learning and exchange, from community-and-skill-building sessions, to “Happy Office Hours” (kind of like coffee breaks at an in-person ISH conference, but taking place inside a 1980s video game), to a virtual banquet.

Reimagining an ISH conference for the online world has been no small feat. For rising to the occasion so imaginatively and energetically, I'd like to extend deepest thanks, on behalf of the Society, to David Stewart and his team at Cold Spring Harbor Laboratory; to our Program Committee, chaired by Luis Campos and Roberta Millstein; and to our Virtual Local Organizing Committee, chaired by Matt Haber. Finally, I'd like to thank you, for the leap of faith you've made in joining us for this first virtual conference for the Society, and for your help from here in making it a success.

Off we go! Or as they say on Long Island: you comin' or what?

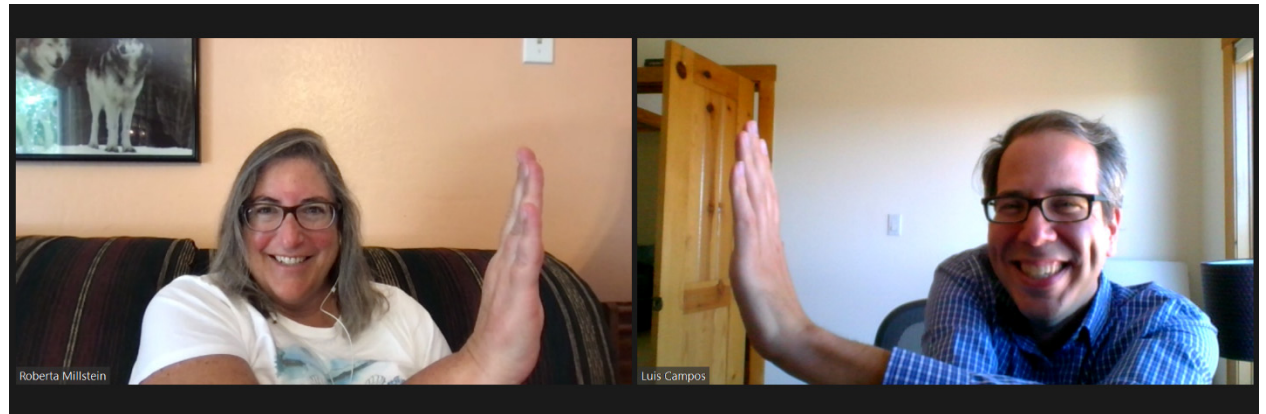
Greg Radick

Welcome from the Program Chairs

Luis Campos and Roberta Millstein entered the maw of program planning for what was supposed to be an in-person ISHPSSB meeting, *long* before the pandemic...



... and celebrate the art of survival in 2021 with the launch of the final program for the virtual meeting!



We would also like to express our gratitude to our hard-working committee members, who have dedicated many hours to making this year's meeting a success!

Program Committee

Carlos Andres Barragán
Christina Brandt
Thierry Hoquet
Eben Kirksey
Celso Neto
Charles Pence
Ciara Staunton
Alex Aylward, assistant to the chairs

Virtual Local Organizing Committee

Matt Haber, chair
Rachel Ankeny
Maria Elice de Brzezinski Prestes
Leonard Finkelman
Javier Suárez
Sophie Veigl

ISHPSSB Officers and Committee Chairs 2019—2021

Council

Officers:

Greg Radick, President
Rachel Ankeny, President-Elect
Sarah Roe, Secretary
Laura Perini, Treasurer
Luis Campos & Roberta Millstein, Program Co-Chairs
Marsha Richmond, Immediate Past President

Elected Members:

Jenny Bangham (2019–23)
Ingo Brigandt (2017–21)
Vivette García Deister (2019–23)
Emily Parke (2017–21)
Jutta Schickore (2017–21)
Joeri Witteveen (2019–23)

Student Representative:

Lúcia Neco

Committee Chairs

Program Committee

Luis Campos
Roberta Millstein

Virtual Local Arrangements Committee

Matt Haber

Communications Committee

Sarah Roe

Education Committee

Charbel El-Hani (Co-Chair)
Isabella Sarto-Jackson (Co-Chair)

Site Selection Committee

Rachel A. Ankeny

Student Advisory Committee

Lucia Neco

Operations Committee

Rachel A. Ankeny

Travel Support Committee

Laura Perini

Off-Year Workshop Committee

Matt Haber

Membership Development Committee

Ingo Brigandt (Co-Chair)
Alan Love (Co-Chair)

Nominations Committee

Marsha Richmond

David L. Hull Prize Committee

Marsha Richmond

Marjorie Grene and Werner Callebaut Prize Committee

Sabina Leonelli

Ad-hoc Bylaws Committee

Marsha Richmond

Many thanks to all of the above, and all the committee members, for their service!

ISHPSSB 2021 Talk Schedule Template

For traditional and individual paper sessions, please use the following template for when to begin and end talks/Q&A.
Diverse format sessions, lightning talks, and other non-traditional sessions will typically break from this format.

Session 1 talks	9:30-10:55		Session 3 talks	14:30-15:55		Session 5 talks	19:00-20:25
9:30-9:55	Paper 1		14:30-14:55	Paper 1		19:00-19:25	Paper 1
10:00-10:25	Paper 2		15:00-15:25	Paper 2		19:30-19:55	Paper 2
10:30-10:55	Paper 3		15:30-15:55	Paper 3		20:00-20:25	Paper 3
Session 2 talks	11:05-12:30		Session 4 talks	16:05-17:30		Session 6 talks	20:35-22:00
11:05-11:30	Paper 1		16:05-16:30	Paper 1		20:35-21:00	Paper 1
11:35-12:00	Paper 2		16:35-17:00	Paper 2		21:05-21:30	Paper 2
12:05-12:30	Paper 3		17:05-17:30	Paper 3		21:35-22:00	Paper 3



Instructions for ISH21 Attendees, Presenters & Chairs

- CSHL has been managing a lot of online conferences and aims to make the mechanics of presenting as easy as possible. To attend or give a talk, simply log in to the zoom link for the meeting and then select the relevant breakout room listed on the program. Once in the breakout room, presenters will be able to share their slides once they are introduced by session chairs. Zoom and other relevant links will be released closer to the start of the conference.
- For sessions without designated chairs (primarily the 'individual papers sessions') we are asking presenters to self-chair as follows: 3rd speaker chairs for the 1st speaker, 1st for the 2nd, and 2nd for the 3rd.

Other tips, tricks, and instructions for attendees, presenters & chairs:

- Chairs will *not* have to manage the technical side of things; that's CSHL's job. Chairs should focus on a more traditional role, i.e., introducing sessions and speakers, helping manage time (with gentle reminders as time is running out), helping with Q&A, etc.
- For regular sessions, talks should run 15 minutes plus 10 minutes for Q&A. There will then be a 5-minute break before the next talk begins. ([Click here for a more detailed breakdown of when talks are scheduled.](#)) We've learned that building in a little time between talks is wise in a virtual conference.
- **Chairs should ask presenters to state their preference for whether their talks may be discussed on social media**, and any constraints or restrictions they might request of those who do, e.g., speakers might be happy for people to post about their talks but ask that no images or recordings of their slides be shared.
- Please read and keep in mind our [ISH21 Social Media and Recording Etiquette Guide](#). Social media can be a fun and great way to promote scholarship, but we ask you to respect speakers' preferences on this. If a speaker grants permission to discuss their talk on social media, please follow our [social media style guide](#). We have attached an image speakers may include on their slides if they do not want them posted on social media.
- At the beginning of Q&A chairs should ask the audience to either post questions in the chat or to electronically 'raise' their hand using the Zoom reaction feature. **Chairs should help the speakers manage Q&A by offering to monitor and read questions that come up in the chat, and by managing the queue as hands are raised 'electronically'.**
- During Q&A please keep in mind the ISHPSSB tradition of prioritizing questions from junior scholars, and aim to include questions from a diverse group of people.
- Please mute your feed while others are presenting; you should only unmute when you are the speaker in a session, chairing a session (i.e., introducing a speaker or session or helping manage Q&A), or asking a question.
- Speakers are encouraged to include a Welcome/Acknowledgement of Country/Land statement in their talks, reflecting their local institutional customs. [Here is an example from the University of Utah.](#)
- To help promote collegiality, we encourage you to turn on your video during talks and Q&A if you are comfortable doing so.

Twitter Styleguide for Online Conference Tweeting

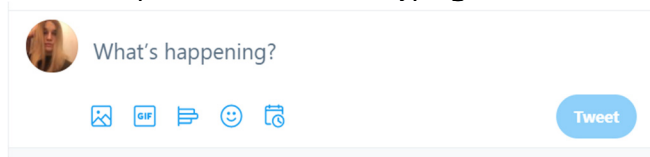
The Structure:

A tweet consists of several elements: main text (up to 280 characters), hashtags (#), mentions (@), a visual object (foto, video, preview to a link, poll)

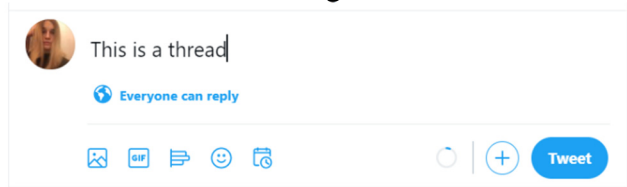
Besides these ‘active’ elements, there are also constitutive elements pertaining to every tweet, such as your account name and twitter handle, the meta-data of the tweet, the engagement-data of the tweet, and a list of ways to engage.

There are several types of tweets: simple tweet, a thread (a series of consecutive tweets that are visually organized to follow each other), a retweet, and a quote-tweet.

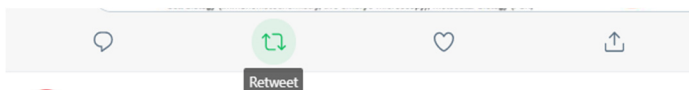
Simple tweet: Just start typing in the “whats happening” box



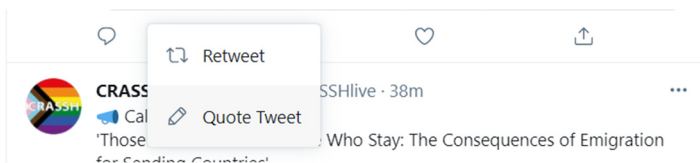
Thread: hit the “+” sign to add more tweets



Retweet: hit the retweet button to share a tweet in your timeline



Quotetweet: hit the quote tweet button and comment on a tweet that you added to your timeline



The Content:

Social media reporting from conferences consists in a diverse array of different activities and practices. There are certain standards and rules of what makes a good conference tweet, but - as with any set of rules - once these rules are mastered most of them can be (consciously) broken.

Here, we will focus on some basic rules when twittering from a conference talk, but of course, every aspect of conference-life is tweetable. Reporting from a talk might however be the most regulated activity, as it concerns the professional lives of the presenters. Thus, conference talk-tweeting deserves the most care.

- Make sure you tag the presenter, and their affiliation (@) if they are on twitter.
- Hashtags: use the conference hashtag (e.g., #ISH21) and other hashtags that match the topic of the talk (e.g., #ecoevodevo, #feministphilsci, #explanatorypluralism, #sts, #histSTEM...)
- Use the title of the talk in your description, or paraphrase the content of the talk in your own words
- photos: make sure not to take photos of the presentation if the speaker indicates a no-tweeting preference. Watch out for no-tweeting signs on individual slides of the presentation
- you can use polls or surveys to increase engagement
- threads: you can choose to make the tweeting from a talk more extensive by creating a thread by, e.g., real-time summarizing the flow of the argument in several sub-tweets
- stay polite and constructive at all times!

Code of Conduct and CSHL Policies

Please pay attention to Cold Spring Harbor Laboratory (CSHL) [regular policies and code of conduct](#). We have agreed to follow these as part of our agreement with CSHL to virtually host our meeting and expect participants to follow these standards. Please note that [CSHL provides mechanisms for reporting violations of their code of conduct](#), and we will support CSHL in their handling of any such issues. Finally, in addition to the CSHL policies and code of conduct, ISHPSSB has drawn up some etiquette around social media, recording talks, and other virtual aspects of our media that we ask you to become familiar with and abide by.

Social Media and Recording Etiquette

We ask all attendees to keep in mind the value of ephemerality of conference presentations. ISHPSSB presentations often feature works-in-progress or very early-stage work. What you are seeing is typically unpublished, and the culture of ISHPSSB is to provide critical yet constructive feedback aimed at helping people develop their projects.

ISHPSSB presentations are not intended to be archived or taken as finished projects; an important component of the spirit of ISHPSSB meetings is the opportunity to workshop projects with an interdisciplinary audience. Many members that feel comfortable doing this in a room at an in-person conference may have hesitations about their presentation being recorded or shared over social media. We recognize that the etiquette around this is developing—especially for virtual conferences—and offer the following guides as we navigate this during ISHPSSB 2021.

Recording Talks:

Background

ISHPSSB 2021 will be attended by scholars from around the world. To help increase accessibility, CSHL has offered to record the talks being given and post them to an archive for a short period of time (most likely July 21-31). This archive will be made available *only* to registered attendees. This will help increase accessibility to the meeting, especially for attendees that may have difficulty viewing the talk live in their time zone.

Policy and Etiquette

CSHL will automatically record all talks but will **only post recorded talks to the archive on permission of speakers**. Presenters were asked prior to the meeting to opt-in if they grant this permission; the default option is to not post talks to the archive.

The archive of talks will *only* be made available to people that have registered to attend ISHPSSB 2021 and will only be archived for a short time (until July 31). At the end of this period, the recordings will be deleted.

Unless expressly permitted, individual attendees should *not* record talks with the intent of sharing that material (be it over social media or otherwise). This includes—but is not limited to—video recordings and screenshots of slides. Please keep in mind that ISHPSSB meetings encourage presenters to workshop unpublished and early stage material that they may not want publicized out of context of a live talk.

Social Media Etiquette:

Background

Increasingly, members of academic disciplines are using Twitter, Facebook, and other social media platforms to broadcast information from professional conferences to a wider audience. However, norms around the use of social media tools at professional conferences have not yet solidified, and some conference participants may feel uneasy at the potential for social media coverage to misrepresent their claims, to present in-progress work as finished material, or to broaden their audience in an unwelcome way.

Policy and Etiquette

ISHPSSB 2021 is an opportunity for attendees to share their work with a wider audience. Social media can help extend that audience to people not at the meeting, and to the public. Norms around the use of social media in academic culture are still emerging. Meeting attendees using social media to broadcast content from the conference to a broader audience are asked to engage with respect and professionalism. **Do not post images from presentations without consent.** Be clear about when you are posting the words or claims of a presenter and when you are posting your own opinion on a presentation. Be considerate of presenters' requests for no social media coverage; they may be sharing work with their peers at this conference to foster discussion and feedback, but feel that the findings are not ready for wider consumption. If you prefer that your presentation not be shared via social media, communicate that clearly to your audience.

Presenters have been encouraged to express their preference on audience use of social media, and provided with a 'no social media' icon to include on their slides. Chairs will remind audiences to be respectful of presenter preferences on this. If you use social media to comment on ISHPSSB 2021 presentations, we ask you to [follow our social media style guide](#).

CSHL will be providing a dedicated and private Slack channel for use during ISHPSSB 2021. This will only be accessible to registered attendees and provides both an alternative and complement to social media, and a means for participants to discuss talks analogous to how this might happen during breaks at an in-person meeting.

Monday 12 July	
TIME	
10:00-15:30	Zoom Practice Day
13:00-14:00	Opening Social Hour and Asynchronous Banquet Kickoff and Instructions gather.town
16:30	Council Meeting 1



Tuesday 13 July

TIME	Grace Auditorium (webinar)
9:30-10:55	CSHL Welcome Plenary Panel
Break	

Grace Lobby (breakout rooms)							
TIME	Vannevar Bush Hall	Al Hershey Hall	Barbara McClintock Hall	Max Delbrück Hall	Martha Chase Hall	Milislav Demerec Hall	Rich Roberts Hall
11:05-12:30	Individual Papers Session Collections	Individual Papers Session Technical genomics	Individual Papers Session Functions and stochasticity	Traditional Session Aquatic organisms, regeneration, and the utility of "non-traditional," model species	Traditional Session Holobionts, symbionts, and demibionts	Traditional Session Borderline confusion: Unsettled boundaries in the life sciences, Part I	Traditional Session Knowledge coproduction and transdisciplinary practices in ecology and the environment, Part I ID PRIZE CANDIDATE
Break							gather.town
13:00-14:00	Community/Skill Building CSHL Virtual Tours: Cryogenic electron microscopy (cryoEM)	Community/Skill Building Building intellectual community across disciplines	Community/Skill Building Demystifying the journal submission process, I	Community/Skill Building How to write a referee report: Killing your inner referee #2	Community/Skill Building Finding and constructing academic communities on Twitter	Virtual Coffee Break / Social Hour	
Break							
14:30-15:55	Individual Papers Session Molecular biology	Traditional Session Rethinking stress in biology and psychology: What is it good for?	Traditional Session Biodiversity data and modeling	Traditional Session Philosophy of cancer, Part I	Individual Papers Session Replication and reconstruction		
Break							
16:05-17:30	Individual Papers Session Causation	Diverse Format Session The coral reef crisis: Communication and value across senses, species and disciplines	Flashtalks I	Diverse Format Session How can living systems persist: Regeneration, failure, and the future	Traditional Session Understanding complexity: Explanatory strategies at the dawn of evolutionary biology		

TIME	gather.town
17:30-19:00	Coffee Break / Social Hour

Wednesday 14 July

TIME	Grace Auditorium (webinar)
9:30-10:55	PLENARY: Open Science, Data Sharing, and Solidarity: Who Benefits?
Break	

Grace Lobby (breakout rooms)								
TIME	Vannevar Bush Hall	Al Hershey Hall	Barbara McClintock Hall	Max Delbrück Hall	Martha Chase Hall	Rich Roberts Hall	Carol Greider Hall	
11:05-12:30	Individual Papers Session Cognition and values	Individual Papers Session Species and pluralism	Traditional Session The biology and metaphysics of free will	Diverse Format Session Plant data science between policy and technology: Reframing plant research to serve global food security	Traditional Session Borderline confusion: Unsettled boundaries in the life sciences, Part II	Traditional Session History of genetics in Brazil and the Dreyfus' group	Traditional Session Immunological perspectives on evolution: Synthesizing the physiological and the evolutionary individual	
Break								

TIME	Grace Auditorium (webinar)
13:00-14:00	GENERAL MEETING
Break	

Grace Lobby (breakout rooms)					
TIME	Vannevar Bush Hall	Al Hershey Hall	Barbara McClintock Hall	Max Delbrück Hall	Martha Chase Hall
14:30-15:55	Individual Papers Session Evolutionary biology	Individual Papers Session Biodiversity and extinction	Traditional Session Regeneration from cells to limbs	Traditional Session Epistemic practices in developmental biology	Diverse Format Session The social life of trauma biology
Break					
16:05-17:30	Diverse Format Session Reconsidering Gaia	Traditional Session Phylogenetics, evolution and philosophy	Individual Papers Session Life around 1900	Individual Papers Session Conservation	Individual Papers Session Plants
				gather.town	
17:30-19:00	Community/Skill Building Demystifying the journal submission process, II	Community/Skill Building Women in ISHPSSB	Community/Skill Building Cocktail making: Selection, drift, mutations, and libations	Virtual Coffee Break / Social Hour	
19:00-20:25	Individual Papers Session Biology in the 19th century	Individual Papers Session Process ontology	Individual Papers Session Knowing molecular biology	Traditional Session Facts and values in invasion biology, Part I: Perspectives from New Zealand and Australia	
Break					
20:35-22:00	Individual Papers Session Fitness	Individual Papers Session Morality	Individual Papers Session Individuality, I	Traditional Session Facts and values in invasion biology II: Perspectives from North	

Thursday 15 July

Grace Lobby (breakout rooms)								
TIME	Vannevar Bush Hall	Al Hershey Hall	Barbara McClintock Hall	Max Delbrück Hall	Martha Chase Hall	Milislav Demerec Hall	Rich Roberts Hall	Carol Greider Hall
9:30-10:55	Individual Papers Session Fossils and strata	Individual Papers Session Altruism, and harm/values in sci debate	Individual Papers Session Sex, gender, and feminist analysis	Individual Papers Session Controversies	Individual Papers Session Holobionts	Traditional Session Deconstructing Darwinism: Toward A new historiography	Traditional Session Wingspread@30: Birth and development of the endocrine hypothesis, Part I	Diverse Format Session Biologies of the South: Negotiating knowledge and livelihoods. Part I
							ID PRIZE CANDIDATE	ID PRIZE CANDIDATE
Break								
11:05-12:30	Individual Papers Session Individuality, II	Individual Papers Session Open Session I and Flashtalks II	Individual Papers Session Cultural adaptation and evolution	Individual Papers Session Information and immunology	Diverse Format Session A critical discussion of Darwin's Argument by Analogy: From artificial to natural selection	Traditional Session Evolvability across biological disciplines: Recent history and new philosophical approaches	Traditional Session Actors and actors' categories in history, philosophy, and social studies of biology	Diverse Format Session Biologies of the South: Negotiating knowledge and livelihoods, Part II
								ID PRIZE CANDIDATE
Break								
13:00-14:00	Community/Skill Building Diverse Format Session Opportunities for ISHerS at CSHL: A virtual tour of collections, resources, fellowships, and the Center for Humanities & History of Modern Biology	Community/Skill Building Topic modeling and optimization, or how we scheduled ISHPSSB2021	Community/Skill Building How to construct an effective academic poster	Community/Skill Building Open science and publishing	Community/Skill Building Building inter-campus graduate networks	gather.town		
Break								
14:30-15:55	Individual Papers Session Climate science	Individual Papers Session Transmission, treatment, and therapy	Individual Papers Session Eugenics	Traditional Session After the modern synthesis	Diverse Format Session Book panel: Four tales from the world of small things			
Break								

TIME	Grace Auditorium (webinar)
16:05-17:30	PLENARY: Revisiting Darwin's Descent, 1871-2021

TIME	gather.town
17:30-19:00	Coffee Break / Social Hour

Friday 16 July	
TIME	
9:00	<i>Graduate Student Meeting</i>
10:00	<i>Membership Development Committee Meeting</i>
16:30	<i>Council Meeting 2</i>



Monday 19 July

Grace Lobby (breakout rooms)								
TIME	Vannevar Bush Hall	Al Hershey Hall	Barbara McClintock Hall	Max Delbrück Hall	Martha Chase Hall	Milislav Demerec Hall	Rich Roberts Hall	
9:30-10:55	Individual Papers Session Engineering life	Individual Papers Session Evolutionary thought in the 19th century	Traditional Session Anteaters, dolphins, kangaroos. Generating knowledge about exotic animals inside and outside the zoo	Traditional Session Wingspread@30: Birth and development of endocrine disruption science, Part II ID PRIZE CANDIDATE	Diverse Format Session "Your genitals don't lie!" An escorted encounter with the history and philosophy of phallic and cervical measuring ID PRIZE CANDIDATE	Diverse Format Session Norms of conceptual development in the life sciences	Diverse Format Session Varieties of memory	
Break								
11:05-12:30	Individual Papers Session Explanation	Diverse Format Session Theories of carcinogenesis: an interdisciplinary analysis	Traditional Session Knowledge coproduction and transdisciplinary practices in ecology and the environment, Part II ID PRIZE CANDIDATE	Diverse Format Session Neuro-presents and neuro-futures: Neurotech practices imagined and lived	Traditional Session Thinking with microorganisms, 1880-1940: Symbiosis, asepsis and domestication	Traditional Session Adaptation, teleology and function in evolutionary biology		
Break								
13:00-14:00	gather.town							
	Community/Skill Building Happy Office Hours 1							
Break								
14:30-15:55	Individual Papers Session Data	Diverse Format Session Evolutionary cognitive archaeology: Epistemological and methodological issues	Individual Papers Session Beyond the traditional organism	Diverse Format Session The selected effect account of function: Problems, extension, reconciliation and applications, Part I	Traditional Session Reform of the genetics curriculum: Interdisciplinary perspectives			
Break								
16:05-17:30	Individual Papers Session Life and its limits	Individual Papers Session Beyond the archive	Individual Papers Session Cell biology	Diverse Format Session The selected effect account of function: Problems, extension, reconciliation and applications, Part II	Traditional Session What does it mean to value biodiversity? ID PRIZE CANDIDATE			
17:30-19:00	gather.town							
	Community/Skill Building Happy Office Hours 2							
19:00-20:25	Individual Papers Session Open Session, III	Individual Papers Session Mechanistic explanation	Diverse Format Session Corroborative and anticipatory predictions	Traditional Session Muller and mutation				
Break								
20:35-22:00	Individual Papers Session Teleology	Individual Papers Session Birds of a feather: Heredity, species, and taxonomy	Traditional Session Mutational biases and adaptation					

hosted by Cold Spring Harbor Laboratory

Tuesday 20 July

TIME	Grace Auditorium (webinar)
9:30-10:55	PLENARY: Viral Vulnerability: From Permissivity to Pessimism
Break	

Grace Lobby (breakout rooms)								
TIME	Vannevar Bush Hall	Al Hershey Hall	Barbara McClintock Hall	Max Delbrück Hall	Martha Chase Hall	Milislav Demerec Hall	Rich Roberts Hall	Carol Greider Hall
11:05-12:30	Individual Papers Session Primateology and the colonial context	Individual Papers Session Emotion and cognition	Individual Papers Session Race and eugenics	Individual Papers Session Remains of the dead	Individual Papers Session Adaptationism	Traditional Session Conceptualizing homology from Richard Owen to developmental genetics	Diverse Format Session Revisiting H.J. Muller and N. Vavilov in Russian genetics	Traditional Session Life as a planetary process: The earth systems science perspective
Break						gather.town		
13:00-14:00		Community/Skill Building Why you should keep hosting online conferences	Community/Skill Building Interdisciplinary collaboration	Community/Skill Building Teaching by building a Wikipedia page	Community/Skill Building How to turn a conference presentation into a paper	Virtual Coffee Break / Social Hour		
Break								
14:30-15:55	Individual Papers Session Modelling	Traditional Session History of evolutionary biology: Connections with science education	Diverse Format Session Bungtown style: Scientific thought and practice at Cold Spring Harbor	Traditional Session Philosophy of cancer, Part II	Traditional Session Causation in biology	Traditional Session History and philosophy of enzymes		
Break								

TIME	Grace Auditorium (webinar)
16:05-17:30	Awards Meeting and Future ISH Plans

TIME	gather.town
17:30-19:00	Coffee Break / Social Hour

MONDAY 12 July

10:00-15:30 (GMT -4)

Zoom Practice Day

13:00-14:00 (GMT -4)

*Opening Social Hour and Asynchronous Banquet
Kickoff and Instructions*

gather.town

16:30 (GMT -4)

Council Meeting 1

TUESDAY 13 July**9:30-10:55 (GMT -4)****CSHL Welcome Plenary Panel**Grace Auditorium
(Zoom webinar)

Greg Radick, Bruce Stillman, David Spector, Rebecca Leshan, Marsha Richmond, Nathaniel Comfort, Luis Campos

11:05-12:30 (GMT -4)**Individual Papers Session
Collections****Lively stasis: Care, routine, and the imaginaries of scientific collections**
Jenny Bangham, Xan S Chacko**Medical anamnesis: The role of past collections in the future of diagnosis and prognosis**
Karin Tybjerg**Decolonizing the biology archive: Postcolonial approaches to recovering gendered knowledges of life**
Don Opitz, Banu Subramaniam**Grace Lobby
breakout room****Abstract #**

1

Vannevar Bush Hall

2

3

**Individual Papers Session
Technical genomics****Carving the social environment at genetic joints: Can GWAS inform claims about environmental causes?**
Olesya Bondarenko**Is it mine or ours? legal conceptualization of the "singular genome"**
Shelly Simana**Identity by descent (IBD) as an algorithm-and-simulation practice in current human population genomics research**
Carlos Andrés Barragán, James R Griesemer**Grace Lobby
breakout room****Abstract #**

4

Al Hershey Hall

5

6

**Individual Papers Session
Functions and stochasticity****Transitional functionality of genomic segments: From stochasticity to robustness**
Zdenka Brzovic, Predrag Šustar**An organizational account of malfunctioning: A dynamic normative field approach**
Xabier E Barandiaran, Tiago Rama**Dissecting stochasticity in gene expression: New epistemological insights by a multidimensional analysis**
Marco Casali, Francesca Merlin, Alberto Vianelli**Grace Lobby
breakout room****Abstract #**

7

Barbara McClintock Hall

8

9

Traditional Session Aquatic organisms, regeneration, and the utility of "non-traditional," model species Chair: Kathryn Maxson Jones		Grace Lobby breakout room	Abstract #
Cut and paste: the Mexican Axolotl, experimental practices and the long history of regeneration research in amphibians, 1864-present Christian Reiß		Max Delbrück Hall	10
Deciphering regeneration through non-model animals: A century of experiments on cephalopod mollusks and an outlook at the future Pamela Imperadore, Fabio De Sio			11
Experimental organisms, neuron regeneration, and the curious case of the lamprey in the history of the neurosciences, 1870s-present Kathryn G Maxson Jones, Jennifer R Morgan			12
Traditional Session Holobionts, symbionts, and demibionts Chair: Elisabeth A Lloyd		Grace Lobby breakout room	Abstract #
One, two or many? It depends why you're asking John Dupré		Martha Chase Hall	13
A network framework to explain the evolution of host-microbiome associations: System-level engineering adaptations result from mixed modes of inheritance Javier Suárez, Saul Huitzil			14
Why the host-symbiont relationship between Euprymna scolopes and Vibrio fischeri is a demibiont and not a holobiont: Reciprocal and non-reciprocal evolution Michael J Wade, Elisabeth A Lloyd			15
Traditional Session Borderline confusion: Unsettled boundaries in the life sciences, Part I Chair: Jan Baedke		Grace Lobby breakout room	Abstract #
Drawn, erased, re-negotiated: The organism-environment boundary in early twentieth-century biology Alejandro Fábregas-Tejeda		Milislav Demerec Hall	16
Membrane, surface, channel, gate, pump, receptor: The cell membrane as exemplary boundary, 1877–2010 Daniel Liu			17
From Bertalanffy to Bunge and beyond: Exploring the unsettled boundaries of living systems Guido I Prieto			18

Traditional Session		
Knowledge coproduction and transdisciplinary practices in ecology and the environment, Part I		Grace Lobby breakout room
Chair: Charbel El-Hani		Abstract #
From basic to applied science: Bioremediation as ecosystem engineering Saliha Bayir		19
Intercultural translation as a kind of knowledge integration: Conservationist projects on seashores of Ecuador Radamés Villagómez-Reséndiz		20

13:00-14:00 (GMT -4)

Community / Skill Building		Grace Lobby breakout room
CSHL Virtual Tours: Cryogenic electron microscopy (cryoEM) Leemor Joshua-Tor		Vannevar Bush Hall
Building intellectual community across disciplines Alan Love & Mark Borello		Al Hershey Hall
Demystifying the journal submission process, I Joeri Witteveen		Barbara McClintock Hall
How to write a referee report: Killing your inner referee #2 Adrian Currie		Max Delbrück Hall
Finding and constructing academic communities on Twitter Sophie Veigl & Lynn Chiu		Martha Chase Hall
Virtual coffee break / social hour		gather.town

14:30-15:55 (GMT -4)

Individual Papers Session		
Molecular biology		Grace Lobby breakout room
How CSHL lost priority for the discovery of RNA splicing? Insights from oral history Pnina G Abir-Am		Abstract #
Molecular biology origins: Max Delbrück and the reductionism debate Vito Balorda		21
A historiographic principle of charity: Retelling the story of Jacques Monod and the history of protein allostery Jacob P Neal		22
		23

Traditional Session		
Rethinking stress in biology and psychology: What is it good for?	Grace Lobby breakout room	Abstract #
Chair: Amanda Corris		
Diverse roles, multiple meanings: Conceptualizing stress in biological research Lauren H Wilson		24
Co-option of stress mechanisms in the origin of evolutionary novelties Alan Love, Günter Wagner	<i>Al Hershey Hall</i>	25
Resilient minds: Stress-adapted cognition in precarious environments Amanda B Corris		26
Traditional Session		
Biodiversity data and modeling	Grace Lobby breakout room	Abstract #
Chair: Robert Lazo		
Ontic risk in species classification for biodiversity conservation Joeri Witteveen		27
A forward-looking theory of biological function for biodiversity modeling Robert S Lazo	<i>Barbara McClintock Hall</i>	28
Making biodiversity data portals FAIR and CARE: Expanding who counts as a participant Beckett Sterner, Steve Elliott		29
Traditional Session		
Philosophy of cancer, Part I	Grace Lobby breakout room	Abstract #
Chair: Thomas Pradeu		
Cancer avatars: The temporality of surrogate models Sara Green, Mie S Dam, Mette N Svendsen		30
Is cancer intrinsic to multicellularity? Thomas Pradeu	<i>Max Delbrück Hall</i>	31
Why don't we get more cancer: The critical role of extracellular matrix and microenvironment in malignancy and dormancy Mina J Bissell		32
Individual Papers Session		
Replication and reconstruction	Grace Lobby breakout room	Abstract #
Citing study mismatches upon failures to replicate: Useful exercise or self-defeating? Davd Colaço, John Bickle, Bradley Walters		33
Forget the midwife toad: Paul Kammerer, acquired characteristics and graft hybridization Matthew Holmes	<i>Martha Chase Hall</i>	34

16:05-17:30 (GMT -4)

Individual Papers Session Causation	Grace Lobby breakout room	Abstract #
Genetic causation Stephen M Downes		35
Demystifying downward causation in evolutionary biology Yasmin Haddad	Vannevar Bush Hall	36
The concept of clone in cancerology: Issues and perspectives Antoine Jourdain		37
Diverse Format Session The coral reef crisis: Communication and value across senses, species and disciplines Chair: Sophie Veigl	Grace Lobby breakout room	Abstract #
Participants: Elis Jones, Tim Gordon, Sonia Levy, Irus Braverman, Stefan Helmreich, Sophie Veigl	Al Hershey Hall	38
Flashtalks I	Grace Lobby breakout room	Abstract #
Immunology in Portugal: Building and consolidating a robust research field in a small country Maria S Almeida, Manuel Vilanova		39
Rethinking the function-accident distinction Brandon A Conley		40
Global organism: The science and politics of holism in the interwar period Abraham H Gibson		41
Why philosophers of biology should look at RNA Stephan Guttinger	Barbara McClintock Hall	42
Biology's Einstein moment Matt Haber		43
5 reasons why philosophers of biology should invest philosophy of interdisciplinarity Kevin Kaiser		44
Is the tube test an appropriate test in the study of model organisms for human neurological diseases Cole C McArthur		45

Flashtalks I	Grace Lobby breakout room	Abstract #
The cultural readiness of paleontological discoveries TJ Perkins	Barbara McClintock Hall	46
Teaching by building a Wikipedia page Aleta Quinn		47
Questioning Darwin's "truly wonderful fact" Mary P Winsor		48
<i>Diverse Format Session</i> How can living systems persist: Regeneration, failure, and the future Chair: Susan Fitzpatrick	Grace Lobby breakout room	Abstract #
Participants: Kate MacCord, S Andrew Inkpen, Jane Maienschein, Manfred Laubichler, Susan Fitzpatrick	Max Delbrück Hall	49
<i>Traditional Session</i> Understanding complexity: Explanatory strategies at the dawn of evolutionary biology Chair: Greg Priest	Grace Lobby breakout room	Abstract #
John Herschel's philosophy of higgledy-piggledy Richard Bellon	Martha Chase Hall	50
Understanding without laws: Charles Darwin's explanatory practices Greg Priest		51
A.R. Wallace's "pure Darwinism": Reinterpreting Darwin's "complexity" for the public Juan M Rodriguez-Caso		52

17:30-19:00 (GMT -4)

Coffee Break / Social Hour
gather.town

WEDNESDAY 14 July**9:30-10:55 (GMT -4)****PLENARY: Open Science, Data Sharing, and Solidarity: Who Benefits?**Grace Auditorium
(Zoom webinar)

Organizers: Ciara Staunton and Andrés Barragan

Panelists: Stefano Canali, Calvin Ho, Sabina Leonelli, Matthew Mayernik, Barbara Prainsack, and Ambroise Wonkam

11:05-12:30 (GMT -4)**Individual Papers Session**
Cognition and valuesGrace Lobby
breakout room**Abstract #****Entrenched values in scientific research: Values beyond the psychological-level**
Morgan Thompson

53

On ecological validity in comparative psychology
Charles A Beasley

Vannevar Bush Hall

54

Super-pleasure
Otniel E Dror

55

Individual Papers Session
Species and pluralismGrace Lobby
breakout room**Abstract #****Epistemically useful and metaphysically adequate pluralist accounts of essentialism**
Christian Culak

56

Differentiating the reference genome: Representation, abstraction and the exploration of variation in genomics and post-genomic research
James Lowe

Al Hershey Hall

57

Traditional Session
The biology and metaphysics of free will
Chair: Anne Sophie MeinckeGrace Lobby
breakout room**Abstract #****Maximising efficiency in an indeterministic world: The free will of biological agents**
Anne Sophie Meincke

58

The neurobiology of probabilistic actions
Björn Brembs

Barbara McClintock Hall

59

The feeling of free will
Eva Jablonka

60

Diverse Format Session Plant data science between policy and technology: Reframing plant research to serve global food security Chair: Sabina Leonelli	Grace Lobby breakout room	Abstract #
Participants: Sabina Leonelli, Hugh Williamson, Rachel A Ankeny, Helen Curry, Paul Thompson	Max Delbrück Hall	61
Traditional Session Borderline confusion: Unsettled boundaries in the life sciences, Part II Chair: Tamar Schneider	Grace Lobby breakout room	Abstract #
Reproductive relations and temporal cross-generation boundaries: The case of eutherian pregnancy Etxeberria Arantza	Martha Chase Hall	62
Where the social meets the biological: Navigating boundaries in the embodiment of race Azita Chellappoo, Jan Baedke		63
Visualizing evolution: Communicating new boundaries Miguel Brun-Usan, Lynn Chiu		64
Traditional Session History of genetics in Brazil and the Dreyfus' group Chair: Aldo Araújo	Grace Lobby breakout room	Abstract #
Dobzhansky and the Brazilians from his letters and reminiscences for the Oral History of Columbia University Aldo M Araujo	Rich Roberts Hall	65
Female researchers at Dreyfus' group: 1943-1960 Lilian Al-Chueyr P Martins, Ana Paula Oliveira Pereira M Brito		66
Perceptions of researchers of the Institute of Biosciences about Dreyfus and Dobzhansky' time and institutionalization of genetics in Brazil Maria Elice B Prestes, José F Sião		67
Traditional Session Immunological perspectives on evolution: Synthesizing the physiological and the evolutionary individual Chair: Elis Jones	Grace Lobby breakout room	Abstract #
Towards a transgenerational perspective on immune systems Sophie Juliane Veigl	Carol Greider Hall	68
When you are forced to being nice: Multicellularity is more about coercion than about altruism Adrian Stencel, Javier Suárez		69
Functions and the immune system: Can immunology impact the way we think about different notions of biological function? Gregor Greslehner		70

13:00-14:00 (GMT -4)

GENERAL MEETINGGrace Auditorium
(Zoom webinar)

14:30-15:55 (GMT -4)

<i>Individual Papers Session</i> Evolutionary biology	Grace Lobby breakout room	Abstract #
Kuhnian incommensurability and evolutionary biology: Are the modern evolutionary synthesis and the extended evolutionary synthesis incommensurable? Juan Gefaell, Cristian Saborido		71
Get costs in everywhere in evolutionary theory! Marion Blute	Vannevar Bush Hall	72
What we can learn from parasites Robert Kok		73
<i>Individual Papers Session</i> Biodiversity and extinction	Grace Lobby breakout room	Abstract #
Song at the end of modernity Rachel Mundy		74
An Aristotelian response to the biodiversity crisis Duncan C Maclean	Al Hershey Hall	75
Where the wild things are classified: Wildness and the nonhuman animals caught in the crosshairs Denise R Hossom		76
<i>Traditional Session</i> Regeneration from cells to limbs Chair: Heiner Fangerau	Grace Lobby breakout room	Abstract #
Democratizing methods? Rhoda Erdmann (1870-1935) and the penumbra of early tissue culture research Heiner M Fangerau		77
Brain regeneration phenomena, morphological research advances, and the practical implications of theory dynamics in modern bio-medicine Frank W Stahnisch	Barbara McClintock Hall	78

Traditional Session Epistemic practices in developmental biology Chair: Stavros Ioannidis		Grace Lobby breakout room	Abstract #
On the concept of biological development Pavlos Silvestros			79
Reconsidering developmental mechanistic explanations Stavros Ioannidis		Max Delbrück Hall	80
What an epistemology of scientific practice should be: The case of developmental biology Konstantina Antiochou			81
Diverse Format Session The social life of trauma biology Chair: Emma Kowal		Grace Lobby breakout room	Abstract #
Participants: Emma Kowal, Michel Dubois, Georgia Samaras, Elsher Lawson-Boyd		Martha Chase Hall	82
16:05-17:30 (GMT -4)			
Diverse Format Session Reconsidering Gaia Chair: S. Andrew Inkpen		Grace Lobby breakout room	Abstract #
Participants: Tim M Lenton, Peter Godfrey-Smith, W Ford Doolittle		Vannevar Bush Hall	83
Traditional Session Phylogenetics, evolution and philosophy Chair: François Papale		Grace Lobby breakout room	Abstract #
Are bacterial lineages feedback systems? From cynical pluralism to meta-pluralism about bacterial species Matthew J Barker			84
What is it that evolves? Celso Neto		Al Hershey Hall	85
Can and should we avoid the notion of natural kind when epistemologically analyzing homologies? François Papale			86
Individual Papers Session Life around 1900		Grace Lobby breakout room	Abstract #
Morphaesthesia, entelechy, and vitalism in early 20th-century biology Ivan Loginov			87
The civic life sciences around 1900: Darwin's legacy in botany and agriculture Giuliano Pancaldi		Barbara McClintock Hall	88

Individual Papers Session Conservation	Grace Lobby breakout room	Abstract #
Keystone species in wildlife management Derek Halm	Max Delbrück Hall	89
Van Parijsian maximin principle in service of soil resource conservation Vivek B Girija		90
Individual Papers Session Plants	Grace Lobby breakout room	Abstract #
Goethe's morphology, the development of plant systematics and the new science of Evo-Devo: Contributions to botany education João Felipe Ginefra Toni	Martha Chase Hall	91
To the victors the spoils: anti-German sentiment in plant biology in the inter-war period as evidenced by textbooks Thomas J McCloughlin		92
The Age of Biology: When plant physiology was the heart of biology David Munns		93

17:30-19:00 (GMT -4)

Community / Skill Building		Grace Lobby breakout room	
Demystifying the journal submission process, II Marsha Richmond		Vannevar Bush Hall	
Women in ISHPSSB Anya Plutynski		Al Hershey Hall	
Cocktail making: Selection, drift, mutations, and libations Jonathan Kaplan		Barbara McClintock Hall	
Virtual coffee break / social hour		gather.town	

19:00-20:25 (GMT -4)

Individual Papers Session Biology in the 19th century		Grace Lobby breakout room	Abstract #
Timothy Lenoir's thesis and the rise of critical idealism in the mid-19th century: A reassessment Ghyslain Bolduc		Vannevar Bush Hall	94
Scientific patronage in the age of Darwin: The curious case of William Boyd Dawkins Henry-James Meiring			95

Individual Papers Session Process ontology		Grace Lobby breakout room	Abstract #
Biological individuals in a process ontology: An objection from biological practice Adam C Smith		Al Hershey Hall	96
How to die slowly: Or, using process ontology to defend the whole brain definition of death Anthony P Smith			97
Representing and intervening in built, biotic, social, and health processes in COVID-19 contexts Hannah Howland			98
Individual Papers Session Knowing molecular biology		Grace Lobby breakout room	Abstract #
Biological clocks and the epistemology of multiple lines of evidence Katherine Valde		Barbara McClintock Hall	99
The generative failures of the central dogma coordinate un-making of epistemic kinds Alok K Srivastava			100
Entangled histories: Karyotyping and population genetics in Cold War Mexico. Armendarces’s and Lisker’s characterization of child and indigenous populations, 1960s-1980s Ana Barahona			101
Traditional Session Facts and values in invasion biology, Part I: Perspectives from New Zealand and Australia Chair: Jay Odenbaugh		Grace Lobby breakout room	Abstract #
Don’t deny it: Invasive species James Russell		Max Delbrück Hall	102
The rediscovery of arguments for biotic colonialism Christopher H Lean			103
How to stop arguing about invasive species Emily C Parke			104
20:35-22:00 (GMT -4)			
Individual Papers Session Fitness		Grace Lobby breakout room	Abstract #
Selection of as selection for: Linkage disequilibrium and fitness Marshall Abrams		Vannevar Bush Hall	105
Finkish trait types and the propensity interpretation of fitness Ryan Kulesa			106
The practice perspective on the inclusive fitness theory debate and its implication Jinkwon Jun			107

Individual Papers Session Morality		Grace Lobby breakout room	Abstract #
From bottom-up: Adaptive act and rule-empathy, game theory and morality Luciana Garbayo			108
Organic circuits, biological complexity, and moral obligation Michael Stingl		Al Hershey Hall	109
Evolutionary psychology of moral <i>phenomenology</i> works fine: A conceptual defense, and empirical support Sam J Woolley			110
Individual Papers Session Individuality, I		Grace Lobby breakout room	Abstract #
The social unit: What kinds of individuals can be social? Lucia C Neco			111
Biological individuality and the intentional stance David Kelley		Barbara McClintock Hall	112
Some reflections on bringing the problem of biological individuality into the field of health sciences. Fiorela R Alassia			113
Traditional Session Facts and values in invasion biology II: Perspectives from North America Chair: Carlos Santana		Grace Lobby breakout room	Abstract #
The biogeographic origin debate in invasion biology: Ecological science and conservation values David M Frank			114
Invasion biology and ecological networks Karen Kovaka, Jacob Barney, Brian Badgley, Bryan Brown, Willandia Chaves, Todd Schenk		Max Delbrück Hall	115
Owls and old-growth: A philosophical examination of a conflict Jay P Odenbaugh			116

THURSDAY 15 July

9:30-10:55 (GMT -4)

Individual Papers Session Fossils and strata		Grace Lobby breakout room	Abstract #
Converging histories in the Anthropocene Jason M Zinser		Vannevar Bush Hall	117
The logic of biological proxies William C Bausman			118
Individual Papers Session Altruism, and harm/values in sci debate		Grace Lobby breakout room	Abstract #
Can genuine altruism evolve or are we condemned to egoism? The case for (and against) the evolution of psychological altruism Jorge Piaia Mendonca Junior		Al Hershey Hall	119
Cultural evolution in the court: Ontological imposition and downstream harm Andrew Buskell			120
Cows, COVID and concerns: Why is the history of vaccination hesitancy repeating itself? Marietjie M Botes			121
Individual Papers Session Sex, gender, and feminist analysis		Grace Lobby breakout room	Abstract #
The future of sperm: A biovariability framework for understanding global sperm count trends Sarah S Richardson, Marion Boulicault		Barbara McClintock Hall	122
Understanding biological sex pluralistically Natasha M Haddal			123
Can applying feminist standpoint theory address gender disparity in biomedical research? Lida Sarafranz			124
Individual Papers Session Controversies		Grace Lobby breakout room	Abstract #
Relative significance controversies in evolutionary biology Katie Deaven		Max Delbrück Hall	125
Unpacking ‘care’ and conflict in public knowledge controversies Angela Cassidy			126
Ecological neutrality and ecological niche-theory Topaz Halperin			127

Individual Papers Session Holobionts		Grace Lobby breakout room	Abstract #
Inhabiting the holobiont: The role of visual and verbal imagery Joana Formosinho			128
Ecological community of holobionts: Ecology in size scales Tamar Schneider		Martha Chase Hall	129
Who is the biological patient? A gradual, dynamic model of organism-environment Yael Friedman			130
Traditional Session Deconstructing Darwinism: Toward a new historiography Chair: Richard Delisle		Grace Lobby breakout room	Abstract #
Beyond Darwin: Towards a new historiography of evolutionary biology Maurizio Esposito			131
Moving the borders of Darwinism: A comparative examination of Darwin's evolutionary theory in Darwin's celebrations, 1909-1959-2009 David Ceccarelli		Milislav Demerec Hall	132
Darwin's static arrow of time: Why we need to find new concepts of time and causality in an evolutionary worldview Patrick Hoburg			133
Traditional Session Wingspread@30: Birth and development of the endocrine hypothesis, Part I Chair: Marsha Richmond		Grace Lobby breakout room	Abstract #
The road to Wingspread: Theo Colborn and developmental disorders in Great Lakes fauna Marsha L Richmond			134
The construction of a sentinel species: Louis Guillette and Lake Apopka's alligators Mark V Barrow		Rich Roberts Hall	135
Mixed reception of the environmental endocrine hypothesis within science and the media: From 1991 to the present Sheldon Krinsky			136
Diverse Format Session Biologies of the South: Negotiating knowledge and livelihoods. Part I Chair: Abigail Nieves Delgado		Grace Lobby breakout room	Abstract #
Participants: Aadita Chaudhury, Nadya Karimasari, Zinhle Mncube, Jairo RoblesPiñeros, Abigail Nieves Delgado, Arturo Vallejo, David Ludwig		Carol Greider Hall	137

11:05-12:30 (GMT -4)

Individual Papers Session Individuality, II		Grace Lobby breakout room	Abstract #
The problem of character individuality James DiFrisco		Vannevar Bush Hall	138
Can scientists study individuals? Rose Trappes			139
From oviparity to viviparity: An organismic approach to the transition David Cortés-García			140
Individual Papers Session Open Session I and Flashtalks II		Grace Lobby breakout room	Abstract #
Trade-offs, pluralism and evolutionary accounts of death Philippe Huneman		Al Hershey Hall	141
Mechanistic causation and explorative strategy in microbiota-gut-brain axis research Yin Chung Au			142
The cognitive map debate in insects: A historical perspective on what is at stake Kelle Dhein	Flashtalk		143
Irene Manton, the cell and the electron microscope: Scientific seeing with an artist’s eye Nicola Williams	Flashtalk		144
Biofictional entities: Or, how to imagine the bewildering powers of life Thierry Hoquet	Flashtalk		145
Individual Papers Session Cultural adaptation and evolution		Grace Lobby breakout room	Abstract #
In between two niches: Cognitive parsimony in cultural adaptation Mathieu Charbonneau		Barbara McClintock Hall	146
Population as a distributed memory system: The species-environment complex and its implications for stability and long-term evolution Ehud Lamm, Oren Kolodny			147
Rethinking evolutionary progress in the light of cultural evolution Alejandro Gordillo Garcia			148

Individual Papers Session Information and immunology	Grace Lobby breakout room	Abstract #
A pragmatic model for the notion of “information” Martina Blečić		149
The evolution of information sharing Rafael Ventura		150
How to think about the immune system in times of COVID-19 and beyond: Why stronger isn’t always better and other misleading metaphors Martin Zach, Gregor Greslehner	<i>Max Delbrück Hall</i>	151
Diverse Format Session A critical discussion of Darwin's Argument by Analogy: From Artificial to Natural Selection Chair: Gregory Radick	Grace Lobby breakout room	Abstract #
Participants: Hayley Clatterbuck, Jonathan Hodge, Gregory Radick, Andrea Sullivan Clarke	<i>Martha Chase Hall</i>	152
Traditional Session Evolvability across biological disciplines: Recent history and new philosophical approaches Chair: Cristina Villegas	Grace Lobby breakout room	Abstract #
History of evolvability: Reconstructing and explaining the origin of a research agenda Laura Nuño de la Rosa		153
Evolvability as a disposition: Philosophical distinctions, scientific implications Ingo Brigandt	<i>Milislav Demerec Hall</i>	154
The conceptual roles of evolvability across evolutionary biology: Between diversity and unification Cristina Villegas, Alan C Love		155
Traditional Session Actors and actors' categories in history, philosophy, and social studies of biology Chair: Robert Meunier	Grace Lobby breakout room	Abstract #
What is an approach in biology? A case study from behavioral biology Robert Meunier		156
Reflections on the use of actors' categories as instruments of historical and epistemological analysis Hans-Jörg Rheinberger	<i>Rich Roberts Hall</i>	157
Diverse Format Session Biologies of the South: Negotiating knowledge and livelihoods, Part II Chair: Abigail Nieves Delgado	Grace Lobby breakout room	Abstract #
Participants: Aadita Chaudhury, Nadya Karimasari, Zinhle Mncube, Jairo Robles-Piñeros, Abigail Nieves Delgado, Arturo Vallejo, David Ludwig	<i>Carol Greider Hall</i>	158

13:00-14:00 (GMT -4)

<i>Community / Skill Building</i>	<i>Grace Lobby breakout room</i>	<i>Abstract #</i>
Diverse Format Session: Opportunities for ISHERs at CSHL: A virtual tour of collections, resources, fellowships, and the Center for Humanities and History of Modern Biology Chair: Alistair Sponsel Participants: Alistair Sponsel, Ludmila Pollock, Stephanie Satalino, Antoinette Sutto, Miriam Rich, Daniel Liu. Alistair Sponsel	Vannevar Bush Hall	159
Topic modeling and optimization, or how we scheduled ISHPSSB2021 Charles Pence	Al Hershey Hall	
How to construct an effective academic poster Sophie Veigl	Barbara McClintock Hall	
Open science and publishing Sabina Leonelli	Max Delbrück Hall	
Building inter-campus graduate networks Jenny Bangham	Martha Chase Hall	
Virtual coffee break / social hour	gather.town	

14:30-15:55 (GMT -4)

<i>Individual Papers Session Climate science</i>	<i>Grace Lobby breakout room</i>	<i>Abstract #</i>
Plant phenomes and climate change Özlem Yilmaz	Vannevar Bush Hall	160
Incorporating a feminist understanding of mobilities into quantitative gendered disaster mobility research Arthur Vandervoort		162
<i>Individual Papers Session Transmission, treatment, and therapy</i>	<i>Grace Lobby breakout room</i>	<i>Abstract #</i>
The elastic ruler: Placebo responses, clinical trials, and medical epistemology Shane N Glackin	Al Hershey Hall	163
Louis Daniel Beauperthuy: His reflections on the causation and transmission of tropical diseases from 1838 to 1871 Irene Bosch		164
An epistemological inquiry into phage therapy: Results and findings Thomas Bonnini		165

Individual Papers Session Eugenics	Grace Lobby breakout room	Abstract #
The Genetical Theory of Natural Selection and the controversy over R.A. Fisher's eugenics Alex Aylward	Barbara McClintock Hall	166
Heredity mobilized: From Mendelism to eugenics in the name of the Greek race Ageliki Lefkaditou		167
Teaching science through eugenics and the expansion of semen banks in USA Ma-Alicia Villela		168
Traditional Session After the modern synthesis Organizer: Alison McConwell Chair: James Griesemer	Grace Lobby breakout room	Abstract #
The extended evolutionary synthesis: A Gouldian perspective Max Dresow	Max Delbrück Hall	169
Shifting problem structures and the rebundling of specialties Elihu M Gerson		170
G.G. Simpson and S.J. Gould on values: Shifting normative frameworks in historical context Alison K McConwell		171
Diverse Format Session Book panel: Four tales from the world of small things Chair: Victoria Lee	Grace Lobby breakout room	Abstract #
Participants: Claas Kirchhelle, Victoria Lee, Neeraja Sankaran, Robin Scheffler	Martha Chase Hall	172

16:05-17:30 (GMT -4)

PLENARY: Revisiting Darwin's Descent (1871–2021)Grace Auditorium
(Zoom webinar)Organizer and Chair: **Thierry Hoquet**
Panelists: **Ross Brooks, Peter Godfrey Smith, Kimberly Hamlin, Christa Kuljian, Zuleyma Tang Martinez**

17:30 – 19:00 (GMT -4)

Coffee Break / Social Hour
gather.town

FRIDAY 16 July

9:00 (GMT -4)

Graduate Student Meeting

10:00 (GMT -4)

Membership Development Committee Meeting

16:30 (GMT -4)

Council Meeting 2

MONDAY 19 July**9:30-10:55 (GMT -4)**

Individual Papers Session Engineering life		Grace Lobby breakout room	Abstract #
A turn to the organism in synthetic biology? Erika Szymanski, Jane Calvert		Vannevar Bush Hall	173
Biological ownership and open source: Peculiarities seen through DIYbio Daphne Esquivel-Sada			174
Notions of microenvironment in organoids and organs-on-a-chip Silvia Caianiello, Marta Bertolaso			175
Individual Papers Session Evolutionary thought in the 19th century		Grace Lobby breakout room	Abstract #
Modalizing Darwin: Rhetoric across the editions of <i>On the Origin of species</i> Pedro L Navarro		Al Hershey Hall	176
Antoinette Brown Blackwell on women’s rights, metaphysics, and evolution Trevor Pearce			177
Traditional Session Anteaters, dolphins, kangaroos: Generating knowledge about exotic animals inside and outside the zoo Chair: Christian Reiss		Grace Lobby breakout room	Abstract #
A tale of two anteaters: Madrid 1776 and London 1853 Helen L Cowie		Barbara McClintock Hall	178
How to get into the pouch: Research on the riddle of the kangaroo birth inside and outside the zoo (1823-1926) Oliver Hochadel			179
Mediterranean dolphins from Miami: Knowledge and practices in Aquarama of the Barcelona Zoo in the 1960s Miquel Carandell Baruzzi			180
Traditional Session Wingspread@30: Birth and development of endocrine disruption science, Part II Chair: Ana Soto		Grace Lobby breakout room	Abstract #
Endocrine disruptors: From the Wingspread Conference (1991) to the EU comprehensive chemicals strategy for sustainability (2020), 30 years of scientific research Ana M Soto, Carlos Sonnenschein		Max Delbrück Hall	181
Theorizing biological disruptions: The case of endocrine disruptors Maël Montévil			182
Another trajectory: Endocrine disruptors in France Nathalie Jas, Jean-Paul Gaudillière			183

Diverse Format Session "Your genitals don't lie!" An escorted encounter with the history and philosophy of phallic and cervical measuring Chair: Caterina Schürch	Grace Lobby breakout room	Abstract #
Participants: Merlin Wassermann, Rebecca Jackson, Caterina Schürch, Kärin Nickelsen, Jutta Schickore	Martha Chase Hall	184
Diverse Format Session Norms of conceptual development in the life sciences Chair: Philipp Haueis	Grace Lobby breakout room	Abstract #
Participants: Philipp Haueis, Corinne Bloch-Mullins, Uljana Feest	Milislav Demerec Hall	185
Diverse Format Session Varieties of memory Chair: Eva Jablonka	Grace Lobby breakout room	Abstract #
Participants: Snait B Gissis, Cornelius Borck, Michael Levin, Eva Jablonka	Rich Roberts Hall	186
11:05-12:30 (GMT -4)		
Individual Papers Session Explanation	Grace Lobby breakout room	Abstract #
Idealization and non-ideal vaginal microbes: Applying Angela Potochnik's account of idealization in science Jacqueline M Wallis	Vannevar Bush Hall	187
Biological proportionality contests Marina DiMarco		188
Darwin, natural history, and explanatory breadth Charles H Pence		189
Diverse Format Session Theories of carcinogenesis: An interdisciplinary analysis Chair: Carlos Sonnenschein	Grace Lobby breakout room	Abstract #
Participants: Carlos Sonnenschein, Marta Bertolaso, Sui Huang	Al Hershey Hall	190

Traditional Session Knowledge coproduction and transdisciplinary practices in ecology and the environment, Part II Chair: Saliha Bayir		Grace Lobby breakout room	Abstract #
The nature of togetherness and togetherness in nature Julia J Turska			191
Knowledge coproduction or integration for conservation: can we go beyond overlaps? Charbel N El-Hani		Barbara McClintock Hall	192
Diverse Format Session Neuro-presents and neuro-futures: Neurotech practices imagined and lived Chair: Sandra Youssef		Grace Lobby breakout room	Abstract #
Participants: Markus Schmidt, Günter Seyfried, Sandra Youssef		Max Delbrück Hall	193
Traditional Session Thinking with microorganisms, 1880-1940: Symbiosis, asepsis and domestication Chair: Daniel Liu		Grace Lobby breakout room	Abstract #
Parasites or symbionts?: Women algologists and the microscopic study of algae in interspecies pairings, 1887-1899 Emily S Hutcheson			194
Domesticating the biochemical bacterium: Balance sheets, resting cultures, and microbial households in Marjory Stephenson's "General Microbiology" Charles A Kollmer		Martha Chase Hall	195
Analogous injections: Vaccines, glandular therapeutics and filters in Paris (1890s) Patrick M Walsh			196
Traditional Session Adaptation, teleology and function in evolutionary biology Chair: Nicola Bertoldi		Grace Lobby breakout room	Abstract #
Adaptation without adaptationism? Adaptations, functions, teleology and organic progress in G. G. Simpson's theory of macroevolution Nicola Bertoldi			197
Adaptation as a criterion for organic progress Silvia De Cesare		Milislav Demerec Hall	198
Evolution is goal directed Dan McShea			199

13:00-14:00 (GMT -4)

<i>Community / Skill Building</i>	Grace Lobby breakout room	
Happy Office Hours 1 Janet Browne, Maria Elice de Brzezinski Prestes, Vivette García Deister, John Dupré, Charbel El-Hani, Sabina Leonelli, Lisa Lloyd, Alan Love, Greg Radick, Elliott Sober	gather.town	

14:30-15:55 (GMT -4)

<i>Individual Papers Session</i> Data	Grace Lobby breakout room	Abstract #
The power of bibliometrics for historical epistemology of 20th century life sciences Hanna L Worliczek		200
How can highly contextual data such as metabarcoding data relate to the world? Aline Potiron	Vannevar Bush Hall	201
Producing social dis/order: Toward an epistemology of biobanking in big data genomics Kathryne Metcalf		202
<i>Diverse Format Session</i> Evolutionary cognitive archaeology: Epistemological and methodological issues Chair: Adrian Currie	Grace Lobby breakout room	Abstract #
Participants: Adrian Currie, Anton Killin, Andra Meneganzin, Ross Pain	Al Hershey Hall	203
<i>Individual Papers Session</i> Beyond the traditional organism	Grace Lobby breakout room	Abstract #
Two out of three: Diversity, heterogeneity and collectivity Ayelet Shavit		204
Multispecies ethnography, philosophy of biology, and 'Anthropocene onsets' in the Americas Francisco Vergara-Silva	Barbara McClintock Hall	205
Gaia: The earth is an organism (not a Darwinian individual) Letitia Meynell		206
<i>Diverse Format Session</i> The selected effect account of function: Problems, extension, reconciliation and applications, Part I Chair: Pierrick Bourrat	Grace Lobby breakout room	Abstract #
Participants: Subrena Smith, Paul Griffiths, Justin Garson, Peter Takacs, Pierrick Bourrat	Max Delbrück Hall	207

Traditional Session Reform of the genetics curriculum: Interdisciplinary perspectives Chair: Dennis Lee		Grace Lobby breakout room	Abstract #
Must genetics education start with Mendel? Two attempts to do otherwise in the 1970s and 80s Hannah Bapty			208
Undergraduate genetics assessments: What are we assessing and how? Kelly M Schmid, Dennis Lee, Monica Weindling, Awais Syed, Stephanie-Louise Yacoba Agyemang, Michelle K Smith		Martha Chase Hall	209
Fostering complex genetics literacy: Effects of a Weldonian curriculum on year ten students' genetics knowledge and social views Oliver S Brown			210
16:05-17:30 (GMT -4)			
Individual Papers Session Life and its limits		Grace Lobby breakout room	Abstract #
Probing the "grey area": Natural kinds and extraterrestrial life Aleksandar V Božić			211
The new N=1 problem Carlos Mariscal		Vannevar Bush Hall	212
Are viruses alive and should we care? Gregory J Morgan			213
Individual Papers Session Beyond the archive		Grace Lobby breakout room	Abstract #
Interface pedagogy-biology-medicine in home education in the GDR: Transdisciplinary logics of action in the mirror of biographical interviews Felicitas P Söhner			214
An animal history of biology: Questioning the place of biologists and historians Quentin Lade		Al Hershey Hall	215
Once upon a time the construction of molecular genetics of bacteria in Mexico: Interviews from the past Marco Ornelas-Cruces			216
Individual Papers Session Cell biology		Grace Lobby breakout room	Abstract #
Roles of scientific generalizations beyond explanation: The case of collective cell migration Yoshinari Yoshida			217
Monads and cells: Investigating on simplicity and complexity in simple biological entities Caroline Angleraux		Barbara McClintock Hall	218

Diverse Format Session		Grace Lobby breakout room	Abstract #
The selected effect account of function: Problems, extension, reconciliation and applications, Part II Chair: Carl Brusse			
Participants: Daniel J Nicholson, Carl Brusse, John Matthewson, Justine Kingsbury		Max Delbrück Hall	219
Traditional Session		Grace Lobby breakout room	Abstract #
What does it mean to value biodiversity? Chair: Michael Dietrich			
Is global biodiversity loss bad? Katie Morrow			220
Aldo Leopold and the biodiversity-stability connection Roberta L Millstein		Martha Chase Hall	221
Research biodiversity and the presumption of generality in the life sciences Michael R Dietrich			222
17:30-19:00 (GMT -4)			
Community / Skill Building		Grace Lobby breakout room	
Happy Office Hours 2 Lisa Lloyd, Alan Love, Roberta Millstein, Lynn Nyhart, Anya Plutynski, Thomas Pradeu, Greg Radick, Betty Smocovitis, ASU Faculty		gather.town	
19:00-20:25 (GMT -4)			
Individual Papers Session		Grace Lobby breakout room	Abstract #
Open Session, III			
A novel argument for a progenerative view of kinship Rob Wilson			223
Pathological complexity and the evolution of consciousness Walter Veit		Vannevar Bush Hall	224
Issues when applying structuralism to biology Angella Yamamoto			225

Individual Papers Session Mechanistic explanation		Grace Lobby breakout room	Abstract #
Lessons from history: What Schelling might add to the New Mechanistic approach and contemporary biological science Sarah M Roe, Steven M Brown			226
Principled mechanistic explanations in biology: A case study of Alzheimer's disease Sepehr Ehsani		Al Hershey Hall	227
Epistemic progress in animal models of mental disorders: From the depressed mouse to the mouse with aspects of depression Derek W Braverman			228
Diverse Format Session Corroborative and anticipatory predictions Chair: Solange Haas		Grace Lobby breakout room	Abstract #
Participants: Solange Haas, Philippe Huneman, Philippe Jarne, Virginie Maris, Sonia Kéfi		Barbara McClintock Hall	229
Traditional Session Muller and mutation Chair: Sander Gliboff		Grace Lobby breakout room	Abstract #
The origins of Muller's mutation concept Sander Gliboff			230
The vexed question of human genetic load Evan Arnet		Max Delbrück Hall	231
Gradualism, natural selection, and randomness of mutation: Darwin, Fisher, and connecting the dots Matthew J Maxwell, Elliott Sober			232
20:35-22:00 (GMT -4)			
Individual Papers Session Teleology		Grace Lobby breakout room	Abstract #
Teleonomy and teleology revisited: The continental critique of cybernetics Auguste A Nahas			233
Understanding teleology: A strategy for the study of value on biological systems David Suárez Pascal		Vannevar Bush Hall	234

Individual Papers Session		
Birds of a feather: Heredity, species, and taxonomy		
Generations and heredity: The social and biological careers of ‘intergenerational’ and ‘transgenerational’ inheritance Tatjana Buklijas	Grace Lobby breakout room	Abstract # 235
The good species John S Wilkins	<i>Al Hershey Hall</i>	236
Ornithology and the “Empire of Nature”: The classification of birds in eighteenth-century France Yotam A Tsal		237
Traditional Session		
Mutational biases and adaptation		
Chair: David McCandlish		
The anomaly of a basic population-genetic cause missing from the Modern Synthesis Arlin B Stoltzfus	Grace Lobby breakout room	Abstract # 238
The role of theoretical population genetics in mutation-biased adaptation Kevin Gomez, Jason Bertram, Joanna Masel	<i>Barbara McClintock Hall</i>	239
Do mutational biases influence adaptive evolution? David M McCandlish		240

TUESDAY 20 July**9:30-10:55 (GMT -4)****PLENARY: Viral Vulnerability: From Permissivity to Pessimism**Grace Auditorium
(Zoom webinar)Organizer and Chair: **Eben Kirksey**Panelists: **Sria Chatterjee, Alexander Gorbalenya, Steve Hinchliffe, and Anthony Ryan Hatch****11:05-12:30 (GMT -4)****Individual Papers Session****Primates and the colonial context****When did we first talk about "primatology" ?**

Marie L Lacomme

Out of Africa: Yerkes and Nissen's primate field studies in French Guinea (1920s-1930s)

Marion C Thomas

Vector biology network: Bringing innovations in modern biology to the field of vector borne diseases

Kulash Zhumadilova

Grace Lobby
breakout room**Abstract #**

241

Vannevar Bush Hall

242

243

Individual Papers Session**Emotion and cognition****Cognitive norms in autonomous systems: Rooting teleosemantics within organicism**

Tiago Rama, Xabier Barandiaran

Emotional appraisal is not memory

Isaac Wiegman

The evolution of imaginative consciousness

Oryan Zacks

Grace Lobby
breakout room**Abstract #**

244

Al Hershey Hall

245

246

Individual Papers Session**Race and eugenics****Epigenetics and the biology of race: Naturalism, environmentalism, constructivism**

Gaëlle Pontarotti

Race eliminated

Tarik D LaCour

Liberal eugenics and the enhancement technologies

Tomás M Hernández Mora

Grace Lobby
breakout room**Abstract #**

247

Barbara McClintock Hall

248

249

Individual Papers Session Remains of the dead		Grace Lobby breakout room	Abstract #
Taphonomy as planetary science Ana María Gómez López			250
Analogue models in paleontology Aja Watkins		Max Delbrück Hall	251
Proximate and distant ancestry in forensic genetics Vivette Garcia-Deister			252
Individual Papers Session Adaptationism		Grace Lobby breakout room	Abstract #
Making sense of the relationship between adaptive thinking and heuristics in evolutionary psychology Shunkichi Matsumoto			253
Intelligence is not reason: Adaptationist biology and the psychology of the in-between David I Delano		Martha Chase Hall	254
Adaptationism and its limitations in biology and machine learning Richard Ngo			255
Traditional Session Conceptualizing homology from Richard Owen to developmental genetics Chair: Devin Gouvêa		Grace Lobby breakout room	Abstract #
Reference and ignorance Aaron Novick			256
Approaching avian digit homology Devin Gouvêa		Milislav Demerec Hall	257
The link between historical continuity and molecular mechanisms: Traceability and individuation Günter Wagner			258
Diverse Format Session Revisiting H.J. Muller and N. Vavilov in Russian genetics Chair: Garland E Allen		Grace Lobby breakout room	Abstract #
Participants: Garland E Allen, Victor E Spangenberg, Helen J Muller		Rich Roberts Hall	259

<i>Traditional Session</i>		
Life as a planetary process: The earth systems science perspective	Grace Lobby breakout room	Abstract #
Chair: Alejandro Merlo		
Gaia: controversial hypothesis, research programme or philosophy of nature? Sébastien Dutreuil		260
Gaia in the mud Leah Aronowsky	Carol Greider Hall	261
On the contribution of earth system science to the thermodynamic account of life Alejandro Merlo, Xabier E Barandiaran		262
13:00-14:00 (GMT -4)		
Community / Skill Building	Grace Lobby breakout room	
Why you should keep hosting online conferences Rose Trappes & TJ Perkins	Al Hershey Hall	
Interdisciplinary collaboration Isabella Sarto-Jackson	Barbara McClintock Hall	
Teaching by building a Wikipedia page Aleta Quinn	Max Delbrück Hall	
How to turn a conference presentation into a paper Greg Radick	Martha Chase Hall	
Virtual coffee break / social hour	gather.town	
14:30-15:55 (GMT -4)		
Individual Papers Session Modelling	Grace Lobby breakout room	Abstract #
The dynamics of modeling and empirical techniques in the history of protein crystallography Dana Matthiessen		263
Integrating-for-purposes: The aims-based approach to scientific integration in biology Alican Basdemir	Vannevar Bush Hall	264
What (and how) can we learn from divergent experimental results? Sandra D Mitchell		265

Traditional Session History of evolutionary biology: Connections with science education Chair: Gerda Jensen		Grace Lobby breakout room	Abstract #
Darwin's discussion of the origin of electric fish: A teaching and learning sequence in Brazilian youth and adult education Gerda Jensen, Maria Elice Prestes		Al Hershey Hall	266
Fritz Müller 200 years and the teaching of Brazilian biodiversity and evolution Leonardo Augusto L Araújo, Nelio Bizzo			267
Diverse Format Session Bungtown style: Scientific thought and practice at Cold Spring Harbor Chair: Nathaniel Comfort		Grace Lobby breakout room	Abstract #
Participants: Nathaniel Comfort, Vassiliki B Smocovitis, Robin Scheffler		Barbara McClintock Hall	268
Traditional Session Philosophy of Cancer, Part II Chair: Lucie Laplane		Grace Lobby breakout room	Abstract #
Clonal evolution: Toward a new view of clones Lucie Laplane			269
Going big by going small: Tradeoffs in microbiome explanations of cancer Anya Plutynski, Emily C Parke		Max Delbrück Hall	270
What does 'aging causes cancer' mean? Mael Lemoine			271
Traditional Session Causation in biology Chair: Ehud Lamm		Grace Lobby breakout room	Abstract #
Generalized Darwinism and the causal structure of natural selection Adam Krashniak			272
The causal decomposition of evolutionary change revisited Samir Okasha		Martha Chase Hall	273
Disambiguating proximate and ultimate "causes" Yafeng Shan			274

Traditional Session History and philosophy of enzymes Chair: Andrew Reynolds	Grace Lobby breakout room	Abstract #
Enzymes and substrates: Practices of relational modeling before and after the introduction of quantum chemical methods Rebecca Mertens		275
A historical approach to enzymes and their functions: Genetics, biochemistry, and infection Maria J Santesmases	<i>Milislav Demerec Hall</i>	276
Enzyme establishments: Examples from three centers of research in the United States, 1940–1955 Gina Surita		277

16:05-17:30 (GMT -4)

Awards Meeting and Future ISH Plans
[Grace Auditorium](#)
(Zoom webinar)

17:30-19:00 (GMT -4)

Coffee Break / Social Hour
[gather.town](#)

Lively stasis: Care, routine, and the imaginaries of scientific collections

Jenny Bangham¹, Xan S Chacko²

¹Queen Mary University of London, School of History, London, United Kingdom

²Wellesley College, Women's and Gender Studies, Wellesley, MA

Collections of living organisms are reservoirs of biological knowledge that operate across times and places. From the mid-twentieth century, institutions dedicated to such living, dynamic, unruly collections have routinized and professionalized their care. But the target of that care is not just individual organisms--rather, care is also focused on the integrity of the 'strain,' 'variety,' 'line,' or 'stock', and the composition of the collection as a whole. What kinds of human and non-human care labour stabilize (and disrupt) these entities? Drawing comparisons between two strikingly different kinds of living scientific collection--seed banks and *Drosophila* stock centers--the authors explore how forms of temporal stasis are enacted. The collections create the conditions for routine care labour, and also constitute a 'past' that is only able to exist because of that care. What kinds of work go into managing the identities of such entities, and the information attached to them?

Seed banks and biological stock centres take the maintenance of stability very seriously. What does monitoring and surveillance look like, and how do these maintain the integrity of the strains and stocks, and the collections themselves? What kinds of value are created through these labours? Since the aim of these collections is to endure such that they can support scientific research in an unknown future, what are the imaginaries of the future that undergird their practices and ideologies of acquisition and maintenance? Finally, how are the future imaginaries rhetorically drawn into the funding strategies of these collections, how do they envision future use, ownership, and control?

Medical anamnesis: The role of past collections in the future of diagnosis and prognosis

Karin Tybjerg²

¹University of Copenhagen, Medical Museion, Copenhagen, Denmark

²University of Copenhagen, Novo Nordisk Foundation Center for Basic Metabolic Research, Copenhagen, Denmark

Anamnesis is the medical history of a patient's disease taken by the doctor when he or she meets the patient as part of the diagnostic process. The term anamnesis comes from Greek, aná "open" plus mnesis "memory". This paper will "open the memory" of medical diagnosis itself showing the role played by collections of historical cases in the establishment of diagnostic categories. And how timelines being extended into the future with prognostics necessitates a deeper delving into the past.

Understandings of disease, disease categories and diagnosis change over time. While diagnosis today increasingly seems to concern the future with an interest in prognoses, early detection and pre-disease, this paper will outline how concepts of diagnosis are always anchored in past cases and collections, as much diagnostic practice in essence is about using past cases, specimens and samples to understand present and future disease. As Daston in her *Sciences of the Archive* pointed to the role of historical archives in the sciences, this paper will focus on the role of historical specimen and cases in medicine.

"Medical Anamnesis" will trace historically how diagnostics have relied on collected material of diseased bodies from the 18th and 19th centuries when disease was localized and generalized on the basis of collections of specimens, to a related process in 21st research projects based on slides and tissue samples from biobanks. At the same time the paper will investigate the inherent tension between describing trajectories of disease or evolution while also establishing a category system – a tension between time and taxonomy.

Decolonizing the biology archive: Postcolonial approaches to recovering gendered knowledges of life

Don Opitz¹, Banu Subramaniam²

¹DePaul University, School of Continuing and Professional Studies, Chicago, IL, ²University of Massachusetts, Amherst, Women, Gender, Sexuality Studies, Amherst, MA

How do we recover ‘hidden’ voices of the past, buried beneath masculinist, Western epistemological layers that have squelched feminist, queer, and indigenous ways of knowing? How do we interrogate ‘the archive’ to access past knowledges of the living world, illuminating the complexity of global histories and accounting for the suppression and erasure of historical agents? How do we retrieve, re-read, and engage archive sources in our decolonization projects, such that we acknowledge colonial hegemonies and their legacies in the very acts of extracting, collecting, preserving, organizing, and archiving? How do we uncover the colonial legacies of race, gender, and sexuality? And how do we ‘break open’ the archive in a digital age, such that we deal with structural barriers that impose differential access among users?

In this paper, we consider these questions and how postcolonial approaches informed by gender, queer, and critical ethnic studies may offer possibilities for recovering gendered knowledges of the living world that span global geographies during the past few centuries. Our questions are motivated by our current work-in-progress: the publication of a cross-cultural compendium of primary sources that will make more widely available diverse ways of knowing, particularly among women, transpersons, and indigenous scholars across colonial and postcolonial contexts from the eighteenth through the twentieth centuries. As we explore these approaches, we review the efforts underway among similar scholarly projects also engaging in this work, for example the decolonization efforts at Kew Archives and curated collections among digital archives like the online Biodiversity Heritage Library. As this is a work-in-progress, we invite critical discussions that highlight both the challenges and yet possible pathways forward for decolonizing the biology archive.

Carving the social environment at genetic joints: Can GWAS inform claims about environmental causes?

Olesya Bondarenko¹

¹University of Cambridge, History and Philosophy of Science, Cambridge, United Kingdom

This paper examines the epistemic strategy which relies on the findings from genome-wide association studies (GWAS) to make claims about the causal role of socio-environmental factors in individual behavioural outcomes, such as educational attainment or subjective well-being. Such a strategy has been proposed in what is known as social science genomics – a research program that aims to address questions in the social sciences with the help of novel genomic designs. I offer an evaluation of the strategy by highlighting the role of intermediate phenotypes identified through GWAS and drawing on a comparison case from epidemiological research, where similar uses of GWAS have been suggested. I argue that, in the context of social science genomics, the study of intermediate phenotypes has relied on “unstable” psychometric constructs which permit of different operationalisations and ways of measurement. One implication of this instability is that they can support divergent inferences about the causal role of environmental factors. Hence, I argue that scientists should proceed with caution when using the information yielded by GWAS mapping to make causal claims about the social environment, as there may be alternative inferences about higher-level behavioural phenomena (and, correspondingly, environmental factors) that can be drawn from the same genetic data.

Is It mine or ours? Legal conceptualization of the "singular genome"

Shelly Simana¹

¹Harvard University, Harvard Law School, Cambridge, MA

The Article focuses on “nonconsensual genetic use.” This means the use of what I term the “singular genome”—that is, the genome of a single individual—by other individuals, without the knowledge or consent of the person from whom it was taken.

The Article begins by mapping out what forms the genome. It shows that the genome has tangible and intangible components and that it has individual, familial, and collective aspects. Moreover, the genome encompasses opposites: it is both excludable and non-excludable; subtractable and non-subtractable. The Article then investigates whether law-making institutions and parties in court proceedings consider the genome’s unique nature. For this purpose, the Article maps the legal landscape in the United States and explores how the genome is conceptualized and which ideologies are presented in briefs, court decisions, and legislation. The legislation and court proceedings are grouped into two arenas: “research” and “other personal interactions.” The former concerns use in the context of scientific research and the latter concerns use in the context of other personal interactions, like with DTC genetic companies or private individuals.

When analyzing the two arenas, there are two main findings. The first finding is that the legislation and court proceedings are overly narrow. The research arena exhibits an altruistic ideology, one that justifies treating the genome as a “public good,” governed by an “open-access commons” regime. The other personal interactions arena exhibits an individualistic ideology, one that justifies treating the genome as a “private good,” governed by a “propertization-through-control” regime. This binary division is superficial. Despite its unique ontology, the genome is positioned in relation to manageable categories—it is conceived as either a resource that is owned by everyone or as a resource that is exclusively owned by individuals. In addition, the binary division fails to properly balance respect for individuals and family members with the promotion of public goals. The second finding is that within each arena, parties in court proceedings, judges, and legislatures are using the legislation and court proceedings to negotiate the value of the genome. In their attempt to advance one conceptualization over another, they seem to employ different strategies.

Identity by descent (IBD) as an algorithm-and-simulation practice in current human population genomics research

[Carlos Andrés Barragán](#)¹, James R Griesemer¹

¹University of California, Davis, Science & Technology Studies Program / Department of Philosophy, Davis, CA

We present findings from in-progress archival, ethnographical, and conceptual analyses of how life-scientists currently frame and implement the concept of *identity by descent* (IBD) as a model to predict biological events for “recent” or “regional” human ancestry. Although IBD can be contextualized to have multiple histories, here we focus on how the concept is used in research programs in population genomics and biomedicine to describe a DNA segment shared by two or more individuals inherited from a common ancestor. We argue that the use of IBD to substantiate relatedness through time and space is a less than straightforward modeling and rendering practice following a well-described concept from population genetics. From a bioinformatics point of view, the use of DNA microarrays to measure genetic similarity involves a considerable risk of misinterpretation of false indications of relatedness, e.g., due to recombination, complicating the understanding of “recent” and “deep” ancestry. A practice scientists seem increasingly to use in order to overcome such challenges is to devote more effort and resources toward building tailored analytical tools, such as algorithms and software packages, as means of exploring alternative modeling strategies for identifying genetic population structure. Framed by scientists as a key form of scientific innovation, these tools are valued not only for helping researchers to address false positives, but more importantly, for allowing them to answer specific questions about contemporary human populations. The landscape of datasets to which scientists seek to apply these tools is dynamic and ever-changing. New models developed through algorithm-and-simulation practices must be applied while relying on a palimpsest of datasets produced in various contexts (e.g., ancestry studies and biomedicine for new and different uses). We argue that IBD, now understood as a tool, can embody models, predictions and datasets as they are re-situated and re-used by multiple actors. In order to illustrate how scientific knowledge about human heredity and ancestry is re-situated among contexts we analyze some recent research outcomes from several university research laboratories in California.

Transitional functionality of genomic segments: From stochasticity to robustness

Zdenka Brzović¹, Predrag Šustar¹

¹University of Rijeka, Department of Philosophy, Rijeka, Croatia, ²University of Rijeka, Department of Philosophy, Rijeka, Croatia

Current theories and their explanatory models accounting for the origin of new genes in a genome stir the traditional function debate and its impact on some other philosophical issues. In this paper, we focus in that regard on the following two questions: the temporal question (TQ), i.e., at which point(s) a previously nonfunctional genomic segment or its activity acquires functionality; and the mechanistic question (MQ), i.e., how the function notions, such as those used in the abovementioned areas of molecular biology, are related to the mechanism notions. More specifically, how the origin of a new functional gene, most frequently, a polypeptide producing gene, relates to apparently contrasting features of the mechanism of protein synthesis; namely, the resilience and noise or stochasticity. We respond to TQ by arguing for a transitioning functionality framework for genomic objects. As to MQ, we advocate in the present paper a strengthening of the link between functions and mechanisms, not only in the sense that biological mechanisms must have a determined function (see Garson 2019), but also that mechanistic arrangements are important for establishing the regularity of the functional outcomes here under consideration.

References:

Garson, Justin (2019), *What Biological Functions Are and Why They Matter* (Cambridge, CUP).

An organizational account of malfunctioning: A dynamic normative field approach

Xabier E Barandiaran¹, Tiago Rama²

¹University of the Basque Country (UPV/EHU), Philosophy Department, Vitoria-Gasteiz, Spain, ²Autonomous University of Barcelona, Philosophy Department, Barcelona, Spain

The notion of malfunction is critical to functional explanations of biological systems for it provides a test-bed for the normative character of functional attribution. Under some circumstances theories of biological functioning must permit that traits be able to operate but at the same time be judged as malfunctioning (in some naturalized, non-arbitrary sense). Whereas malfunctioning (and semantic error) has attracted most attention and discussion in evolutionary etiological approaches, organizational ones have been less discussed. Saborido (2011) and latter Mossio and Moreno (2015) provide an organizational account of biological function in which “malfunctions are a subset of functions that fit first-order norms (of the first-order ongoing organization in which they match functional presuppositions), but not second-order ones (since they do not obey to second-order regulatory functions, and prevent the shift to another first-order organization).” (Moreno & Mossio 2015: 85). We argue that this conception is unnecessarily complicated (malfunctions, we argue, do not need to arise as a result of two conflicting levels of norms) and too narrow (it excludes cases failure to comply with first or second order norms independently of each other and leaves out cases of malfunctioning within a specific self-maintaining regime).

We provide a notion of biological malfunctioning grounded on viability theory as modelled by Barandiaran & Egbert (2014) solving the problems mentioned above. The operations of the traits that constitute an organism define the normative field of its viability space: sugar must be replaced at certain rate, blood must be pumped at a certain pace, etc. A trait operates normatively when its effects on the viability space correlate with the normative field. Three sense of dysfunctionality might be distinguished: a) subfunctional operations are those that positively correlate with the normative field but quantitatively fail to match the required speed, b) malfunctional operations are those that negatively correlate with the normative field and c) nonfunctional traits either don't operate at all or operate with no correlation effect on the normative field. We illustrate these cases with examples of bacterial metabolism and chemotaxis.

Dissecting stochasticity in gene expression: New epistemological insights by a multidimensional analysis

Marco Casali^{1,2}, Francesca Merlin², Alberto Vianelli³

¹University of Rome Sapienza, Philosophy, Rome, Italy, ²IHPST, CNRS & University of Paris 1, Philosophy, Paris, France, ³University of Insubria, Department of Theoretical and Applied Sciences, Varese, Italy

Since the 1990s, researches dealing with stochasticity in molecular and cellular biology have been mainly focused on the process of gene expression, especially on transcription. In this context, stochasticity is conceived as noise, and is defined and measured as random variation around the mean value of a given gene expression parameter (i.e., the concentration/number of RNAs or proteins produced; see Elowitz 2002). The focus here is thus on what we call “quantitative stochasticity” (QTS), i.e., stochastic processes whose effects influence the amount of genetic products synthesized from the same DNA sequence (e.g., Pilpel 2011). More and more research studies suggest that QTS in transcription is not just mere noise (i.e., a perturbation or error with respect to some expected result), but can be a relevant parameter likely to play a role in the explanation of cell differentiation and development (cf. Casali & Merlin 2020). What about stochasticity in translation? This other step of gene expression, and stochasticity affecting it, have seldom been studied. Recent experimental researches clearly show the pervasive influence of stochasticity on translation too, in particular on the type of protein(s) produced (e.g., Boersma et al 2019). We talk about “qualitative stochasticity” (QLS) to refer to stochastic processes whose effects influence the diversity (type) of genetic products synthesized from the same DNA sequence. By focusing on a case of “noncanonical translational events”, namely alternative start-codon selection events, we argue that QLS in translation is not mere noise but can make a difference in gene expression, and further in cell differentiation and development. Thus, it can have an explanatory role to account for these processes. Our argument relies on the distinction of various dimensions where stochasticity takes place: two temporal dimensions (time as order and time as duration), and two spatial dimensions (homogeneous and heterogeneous intracellular space), coupled with considerations based on the law of large numbers. Taking into account all these dimensions, we argue, allow for a better evaluation and understanding of the ways QLS affects translation dynamics, and its very role in the explanation of gene expression results.

Cut and paste: The Mexican Axolotl, experimental practices and the long history of regeneration research in amphibians, 1864-present

Christian Reiß¹

¹Regensburg University, History of Science Unit, Regensburg, Germany

The Mexican axolotl (*Ambystoma mexicanum*) is an important model in contemporary regeneration research and regenerative medicine. The species also has a long history as an experimental and laboratory-bred animal. The species' astonishing ability to regenerate tissues and entire body parts became apparent shortly after the first 34 living axolotls were brought from Mexico to Europe in 1864. Nevertheless, only at the beginning of the 20th century did regeneration become a research focus. In the flourishing field of experimental embryology, regeneration in axolotls was used in three different ways: First, it was studied as a phenomenon in its own right. But more importantly, and second, it served as a macroscopic model for normal development and, together with other techniques like grafting, became an experimental tool or technical object in the experimental systems of experimental embryologists. In my presentation, I will show how the Mexican axolotl became a model for regeneration research. By revisiting the different moments in which regeneration was studied since the first axolotls came to Europe, I will demonstrate how regeneration was used in various conceptual and experimental settings and how the Mexican axolotl was molded into a model for these processes. Beyond the example of the axolotl, this history offers a window into the history of the experimental practices and organisms of regeneration research.

Deciphering regeneration through non-model animals: A century of experiments on cephalopod mollusks and an outlook at the future

Pamela Imperadore¹, [Fabio De Sio](#)²

¹Stazione Zoologica Anton Dohrn, Biology and Evolution of Marine Organisms, Naples, Italy, ²Heinrich Heine Universität, Institut für Geschichte, Theorie und Ethik der Medizin, Centre for Health and Society, Medizinische Fakultät, Düsseldorf, Germany

The advent of marine stations in the last quarter of the 19th century has given biologists the possibility of experimenting upon myriad marine organisms. Among them, cephalopod mollusks have attracted great attention, thanks to a number of biologically unique features including a sophisticated behavioral repertoire, remarkable body patterning capacities, and complexity of the nervous system. Surprisingly, the capacity to regenerate appendages and tissues, including in the central nervous system, has been understudied over the decades.

Here, we will first review the studies on the subject published between 1920 and 1970, which set the base for the study of regeneration in the taxon, in their epistemic and disciplinary contexts.

We will then explore the potential and growing relevance of cephalopods as prospective models of regeneration in recent times, in the light of the novel opportunities provided by technological and methodological advances, to reconsider old problems and explore new ones. The recent development of cutting-edge technologies made available for cephalopods, like genome editing, is allowing for a number of important findings and opening the way toward new promising avenues. Through the dialogue between experimental and historical perspectives, this article will stimulate a discussion around the changing epistemic and historical relations between the model-based and the comparative approach 20th-century biology and medicine.

Experimental organisms, neuron regeneration, and the curious case of the lamprey in the history of the neurosciences, 1870s-present

Kathryn G Maxson Jones¹, Jennifer R Morgan²

¹Baylor College of Medicine, Center for Medical Ethics & Health Policy, Houston, TX, ²Marine Biological Laboratory, Eugene Bell Center for Regenerative Biology & Tissue Engineering, Woods Hole, MA

This paper explores the history of lampreys in neurobiology since the 19th c. Three attributes have enabled lampreys' staying power as experimental organisms: the large neurons in their central nervous systems (CNS); the robust structural and functional regeneration that larvae exhibit after spinal cord injuries; and their early branching position in the vertebrate phylogeny.

From the 1870s to the 1960s, identifiable cells in the lamprey CNS helped to prove the very existence of neurons. Then, from the 1960s to the 1980s, biologists characterized structural regeneration in the spinal cord, offering a comparative perspective next to the robust CNS regeneration in many invertebrates yet poor such ability in most mammals, including humans. Finally, since the 1980s, biologists have employed multiple methods to explore functional regeneration, including recovery of swimming after CNS injuries in tandem with physiological recordings in cells and molecular tools. In this work, biologists have especially leveraged the evolutionary place of lampreys, providing comparative insights into humans' limitations.

At each point in this history, lampreys have helped elucidate problems of biological and medical relevance. Yet, this relevance has depended on comparison, from the cellular to phylogenetic levels. Thus, the lamprey story tells us that “translational” research, including in regenerative medicine, must also be comparative, to maximize insights and applications from lab to clinic.

One, two or many? It depends why you're asking

John Dupre¹

¹University of Exeter, Egenis, Exeter, United Kingdom

The realisation of the near omnipresence of symbiosis has given rise to an active debate about what are the “real” biological individuals. A growing number of theorists are opting for the holobiont, a macrobe and all its associated microbes. Conservatives still defend what I have called the monogenomic differentiated cell lineage (MDCL) as the paradigm multicellular individual. Lisa Lloyd will discuss the demibiont.

My argument today will be let a thousand flowers bloom. Within a process ontology, which I endorse, reality is not restrictive in the individuals it allows us to identify. The MDCL is a distinguishable flow of biological activity, intertwined at any one point with many other such flows provided by partners ranging from the obligate symbiont to the dangerous pathogen. The more long-lasting the association and the more it is required for the functioning of both partners, the stronger the grounds for including both within the same individual. But there is no absolute criterion for such conjunction, and no obstacle to distinguishing the minimal organismic parts as individuals when theoretical purposes demand.

In this talk I shall sketch what I mean by a process ontology and then consider how it applies to multicellular and multilineage biological individuals. A starting point will be the thesis of Dupré and O'Malley (2009) that life generally occurs when lineages intersect and interact metabolically. I shall then consider what is involved in identifying all or part of such interactions as an individual or as an organism.

A network framework to explain the evolution of host-microbiome associations: System-level engineering adaptations result from mixed modes of inheritance

Javier Suárez¹, Saul Huitzil²

¹Jagiellonian University, Philosophy Of The Natural Sciences, Krakow, Poland, ²universidad Nacional Autónoma De México, Institute Of Physics, Mexico, Mexico

It has recently been proposed that holobionts (host-microbiome systems) act as a level of selection in evolution, because they can act as interactors, reproducers, and manifestors of adaptation (Lloyd 2017; Lloyd & Wade 2019). In this line, recent research has shown that some taxa have evolved hologenomic (engineering) adaptations (manifestors of adaptation), proving that natural selection can generate engineering adaptations in some host-microbiome lineages (Suárez & Triviño 2020). However, a question remains about the conditions that make the evolution of hologenomic (engineering) adaptations feasible, especially as holobiont selection is believed to be disrupted due to the abundant of horizontal transfer of microbes between host lineages (Moran & Sloan 2015). To investigate the conditions under which hologenomic (engineering) adaptations can evolve even when horizontal transfer is common, we modelled the host-microbiome as a Boolean network and explored how the adaptability of the host and of the microbiome changed over several generations. Our model shows that if the task assigned to the network remains constant, horizontal transfer of symbionts does not erode adaptation at the host-microbiome system, but reinforces it, whenever it is kept in a specific proportionality vis à vis vertical transmission. We interpret this result biologically and conclude that host-microbiome joint adaptation will not be eroded by horizontal transmission when the environmental conditions that the system faces are extreme and relatively rare in relation to the conditions encountered by other taxa.

Why the host-symbiont relationship between *Euprymna scolopes* and *Vibrio fischeri* is a demibiont and not a holobiont: Reciprocal and non-reciprocal evolution

Michael J Wade¹, Elisabeth A Lloyd^{2,1}

¹Indiana University, Biology, Bloomington, IN, ²Indiana University, History and Philosophy of Sci, Bloomington, IN

In the context of the discussions concerning holobionts, numerous critiques of the arguments have identified the bobtail squid-*Vibrio* species pair (*Euprymna scolopes* host and *Vibrio fischeri* symbiont) as an example of a holobiont. In a prior work (Lloyd and Wade 2019), we provided a critique in the context of a conceptual framework involving coevolutionary genetic processes that we think can be helpful in many other studies of a host and its symbionts. Our method requires that we examine not only the interaction between squid and *Vibrio* but also address the evolutionary genetic consequences when there is a fundamental asymmetry in the association: all *E. scolopes* are associated with *V. fischeri*, but few *V. fischeri* are associated with *E. scolopes*. Moreover, the small numbers of *V. fischeri* that become squid-associated by colonizing a host come from the larger pool of non-host associated *V. fischeri*, free-living in the water column. There are still other populations of *V. fischeri* that are associated with the hind guts of some fishes and with marine sediments. Migration or gene flow across heterogeneous selective environments tends to slow the rate of local adaptation (i.e., *E. scolopes*; Lenormand 2002), especially when selection acts differently in different environments. It is yet more difficult to achieve adaptation to a rare environment, when the direction of gene flow is predominantly from the environments where individuals are more abundant (free-living or in hind-guts of fishes) into the one in which they are scarcer (squid-associated). When there are fitness trade-offs, so that adaptation to one environment compromises fit to another, gene flow between environments, especially when asymmetric, presents a daunting challenge to local adaptation to a rare environment. In sum, we use this squid/*Vibrio* case to illustrate the difference between demibionts and holobionts. We propose that this is a case where philosophy of science can aid biology in practice.

Drawn, erased, re-negotiated: The organism-environment boundary in early twentieth-century biology

Alejandro Fábregas-Tejeda¹

¹Ruhr University Bochum, Department of Philosophy I, Bochum, Germany

Recent historiographical work has shown that ‘organism’ and ‘environment’ were two important *loci* of ontological, epistemological and methodological debates in early twentieth-century life sciences. Manifold organism-centered perspectives flourished in the interwar period, and discussions on the relationship between organisms and environments extended to other fields of inquiry (e.g., philosophy and psychology). Here, I will focus on a hitherto uncharted component of these debates: the nature of the organism-environment (O-E) boundary. In particular, I will explore how this ‘boundary’ was framed, expunged and re-negotiated by biologists from different disciplinary orientations and theoretical standpoints. First, I will illustrate diverse views on how the O-E boundary was drawn, appealing to examples that include metabolic gradients in development (C.M. Child) and the experiential delimitation of organisms as agents with a point of view in the world (E.S. Russell), among others. Second, I will cover some stances that disavowed the existence of an O-E boundary due to the inextricable causal reciprocity between these *relata* (e.g., the works of J.S. Haldane and M. Prenant). Third, I will recount how certain positions did not abide this dichotomy and, instead, reframed the organismal boundary between the external and the internal through novel lenses (e.g., the complementary principle of A. Meyer-Abich, whereby the whole organism is, in itself, the mediating interface).

Membrane, surface, channel, gate, pump, receptor: The cell membrane as exemplary boundary, 1877–2010

Daniel Liu¹

¹Max-Planck-Institut für Wissenschaftsgeschichte, Department III, Berlin, Germany

While the membrane is *visually* an obvious delimiter of the cell's individuality, biologists since 1877 have discovered several classes of functional activity that are carried out at the cell surface that could not occur anywhere else. These types of activities in turn can be considered to be generalizable modalities of boundary-mediated relations, which are best captured in mechanistic terms. Such a mechanistic, generalized conception has the advantage of describing mutual permeability of relata in more specific and nuanced ways than simply describing bodies as “porous” or “relational.” Drawing on recent work by Andrew Reynolds (2018) and Mathias Grote (2019), this paper will present four brief case studies in the history of cell membrane biophysics: 1) the modern conceptualization of the cell membrane as a semi-permeable boundary, ca. 1877–1887; 2) the discovery of the lipid bilayer as a colloidal surface, ca. 1917–1933; the development of the patch clamp technique to the electrophysiology of membrane ion channels in ca. 1976–1991; and ongoing research in G-protein coupled receptor physiology since 1980.

From Bertalanffy to Bunge and beyond: Exploring the unsettled boundaries of living systemsGuido I Prieto¹¹Ruhr University Bochum, Department of Philosophy I, Bochum, Germany

Focusing on organization as the key to understanding the identity and behavior of living beings is an enduring standpoint in philosophy of biology. A particular kind of organizational approach consists in conceptualizing organisms and other kinds of biological individuals as nested systems emerging at different levels in a hierarchy of biological organization. Within this framework, demarcating living beings from their surroundings involves identifying the sets of interacting components that form autonomous or quasi-independent systems with peculiar dynamics that contrast with the dynamics of their environments. A much-overlooked problem, however, is that of the nature of the boundary between living systems and their environments. Is the boundary a part of the living system, of the environment, or a third player somewhere in between them? Is it physical or functional? Is it static or dynamic? Here, I will first explore the ways in which the living system-environment boundary has been conceptualized by prominent figures in the 'systemic camp' (L. von Bertalanffy, J. H. Woodger, and M. Bunge) and by contemporary authors. Then, I will present a dynamic, level-dependent, and functional notion of boundary in tune with the systemic perspective. I will show that this notion of boundary as a 'third party' or interface through which the system acts on and is acted upon by its environment plays specific explanatory roles, and thus it is worthy of attention in itself.

From basic to applied science: Bioremediation as ecosystem engineeringSaliha Bayir¹¹University of Kassel, Department of Philosophy, Kassel, Germany

Bioremediation is an applied scientific field that works on treating contaminated habitats, including marine, lake, soil, and other natural sites. In order to make the polluted environments more sustainable, researchers use the main principles of microbial ecology and apply them on site. Inducing the growth of microbes that would degrade target contaminants such as petrol spills and heavy metals, scientists aim at processing the pollutants in a more sustainable and feasible way. As bioremediation research mainly emerged from microbiological experiments of petroleum engineers, the application of microbial ecology principles in the field by engineers and their knowledge-making practices provide a rich ground for philosophical and historical analysis. In this paper, I aim to show how certain research questions, practices, and concepts are taken from basic science and resituated in order to overcome real-world issues with organizational, economic, and political constraints by focusing on the epistemic practices of researchers starting from the 1970s.

Intercultural translation as a kind of knowledge integration: Conservationist projects on seashores of Ecuador

Radamés R Villagómez-Reséndiz¹

¹CRIM-UNAM, Socioenvironmental Studies, Cuernavaca, Mexico

Knowledge integration has become an important issue, not exclusively in philosophical terms, but in practical spheres where different stakeholders interact to accomplish conservationist projects. From political ecology to ethnobiology, researchers have mobilized analytical tools from the philosophy of science to cope with a deconstructive view of scientific knowledge face to other kinds of knowledge systems (Villagómez-Reséndiz 2020). Beyond epistemological conundrums, interdisciplinary stances involving environmental understanding have deepened the nuances of different integration projects, taking into account several dimensions such as policy and value theory, among others (Ludwig and El-Hani 2020).

Departing from the recognition, established by Ludwig and el-Hani (2020), that concerning overlap and differences in local knowledge systems and academic knowledge, ethnobiologist and other stakeholders have to deal with the problem of how to address these differences in policy and practice, I brought to discussion the role of juridical and militant anthropology. This research area becomes interesting to offer new venues to understand knowledge integration, moving beyond partial overlaps without incurring logical alternatives of universalism or incommensurability. Juridical and militant anthropology emerges from approaches of alternatives epistemologies (Santos 2009), and seeks to develop an ecology of knowledge(s), understood as inter-cultural translation in juridical terms (Santos 2003b, Aragón Andrade 2019).

Considering juridical anthropology in philosophical debates about knowledge integration could contribute significantly in a twofold manner; the first one concerns enriching discussions of political dimensions underlying diverse knowledge systems within multi-stakeholder processes. Since juridical knowledge represents a third party involved as a normative stance between TEK holders and biologists, it could disentangle notions of assimilation and integration. Hence, it could be an alternative to the challenge posed by Ludwig and El-Hani (2020) about that partial overlap toward value systems needs to distinguish from an illusionary co-creative process that is an assimilation of TEK into normative agendas of conservation management, which in the ground reproduce unequal power relations.

How CSHL lost priority for the discovery of RNA splicing? Insights from oral history

Pnina G Abir-Am¹

¹Brandeis University, WSRC, Belmont, MA

The discovery of RNA splicing, (1977) has major ramifications for our understanding of the molecular basis of biological diversity, especially how the large number of proteins (~150,000) needed to maintain life are coded by a much smaller number of genes. (~20,000) In the year or so preceding the publication of the discovery of RNA splicing in 8&9/1977, several research teams focused on anomalies in mRNA processing. Based at CSHL, MIT-CRC, NIH, Rockefeller University, and the Weizmann Institute, these teams published discovery claims in the second half of 1977 but only two of them, CSHL & MIT-CRC, provided the so-called "discovery proof", or EM generated visual evidence for the splicing phenomenon in the form of several loops of DNA displaced by mRNA at specific sites where splicing occurred.

This talk explores the circumstances which led CSHL to lose priority by publishing its findings later than the MIT-CRC team. This occurred as a result of opting to publish its "proof of discovery" simultaneously with three other supportive papers. As a result, not only is the discovery often seen as having been done at MIT-CRC only, but the scientist who produced the discovery proof at CSHL remains largely unknown. This loss of priority precipitated the epistemic injustice at the heart of the public memory of this discovery. The role of gender and ethnicity bias in obscuring the role of the scientist who produced the discovery proof was discussed elsewhere. (Abir-Am 2020)

This talk seeks to illuminate the circumstances which led to CSHL's loss of priority in publication, by clarifying the conduct of discoverers, lab directors, institutional directors, and other scientists who had input into the publication process. The aim is to illuminate the forces producing and sustaining epistemic injustice for decades, and those which might eventually lead to a corrective allocation of credit.

Molecular biology origins: Max Delbrück and the reductionism debate

Vito Balorda¹

¹University of Rijeka, Department of Philosophy, Rijeka, Croatia

In this paper, I examine the molecular biology (henceforth MB) origins by investigating the two following points: (i) Max Delbrück and his importance for MB origins, and (ii) Delbrück's complementarity approach and its consequences for the reductionism debate regarding MB.

In (i) I examine Delbrück's migration from physics to biology, and thus his impact in the development of MB. I emphasize his role as the central figure of "The Phage Group", that is, an informal group of scientists, i.e., physicists, biochemists, geneticists, and biologists that used bacteriophages as experimental models to unravel the mysteries behind the origin and heredity of life. Delbrück and "The Phage Group" had an enormous impact in the development of MB that culminated with the 1969 Nobel prize for the discoveries concerning the replication mechanism and the genetic structure of viruses, shared by Max Delbrück, Salvador Luria, and Alfred Hershey.

In (ii) I examine Delbrück's complementarity approach towards biological explanations and argue that it was unsuccessful, thus I advocate for the reductive approach towards explanations in MB. Delbrück was highly influenced by Niels Bohr's 1932 lecture entitled "Light and Life". Bohr was vocal on the complementarity approach towards physics and biology, which was another application of the principle of complementarity that he introduced as part of his interpretation of quantum mechanics. Delbrück followed Bohr's approach and later described the lecture as an event that changed the course of his life and, consequently, motivated his interest in biology and shaped his research projects. However, the complementarity was never discovered, thus the approach is deemed unsuccessful. Instead, I argue for an alternative approach towards biological explanations, that is, the reductive approach towards explanations in MB.

The paper is structured as follows: in Section 2, I examine Max Delbrück and his role for the development of MB, and as a central figure in "The Phage Group". In Section 3, I examine the complementarity approach towards biological explanations argued by Max Delbrück. In Section 4, I argue for an alternative approach towards biological explanations, namely the reductive approach, based on the unsuccessfulness of the complementarity approach.

A historiographic principle of charity: Retelling the story of Jacques Monod and the history of protein allostery

Jacob P Neal¹

¹University of Pittsburgh, History and Philosophy of Science, Pittsburgh, PA

With his discovery of “allosteric inhibition,” Jacques Monod claimed to have “discovered the second secret of life.” He first introduced the concept in his conclusion to the 1961 Cold Spring Harbor Symposium, as a generalization of feedback inhibition. From this origin in feedback inhibition, the concept of allostery would come to have a life of its own. It remained the focus of Monod’s work for the remainder of his career, and he helped make it a core topic of structural biology by publishing a review of allosteric enzymes in 1963 and the highly influential Monod-Wyman-Changeux (MWC) model in 1965.

The primary aim of this paper is to develop a historical account of the conceptual development of allostery from 1961 to 1965, from its prehistory in feedback inhibition to the MWC model. My target is the interpretation by Angela Creager and Jean-Paul Gaudilliere (1996), the only historians of science to carefully study this episode. They argue that the shift from a biological-functional to a structural-mechanistic concept occurred not with Monod’s introduction of allosteric inhibition in 1961 but rather in 1963 with the publication of the review. Contrary to their account of conceptual discontinuity, I argue that Monod caused the conceptual shift from biological regulation to protein structure with his substitution of “allosteric inhibition” for “feedback inhibition” in 1961. Once we acknowledge that allosteric inhibition was a structural-mechanistic concept from the start, we can recognize legitimate scientific reasons for its introduction in 1961. Thus, my account shows that we do not need to rely on extrinsic factors—such as Monod’s desire to cement his place in the history of feedback inhibition—in order to explain why he introduced the new concept. Although we cannot rule out the possibility that Monod was seeking scientific credit and priority, as Creager and Gaudilliere suggest, we have an alternative, more charitable interpretation of this history that accords with Monod’s own justification in his published remarks. My interpretation therefore has the dual advantages of presenting the conceptual development of allostery from 1961 to 1965 as continuous and providing a charitable interpretation of Monod’s motives for introducing the new concept.

Diverse roles, multiple meanings: Conceptualizing stress in biological research

Lauren H Wilson¹

¹University of Minnesota, Philosophy, Minneapolis, MN

Many scientists worry that the diversity of meanings of stress creates ambiguity in research and therefore have offered a single general definition of stress. Their goal is to unify investigations of stress across multiple levels of organization by using a predominant theoretical framework, such as from classical physics or control theory. However, recent philosophical work offers an alternative approach: concepts can play more than one role in research. Diverse definitions of stress often correspond to different conceptual roles in scientific research programs. Given that multiple conceptions of stress appear in successful empirical studies, it is critical to explore whether they might contribute positively to scientific investigation through fulfilling different roles. To address this issue, I explore how stress is conceptualized when investigating the impact of temperature on canalization to show that biologists use the concept of stress to do different kinds of investigative work. The ability of different conceptions of stress to play multiple conceptual roles in scientific reasoning serves different investigative and explanatory purposes. Attempts to limit stress to a single conception or role would fail to do so. These findings provide further confirmation from practice-oriented philosophy of science that successful practices often involve terms (e.g., hardness, living fossil, or novelty) which exhibit polysemy and play different roles depending on researchers aims.

Co-option of stress mechanisms in the origin of evolutionary novelties

Alan Love¹, Günter Wagner²

¹University of Minnesota, Philosophy, Minneapolis, MN, ²Yale University, Ecology and Evolutionary Biology, New Haven, CT

It is widely accepted that stressful conditions facilitate evolutionary change through a *generic* increase in heritable variation, leading to rapid adaptive evolution. Through attention to different meanings of stress and a recognition that stressors must be characterized with respect to their effect on an entity that maintains its functioning and integrity, we distinguish between: (1) previously identified stress responses that indicate how traits change to maintain an adaptive fit with the environment, and (2) the co-option of stress-responsive mechanisms for the origin of novelties. The latter involves a *specific* correspondence between particular stressors and the compensatory mechanisms that originate evolutionarily. Unlike accounts of gene co-option that retrospectively identify component sources of evolutionary change, our model documents the cost-benefit trade-offs and thereby explains how one mechanism—an immediate response to acute stress—is transformed evolutionarily into another—routine protection from recurring stressors. We illustrate our argument with examples from cell type origination in diverse taxa and abstract from the patterns manifested in these examples to formulate a putative, phylogenetically universal principle—a “rule of life”—for stress-induced evolutionary innovation.

Resilient minds: Stress-adapted cognition in precarious environments

Amanda B Corris¹

¹University of Minnesota, Minnesota Center for Philosophy of Science, Minneapolis, MN

Models of cognitive development in adverse conditions typically focus on dysregulation and pathology. Individuals who are exposed to harsh and unstable environments may develop deficiencies in skills and abilities. Research on the impact of stress on cognition has led to what is referred to as the ‘deficit model’ of stress-induced mental impairment. However, some researchers have suggested that while cognitive development may be impaired along some dimensions, there may be adaptive effects as well, and these adaptive effects have been understudied. The ‘hidden talents’ approach, for example, complements and augments the standard deficit model by investigating how stress-adapted abilities may also aid individuals in coping with adverse conditions.

This paper discusses the call for a shift toward evaluating the advantageous aspects of cognitive abilities that develop in precarious environments. I argue that this new line of research illustrates the importance of analyzing the specific coupling between cognitive strategies and environment contexts. A focus on the ecological relevance of cognitive behaviors highlights how “stress-adapted cognition” develops in relation to local factors. Stressful conditions can induce context-specific and context-dependent adaptive strategies. Strategies may be adaptive in the context in which they develop yet maladaptive outside of that context.

Ontic risk in species classification for biodiversity conservation

Joeri Witteveen¹

¹University of Copenhagen, Department of Science Education (Section for History and Philosophy of Science), Copenhagen, Denmark

With mounting evidence that life on earth has entered a sixth mass extinction, the age-old ‘species problem’ is gaining renewed attention at the junction of biodiversity science and conservation action. Debates among taxonomists about whether a certain (meta)population ought to be recognized as a species or subspecies can affect whether it is considered threatened and requires conservation action. This paper offers a new take on the nature of disputes about species at the science-policy interface.

The practical issues that prompt this philosophical discussion are illustrated by the ongoing debate over the classification of African ungulates. An influential revision of this group, based on a version of the Phylogenetic Species Concept, more than doubled the number of recognized species compared to earlier classifications, which were rooted in the Biological Species Concept. This stirred up discussion among zoological taxonomists about whether and in what sense a PSC-based classification of ungulates is ‘better’ than a BSC-based one. The outcome of this debate has potentially significant implications for which groups become a focal point of conservation policy making and management. Recently, several taxonomists have suggested that the dispute over which classification of animal species is ‘right’ should be parsed as an epistemic problem about minimizing different types of error. The PSC is said to minimize false negatives in the attribution of species hood to metapopulations (at the cost of increased false positives), whereas the BSC and its cognates is said to minimize false positives (at the cost of increased false negatives). While reflections of this sort bring the taxonomic literature in touch with the philosophical literature on inductive and epistemic risk, this literature leaves an explanatory residue concerning the particular implications of classificatory choices at the taxonomy-conservation interface. This talk addresses this lacuna by introducing the notion of *ontic risk* in the context of biological taxonomy. Central to this account will be a philosophical analysis of the performative consequences of classificatory choices in shaping (and foreclosing) the *ontological futures* of evolving lineages through conservation action.

A forward-looking theory of biological function for biodiversity modeling

Robert S Lazo¹

¹University of Arizona, Philosophy, Tucson, AZ

Forward-looking theories of biological function have been the subject of two sustained and, by my lights, successful critiques. First, if we think that functional explanations are meant to explain the presence of some trait in a population, then forward-looking functions get the causal order all wrong. Second, forward-looking theories have been said to overgenerate, attributing functions to obviously nonfunctional things. However, recent work in biodiversity modeling and conservation relies on forward-looking attributions of function. When we ask whether or not some organism could successfully inhabit an environment as the climate changes, we are really asking for a summary of claims about mechanisms and their future functions: will this organism's suite of traits have the right functions such that the organism will, on average, survive and reproduce in the expected future environmental conditions, or not? I propose the following theory of forward-looking function, which I believe both captures the work being done in conservation and evades the old objections: some trait x has the forward-looking function f at time t just in case an organism or population can do f at t because it has x , it is on a pathway at t to occupy some part y of its niche, and its ability to do f helps to explain why it could successfully inhabit y if it reached that environment or why it is able to traverse the distance between its present range and y . This definition avoids the first objection above because, unlike some past iterations of forward-looking theories (e.g. the propensity account of function), it isn't interested in explaining the presence of traits in a population. It is instead concerned with how present traits can help to explain the future success or failure of a population. The theory's appeal to the niche - more particularly, to a set of niche concepts suggested by work in ecological niche modeling - enables it to evade the second objection: it only attributes functions to traits that help organisms to fit into their niches. It may, however, be subject to a nearby worry about indeterminacy of function. Because the definition does not settle how far into the future one might look, different applications can produce very different sets of forward-looking functions.

Making biodiversity data portals FAIR and CARE: Expanding who counts as a participant

Beckett Sterner¹, Steve Elliott²

¹Arizona State University, School of Life Sciences, Tempe, AZ, ²Arizona State University, Center for Gender Equity in Science and Technology, Tempe, AZ

When people speak of participatory biodiversity science, who counts as a participant and who gets to decide? The typical answer to the first question is that a participant is someone who contributes data records, or maybe metadata curation, to a project. This view, understandable at first glance, is problematic when we consider the broader scope of who contributed to or is affected by a project's origins, activities, and consequences. To show how and why the typical answer is problematic, we discuss some historical and contemporary relations between Indigenous peoples and biodiversity science.

The open data movement increasingly and implicitly decides who participates in open data as a matter of institutional governance. Against this background, the recent development of the FAIR and CARE Principles for scientific data management and governance provides a new context for addressing enduring problems created by the Western tradition of natural history collecting. Since their publication in 2016, the FAIR Principles (Findable, Accessible, Interoperable, Reusable) have become across the sciences the leading community standard for open data repositories. The FAIR Principles are broadly motivated by concerns among industry, science funders, governments, and scientists that "the existing digital ecosystem surrounding scholarly data publication prevents us from extracting maximum benefit from our research investments." More recently, the Indigenous Data Governance Working Group has noted that the FAIR Principles alone don't guarantee, and may forestall, equity of benefits for, and the sovereignty of, Indigenous peoples. The Working Group developed the CARE Principles (Collective Benefit, Authority, Responsibility, Ethics) to highlight how open data can impact people.

While the FAIR Principles provide a basis for setting standards about what counts as open data, these principles also leave structural opportunities for data sharing to lead to exploitation and failures of collective benefit. By focusing on the features of open data, the FAIR Principles cannot enable scrutiny of who is benefited or harmed by the collection, storage, publication, and use of open data. The CARE Principles provide a complementary set of normative resources that direct people to look beyond what makes data machine actionable, and to consider specific groups of people who are implicated and affected by data use.

Cancer avatars: The temporality of surrogate models

Sara Green^{1,2}, Mie S Dam², Mette N Svendsen²

¹University of Copenhagen, Department of Science Education, Copenhagen, Denmark, ²University of Copenhagen, Department of Public Health, Copenhagen, Denmark

This paper explores how organism choice intersects with questions about the most salient features of cancer. Precision oncology highlights the importance of tumour heterogeneity and thus comes with an increasing demand for translational models to account for patient variation. We explore the use of patient-derived xenografts (PDXs), or “mouse avatars”, as *surrogate models* that stand in for specific patients. PDXs are hoped to allow for instant translation from preclinical drug screening to clinical decision making. As a consequence, the translational potential of PDXs not only depends on representational matching of model and target, but also on *temporal alignment* of the lab and the clinic. We examine strategies to manage this challenge, including cryopreservation, biobanking, as well as exploration of organisms that develop faster and thus speed up translation. Murine models have long been seen as the ideal organism for patient-specific drug screening due to their ability to mimic the physiological context of human tumours. But the temporal challenge currently paves the way for “personalizing” organisms which seem very far from cancer patients from a physiological perspective. Examples are zebrafish xenografts (zPDXs) and “fly avatars”, i.e., genetically personalized fruit flies used for high-throughput screening of drug combinations. We end with reflections on the need to combine different animal models to account for the complexity of cancer.

Is cancer intrinsic to multicellularity?

Thomas Pradeu¹

¹CNRS & University of Bordeaux, Life & Health Sciences, Bordeaux, France

Many biologists and philosophers describe cancer as a breakdown of multicellularity. Yet, to make this idea precise and scientifically useful, three clarifications are needed.

First, it is essential to explain whether multicellularity breakdown is supposed to be a description, a cause, or a consequence of cancer. Second, some characteristics of cancer appear as a complete loss of features of multicellularity, while others appear as alterations of such features. Third, although some claim that multicellularity is a necessary and sufficient condition for cancer, some multicellular organisms almost never develop cancer, often exhibiting potent anti-cancer mechanisms.

Scientifically and therapeutically, the question crucial: should we invest time studying multicellularity to better understand cancer? We can respond positively, provided that we focus on multicellularity breakdown as a cause of cancer, and we connect cancer to specific features of multicellularity. Three avenues should be explored, via collaborations between biologists and philosophers: the study of multicellular organisms that do not develop cancer, the exploration of both cancer-suppressive and cancer-eliminative mechanisms across multicellular organisms, and the conceptual and experimental examination, via a comparison of the literatures on multicellularity and on cancer hallmarks, of exactly which characteristics of multicellularity, when disrupted, lead to cancer.

Why don't we get more cancer: The critical role of extracellular matrix and microenvironment in malignancy and dormancy

Mina J Bissell¹

¹E. O. Lawrence Berkeley National Laboratory, Biological Systems & Engineering Division, Berkeley, CA

Cancer is an organ-specific disease. To understand cancer, one must know the biology of the normal tissue from which the malignant tumors develop.

The overall questions are:

- 1- Even though we have 10-70 trillion cells all essentially with the same genetic information, what is the basis of tissue and organ specificity?
- 2- Why don't we get more cancer?

The work in my laboratory in the last few decades point to an important role for the extracellular matrix and their tissue's specific architecture. I will discuss the results that have led us to postulate that the "ECM" outside the cell actually signals to the nucleus and the nucleus signals back leading to gene expression that is tissue-specific.

Citing study mismatches upon failures to replicate: Useful exercise or self-defeating?

David Colaço¹, John Bickle², Bradley Walters³

¹Tulane University, Philosophy, New Orleans, LA, ²Mississippi State University, Philosophy and Religion, Starkville, MS, ³University of Mississippi Medical Center, Neurobiology and Anatomical Sciences, Jackson, MS

A “crisis” has led to increased scrutiny of the role of replication in science. This scrutiny includes debates about the relative importance of replication over other epistemic practices, how to promote replication, and even the meaning of ‘replication’ itself. Relevant to each debate, a multiplicity of uses of ‘replication’ has been the impetus for philosophers and scientists to supplant vernacular uses of this notion with a concept that corresponds to a well-defined epistemic practice. Worries about replication are present in other scientific fields. For instance, a program called “Facilities of Research Excellence – Spinal Cord Injury” (FORE-SCI) was developed after failures to translate results in animal studies of spinal cord injury to human participants. FORE-SCI was instituted to replicate several notable spinal cord animal studies but resulted in a “surprising preponderance of failures to replicate,” with “reasons for a failure to replicate” proposed by the researchers (Steward et al. 2012).

While these neuroscientists assign importance to replication, their reactions to failures focus on explanations that cite mismatches between the components of the original and replication studies. We call these *mismatch explanations*. While concerns over the “exactness” of replications are common, we question whether citing mismatches is an epistemically justifiable explanation. In this talk, we argue that mismatches are sometimes epistemically justified explanations, as alleged failures to replicate can be due to a mismatch of components and the identification of those mismatches is important. However, we also argue that researchers should not focus on mismatch explanations at the expense of other epistemic concerns of the field. Solely addressing mismatches all too often results in focusing on the minutiae of individual experiments rather than systematic issues of a field. While this focus can “save” a replication, it achieves this at the expense of defeating epistemic aims like translation. We end by speculating that mismatch explanations may reflect worries about blame: after a failure to replicate, the search for mismatches is a search for a target of blame aside from the original researchers.

Forget the midwife toad: Paul Kammerer, acquired characteristics and graft hybridization

Matthew Holmes¹

¹University of Cambridge, CRASSH, Cambridge, United Kingdom

The life and legacy of Viennese zoologist Paul Kammerer is defined by the midwife toad controversy and revelations of scientific fraud. Analysis of Kammerer's work has consequently operated under the suspicion that all of his results may have been fraudulent. Yet historians have increasingly recognized that his interwar arguments in favour of Lamarckian inheritance were based on several experimental demonstrations with different organisms. In this paper, I discuss the development and reception of Kammerer's grafting experiments on salamanders. By exchanging the ovaries of different varieties of salamander, Kammerer was able to obtain hybrid offspring. This result seemingly violated the Weismann barrier and suggested that the cells of the body played a significant role in heredity. The salamander experiments, however, did not play a prominent role in the controversy surrounding Kammerer. Whilst one of his most prominent critics, British geneticist William Bateson, preferred to focus on the midwife toad, a leading critic of Kammerer's salamanders was fellow neo-Lamarckian Joseph Thomas Cunningham. In a 1923 rebuke, Cunningham argued that Kammerer lacked basic knowledge of salamander anatomy. The ovarian transplants, argued Cunningham, had failed and the original organs had regenerated. Drawing upon these exchanges, I argue that experimental error, rather than fraud, is the most likely explanation for Kammerer's results. Ironically, Kammerer had previously accused another graft hybridizer, American physiologist Charles Guthrie, of making identical mistakes in his grafting experiments on chickens. Drawing upon his extensive surgical expertise, however, Guthrie had been able to defend his results in a way that Kammerer could not.

Genetic causation

Stephen M Downes¹

¹University of Utah, Philosophy, Salt Lake City, UT

My aim in this talk is to compare and contrast the way in which philosophers address genetic causation in two different areas of biology. I will argue that there is no single problem of genetic causation, rather, scientists' causal claims about genes require appraisal against the background of the relevant scientific context. Philosophers have examined genetic causation in the context of work in human behavioral genetics where causal claims are generated from statistical work on the analysis of variance. This work is familiar from debates over the genetic basis of IQ. The variance in IQ (range of IQ scores) is attributed to both our genes and environment but the proportion of the variance attributed to genes is said to license an inference about the genetic cause(s) of differences in IQ. Philosophers have also examined genetic causation in the context of work in developmental biology where one issue is whether or not genes play the primary causal role in development. Numerous philosophical issues arise from the inferences from statistical work to causal claims and from invoking genes as the most important causal factor in the development of traits. Here I introduce some of the relevant philosophical work and distinguish a few of the different ways in which genetic causation is invoked in the sciences. Finally, I make the case that work of the kind outlined here is necessary before we start the attempt to understand genetic causation from the perspective of alternate specific accounts of causation.

Demystifying downward causation in evolutionary biology

Yasmin Haddad¹

¹McGill University, Department of Philosophy, Montreal, Canada

Despite the hesitancy of philosophers towards the notion of downward causation (DC), it is a widespread relation frequently used in an explanatory capacity to account for certain regularities and processes. In this paper, I propose a conceptual framework that should contribute to demystify what is meant by ‘downward causation’ (DC) as this term applies to evolutionary biology. DC in biology is thought to be problematic because it relies on the assumption that entities are synchronically connected by nested hierarchies of levels of organization. Although the concept of levels of organization is epistemically useful and pervasive in biology, my analysis questions the more specific notion of compositional levels to describe biological reality. I aim to demonstrate that DC in evolutionary biology is an altogether different concept than the one relying on compositional levels. I argue that in biology, the use of the concept of DC becomes unproblematic if we use an interventionist framework for causation dropping the compositional assumption. I argue that we can account for examples of DC in evolutionary biology perfectly coherently in terms of causes drawing from interventionist theories such as those defended by James Woodward (2004). I analyze two empirical examples that support my view: feedback loops in the glucose metabolism and parallel evolution of a phenotype in *Pseudomonas*.

The concept of clone in cancerology: Issues and perspectives

Antoine Jourdain¹

¹Ecole Normale Supérieure, Philosophy, Paris, France, ²Université de Paris, Medicine, Paris, France

Evolutionist approaches of cancer tend to grow in oncology. They describe oncogenesis and tumor progression as a Darwinian process of evolution by natural selection. In the model of clonal evolution, cancer cells grow differentially depending on the mutations they possess, which are inherited by the descendant cells. The clone is defined as a population of cells sharing a common ancestor and thus the same genetic mutations. Identifying the clones and studying their dynamics in a tumor helps choosing the right treatment, preventing resistance and relapse. However, the concept of clone is not used in a unified manner by the scientists, which infringes research on cancer. I will 1) show that the use of the clone is polysemic, 2) show that there exists a tension between two conceptions of the identity of the clone, typological and qualitative identity, and 3) propose to resolve this tension by a new categorization of the clone. The aim of this talk will be to show that the cells of a clone can't be considered as pure replicates (typological), and must be considered as identical regarding certain traits (qualitative). Choosing the best trait to support clonal identity requires a causal hierarchization of the traits that explain the common behavior of the cells in the clone. I will suggest that Woodward's criteria of causal selection can help defining the most accurate clone category for each scientific study.

The coral reef crisis: Communication and value across senses, species and disciplines

Elis Jones¹

¹University of Exeter, Exeter, United Kingdom

Format: 3 speakers x 20 mins (15 mins presentation, 5 mins questions each) followed by commentary, discussion and Q&A (30 mins) – 90 mins total

Participants: Elis Jones¹, Dr Tim Gordon^{2,3}; Sonia Levy⁴, Professor Irus Braverman⁵; Professor Stefan Helmreich⁶; Dr Sophie Veigl⁷ (session chair).

¹Egenis Centre for the Study of Life Sciences/Sociology, Philosophy & Anthropology Dept., University of Exeter, UK; ²Biosciences, College of Life and Environmental Sciences, University of Exeter, UK; ³MARS Coral Restoration Programme; ⁴Independent Artist; ⁵University at Buffalo School of Law, The State University of New York, NY, USA; ⁶Department of Anthropology, Massachusetts Institute of Technology, MA, USA; ⁷Cohn Institute for The History and Philosophy of Science and Ideas, Tel Aviv University.

Session Description: Coral reefs across the world are in crisis, their environments pushed to the edge of habitability by human stressors. Understanding, responding to and reducing these stressors requires communication between coral organisms, publics and scientists. These communication channels may operate through different social, ecological and physiological routes. This session explores some of the channels of communication available to these three groups and the sub-groups within them. It brings together people from coral science, sociology, philosophy, art and anthropology who are interested in understanding how marine organisms communicate with and perceive the world, and in furthering our efforts to understand and protect them. Part of this involves opening up new channels of communication, such as acoustic and artistic ones, between corals, scientists and publics in order for them to better listen, understand and respond to one another. These channels tell us much about the value of coral reefs across different contexts, and better enable communication of this value: for scientists, for other societal groups, and for the reef organisms themselves.

Immunology in Portugal: Building and consolidating a robust research field in a small country

Maria S Almeida¹, Manuel Vilanova^{1,2,3}

¹ICBAS, Universidade do Porto, Porto, Portugal, ²3S, Universidade do Porto, Porto, Portugal, ³IBMC, Universidade do Porto, Porto, Portugal

The present paper explores the growth and consolidation of the research field of immunology in Portugal. In 2014, the singularity of the field with regards to the growing impact of publications and the relation of this measure with the European average (UE15) was highlighted in the news of a daily national newspaper of high circulation and specially the fact of being above that average elicited our interest. The study here reported develops from that fact and aims at exploring the dynamics of the field trying to understand the mentioned particularity. Drawing from scientometric materials – mapping networks of collaboration and of studied topics – as well as from a series of semi structured interviews with privileged informants – ten prominent Portuguese immunologists – we present a first analysis of the dynamics of the area. The growth of immunology in Portugal followed the evolution of national science policies, mostly implemented after the Carnation Revolution in 1974 (which brought the end of the dictatorship regime) and, later, after the integration in the European Union. It was fostered by the fact that key Portuguese researchers working abroad as team leaders in renowned research institutes were simultaneously active within the emerging national community of immunologists from the early 1970s onwards. The implementation of diverse graduate training programs in the 1990s was deemed influential both in growth and consolidation of the area. This study illustrates how the evolution of the Portuguese scientific system and the implemented science policies, at national and European levels, as well as the existing networks of international collaboration framed the evolution of this biomedical field in the country. How this portrait might extend to the building of a research field in a small country with limited financial resources will be discussed.

Rethinking the function-accident distinction

Brandon A Conley¹

¹Colgate University, Philosophy, Hamilton, NY

It is a widely recognized desideratum on a theory of biological functions that it draw a distinction between functions and accidents. While pumping is a function of hearts, making "glug glug" noises is an accidental effect, rather than a function. One of the claimed advantages of selected effect, and more recently organizational, approaches to function over dispositionalist accounts is that dispositionalists fail to capture the function-accident distinction. However, I suggest that the function-accident distinction, while quite real, is not best conceived as a special feature of functions that should be explained by a theory of functions. Rather, the distinction between functions and accidents is a special case of a broader phenomenon already well recognized in philosophy of science, namely the distinction between law-like and accidental generalizations. Considered in this light, the function-accident distinction emerges from the combination of a theory of functions and a theory of law-like scientific generalizations—in my view, the best candidate is a theory of natural kinds. Insofar as selected effect and organizational accounts build the function-accident distinction into the theory of functions, they conflate the issue of what functions are with the questions of what processes explain law-like generalizations about functions. With these two questions separated, many issues surrounding functions appear much less puzzling, or so I argue, including the nature of dysfunction, the teleological character of function attributions, and the relationship between dispositionalist functional analysis, organization, and natural selection.

Global organism: The science and politics of holism in the interwar period

Abraham H Gibson¹

¹Arizona State University, Center for Biology and Society, Tempe, AZ

My next project examines the emergence of globalism in the wake of WWI, and its popularity in many different nations during the interwar years. Adherents included world leaders, scientists, artists, athletes, activists, musicians, missionaries, and opium addicts. These globalists lived in different nations, occupied different stations, and promoted different ideologies, but they nevertheless agreed that a single “world state” loomed in the near future. What is more, they all cited evidence from the biological sciences when justifying their vision of the global future. For example, they all agreed that globalism was the inevitable culmination of a long evolutionary process. Just as individual cells organized to form multicellular organisms, so too would nations inevitably integrate to form a global organism. This was more than just hyperbole. Globalists increasingly referred to nation-states as true organisms, rather than mere analogues. This meant that nations were bound by the same laws of growth and integration that governed other organisms.

This project helps reframe the history of science. Popular narratives often portray the scientific enterprise as one long march toward reductionism, but many interwar biologists rejected that narrative. Having just endured the deadliest war of all time, they instead sought to understand how organisms cooperate and integrate with one another. They were generally antagonistic toward the new science of genetics, which they deemed too atomistic. In any given system, the whole is always more than the sum of its parts, they explained. They invoked or invented a variety of labels to describe this phenomenon (holism, gestalt, organicism, symbiogenesis, symbiontism, superorganism, and emergent evolution, among others), but they agreed that an integrative tendency permeated the universe from atoms to human societies. This project also provides nuance to the nationalism-vs.-globalism debate. Just as there were many different types of nationalism, so too were there many different types of globalism. My project shows that these global visions invariably reflected national (and even local) contexts.

Why philosophers of biology should look at RNA

Stephan Guttinger¹

¹Durham University, Philosophy, Durham, United Kingdom

In philosophy of biology there has been a lot of focus on DNA and its role in biological systems. This has happened for good reason, as DNA is central to the development and the maintenance of living systems. Its sister (or mother?) molecule RNA has, in comparison, received little attention. This might be connected to the fact that for most of the 20th century RNA was seen as a mere go-between between DNA and proteins, connecting DNA with the protein production machinery in the form of “messenger” (and “transfer”) RNAs.

However, in the 1990s, scientists slowly came to realise how diverse the structures, dynamics and functional roles of RNA are within living systems. From small non-coding RNAs that form part of gene-regulatory networks to intricately folded RNAs that function as enzymes, RNA emerged as a key pillar of most living systems (including viruses). These insights not only changed the position that RNA takes up in scientific theory but also the role it plays in scientific practice. For instance, once it became clear that RNA molecules can regulate both the DNA transcription and the protein translation machineries, researchers started to co-opt this molecule in order to revolutionise the way in which they interfere in living systems. In this lightening talk I will highlight three reasons why RNA is important and argue that in order to grasp the dynamics, the power, and the limitations of the contemporary life sciences philosophers also need to take into account RNA biology.

Biology's Einstein moment

Matt Haber^{1,2,3}

¹University of Utah, Philosophy, Salt Lake City, UT, ²University of Utah, School of Biology, Salt Lake City, UT, ³University of Utah, Center for Quantitative Biology, Salt Lake City, UT

I have previously argued for the rejection of what I call an 'absolute phylogeny' (Haber 2012, 2016, 2019), suggesting it is analogous to Einstein's rejection of Newton's notion of absolute space. Here I will consider some of the upshots of rejecting absolute phylogeny, including (i) identifying how this accords with recent work in biology and (ii) noting advantages of adopting this stance. Like its famous physics counterpart, the rejection of absolute phylogeny is the rejection of a fixed frame of reference, only in the biological case that frame of reference is historical, rather than spatial. It means there is no privileged biological history against which all others are measured. Instead, we ought to recognize that there are multiple incongruent biological histories, and the relevant biological 'frame of reference' must be specified. No one biological frame of reference is privileged, except in the context of a specified research context. I will argue that adopting this stance promotes an interdisciplinary approach in biology, offers explanatory resources useful for explaining biological historical incongruence, and provides a useful theoretical and empirical context for framing research projects in biology and philosophy of biology.

5 reasons why philosophers of biology should invest philosophy of interdisciplinarity

Kevin Kaiser¹

¹Université de Montréal, Philosophy, Montréal, Canada

Philosophy of interdisciplinarity is an emerging field in philosophy of science. It aims at systematically understand the growing phenomena of interdisciplinarity research in science, both descriptively and normatively. However, that subfield of philosophy of science is having a slow development, at least compared to some other disciplines that have been working on the topic for at least 30 years.

For this lightning talk, 5 reasons why philosophers of biology should invest philosophy of interdisciplinarity will be outlined. Succinctly put, first, the object of study of both philosophy of biology and philosophy of interdisciplinarity share some structural similarities. Second, philosophy of biology has produced many tools to address situations similar to those encountered by philosophers of interdisciplinarity. Third, philosophy of biology has studied dozens of case studies in biology, some of which are even cases of proximal interdisciplinarity. Fourth, interdisciplinarity theorists are having plenty of conceptual needs, especially on how to justify the use of tools from others fields of science in a particular field, a topic that philosophy of biology has well explored. Fifth, philosophy of biology could benefit from this interaction by having a new playground to test and refine its own conceptual models.

Is the tube test an appropriate test in the study of model organisms for human neurological diseases?

Cole C McArthur¹

¹The University of Auckland , Biological Sciences, Auckland, New Zealand

The tube test for social dominance is a test commonly used in the study of mice and model mice that tests mice on their relative dominance over conspecifics with a similar goal. Simply, two mice beginning on opposite ends compete to exit the tube and get a reward; to be successful the winning mouse must push the losing mouse backwards through the tube and out the other end. The tube test for social dominance in mice was described in 1961 by Gardner Lindzey's lab at the University of Minnesota, Minneapolis; social dominance is described in G Lindzey's 1961 paper as "the tendency of an animal to make a goal response when this response involves overcoming the competing response of another animal similarly motivated". Since then the tube test has been used broadly in psychology to assess the temperament and social aptitude of mice in studies.

My goal in this talk is to explain ways in which a common behavioural test in mice, the tube test, is used in model studies of neurodevelopmental diseases (NDDs) such as Autism Spectrum Conditions (ASC). As a key behavioural test for the study of NDDs the tube test is an interesting reflection of how scientific research frames perceptions in its attempt to model communities in a study. I think that by looking at the history and application of the tube test we can learn something about the effects of a behavioural test on both the researcher and the researcher. Questions I think it is important to ask about are: What specific information does the tube test contribute to research into NDDs? Is this information about social features of model mice different from other tests? And how does a measure of social dominance map to broader discussions of neurodiverse conditions like ASC or other NDDs?

The cultural readiness of paleontological discoveries

TJ Perkins¹

¹University of Utah, Philosophy, Salt Lake City, UT

The picture of the historical sciences that emerges from the *philosophy* of science is mainly one showcasing methodological and evidential ingenuity lending to historical reconstruction. Recent *history* and *anthropology* of historical science paints a different picture, however; one which ties some significant paleontological discoveries to the broader cultural context of the time. Paleontologist David Fastovsky argues that the Alvarez hypothesis regarding the extinction of the dinosaurs, “gained a foothold not only because the interpretations were supported by discoveries, but because the social climate was ripe for these kinds of inferences” (2009, 240). He shows that the broader socio-political context influenced the culture of historical scientific communities to such a degree that they were (or were not) “culturally ready” (248/249) to accept some historical explanations. This suggests some role for social value preferences and judgements in paleontological research.

As the received view shows, paleontologists face high levels of uncertainty, and so engage in careful evidential reasoning about degraded traces to decide between competing hypotheses about past events. They utilize inference to the best explanation, wherein explanations are formed and judged on their ability to, e.g., broadly or elegantly unify traces. These inferences leave open a space for social values to play an indirect role in theory choice. In many sciences there is uncertainty in choosing between competing hypotheses, which sometimes runs beyond the material evidence to include such considerations as aesthetic preference, public health and economy (Douglas 2000), or anxieties of nuclear annihilation (Fastovsky 2009). Paleontologists – influenced by their scientific culture and by the broader political context – make or fail to make culturally-(un)informed theoretical decisions.

In this paper I aim to characterize this phenomenon – the notion of cultural readiness – to assess paleontological discoveries and interpretations, addressing why fossil discoveries in particular seem to lend themselves to this kind of assessment: the kind that uses cultural values to fill the gap left by uncertain inferences of historical explanation.

Douglas, H. 2000. “Inductive Risk and Values in Science,” *Philosophy of Science* 67: 559–579.

Fastovsky, D. 2009. *Ideas in Dinosaur Paleontology*. in Sepkoski, David & Michael Ruse. 2009. *The Paleobiological Revolution*. Chicago: University of Chicago Press

Teaching by building a Wikipedia page

Aleta Quinn¹

¹University of Idaho, Politics & Philosophy, Moscow, ID

Online classes are increasing in popularity, but present unique and serious pedagogical challenges. In an effort to improve my online Environmental Philosophy course, in Fall 2019 I assigned the online class to develop (or radically overhaul) a Wikipedia page. I built on the successful experience reported by Hubbs (2016) (in *Experiential Learning in Philosophy*). Expected benefits included students learning to engage philosophical research beyond the classroom walls, students developing solidarity through responsibility for a shared project, and students focusing in-depth for a sustained period of time on a contemporary philosophical issue.

From six options, students chose to develop Earth Optimism, a Smithsonian-sponsored initiative to promote positive scientific, social, and technological approaches to environmental problems. The initiative aims to complement “doom and gloom” narratives that may discourage environmental activism, and to highlight diverse new approaches.

Students reported weekly via BlackBoard, and I monitored activity through Wikipedia’s page edits. Small groups produced draft text for each of 8 sections, and then students individually critiqued, copy-edited, and provided references and images. The page went live just before Thanksgiving, enabling students to evaluate and uptake feedback from the public in the last two weeks of the course. At the time of this writing, the page has been viewed 1003 times (median 6 views per day), and edited 283 times by a total of 47 editors.

The poster will explain pedagogical motivation, methodology, and results, with recommendations for other instructors who may develop similar courses in the future. The poster will include screenshots of portions of the Wikipedia page and charts of data about page authorship and traffic.

The project experience required students to demonstrate understanding and analysis of the course material beyond what is easily captured by quiz and test formats. Forum and page editing assignments required substantive participation, avoiding the trap of students’ providing platitudes in forum responses. Grading was relatively stream-lined compared to traditional writing assignments, which can be vital in the face of institutional pressures to increase class enrollments. Building a Wikipedia page can be a valuable complement to traditional pedagogical methods.

Questioning Darwin's “truly wonderful fact”

Mary P Winsor¹

¹University of Toronto, Institute for the History and Philosophy of Science and Technology, Toronto, Canada

Darwin declared that “living things resemble each other in descending degrees, so that they can be classed in groups under groups.” These groups, which modern systematists call taxa, were the hundreds of families, orders and classes to which taxonomists had given proper names. Because Darwin's book focussed on the process of speciation, a focus reinforced by Ernst Mayr in the twentieth century, historical discussions of classification mostly consider the so-called lower groups: varieties, species, and genera. The existence of the higher groups has received little attention, even though, for Darwin, it constituted powerful evidence for evolution. In the *Origin of Species* he called it, twice, a “truly wonderful fact.” He furthermore claimed that because it was so familiar, this great fact was generally overlooked.

Those of us who are admirers of Darwin ought to beware of our bias in his favour. He wrote in such a sober tone, and conveyed such an attractive humility, that we rarely apply a healthy scepticism to his claims. His declaration of the TWF that “living things resemble each other in descending degrees,” has become the accepted portrait in the history of systematics. In the twentieth century it was christened with a new name, pattern, said to be the explanandum (thing to be explained) of which the explanans was evolution. In coining the phrase “the shape of nature” I long ago endorsed Darwin's claim. In doing so I was ignoring the historical fact that many Victorian naturalists regarded taxonomic groups above the genus level as human inventions rather than entities in nature. Louis Agassiz in 1857 complained that higher groups were “universally considered as convenient devices.” If his testimony is correct, naturalists cannot be said to have overlooked the TWF, for what they were doing was refusing to accord it the status of fact. In that case, it makes no sense for us today to claim that a pattern awaiting explanation existed.

How can living systems persist: Regeneration, failure, and the future

Kate MacCord^{1,2}, S. Andrew Inkpen³, Jane Maienschein^{1,2}, Manfred Laubichler², Susan Fitzpatrick⁴

¹Marine Biological Laboratory, Eugene Bell Center for Regenerative Biology and Tissue Engineering, Woods Hole, MA, ²Arizona State University, Tempe, AZ, ³Mount Allison University, Philosophy, Sackville, Canada, ⁴James S. McDonnell Foundation, N/A, St. Louis, MO

Persistence within living systems relies on a system's ability to regenerate—to recover all or some of their parts and/or functions following disturbance. Sometimes this regenerative capacity is successful; sometimes it is interrupted or unable to cope with the scale of damage, leading to systems failure and death. Faced with the literal and existential threat of climate change, failing ecosystems, and the limited ability of most human living systems to regenerate in the face of traumatic injury, understanding the conditions under which living systems successfully regenerate and the factors involved in failure thereof, would benefit science and society by enhancing our ability to effect persistence and sustainability within living systems. However, scientists have yet to investigate regeneration as a property of biological systems that operates regardless of scale, and historians and philosophers have yet to turn cross-cutting attention to the topic of regeneration and its failure within living systems.

In this roundtable we will explore the idea that regeneration and failure are linked properties of all living systems, regardless of scale—from microbial communities, to the cells within our bodies, to our global ecosystem—and how what we know at one scale of living systems can inform others. Our exploration will highlight big, open questions and areas for further investigation within history, philosophy, and the life sciences.

John Herschel's philosophy of higgledy-piggledy

Richard Bellon¹

¹Michigan State University, Department of History / Lyman Briggs College, East Lansing, MI

Word reached Charles Darwin that John Herschel had described natural selection as "the law of higgledy-piggledy." "What this exactly means I do not know," Darwin remarked, "but it is evidently very contemptuous." My talk examines "higgledy-piggledy" as Herschel understood it. He reacted warily to natural selection from a deep philosophical commitment to a calm regularity underlying the apparent messiness of the natural world. Randomness -- "higgledy-piggledy" -- is the local, temporary, and bounded manifestation of the interactions of orderly laws. While ocean waves could, as he found during his stomach-churning voyage to South Africa, "throw everything about off the tables, chairs &c higgledy piggledy," the ocean's seeming caprice reduced to the geometrical certainties of simple, unvarying, and comprehensible natural law. This view informed his understanding of biological variation. The diversity of life, no less than ocean waves, must reduce to stable, law-governed regularities, much like Richard Owen's archetypes. Darwin pitched Herschel's understanding of natural order on its philosophical head. The structural regularities that Owen elevated to archetypes were, in the logic of natural selection, impermanent manifestations of previously selected random variations. In the *Origin*, higgledy-piggledy coalesced into order, which violated Herschel's philosophy of the universe.

Understanding without laws: Charles Darwin's explanatory practices

Greg Priest¹

¹Stanford University, History, Stanford, CA

After disembarking from *HMS Beagle* after its voyage around the globe, Charles Darwin set himself a lofty goal: he would discover the “laws of life.” Just as Isaac Newton had unified a vast array of physical phenomena by means of simple, invariant laws, Darwin would do the same for living nature. But it was not to be. Over the ensuing decades, Darwin came to believe that evolutionary processes are so ineluctably complex that they cannot be explained by the operation of simple, invariant laws. Moreover, because the human mind is not a perfect engine of ratiocination but an evolved bodily system, scientific explanation is not a matter of formal rigor, but of bringing phenomena into the light of human understanding.

Because he deemed laws insufficient to generate understanding of living nature, Darwin developed conceptual and explanatory practices he deemed better suited to the inherent complexity of evolutionary dynamics. In this talk, I examine four examples of such practices: a diagram, a conjectural narrative, an account of an experiment, and the remaking of a concept Darwin had appropriated from earlier naturalists. Darwin’s approach to explanation was pluralistic and perspectival. It demanded, and rewarded, imaginative engagement on the part of the investigator. And it was a hermeneutic enterprise, a process of seeking to make the forms and behaviors of living beings perspicuous to us not by reducing them to formulae but by asking what they *mean*.

A.R. Wallace's "pure Darwinism": Reinterpreting Darwin's "complexity" for the public

Juan M Rodriguez-Caso¹

¹National Autonomous University of Mexico, School of Philosophy and Letters, Mexico City, Mexico

Alfred R. Wallace (1823-1913) is a Victorian figure renowned for his more than diverse interests. However, little has been said about his role as a populariser of evolution. One of his best known but little analysed works is *Darwinism* (1889), written as a result of his travels in Canada and the United States (1886-1887). One of Wallace's motivations for "actualising" Charles Darwin's original proposal was to present contemporary discussions of evolution in a "simple" way for the public. This paper aims to show Wallace's strategies in *Darwinism* to present his vision. Despite following a similar argumentative structure as the one presented in Darwin's *Origin* (1859), he made not very subtle changes in his desire to present a proposal suitable for the non-specialist public. Revisiting Wallace's proposal also allows us to show an explanation distant from the methodologies proposed by philosophers such as J. Herschel and W. Whewell, which entails an alternative philosophical background, rarely appreciated by historians and philosophers. Another point of interest is the value of a work explicitly intended for the public, which implies little-recognised dissemination strategies. Wallace's *Darwinism* thus serves to recognise undervalued argumentative strategies within the Victorian context.

Entrenched values in scientific research: Values beyond the psychological-level

Morgan Thompson¹

¹Bielefeld University, Philosophy, Bielefeld, Germany

Determining whether social, political, and ethical (i.e., non-epistemic) values do and ought to play a role in scientific research is important for contemporary philosophy of science. However, this debate is primarily framed in terms of when scientific decision-making is value-laden, which obscures that the material and epistemic tools of scientific research can be value-laden.

Zina Ward (in press) distinguishes between motivating and justifying values. Values act as motivating reasons when they directly motivate an agent to make some choice. Values can also be said to act as justifying reasons when they provide a reason for or against some action. According to Ward, philosophers of science sometimes take science to be value-laden when values act as motivating reasons and others when values act as justifying reasons, which can cause cross-talk.

My view is that Ward's distinctions provide a useful way of organizing different but implicit views in the values in science debate. However, her distinction does not exhaust the range of possible views on value-laden science due to its focus on the psychological level of scientific decision-making. Instead, I argue that values can be entrenched into the epistemic and material products generated in scientific research. For example, a survey that operationalizes racism in terms of racial differences in reports of discriminatory experiences, then it has entrenched values such as the primacy of interpersonal racism. When these epistemic tools are used in new contexts (for practical, sociological, and/or epistemic reasons), the values travel with them.

One major consequence of distinguishing the values as psychological reasons and value entrenchment in epistemic tools is that we can now consider whether some scientific project can be value-laden without any appeal to values playing either a motivating or justifying role in scientific decision-making. I argue that these cases do occur and have implications for normative and prescriptive claims about values in science. For example, in psychology much research uses surveys and structured interview questions. These survey instruments, such as the Everyday Discrimination Scale (Williams, Yu, Jackson, & Anderson, 1997), are evaluated by examining their psychometric properties. In cases where the survey instrument has appropriate psychometric properties, then the instrument may well be exported to different domains of study by researchers rather than attempting to develop their own studies.

On ecological validity in comparative psychology

Charles A Beasley¹

¹London School of Economics and Political Science, Philosophy, Logic, and Scientific Method, London, United Kingdom

In the late 19th century, as comparative psychology was flush with unprincipled anecdotes and spiritualism, the young discipline began to take its first steps out of the wild and into the lab. While this introduced a new kind of methodological rigor that promised to overcome many of the discipline's clear difficulties, lab based comparative psychology's use of 'artificial' stimuli in 'artificial' environments (i.e. Thorndike's (1898) puzzle-boxes) also introduced new methodological questions (Mills 1904). Most pressing, how is it that highly artificial lab experiments are able to provide evidence of the cognitive capacities that animals possess in wild? Over a century later, this question remains central to the discipline, and is often framed as a trade-off between the ability to control for extraneous variables, and achieving what is referred to as ecological validity. The task of my talk will be two-fold. First, to clarify the concept of ecological validity, and second to determine what implications this has for experimental design and the interpretation of data in comparative psychology. I begin by distinguishing between two types of ecological validity. A study is task ecologically valid if it recreates a task that a member of a species would genuinely and frequently face in the environment it evolved in. By contrast, a study is capacity ecologically valid if the capacity shown in the lab is one that wild animals are also likely to possess. This results in two types of ecological validity based objections that can be made to a given study. First, objections rooted in task ecological validity failures can be used to explain why a given animal might have failed a task. Second, objections rooted in capacity ecological validity failures, can be used as a marker of caution in the interpretation of the successful completion of a task. I then raise a concern about the degree to which cognitive flexibility should be seen to shape how capacity ecological validity is determined, and how preconceptions regarding this might lead to a vicious cycle in which current knowledge of an animal's cognitive capacities determine what is considered to be capacity ecologically valid. In doing this, I highlight the way in which cognitive flexibility must be thought in tandem with ecological validity to determine the appropriate level of abstraction at which these two types of ecological validity should be characterized.

Super-pleasure

Otniel E Dror¹

¹The Hebrew University of Jerusalem, History of Medicine, Jerusalem, Israel

In 1954, James Olds and Peter Milner discovered pleasure in the brain of a laboratory rat. Pleasure, which had been ostracized as a nameable experience by the behaviorist sciences and which had been de-ontologized during the early twentieth-century as merely aponia—as only an absence of pain, returned with a vengeance. The return of pleasure inaugurated a major transformation whose repercussions and off-shoots are very much still with us today.

In this presentation, I will focus on the first decade or decade and a half of the discovery of this new super-pleasure in the brain. I will reconstruct the laboratory enactments and models that constituted this new pleasure as “supramaximal,” instant, and insatiable. I will argue that “pure” “supramaximal” “super-pleasure” was the immediate product of experimental enactments. These enactments of the laboratory made pleasure and made it supramaximal. The laboratory construction of an instantaneously-produced insatiable self-perpetuating super-pleasure captured the imagination of contemporaries and of generations to come. I will briefly discuss the reactions to the new discovery. One of the major preoccupations of contemporaries was where to position the newly discovered super-pleasure in the social and natural orders.

Epistemically useful and metaphysically adequate pluralist accounts of essentialismChristian Culak¹¹University of Missouri, Department of Philosophy, Columbia, MO

Intrinsic biological essentialists claim that essential properties adequately explain species membership, but this is overwhelmingly rejected by philosophers of biology. Rejections arise from metaphysical and epistemic worries: Can species have an essence? Are essences metaphysically useful for explaining species membership? The big question—What is a species? —is too ambiguous to be adequately answered. I argue essentialism is epistemically useful, but metaphysically deficient, for answering four interpretations of the big question. I propose pluralist accounts—essentialism with species concepts—to supplement essentialism's metaphysical deficiency. Ultimately, I argue essentialism with phylogenetic-cladistic concepts and essentialism with biological species concepts are the best candidates.

Differentiating the reference genome: Representation, abstraction and the exploration of variation in genomics and post-genomic research

James Lowe¹

¹University of Edinburgh, Science, Technology and Innovation Studies, Edinburgh, United Kingdom

A key resource in genomics is the reference genome, a consensus DNA sequence for a given species or sub-species. It can be used for the recording of genomic features, discovering variants, as a scaffold on which to construct other sequences, and as a point of comparison. There has been criticism of the representativeness of reference genomes, especially the human one. Critiques focus on the extent and source of the variation that they incorporate and the implications this has for their use. This has prompted the ongoing improvement of reference genomes, the creation of population-specific reference sequences, and the production of pangenomes incorporating multitudes of sequences. I discuss the basis for these critiques in particular conceptualisations of “representation”, and the way in which reference genomes “stand-in” for a species or sub-species. I argue that a reference genome should not be assessed on the criterion that it represents the variation of a given species or sub-species, but instead that it – and associated resources, infrastructures and institutions – should enable the creation of a web of linked references and resources across the multi-dimensional variational state space of the type. This has implications for how we evaluate the utility of particular abstractions of variation and how we can understand differences in the processes of creating and refining standards in the life sciences, as well as indicating a fruitful way of thinking about translation.

Maximising efficiency in an indeterministic world: The free will of biological agents

Anne Sophie Meincke¹

¹University of Vienna, Philosophy, Vienna, Austria

Traditional Session: The Biology and Metaphysics of Free Will / Chair: Anne Sophie Meincke

Are we free to want what we do when we do what we want? Could we have wanted and, hence, acted differently than we actually did? There are three main ways metaphysicians think about this. The so-called ‘hard incompatibilists’ deny free will on account of the supposed truth of universal determinism. The so-called ‘compatibilists’, too, subscribe to determinism but try to sell us as ‘free will’ what actually is mere ‘freedom of action’, i.e., the absence of coercion. And, finally, a minority of so-called libertarians audaciously postulates that universal determinism be wrong since we do have free will, while facing a new challenge: Is what we want, and how we accordingly act, a matter of mere chance?

In this talk, I want to make a fresh start by assuming that the world is indeterministic as a matter of fact, and by considering free will in the context in which it seems naturally to occur: the agency of organisms, human and non-human. Organisms, I argue, are stabilised higher-order processes whose stability results from their continuous interaction with processes in the environment. Actions are a particular form of such self-stabilising interactions; and they are minimally freely willed insofar as they are chosen over alternatives. These alternatives need not be conceptualised; implicit affective presence suffices. Free will maximises the efficiency of agency, which, qua adaptive, is never merely random.

The neurobiology of probabilistic actions

Björn Brembs¹

¹Universität Regensburg, Institut für Zoologie - Neurogenetik, Regensburg, Germany

Perhaps physics still struggles with the concept of chance as a fundamental component of the universe because it lacks the additional 50 years of scientific progress biology has had to come to terms with indeterminate variability as the core creative element in evolution? While initial evolutionary discussions meandered between variously overemphasizing the deterministic or the random processes, today, the concept of a tight interaction between chance and necessity not only in evolution but in many areas of biology is commonplace. Stochastic resonance, the neuronal trick to increase sensory sensitivity; stochastic gene expression as a source of phenotypic variation in bacteria or in the developing multicellular organism, are well-studied phenomena that require indeterminacy. At the same time, this indeterminacy does not entail complete chaos and unpredictability. On the contrary, indeterminacy has become a central component in many functional principles throughout biology and, as such, its role as a creative, constructive element is under constant scientific investigation. For instance, in neuroscience, we are now discovering neurons and circuits incorporating indeterminacy in order to not only render animal behavior less predictable for competitors, prey or predators, but also to solve problems by trial and error, or to detect which component of the incoming sensory stream is under the control of the individual. The observation that we cannot tickle ourselves is one outcome of such a process. Under complete sensory deprivation, such neurons and circuits generate constantly varying output and the emerging mechanisms point towards unstable nonlinear processes at the core. It is currently under investigation if these nonlinear processes are sufficiently sensitive to amplify quantum-level indeterminacy to the macroscopic level.

The feeling of free will

Eva Jablonka¹

¹Tel-Aviv University, Cohn Institute, Tel-Aviv, Israel, ²Lodnon University, CPNSS, London, United Kingdom

A feeling of free-will, which is entangled with a concept of free choice, seems ubiquitous among humans and has been suggested to be a basis of the human moral sense. I discuss the concept of free will and its relation to notions of agency and choice, and suggest that the human feeling of free will is the outcome of the interaction, sometimes the conflict, between imagined and internalized collective societal norms (a super-ego, which provides the “ought”) on the one hand, and the individual’s feelings of agency and choice, which stem from humans’ ability to imagine themselves in endless situations, with endless goals, on the other hand. The evolutionary origins of the human feeling of free-will are therefore to be sought in the evolutionary extension of social animals’ subjectively-felt agency and decision-making, which are the outcomes of the evolution of imaginative animals’ cognition, self-control and emotions. Humans’ feeling of free-will emerged on these foundations, in the context of culturally-driven evolution of new norms, new representation of the self and new social and individual emotions.

Plant data science between policy and technology: Reframing plant research to serve global food security

Sabina Leonelli¹, Hugh Williamson¹, Rachel A Ankeny³, Helen Curry⁴, Paul Thompson²

¹University of Exeter, Egenis, Exeter, United Kingdom, ²MSU, Philosophy, Lansing, United Kingdom, ³University of Adelaide, History, Adelaide, Australia, ⁴University of Cambridge, HPS, Cambridge, United Kingdom

Research on plants and crops is crucial to informing innovation and policy relating to food security around the world, yet the development of efficient systems to link and interpret data acquired through such research has lagged behind other fields such as climate or human health. Such data management systems are viewed as indispensable to developing an evidence base for a range of technologies and interventions that include crop breeding, genetic modification and synthetic biology, modelling, decision support systems and growing procedures. Unsurprisingly, this means engaging with a highly fragmented landscape with multiple levels of locality and coordination, ranging from institution- and experimental system-specific solutions to international research projects, breeder- and farmer-led groups, transnational communities of practice. This panel explores the challenges encountered by philosophers, social scientists and historians collaborating with stakeholders across this complex landscape, and the lessons learnt from qualitative empirical engagement with these various dimensions of plant and crop research, which bring into sharp relief some of the most urgent concerns underpinning global approaches to food security.

Reproductive relations and temporal cross-generation boundaries. The case of eutherian pregnancy

Arantza Etxeberria¹

¹University of the Basque Country, Philosophy, Donostia-San Sebastian, Spain

Beyond the organization of an individual being, reproductive phenomena are relational. In biology, some authors (e.g., Buffon, Jacob) view reproduction as essential for life, as generating a continuous chain of organic beings, whereas for others (e.g., Maturana and Varela), reproduction is secondary and derived from organization. Received views have characterized reproduction as a formal process in which preexistent units are copied; thus, the complexity and diversity of the relations involved has been concealed. Understanding the evolved relations, distributed agencies, and emergent individualities of reproduction requires considering material overlapping, temporal continuities/discontinuities and strong developmental interactions.

The aim of this paper is to examine how boundaries between individuals emerge in reproduction, particularly in eutherian pregnancy (Nuño de la Rosa et al. 2021), as a result of the temporal transformations of individualities and appearance of boundaries and limits. The following questions are addressed: 1) the role of reproduction in the organization of life and of individual living organisms and the contribution of physiology to reproduction (for example, how female physiologies accommodate developing embryos in a new organismal organization; how boundaries between individual organisms are constituted), 2) how boundaries can be conceptualized in different kinds of reproductive strategies (oviparity vs. viviparity). Unlike individualist frameworks in which boundaries between individual entities are presupposed, this kind of framework enables a developmental view of reproductive relations in which boundaries are blurred and established.

Where the social meets the biological: Navigating boundaries in the embodiment of race

Azita Chellappoo¹, Jan Baedke¹

¹Ruhr Universität Bochum, Institut für Philosophie I, Bochum, Germany

Where the boundary between the biological and the social lies has long been debated, although the nature of the boundary itself has been under-attended to. Recent postgenomic research in fields like epigenetics and microbiome research appears to suggest a dissolution of the boundary, driving a view of the biological and social as inextricably interlinked and co-constituted. In contrast, we argue that postgenomic narratives indicate a re-conception of this boundary, rather than its complete abandonment. The postgenomic biosocial boundary emerges as selectively permeable: only a small set of features of the social environment (e.g., stress and diet) are able to reach into the body and enact particular effects. We focus on this boundary in the context of postgenomic work on race.

We identify four characteristics of how the new biosocial boundary is conceptualised, in terms of which features of the social environment are allowed to permeate this boundary: (1) there is a strong focus on the negative social environment of racialised groups and (2) the social environment is only allowed to permeate if it becomes fragmented or (3) if social phenomena are reduced to simple proxies. In addition, (4) for the social environment to pass the boundary it needs to be highly stable, both across time and across different national settings. We argue that these problematic assumptions lead to a distorted view of the biosocial boundary, arising in part from the greater control that scientists exert over what this boundary looks like. We suggest ways in which social science work could inform a more nuanced conception of the social environment, and thus contribute to a more complex and less biased understanding of the biosocial boundary itself.

Visualizing evolution: Communicating new boundaries

Miguel Brun-Usan¹, Lynn Chiu^{2,3}

¹Lund University, Lund, Sweden, ²University of St. Andrews, School of Biology, Fife, United Kingdom, ³KLI, Klosterneuburg, Austria,

The transition from the Modern Synthesis (MS) to the Extended Evolutionary Synthesis (EES) is often seen as a conceptual shift from a framework that relies on strict dichotomous boundaries between evolutionary agents and processes to one with fluid, intermingled boundaries. In this talk, we first investigate this claim by examining the conceptual and visual metaphors used in MS and EES explanations. We show that MS metaphors assume and harden distinct boundaries between the different individuals, levels and processes involved in evolutionary dynamics. The EES aims to break such boundaries by taking a wider set of evolutionary causes, entities and levels into consideration. Since this complexity is hard to conceptualize and communicate using classical schemas, new metaphors are needed. But which ones? Here, we provide some art-based representational tool kits that can help represent multi-level, or feedback causal chains. Boundaries are still used, but as visual guidelines rather than real-world compartments. Some of these tools are based on artistic principles developed by artists such as Escher or Arcimboldo, which are presented as case studies. This exercise shows how artistic principles can help us overcome the cognitive tendencies that perpetuate misleading metaphors in evolutionary theorizing, illustrating the epistemic value of the arts in evolutionary thinking.

Dobzhansky and the Brazilians from his letters and reminiscences for the Oral History of Columbia University

Aldo M Araujo¹

¹Universidade Federal do Rio Grande do Sul, Dept of Genetics, Porto Alegre, Brazil

Theodosius Dobzhansky (1900 – 1975) was a prolific writer, not only of books and papers, but also of letters to his friends and collaborators. He came to Brazil many times, the first being in 1943, staying there for periods of one year or some months (his final visit to Brazil was in 1966, during the International Symposium on Genetics, where he was the Honorary President). In his interviews to Barbara Land for the Oral History Memoir of the Columbia University, he dedicated around 90 pages, in a total of 639 pages (14%) to the “Brazilian venture” as he said in a letter to Sewall Wright. In the present communication it will be discussed some of his letters and comments on Brazil and Brazilians which reveal his enthusiasm for some of his friends as well as for the country but also his disappointment and even prejudice about his fellow researchers and people in general. The following represents just two examples, one from his reminiscences, the other from a letter: “Now, I probably sound as saying Portugal and Brazil are 100 percent wonderful, the rest 100 percent bad. I don’t mean to say that at all. Of course, this dedication to pleasure has clearly disadvantages. The dedication to pleasure makes very frequently sad results if you have to do any work. Everybody is tremendously enthusiastic to start with, but when it comes to work, it just isn’t done. In particular, nothing is every prepared in advance, even when a preparation is necessary. My very good friend, Professor Pavan, - he’s of pure Italian descent but culturally 100 percent Brazilian – cannot do anything for tomorrow. Tomorrow will take care of itself. It quite often doesn’t take care of itself. That has some disadvantages, but there exists this difference” (Oral History Memoir 1962, p. 524). In 1966 he exchanged a series of letters with a doctoral student from Faculdade de Filosofia Ciências e Letras, São José do Rio Preto, state of São Paulo. This student was planning to stay one year with him at Columbia University, after receiving the doctoral degree. In December the 7th, 1966, Dobzhansky sent him a letter which starts as this: “Let me congratulate you with your doctorate, and wish you that this achievement be the beginning, not the end, of a long, productive, and successful scientific career. It so often happens to be the end; this happens everywhere, but as you know and I know it happens to be the end most often in Brazil, because of the characteristics of the ‘ambiente’ (environment)”

Female researchers at Dreyfus' group: 1943-1960

Lilian Al-Chueyr P Martins¹, Ana Paula Oliveira Pereira M Brito²

¹University of São Paulo , Biology, Ribeirão Preto , Brazil, ²University Nine July , Psychology, São Paulo, Brazil

One of the main biological centres from which genetics started and developed in Brazil was situated at the Faculty of Philosophy, Sciences and Linguistics at the University of São Paulo and led by André Dreyfus (1897-1952). From 1943 until 1956, Theodosius Dobzhansky (1900-1975) visited it four times and introduced natural population genetics studies. Several of its members, such as Crodowaldo Pavan (1919-2009), Antônio Brito da Cunha and Luiz Edmundo Magalhães (1927- 2012) are well known for their contributions. On the other hand, there is not much information about the women who joined Dreyfus' group during the relevant period. This communication aims to discuss the role of women in the Dreyfus' group, taking into account, among other aspects, the visibility of their contributions. This research shows that as the authors' first names usually appear in the paper's bibliographical references in an abbreviated form, it is impossible to identify which authors are women. Besides that, except for Rosina de Barros, women did not appear as the first authors in most English articles. For instance, Marta Erps Breuer (1902-1977), who investigated the male genitalia of *Drosophila* as an essential tool for the identification of species, was not the first author in the papers on the subject written with Pavan. The same occurred with Elisa do Nascimento Knapp and Marta Wedel, who worked with natural populations of *Drosophila willistoni*. Natasha Dobzhansky's name appears once as the third author of a paper. Historiographical studies of genetics in Brazil scarcely mention their names or contributions. This situation is similar to the one reported in other studies (Richmond, 2007; Dietrich & Tambasco, 2007): from 1934 to 1970, most women working with *Drosophila* were technical assistants and remained invisible in the historiography of genetics.

Perceptions of researchers of the Institute of Biosciences about Dreyfus and Dobzhansky' time and institutionalization of genetics in Brazil

Maria Elice B Prestes¹, José F Sião²

¹University of São Paulo, Genetics and Evolutionary Biology, São Paulo, Brazil, ²State Secretary of Education, Education, São Paulo, Brazil

The institutionalization of genetics in Brazil occurred in the decades of 1940s and 1950s, in the so-called Department of General Biology, of the old School of Philosophy, Literature and Human Sciences of the University of São Paulo (FFLCH/USP). In this presentation, we will learn the perceptions about that period of five faculty members from the current Department of Genetics and Evolutionary Biology. They had some contact with its first institutional leader, André Dreyfus (1897-1952), and with the visiting professor, Theodosius Dobzhansky (1900-1975). The second author of this work did the interviews with the five collaborators, as they are called by the methodology of Oral History, between May and August 2011, and focused on: a) their historical trajectory in the Department; their perception about the partnership between Dobzhansky and Dreyfus for the development of the genetics at the Institute of Biosciences and in Brazil, in the 1940s and 1950s; the specific contributions that the whole group should have made in that period; the role of the population genetics and the History of Science in Brazil Science Education. The collaborators, including those who had no direct contact with the researchers of that time, showed considerable knowledge about the Department's history, including Dreyfus and Dobzhansky's role. However, they pointed out other researchers that they considered equally relevant to the consolidation of the group and the field of Animal Genetics in Brazil. All collaborators said that the History of Science plays an essential role in science education. The narratives that emerged from the three phases of the Oral History (transcription, textualization, and transcreation) become sources for research and teaching the History of Science in Brazil.

Towards a transgenerational perspective on immune systems

Sophie Juliane Veigl¹

¹Tel Aviv University, Cohn Institute, Tel Aviv, Israel

The question of how the border between organism and environment is negotiated is a critical problem in cutting-edge philosophy of biology. While both philosophers of evolutionary biology as well as philosophers of immunology place the organism at center stage, these investigative endeavours rarely interact. Whereas evolutionary biology takes interest in how organism and environment interact transgenerationally, immunologists investigate these equilibria within one generation, presupposing an immunological discontinuity in the succession of physiological individuals.

This presupposition might be warranted when describing mammalian immune systems. It is my aim, however, to show that other phyla have developed immune responses that persist transgenerationally. As an example, I will introduce the inheritance of stress-responsive small RNAs in the roundworm *C. elegans* as an instantiation of a transgenerational and adaptive immune response. I will further discuss how cues from the environment change which nucleic acids are recognized as organismic or environmental. In particular, I will demonstrate how immunological interactions between organism and environment shape the trajectory of the evolutionary individual. I will conclude by proposing how a perspective that is not primarily focused on mammals, but considers a broader range of immune systems contributes to philosophical questions such as those regarding theories of immunogenicity.

When you are forced to being nice: Multicellularity is more about coercion than about altruism

Adrian Stencel¹, Javier Suarez¹

¹Jagiellonian, Department of Philosophy, Krakov, Poland

The use of agency metaphors in biology is a popular tool as they help guiding research. For instance, in evolutionary biology researchers often say that genes are “selfish” units that pursue their aims and goals. The work of philosophers is to analyze the adequacy of these metaphors. A popular agential idea is to think that somatic cells, responsible for maintaining the functionality of the organism, but incapable of transmitting their genes to the next generation, are altruists. They sacrifice their life on behalf of the germline cells, where the capacity to transmit genes to the next generation ultimately lies.

What explains the use of this metaphor? One conventional answer refers to inclusive fitness (or kin selection) theory, according to which somatic cells sacrifice themselves altruistically, because they are genetically related to germline cells. Given this genetic relatedness, their sacrifice enhances the transmission of their genes to the next generation, insofar as they are genetic clones of the germline cells. In this talk, we analyze kin selection theory and the mechanisms of the development of multicellular organisms and conclude that this explanation ignores the key role of policing mechanisms in maintaining the germ/soma divide. We conclude that it is better to think of somatic cells as victims of coercion that are forced to sacrifice, rather than as altruists.

Functions and the immune system: Can immunology impact the way we think about different notions of biological function?

Gregor Greslehner¹

¹University of Vienna, Department of Philosophy, Vienna, Austria

It is a long-standing tradition in philosophy of biology to distinguish between functions as causal roles and selected effects - according to Robert Cummins and Larry Wright, respectively. While there are recent efforts by Justin Garson to unify them under a “generalized selected effects” account, there is a case to be made for the independent conceptual and explanatory importance of the causal role notion. I believe immunology offers a rather different perspective in which a selection account appears somewhat arbitrary. The immune system monitors most physiological activities, including its interactions with the microbiota, delicately adjusting its response to their structural and functional aspects and can trigger immune responses in particular contexts, in which the selection perspective simply does not fit. There is no differential persistence, fitness advantage, evolutionary or teleological element to be explained; rather, the physiological effects of microbiota can directly be the object of immunological recognition. This is in contrast to a major criticism against function understood as a causal role, that it would depend on an observer’s subjective decision what and what not to consider a function in the first place. The immune system’s ability to recognize causal role functions thus provides a new objective and realist interpretation, opening interesting questions about physiological and evolutionary notions of function.

Kuhnian incommensurability and evolutionary biology: Are the modern evolutionary synthesis and the extended evolutionary synthesis incommensurable?

Juan Gefaell¹, Cristian Saborido²

¹University of Vigo, Biochemistry, Genetics, and Immunology, Vigo, Spain, ²National Distance Education University, Logic, History, and Philosophy of Science, Madrid, Spain

In recent years, several evolutionary biologists have suggested that the Standard Evolutionary Theory, also known as the Modern Evolutionary Synthesis (MES), needs to be revised in order to incorporate new biological findings such as epigenetic inheritance, developmental bias, phenotypic plasticity, niche construction, or evolvability. In particular, these evolutionary biologists have proposed an alternative evolutionary framework, usually known as the Extended Evolutionary Synthesis (EES), to fully account for these findings. However, not all evolutionary biologists agree, and many of them think that the MES doesn't need to be revised at all, and that the EES is therefore not necessary. This controversy has prompted a debate among evolutionary scientists over the relationship between the MES and the EES. This debate constitutes a perfect case study for those philosophers of science interested in the topic of Scientific Change. Given that many evolutionary biologists use Kuhnian terms in the debate (such as “scientific revolution”, “paradigm” or “incommensurability”), in this talk we apply Kuhn's theoretical framework for scientific change to the contemporary discussion in evolutionary biology. In particular, we explore to what extent the Extended Evolutionary Synthesis is in fact incommensurable with the Modern Evolutionary Synthesis. We claim that this issue depends on the characterization that one adopts of the notion of “incommensurability”. Here, we show that throughout the work of Thomas S. Kuhn it is possible to distinguish at least two different meanings of the concept of incommensurability. Each of these interpretations involves different characterizations of scientific change. This distinction between two Kuhnian interpretations of incommensurability allows us to assess the different positions of the debate in evolutionary biology in order to shed light on the particularities and implications of the current scientific scenario.

Get costs in everywhere in evolutionary theory!

Marion Blute¹

¹University of Toronto, Sociology, Toronto, Canada

A lesson can be drawn from Rick Charnov (1982) who transformed Fisher's sex ratio theory into sex allocation theory, but unfortunately the lesson has not spread far enough within evolutionary theory. The lesson is that costs as well as frequencies have to be included. Every time one dives deeper, one finds both. That is so whether we are talking about evolutionary ecology (e.g. density-dependence), social evolution (e.g. sexual selection), the origin of life, the extended synthesis or whatever. The two dimensions are expressed in a variety of ways - costs as well as frequencies, quality as well as quantity, investing as well as spending, somatic as well as reproductive functions, etc. Both are needed for explanation at all levels of evolutionary theory.

E.g. density dependence traditionally is quantity (r , at low density) versus quality (K , at high density) but then we need quantity and quality at both.

E.g. sexual selection theories are frequency (e.g. male Intrasexual mate/sperm competition) or quality (e.g. female intersexual mate/cryptic choice competition) but we need both frequency and quality for natural as well as for sexual selection).

E.g. the "originals" grew and developed (quality) as well as doing so competitively (quantity).

E.g. development (quality) as well as evolution (quantity) along with ecology must become part of the modern evolutionary synthesis.

What we can learn from parasites

Robert Kok¹

¹University of Utah, Philosophy, Salt Lake City, UT

Symbiotic relationships are widespread in the biological world. Discovered at multiple hierarchical levels, its ubiquity challenges the notion of discrete, linear evolutionary progress within taxonomic boundaries and our views of inheritance. However, philosophers of biology have focused primarily on mutualisms as the dominant symbiotic relationship in nature with microbial associations taking center stage. This *mutualistic perspective* in symbiotic analysis has reshaped and reformed our understanding about reticulate evolutionary patterns and processes, the co-evolution of diverse organisms, and ideal models for non-Darwinian individuals. In contrast to highly researched mutualistic associations between free-living organisms, parasitism is often considered by philosophers a deviant form of symbiosis and a substandard evolutionary strategy. In this paper, I explore recent studies into parasite evolution that challenge this bias and argue that major insights are to be gained by adopting a *parasitological perspective* in biological research. To be gained are insights into co-evolution, phylogenomic entanglement, origins of novel strategies, and host immunology. To show this, I focus on the evolutionary history of two much researched parasite lineages: nematodes, the most abundant animal on the planet, and *Plasmodium falciparum*, the parasite responsible for malaria in humans.

Song at the end of modernity

Rachel Mundy¹

¹Rutgers University, Newark, Arts, Culture, and Media, Newark, NJ

John James Audubon's *Birds of America*, printed between 1827 and 1838, is understood as being about what Audubon called the birds of "our country," the United States. Yet like Audubon himself, who was born in Haiti in 1785 before moving northward, the most vocal birds in Audubon's book, including mockingbirds, migrate regularly across national boundaries. Today, these migrations are often described using an environmentalist language of survival and extinction.

In my talk today, I want to link the stories we tell about Audubon's ears and birds' songs to two seemingly unrelated topics: the way we talk about species extinction, and the way we talk about human worth. The language of survival, extinction, protection, and conservation connects modern-day environmentalism to much older traditions of hearing nature through tropes of national identity. In this talk, I argue that the connection between nature and nation is part of a much broader and very difficult inheritance that predisposes Western listeners to frame the rights of animals in terms of the right to human life. And in this moment, the right to human life is not a general right, but reveals to listeners the role of nationality, race, gender, sexuality, and other factors matter, including species, in determining life's privileges.

An Aristotelian response to the biodiversity crisis

Duncan C Maclean¹

¹St. Mary's University, Humanities, Calgary, Canada

Ancient Greek ethics is not a typical resource for environmental ethics. Classical Greek ethics can be characterized as a series of investigations into the inner life of human beings and how one might acquire the virtues needed to succeed in city-state living. As well, besides Aristotle's biology, ancient Greek philosophers did not conduct empirical research into the rich diversity among plant and animal species. Thus, the Greeks showed little interest in how humans related to the wilderness beyond the city walls.

Of what use, then, could Aristotle's ethics be to the current debate on the biodiversity crisis? I argue that Aristotle's virtue ethics says that we must preserve plant and animal species or risk losing our own eudaimonia or happiness. Aristotle argues in the *Nicomachean Ethics* that true human flourishing consists of a life dedicated to the employment of theoretical reason, which includes the scientific understanding of nature. But today with the extinction of species, there are fewer species for biologists to work on and fewer species for the general public to learn about. For Aristotle, the loss of biodiversity amounts to the undermining of reason and our innate curiosity about the world. We must, then, protect biodiversity so that we may continue to fully realize our natures as knowers of nature.

In the second part of the paper, I argue that an Aristotelian environmental virtue ethics is better at considering the interests of plant and animal species than deontological and utilitarian attempts. I also defend the proposal from charges of anthropocentrism and that arguments from theoretical reason would fail to motivate people to protect species diversity.

Where the wild things are classified: Wildness and the nonhuman animals caught in the crosshairs

Denise R Hossom¹

¹University of California, Davis, Philosophy, Davis, CA

My dissertation analyzes nonhuman animal classification practices across the biological sciences for the following interrelated concepts and distinctions; wild, domestic, feral, tame, captive, free-roaming, pest, vermin, varmint, pet, and livestock. I term these concepts the “Wild-Domestic Classification System” (WDCS). Analysis of classification practices spans evolutionary biology, animal behavior, ecology, conservation biology, zoology, agricultural science, and veterinary science, and is approached through a case-based methodology. This enables an analysis of concepts as they materialize in particular cases of human, nonhuman animal, and environmental stakeholder group conflict. Examined cases display what I term a “zone of conflict”; a the tangled web of human, nonhuman animal, and environmental stakeholder interests extending into a unique spatiotemporal context and boundary, tangible and intangible. The zone of conflict conceptual schema aims to uncover where classification can weaponize or safeguard stakeholder groups through specific confluences of value-interactions, boundary-drawing tactics, and value-tradeoffs amongst stakeholders.

The focal case study for this paper examines “wild horse problems”; the American Mustang and Australian Brumby demonstrate national zone of conflict contexts, and the Przewalskii horse a transnational context. Examination of how constitutive and contextual values shape classification across a case study’s diverse scientific and social contexts, both historical and contemporary, is vital to the project. The ‘problem taxa’ of “wild horses” demonstrates how every concept and distinction from the WDCS can be applied to one taxa. The mustang and brumby horse present strong scientific and social stakeholder group interaction, with biodiversity featuring as a central tension. The transnational conservation programs for Przewalskii horses contends with the debate over its status as a “true” wild horse, with the main conflict over biodiversity predominantly occurring in scientific contexts. “Wild horse problems” illuminate the complexity of biodiversity from the perspective of a zone of conflict schematic. This offers a contextualized picture engaging particular stakeholder lenses, in order to best represent the scientific, social, and nonhuman actors involved.

Democratizing methods? Rhoda Erdmann (1870-1935) and the penumbra of early tissue culture research

Heiner M Fangerau¹

¹University of Duesseldorf, History, Philosophy and Ethics of Medicine, Düsseldorf, Germany

In the years after Ross Harrison published his seminal paper on nerve fiber regeneration in 1907, researchers following his line of research presented tissue culture techniques as an extremely difficult and almost occult methodology. Alexis Carrel, for one, is known to have contributed to the image of cell culture techniques as an esoteric practice. As late as 1954, Philip R. White introduced his manual of tissue culture as an attempt at dispelling “its former atmosphere of mystery and complication” (Witkowski 1979). 32 years before, the German zoologist Rhoda Erdmann had published a similar manual, with an analogous intent. She sought to make the method “a common property of those who want to do biological research in the future”. In a period of transition from little to big science, Erdmann tried to democratize tissue culture knowledge.

Erdmann was an extraordinary scholar in many ways. One of the few women in the field, she worked as a low-level assistant at the Robert Koch Institute in Berlin before taking the opportunity of a research fellowship with Ross Harrison in Yale. She was imprisoned during the WW1 on suspicion of espionage. After she could return to Germany in 1919 she established a laboratory for experimental cell research in Berlin. In 1929 she was one of the first women to be appointed professor in Germany.

The proposed paper focusses on Rhoda Erdmann’s attempts at distributing practical tissue culturing knowledge. On the basis of her and other scholars research on nutrient solutions or soils for cell cultures, the paper follows the hypothesis that much of this work was eclipsed by the final results of tissue growing experiments. In the early days of tissue culture, the appeal of cultured cells was much higher than that of the material they grew upon and academic recognition was rather attributed for fancy results than for working on cell nurturing methodology. Scientists developing and producing nutrient soils tended to be forgotten. The paper will explore the epistemic relations between Erdmann’s own outsider position and certain “niches” in the academic world (topics, places, techniques, communities) that represented her research Umwelt. It will also enquire whether Erdmann’s attempts at democratising techniques can be read as part of a more general attempt to move these niches from the periphery to the centre of academic attention.

Brain regeneration phenomena, morphological research advances, and the practical implications of theory dynamics in modern bio-medicine

Frank W Stahnisch¹

¹University of Calgary, History, Calgary, Canada

The modern thesis of structural plasticity of the brain, as a deliberate reaction to traumata, tissue damage, and degenerative cell death, is hardly expansible for clinical neurology and allied disciplines. It has been termed by Peter R. Huttenlocher “a critically important phenomenon for both neuroscience and psychology. Increasing evidence about the extent of plasticity – long past the supposedly critical first three years [of childhood] – has recently emerged” (2002).

This paper explores the history of phenomena connected with the thesis of brain plasticity from the 1950s to the 1990s, while analyzing the neuroanatomical interpretations regarding the Central Nervous System. These phenomena currently have significant implications for the burgeoning field of regenerative medicine, while also posing severe ethical challenges for related research endeavors.

After first describing early precursors of research into brain plasticity phenomena in non-vertebrates at the beginning of the 20th century, such as the light microscopic studies by Morgan (1901), Korschelt (1907), and Przibram (1909), I will then focus on hippocampus models in rat and mouse brains by Palay (1956) and Gray (1963), whose electron microscopic findings substantiated the existence of structural neuroplastic phenomena in higher cortical substrates.

Experimental physiological research in hippocampal regenerative in vivo models by Gage (1992) and Rakic (1994) substantiated clinical physiological views that structural plasticity can be seen as positive regenerative CNS responses to brain damage and degeneration. Yet the underlying mechanisms still remained to be established and became advocated for through the discovery of neuronal stem cells in the brains of adult mammals by Reynolds and Weiss (1992).

Applying an analytical framework developed by Polish-Israeli historian and philosopher of science Ludwik Fleck (1896-1961) in his "Genesis and Development of a Scientific Fact" (originally published in 1935), this paper examines the practical implications of theory dynamics regarding (new) model organisms of regeneration that determined morphological research advances and scientific trajectories at the modern bio-medical interface.

On the concept of biological development

Pavlos Silvestros¹

¹National & Kapodistrian University of Athens, History and Philosophy of Science, Athens, Greece

The aim of this paper is to propose and defend a general characterization of development in the context of developmental biology. Historically, the term ‘developmental biology’ emerged right after the Second World War, gained popularity in the late 1950s, and till the end of 1960s became the dominant label in scientific societies and journals for referring to the research previously done mainly under the older label of ‘embryology’ (Burian & Thieffry 2000). However, despite the undeniable successes of developmental biology from the second half of the 20th century to the present day there has been a surprising lack of consensus about the notion of development (Minelli 2003). This scientific discipline is not unsuccessful nor immature, thus the persistent lack of consensus on its most central concept raises some questions: is there any need to define comprehensively biological development, and if so, what content should be given? These puzzling issues will be tackled here through scientifically informed philosophy and constrained by the principle of epistemic transparency, namely that an account of scientific investigation must be accessible to scientists’ perspective. First, I will argue that an exact definition of development is very much required for overcoming implicit assumptions and delineating the domain of inquiry of developmental biology (Pradeu et al. 2016). Second, by examining a representative sample of the most common definitions I will show that they are unsatisfactory on both conceptual and empirical grounds. Lastly, I will put forth an improved general characterization of biological development that addresses the main objections while being descriptively adequate. According to this, *biological development is the causal pathway that starts from a cell and through a variety of coupled mechanisms gradually produces or alters an organism's shape, size and structural features throughout its life cycle.*

References

- Burian, R., & Thieffry, D. (2000). “Introduction to the special issue. ‘From embryology to developmental biology’”. *History and Philosophy of the Life Sciences* 3: 313-323.
- Minelli, A. (2003). *The Development of Animal Form: Ontogeny, Morphology, and Evolution*. (CUP).
- Pradeu, T., et al. (2016). “Defining ‘Development’”. *In Current Topics in Developmental Biology* 117: 171-183.

Reconsidering developmental mechanistic explanations

Stavros Ioannidis¹

¹National & Kapodistrian University of Athens, History & Philosophy of Science, Athens, Greece

The mechanistic framework has been widely adopted by philosophers of biology as a general perspective for understanding the epistemology and metaphysics of life sciences in areas such as molecular biology and neurobiology. However, the case of developmental biology in relation to the mechanistic framework has not been sufficiently explored (cf. McManus 2012). This is an important omission, since the notion of a developmental mechanism has become central in contemporary biology, as developmental biologists have discovered that a lot of the diversity of developmental processes can be accounted for by common developmental mechanisms that make use of very similar basic regulatory components in different ways. The main aim of the paper is to examine the explanatory practices of contemporary developmental biology by focusing on the concept of a ‘developmental mechanism’. Two examples of developmental mechanisms will be discussed: axis formation and determination mechanisms, and mechanisms for the generation of the tetrapod limb. It is widely accepted among new mechanists that (i) biological systems contain a hierarchy of nested mechanisms and that (ii) many explanations in biology are constitutive mechanistic explanations. These two claims lead to a view about multi-level mechanistic explanation, where such an explanation involves the identification of a nested hierarchy of constitutive mechanisms (Craver 2007). In the paper it will be argued that this account of multi-level explanation does not fit with the explanatory practices of developmental biology. A key point will be that levels of organisation are themselves constructed during development. This diachronic viewpoint on the construction of levels leads to an alternative account of multi-level explanation in developmental biology, where such explanations identify causal pathways that contain entities from various levels of organisation. The paper will thus illuminate the explanatory practices of developmental biology and develop a practice-based account of the notion of a developmental mechanism.

References

- Craver, C.F. (2007) *Explaining the Brain: Mechanisms and the Mosaic Unity of Neuroscience*, New York: Oxford University Press.
 McManus, F. (2012) “Development and mechanistic explanation”, *Studies in History and Philosophy of Biological and Biomedical Sciences* 43: 532–541.

What an epistemology of scientific practice should be: The case of developmental biology

Konstantina Antiochou¹

¹University of Athens, Department of History and Philosophy of Science, Athens, Greece

According to an increasingly influential view among biologists and philosophers of biology, philosophy of science, in general, and of developmental biology, in particular, should focus on a thorough investigation of what scientists do. The turn to the practice of science is not something new in the philosophy of science. In the case, however, of developmental biology what seems to necessitate this choice is the lack of a (unified) theory of development (Minelli & Pradeu 2014). The aim of this paper is to discuss the scope of this view and defend a broad conception of biological practice which essentially involves (argumentative) reasoning and theory building. It argues, first, that it is not so clear what ‘scientific practice’ means or involves for those prioritizing the actual scientific practice over theory. While the description of scientific practice is understood in contrast to normative accounts of science, on the one hand, and theory-based analyses of science, on the other, the role of both norms and theories, as well as the data that need to be taken into account and captured in this context are not clearly specified. The argument from the complexity of developmental phenomena is probably the strongest one provided against the possibility and/or desirability of a theory of development. It is often combined with an argument for pluralism - in both science and philosophy - which is supposedly undermined by the ontological commitments of theories or the search for a unified theory (cf. Kaiser 2015, Waters 2019). But as it is argued in the second part of the paper, this argument is based on a strong and rather demanding conception of theory. Naturalism is not rejected. It is argued, however, that the practice of science cannot be conceived in opposition to theory (building) or theorization. For the role of theory is indispensable in the context of justification of knowledge claims.

References

- Kaiser, M.I., 2015, *Reductive Explanation in the Biological Sciences*, Cham: Springer.
 Minelli, A. & Pradeu T. (eds.), 2014, *Towards a Theory of Development*, Oxford: Oxford University Press.
 Waters, C.K., 2019, “An Epistemology of Scientific Practice”, *Philosophy of Science*, 86: 585–611.

Keywords: developmental biology, scientific practice, theory/theorizing, norms

The social life of trauma biology

Emma Kowal¹, Michel Dubois², Georgia Samaras³, Elsher Lawson-Boyd¹

¹Deakin University , Alfred Deakin Institute, Melbourne, Australia, ²CNRS/Sorbonne University, EPIDAPO, Paris, France, ³Technical University of Munich, Science and Technology Policy, Munich, Germany

The biology of trauma has animated recent scientific work across many fields including neuroscience, psychiatry, epigenetics, biological anthropology, and the developmental origins of health and disease (DOHaD). Findings related to ‘historical’ or ‘transgenerational’ trauma have generated huge interest among historically marginalized groups and the social scientists interested in their experiences. Roundtable participants will present on their work in scientific and social settings where trauma science is enacted, including the environmental epigenetics of PTSD, neuroepigenetics, and the epigenetics of historical trauma. The discussion will inquire into the new alliances we see between different scientific and social actors. How are trauma and stress defined, studied and reformulated across these arenas? What are the social hype and political stakes of trauma-informed practices? What forms of temporality, identity, embodiment and justice do they produce?

Emma Kowal is Professor of Anthropology at Deakin University. With a background in clinical medicine, her research interests lie at the intersection of STS and Indigenous studies and have recently focused on the many iterations and resonances of ‘Indigenous DNA’ in Australia. Her projects include the Australian Research Council-funded project ‘The politics of epigenetic hype and hope in Indigenous Australia’. Michel Dubois is a CNRS senior research fellow and associate director of EPIDAPO - (Epi)Genetics, Data & Politics – a collaboration between CNRS and George Washington University. He is teaching and publishing mainly on issues of sociology of science and technology, epistemology and methodology of social research, sociological history and theory. Georgia Samaras is a postdoctoral researcher at the Technological University of Munich working on the DFG-funded project “Situating Environmental Epigenetics. A Comparative, Actor-Centered Study of Environmental Epigenetics as an Emergent Research Approach in Three Research Fields”. Elsher Lawson-Boyd is completing a PhD at the Alfred Deakin Institute of Globalisation and Citizenship, Deakin University. Her research is on emerging postgenomic models of trauma in neuroscience and epigenetics.

Reconsidering Gaia

Tim M Lenton¹, Peter Godfrey-Smith², W. Ford Doolittle³

¹University of Exeter, Global Systems Institute, Exeter, United Kingdom, ²University of Sydney, History/Philosophy of Science, Sydney, Australia, ³Dalhousie University, Biochem/Mol Biol and Philosophy, Halifax, Canada

James Lovelock, often working with Lynn Margulis, proposed the Gaia Hypothesis – that the biosphere is “an active adaptive control system able to maintain the Earth in homeostasis” and suitable for life over 4 billion years. The hypothesis was instrumental in establishing Earth System Science as a discipline, but many of its implications for theories of evolution by natural selection (ENS) are controversial. Our three panelists have three very different takes on this hypothesis. Peter Godfrey-Smith, a philosopher of evolution, holds that while the systematic organismic transformation of environments is important and feedback is ubiquitous, there is little chance that the Earth as a whole acts as an organismal system, given the kind of placement it has within evolutionary processes. Tim Lenton, an evolutionary modeler, argues that there are different forms of selection for Gaia across multiple scales, including ENS, sequential selection of self-stabilising feedbacks, and accumulating of those feedbacks through persistence-based selection. Ford Doolittle, an evolutionary biologist, is trying to “Darwinize Gaia”, reworking traditional ENS theory in an expanded replicator/interactor framework to legitimize claims for Gaian adaptations. Each will present for 20 minutes and we will then have 30 minutes of discussion among them and with the audience, hoping for some sort of principled agreement.

Are bacterial lineages feedback systems? From cynical pluralism to meta-pluralism about bacterial species

Matthew J Barker¹

¹Concordia University, Department of Philosophy, Montreal, Canada

Historical, philosophical, and sociological work has shown great diversity in methods, practices, and concepts of prokaryotic systematics. From this pluralism, some have cynically inferred that no single account of the nature of bacterial species will or should enjoy consensus across most disciplines involved. As tempting and liberating as that inference from pluralism to cynicism may be, it is not yet justified. Compared to the glacial pace of some conceptual advances in the history of science, it may also be premature by many centuries. But it is hard to slow cynical pluralism without proposing a more integrative alternative that could attract consensus. This paper outlines such an alternative. It applies the new view that some evolving lineages are metapopulation feedback systems, to bacterial groups. Such systems have metapopulation feedback cohesion, M , which varies dynamically with the magnitude and frequency of feedback relations between causal variables at lower levels. This paper outlines ways of empirically testing this model for bacteria, by experiments on transformation and whole genome sequence comparisons. Tests may eventually be unfavourable. But having the motivation provided here for testing it all (or analogous views) suggests that a less cynical form of pluralism should prevail at the level of whole research communities, for now. This would be a type of meta-pluralism, encouraging some to seek integration, and others to remain cynical or disinterested.

What is it that evolves?Celso Neto^{1,2}¹Dalhousie University, Philosophy, Halifax, Canada, ²Dalhousie University, Biochemistry and Molecular Biology, Halifax, Canada

Traditional formulations of natural selection assume that entities undergoing selection form lineages. This assumption motivates recent claims that multispecies microbial communities do not undergo selection. Yet, these claims are controversial in part because the role and nature of lineages are poorly understood. In this paper, I clarify these issues by revisiting David Hull's notion of units of evolution. Lineages are units of evolution in traditional formulations of natural selection, while the entities that form lineages are units of selection. I revise this idea in two ways. First, we argue that lineages can also be units of selection. Second, I argue that units of evolution do not have to form clear parent-offspring relations. With this aim in mind, I analyze a set of borderline cases of lineage and the underlying notions of reproduction and inheritance. Our analysis offers a framework to compare traditional and more recent formulations of evolution by natural selection. It also helps to clarify how multispecies microbial communities might evolve.

Can and should we avoid the notion of natural kind when epistemologically analyzing homologies?

François Papale^{1,2}

¹Université de Montréal, Département de philosophie, Montréal, Canada, ²Muséum National d'Histoire Naturelle, L'Institut de Systématique, Évolution, Biodiversité, Paris, France

It is common among philosophers of science to hold that describing scientific categories as natural kinds can provide insights into the workings of classificatory practices. In this presentation, I show that while this might be the case, natural kinds-based approaches are nonetheless insufficient to account for the rich inferential processes that underly classification. I will focus my argument on phylogenetic systematics as a case study. More specifically, I will analyze how natural kinds-based accounts of the notion of homology deflect epistemological analysis of phylogenetic endeavours away from important inferential processes of the field.

To achieve this, I will present a typical workflow leading to the reconstruction of phylogenetic trees, which are in turn used to generate hierarchical classifications (Assis 2015; Farris 1983; Kapli, Yang, et Telford 2020; Kearney and Rieppel 2006; Rieppel 2015). Analyzing this inferential process shows that there is a variety of epistemologically important issues arising at every step. I will then review a natural kind accounts of the notion of homology based on the homeostatic property cluster theory of natural kinds (Assis et Brigandt 2009; Boyd 1999; Griffiths 2007; Pearson 2019), and show that it provides tools to analyze only a limited amount of these epistemic questions since they focus only on categories *per se*. This will help me conclude that alternative approaches to natural kinds theories (Brigandt 2020; Chang 2007; 2017; Ereshefsky and Reydon 2015) must be developed and pushed forward in order to provide a better understanding of classificatory practices in science.

Morphaesthesia, entelechy, and vitalism in early 20th-century biology

Ivan Loginov^{1,2}

¹Charles University, Department of Philosophy and History of Science, Prague, Czech Republic, ²Charles University, Center for Theoretical Study, Prague, Czech Republic

The questions of morphogenesis and regeneration bothered biologists and philosophers for generations. At the turn of the 20th century, many researchers considered the complexity of life unexplainable by contemporary mechanistic scientific methods and resorted to (neo)vitalism or at least some teleological explanation. To explain the regeneration in organisms, German embryologist Hans Driesch utilized the Aristotelian concept of *entelechy*. Although not as well known today, at the beginning of the 20th century, *morphaesthesia* was often quoted in connection to entelechy. It was coined by German botanist Fritz Noll in 1900, who defined it as the irritability of an organism (plant) due to perception of stimuli dependent upon its own body's shape and posture. Conceptually, he built on the terminology created by Austrian botanist Friedrich J. F. Czapek, who described plants' ability to perceive physical stimuli as -aesthesia (e. g., fotoaesthesia for light perception). Noll would not consider himself a vitalist per se, neither did he create the advanced philosophical background to situate his concept. Nevertheless, Driesch himself compared entelechy to morphaesthesia. Others tied those two terms together in texts, both criticizing and drawing inspiration from them. Morphaesthesia can be found mentioned by plant scientists, embryologists, psychiatrists, philosophers alike, from Eugen Bleuler to Bohumil Němec and Alexander Gurwitsch. Despite that, at some point, it disappeared from academic writing altogether. This paper aims to demonstrate and explain morphaesthesia in its contemporary context, compare it to Driesch's entelechy, and show its influence over later studies in morphogenesis.

The civic life sciences around 1900: Darwin's legacy in botany and agriculture

Giuliano Pancaldi¹

¹University of Bologna, Philosophy, Bologna, Italy

It has been argued, convincingly, that the botanical works to which Darwin devoted most of his efforts in the last two decades of his life were decisive in conquering him substantial scientific approval among his peers. It is likewise well known that the subsequent two decades were marked by momentous vicissitudes for Darwin's legacy, affecting both Darwin's evolution theory and the many varieties of Darwinism connected with fin de siècle nationalisms and colonialism. Historians seem to have neglected another thread potentially relevant for an understanding of the life sciences ca. 1900: Darwin's little-explored attempts to encourage the application of his views on the cross-fertilization of plants, hybrids' vigor, and selection to improve agriculture and prevent famine. Such attempts were concomitant with the rise of a figure that contemporaries occasionally described as "the civic scientist". This paper explores the work of researchers in botany and agriculture who, like Darwin, felt engaged in a civic mission vis à vis food production and famine prevention. It argues that the range of institutional, entrepreneurial, and political goals thus pursued may shed some fresh light on scientific change in the life sciences around 1900.

Keystone species in wildlife management

Derek Halm¹

¹University of Utah, Philosophy, Salt Lake City, UT

A keystone species' purported ecological role can justify reintroduction or heightened attention, depending on the conservation paradigm in use. However, for wildlife management, a distinct conservation paradigm, whether or not a species is a keystone is not necessarily meaningful for conservation; the keystone status of a species may not enter into conservation decision-making. To make sense of this, I survey several keystone species cases and use current Wildlife Action Plans to see what value the concept has for wildlife managers and to what extent it is used to justify conservation. Because the concept is applied inconsistently by wildlife managers, the keystone concept can be used to understand wildlife managers' values and conservation priorities.

Van Parijsian maximin principle in service of soil resource conservation

Vivek B Girija^{1,2}

¹M S Swaminathan Research Foundation, J R D Tata Ecotechnology Centre, Chennai, Tamil Nadu, India, ²BPTAbC-MSSRF, Bija Patnaik Tribal Agrobiodiversity Centre, Jeypore, Odisha, India

Phillippe Van Parijs propounded the maximin principle's novel variant as the maxi-min criterion, by maximizing it as "maximal, minimal competence". This "maximal, minimal competence" (lingua-franca understood minimally by a maximum number of people) characterized as the criterion, which minimizes effort or the one that offers the least laborious solution for enhanced communication between speaker and audience. Van Parijs also discusses the ego-centric criterion, which means expressing in a language that is more comfortable and most elegant for the speaker.

Situated in an uncertain socio-ecological/environmental system, farmers are facing the urgent need for implementing soil conservation practices. Should one, depend only on techno-fixes (ego-centric) or complementarily should use facilitative learning environments (Village Knowledge Centres - VKC) to hone the agent's cognitive-behavioural capabilities. Because, the cognitive-behavioural capabilities are the most persistently (across space & time), swiftly (continuous/instantaneous monitoring), accessible/available (least laborious/effort) and importantly observable.

Also, while emphasising the difference between the maximin principle and the maxi-min criterion, Van Parijs had discussed that the former is in response to "uncertainty". In contrast, the latter is used based on the "certainty" that as many numbers of agents are at the least minimally competent in using a particular tool. One could elaborate this distinction using the ecological rationality framework, i.e., the maximin principle addresses the uncertainty in the "structure of the environment" whereas the "Van Parijsian Maximin - VPM" principle seeks for utilising or nurturing the certainty of human cognitive-behavioural (CB) capabilities.

Further by using Van Fraassen's observable and unobservable distinction, I try to investigate how data, surface & theoretical models could inform the foundational models, i.e., the CB evaluation/decision models, through feedback between them. So, I propose the VPM principle, which is distinct from the commonly known maximin principle and it calls for the development of grounded evaluation and implementation tools for soil conservation.

Goethe's morphology, the development of plant systematics and the new science of evo-devo: Contributions to botany education

João Felipe Ginefra Toni^{1,2}

¹Friedrich-Schiller University of Jena, Faculty of Biosciences, Jena, Germany, ²Research Institute of the Goetheanum, Natural Science Department, Dornach, Switzerland

Goethe's morphological writings have been subject of reappraisal by several historians of biology and Goethean biologists. From a Goethean perspective, comparative morphology is not only descriptive but also explanatory, and complements molecular approaches in the study of Evolutionary Developmental Biology (Riegner 2013; Minelli 2018; Ledford 2018; Ginefra Toni 2018; Rutishauser 2018). Another related problem, namely, that the morphology practiced by Goethe could contribute to plant systematics should be also further investigated here. In 1794 Goethe implemented two gardens for his botanical investigations: one in his own house at Frauenplan in Weimar with the collaboration of the botanist and gardener Dr. Friederich Gottlieb Dietrich and the other one at the University of Jena in association with Prof. Dr. August Karl Batsch (Ahrendt & Aepfler 1994; Robin 2006). It was originally Goethe's intention to establish a new systematics, by writing a second essay on the metamorphosis of plants, in order to arrive at an inner relationship between the plant families through his morphological considerations. In his essay *Nacharbeiten und Sammlungen (Zur Morphologie 1820)* he describes further this purpose: "Through stimulating association with Batsch, the importance of relationships between plant families had become clearer to me and now Usteri's edition of Jussieu's work proved extremely useful" and later he reported that what he had undertaken was nothing less than: "... to present to the physical eye, step by step, a detailed, graphic, orderly version of what I had previously presented to the inner eye conceptually and in words alone, and to demonstrate that the seed of this concept (metamorphosis) might easily and happily develop into a botanical tree overshadowing the entire world " (Goethe 1989, p. 97). The present research project should enable, on one hand, a reassessment of the importance of Goethe's morphology to the systematics and evo-devo of flowering plants, and on another hand to develop a didactic activities using a Goethean garden as a place for teaching and learning such topics in botany.

To the victors the spoils: Anti-German sentiment in plant biology in the inter-war period as evidenced by textbooks

Thomas J McCloughlin¹

¹Dublin City University, DCU Science Archive & Herbarium, Dublin, Ireland

In the history of biology and botany, in particular, the 19th century was a golden age and in spite of the lack of a single German state, German-speaking scientists were pre-eminent in the major breakthroughs in understanding plant growth and development often with the invention and innovation in apparatus invention. As expected, textbooks of botany in the 19th century presented discoveries, innovations and inventions of German botanists by name. However, following the defeat of the German Empire in 1918, references to German botanists disappeared from textbooks and school textbooks in particular. The effect of this was that the history of botany was de-Germanised in the anglophone world. Furthermore, the German language ceased to hold esteem as a language of science, and German scientists were ostracized on the international stage. However, the picture is in fact more nuanced than summarised above. Anglo-German relations had been see-sawing in the latter 19th century, and the two “Great Powers” were both vying for international domination in Africa, and relations reached an all-time low in “peacetime” concerning the second South African (“Boer”) War (1899 - 1902). However, German science, especially in the area of botany was ascendant. Prior to the 19th century, a few scientists such as Junge (17th century) had established plants as worthy of study. von Sachs’ invention of the klinostat [sic] and his formulae of plant growth media, followed by Pfeffer’s recording auxanometer which led the way to understand plant growth, Eichler’s formalization of the structure of flowers - as influential in evolution as Haeckel; Fehling’s chemistry of organisms became de rigeur in biology. The de-Germanization of biology was never fully realized however since Fehling’s solutions continued to be known as such, but von Sachs became merely Sachs. Eichler’s work was never translated and side-lined - to the detriment of biology, and Haeckel is not given his due in the history of evolution and ecology. Evidence from the above assertions comes from a survey of anglophone textbooks from the 19th and 20th centuries. This paper recommends a revision in the teaching of botany, with a full history acknowledging the ethnicity of the innovators.

The Age of Biology: When plant physiology was the heart of biology

David Munns¹

¹John Jay College, CUNY, History, New York, NY

For much of the twentieth century, plant physiologists considered themselves in an ideal position to study and explain the functions and processes of plants. Much of that authority stemmed from plant physiologists long-standing commitment to experimental control and the integration of the physical sciences into biological practice. This talk places plant physiology back in the center of the story of the recent life sciences. It describes the development of parallel experimental research programs into environmental as well as genetic effects on growth and development in plant physiology. It notes that the pursuit of an experimental environment was as celebrated as much as (and occasionally more than) a molecular vision of life throughout most of the twentieth century by much of the plant science community. Thus talk argues that the history of the recent life sciences needs new complementary narratives of plant physiology with genetics, new concepts with technological tools, and plant-sized scales with the molecular. The history of the ‘Age of Biology,’ as the plant scientists saw it, helps confront the issue first posed by Evelyn Fox Keller, namely that the history of genetics has overshadowed a larger history of experimental life science. My answer here is through a larger narrative of the rise of the complimentary experimental sciences of genes and environments in the life sciences.

Timothy Lenoir's thesis and the rise of critical idealism in the mid-19th century: A reassessment

Ghyslain Bolduc¹

¹IHPST, Paris, France

One of the most influential and controversial theses in the history of biology is Timothy Lenoir's idea that a Kantian research program dominated the biological sciences in Germany from the turn of the 19th century to the 1860s. Lenoir have often been criticized for underestimating the gap between Kant's notion of formative force or "drive" (Bildungstrieb) as a regulative principle, and its constitutive use by the main representatives of the "teleomechanistic" approach, such as Johann F. Blumenbach, Johannes Müller and Karl E. von Baer. Commentators have mainly based their critiques on the early phases of teleomechanism, but rarely addressed the advent of "functional morphology" in the 1840s, the presumed death of the teleomechanistic program in the 1860s and its alleged "resurrection" with Hans Driesch's vitalism. In this talk I will intent to partly fill this gap. While Hermann von Helmholtz's physiological investigations were openly inspired in the 1850s by Kant's transcendental philosophy, did a "Back to Kant!" avant la lettre also have taken place in the morphological sciences of that time? I will argue that it was rather Hermann Lotze, who indeed integrated core ideas of Kant's Critique of the Power of Judgment in his own critical-idealistic system, that provided key heuristic principles such as "mechanistic teleology" to morphological research programs like Rudolph Leuckart's functional morphology and Hans Driesch's first program of experimental embryology (1890-1899). The relationship between Darwinism and these programs will also be addressed. The analysis of Driesch's vitalistic reform of the Kantian categories (1911) finally leads to a fruitful perspective on the fate in biology of Kant's reflection on the conditions of our knowledge of organic nature.

Scientific patronage in the age of Darwin: The curious case of William Boyd Dawkins

Henry-James Meiring¹

¹The University of Queensland, Institute for Advanced Studies in the Humanities, Brisbane, Australia

This paper examines the curious relationship between Charles Darwin and the palaeontologist William Boyd Dawkins (1837-1929). Dawkins was a beneficiary of Darwin's patronage and styled himself as a Darwinian to Darwin and the public, yet viciously attacked Darwin and his theory in anonymous reviews. This has confused historians who have misunderstood the exact nature of Dawkins's attitude towards evolution and his relationship to Darwin. The present study explains both the reasons for Dawkins's contradictory statements and his relationship with Darwin. I introduce Batesian mimicry as a conceptual framework to make sense of Dawkins's actions, suggesting that Dawkins mimicked a Darwinian persona in order to secure advancement in the world of Victorian science. Dawkins's pro-Darwinian stance, therefore, was a façade, an act of mimicry. I argue that Dawkins exploited Darwin for his patronage – which took the form of advice, support from Darwin's well-placed friends, and monetary assistance – while safely expressing his dissent from Darwinian orthodoxy in the form of anonymous reviews. This is, therefore, a case study in how scientific authority and power could be gained and maintained in Victorian science by professing allegiance to Darwin and Darwinism.

Biological individuals in a process ontology: An objection from biological practice

Adam C Smith¹

¹University of Utah, Philosophy, Salt Lake City, UT

David Nicholson and John Dupré (2018) have recently argued for a process ontology of biology. This view calls for a radical change in the metaphysics of biology, holding that the living world is not made up of things and substances, but of processes (i.e. activities) interacting with other processes which create entities that are stable over a period of time. For example, biological individuals under a process ontology are in a state of constant change and are constituted by the interactions of processes. Dupré and Nicholson contrast this with what they call the traditional view of substance ontology, where biological individuals do not change, do not rely on other individuals for their existence, and are constituted by substances (or things).

I will argue that modern biologists hold what I call a dynamic substance ontology, not the so-called traditional substance ontology. According to this dynamic substance ontology, biological individuals undergo changes, rely on other individuals for their existence to varying degrees, and are constituted by substances (or things). I will then argue that process ontology does no better than a dynamic substance ontology in explaining the three cases that Nicholson and Dupré use to support their process ontology: metabolism, life cycles, and ecological interdependence. Because process ontology does not improve upon the dynamic substance ontology currently used by biologists and comes with the high cost of completely altering the field's metaphysics, I conclude that Nicholson and Dupré have yet to offer sufficient reason for biology to switch to a process ontology.

Works Cited

Nicholson, Daniel J. & Dupré, John (eds.). 2018. *Everything Flows: Towards a Processual View of Biology*. New York, NY: Oxford University Press.

How to die slowly: Or, using process ontology to defend the whole brain definition of death

Anthony P Smith^{1,2}

¹Snow College, Department of English & Philosophy, Ephraim, UT, ²University of Utah, Department of Philosophy, Salt Lake City, UT

The President's Commission on Bioethics defines death as the cessation of functioning of the whole brain. James Bernat (and his colleagues) defends the Commission's definition by arguing that death occurs with the cessation of integrated biological function. The entire brain is responsible for controlling and maintaining this function. Death, then, occurs when the whole brain ceases to function. Bernat's account is not without its detractor. The most poignant of these criticisms is given by Alan Shewmon. Shewmon (and his colleagues) argues that such certain biological functioning can continue after the loss of whole brain function, like digestion and skin, hair, and nail growth. Such biological functioning occurring after whole brain death appears to be at odds with the notion that the whole brain is required for integrated biological functioning. In the most striking example, a pregnant woman properly diagnosed as brain dead was able to successfully maintain the pregnancy with the help of life support. It is difficult to say that a woman whose body is capable of maintaining a pregnancy is dead even if she is, technically, brain dead. As such, the whole brain definition of death seems to be medically and biologically inaccurate.

However, drawing from John Dupré and others' development of process ontology for biology such criticism can be dealt with. Just like integrated functioning is a biological process, death, too, is a process. Shewmon's criticisms rest on a substance ontology. Death on this prior ontology marks a substantial change in the person. Shewmon's criticisms raise worries that such a change has not occurred. However, in moving to a process ontology, no such worry occurs. Rather, death marks the end of a process, the processes involved in integrated bodily function, and the beginning of a new one, the breakdown of the body. This new process can be slowed or stalled through artificial means, but it cannot be reversed, nor can the old processes be restarted. The loss of whole brain function, then, defines death because the functioning of the whole brain is required to maintain the processes necessary to sustain life. The processes of integrated bodily function end when the whole brain ceases to function. Thus, process ontology provides the needed philosophical support for the standard medical definition of death—whole brain death.

Representing and intervening in built, biotic, social, and health processes in COVID-19 contexts

Hannah Howland¹

¹Pyatok, Applied Ecological Design, Oakland, CA

A transdisciplinary lens is applied to generate a process-based approach to representing and intervening in COVID-19 pandemic contexts. This process-view is located relative to recent conceptual developments that focus on social and environmental relations and the entanglement between biotic, social, built, and health processes. It is argued that a new conceptual infrastructure is necessary to adequately represent ‘unacknowledged process-intersections’ between biotic, built and social processes, and that such an infrastructure can be used to develop new methods for equitable data-generation, modeling, and resilience-promoting interventions. Two performative goals are presented: First, how to conceptualize a transdisciplinary approach to adequately represent complex, dynamical relations; Second, how to intervene in COVID-19 environments. To address the first goal, a relation-based modeling approach (RMA) is presented. RMA is used to analyze the complex relations within COVID-19 pandemic contexts, in order to show the entangled and co-regulatory relationships between built environment processes (BEP’s), biotic/ecological processes (EP’s), social processes (SP’s), and health processes (HP’s). RMA draws on concepts and methods from architecture and design, philosophy, sociology, systems biology, ecology, and public health—notably, drawing on relational approaches such as, ‘place perspectives’, ‘affordances’, and Leopold’s ‘land ethic’. RMA is visualized in a series of diagrams, showing built, biotic, social, and health contexts as overlaid interfaces that regulate process pathways. RMA is used to illuminate ‘unacknowledged process-intersections’, where inequitable built environments and environmental racism in social processes moderate biotic and public health processes. This transitions into the second performative goal. A case study of airflow processes and inequitable access to biotic resources is presented in order to show how adequate representation can lead to effective interventions. The point is to show how complex, dynamical representations of COVID-19 contexts can be approached through precise, ‘difference-making’ interventions. The focus of these interventions is not top-down, but rather it is co-mediating. By presenting how built environments can co-mediate along with biotic and social processes, the autonomy of biotic and social processes is recognized as a necessary conceptual consideration for shaping COVID-19 environments.

Biological clocks and the epistemology of multiple lines of evidence

Katherine Valde¹

¹Wofford College, Philosophy, Spartanburg, SC

Biologists rely on indirect measures, such as the accumulations of genetic mutations (the "molecular clock") or fossil locations in layers of sediment (the "biostratigraphic clock"), to infer temporal information about events in the deep past. Unfortunately, each of these biological clocks can only provide partial and imperfect information. For example, the fossil record is known to be incomplete and biased in various respects. Similarly, while statistically speaking neutral mutations can accumulate in DNA sequences at predictable rates, understanding neutral mutations or how often they occur in actual populations poses substantial difficulty. This talk will explore how these methods work, the ongoing process of refining them, and the lessons we can learn about evidence from this case study.

One key challenge is that these molecular and biostratigraphic clocks don't always agree (i.e. they are discordant). Notably, they fail to agree for some key events such as dating the divergences of avian birds, vascular plants, and placental mammals. Since both of these methods have important limitations, scientists have started using them in conjunction with one another to develop even better date estimates. Understanding the reasons for these disagreements allows scientists to identify assumptions that go into the reading of these molecular and biostratigraphic clocks. This process of trying to synchronize and recalibrate allows scientists to generate improved systems of time telling. Although these clocks might never have read time correctly, through iterative recalibration scientists are able to improve these biological clocks, even in the absence of a reliable independent standard.

This story seems to contradict some of the received view on the epistemic importance of multiple lines of evidence. Some have argued that discordant lines of evidence cannot be jointly epistemically useful (Stegenga 2009), and other have argued that different lines of evidence need to be independent in order to be jointly epistemically useful (Wylie 1999; Forber and Griffith 2011; Stegenga 2009). I will argue, using these biological clocks as a case study, that discordant lines of evidence can jointly support a single hypothesis, and that interdependent lines of evidence can jointly increase the reliability of a particular hypothesis.

The generative failures of the central dogma coordinate un-making of epistemic kinds

Alok K Srivastava¹

¹Independent Scholar, -, San Francisco, CA

The late Richard Boyd developed the concept of Homeostatic Property Clusters (HPCs) in a 1979 paper. I will use Boyd's construction to explore the many generative failures of The Central Dogma of Biology after it was first proposed by Francis Crick in 1958. The Central Dogma diagrams the relations between molecular kinds presumed to be at the heart of the physiology of cells. It was built using the notions of information and code coming from linear sequences of common written languages and the early formalisms of computing machines. This diagram was used to coordinate studies of molecular physiology of cells in organisms. However as research programs progressed, surprises became salient and several non-conforming kinds with alternative homeostatic property clusters (HPCs) were characterized. Virus genomes coded for Reverse Transcriptase Polymerase Enzymes to transcribe their RNA genomes into DNA. Nuclear RNA could act as catalytic enzymes. Genes were interrupted with sequences that have to be edited by protein-RNA complexes so that edited mRNA could produce functional proteins. Non-coding RNAs have gene regulatory roles. Sahotra Sarkar collects several similar cases in his 1996 paper "Decoding 'Coding': Information and DNA".

The Central Dogma has functioned like a book-keeping device in the growth and evolution of research projects in the community of molecular biologists. Its book-keeping of epistemic kinds encountered in experiments has made salient novel and aberrant kinds. The marking of novel constellations of property clusters un-made the most recent conventions of epistemic kinds. This historical record of repeatedly un-making previous epistemic kinds serves to historicize the epistemic spaces of molecular biology research programs.

In this paper I will explore how the discursive and material practices of a community of practice—Molecular Biologists in this case—are regulated by the materials being studied in their research programs. The discursive and epistemic practices encoded in The Central Dogma had to be repeatedly re-worked to accommodate the breakdowns in the conventionalized HPCs of its epistemic objects. I will use this historical landscape of surprises to conceptualize the inter-regulation between discursive and material practices in communities of scientific practice.

Entangled histories: karyotyping and population genetics in Cold War Mexico: Armendarés's and Lisker's characterization of child and indigenous populations, 1960s-1980s

Ana Barahona¹

¹UNAM, Evolutionary Biology, Mexico City, Mexico

This paper focuses on Mexican geneticists Salvador Armendarés's and Rubén Lisker's studies from the 1960s to the 1980s, to explore how their work fits into the larger tapestry of post-1945 human biological studies, and also how the populations they studied, child and indigenous, can be considered laboratories of knowledge production. This paper describes how populations were considered specific entities for different purposes: scientific inquiry, the standardization of medical practices, and the production or application of medicines. Through the narrative of the different trajectories and collaborations between Armendarés and Lisker, this paper also attempts to show the contact of their scientific practices, which brought cytogenetics and population genetics together at the local and global levels from a transnational perspective.

Don't deny it: Invasive species

James Russell¹

¹University of Auckland, Biology & Statistics, Auckland, New Zealand

Invasive species are the leading cause of species extinctions on islands and the third highest ranked threat for extant species. Thousands of species have been wiped from the face of the earth by invasion. With such clear evidence of determinantal impact to species richness vis-à-vis biodiversity, why is this form of global change not more greatly acknowledged? The answer lies at the turbulent interface of science and values traversing zealousness through indifference, disagreement and outright denial. Drawing on my motivation and experience as a conservation biologist in New Zealand, the last major archipelago in the world colonised by humans, I will lay out the case for invasive species control if not eradication, drawing broadly from the natural and social sciences, culminating in the case for a Predator Free New Zealand. The arguments raised include consideration of welfare and rights of, and duties and responsibilities to, the varying ecological collectives of individuals, populations, species and communities, while weighing the consequences of human action versus inaction. Debate on these topics is often inconclusive, but the practical actions required nevertheless seem starkly obvious.

The rediscovery of arguments for biotic colonialism

Christopher H Lean¹

¹Dalhousie University, Philosophy/ Biochemistry, Halifax, Canada

Recently, there has been increasing scepticism towards the control of invasive species. This has not simply been an academic debate, there has been strong criticism of Predator-Free New Zealand and Australia's Feral Cat policies, particularly by USA and UK-based academics. While many of the arguments against controlling invasive species were originally on animal welfare grounds, a new form of argument built around normative economic assumptions has emerged. This is what I have referred to as ecological neoliberalism. The position that we should not control the free movement of species. When species can move and interact with new ecological systems, they create novel ecosystems. These novel arrangements create experimental markets in nature's economy, providing opportunities for the efficient production of goods for humans (ecosystem services). When invasives supersede local populations, it indicates previous biotic systems were inefficient, which is why they were replaced, and therefore it is wrong to protect indigenous 'losers' from extinction. In this talk, I will indicate how this argument recreates many of the key assumptions that grounded the initial introduction of European species to Australasia by 19th-century acclimatisation societies. Using historical records of the arguments forwarded by the Victorian Acclimatisation society before the introduction of rabbits to Australia, I will show how modern critics of invasive species control have converged on the original position of biological colonialism.

How to stop arguing about invasive species

Emily C Parke¹

¹University of Auckland, Philosophy, Auckland, New Zealand

Global debates about invasive species have come to a head recently with some extreme positions regarding skepticism or denial of invasive species' impacts. A problem with these debates is that they often fail to rest on clear shared assumptions about what qualifies as 'native' and 'invasive', and why we value or disvalue these populations, respectively. This has led to confusion and people talking past each other, on matters terminological, conceptual, empirical, social, ethical, and cultural. Which populations qualify as 'native' and 'invasive', and associated value judgments and conservation decisions, are often quite contextual and nuanced. This gets glossed over in some attempts to pass high-level generic judgments about invasive species and their impacts (or lack thereof).

While clarifying the terminological and conceptual foundations of invasion biology is important (for example, in the interest of prediction), I suggest that certain aspects of these debates would be more productive if we set aside the 'invasive versus native' framing, and instead zoomed in on the underlying issues, which are a tightly interwoven mix of science and values. Using the Predator Free New Zealand movement as a guiding example, I suggest some strategies for capturing important nuances, and clarifying some more reasonable stances for those inclined towards invasive species skepticism.

Selection of as selection for: Linkage disequilibrium and fitness

Marshall Abrams¹

¹University of Alabama at Birmingham, Philosophy, Birmingham, AL

Elliott Sober's well known distinction between *selection for* and *selection of* is a generalization of *genetic hitchhiking* due to linkage disequilibrium (LD). If trait T₁ is fitter than competing trait T₂, and most individuals with T₁ happen to have an unrelated neutral trait U₁ rather than alternative trait U₂, then there will be *selection for* T₁ over T₂, but only *selection of* U₁ over U₂. If A and B are two loci with respective alleles A₁ and A₂, and B₁ and B₂, we say that their alleles have a high level of LD when the frequencies of e.g. B₁ among A₁ individuals is greater or less than would be expected if the alleles had been randomly combined. If A₁ usually produces fitter phenotypes than A₂, but the B locus is neutral, then B₁ may "hitchhike" to a higher frequency due to selection on A₁. In Sober's terms, again, there is selection for A₁ but selection of B₁. This kind of influence can occur even if B is not neutral.

These facts fit poorly with the common assumption among philosophers of biology that causal fitness properties are based on properties of particular token organisms. Linkage disequilibrium or trait correlations are fundamentally population-level, since correlations between alleles or traits can only be defined in terms of a population. This is one reason why views like those of Pence and Ramsey, who define fitness for token organisms in terms of probabilities of representation in future generations, turn out to depend on population-level properties.

This particular challenge can be avoided by views that treat allele fitnesses that are causally relevant to evolution as, fundamentally, properties of populations in environments. However, hitchhiking still presents a challenge for such views, if trait fitness depends on probabilities of future interactions with conspecifics, since others' traits may be influenced by LD between selected loci rather than effects of alleles themselves. This makes allele fitness a function of loci that are unrelated, i.e. without epistatic interactions.

However, if trait fitness is a population property, we can understand an allele B₁ in LD with an allele A₁ at another locus as having—in addition to the usual influences on phenotypes—a relational property due to correlation with A₁, giving B₁ an additional component of fitness via its relation to A₁. Seeing LD as generating such "linkage fitnesses" treats hitchhiking in terms of well-known phenomena of pleiotropy and epistasis. Similar points can be made about Sober's distinction.

Finkish trait types and the propensity interpretation of fitness

Ryan Kulesa¹

¹University of Missouri, Philosophy, Columbia, MO

The propensity interpretation of fitness – from here on, PIF – is a popular way of understanding the fitness of a trait type which, under certain views (Brandon 1978; Beatty and Mills 1979; and Pence and Ramsey 2013), roughly asserts that, given a certain environment, a trait type will lead to an average expected number of offspring. As suggested by the foregoing definition, propensities in this view are probabilistic dispositions. In other words, in some environment, the fitness of a trait is its disposition to produce, on average, a certain number of offspring.

The literature on issues presented for conditional analyses of dispositions has been surprisingly neglected. In particular, finkish dispositions provide counterexamples to understanding dispositions as conditional causal statements. In this paper, I suggest that an example of plant disease and resistance genes provide instances of biological finks with regard to trait fitness, thereby providing counterexamples to PIF. In short, I argue, the statement ‘if an organism, x , is in environment, E , then x will produce O number of expected offspring’ is false; thus, PIF cannot accurately determine fitness values in biological fink cases.

Roughly, barley with a particular set of disease resistant genes has a disposition to produce a certain average number of offspring in E , which it in fact does not produce given the presence of typically harmless microbes on its leaves surface. Since the barley has a disposition to produce a certain average number of offspring in E which it does not actually produce once in E , barley with disease resistance genes provides an example of a finkish genotypic disposition.

The practice perspective on the inclusive fitness theory debate and its implication

Jinkwon Jun¹

¹Myoung-Ji University, General Education, Seoul, South Korea

According to the traditional view, scientific theory is considered well-organized and unified. However, the recent controversy surrounding the inclusive fitness theory, which is difficult to organize in a single way, shows the limitations of the traditional view. This presentation suggests the practice view as an alternative. Here, “practice” refers to the action of a scientist, and the practice view emphasizes that the non-verbal and non-propositional contents are also important for understanding scientific theory. Following this perspective, W.D Hamilton's theorizing practice of inclusive fitness theory was analyzed. The result shows that the theory has a multi-layered structure, and its inherent complexity opens up a variety of interpretations. In the end, it turns out that many of the problems raised in the debate arise from the confusion of the layers of interpretation. Clarifying these confusions will be the starting point for resolution. In conclusion, it is recommended to change the traditional view to a practice view on the inclusive fitness theory debate.

From bottom-up: Adaptive act and rule-empathy, game theory and morality

Luciana Garbayo¹

¹University of Central Florida, Philosophy and Medical Education, Orlando, FL

In this work I propose a naturalistic dual theory of empathy as act-empathy and rule-empathy associated fundamentally to the prosocial phenomena of cooperation, grounded in both distal (evolutionary) and proximal (psychosocial) types of explanation. I discuss how standard and evolutionary game-theory, in the context of philosophy of biology, might allow us to consider empathy as having strong adaptive and developmental components, and how it might impact other events, such as the emergence of social norms and ethical communication, modeled in signaling games. I suggest that empathy might be interpreted as the disposition that enables us to be aware of other players' utilities and strategies in the context of interaction. It manifests itself by the variable ability to put oneself on the place of others. When other-regarding, it implies sharing the "utilities" of another player. The continuum between two types of empathy in the context of a game is a crucial one to consider the transition from merely understanding others to cooperating with them or not. The first is regarding empathic pre-reflective players – and the range of their possible games they are constrained to – and the second, is regarding empathic reflective players, who expand on the possible ranges of games to be played, cooperatively. In the case of pre-reflective players, I suggest a rule-following modality of adaptive rule-empathy is mainly operative, founded distally in the Hamiltonian rule for kin selection, meaning, to the preference for closest kin, and in past record of reciprocity. As such, agents may tend to reinforce norms of conformity and coalition formation in cooperative games, by strengthening parochial sympathetic preferences. In the case of empathic reflective players, I propose a quasi-spontaneous act-empathy is mainly operative through the pursuit of improved communication. Such behavior would be founded in a non-specified cooperative inclusive altruistic interest of the individual (no kin target), leading to the understanding of moral strangers and to cooperating on what should be the rules to be applied in any game, in order for it to be potentially normatively inclusive.

Organic circuits, biological complexity, and moral obligation

Michael Stingl¹

¹University of Lethbridge, Philosophy, Lethbridge, Canada

Collier and Stingl (2020) argues that moral values are regularly recurring structural features in the environments of creatures that are both social and intelligent. This means that the human moral sense is not simply the result of the right mutation in the right environment, or of the right series of the right mutations in the right environments. But according to Agosta and Brooks (2020), the Hardened Synthesis assumes that this is mainly how evolution works. Agosta and Brooks go on to argue that the Hardened Synthesis is importantly wrong about how evolution works. On their alternative model of evolutionary processes, the Collier and Stingl approach to morality is much more plausible as an empirical approach to morality than it otherwise might be. This paper looks at the main arguments of both books, in combination, to see what they might tell us about what moral values really might be. Since moral values without moral obligation would seem to be morally inert, this paper will move beyond Collier and Stingl to develop a more careful biological approach to the concept of moral obligation. Its main conclusion will be that we cannot understand what moral obligation is without first understanding what in fact moral values are.

Agosta, Salvatore J., and Daniel R. Brooks. 2020. *The major metaphors of evolution: Darwinism then and now*. Switzerland: Springer Nature.

Collier, John, and Michael Stingl. 2020. *Evolutionary moral realism*. London: Routledge.

Evolutionary psychology of moral *phenomenology* works fine: A conceptual defense, and empirical support

Sam J Woolley¹

¹The University of Auckland, Philosophy, Auckland, New Zealand

Some writers have argued that explanations of morality treating it as a biological adaptation fall flat, lacking conceptual clarity and/or empirical rigour.* Sometimes, this is because what counts as “morality” is characterised idiosyncratically, and so it doesn’t stack up against our intuitions when it comes to assessing what counts as a “moral” (as opposed to “non-moral”) judgement, value, or norm. In other cases, it’s because a characterisation that appropriately captures how and when we make “moral” judgements (for instance) is so strange a phenomenon to try to explain that it lacks the kind of empirical support needed to justify its status as a biological adaptation. It might even be unclear what could support that claim, a criticism oft-levied at ‘unfalsifiable’ evolutionary psychological accounts.

I argue we can have it both ways. We can characterize morality in such a way that we preserve what we (most of us, anyway) actually care about regarding moral claims, values, and norms, by appealing to the phenomenology of morality – the first-hand experience of issuing moral judgements; holding a moral value; acting according to a moral norm – as opposed to the typical content of those kinds of judgements, values, and norms. But, we can also give a plausible empirical account in support of the claim that moral phenomenology is a biological adaptation – that being able to feel the way we feel when issuing moral judgements, say, very likely had reproductive benefits for those humans who could versus those humans who could not. I draw mainly on anthropological cross-cultural accounts of moral psychology, the child developmental literature, to support this claim.

* For an example of the former, see J. Prinz, "Against Moral Nativism," in M. Bishop and D. Murphy (eds.), *Stich and his Critics* (Malden, MA: Wiley-Blackwell, 2009): 167-189 (168); for the latter, see E. Machery and R. Mallon, “Evolution of Morality” in J. Doris (ed.), *The Moral Psychology Handbook* (Oxford: Oxford University Press, 2010), 3-46 (20-36).

The social unit: What kinds of individuals can be social?Lucia C. Neco¹¹University of Western Australia, School of Humanities, Perth, Australia

Interactions are being chiefly used as components in descriptive models of social complexity. Their use opens a discussion about expanding the spectrum of individuals that we would consider to be social, usually restricted to animal organisms. This expansion introduces the need to clarify the actors, the structure and the processes involved in social behavior. In this paper, I propose an account of “social individuality” that would be useful to identify the interacting individuals in a social system, the social units. To do so, I first consider the literature on biological individuals. Given its pluralistic nature, I will discuss helpful definitions to identify the social individuals, in particular. I then analyze the concept of organism and argue that autonomy is the best criterion to identify the interacting individual in a social system. Since sensing and responding to the world would be necessary features of social interaction, cognition seems to be a key concept to understand the autonomy of the social individuals. Accordingly, I develop an account of cognitively autonomous individuals arguing for two complementary definitions that describe the organization of a cognitive cohesive unit and its function. I conclude that social systems must be composed of cognitively autonomous individuals, their social units. This opens the possibility of entities other than animal organisms to be social units and unlocks more questions about the nature of sociality.

Biological individuality and the intentional stance

David Kelley¹

¹University of Auckland, Philosophy, Auckland, New Zealand

The subjects of biological individuality (within the philosophy of biology) and group agency (within moral and political philosophy) can be mutually informative - for example, when each is used to challenge the presumptions of the other.

Pre-theoretically, in the case of group agents (e.g. corporations), we have no need to remind ourselves that the lower level units (i.e. people) are themselves agents. This is because, from our vantage, individual agents are paradigmatic agents.

Pre-theoretically, in the case of biological individuals, we have no need to remind ourselves that e.g. a multicellular organism is an individual in addition to the individual cells that comprise it. This is because, from our vantage, the multicellular organism is a paradigm individual.

What I will call “the multilevel intentional stance” (following Dennett) is ubiquitous yet largely invisible in our everyday reasoning about groups and individuals in society. Yet when imported into our theorizing about biological individuals, it becomes natural to conceptualize individuality as a group achievement more or less maintained to the extent that incentive structures remain compatible among biological agents, some nested within others.

With a plurality of biological “individuals” currently on offer within the philosophy of biology literature, a focus on multi-level agency may offer a fresh perspective and supplement existing explanations of biological individuality which otherwise seem lacking.

Some reflections on bringing the problem of biological individuality into the field of health sciences

Fiorela R Alassia¹

¹National University of Patagonia San Juan Bosco, Department of Chemistry and Department of Pharmacy, Comodoro Rivadavia, Argentina

Within the philosophy of biology, some questions around the concept of biological individuality have been extensively worked. In a recent work, Kaiser and Trappes (2021) claim that it would be necessary to broaden this philosophical agenda to include other questions that have not been sufficiently addressed, such as the philosophical questions about biological uniqueness and temporality. In many research areas of biology, questions are raised about what underlies the differences between individuals and what makes a biological individual unique. Many of these issues concerning biological individuality are also of interest in the framework of human health sciences (medicine, clinical laboratory, biochemistry, pharmacology, etc.). Then, it becomes necessary to clarify these concepts and their relationships with scientific problems, such as the causes of biochemical individuality, the distinction between healthy-diseased individuals, or the interpretation of reference values in light of precision medicine, among others. This work aims to bring the philosophical discussion of biological individuality into the field of health sciences to show why and how these issues are important in these disciplines.

The biogeographic origin debate in invasion biology: Ecological science and conservation values

David M Frank¹

¹Brown University, Philosophy, Providence, RI

Invasion biology is the field of ecology and conservation biology that interacts with introduced and invasive species. Introduced species are usually biogeographically “non-native,” requiring anthropogenic or human-aided dispersal to cross geographic barriers, and those introduced species that have undesirable economic, environmental, or public health effects are usually those labelled “invasive.” Critics of invasion biology often point out that native species can also become ecologically problematic weeds or pests, and furthermore that most introduced species fail to establish, and of those that do establish, only a small minority become invasive. Some of these critics go further, arguing that the field’s emphasis on biogeographic origin—the risks of introducing non-native species—is questionable on scientific and ethical grounds. This presentation will evaluate arguments for and against the relevance of biogeographic origin for decision-making in invasion biology, distinguishing debates in ecological science and biogeography from concerns that stem from diverse conservation values, especially risk attitudes, the value of ecological diversity and ecological novelty. I argue that a nuanced view about the relevance of biogeographic origin for decision-making about introduced species is warranted.

Invasion biology and ecological networks

Karen Kovaka¹, Jacob Barney², Brian Badgley², Bryan Brown², Willandia Chaves³, Todd Schenk⁴

¹Virginia Tech, Philosophy, Blacksburg, VA, ²Virginia Tech, School of Plant and Environmental Sciences, Blacksburg, VA, ³Virginia Tech, Fish and Wildlife Conservation, Blacksburg, VA, ⁴Virginia Tech, School of Public and International Affairs, Blacksburg, VA

Most studies in invasion biology focus on the effects that a single invasive species has on a single (or very few) native species. This approach fails to capture the real-world complexity of biological invasions. Specifically, it does not account for the community context into which invaders are inserted, nor the compounded effects of multiple invading species across multiple scales. Our project is to develop an alternative approach, one that views invasive species as members of a dynamic ecological network that collectively shapes the pools and fluxes of matter and energy. In this talk, we argue that modeling strategies from community ecology can be used to understand the ecological networks of invaded systems that span levels of biological organization, and to identify emergent properties of these systems. We also show how our network-centric approach can speak to controversies about (a) evidence in invasion biology, (b) the impacts of invasions, and (c) policy and management strategies.

Owls and old-growth: A philosophical examination of a conflict

Jay P Odenbaugh¹

¹Lewis & Clark College, Philosophy, Portland, OR

In the Pacific Northwest, a variety of scientific and ethical controversies surround the northern spotted owl. I consider the recent interspecific competition between the northern spotted owl and barred owl. The latter was mostly likely introduced by human activity into old growth temperate rainforests where it outcompetes the former. The northern spotted owl is a threatened subspecies of the spotted owl that is protected under the Endangered Species Act (ESA). It is also an indicator species of old growth forest, and thus its being listed under the ESA is thought to be especially crucial to protecting old growth. In the 2000s, the U. S. Fish & Wildlife Service conducted removal experiments killing the barred owl to conserve the northern spotted owl. These experiments have stabilized and sometimes increased in population size of the northern spotted owl. However, many people question the morality of perpetually killing of one owl to save another. I argue that we should be directly protecting endangered ecosystems such as old-growth temperate rainforest for a variety of pragmatic reasons. For example, this would reduce the labor in creating species by species habitation conservation plans. This would have as a side-effect eliminating the need to kill the barred owl to save old-growth forest. But it raises questions about the nature of ecosystems and biomes; most importantly, in what sense can a kind of ecosystem – a biome – be endangered? In this talk, I sketch the above argument and provide an account of how biomes can be endangered.

Converging histories in the Anthropocene

Jason M Zinser¹

¹University of Wisconsin - Stevens Point, Philosophy, Stevens Point, WI

A proposal to designate a new geological epoch, the Anthropocene, has been approved by the Anthropocene working group and is working its way to a final vote by the International Union of Geological Sciences. This is not to say that the proposal is without criticism. Santana (2018) argues that present stratigraphic changes do not meet the threshold for demarcating a new epoch. The effects of climate change and other anthropogenic activities reflected in the geological record may eventually warrant a designating a new epoch, Santana argues, but only future geologists would be in a position to know if these changes will be “set in stone,” or if they will be mitigated or reversed.

I will respond to Santana’s criticisms in a two-fold manner. First, I will outline a counterfactual account of the scientific designation of the Anthropocene by arguing that given the global trajectory of greenhouse gas emissions, along with the stratigraphic markers already present, we are at an inflection point in geologic history, worthy of a new designation. A second, and related, strategy is to identify that the extant stratigraphic changes, while perhaps not significant enough to warrant a change on their own merits, were caused by a novel geological force, and as such could justify designating a new epoch. Clearly, we are not the first species to change earth history, earth systems, atmospheric chemistry, or the stratigraphic record. However, we are the first to knowingly do so, and I argue that this distinction is significant. To borrow from Santana, in order to understand the geological history of earth, future geologists will not only have to understand traditional causal forces, such as those that have shaped previous chronostratigraphic delineations, but also the politics, science, and psychology of a curious species of primates. Finally, the recognition of human agency as a geological force will collapse a distinction, articulated by Collingwood (1936), that natural history should be conceptually separate from human history. Chakrabarty (2009) argued that the Anthropocene means that human history is now conceptually intermingled with natural history. I extend this view by arguing that natural history, too, cannot be separated from human history.

The logic of biological proxies

William C Bausman¹

¹University of Wisconsin, Madison, Philosophy, Madison, WI

Given the turn to the epistemology of scientific practice, it has been fashionable to disparage the Logical Empiricist's context of discovery vs. justification distinction. But these ideas are useful for the practice of science.

Biologists use proxies to learn about inaccessible parts of the world, but we haven't paid much attention to how they do it. They use tree rings as proxies for past temperature based on conditions favoring and disfavoring growth. Alfred Russel Wallace used the long nectary spur of an orchid from Madagascar as a proxy to infer that a pollinator moth with a long proboscis sucks it based on adaptation by natural selection. Here I focus on a contemporary case study of fossil teeth as a paleoclimate proxy.

Using Reichenbach's original context of discovery vs. justification distinction (why people believe something vs. whether they should believe it) I argue that scientists do and should consider the context of justification of their work while operating in the context of discovery. While the justification for trusting the decisions of scientists is not based on the reasons the scientists used for making those decisions, scientists do well to consider the potential justification of their approach in their decision making. While reconstructing how proxies are established and used, I suggest how to modify the logic of justification to concern practices using Chang's idea of operational coherence.

Can genuine altruism evolve or are we condemned to egoism? The case for (and against) the evolution of psychological altruism

Jorge Piaia Mendonca Junior¹

¹The University of Western Australia, Philosophy, Perth, Australia

Altruism is a term with multiple meanings. In everyday language, we use it to refer to certain motivations to help others. The notion of psychological altruism aims to represent this motivational account, defining altruism in terms of ultimate desires to increase the welfare of others. By contrast, in evolutionary altruism, this motivational character is detached from altruism — evolutionary altruism is defined purely in terms of the lifetime direct fitness consequences of behaviors. Given that these two kinds of altruism are independent of each other (the existence of one does not imply the existence of the other), research on one kind usually does not have much to say about the other. Evolutionary biology offers a sophisticated discussion on evolutionary altruism, while the arguments supporting psychological altruism are often based on a priori reasoning or empirical research in social psychology, with inconclusive results. However, in this paper, I will address psychological altruism from an evolutionary perspective. Psychological altruism can be seen as a proximate mechanism, and, as such, it is also subjected to natural selection. The strategy of addressing psychological altruism from an evolutionary point of view was recently adopted by authors arguing for the claim that we humans are capable of genuine altruistic motivation. I discuss the most influential arguments and the criticism directed towards them. I argue that the flaws we see in these evolutionary cases for psychological altruism are no evidence of a selfish nature. They follow from the fact that we restrict psychological altruism to ultimate desires. I will argue against this emphasis on desires, showing that we can justifiably define psychological altruism in terms of other motivational states, such as emotions. If we do so, the criticism against the evolution of psychological altruism, which is compelling, becomes much weaker. Perhaps much of the difficulties in supporting psychological altruism might follow from the overly restrictive definition which accounts only for ultimate desires.

Cultural evolution in the court: Ontological imposition and downstream harm

Andrew Buskell¹

¹University of Cambridge, Department of History and Philosophy of Science, Cambridge, United Kingdom

The reflexive turn in anthropology was a critical project that drew attention to how the perspective of the anthropologist—typically a Western-trained white male whose work spoke to academic audiences—was built into the concepts and distinctions used and the objects they purported to study. One aspect of the critique was the claim that “culture” and “cultures” were not objects in the world waiting to be discovered, but constructs imposed upon different peoples. The corollary to this was that such impositions were metaphysically, ontologically, and empirically wrongheaded.

My focus in this paper is on how this plays out for “cultures”—understood as a class that gathers specific “cultural groups” as instances. The overall aim is to identify *ontological imposition* as a distinctive kind of problem—one that has pressing implications for real-world populations. To show this, I employ a historical case study drawing on the influence of Julian Steward on judicial decision-making in what is now North America. Steward's work on “sociocultural integration” postulated distinct kinds of cultural groups—and he and later researchers used this framework to argue against Indigenous groups in title and rights cases. As I argue, cases like this should motivate researchers to shift focus from metaphysical issues (typically around essentialism) that have dominated the theoretical literature on “cultures” to focus on ontological ones. Because of the potential for downstream harm, greater attention is needed on how ontologies of “cultures” are constructed and applied to populations across the sciences, humanities and policy spheres.

Cows, COVID and concerns: Why is the history of vaccination hesitancy repeating itself?

Marietjie M Botes¹

¹University of Luxembourg, SnT Interdisciplinary Centre, Luxembourg City, Luxembourg

Despite advances made in vaccinations, people are still hesitant to get vaccinated against COVID-19. History is merely repeating itself since Dr Jenner successfully vaccinated the first patient against “cow” pox 225 years ago. Like the scepticism with which some of the COVID vaccines has been received, Dr Jenner’s smallpox vaccine was similarly scoffed at and initially not accepted. But regardless of these tribulations the WHO declared smallpox eradicated from the face of the Earth 150 years after Dr Jenner’s death. But why could vaccine hesitancy not be resolved since then and in light of this success?

Considering the origins of vaccines and that COVID-19 and many other infectious diseases with pandemic potential originated from wild animals, it is necessary to contextualise the importance of the interdependence between human and animal vaccinations, including the repercussions of the extended use of the BCG tuberculosis vaccination that led to the death of more than a hundred children resulting in the landmark Lübeck court case. Despite scientific developments vaccines continued to be met with defiance from the 1700’s until now by anti-vax sentiments, which gained serious momentum during the so-called MMR vaccine saga.

Depending on social and epidemiological conditions, mathematical models indicated that social norms can either boost vaccine coverage or drag it below levels that are optimal either from a social perspective or from the perspective of a purely rational individual who is not influenced by social norms. If social pressure is strong enough, a temporary vaccine scare caused by heightened risk perception can be transformed into an extended period of depressed vaccine coverage. An exploration of how social norms interact with interventions such as public health messaging strategies may play a decisive role in the successful management of COVID-19. Social media platforms give the public a voice to exchange information, and the most common sources of vaccine information are often non-experts. The false information pandemic that followed on the heels of COVID-19, and was even criminalised in some countries, may also be to blame for vaccine hesitancy in the current climate. Science communication needs to be aligned with all these complex socioeconomic issues to have real value and impact – to prevent future disease outbreaks.

The future of sperm: A biovariability framework for understanding global sperm count trends

Sarah S Richardson^{1,2}, Marion Boulicault^{3,4}

¹Harvard University, Department of the History of Science, Cambridge, MA, ²Harvard University, Studies of Women, Gender, and Sexuality, Cambridge, MA, ³MIT, Department of Philosophy, Cambridge, MA, ⁴University of Adelaide, Department of Philosophy, Adelaide, Australia

The past 50 years have seen heated debate in the reproductive sciences about global trends in human sperm count. In 2017, Levine and colleagues published the most methodologically rigorous and largest meta-regression analysis to date and reported that average total sperm concentration among men from “Western” countries has decreased by 59.3% since 1973, with no sign of halting. These results reverberated in the scientific community and in public discussions about men and masculinity in the modern world, in part because of scientists’ public-facing claims about the societal implications of the decline of male fertility. We find that existing research follows a set of implicit and explicit assumptions about how to measure and interpret sperm counts, which collectively form what we term the Sperm Count Decline hypothesis (SCD). Using the study by Levine and colleagues, we identify weaknesses and inconsistencies in the SCD, and propose an alternative framework to guide research on sperm count trends, the Sperm Count Biovariability hypothesis (SCB). SCB asserts that sperm count varies within a wide range, much of which can be considered non-pathological and species-typical. Knowledge about the relationship between individual and population sperm count and life-historical and ecological factors is critical to interpreting trends in average sperm counts and their relationships to health and fertility.

Understanding biological sex pluralistically

Natasha M Haddal¹

¹University of California, Davis, Philosophy , Davis, CA

There are three key connected concepts which have been a source of public debate: human sexuality, gender, and biological sex. This project aims to place an extended spotlight on the domain of this discourse and amplify the more limited work being done on biological sex. There are deep, though largely un-argued for, intuitions surrounding biological sex in the public domain, in that unlike gender—which is a fluid social kind— sex is “real”. Moreover, there are rigidly two types, male and female. I push back against these intuitions and intend to argue for a pluralist-realist view (Glennan, 93, Mitchell 2009, 13) with respect to biological sex.

As a preliminary to developing my argument, I will examine more closely Sarah Richardson’s paper *Sexes, species, and genomes: why males and females are not like humans and chimpanzees* (2010). I will provide an exegesis of her arguments against biological sex—male and female—as individual kinds and then her own proposal of biological sex as a dyadic kind. Richardson draws on genomic research of the sequencing of the human sex chromosomes, which seemed to suggest the genetic differences between male and female were akin to genomic differences between species. In other words, on this account we would separate biological sexes as we would separate species. Richardson argues that such accounts are flawed and, as a result, offers her own account of biological sexes as a dyadic kind.

In this essay, I do not intend to argue against her account. Instead, I argue that her framework of the sexes is best understood as a mechanism that explains a recurrent phenomenon, namely reproduction. I will then argue that this framework does not fit every role biological sexes might play, and so we should become more comfortable with a pluralist-realist view of biological sex, and take seriously the context of evaluation in determining biological sexes.

I aim to explore the following questions: To what extent do we need to draw the boundaries of the sexes as two in some way? What role does infertility, intersex, social dynamics, and historical attitudes play in understanding biological sex?

Can applying feminist standpoint theory address gender disparity in biomedical research?

Lida Sarafraz¹

¹University of Utah, Philosophy, Salt Lake City, UT

Ample academic attention has been focused on gender bias in biomedical research where the disproportionate use of male human subjects and animal models have ongoing negative impacts on women's health.

In this paper, I argue this disparity causes epistemic harm. In these trials, the researchers discriminate based on sex/gender to qualify research participants. As a result, researchers and physicians do not have sufficient data about the effects of drugs on the female body. Consequently, women will experience more pain and adverse effects, which would threaten their health. Besides, the lack of sufficient data about female physiology and drug metabolism in women's bodies would be an epistemic harm for biomedical science.

In this paper, first, I will analyze the problem from the feminist standpoint theory's perspective. Applying feminist standpoint theory to analyze this case, helps us to understand the experiences, needs, and values of women have been ignored in the production of biomedical knowledge. Feminist philosophers of science such as Sandra Harding suggest to overcome biases in scientific methodology, there is a need to start from the standpoint of underrepresented groups in research. I will argue Sandra Harding's suggestions about "strong objectivity" will be helpful to overcome gender biases in biomedical research.

Relative significance controversies in evolutionary biology

Katie Deaven¹

¹University of Wisconsin-Madison, Philosophy, Madison, WI

Scientists engage in relative significance controversies when they investigate the importance of a cause in producing a phenomenon of interest. Some philosophers have questioned the epistemic value of engaging in these controversies. In this paper, I present a taxonomy outlining the conditions under which questions of causal importance may arise. I then show how engaging in these different kinds of controversies may inform scientists' research. Using the group selection controversy, I illustrate how these controversies help scientists form predictions about new instances of the phenomenon of interest, refine our understanding of causes of the phenomenon of interest, and improve upon explanations of causal structures.

Unpacking ‘care’ and conflict in public knowledge controversies

Angela Cassidy¹

¹University of Exeter, Sociology, Philosophy and Anthropology, Exeter, United Kingdom

What does it mean to ‘care’? In this paper, I will explore the multiple meanings and rhetorical usages of care that manifest in public knowledge controversies. A proliferation of scholarship on care in the life and environmental sciences has tended to focus on its positive aspects fostering relationships between humans (e.g. in collaborative research); between humans and other animals; and in encouraging co-existence, restoration and resilience in people seeing themselves as part of wider ecosystems or environments. Van Dooren (2019), Haraway (2016) Giraud (2019) and others have explored the ambiguities, contradictions and conflicts inherent in caring practices. This paper explores how such conflicts play out in the wider public sphere during knowledge controversies. I argue that care is a critical yet overlooked aspect of such controversies, shaping arguments about what should or should not be done; framings of what the problem is in the first place; and what knowledge and expertise can be brought to bear on the issue. The longstanding controversy over culling wild badgers to control the spread of bovine tuberculosis (bTB) in British cattle herds will be used as an exemplar. Three intersecting ‘cultures of care’ (Davies et al, 2018) have engaged in these debates since the 1970s: *animal health*, *disease ecology* and *badger protection*. Over this time, changing intersections, alliances and divergences between these three have shaped and reshaped public debates and policy decisions. Those involved care deeply, but who or what they care about and indeed what practices constitute ‘care’ in the first place are very different. A sense of shared care *within* these communities is co-constituted with beliefs in an absence of care *between* them, fostering mutual hostility and at times driving public polarisation. I will use this case – and other examples from across the life sciences – to analyse the multiple dimensions of care present in such controversies, including individual-collective; life-death; and suffering-flourishing. Understanding differences across these dimensions of care not only provides critical insight into the emotional and moral drivers of knowledge controversies, but also opens possibilities for using them to explore otherwise invisible common ground in ‘intractable’ (Grant, 2009) policy and public debates.

Ecological neutrality and ecological niche-theory

Topaz Halperin¹

¹The Hebrew University, Philosophy, Jerusalem, Israel

Approximately twenty years ago, the field of community ecology was shaken by a new, so-called ‘neutral’ theory of biodiversity. This theory aims to explain the relative abundance of species in an ecological community (not to confuse with the neutral theory of molecular evolution, which focuses on variation at the molecular level). The neutral theory in ecology treats all species in a given community as ecologically-equivalent. Thus, in effect, it suggests that differences in species abundance are entirely stochastic: the fact that a given species is more common than another does not imply that it is better adapted; rather, it became more prevalent by chance. Many ecologists interpret the neutral theory as a radical alternative to the traditional niche-based approach, which highlights the importance of inter-species competition and assumes that differences between species determine their relative abundance. In my talk, I argue that the conceptual relationship between ecological neutrality and ecological niche-theory is much more entangled than ecologists and philosophers of biology have hitherto appreciated. In fact, there are various concepts of both ‘neutrality’ and ‘niche’, and some of them even depend on one another. More specifically, I identify three different notions of neutrality: functional-neutrality, adaptedness-neutrality and demographic-neutrality. I then discuss how these notions of neutrality relate to each other and to different notions of niche. Special attention is paid to the explanatory roles of the concepts discussed and to the problems generated by confounding them. The overall goal is to further our understanding of what ecological neutrality and ecological niche are, and thereby to enhance our understanding of explanation in ecology.

Inhabiting the holobiont: The role of visual and verbal imagery

Joana Formosinho¹

¹University of Copenhagen, Medical Museion, Department of Public Health/ CBMR, Copenhagen, Denmark

I begin this talk by arguing that the holobiont is a concept of perceptual value, beyond controversies of usage within disciplines. It invites us to encounter anew the human body and selfhood, in an attempt to make representational sense of microbiome research. The holobiont is often defined as the functional unit comprised of a host macro-organism plus micro-organisms living on or inside the host (the microbiota). Its multi-genomic composition is highly dynamic: it varies from individual to individual, and changes throughout the lifespan of an individual according to factors such as age, food ingestion, social relations and physical surroundings. As a term, the holobiont invites re-drawing of the boundaries of biological self, and re-imagining of the relational pathways between human and non-human; human and environment. In this talk, I review visual imagery associated with the holobiont within scientific and popular science discourse, and identify recurring patterns. I hypothesize that these patterns may indicate perceptual challenges—challenges of categorisation and organisation of thought. There has been some attention lately on the role of cross-disciplinary collaboration in addressing translational challenges posed by the complexity sciences. Notably, Latour and Lenton’s work on the critical zones, which emphasizes that the climate crisis is a crisis of the imagination, of the capacity to inhabit scientific knowledge. Latour and Weibel (2020) argue that enlightenment cosmologies of the Earth as a body made up of separate constituent parts that can be ‘added up’ to a coherent whole are no longer adequate—a “new metric” is needed. I argue that this ‘cosmological problem’ extends to microbiome research which, at a different perceptual scale, has similar implications for representations and metrics of the human body and society. Attention to imagery arising within the field of discourse can help us understand some of the challenges inherent in re-conceptualising the human and its relations with microbes. I also argue that verbal imagery arising within STS may facilitate holobiont-adequate perceptual shifts, and shifts in metrics of thinking—e.g. terms such as Isabelle Stengers’ ‘reciprocal captures’, Pickering’s ‘dances of agency’, and Haraway’s ‘sympoiesis’.

Ecological community of holobionts: Ecology in size scales

Tamar Schneider¹

¹Tel Aviv University, Cohn Institute, Tel Aviv, Israel

In any given ecosystem, we have two different size scales of examination, the macroorganism ecology, and the microorganism ecology. But with such a scale difference, it is difficult to find a satisfying theoretical framework for both (Konopka 2006). My talk examines the concepts of stability, resilience, and equilibrium in microbial ecology (or microbial ecosystems) in comparison with the understanding of these concepts in macrobial ecology. I ask about the relationship between these two different scales and their mutual epistemic influences. In particular, I examine the possible impact the microbial ecosystems have on macrobial ecosystems' paradigm as they are significant and influential part of the latter.

In microbial ecology, the microbial ecosystem is characterized by their biogeochemical functions, and the microbial composition or diversity examined through their biochemical capacities. Thus, they are identified not by their taxa alone but through their functions. Furthermore, microbial function in their ecosystem is the result of their interactions and metabolism, such that different compositions can have similar functions (Burke et al. 2011). Thus, the taxonomic composition, biodiversity, and mass are regarded in a non-specific way as opposed to animals and plant communities.

This characterization is different from ways of thinking about macroorganismal ecosystems and communities. In particularly thinking about concepts such as stability, resilience, and equilibrium, the difference is on the emphasis on species vs. function (Green et al. 2008; O'Malley 2014).

My talk examines the relations between these two different frameworks and in what ways they connect when thinking of macroorganisms ecology from the perspective of holobionts' ecology, as the latter are also a part of an ecological community or ecosystem. That is, I ask in what way we need to include the small-scale microbial world in the larger animal and plant world in addition to the studies of their biochemical functions. Particularly, in what ways the ecology and evolutionary processes of microbial distribution and transmission are essential in the macrobiotic ecological studies of communities and ecosystems. These relations are essential in the understanding of ecosystems and their characterizations of stability or resilience, which is not individualist but instead focuses on the processes of mutual interactions and the microbial environmental niche.

Who is the biological patient? A gradual, dynamic model of organism-environment

Yael Friedman¹

¹University of Oslo, Department of Philosophy, Classics, History of Art and Ideas, Oslo, Norway

In biomedical contexts, patients are typically viewed as individual organisms. Simultaneously, in Public Health, Epidemiology, and One Health Medicine, one can detect more inclusive ways of understanding patients as biological units, e.g. as a population or an ecosystem. The growing literature on symbionts also contributes to the variety of patient definitions, e.g. by seeing humans as holobionts. While there is a lively discourse in the life sciences about how to delineate different forms of living beings depending on scientific contexts, everything outside of them is often understood simply as environment, a broad concept that has stayed as a relic from the exclusively organism-focused past. On the backdrop of current discussions on symbionts and the global epidemiological and ecological crises, I rethink the traditional dichotomic model of organism-environment. I present a new gradual model of the living being and its exterior, i.e. the different ways of 'being outside the organism' that correspond to various definitions of living beings. The model is formed as nested domains that create a spectrum of boundaries between the living being and its exterior that are part of the same whole. The model allows a dynamic understanding of life and more precise definitions of biological patients.

Beyond Darwin: Towards a new historiography of evolutionary biology

Maurizio M Esposito¹

¹University of Lisbon , Department of History and Philosophy of Science, Lisbon, Portugal

In the last two decades, historians have increasingly questioned many historiographical categories underpinning Darwinian narratives of evolutionary biology. Like those old monuments pulled down after a revolution, labels such as “Darwinian revolution”, “neo-Darwinism” and “Modern synthesis” are collapsing under persistent criticism. Yet, while we might be on the verge of an historiographical revolution, we still ignore how the old “monuments” would be replaced by new ones. With the proliferation of alternative views, a general discontent about past accounts, and the need of philosophical inquiries probing the tenets of historians’ craft, we might be in the middle of a Kuhnian historiographic “paradigm shift”. Against this backdrop, the talk aims to draw attention over three related questions:

- a) What were the rationales and goals underpinning some of the old historiographical categories?
- b) Why do we need to reconsider these categories and the narratives they support?
- c) How can we rethink a new historiography of evolutionary biology without these categories?

I argue that a serious consideration of these questions can provide us with some insights for reorganizing the history of evolutionary biology around figures and themes that are not necessarily “Darwin” and “Darwinism”.

Moving the borders of Darwinism: A comparative examination of Darwin's evolutionary theory in Darwin's celebrations, 1909-1959-2009

David Ceccarelli¹

¹University of Rome Tor Vergata, Department of History, Cultural Heritage, Education and Society, Rome, Italy

Since the publication of *On the Origin of Species* by means of Natural Selection (1859), the narratives of Charles Darwin's theory of evolution have significantly changed. Indeed, the very meaning of the concept of "Darwinian evolution" has been disassembled and assembled in response to the debates in evolutionary biology, and thus seems to be the product of a long and complex interplay between historiographical and scientific needs. This clearly appears when considering the way evolutionary biologists, historians and philosophers of biology commented on Darwin's attitude toward theoretical issues that proved to be objects of great debate in twentieth-century evolutionary biology such as soft inheritance. The paper examines how scholars depicted Darwin's views on soft inheritance on the occasion of the three main anniversaries of his birth: 1909, 1959 and 2009. Indeed, not only did these represent a symbolic occasion for evolutionary biologists to take the stock of the situation within their research field, but also were an opportunity to assess Darwin's legacy. This analysis will show: a) that the border between "Darwinian" and "non-Darwinian" theories of evolution has been moved over time; b) that evolutionary biologists have often had concern for identifying what is in and out of the Darwinian research program, making up research traditions and confining inconvenient ideas.

Darwin's static arrow of time: Why we need to find new concepts of time and causality in an evolutionary worldview

Patrick Hoburg¹

¹Purdue University, West Lafayette, IN

The persistent role of mechanistic reasoning in debates over the nature of evolution owes to the continued influence of the Scientific Revolution's etiological orientation, a pursuit of the *real causes* of observable phenomena. Contemporary evolutionary syntheses adopt mechanistic approaches to evolutionary causality in the construction of their components, but the scope and efficacy of these mechanistic components demand epistemological scrutiny. I examine mechanistic accounts of evolutionary causality, focusing on Charles Darwin's underlying commitment to a predominately *static worldview* in the *Origin of Species* (1859). The mechanistic concepts of space, time, and causality constitutive of this worldview, from Darwin to extended syntheses, are no longer tenable. I deconstruct the rationalist eclipse of the problem of time in Darwin and its tight connection to the preeminent role of natural selection as a case of *the chronometric subordination of time to motion in philosophy, science, and society*. The causal components of evolutionary syntheses and their connections will remain weak and diffuse until the lineaments of an *evolutionary worldview* bring them into focus. The most constructive way to conceptualize evolutionary causality is in light of a new concept of evolutionary time, one attentive to time in physics and philosophy, as well as in the earth and life sciences. I consider the strengths and weaknesses of various conceptual options.

The road to Wingspread: Theo Colborn and developmental disorders in Great Lakes fauna

Marsha L Richmond¹

¹Wayne State University, History, Detroit, MI

By the 1970s in the US, decades of poorly regulated industrial wastes discharged into the nation's water and air came to the public's attention. In the 1980s, new concerns arose after the discovery that the industrial chemical, PCBs, was not only environmentally persistent but caused health problems in fish, wildlife, and humans. In 1988, Canadian biologists studying the Great Lakes engaged Theo Colborn, scientific consultant for the Conservation Foundation of Washington, DC, to prepare a report on problems US biologists had identified in Great Lakes fauna. Analyzing a dozen keystone species, Colborn made the surprising discovery that rather than causing cancer, chemical pollutants appeared to trigger developmental abnormalities. Colborn presented her preliminary findings in a 1989 working paper and more fully in *Great Lakes, Great Legacy?* (1990). Searching for causes of these disorders, Colborn convened a meeting of biomedical scientists and researchers at the Wingspread Conference Center in July 1991. The outcome was the Wingspread Consensus Statement (1992), which proclaimed that environmental chemicals could trigger "endocrine disruption." Following in the footsteps of Rachel Carson's *Silent Spring* (1962), Colborn, Dianne Dumanoski, and John Peterson Myers published the popular book *Our Stolen Future* (1996), which warned the public about dangers posed by endocrine disrupting chemicals (EDCs). This paper explores how worries about Great Lakes pollution among scientists, government bodies, NGOs, and environmental activists led to a new area of scientific research and widespread concern.

The construction of a sentinel species: Louis Guillette and Lake Apopka's alligators

Mark V Barrow¹

¹Virginia Tech, History, Blacksburg, VA

This paper examines the scientific research and public activism of the American biologist Louis Guillette, a prominent supporter of the endocrine disruptor hypothesis and a strong advocate for the idea of sentinel species. While researching the reproductive biology of the endangered American alligator in the late 1980s and early 1990s, Guillette discovered that the population at one of his study sites, Lake Apopka, Florida, was displaying numerous abnormalities, including low reproductive rates, males with high estrogen levels, females with high testosterone levels, and excessive rates of juvenile mortality. The lake had been a premier bass fishing site up until the 1960s and 1970s, after its north shores began experiencing intensive agricultural development. Guillette discovered that its waters were burdened not only with significant run-off from agricultural chemicals but also a 1980 spill from the Tower Chemical Company, which manufactured synthetic pesticides. After learning of the work of Theo Colburn, he became convinced that environmental contaminants acting like hormones were responsible for the troubling symptoms he was observing in his study subjects. Guillette's research, and his many appearances in the media and before Congress, became a key source of support for the endocrine disruption hypothesis that was being debated in scientific, environmental, and regulatory circles in the 1990s and that became popularized in the bestselling book, *Our Stolen Future* (1996). Until his death in 2015, the passionate, energetic, and charismatic Guillette also argued repeatedly that the alligator served as a sentinel species, a warning that continued exposure to modern synthetic chemicals, even what seemed like very low levels, posed a dire threat not only to wildlife populations, but also to humans.

Mixed reception of the environmental endocrine hypothesis within science and the media: From 1991 to the present

Sheldon Krimsky¹

¹Tufts University, Medford, MA

Any new theory of the etiology of human disease is likely to be met with skepticism among scientists. Science is a conservative body that resists new theories, which when published in scholarly journals are cast in the backwaters of a discipline. So it was with Mendel's pea experiments, Darwin's Theory of Evolution, and the Theory of Continental Drift, to name a few.

The term endocrine disruptor and the theory behind it was first introduced in the Consensus Statement from a work session organized by Theo Colborn in July 1991. From that point on it became the chosen term to describe the impact of chemicals on the endocrine system of humans and wildlife affecting development.

My talk will discuss the initial reticence of the broad scientific community, including journal editors, and the media to accept endocrine disruption as a new etiology of disease and mechanism of toxicology. I will examine the transitional stage when the Environmental Endocrine Hypothesis was finally adopted by the major journals and the media. Today there are over 3,500 scientific papers with "endocrine disruptor" in the title. I will discuss Colborn's role in raising the visibility of the hypothesis among scientists, government agencies, the media and the general public.

Biologies of the South: Negotiating knowledge and livelihoods, Part 1

Aadita Chaudhury¹, Nadya Karimasari², Zinhle Mncube³, Jairo Robles-Piñeros⁴, Abigail Nieves Delgado⁵, Arturo Vallejo⁶, David Ludwig⁷
¹PhD Candidate, York University, Toronto, Canada, ²PhD Candidate, Dept. of Sociology and Anthropology of Development, Wageningen University, the Netherlands, ³Lecturer in Dept. of Philosophy, University of Johannesburg and PhD Candidate, Dept. of History and Philosophy of Science, University of Cambridge, United Kingdom, ⁴PhD Candidate, History, Philosophy, and Science Teaching, Federal University of Bahia and UDFJC-Columbia, ⁵Assistant Professor, Utrecht University, the Netherlands, ⁶PhD Candidate, Philosophy of Science/Social Studies of Science, National Autonomous University of Mexico, ⁷Associate Professor, Wageningen University and PI of the "Global Epistemologies and Ontologies" project, the Netherlands

Knowledge about the biological world is produced in heterogeneous geographic contexts and by diverse communities such as smallholder farmers, population geneticists, Indigenous herbalists, or medical practitioners. Addressing this heterogeneity is especially pressing where it relates to local livelihoods in areas such as conservation management, food security/sovereignty, or public health. History, philosophy, and social studies of biology (HPSSB) can contribute to understanding the methodological, ontological, and political dimensions of negotiations between different forms of knowledge production. At the same time, by facing these different biologies, HPSSB can positively expand its methodological, thematic, and theoretical perspectives. This session highlights the potential of HPSSB but also the need for more explicit engagement with global tensions surrounding biological knowledge production. Rather than presenting separate papers, we proceed in four connected steps and answer the following questions:

1. Introduction of 6 case studies.
2. How does HPSSB contribute to better understand each case study?
3. How does each case study challenge HPSSB epistemological resources?
4. Final discussion on the role of HPSSB in negotiating biological knowledge production from a global epistemically diverse perspective.

Case studies and participants:

1. **Unravelling the threads of Dhaka Muslim: colonial ecologies and revivalism.** Aadita Chaudhury, PhD candidate, York University.
2. **The Politics of Taxonomy - The Tapanuli orangutan in Indonesia.** Nadya Karimasari, PhD candidate, Department of Sociology and Anthropology of Development, Wageningen University. David Ludwig, associate professor, Wageningen University
3. **Decolonising Medicine: On the African Traditional Medicine Case.** Zinhle Mncube, lecturer in University of Johannesburg and PhD candidate, University of Cambridge.
4. **Creating livelihoods: History and methods of Mexican ethnobiology.** Abigail Nieves Delgado, assistant professor, Utrecht University.
5. **Techno-Sciences and Tensions between Agrarian Knowledge Systems. A Case Study in the Northeast of Brazil.** Jairo Robles-Piñeros, Ph.D. candidate, Federal University of Bahia and UDFJC-Colombia.
6. **Chinto Tour 2021: Technoscientific narratives of urgency and compulsion in Mexican citizen science birding.** Arturo Vallejo, PhD candidate, National Autonomous University of Mexico.

The problem of character individuality

James DiFrisco¹

¹KU Leuven, Institute of Philosophy, Leuven, Belgium

Characters are the modular building blocks of organisms. Biology depends on being able to partition organisms into characters in order to differentiate and compare taxonomic groups, track and explain evolutionary change, study subsystems separately from the whole organism, and much more. How should this partitioning be done so that the resultant characters are natural units of biological processes, rather than being arbitrary or reified constructs? This is the problem of character individuality. In this presentation, I introduce and frame this critically under-theorized problem. One idea proposed by some theorists in evo-devo is that the identification of characters should be grounded on underlying modular mechanisms controlling their development. At the same time, the individuation of characters is not only a matter of how they develop, but of their ecological interactions with other organisms and environments. In ecological processes like sexual selection, predation, and mimicry, the identity of a trait is not only fixed by the way it develops, but by the way it is perceived and acted upon by other organisms. Conceptually disentangling the complex and shifting overlaps between the units of these two processes—between developmental and ecological character individuation—is one path toward addressing the problem of identifying the true characters at work in evolution.

Can scientists study individuals?

Rose Trappes¹

¹Bielefeld University, Philosophy Department, Bielefeld, Germany

Scientists usually aim for generalisations. Description, explanation and prediction rely, if not always on universal laws, then on knowledge of general patterns across cases, in different populations, or over time. But what about studying particular cases? Can individuals be the object of scientific study? There are of course ways to apply general knowledge to particular individuals. More difficult is gaining scientific knowledge about individuals themselves, especially when we consider that individuals are unique. For instance, health sciences face the challenge of patients' sometimes unique symptoms, comorbidities, and responsiveness to treatments. Non-human animals are also unique, and behavioural biologists, ecologists and conservation biologists grapple with the sometimes extreme variation in behaviour, social relations, resource requirements and habitat choices in the populations they study. The uniqueness of individuals is problematic for diagnosis and description, since accurate measurement requires repeated observation of stable properties. It is also challenging for gaining causal knowledge, which usually requires generalisation across multiple cases, for instance through group-based experimentation or statistics. In this talk I present these challenges for studying individuals in science. In addition, based on a case study in behavioural ecology, I consider some of the solutions and workarounds for dealing with unique individuals, including decomposition, quantification and approximation. I argue that, while these solutions are often very effective, they always leave a remainder of individuality undescribed and unexplained.

From oviparity to viviparity: An organismic approach to the transition

David Cortés-García¹

¹University of the Basque Country, Department of Logic and Philosophy of Science, San Sebastian, Spain

The evolution of viviparity is a particularly puzzling innovation that intrigues both biologists and philosophers of biology, and is receiving an increased attention during the last decades. Here, we distinguish three features of the evolution of viviparity across Animalia that require an explanation: (i) its *prevalence*, viviparity is present in 20 of 32 animal phyla (Ostrovsky et al., 2016); (ii) its *homoplastic character*, over 150 independent origins have been described only within vertebrates (Blackburn, 2015); and (iii) its *multiple realizability*, viviparity encompasses a great diversity of specializations (Fusco & Minelli, 2019). These three features raise the question of whether the evolution of viviparity responds to internal demands of the autonomous organism (e.g.: developmental limitations, constraints, pre-adaptations) or it is rather conditioned by environmental factors (e.g.: shared selective pressures). It has been argued that the novelties involved in the evolution of viviparity –namely the internalization of embryonic development and separation from environmental influences– reflect a wider evolutionary tendency towards an increased autonomy, so that the influences of the environmental fluctuations on the individual organism are gradually reduced (Rosslenbroich, 2014). The evolution of eutherian viviparity and pregnancy is a preeminent instantiation of this tendency, which involves the appearance of novel cell types and functional innovations. In particular, a previous environmentally induced stress response occurring in the mother is *internalized* giving rise to a physiologically regulated process that permits the implantation of the embryo (Wagner et al., 2019). The evolutionary origin of eutherian viviparity has recently been argued to imply the emergence of a novel *historical individual*: the pregnant female. Pregnancy is hence understood as a relational novelty (Nuño de la Rosa et al., 2021). This raises the question of the appropriateness of addressing the origin of eutherian viviparity as a major transition, which are commonly understood as transitions of individualities.

Trade-offs, pluralism and evolutionary accounts of death

Philippe Huneman¹

¹CNRS, IHPST, Paris, France

Why do organisms die ? And why do they live a limited but species-specific average lifespan ? Philosophers often answered this question by providing metaphysical reasons, such as finiteness of the individual understood as its inadequacy to its universal concept. Death was an essential property of living beings.

As many other key features of life (e.g. sex or inheritance), Darwinians intend to explain these facts of death on the basis of evolution. Unicellular organisms were thought to be immortal, while multicellular organisms had to die, so death must have had evolved. Senescence, as an increased probability of death with age, should have evolved too. But why ? The intuitive argument that death evolved because it's good for the species, used by Weismann initially, appeals to group selection and therefore faces the usual objections raised by this concept since Williams (1966). Williams and Medawar came up in the late 1950s with two different theories that both explain death and senescence through an appeal to individual natural selection, but indirect, based on the idea that the force of selection declines with age. Hence, either genes with deleterious effect at late age accumulate (Medawar's "mutation accumulation" (MA)) and finally kills the organism, or genes enhancing fitness at a younger age but decrease survival later are advantaged over genes increasing longevity late in life - thus the former, which imply increased probability of death, are selected (Williams' "antagonistic pleiotropy" (AP)). In the 1970s the Disposable Soma Theory (DST) (Kirkwood) explained senescence by a trade-off between reproduction and gene-based repair. Those three accounts generated te hundreds of rival theories of death that today compete.

I'll highlight the shift in understanding achieved by evolutionary accounts, in which death appears as an adaptation to accidental deaths caused by the environment (and their specific age-related distribution) rather than as an intrinsic property of life. I'll then defend an explanatory pluralism about death, because each theory explains either longevity, or aging itself, or a pattern of senescence - thus they can hold at the same time. Finally I'll analyse the various trade-offs referred to by DST and AP in terms of rates of temporal discounting in an environment, and question the commensurability of these trade-offs.

Mechanistic causation and explorative strategy in microbiota-gut-brain axis research

Yin Chung Au¹

¹National Cheng Kung University, History, Tainan, Taiwan

This study explores possible interactions between mechanistic and exploratory strategies in the microbiota-gut-brain axis research field. Mechanism research has been the trajectory practice in life sciences since the late twentieth century. It determines the components of mechanistic explanations of phenomena of interest mainly by intervening in candidate components and their relationships based on hypotheses derived from established theories. Nonetheless, in the practice of understanding biological complexity, factors that contribute to the occurrence of phenomena of interest may not be able to determine by hypothesis-driven interventions. Previous historical and philosophical studies have argued that researchers may explore empirical regularities by either experiments that do not aim to test specific hypotheses or employing screening techniques that do not directly intervene in the relationships between factors and phenomena. Given the dominance of mechanism-oriented thinking in contemporary biology, how the exploratory strategy interacts with mechanism research in building causal knowledge of complex phenomena needs a philosophical analysis. The microbiota-gut-brain field contains epistemic activities that seem to respectively fall in mechanism research and exploratory research, as well as somewhere in between. While the former helps to determine upward causation, namely the contributions of specific components at lower levels to phenomena at higher levels, the latter sheds light on downward causation from a higher-level coherent whole to its constituent entities such as neural and immune systems and bacteria. This study assumes that evidence required for these two kinds of causation is combined in the actual practice of scientific reasoning. Two possibilities are examined: first, if evidence obtained by exploration is used to determine causal relevance, which is considered by some mechanical philosophers as a prior step to the determination of causal production in mechanisms, exploration can be discussed in the vein of mechanisms. Second, and perhaps in many cases, when exploration does not discover causal relevance, exploratory evidence is used to formulate idealisations of empirical regularities. The relationship between such idealisations and the target phenomena is flexible for accommodating new phenomena. hypothesis-driven research enters when this flexible relationship incorporates a phenomenon that has been mechanistically explained.

The cognitive map debate in insects: a historical perspective on what is at stake

Kelle Dhein^{1,2}

¹Arizona State University, Center for Biology & Society, Tempe, AZ, ²University of Minnesota, Minnesota Center for Philosophy of Science, Minneapolis, MN

The cognitive map hypothesis has been called “one of the holy grails of cognition” (Breed 2017), “an unwarranted exercise of anthropomorphism” (Shettleworth 2010), “one of the most important neuroscientific results in recent decades” (Shea 2018), and an “a priori assumption” that “should be abandoned” (Benhamou 1995). In mammalian navigation research, the cognitive map is an established fact. But in insect navigation research, the hypothesis has engendered a decades long debate. Contrary to existing commentary that implies the cognitive map debate in insects persists due to definitional confusion, I argue that the debate persists because competing research groups are guided by different constellations of epistemic aims, theoretical commitments, preferred animal subjects, and investigative practices when justifying claims about how insects utilize neurosensory representations. I then examine the history of the cognitive map hypothesis and the biographies of the leading debaters to situate those different epistemic aims, theoretical assumptions, investigative practices, and evidential norms within the broader history of animal behavior research. From a historical and sociological perspective, the heads of the pro-cognitive map group and the anti-cognitive map group in insects have an interesting relationship. Rüdiger Wehner (b. 1940–) and Randolph Menzel (b. 1940–) were trained in the same ethological research tradition by the same mentor at the same time, and in 1990, they agreed that ants and honeybees do not possess a cognitive map. But as the scientists continued to develop their own prominent research programs through the 2000s, Menzel changed his position and began to argue that honeybees do possess a cognitive map while Wehner continued to challenge the cognitive map by developing alternative hypotheses. By relating Wehner’s and Menzel’s justificatory practices to larger disciplinary themes in the history of animal behavior research, I show that more is at stake in the cognitive map debate than the truth value of propositions characterizing insect cognition. Wehner and Menzel’s competing ways of knowing animals represent competing visions for the future of their shared research tradition.

Irene Manton, the cell and the electron microscope: Scientific seeing with an artist's eye

Nicola Williams¹

¹Post-doctoral fellow, Leeds Arts and Humanities Research Institute, Leeds, United Kingdom

The invention of the electron microscope was integral to the development of cell biology. Thus far, historical discussion has focused on 1954 as a watershed moment in the inception of this postwar discipline. It's well known that in the 1940s and early 1950s, international researchers worked to overcome some abiding and vexatious technical challenges, necessitating the invention of new and auxiliary technologies, for optimal use of this new kind of microscope. Only then was it possible to secure access to the cell. Lesser known is that in the preamble to this technical feat, a British evolutionary botanist and cytologist had already beaten a path to the treasures of the cell, heretofore beckoned forth only by the electron microscope.

In the early 1950s, Leeds-based Professor of Botany, Irene Manton (1904-1988), FRS, found a way to circumvent the technical difficulties of the age, and to demonstrate the fine structural details of the cell. But how did she come to 'see' inside the cell? And without recourse to newly invented auxiliary technologies? It is argued here that key to Manton's achievement was the opportunistic merger of light and electron microscopy, and her background as botanist, artist and collector of fine art. Manton found a way to merge the oft perceived dichotomous areas of art and science to 'see' a scientific object with an artistic eye. She was able to reconstruct this object in its three-dimensional form and, in so doing, she pre-empted the work of her fellow workers in cell biology by years.

In the long durée of an 'observational science,' like botany, it's possible to lament a 'lost art.' A botanist's craft is traditionally based upon observation and meticulous illustration. But following the advent of photography and the professionalisation of science, in the late 19th and early 20th centuries, botanists succumbed to a drive toward efficiency. Meanwhile Manton garnered familiarity with scientific objects through repeated observation and the process of drawing results by hand. Here I argue Manton's early 1950s work with the electron microscope shows us that this 'lost art' was, in fact, never really lost at all: rather it was simply reconfigured into a modern format.

Biofictional entities: Or how to imagine the bewildering powers of life

Thierry Hoquet¹

¹Paris Nanterre University, Philosophy, Nanterre, France

From Mary Shelley's *Frankenstein; or, The Modern Prometheus* (1818) to Daniel Espinosa's *Life* in 2017, numerous fictions have imagined the amazing powers of living matter and the way they affect human beings. Instead of a piecemeal approach to selected examples, I will offer a synoptic table, presenting twelve different types of “almost-but-not-quite human” characters.

In between two niches: Cognitive parsimony in cultural adaptation

Mathieu Charbonneau¹

¹Central European University, Philosophy and Cognitive Science, Budapest, Hungary

The cultural transmission of technical skills has proved essential to the success of the human species in populating all but the most hostile ecosystems on the planet. There is an ongoing controversy, however, about the origins of human-specific ingenuity and its expression in terms of cultural adaptations. On the Cognitive Niche side, cultural adaptations are to be explained by human-specific cognitive capacities for intelligent problem-solving, either in the form of general (improvisational) intelligence, or in the form of technical intelligence. In contrast, the Cultural Niche side explains cultural adaptations by the human-specific capacity for cumulative cultural evolution, where small inventions are incrementally modified and selected through social processes. Instead of being the result of evolved individual intelligence, as the Cognitive Niche would have it, cultural adaptations would be the product of a collective, historically-distributed form of intelligence. While at first sight the contrast between the two positions couldn't seem sharper—one situates intelligence at the level of the individual, the other at the level of the collective—a closer look reveals a much blurrier picture. Proponents of the Cognitive Niche clearly embrace cumulative culture as essential for cultural adaptation, and those of the Cultural Niche agree individual intelligence plays a fundamental role in cumulative culture. Yet, rather than agreeing on a complementary view, the controversy has persisted, for over a decade now.

In this paper, I argue that the key contention between the two sides resides in their different understanding of the ontology of individual intelligence. While the Cognitive Niche approaches improvisational (or technical) intelligence as a discrete, yet complex cognitive capacity, the Cultural Niche adopts a quantitative account of individual intelligence, such as IQ, which is historically well-documented to gradually evolve on a continuous scale. I defend a discrete ontology for intelligence as a family of problem-solving capacities, yet one that permits a gradualistic, cultural evolution of those capacities. My proposed solution moves the debate away from the issue of determining which form of intelligence, individual or collective, best serves as the general driver of cultural adaptations. Instead, the debate is relocated at the level of specific cultural traditions, for which clearly nuanced empirical solutions can be provided.

Population as a distributed memory system: The species-environment complex and its implications for stability and long-term evolution

Ehud Lamm¹, Oren Kolodny²

¹Tel Aviv University, Cohn Institute for History & Philosophy of Science, Tel Aviv, Israel, ²Hebrew University, Ecology, Evolution & Behavior, Jerusalem, Israel

Species' adaptation to their environments occurs both via genetic adaptation and via non-genetic mechanisms of adaptation. We propose a third category: cases in which adaptation to the environment occurs via “conformational adaptation” (CA), in which the adaptation is conferred via structural or compositional structure of the population.

Consider the following example. Individuals may need to find suitable habitat to breed or dwell when they mature. Adaptations that are carried by the individual may include innate knowledge about environmental cues for finding a suitable site, or learned knowledge about where such sites are found. These solutions rely on *individual-level adaptive information*. Alternatively, a CA, comprising *population-level adaptive information*, may involve individuals relying on searching for other individuals, and joining them. Such a strategy would be adaptive, since the locations in which multiple individuals are found are highly likely to be habitable. In this case, the information necessary for survival is found in the spatial distribution of the individuals (coupled with their aggregating behavior) and cannot be reduced to information possessed by a single individual.

While human culture is presumably like this, we argue that there are other cases that belong to this category. We explore when and how such adaptations will evolve and provide various examples to show that they are probably less rare than may be expected and how their evolutionary origins are distinct from issues related to the level of selection. We analyze the notion in relation to related concepts, in particular division of labor, strategy choice, and collective memory. We also explain how CAs differ from niche construction. CAs may be part of the explanation of a variety of phenomena potentially including communal breeding, obligatory schooling, distributed skills in bands. Finally, we suggest that they may help explain Allee effects, i.e. positive correlation between population size or density and the mean individual fitness, for which the causality is often unclear, and hence may be significant for species conservation and re-introduction.

Rethinking evolutionary progress in the light of cultural evolution

Alejandro Gordillo Garcia¹

¹KU Leuven, Institute of Philosophy, Leuven, Belgium

Is humanity progressing? Cultural evolutionists have inadvertently refrained from addressing this kind of questions by explicitly opposing their evolutionary approach to human history with so-called progressivist (or Spencerian) theories of sociocultural evolution on grounds of inherent incompatibilities with Darwinism regarding teleological thinking and immutability. However, this maneuver dismisses potential alternative understandings of evolutionary progress consistent with a Darwinian treatment of culture, impeding the development of an otherwise interesting line of enquiry into the trends of human cultural evolution.

In this work, I argue that ‘evolutionary progress’ can be a valuable operational concept for cultural evolutionary theory if it is well defined. After a discussion of the concept of progress in evolutionary biology and philosophy of biology, I argue that, when applied in the cultural realm, ‘evolutionary progress’ needs to be operationalized in a more precise manner. What we need in this context is an account that (1) gives a value-free description of the cultural evolution process; (2) considers an objective and quantifiable criterion (i.e., one that can be empirically tested); and (3) that is compatible with the Darwinian approach. I then propose an operationalization of cultural evolutionary progress that meets these requirements. I suggest that cultural evolutionary progress should be understood as the outcome resulting from minimizing the use of cultural information to maximize adaptively relevant effects at the phenotypic level, where these effects increase the average fitness values of the cultural populations in question. Cultural fitness is defined in terms of average survival and reproduction of individuals. Finally, I show the advantages of this concept of cultural progress to advance our understanding of the directions of human cultural evolution.

A pragmatic model for the notion of “information”

Martina Blečić¹

¹University of Rijeka, Department of Philosophy, Rijeka, Croatia

I suggest a pragmalinguistic model for the notion of “information” used in molecular biology to describe protein synthesis. Discarding any ontological commitments of the term “information” and treating it as a metaphor whose role is to aid our understanding of genetic processes, I propose a view of information based on an analogy with communication as seen by pragmatics, esp. speech act theory, that emphasizes the procedural nature of the genome. The motivation is twofold. (i) If the role of metaphors is to help understand molecular phenomena they should be revised when their explicatory power fades. The information metaphor is based on early computer technology, which many today find unfamiliar, making it flawed as a means for the understanding of gene action. (ii) A metaphor based on early computers and punched cards creates a linear picture of genetic processes that ignores context.

This view is based on pragmatics, the study of language in use, especially on the theory of speech acts proposed by J. L. Austin. L. Floridi has passingly compared genes to performatives, but has not developed this idea any further. My aim is to work on his suggestion focusing on the role of the information metaphor in understanding. According to Floridi (2010), genes are dynamic procedural structures that contribute, together with other indispensable environmental factors, to control and guide the development of an organism. This account interprets genes as instructions that require the full collaboration of the relevant components of the organism and of its environment to be carried out successfully. I suggest this view as the starting point of a broader pragmatic notion of “information”, albeit one that will consider genes as performatives only in a metaphorical sense. A pragmatic metaphor, based on the analogy between protein synthesis and human communication could explain this process in a way accessible to non-experts and provide a model for experts to make their findings more understandable, but it could also help them consider different aspects of protein synthesis.

To conclude, this approach will focus on the role of the informational metaphor in understanding genetic processes and not on the ontological status of “information” that will be held as a metaphorical heuristic, useful if correctly modeled.

The evolution of information sharing

Rafael Ventura¹

¹University of Pennsylvania, Biology, Linguistics, Philadelphia, PA

Mechanisms for information gathering and social learning have rightly been the focus of much work in cultural evolution. But information-sharing mechanisms—mechanisms that determine what information is available for learners to learn in the first place—are equally important to cultural evolution.

Information-sharing mechanisms are common in humans and have been found in many non-human animals. In the 1950s, for example, a troop of Japanese macaques living on the island of Kojima in Japan were reported to wash sweet potatoes before eating. As potato washing was not observed in other troops, it soon became clear that this skill spread through social learning: after observing a macaque wash a potato before eating it, other macaques were more likely to perform the same behavior in the presence of similar food items. Other skills, such as tool handling, were subsequently shown to likewise spread and persist through social learning among Japanese macaques. Socially transmitted skills have also been documented in other animal species—for notable examples, see termite fishing in chimpanzees, prey handling in meerkats, tool use in corvids, and foraging patterns among some social insects.

In this talk, we propose a simple model that integrates cognitive and evolutionary aspects of information sharing. Our model represents a dual-inheritance process: individuals acquire and share information about valuable skills at the same time that their capacity to share information about such skills is under control of genes that evolve by natural selection. Our model therefore allows us to simultaneously study the cognitive faculties that transmit skills and the evolutionary dynamics that shape these cognitive faculties. Results show that information sharing can give rise to an opportunity cost that goes beyond any direct cost that it may also entail. We then discuss how this opportunity cost can cause information-sharing mechanisms to be self-limiting, suggesting that such mechanisms may nevertheless play an important role in the evolution of cumulative culture in humans. Finally, we conclude with brief thoughts on the co-evolution of information sharing and information gathering.

How to think about the immune system in times of COVID-19 and beyond: Why stronger isn't always better and other misleading metaphors

Martin Zach^{1,2}, Gregor Greslehner³

¹Czech Academy of Sciences, Department of Analytic Philosophy, Institute of Philosophy, Prague, Czech Republic, ²Charles University in Prague, Department of Philosophy and Religious Studies, Faculty of Arts, Prague, Czech Republic, ³University of Vienna, Department of Philosophy, Vienna, Austria

In light of the worldwide pandemic crisis, both the wider public as well as researchers from biological domains are operating with immunological terms and concepts which are also the scholarly focus of philosophy of immunology (Pradeu 2020; Swiatczak and Tauber 2020).

We propose to think of the immune system in terms of three key features: contextuality, regulation and trade-offs.

Contextuality concerns both the compartmental nature of the immune system and its environment at large including microorganisms, many of which are pathogenic only under certain circumstances. Regulation pertains to the fact that (feedback) mechanisms ensure that the immune response is neither too vigorous, nor too permissive, but just right for the given task. Dysregulation is often at the heart of pathology, including in COVID-19. Given the sheer complexity of the immune system, trade-offs are to be expected: e.g. a specific HLA allele confers resistance against certain pathogens but leaves the host susceptible to another, or in risk of developing an autoimmune disease.

Unfortunately, the discourse on the immune system is often riddled with metaphors that give rise to intuitions that are, to a large extent, misguided. The idea that one's immune system is somewhere on the continuum between weak and strong is a misconception. It is based on the assumption that the immune system is primarily a defense mechanism against anything foreign or harmful which does not take into account a variety of other processes in which the immune system is involved. This neglects the fact that the immune response which is optimal for an organism under certain conditions is something very specific, context-dependent, and heavily regulated by (feedback) mechanisms. Neglecting the three key features noted above contributes to missing on the fundamental principles of the immune system and gives rise to misleading metaphors which abound in immunology. Instead, we show that often the immune system works counterintuitively.

A critical discussion of *Darwin's Argument by Analogy: From Artificial to Natural Selection*

Hayley Clatterbuck¹, Jonathan Hodge², Gregory Radick², Andrea Sullivan-Clarke³

¹University of Wisconsin-Madison, Philosophy, Madison, WI, ²University of Leeds, Philosophy, Religion and History of Science, Leeds, United Kingdom, ³University of Windsor, Philosophy, Windsor, Canada

In *On the Origin of Species* (1859), Charles Darwin put forward his theory of natural selection. Conventionally, Darwin's argument for this theory has been understood as based on an analogy with artificial selection. But there has been no consensus on how, exactly, this analogical argument is supposed to work – and some suspicion too that analogical arguments on the whole are embarrassingly weak. In *Darwin's Argument by Analogy: From Artificial to Natural Selection*, to be published in July 2021 by Cambridge University Press, Roger White, Jon Hodge and Greg Radick offer an original perspective on Darwin's argument. Drawing on new insights into the history of analogical argumentation from the ancient Greeks onward, as well as on in-depth studies of Darwin's public and private writings, they attempt to restore to view the intellectual traditions which Darwin took for granted in arguing as he did, notably the distinction between Aristotelian analogy as proportionality versus Reidian analogy as similitude. From an understanding of Darwin's analogical argument as Aristotelian rather than Reidian in style, they argue, come new appreciations not only of Darwin's argument but of the metaphors based on it, the range of wider traditions the argument touched upon, and its legacies for science after the *Origin*.

This session will introduce, examine and explore the main claims and themes of the book with help from two expert commentators on Darwin's *Origin* reasoning and its contexts, Hayley Clatterbuck (UW-Madison) and Andrea Sullivan-Clarke (Windsor). The session will begin with an overview of the book from Jon Hodge (Leeds), then proceed to commentaries from Prof. Clatterbuck and Prof. Sullivan-Clarke. After some discussion among the panellists, the virtual floor will be open for questions and comments from everyone, with Greg Radick (Leeds) serving as chair throughout. No previous knowledge of the primary or secondary literatures will be presumed. All are welcome!

History of evolvability: Reconstructing and explaining the origin of a research agenda

Laura Nuño de la Rosa¹

¹Complutense University of Madrid, Logic and Theoretical Philosophy, Madrid, Spain

While several aspects of evolvability were investigated before the 1990s, evolvability as a research agenda only emerged in the mid-late 1990s. Since then it has increased exponentially in several domains of evolutionary biology, being considered by many as one of the main ‘expanders’ of the Evolutionary Synthesis. This talk addresses the historical origination of evolvability research with the aim of contributing more generally to the reconstruction and explanation of the recent history of evolutionary biology. In the first part, I combine co-citation analysis and first-person reconstructions of the history of the field obtained from a series of interviews with evolutionary biologists, to discuss the historical novelty of the evolvability research agenda. In the second part, I apply some conceptual tools from evolutionary biology itself to present three causal hypotheses explaining this distinctive historical pattern. These are (1) the contingency hypothesis, pointing to accidental factors which had an effect in the explosion of the relative interest in evolvability; (2) the innovation hypothesis, focusing on aspects of the intellectual landscape which promoted the acceptability and diffusion of the evolvability perspective; and (3) the evolvability hypothesis, concerning the consequences for empirical research of the relative autonomisation of theoretical components.

Evolvability as a disposition: Philosophical distinctions, scientific implications

Ingo Brigandt¹

¹University of Alberta, Department of Philosophy, Edmonton, Canada

While it has been noted that evolvability as the ability to evolve is a dispositional property, the significance of this yet has to be analyzed. This talk discusses why the dispositional nature of evolvability matters to evolutionary research, including why philosophical distinctions about dispositions can have scientific implications. To that end, I lay out a conceptual toolkit on dispositions that is also useful for biologists to reason about dispositions on biology. I then apply this toolkit to address several methodological questions related to evolvability. What entities are the bearers of evolvability? What features causally contribute to the disposition of evolvability? How does evolvability manifest? The various possible answers to these questions available from our philosophical distinctions suggest key implications for why the concept of evolvability as a disposition is useful in evolutionary research. These include (1) securing scientific virtues (e.g., explanatory depth and generalization, prediction or retrodiction, and control or manipulation) and (2) fostering interdisciplinary collaboration through the coordination of definitional diversity and different types of inquiry. Together these facilitate concentration on a variety of research questions at different levels of organization and on distinct time scales, all of which should be expected for a complex dispositional property such as evolvability.

The conceptual roles of evolvability across evolutionary biology: Between diversity and unification

[Cristina Villegas](#)¹, Alan C Love²

¹Complutense University of Madrid, Department of Logic and Theoretical Philosophy, Madrid, Spain, ²University of Minnesota, Minnesota Center for Philosophy of Science, Minneapolis, MN

A number of biologists and philosophers have noted the diversity of interpretations of evolvability in contemporary evolutionary research. Different clusters of research—defined by shared methodological orientation or co-citation patterns—sometimes concentrate on distinct conceptions of evolvability, which suggests that at least some of this diversity may be associated with differences in the conceptual roles that evolvability may play within particular evolutionary domains. In this talk we analyze this diversity and what these different conceptualizations accomplish in scientific reasoning. We first examine five different research contexts where evolvability plays roles in evolutionary biological investigation: setting a research agenda, characterization, explanation, prediction, and control. Our analysis of representative examples suggests that the concept of evolvability often plays a role both as a target and as a tool in these contexts, and demonstrates how these roles are crucial for current evolutionary inquiry. We then argue that while these uses of evolvability indicate important relationships across research contexts and conceptual roles, there is still a quasi-independence of roles and conceptualizations—no single conceptual role is most fundamental. This conclusion provides us with the resources to detail two distinct strategies for how evolvability might help to synthesize disparate areas of research and thereby serve as a unifying notion in evolutionary biology.

What is an approach in biology? A case study from behavioral biology

Robert Meunier¹

¹University of Kassel, Institute of Philosophy, Kassel, Germany

Researchers routinely speak of “approaches”. They promote their approach to a phenomenon in their writings and they distinguish their approach from others in the field. Given the prominence of the category in the language of scientists, it seems worthwhile to ask from a philosophical perspective what an approach is. Philosophers occasionally use the term to refer to the work of researchers, often in a contrastive manner. However, in most cases the concept remains unanalyzed. Waters (2004) identifies the genetic approach as an actors’ category central to the work of classical geneticists. He characterizes an approach as an “investigative strategy” or a “pattern of investigative reasoning”. He shows that these geneticists did not merely aim to confirm the theory of transmission genetics, but to put it to use, to generate more knowledge on biological phenomena. In my contribution, I will draw on a case study from behavioral genetics, in particular the work of Jerry Hirsch around 1960, to further characterize what an approach is in experimental biology, and how researchers develop an approach and distinguish it from others, and how it shapes the resulting knowledge. As a first approximation, I will explicate approaches as mediating between a problem and an experimental system. Researchers, when developing an approach, interpret a broader problem pertaining to a realm of phenomena and recognized in a given community, to arrive at a question that can be answered by engaging an experimental system. To understand the way in which an approach shapes the knowledge resulting from taking it, an analogy with perspectives is helpful: Theoretical representations have been described as perspectival, in that they denote aspects of the world to the expense of others (Giere 2006). Interaction with phenomena – like perception – always has a direction and it involves a particular mode of action. To approach a phenomenon then involves moving towards it from a vantage point and to access it in a specific and selective manner. That phenomena are understood from a theoretical point of view requires that they are made accessible from a ‘point of action’. To take an approach also implies that actors position themselves within the community in question. In this way, the actors’ category of an approach can be developed to address pluralism in science on the level of material practice.

Reflections on the use of actors' categories as instruments of historical and epistemological analysis

Hans-Joerg Rheinberger¹

¹Max Planck Institute for the History of Science, Rheinberger, Berlin, Germany

The use of actors categories for historical and social studies of science is not uncontested. In the worst case, it can lead to tautological reconstructions that are of no analytical value. And yet, they have a potential. It consists in bringing conceptualization and the objects of inquiry into closer connection with each other. However, there remains a tension that cannot be resolved. I will argue that it is precisely this tension that has the potential to promote new insights. I will try to exemplify and contextualize this argument by presenting the notion of “experimental system” that I have used as a central category for coping with the dynamics of the modern empirical research process.

Biologies of the South: Negotiating knowledge and livelihoods Part 2

Aadita Chaudhury¹, Nadya Karimasari², Zinhle Mncube³, Jairo Robles-Piñeros⁴, Abigail Nieves Delgado⁵, Arturo Vallejo⁶, David Ludwig⁷
¹PhD Candidate, York University, Toronto, Canada, ²PhD Candidate, Dept. of Sociology and Anthropology of Development, Wageningen University, the Netherlands, ³Lecturer in Dept. of Philosophy, University of Johannesburg and PhD Candidate, Dept. of History and Philosophy of Science, University of Cambridge, United Kingdom, ⁴PhD Candidate, History, Philosophy, and Science Teaching, Federal University of Bahia and UDFJC-Columbia, ⁵Assistant Professor, Utrecht University, the Netherlands, ⁶PhD Candidate, Philosophy of Science/Social Studies of Science, National Autonomous University of Mexico, ⁷Associate Professor, Wageningen University and PI of the "Global Epistemologies and Ontologies" project, the Netherlands

Knowledge about the biological world is produced in heterogeneous geographic contexts and by diverse communities such as smallholder farmers, population geneticists, Indigenous herbalists, or medical practitioners. Addressing this heterogeneity is especially pressing where it relates to local livelihoods in areas such as conservation management, food security/sovereignty, or public health. History, philosophy, and social studies of biology (HPSSB) can contribute to understanding the methodological, ontological, and political dimensions of negotiations between different forms of knowledge production. At the same time, by facing these different biologies, HPSSB can positively expand its methodological, thematic, and theoretical perspectives. This session highlights the potential of HPSSB but also the need for more explicit engagement with global tensions surrounding biological knowledge production. Rather than presenting separate papers, we proceed in four connected steps and answer the following questions:

1. Introduction of 6 case studies.
2. How does HPSSB contribute to better understand each case study?
3. How does each case study challenge HPSSB epistemological resources?
4. Final discussion on the role of HPSSB in negotiating biological knowledge production from a global epistemically diverse perspective.

Case studies and participants:

1. **Unravelling the threads of Dhaka Muslim: colonial ecologies and revivalism.** Aadita Chaudhury, PhD candidate, York University.
2. **The Politics of Taxonomy - The Tapanuli orangutan in Indonesia.** Nadya Karimasari, PhD candidate, Wageningen University. David Ludwig, associate professor, Wageningen University
3. **Decolonising Medicine: On the African Traditional Medicine Case.** Zinhle Mncube, lecturer in University of Johannesburg and PhD candidate, University of Cambridge.
4. **Creating livelihoods: History and methods of Mexican ethnobiology.** Abigail Nieves Delgado, assistant professor, Utrecht University.
5. **Techno-Sciences and Tensions between Agrarian Knowledge Systems. A Case Study in the Northeast of Brazil.** Jairo Robles-Piñeros, Ph.D. candidate, Federal University of Bahia and UDFJC-Colombia.
6. **Chinto Tour 2021: Technoscientific narratives of urgency and compulsion in Mexican citizen science birding.** Arturo Vallejo, PhD candidate, National Autonomous University of Mexico.

Opportunities for ISHers at CSHL: A virtual tour of collections, resources, fellowships, and the Center for Humanities & History of Modern Biology

Alistair Sponsel^{1,2}, Ludmila Pollock¹, Stephanie Satalino¹, Antoinette Sutto¹, Miriam Rich³, Daniel Liu⁴

¹Cold Spring Harbor Laboratory Archives and Center for Humanities & History of Modern Biology, Cold Spring Harbor, NY, ²Harvard University, Program in Science, Technology & Society, Cambridge, MA, ³Yale University, Program in the History of Science and Medicine, New Haven, CT, ⁴Max Planck Institute for the History of Science, Department III, Berlin, Germany

In recognition of ISPHSSB's virtual visit to Cold Spring Harbor, this session invites attendees to learn more about the opportunities for research, collaboration, and funding at CSHL's Library and Archives and the CSHL Center for Humanities & History of Modern Biology. Executive Director Mila Pollock will provide a welcome. She and CSHL Archivist Stephanie Satalino will give a virtual tour of the lab's historic library building and show highlights from the archives. CSHL Historian of the Life Sciences Alistair Sponsel will introduce the recently created "Guide to the CSHL Historical Collections" and other online resources. Sponsel and Pollock will discuss opportunities offered by the Center for Humanities, including research fellowships, public events, and history of science meetings. Three scholars will discuss their experiences doing research in CSHL collections: former CSHL Ellen Brenner fellow Antoinette Sutto, former CSHL Sydney Brenner scholar Miriam Rich, and former CSHL digital humanities historian Daniel Liu. The session will end with an opportunity for Q&A and discussion with attendees.

Plant phenomes and climate change

Özlem Yilmaz¹

¹University of Exeter, Sociology, Philosophy and Anthropology, Exeter, United Kingdom

One of the main driving forces of current plant phenome research is the aim to understand plant responses to climate change for the purpose of increasing crop yields. Without a doubt, this is a very crucial aim; it is also a hugely complex matter that needs involvement of many experts from different areas. In this talk, I will be focusing on plant physiology research related to elevated carbon dioxide (e-CO₂). I will consider which phenotypic traits, what type of other environmental parameters in combination with e-CO₂ and what kind of plants are investigated and why physiological parameters are specifically important for understanding plant responses to changing climate. Physiological parameters like shoot and root weight, shoot to root ratio, photosynthetic rate, stomatal conductivity, root branching etc. are widely measured phenotypic traits. They represent plants' state very informatively and also enable us to create a valuable structure in which to place data coming from other parameters. Plants give various kinds of responses to different combinations of stressors: for example young wheat plants grown in nutrient solution show an increase in shoot weight in e-CO₂ conditions whereas if the growth condition involves both e-CO₂ and Mg deficiency they show decreased shoot weight that is much lower than the plants that are grown in Mg deficient and ambient CO₂ (Yilmaz et al. 2016). No doubt the same cultivar of wheat plants would give different responses to those conditions if they were exposed to them at other stages of their development or if they were grown in different types of soil that has different microbial communities. This is just one example of plant-environment interaction and how it is highly dynamic and complex. Plant phenome research requires meticulous observation and measurement activities in controlled experiment conditions which would be designed in various kinds of ways in hope for better understanding plant interactions with “real” conditions. These conditions are of course vary depending on different areas of the world and also changing with the changing climate. The nature of plant-environment interaction shows that adapting crops to climate change needs specific research that considers local conditions, and that cannot be replaced by the production of “optimal” varieties by big agrobusiness.

Metadata and contextualist epistemology in biology and climate science

David Montminy¹

¹U of Montreal, Philosophy, Montreal, Canada

While the importance of metadata in data intensive science is well recognized, its relation with underdetermination and interpretation is not always clearly defined. In her 2016 book on data and biology, Sabina Leonelli refers to Chang (2004) and says that “... underdetermination is the epistemological motor of data-centric research and grounds the contemporary emphasis on both ‘big’ and ‘open’ data.” She also claims that in order to fully appreciate the evidential value of a given dataset, one must take into account the context in which these data are produced, shared and re-used. This contextualist approach to epistemology can be used to analyze data management practices in another data intensive discipline, i.e. climate science, and more specifically to analyze what the World Meteorological Organization calls “discovery metadata”. Such metadata, unlike observational metadata, for example, “... are intended to facilitate the discovery and assessment of a spatial dataset to determine if it is fit for reuse for a purpose that may be at odds with the reason for which it was originally created” (CDMS 2014). Using Leonelli’s insights and Winter’s (2015) description of the pragmatic structure of scientific theories we can show that climate scientists are indeed giving metadata its epistemological dues, however a review of various databanks and data repository guidelines indicate a significant disparity in the availability and depth of such “discovery metadata”. Finally, we will discuss the topic of shared epistemic responsibility with regards to underdetermination in such large-scale enterprise as the IPCC and its use of metadata, all the while highlighting the differences with projects in data intensive biology (Zumwald et al 2020).

Keywords: Contextualism; IPCC; data repository guidelines; Interpretation; underdetermination; Metadata

Incorporating a feminist understanding of mobilities into quantitative gendered disaster mobility research

Arthur Vandervoort¹

¹University of Exeter, UKRI CDT in Environmental Intelligence, Exeter, United Kingdom

As digital trace data are increasingly leveraged to measure environmental phenomena and their impacts on individuals and communities, their application to disaster mobility research is becoming increasingly commonplace. This is not for nothing – the use of mobile phone data in disaster settings allows for more longitudinal analyses of mobility at an unprecedented scale and granularity, leading to the identification of so-called “hidden” migration and mobility patterns (Lu et al., 2016), as well as tentative attempts to identify gendered differences in such patterns (Bosco et al., 2019). Within this paper, I respond to a call for more feminist conversations within big gender data work (Vaitla et al., 2020) by arguing that the recent development of a discursive subjectivities-based approach with the purpose of investigating climate-induced (im)mobility has significant implications for quantitative analyses of (gendered) disaster mobility research. Arguing from a poststructural feminist perspective, I argue that a discursive subjectivities approach can add to quantitative gendered mobility research by providing crucial information on the socio-psychological factors which co-constitute mobility, helping incorporate an understanding of immobility into mobility analyses. Furthermore, discursive subjectivities provide a meaningful counterpoint to the disembodied objective framing of mobility flow analyses, refocusing attention on the research subject and inviting investigation into which aspects of an individual’s mobility are represented by the digital trace data, and which are not. Finally, discursive subjectivities can serve to turn the tools of research inward, helping to uncover the often unstated ontologies and epistemologies present in quantitative mobility research, encouraging a more negotiated form of empiricism cognisant of its own epistemological position (Code, 2006). Positioning itself between the emerging literatures around quantitative disaster mobility and gendered disaster (im)mobility, this paper provides an investigation into how feminist poststructural work can provide a meaningful contribution to research looking to use digital trace data in order to identify and quantify environmental phenomena and the way individuals and communities respond to them.

The elastic ruler: Placebo responses, clinical trials, and medical epistemology

Shane N Glackin¹

¹University of Exeter, EGENIS/Department of Sociology, Philosophy, & Anthropology, Exeter, United Kingdom

An elastic ruler, Wittgenstein writes, would be useless for purposes of measurement. But this is the situation of most modern medical knowledge. The “gold standard” for measuring efficacy of medical therapies is double blind testing against placebo; therapeutic response to placebo is the “zero point” against which treatments are measured. But this zero is not constant; it varies with a host of demographic and genetic factors. Medicine, in short, is measured with an elastic ruler.

As so often, Wittgenstein's phrasing masks an engineer's technical precision. Following Stevens' classic schema, Measurement Theory distinguishes between four kinds of scale; nominal, ordinal, interval and ratio. Nominal scales distinguish categories but are not ordered, whereas ordinal scales are; they allow objects to be compared and ranked but do not permit arithmetical operations on values (e.g. the Beaufort Wind Scale). Interval scales permit such operations on intervals between values, but not on values themselves, since their zero-point is arbitrary (e.g. Celsius and Fahrenheit); ratio scales, with a non-arbitrary zero (e.g. Kelvin, or km/h), have the same algebraic structure as the real numbers, with meaningful sums and ratios.

Medical intervention is treated, in short, as if its empirical structure maps to a ratio or interval scale; in fact, lacking even a fixed zero-point, it maps at best to an ordinal scale which may not properly qualify as “measurement” at all. Moreover, since the absence of a fixed point may preclude a consistent transitive ordering, even a true ordinal scale may be unavailable. Put another way, if RCTs are an instrument for measuring medical efficacy, we have no way of calibrating it.

Fortunately, all is not lost. As Peter Hacker has pointed out, measurement in “elastic ruler” systems with no fixed point is intelligible in some circumstances, e.g. currency exchanges. Because the magnitude of placebo responses, though dynamic, is relatively stable (like the actual gold standard in currency systems), a “sceptical solution” to the problem is possible; we accept the lack of an objective measure for medical efficacy, but show we can do without one.

Louis Daniel Beauperthuy: His reflections on the causation and transmission of tropical diseases from 1838 to 1871

Irene Bosch¹

¹Massachusetts Institute of Technology, IMES, Cambridge, MA

Louis-Daniel Beauperthuy (1807-1871) was a naturalist researcher and a medical doctor born on the Island of Guadalupe (French Antilles) who graduated from the Medical School in Paris. He established himself with his family in the city of Cumaná, in eastern Venezuela, where he led an intense life as a Naturalist Traveller of the Muséum National d'Histoire Naturelle (MNHN) in Paris, France and as a medical doctor from Venezuela and France. In 1853, during a Yellow Fever epidemic in Cumaná, Beauperthuy proposed the connection between mosquitos and the spread of the diseases, including fevers like Yellow Fever, malaria, and other tropical fever diseases. This was almost fifty years before the experimental confirmation was carried out by the U.S. Yellow Fever Commission. Among other observations of Beauperthuy were those relating to Cholera and Leprosy. In 1853, after a large magnitude earthquake, a cholera epidemic occurred in the city of Cumaná, Venezuela where Beauperthuy was working as a medical doctor. He observed in patients' stools a great number of vibrios using the highest power lens in the microscope. These observations were published in the *Gaceta Oficial de Cumaná* (1854) almost simultaneously and independently with Pacini's work in Italy, he published in the *Comptes Rendus des Séances de l'Académie des Sciences* of Paris. His goal was to travel throughout the different provinces of Venezuela, through the Caribbean islands and in the surrounding parts of South America so as to collect samples in these three regions representing the different branches of the local natural history. He worked for the MNHN between 1838 and 1841 and able to classify, catalogue and ship a large number of samples from different Caribbean islands and from the mainland Venezuela (Tierra Firme or Gran Colombia). Yellow Fever work was documented travelled in the Caribbean, Cuba, according to medical Cuban doctor Louis Perna. We analyzed the scientific notebook of Jesse Lazear written in Cuba, Columbia Barracks, with detailed information of the mosquito transmission of Malaria and Yellow Fever. Due to self experimentation and becoming the Guina Pig No.1, Lazear succumbs, defending his idea of the insect transmission of Yellow Fever.

An epistemological inquiry into phage therapy: Results and findings

Thomas Bonnin¹

¹Universite Clermont Auvergne, Philosophie et Rationalites, Clermont-Ferrand, France

Bacteriophages (or phages) are viruses that have bacteria as their hosts. Their therapeutic use, "phage therapy", is a century-old strategy against bacterial diseases.

Briefly put, phage therapy's history follows three stages: (a) initial enthusiasm and interest in a time of "powerlessness" against bacterial infections (the 1920s-1940s); (b) phage therapy is "eclipsed" by antibiotics, with anecdotal production and use, except for the Soviet bloc (1940s-1990s), and (c) rekindling of interest over the increasing concern for antimicrobial resistance (1990s-now).

The rich history of phage therapy is a reservoir of epistemological inquiries. One concerns the development of clinical knowledge about phage therapy. A common trope in contemporary advocates for phage therapy is to highlight how little was known about bacteriophages during the first wave of interest. In this view, contemporary phage therapy would be grounded on a much-firmer understanding of phages' in vivo behaviour. How much is actually known today? How comparatively extensive is it compared to pre-WWII knowledge? A survey of the contemporary pharmacokinetic and pharmacodynamic knowledge about phages enables the identification of lurking unknowns and knowledge that define a clearer (albeit more restricted) scope of application for phages.

A second, related, topic is tied to the clinical evaluation of the efficiency of phage. The first phase of interest ended with agnostic reviews about phage therapy. Specially-commissioned reports by the US Council of Pharmacy and Chemistry concluded that the current contradictory clinical evidence was of insufficient quality to warrant any (positive or negative) conclusion about the therapeutic efficiency of phages. This means, among other things, that phage therapy posed a problem which pre-WWII method of evaluation was unable to overcome. The second half of the 20th century witnessed the rise in prevalence of a "gold standard" for the scientific evaluation of therapeutic strategy: the randomized controlled trial. Has this created the condition for unequivocal evaluation of phage therapy? The examination of recent clinical trials shows that there remain scientific, ontological, as well as infrastructural challenges. This has not yet permitted a conclusive evaluation of phage therapy.

***The Genetical Theory of Natural Selection* and the controversy over R. A. Fisher's eugenics**

Alex Aylward¹

¹University of Leeds, School of Philosophy, Religion and History of Science, Leeds, United Kingdom

In June 2020, students at Gonville & Caius College Cambridge launched a petition calling for the removal of a stained-glass window commemorating a former student and Fellow, the statistician and geneticist Ronald Aylmer Fisher (1890–1962). The petition, which cited Fisher's troubling views on race and his lifelong support for eugenics, was a success. The College's Council voted in favour and within a few weeks, the window had been removed.

Whilst the recent #FisherMustFall campaign was catalysed by the global BLM movement and the recent Inquiry into eugenics at University College London, the controversy over Fisher's eugenics has a much longer history. Since the 1970s, several prominent historians and sociologists of science have argued that Fisher's eugenical commitments were crucial in motivating and shaping his vaunted scientific contributions to population genetics and evolutionary theory. Many biologists (several of whom worked with or under Fisher) have steadfastly denied this claim, either by questioning the extent of Fisher's eugenic commitments, or otherwise denying their relevance to his scientific work.

A consistent focus in this long-term controversy, as well as in the recent #FisherMustFall campaign, has been Fisher's celebrated book of 1930, *The Genetical Theory of Natural Selection*, which notoriously closes with five eugenical chapters on the decay of civilisations. My doctoral research project takes this book as its focus, examining *The Genetical Theory's* composition, publication, reception, and legacies. In this talk, I will discuss some of the major novel findings of my research, demonstrating how they shed new and important light on the ongoing controversy over Fisher's eugenics.

Heredity mobilized: From Mendelism to eugenics in the name of the Greek race

Ageliki Lefkaditou^{1,2}

¹University of Oslo, Museum of University History, Oslo, Norway, ²University of Leeds, School of Philosophy, Religion and History of Science, Leeds, United Kingdom

“They are fatal and relentless for humans too, the laws of heredity first discovered by the monk Gregor Mendel,” wrote the Greek anthropologist John Koumaris in 1939 in a newspaper article entitled “Mendelism and Humanity”. While seemingly out of date with leading geneticists who by that time were emphasizing genetic complexity, Koumaris’ views capture eloquently the kind of double language employed by those scholars working at the intersection of anthropology, genetics and eugenics. Indeed, when Koumaris was writing this article, the idea that hereditary traits were passed on in a simple recessive/dominant fashion had given way to more complex understandings of possible interactions between multiple genes, or even between genes and the external environment. Geneticists at the Kaiser Wilhelm Institute for Anthropology, Human Heredity, and Eugenics, with whom Koumaris was closely affiliated, had coined the term “higher Mendelism” to describe this complexity. As his article reveals, despite proclamations such as the above quote, he was mindful of the negotiations between an ever-increasing understanding of genetic complexity and the requirements for its simplified application through eugenic measures.

Here, I examine the origins of Koumaris’s thinking, both within Greece and internationally, by looking at how Mendelism, and even anti-Mendelism, developed a symbiotic relationship with eugenics. Through a close reading of works by members of the Hellenic Anthropological Society, that Koumaris led as a lifetime secretary, I focus on how mobilizing hereditary knowledge for the benefit of society led a number of these actors to discuss and suggest eugenic measures as the long-term solution to social ailments. In the course of these discussions, Mendelism and heredity—often treated as synonymous—operated as both a research question and an assumption or interpretative scheme not to be tested. While transnational networks supported the whole enterprise, the transdisciplinary discussion within Greece created an intellectual atmosphere of unity and common cause despite diverging views. In this sense, anthropology became again a science in the service of the nation, but now looking inside that community and even—figuratively and literally—under its skin to improve its qualities.

Teaching science through eugenics and the expansion of semen banks in USA

Ma-Alicia Villela¹

¹National University of Mexico, Evolutionary Biology Department, School of Sciences, Mexico, Mexico

Education is not neutral and it always has a value, a position or a political point of view. This work shows how to use some elements of the history of science with the eugenic movement in USA to explain which where some theories of understanding about biological inheritance.

Perhaps no theory in modern times has had so great a social impact and has been researched as many diverse perspectives as the eugenics movement is being studied now within the history of science.

The history of the eugenics movement in the United States is a remarkable case study showing how eugenicists convinced that the future of the United States depended on the protection of “the race” used involuntary sterilization. I begin my lecture with eugenic sterilization in California institutions and I have students read portions of primary sources to help them to understand those explanations in their own historical context and together we explore how and why eugenics took different responses around the world.

One of the main questions that are addressed using the history of science in science education is whether eugenics continues to influence the views and policies of some reproductive sperm banks, because interpretations of biological inheritance and race matters match well with social popular beliefs, moving away from genuinely scientific conceptions. Students examine and debate how the concept of “race” gained its modern currency in popular and scientific discourse and has evolved into an organizing principle for political theory and social policies. This project shows the existence of eugenics ideas in school education. The purpose of this education project is to uncover eugenics ideology in the currently sperm banks.

The extended evolutionary synthesis: A Gouldian perspective

Max Dresow¹

¹University of Minnesota, Philosophy, Minneapolis, MN

Calls for an enlarged evolutionary theory have been around for many decades, but for much of this time, they have cut virtually no scientific ice. In 1980, Stephen Jay Gould asked whether “a new and general theory of evolution [was] emerging,” and was roundly criticized for suggesting that it was. Then, four years later, a volume called *Beyond Neo-Darwinism: An Introduction to the New Scientific Paradigm* fell from the presses with a thud. Scattered calls for an extended evolutionary theory were heard over the next twenty years, but the issue lay mostly dormant until 2008, when a now-infamous meeting was held in Altenberg under the name “Towards an Extended Evolutionary Synthesis.” The meeting grabbed headlines, in part because it quickly became the subject of creationist misrepresentation. Still, it achieved its goal of stimulating interest in an “extended evolutionary synthesis” (EES), and since that time, the issue has been more-or-less continuously under discussion, helped along by a generous grant from the John Templeton Foundation. The results of these discussions have been decidedly ambiguous. Advocates of an EES maintain that “standard evolutionary theory” (SET) needs a significant overhaul, reaching all the way to its metaphysical building-blocks. Their interlocutors deny this. The EES merely puts old wine in new bottles, they say. As such, there is no need to revise the conceptual structure of evolutionary theory, still less to raze it to the ground.

The goal of this paper is to explore the space between these polarized positions. To do this, I will pursue a twofold strategy. First, I will argue that there is no such thing as SET, even though there is something we might easily confuse for it: a set of increasingly abstract theoretical commitments that can claim a sort of retrospective stability. Second, I will argue that the challenge posed by the EES can be understood as a set of smaller (and mostly independent) challenges directed at different “themes of Darwinian logic” (Gould 2002, 13). Using resources from Gould’s *Structure of Evolutionary Theory*, I will analyze these challenges and compare them to past challenges to mainstream evolutionary theory, including Gould’s own. In addition, I will draw a normative conclusion from the bundle structure of the EES regarding the appropriate goal for critics of “SET.”

Shifting problem structures and the rebundling of specialties

Elihu M Gerson¹

¹Tremont Research Institute, San Francisco, CA

The Modern Evolutionary Synthesis (MES) organized evolutionary research along two major lines of cleavage: physical scale (molecular to macroevolution), and perceived independence of phenomena (e.g., transmission vs development, environment vs organism). As a side effect, specialties focused on the way things fit together were largely excluded from the MES. Since the late 1970s, multiple lines of research have been recasting these lines of cleavage. Boundaries among specialties delimited by physical scale (molecules, cells, populations, clades, etc.) are weakening; emerging problems (e.g., plasticity and evolvability) routinely span two or more levels of scale. At the same time, concern with interdependence among phenomena has been increasing, as exemplified by work on evo-devo, symbiosis, coevolution, niche construction, and other problems.

The weakening, shifting, and reforming of specialty boundaries is transforming the character and scope of evolutionary biology. New ways of acquiring and working with data have been very important. Molecularization has transformed almost every line of evolutionary research, leading to the discovery of new phenomena and their characterization (e.g., the three domains hypothesis; holobionts). The use of computing has become pervasive, and many lines of research (e.g., modern forms of classification and phylogeny; genomics) are dependent upon it. Third, the development of many new and more powerful instruments (e.g., various forms of advanced microscopy) and other laboratory techniques have enabled far greater detail and precision in data collection and analysis. Shifting specialty boundaries also reflect changing theoretical concerns, such as the reconceptualization of, and increased concern with, inheritance of acquired characters, and the nature and limits of selection and adaptation. There has also been extensive recharacterization of phenomena (e.g., genotype-phenotype mapping), and reformulation of problem agendas.

As a result of these changes, the boundary lines among specialties of evolutionary biology are in the midst of a major realignment. The outcome of this process is not yet clear, but it seems likely that future work will be organized in part around system/environment interdependence at many levels, and a continuing shift away from focus on understanding how similar things form aggregates, to understanding how dissimilar things form compositions.

G.G. Simpson & S.J. Gould on values: Shifting normative frameworks in historical context

Alison K McConwell^{1,2,3}

¹University of British Columbia, Philosophy, Vancouver, Canada, ²UC Davis (Visiting), Philosophy, Davis, CA, ³Stanford (Visiting), Philosophy, Stanford, CA

George G. Simpson (1902-1984) and Stephen J. Gould (1941-2002) were both engaged with the normative—social, cultural, political, and even ethical—consequences of their evolutionary theorizing, however, there is a point of departure between Simpson and Gould’s work that has received little attention. That departure, I contend, exemplifies a shift in normative framework that occurred more than a decade after the peak of the modern synthesis. Leading up to and during what Gould dubbed the “hardening” of the synthesis in the 1950s, Simpson (1941, 1952) continued to frame his work on evolution by attempting to draw value-laden consequences, such as existential questions about human improbability, social impact in terms of (political) organization, and the desirability of a synthesis between behavior and evolution. In his autobiography (1978, 274) published just six years before his death, Simpson proudly took his work to have honorably entered the arena on such matters. However, Gould (1986, 1999) was well known for his concerns over safely drawing lessons about culture and society from evolution. Gould thought that emphasis on the biological basis of socially-charged issues like behavior, culture, psychology, etc. were fraught with assumptions about biological determinism, and as such were dangerous in their implicit justification of discriminatory prejudices. Gould, unlike Simpson, distanced himself from drawing normative consequences about his own work and publicly denounced attempts to do so (e.g. Wilson 1975, Gould 1986). There is, however, archival evidence that throughout his time at university, and perhaps even very early career, Gould was mining for some way to connect evolution and ethics/values, and later abandoned that search. If Simpson and Gould roughly exemplify modern and extended (or developing) synthesis work, respectively, then the shift in normative tendencies arguably tracks a shift in thinking about values, ethics, and society in relation to biology after the heyday of the modern synthesis.

Book panel: Four tales from the world of small things

Claas Kirchhelle¹, Victoria Lee², Neeraja Sankaran³, Robin Scheffler⁴

¹University College Dublin, School of History, Dublin, Ireland, ²Ohio University, Department of History, Athens, OH, ³Utrecht University, Descartes Centre for the History and Philosophy of the Sciences and the Humanities, Utrecht, Netherlands, ⁴Massachusetts Institute of Technology, Program in Science, Technology, and Society, Cambridge, MA

The individuals may be tiny, but the microbial world is vast, as is the history. In this book panel, the authors of four new works discuss how the history of microbiology goes far beyond the germ theory, looking into the twentieth century and to various aspects of different kinds of microbes, and linking them in diverse ways to macrolevel history. Viruses, entities at the most fundamental level of life, are the focus of Scheffler's and Sankaran's books. Scheffler's *A Contagious Cause* (2019) traces the century-long hunt for a human cancer virus in America, illuminating how the endeavor to translate laboratory discoveries into useful medical therapies merged the worlds of molecular biology, public health, and military planning. In *A Tale of Two Viruses* (2021), Sankaran draws parallels in the research lives of two groups of medically important viruses: bacteriophages, which infect bacteria, and sarcoma agents, which cause cancer. They highlight the flux in scientific concepts over time, as the discovery of the viral identity of bacteriophages and certain types of cancer faced opposition from researchers until the 1970s. Turning to bacteria and fungi, Kirchhelle's and Lee's books focus on agriculture and industry, respectively. Kirchhelle's *Pyrrhic Progress* (2020) shows how antibiotics helped revolutionize US and British food production after 1945, but it came at a price. His analysis reconstructs the negotiations between consumers, farmers, and regulators to provide insights for current debates on the global burden of antimicrobial resistance. Lee's *The Arts of the Microbial World* (forthcoming 2021) showcases the role of indigenous techniques in twentieth-century Japanese fermentation science. At a moment when twenty-first-century developments in the fields of antibiotic resistance, the microbiome, and green chemistry suggest that the traditional eradication-based approach to the microbial world is unsustainable, it provides a broader vantage for understanding microbial interactions with society.

A turn to the organism in synthetic biology?

Erika A Szymanski¹, Jane Calvert²

¹Colorado State University, English, Fort Collins, CO, ²University of Edinburgh, Science, Technology and Innovation Studies, Edinburgh, United Kingdom

The organism is often notably absent from synthetic biology. Some synthetic biologists even pride themselves on their ‘organism agnosticism’, aiming to construct standardized biological ‘parts’ that can be inserted into any stripped-down cellular ‘chassis’. But does the situation change when whole genomes are synthesized? Our study of the synthetic yeast project suggests it does: the yeast and its distinctive characteristics figure centrally in this project, and the scientists often describe themselves as working with the yeast to achieve their design goals. We present the early stages of a social scientific research project asking whether there is a similar ‘turn to the organism’ in other whole genome synthesis projects. Such a turn is potentially significant because organisms come with established relations to social worlds both inside and outside the lab, relations that could be reconfigured if new types of organism are synthesized in the future. Moreover, the particular and affective relationships that scientists form with the organisms with which they work challenge the assumption that synthetic biology is a strictly reductionist science and may make space for broader conversations about its objectives.

Biological ownership and open source: Peculiarities seen through DIYbio

Daphne Esquivel-Sada¹

¹University of Ottawa, School of Sociological & Anthropological Studies, Ottawa, Canada

This communication aims to shed some light on an usually overlooked yet crucial dimension in scholarship about the open source regime, namely, the peculiar and paradoxical relation of this model to ownership, all the more when it is transposed into biotechnosciences. To do so, I explore the case of Do-it-yourself bio (DIYbio). Seen as an embodiment of “open science” and “open innovation”, DIYbio endeavours to bring molecular biology and biotechnological tools to the hands of the “public” for individual autonomous use, freeing these tools of political, social, and normative institutional grips. Because of the proximity of DIYbio to hacker ethos and the open source development model, the tendency is to believe, more or less implicitly, that DIYbio epitomizes a movement of opposition to the patent system on biotic entities, or at least that it holds a critical distance from the intellectual property (IP) regime underlying such system.

The reality appears to be rather well more nuanced and complex, according to the results of an empirical qualitative study of the DIYbio network, based on discourse analysis of 25 qualitative interviews, conducted mostly in North America, with members of the network. Drawing on interdisciplinary science studies scholarship, especially around hacker culture and biotechnologies, the analysis unravels how IP and patent rights over biological entities are seen by the participants. It shows that even though adepts of DIYbio do tend to express eminently discordant visions with regards to the traditional patent system and sympathetic ones to the open source model, the overwhelming majority of them remain attached to the application of intellectual property rights to living organisms for distinct reasons. Lastly, the analysis reveals that the open source system can coexist functionally with the traditional IP system, while pushing to its paroxysm the sense of ownership over living entities, leveraging a symbolic regime of ownership.

Notions of microenvironment in organoids and organs-on-a-chip

Silvia Caianiello¹, Marta Bertolaso¹

¹CNR, Institute for the History of Philosophy and Science in Modern Age, Dept. Human Sciences, Naples, Italy, ²Università Campus Bio-Medico di Roma, Faculty of Science and Technology for Humans and the Environment, Rome, Italy

In the last decade, the new 3D microphysiological systems in vitro have raised hope to steer the virtuous cycling between wet and dry experimentation, characteristic of Systems Biology, at a higher level of resolution, fostering a multilevel approach both in the dry and in the wet lab. We will argue that the two major families of 3D advanced in vitro organotypic models, organoid and organs- and body-on-a-chip, move from two different notions of microenvironment, stemming respectively from stem cell research and tissue engineering. Consequently, they adopt two different strategies of selective “recapitulation” of the microenvironment, which entail a different choice in the appropriate level of control of the experimental system. On this basis, we will argue that the current systematic effort for their merging entails not only innovative “synergistic” engineering solutions (Takebe et al 2017), but also conceptual negotiations among epistemic and ontic dimensions of biological integration’s processes.

Modalizing Darwin: Rhetoric across the editions of *On the Origin of species*

Pedro L Navarro¹

¹University of São Paulo, FFCLRP, Ribeirão Preto, Brazil

Charles R. Darwin (1809-1882) travelled a long and bumpy road from the first sparks of his theory in 1839 until the publication of *On the Origin of Species* in 1859. However, this was not the only iteration of his text. Due to the urgency caused by the arrival of Alfred R. Wallace (1823-1913) manuscript, John Murray's (1808-1892) publication practices, and the impact the book had on Victorian society, Darwin followed with five more editions until 1872. Each edition was more revised and augmented than the last, which naturally made the comparison of their texts an exciting and necessary research question. After the first physical variorum was published in 1959 by Morse Peckham, Barbara Bordalejo used digital collation techniques to launch the *Online Variorum of Darwin's Origin of Species* in 2009. This tool made the study of the *Origin's* editions more practical and made it possible to identify Darwin's specific behavioural trends while revising his book. In this communication, we aim to look at these trends through Bruno Latour's approach concerning rhetoric in scientific literature. In his *Science in Action* (1987), Latour proposed that scientists can modalize a statement positively to present it as a fact or negatively to show that it is still open to discussion. After a preliminary comparison of all editions, we could detect a trend of positive modalization in the *Origin*, which may be explained by the growing acceptance of Darwin's theory towards the following decades of the 19th century, reflecting in a more confident author and consequently his text.

Antoinette Brown Blackwell on women's rights, metaphysics, and evolution

Trevor Pearce¹

¹University of North Carolina at Charlotte, Philosophy, Charlotte, NC

Antoinette Brown Blackwell was one of the first women to be ordained as a minister in the USA; she was also one of its first feminist philosophers of science. In this chapter I will show that Blackwell's early writings, despite being committed to the reconciliation of biology and philosophy, rejected the agnostic and quasi-materialist evolutionary philosophy of Herbert Spencer and others. Her position contrasted with that of the physician and philosopher Frances Emily White. Although both White and Blackwell wrote feminist critiques of Darwin and Spencer in the 1870s, White did so from the perspective of a strict materialism, whereas Blackwell argued that evolution was compatible with dualism and personal immortality.

A tale of two anteaters: Madrid 1776 and London 1853.

Helen L Cowie¹

¹University of York, History, York, United Kingdom

In 1776, the first living giant anteater to reach Europe arrived in Madrid from Buenos Aires. It survived six months in the Real Sitio del Buen Retiro before being transferred to the newly-founded Real Gabinete de Historia Natural. Seventy-seven years later, a second anteater was brought to London by two German showmen and exhibited at a shop in Bloomsbury, where it was visited by the novelist Charles Dickens. The animal was subsequently purchased by the Zoological Society of London, which classed it ‘by far the most important addition, in a scientific point of view, which has been made to the collection since its commencement’. Drawing on recent work in animal biography, this article assesses the reception of the two anteaters and considers their cultural and scientific significance. I examine the logistics of the exotic animal trade and trace the transatlantic networks that permitted anteaters – and knowledge about them – to move between continents. I also study the technologies of representation that enabled the insectivores to reach new audiences – from painting to taxidermy. By focusing in detail on the lives of two exceptional anteaters, the article illuminates understandings of the species more broadly and shows how different spaces and places shaped the creation and dissemination of zoological knowledge. I emphasise, in particular, the tensions that emerged between imperial and colonial science and the competing knowledge regimes of the natural history museum, the menagerie and the field. Who was a more reliable authority on American fauna: the keeper who cared for an insectivore in a zoo, the scholar who studied stuffed anteaters in the metropolitan museum or the travelling naturalist who studied living specimens in Paraguay or Brazil?

How to get into the pouch: Research on the riddle of the kangaroo birth inside and outside the zoo (1823-1926)

Oliver Hochadel¹

¹CSIC, IMF, Barcelona, Spain

Ever since Europeans sighted the first kangaroo in Australia, it posed riddles galore to naturalists. For example: were Marsupials real mammals? One question proved a particularly hard nut to crack and led to a century-long debate: how do kangaroos actually give birth? The advent of the zoo in the first half of the nineteenth century made it possible, at least in principle, to tackle the problem through observation. British naturalist Richard Owen enlisted the Regent's Park Zoo in London to devise a research program. He put forward the hypothesis that the mother put the tiny embryo into the pouch using her lips but could not observe it as such. Naturalists in other European zoos were eager to come up with definite observations such as Theodor Leisering, a veterinarian at the Zoologische Garten in Berlin, and Ernst Pinkert, the owner of a private zoo in Leipzig.

In its first part this paper will analyze the reports published by European naturalists. In what way did they use the zoo as a resource? What was the epistemic value of observations as opposed to the classical anatomical approach (dissection)? What role did the animal keepers play who had been told to observe the pregnant kangaroo day and night?

In the second part this paper will contrast the European zoo-based investigations with the observations made by naturalists, hunters and farmers in Australia in the late nineteenth and early twentieth centuries. The riddle of the kangaroo birth had become a question much debated in the Australian public sphere, in particular in newspapers. In how far was this research conducted outside the zoo different to the European one?

Finally, this paper will ask in what ways information about the reproduction of marsupials circulated between continents - or not.

Mediterranean dolphins from Miami: Knowledge and practices in Aquarama of the Barcelona Zoo in the 1960s

Miquel Carandell Baruzzi^{1,2}

¹History of Science Institute, Universitat Autònoma de Barcelona, Barcelona, Spain, ²Natural Sciences Museum Granollers, Heritage and Archive, Granollers, Spain

In May 1965, in the midst of Franco's dictatorship in Spain, four Bottlenose Dolphins travelled by boat from Miami to the Barcelona Zoo. These became the first inhabitants of one of the first dolphinariums in Europe. The construction of the "Aquarama", the name given to the cetaceans' installation, was the pinnacle of a great transformation of the Barcelona Zoo: from an old-fashioned zoo to a larger and "modern" institution. The arrival of the Dolphins was preceded by two trips of the Zoo director, together with an architect and a politician, to visit the installations of the Miami Seaquarium, Sea World San Diego and Los Angeles Marineland. The dolphins, purchased from the Miami Seaquarium, arrived in Barcelona accompanied by a trainer who stayed on for a couple weeks in Barcelona.

In this paper I want to reflect on how knowledge and practices about a completely new animal and its keeping were built in the particular setting of the zoo, the specific geographical conditions of Barcelona, and the political context of the dictatorship. How did the Barcelona Zoo keepers managed to gather information on the building and keeping of a dolphinarium? And how did they gather knowledge on how to feed, care for and exhibit the dolphins? Did they encounter problems to get this information? How did the Barcelona managers relate to the other European new dolphinariums? Beyond, practical knowledge, were they interested in acquiring scientific knowledge? How was the Aquarama integrated into the broader zoo visit? How were dolphins adapted to the climatic conditions of a Southern European Mediterranean city? How did the political aims of the dictatorship shape this knowledge making?

Endocrine disruptors: From the Wingspread Conference (1991) to the EU comprehensive chemicals strategy for sustainability (2020): 30 years of scientific research

Ana M Soto^{1,2}, Carlos Sonnenschein^{1,2}

¹Tufts University School of Medicine, Immunology, Boston, MA, ²Ecole Normale Supérieure, Centre Cavailles, Paris, France

Background: Dr. Theo Colborn and her collaborators' survey on the state of the environment in the Great Lakes area revealed a plethora of adverse health outcomes involving hormones (thyroid function, abnormal gonadal development and hermaphroditism). She wondered whether these devastating health effects were the consequence of the lowering levels of estrogenic chemicals following the introduction of regulations by the EPA in the 1970s. If this was the case, there was nothing else to do but wait for a further lowering of these levels. Instead, the accidental discovery of estrogens in plastics and detergents at that time revealed that there were xenoestrogens in the environment that were yet to be regulated.

The Wingspread Declaration: In 1991 Dr. Colborn brought together a group of scientists to discuss the state of the environment in the Great Lakes area. They unanimously asserted that, "Many compounds introduced into the environment by human activity are capable of disrupting the endocrine system of animals, including fish, wildlife, and humans. Endocrine disruption can be profound because of the crucial role hormones play in controlling development." We will address the scientific bases that led to the concept of "endocrine disruption", the development of this field and the ongoing theoretical work on this subject. Additionally, we will briefly cover the role of industry and certain regulators on the creation of doubt and ignorance that hinder regulatory action.

Conclusions: Sufficient data have been gathered on the deleterious effects of endocrine disruptors to warrant immediate action to decrease human exposure to these agents by means of a well-thought out and enforceable public health policy. To speed up this process we propose to foster theoretical work leading to the identification of fundamental principles both for the sake of finding accurate explanations of phenomena, and to perform regulatory science, informed by a proper theoretical framework. We expect that endocrinologists now armed with rigorous principles and a clear understanding of when "enough is enough" could help to overcome the delaying tactics aiming to derail the EC strategy.

Theorizing biological disruptions: The case of endocrine disruptors

Maël Montévil^{1,2}

¹Université Paris 1, IHPST, Paris, France, ²IRI, Paris, France

The notion of disruption is used broadly in the scientific literature to describe anthropogenic, detrimental effects on living beings, from organisms to ecosystems. However, this notion is missing a proper theoretical and conceptual elaboration. Why do living beings display specific vulnerabilities to some perturbations that are described as triggering disruptions? In particular, what distinguishes endocrine disruptions from mere perturbations?

We discuss the notion of disruption in the case of endocrine disruptors by first building on examples. We contend that disruptions are the randomization of natural history outcomes that contribute to viability. In the case of endocrine disruptions, development complexifies the picture, and it was the first argument for the specificity of this phenomenon. Another critical aspect of the analysis is the technological lineages leading to new molecules from the disrupted biological lineages' perspective.

By conceptualizing and theorizing disruptions further, we hope to contribute to the scientific knowledge of these phenomena, build bridges between different fields studying different kinds of biological disruptions, and facilitate their understanding by the general public.

Another trajectory: Endocrine disruptors in France

Nathalie Jas¹, Jean-Paul Gaudillière²

¹French National Research Institute for Agriculture, Food and Environment , IRISSE, Paris, France, ²Inserm, CERMES3, Paris, France

Originally American, the issue of endocrine disruptors (EDs) has rapidly become international. However, this process remains largely to be understood. In order to explore it, this paper focuses on the double movement of generalization and localization that underlies this internationalization. Based on a comparative study between the United States and France, this paper analyzes the beginnings of the French EDs' trajectory. The events targeted are those that occurred before 2007, that is, well before EDs became an object of visible controversy in France, with the increasingly important investment of a heterogeneous set of activist organizations. The paper will question the common idea that the introduction of EDs in France was solely the result of medical circles interested in male infertility. It will also show that these early developments reveal the existence of a publicly "invisible" phase of appropriation and configuration of the problem of endocrine disruptors, revealing a French regime of expertise in environmental health problems and chemical risk management that relies heavily on collaborations between the State, industry and academic researchers. In doing so, the paper analyzes the characteristics of the first French system of expertise and research on EDCs and its specificities with respect to the American trajectory.

"Your genitals don't lie!" An escorted encounter with the history and philosophy of phallic and cervical measuring

Merlin Wassermann¹, Rebecca Jackson², Caterina Schuerch¹, Kärin Nickelsen¹, Jutta Schickore²

¹Ludwig-Maximilians-University, History of Science, Munich, Germany, ²Indiana University Bloomington, Department of History and Philosophy of Science and Medicine, Bloomington, IN

In this session, we escort you into the baffling and scary world of phallometry and cervimetry: We examine how researchers studied psycho-physiological phenomena by measuring the penis and the cervix. You are introduced to devices that look like modern torture instruments to the uninitiated. These instruments populated the laboratories of obstetricians and sex researchers only a few decades ago, and some are still in use today. They were used to answer questions like: Is this subject's impotence psychologically or biologically caused? Should doctors perform a C-section, or is "natural" labor safer? Or: Is this subject attracted to men, women, or clouds?

We analyze from historical and philosophical perspectives how researchers dealt with the challenges they faced: While the organs to be measured were sensitive and relatively inaccessible, the processes under study – sexual arousal/attraction and labor progress – were complex and often ill-defined. One obvious difficulty was that the instruments (the phallo- and cervimeter) affected the subjects' bodies as well as psychological state and thus interfered with the phenomena to be measured. Another difficulty was that each subject's "normal" varied widely so that deviation from the normal was difficult to ascertain or even define.

As the issues of standardization, validation, and conceptual clarification are problems associated with measuring in general, analyzing how they were identified, overcome or circumvented makes the study of phallo- and cervimetry as interesting as it is bizarre.

Norms of conceptual development in the life sciences

Philipp Haueis¹, Corinne Bloch-Mullins², Uljana Feest³

¹Bielefeld University, Philosophy, Bielefeld, Germany, ²Marquette University, Philosophy, Milwaukee, WI, ³Leibniz University Hannover, Philosophy, Hannover, Germany

Work on scientific concepts have recently taken a practice turn, with philosophers analyzing the role concepts play in experimentation, classification and modeling. This literature implies that scientists modify their concepts to better achieve their epistemic goals. But when does conceptual development lead to more successful science, and when does it fail to foster epistemic goals? This session discusses these questions with regard to conceptual development in the life sciences.

First, Philipp Haueis articulates norms which guide how researchers (I) introduce a concept in a local context, (II) extend it to novel cases, (III) decide when it should be restricted, replaced or abandoned. Using the development of “cortical column” as an example (I) is successful when the concept identifies an *anchoring property* characteristic of the phenomenon studied and when it is *open-ended*—applicable beyond the local context. Second, (II) extending a concept is legitimate when the technique used to apply it is *reliable*, the domain to which it is applied is *homogeneous* and the property it picks out is *significant* to achieve epistemic goals. Third, (III) a concept should be restricted when particular uses fails norms governing (II), replaced if scientists continue to pursue the same epistemic goal as the old concept, and it should be abandoned if that goal is given up altogether.

Second, Corinne Bloch-Mullins critically evaluates this account by examining whether scientific concepts can successfully foster epistemic goals without following these norms, by highlighting the role of contrasting concepts and similarity judgments in conceptual development, and by asking if the account adequately distinguishes synchronic and diachronic evaluation of concepts. This part is followed by a Q&A session on both contributions.

Third, Haueis and Bloch-Mullins hold a panel discussion with Uljana Feest on normativity in philosophical accounts of concepts. How can philosophers can derive normative vocabulary from historical cases of conceptual development? How does conceptual development relates to epistemic norms, what role do norms play in ongoing scientific practice. This part is again followed by a Q&A session.

Varieties of memory

Snait B Gissis¹, Cornelius Borck², Michael Levin³, Eva Jablonka⁴

¹Tel Aviv University, Cohn Institute for the History and Philosophy of Science and Ideas, Tel Aviv, Israel, ²Luebeck University, Institute for Medicine and History of Science, Luebeck, Germany, ³Tufts University, Harvard University, Allen Discovery Center, Wyss Institute, Somerville, Cambridge, MA, ⁴Tel Aviv University, Cohn Institute for the History and Philosophy of Science and Ideas, Tel Aviv, Israel

We suggest a session of three talks and a commentator on diverse views on “memory”, how it has been investigated, analyzed, experimented upon and related to biological systems and processes. Two talks will be historically oriented and the third will discuss present day experimental work.

The first talk by Snait Gissis will discuss how Théodule Ribot, in his endeavor establish ‘scientific psychology’ in late 19th century France constituted memory as primarily biological : “Théodule Ribot and the memory - heredity relationship within an evolutionary (neo-Lamarckian) continuum”

The second talk, by Cornelius Borck, will discuss Penfield and focus on the role of instruments as tools and models in his research practice: “Wilder Penfield operating on mind and memory - media and models in his brain research”.

The third talk, by Michael Levin, will discuss conceptual issues surrounding memory in brains and non-neural tissues undergoing radical remodeling: “Unconventional subjects of memory: beyond neuroscience in brainy model species”.

Eva Jablonka will comment on the juxtaposition of the three talks

Idealization and non-ideal vaginal microbes: Applying Angela Potochnik's account of idealization in science

Jacqueline M Wallis¹

¹University of Pennsylvania, Department of Philosophy, Philadelphia, PA

Angela Potochnik's *Idealization and the Aims of Science* (2017) develops an account of science which centers idealizations, “assumptions made without regard for whether they are true, generally with full knowledge that they are false” (p. 2). Idealizations are, Potochnik argues, both “rampant and unchecked” in science, which has myriad implications for scientific practice – from study design, data collection and modeling to scientific explanation and understanding. Such idealizations play crucial roles in investigating science's target phenomena, which Potochnik identifies to be causal patterns. In this work-in-progress talk, I apply Potochnik's account of idealization in science to a case study from human microbiome research: investigating the correlation between bacterial vaginosis and increased risk of HIV acquisition. I identify target causal patterns in the case study and explore six distinct idealizations in early stages of such biomedical research projects. Finally, in light of my analysis of the case study, I'll return to Potochnik's claim that idealizations are both “rampant and unchecked”. While idealizations are rampant here, I suggest they are not as unchecked as a strong reading of Potochnik might indicate.

Biological proportionality contests

Marina DiMarco¹

¹University of Pittsburgh, History & Philosophy of Science, Pittsburgh, PA

On a relatively minimal notion of causation, we can admit many causes of the same effect. Because of this, biologists, epidemiologists, and philosophers of biology rightly ask: which of these causes should we prioritize in scientific explanations? One way to approach this problem is as a choice among causal variables.

Two candidates have been offered as objective guides to causal variable selection in biology: proportionality and the causal economy account. Proportionality, the appropriate granularity or degree of abstraction, is supposed to tell us something about the right level of explanation with which to describe a cause. Identifying a proportional level of abstraction is supposed to be an empirical, rather than a pragmatic, matter. Similarly, Franklin-Hall's causal economy account recommends selecting causal variables by maximizing the ratio of cost, in terms of details to be included, to benefit, in terms of the extent to which the candidate variables secure the stability or robustness of the effect of interest. Causal economizing is alleged to offer an objective guide to the selection of "narrow" causes from among the innumerable causal determinants of, or influences upon, some effect of interest.

Both proportionalists and causal economists advocate a contest model for causal variable selection: we compare causal variables and choose the variable(s) that best satisfy the norm. Even if we do not choose a single unique winner of such contests, we choose from the candidate variables on hand. I argue that both proportionality and causal economy are properly subject to underconsideration, or "bad lot" concerns. Such concern is a matter of epistemic risk. Underconsideration worries are particularly salient in biology and the health sciences, where our understanding of complex causal structures is often incomplete. Because of this, discussions of both proportionality and causal economy may obfuscate an important role for nonepistemic values in causal variable choice in biology and biomedicine. Since neither guide to causal selection is value-free, my account offers an opportunity to engage with what these values are, or ought to be.

Darwin, natural history, and explanatory breadth

Charles H Pence¹

¹Université Catholique de Louvain, Institut Supérieur de Philosophie, Louvain-la-Neuve, Belgium

As Charles Darwin moved on from the drafting of the *Origin* after its publication in 1859, he sought to bolster the case for his nascent theory of evolution by natural selection. One way in which he did so was to start to marshal a host of other data that we might recognize as natural-historical – detailed treatments of the fertilization of orchids, the workings of insect-eating plants and of climbing plants, and the structures of flowers, to name only a few. In this talk, I want to consider why he would have taken these to be the kinds of data needed to support his view of natural selection. I'll use the example of Darwin as an opportunity to explore a concept that I will call “explanatory breadth.” This notion best stands out against two other, more common features of scientific explanations which have frequently appeared in recent literature. On the one hand, explanatory depth (commonly discussed in the literature on causal mechanisms, for instance) doesn't at all seem to capture the kind of extension of selection that Darwin was after – there is nothing here about the “more fundamental” ways in which natural selection might be taken to act. On the other hand, explanatory scope (often discussed in the literature surrounding the physical sciences) normally involves working on the construction or formulation of the theory itself so as to render its claims more general, applicable to a larger range of target objects. Darwin's pursuit seems to be neither of these – it is a precisely targeted effort to elucidate the way in which natural selection works in particular cases that he thought would cement the strength of his explanation for diversity and adaptation in the living world. This pursuit of explanatory breadth can offer us a lens for understanding the role of natural history both for Darwin and more broadly, including, potentially, current debates over natural history and museum-collection-based biological study.

Theories of carcinogenesis: An interdisciplinary analysis

Carlos Sonnenschein¹

¹Tufts University School of Medicine, Immunology, Boston, MA

SPEAKERS:

1. Carlos Sonnenschein. Tufts University School of Medicine. Boston MA. USA. Email: carlos.sonnenschein@tufts.edu
2. Marta Bertolaso. Università Campus Bio-Medico di Roma. Italy. Email: m.bertolaso@unicampus.it
3. Sui Huang. Institute of Systems Biology. Seattle WA. USA. Email: sui.huang@systemsbiology.org

The three speakers will briefly make a historical and an epistemological overview of the subject covering important milestones that shaped ideas in the field of carcinogenesis to the present day. Brief arguments describing the premises adopted by those favoring either a) the somatic mutation theory (SMT) and its variants or b) the tissue organization field theory (TOFT) will be made. These theories differ on two accounts, namely, i) the SMT is lodged at the cellular level of biological organization while the TOFT is centered at the tissue level of this same hierarchical organization. And ii) while the SMT adopts the premise that quiescence is the default state of cells in metazoans, the TOFT adopts the premise that proliferation and motility is the default of all cells. The SMT considers cancer a disease of the control of cell proliferation and adopts a reductionist approach searching for molecular mechanisms of carcinogenesis. Instead, using an organicist approach, the TOFT posits that cancer is a problem of tissue organization akin to “development gone awry.”

The nature of togetherness and togetherness in nature

Julia J Turska¹

¹Wageningen University & Research, Knowledge, Technology, Innovation, Wageningen, Netherlands

Co-participation, co-production, co-management, co-adaptation. The puzzle this talk will address is crystallised in the meaning of the "co-" prefix, which stands for "together", "with", "mutually". It will do so in the context of environmental challenges, which are widely established as in need of co-llective action. How can goals of coming together to address these issues be achieved in a world perhaps best characterised by the diversity of its environments, languages, practices, ethical frameworks and socio-economic power? The nature of this variety with its affinity for generating conflict or conversely increasing creativity through productive exchanges will be my main interest of my project. In the talk, I will sketch a philosophical theory of alterity which could serve as a framework for navigating negotiations between competing viewpoints on solutions for the pressing problems of ecological well-being. To carve out the space of interest of the talk more precisely, let us consider a negotiation between communities A and B on an environmental problem X. Ludwig and El Hani (2020) argue that a model of such interaction cannot be a simple exchange of pieces of propositional knowledge to in the end arrive at the "best solution". Instead, what needs to be taken into account is a broad spectrum of epistemological, ontological, ethical and political factors which are in play. Similarly, in philosophical tradition there is no easy way to discern between issues of diversity of knowledges and systems of concepts and matters of existence. Knowledge and communication presuppose an ontology. To begin with I will therefore be concerned with ontological considerations and their impact on epistemology, hermeneutics, ethics and political ecology, in the context of cultural alterity. I will briefly go through key aspects of the debates on this topic across multiple disciplines, with a focus on the Ontological Turn within cultural anthropology. In what follows, I will propose an ecological account of cultural alterity grounded in ideas of rejection of the notion of belief and show its relevance for issues regarding co-production of knowledge about the natural world.

Ludwig,D., and Charbel N. El-Hani. "Philosophy of ethnobiology: understanding knowledge integration and its limitations." *Journal of Ethnobiology* 40, no. 1 (2020): 3-20.

Knowledge coproduction or integration for conservation: Can we go beyond overlaps?

Charbel N El-Hani¹

¹Federal University of Bahia, Institute of Biology, Salvador, Brazil

It is currently acknowledged by the academic community and science-policy arenas such as IPBES that building bridges between Indigenous/traditional and academic scientific knowledge contributes to move toward sustainability in terms of knowledge, practice, and ethics. This entails noteworthy concerns, since recognition of traditional knowledge can be merely partial, acknowledging only its contributions in agreement with (ontological, epistemic, value) assumptions of academic researchers. This may lead to extraction of useful facts from a body of knowledge without consideration of its integrity and cultural context. To avoid this consequence, it is instrumental to acknowledge the complex philosophical questions involved in dialoguing or bridging between knowledge systems, recently summarized by Ludwig and El-Hani in terms of epistemological, ontological, ethical, and political challenges. These challenges can be addressed through a perspective of partial overlaps, which harbors a methodology involving analyses of ontological, epistemological and axiological overlaps that may provide common grounds for collaboration and mutual learning among heterogeneous stakeholders, and partialities of overlaps, i.e., substantial differences in these dimensions that likely exist between any two knowledge systems. Learning opportunities provided by overlaps can be conceived, but might mutual learning go beyond overlaps? I will answer affirmatively by considering intercultural translation as involving “controlled equivocation”, i.e., recognizing that translating across knowledge systems necessarily entails intercultural equivocality, even though productive misunderstandings may follow. A key question for learning from partialities is whether there could be a way of going beyond dwelling in the space of equivocation, towards a mutual learning process engaging heterogeneous stakeholders. I will argue that this can happen through relational intercultural empathy in a domain of shared understanding arising from shared experience. I will illustrate this kind of learning by considering relations between Amerindian Indigenous peoples’ ontologies and academic ecological models used for sustainable resource management.

Neuro-presents and neuro-futures: Neurotech practices imagined and lived

Markus Schmidt¹, Günter Seyfried¹, Sandra Youssef¹

¹Biofaction KG, Vienna, Austria

- 1) Presentation (15 mins)
- 2) Films (~40 mins)
- 3) Panel and Audience (zoom) discussion (25 mins)

Neurotechnologies have been historically connected with the medical realm especially in imaging and diagnostics. Today neurotechnologies find applications in non-invasive as well as invasive therapies, from brain-computer-interfaces to cochlear implants, from prostheses to neurostimulation.

Yet, outside the health sector and divorced from therapeutic and medical purposes, neurotechnologies have different roles to play. On the one hand, depicted on our screens, in films imbued with an element of science fiction, they carry with them imaginations of the future – be they dystopian or utopian.

On the other hand, in the present, with lower production costs, easier access, beyond hospitals and academia, neurotechnologies have been adopted and adapted by body artists, neurohackers and hacker collectives in a DIY approach. Individuals from a variety of backgrounds are taking new approaches in tinkering with, modifying, and hacking their bodies, senses, and brains.

This mixed session offers several approaches to gather insight into current neuro-presents and visions of neuro-futures. We introduce our research with current neurohackers and their practices, touching on key themes including their background, development, tools and methods, motivations and identity, ethics and risk perceptions, as well as their outlooks on the future of neurotechnologies. This is followed by a screening of carefully selected short films (from the 2019 BIO·FICTION Science Art Film Festival focused on neurotechnologies), which serve as visual stimulus for a larger panel discussion: what could the future of the human body and mind look like with technologies that affect the nervous system, senses and brain? How is the future of society imagined in these visions?

Films

Paramusical Ensemble

Tim Grabham (2015) Severely motor-impaired patients performing a live musical piece with the help of a Brain-Computer Music Interfacing system.

Reboot

Andrei Thutat Ungur (2019) Depressed man chooses to erase his memory in order to restart his life.

Perfectly Natural

Victor Alonso-Berbel (2018) Future Families is a virtual parenting system that gives the baby allegedly access to a better life.

Parasites or symbionts?: Women algologists and the microscopic study of algae in interspecies pairings, 1887-1899

Emily S Hutcheson¹

¹University of Wisconsin-Madison, History, Madison, WI

Historical attention to the study of algae (algology) has highlighted how women participated through producing artistic work and making natural history collections. These narratives suggest that women were ultimately pushed out of algological practice by professionalizing botanists in the late 19th century. Yet, in the 1880s and 1890s, a handful of women trained in botany and plant physiology engaged in the scientific study of algae, studying species of the primitive plant-like organisms “in life” rather than as part of a collection of dried herbarium sheets. In the context of Swiss botanist Simon Schwendener’s recently discovered “dual organism” and his classification of the relationship as parasitic (1868), this paper traces the microscopic studies of algae completed by Dutch algologist Anna Weber-van Bosse (1852-1942) and Russian algologist Natalie Karsakoff (1863-1941) and shows how their conceptions of cohabiting species changed over time. Weber-van Bosse, who studied algae that inhabited parts of other organisms (e.g., sloth fur, marine zooplankton, freshwater and marine sponges) initially framed algae as part of parasitic interspecies relationships, in accordance with the standard conception of how two species lived together in intimate arrangements. However, as Weber-van Bosse made more studies of codependent species, she would suggest that algae lived symbiotically, that is, the interspecies pairing was mutually beneficial to both kinds of organisms. Karsakoff, in her study of a marine algae that lived epiphytically on other algae, suggested a benign co-existence. This talk examines the fuzzy and dynamic conceptions of parasitism and symbiosis, by considering the social context and scientific work of two women algologists in the late 19th century.

Domesticating the biochemical bacterium: Balance sheets, resting cultures, and microbial households in Marjory Stephenson's "General Microbiology"

Charles A Kollmer¹

¹Caltech, Division of Humanities and Social Sciences, Pasadena, CA

British biochemist and bacteriologist Marjory Stephenson is often remembered for her prominent role in the professionalization of "General Microbiology," a field in which researchers conspicuously distanced themselves from the medical, industrial, and agricultural concerns that had animated many prior studies of microbial life. In this talk, I trace Stephenson's notion of what constituted generality in microbiology to a set of strategies that she took up in the 1920s and 1930s to study the chemical activities of microorganisms *in vitro*. Counterintuitively, for Stephenson, the most effective means to understand microorganisms in their own terms was to domesticate them, both literally and conceptually. At the level of technique, Stephenson employed a metabolic "balance sheet" to account for how bacterial cultures made use of nutrients present in growth media. Additionally, she and her colleagues at Cambridge University adopted a method for preparing "resting" cultures, in which the bacterial cells ceased to divide and reacted with great sensitivity to the addition of new chemicals. These laboratory methods and rhetorical figures combined to frame bacterial cultures as miniature metabolic households that Stephenson characterized with terms derived from human cultures. In the apotheosis of this move, Stephenson came to refer to bacteria as "biochemical experimenters," seeing in them the evolutionary origins of her own scientific vocation. Extant accounts of twentieth-century microbiology have tended to echo uncritically or reify historical actors' demarcations between "general" and "applied" forms of research. This talk offers a corrective by illustrating how microbiologists like Stephenson articulated this distinction through their language and research practices. Significantly, a close reading of Stephenson's work sheds light on a curious tendency of twentieth-century microbiologists, who, in efforts to correct what they saw as rampant anthropocentrism in their field, offered alternatives steeped in anthropomorphism.

Analogous injections: Vaccines, glandular therapeutics and filters in Paris (1890s)

Patrick M Walsh¹

¹UW-Madison, History, Madison, WI

On April 25, 1895, the French government passed a watershed legislation for the regulation of therapeutic serums. It was specifically a reaction to the development of the new diphtheria anti-toxin vaccine, which was formulated in France in 1894 by Emile Roux of the Pasteur Institute at the height of the bacteriological revolution.

The law of 1895 did not just apply to Pasteurian injections. There was another famous therapeutic injection, largely overlooked by historians, which came under the purview of the law: the injection of “organic extracts,” formulated from the glands, tissues and organs of animals. Available in France in the early 1890s were thyroid injections, pancreatic injections, suprarenal capsule injections and, most famously of all, testicular injections spearheaded by one of France’s most eminent physiologists, Charles Brown-Séquard. It was the beginning of modern endocrinology, and these injections were the precursors to twentieth-century hormone replacement therapies. By grouping vaccines and injections of organ extracts under the term “therapeutic serums,” the law of 1895 saw a clear connection between these two technologies.

Histories of microbiology and endocrinology are siloed, which has made it difficult to approach some simple but critical questions: How were bacteriology and endocrinology related in 1890s France, and why were they brought into a legal union? In this paper, I build an argument about how early endocrinology came into being alongside the bacteriological industry. The lynchpin of this relationship, and the reason for their parallel trajectories, was their joint emphasis on aseptic practice and, specifically, filtration. By describing this scientific and therapeutic relationship, the history of early endocrinology takes on new meaning. Not an isolated *fin de siècle* therapeutic movement of glands, which is how it is usually construed, but rather a therapeutic revolution of the “organic” that was defined and advanced by its proximity to the bacteriological.

Adaptation without adaptationism? Adaptations, functions, teleology and organic progress in G. G. Simpson's theory of macroevolution

Nicola Bertoldi¹

¹Université du Québec à Montréal, Philosophy, Montreal, Canada

The concept of function plays a crucial role in G. G. Simpson's (1949, 1974) view of organic progress and teleology in evolution. Simpson defined organic progress as the process of incremental adaptation of a given lineage to its specific environmental conditions resulting from the functional improvement of certain organic traits (De Cesare 2019). He explicitly characterized the utility of a trait for the organisms that possess it and at a given time in evolutionary history as the only possible definition of teleology (or teleonomy) in a naturalistic, materialistic sense (Simpson 1958, 1959). It follows that, although he only understood both concepts in relative terms (i.e. with respect to particular traits, lineages and historical periods), Simpson saw progress and teleology as defining characters of evolution due to the pervasiveness of adaptation in all evolutionary processes. It is precisely for this reason that S. J. Gould's (1983, 1998, 2002) critical appraisal of Simpson's theory of the evolution of higher taxa insists on the increasingly important role played by the concept of adaptation in Simpson's intellectual itinerary. More precisely, Gould described this itinerary as a steady march towards adaptationism, i.e. a research program that boils down to two fundamental tenets, i.e. what might be called a "principle of functional isolation" and a "principle of optimality". Therefore, Gould's analysis of G. G. Simpson's trajectory raises the following question: to which extent does Gould's concept of adaptationism explicate Simpson's views? This communication aims to assess the adequacy of Gould's characterization of the adaptationist program for appraising Simpson's contributions to paleobiology, notably his theory of the evolution of higher taxa as laid out in his later works (Simpson 1953). To this end, it focuses on the relation between Simpson's understanding of adaptation and his characterization of biological functions. This relation is instrumental for interpreting Simpson's evolutionary conception of both teleology and organic progress in nature. It is thus argued that this conception is founded on a "non-adaptationist" theory of adaptation, i.e. a theory of adaptation that does not rely upon Gould's two principles mentioned above.

Adaptation as a criterion for organic progress

Silvia De Cesare¹

¹Université de Genève, Philosophy, Geneva, Switzerland

This contribution aims at conceptually clarifying the relationships between the notion of adaptation and an idea which is complexly interwoven with the history of evolutionary biology: organic progress (Ruse 1996). This idea refers to some kind of “change towards the better” over the history of life or parts of the history of life. Since Darwin, this notion is related to the mechanism of natural selection conceived as a cause of organic improvement, following the reasoning that organism having a competitive advantage in the struggle for life should be somehow “better” (Darwin 1859). However, if one wants to argue that the notion of progress is theoretically consistent with evolutionary theory, she should also clarify the question of the criterion of progress (what exactly has improved?) and of the scope of progress (to which part of the history of life does the improvement apply? De Cesare 2019).

After Darwin, several evolutionary biologists have proposed different criteria of organic progress, e.g. morphological complexity, autonomy from environment or adaptation (Rosslénbroich 2006). I shall argue that only adaptation can be considered as a theoretically sound criterion of organic progress. To do this, I draw on the thought of G. G. Simpson and R. Dawkins and I propose to define adaptation as functional improvement of organic traits. In this definition, referring to the concept of function, the ontology of interest concerns organic traits (parts of organisms), rather than whole organisms. Also, this notion refers to a local scope of improvement, being applicable only to lineages of ancestors and descendants.

I shall argue that this notion of organic progress is theoretically consistent and cannot be ruled out without dismissing some central tenets of evolutionary theory. However, despite this, problems arise when the notion is applied empirically. Thus, it seems hard to claim that adaptive traits – and the related notion of organic progress – represent a general phenomenon in evolutionary history.

Finally, I discuss some attempts to extend the notion of organic progress beyond functional improvement of organic trait. I shall examine arguments considering that whole organisms (and not only parts of them) have somehow improved over the history of life, with a particular focus on arguments based on fitness and organism design.

Evolution is goal directed

Dan McShea¹

¹Duke University, Biology, Durham, NC

Evolution is goal directed. It isn't, of course, if that claim is understood to say that life as a whole is inexorably headed somewhere, deliberately, purposively. But to the extent that individual lineages are guided by selection, there is a good case to be made for calling them goal directed. The process of adaptation has the same physical organization as all other goal-directed systems, from development to organismal tropisms to goal-directed human artifacts, and perhaps to human intentionality. More specifically, these systems have a nested hierarchical structure in which a goal-directed entity behaves persistently and plastically, guided by a larger-scale "field" in which it is immersed. For a goal-directed homing torpedo, the field is the sound field emitted by a target. For adaptation, the field is the local ecology, extended in time and space, within which a lineage evolves. Reasonable people may differ over whether to call selection-guided lineages goal directed, but whether such lineages rise to that level or not, the fact that they share the same architecture as other goal-directed systems at least raises the possibility that goal directedness is a continuous (and probably multidimensional) variable, that it is a matter of degree. It also raises the possibility that the attempt to devise binary necessary and sufficient conditions for goal directedness is misguided. In sum, if the analysis here is correct (and it is), it suggests that systems with some degree of goal directedness are quite common, with natural selection representing just one instance, albeit one with a large domain of application.

The power of bibliometrics for historical epistemology of 20th century life sciences

Hanna L Worliczek¹

¹University of Vienna, Department of History, Vienna, Austria

Historical epistemology of the life sciences in the latter half of the 20th century is frequently challenged by phenomena of abundance. This concerns not only the sheer amount of published scientific papers and the number of scientists, but also the steadily increasing quantity of interdisciplinary research fields – many of them with their own professional societies, conferences, and scientific journals. This abundance raises the question of how to select historical periods, relevant actors, sources, and historical research fields to address particular epistemic interests. This question gains relevance as more and more periodicals make their historical papers available online. These developments raise the necessity for increasingly delicate source selection processes since pragmatic availability or access constraints decrease constantly. These developments may also provoke new challenges when trying to avoid selection bias. Elaborated tools of the digital humanities, including corpus analyses of whole research fields and disciplines, are one way to make systematic use of these digital sources. However, such high-end tools are not universally available due to resource limitations, lack of highly specialized expertise, fragmentary full-text availability, or time-constraints. Easily applicable bibliometric analyses using digital resources may, however, provide an important tool in source-based selection and contextualization processes. By taking the history of modern cell biology as an example, I discuss two low-threshold strategies to tackle the above-mentioned abundance problems bibliometrically. I discuss (1) a bibliometric strategy to identify relevant research fields and historical periods of increased dynamics as a basis for historical-epistemological research, with the introduction of a new microscopic imaging method in cell biological research as an example. I (2) discuss a bibliometric strategy to contextualize narratives about cell biological journals by reconstructing historic publication dynamics and impact factors, and by addressing their explanatory power. To conclude, I will illustrate how knowledge from these low-threshold strategies can inform historical epistemology and how they help weighing conflicting narratives in other sources, exemplified by the case of modern cell biology.

How can highly contextual data such as metabarcoding data relate to the world?

Aline Potiron¹

¹Institute of Philosophy and Scientific Method, Johannes Kepler University, Linz, Austria

This paper aims to reconsider the relationship between scientific data and the world. Data are usually considered as direct “screenshot” of the world. They are thus supposed to be fixed, context-independent and objective. In particular, in the context of modern Big Data-based science, data are supposed to “speak for themselves”. Metabarcoding is one method of modern microbiology that generates such data. Its principle is the DNA sequencing and analysis of a single gene, called a barcode. DNA sequences are thus central in those methods and passed from the world (the microorganisms) to the computer. During the transformation, choices are made which impaired the view of the fixed and objective screen shot. A sequenced barcode uniquely identifies the species of microorganisms in the community of a given environment. Thus, metabarcoding data are highly contextual where “context” is supposed to refer to a particular place, time and/or conditions. Thus, in metabarcoding, the path between data to knowledge is less straightforward than expected.

This paper uses metabarcoding as a case study to develop a new understanding of the relationship between scientific data and the world. Metabarcoding generates millions of sequences, and is considered a data-centered method. Hence, I use the data journey framework developed by Leonelli in her book *Data-centric biology: a philosophical study* (2016).

First, I assess what constitutes data in metabarcoding. I argue that DNA sequences become data not by acquiring the ability to travel but by acquiring the ability to sustain empirical claims. Sequences do so by increasing their reliability, through the interactions between environmental DNA and scientific technologies and through bioinformatics steps performed on sequences retrieved from sequencing platforms.

Second, I evaluate how metabarcoding data can sustain empirical claims. I argue that the biological relevance of these data and conclusions made from them are better understood if we conceive the environment at the same epistemic level as the organism. Biology is usually conceived as gathering data and conclusions about individual organisms or even population. Yet, metabarcoding is about gathering data about a given environment. Projects such as the Earth Microbiome Project, in developing an ontology of studied environments that is more or less inclusive depending on the level of the taxonomy tend to integrate this shift.

Producing social dis/order: Toward an epistemology of biobanking in big data genomics

Kathryne Metcalf¹

¹University of California San Diego, Communication and Science Studies, San Diego, CA

This project seeks to explore the role of biobanking institutions in their role as the data production infrastructure of contemporary human genomic research. Drawing on work from the sociology of expertise and critical data studies, I argue that biobanks serve to organize social relationships between actors including researchers, clinicians, advocacy groups, and patients in the production of biomedical science. By coalescing particular sets of actors around the interpretation of their data, biobanks thus contribute to disciplinary and discursive differences within subsequent research. This has important implications for how biosocial conditions are reproduced through basic research in biobank-driven genomic sciences, which contribute to the formation of “human kinds” (Hacking 1995). To this end, I offer a case study centered on genomic autism research produced using data from two large biobanks: 23andMe and MSSNG. The “data journeys” (Leonelli 2016) that their data undertake through research environments materially shape their contents, and frequently involve recombination with data from other institutions. I map these journeys alongside the theoretical, methodological, and discursive apparatuses employed by the researchers who analyze them. The resulting network charts a provocative series of epistemic and ontological disjunctures regarding what autism is and how it can be understood through genomic investigation, suggesting that biobanks represent a notable influence in the construction of biomedical difference through basic research.

Evolutionary cognitive archaeology: Epistemological and methodological issues

Adrian Currie¹, Anton Killin², Andra Meneganzin³, Ross Pain²

¹University of Exeter, Sociology, Anthropology & Philosophy, Exeter, United Kingdom, ²Australian National University, Philosophy, ACT, Australia, ³University of Padua, Biology, Padua, Italy

This session examines two sets of issues at the crossroads of archaeology and human cognitive/behavioural evolution.

First, Adrian Currie and Andra Meneganzin will dive into issues related to **Behavioural Modernity, Investigative Disintegration, and Rubicon Bias**. ‘Behavioural Modernity’ isn’t what it used to be. No longer conceived as an integrated package of traits, demarcated by a clear archaeological signal in a specific time and place, it is now disparate, archaeologically equivocal, and temporally and spatially spread. This change in our conception of modernity is due to a wealth of surprising discoveries in the material record, as well the reappraisal of old evidence, driving increasingly sophisticated demographic, social and cultural models of inheritance. Currie and Meneganzin develop an account of investigative disintegration to capture these changes. For behavioural modernity, the explanatory weight which once lay on identifying ‘switch-points’ in the innate suite of hominin cognitive capacities, lie now in understanding the social and demographic environments that were capable of sustaining and nourishing more complex material cultures. Currie and Meneganzin will illustrate the importance of disintegration by focusing on ‘Rubicon bias’: classificatory and interpretive practices which look for or assume clear demarcations.

Second, Anton Killin and Ross Pain will turn to **The Challenge to Cognitive Archaeology of Sample Diversity in the Behavioural and Cognitive Sciences**. In their landmark 2010 paper in *BBS*, Heinrich et al. outlined a serious methodological problem for the behavioural sciences. Most of the studies produced in the field use people from Western, Educated, Industrialised, Rich and Democratic (WEIRD) societies, yet inferences are often drawn to the species as a whole. In doing so, researchers implicitly assume that either there is little variation across human populations, or that WEIRD populations are generally representative of the species. Yet neither of these assumptions is justified. Here Killin and Pain extend this problem to the study of ancient humans and their hominin forebears through the strategies of cognitive archaeology. They’ll assess a range of representative arguments and key studies, outlining some WEIRD problems and sketching some potential solutions.

Two out of three: Diversity, heterogeneity and collectivity

Ayelet Shavit²

¹Tel Hai College, Interdisciplinary Studies, Tel Hai, Israel, ²Technion, Humanistic Studies, Haifa, Israel

A Collective holds different parts that “come together” to interact in different ways, and four such types of interaction are described: coordination, cooperation, collaboration and chimerism. The concept of difference holds a well-recognized research tradition, and I explicate two of its meanings - ‘diversity’ and ‘heterogeneity’ - which often surprisingly conflict. I argue that ‘diversity’ can describe a population well enough, but does not describe a collective well, whereas ‘heterogeneity’ better describes a collective and therefore ought to describe it. Moreover, measuring heterogeneity can detect the different developmental and ecological stages an entity passes during its evolutionary transition, from full aggregativity, to kinds of collectivity to a new kind of individuality (an interacting chimera). To conclude, noticing the link between ‘heterogeneity’ and ‘collectivity’ is both practically relevant and theoretically important.

Multispecies ethnography, philosophy of biology, and ‘Anthropocene onsets’ in the Americas

Francisco Vergara-Silva¹

¹Laboratorio de Teoría Evolutiva e Historia de la Ciencia, Instituto de Biología, Universidad Nacional Autónoma de México, Mexico City, Mexico

Multispecies ethnography (ME) has been established throughout the last decade as a salient theoretical concern in the ‘anthropology of non-human agency’, in dialogue with scholar debates around ‘the ontological turn’, as well as in connection to discussions in environmental history and humanities. Viewpoints brought forward in these interdisciplinary scenarios are in turn pertinent to address the diversity of ways in which the so-called ‘Anthropocene’ could/should be defined and studied. The notion of ‘more-than-human assemblages’ stands out at the core of ME as anthropological discourse, revealing the importance that ecological and other kinds of ‘relational’ reasoning have for anthropologists doing fieldwork and writing along these theoretical assumptions. In this paper, I review ways in which philosophy of eco-evo-devo arguments about ‘holobionts’ –as elaborated by Lynn Chiu and Scott Gilbert, among others– have been received by anthropologists investigating multispecies entanglements, paying special attention to relevant interventions by Anna Tsing and Eben Kirksey. I then consider how such philosophy of biology contributions might in turn be fruitful to address, or even complement, criticisms (by Erle Ellis and others) to strict periodizations of the ‘Anthropocene’ and other mostly static understandings of long-term change in socio-environmental systems. Using a model of diachronic transformation in/of the Valley of Anahuac (i.e. ‘Mexico Valley’) before and after the ‘fall of Mexico-Tenochtitlan’ as a case study, I then argue that the ongoing ‘processual turn’ in the philosophy of biology is compatible with EM’s central notion, therefore supporting multispecies-oriented, anthropological interpretations of heterogeneous, diachronically distributed onsets of the ‘Anthropocene’ in the American continent.

Gaia: The earth is an organism (not a Darwinian individual)

Letitia Meynell¹

¹Dalhousie University, Philosophy, Halifax, Canada

When James Lovelock and Lynn Margulis first suggested the Gaia hypothesis (1974; Lovelock 1979) they were roundly criticized by a number of evolutionary biologists, who maintained that no plausible evolutionary account was compatible with the idea that the Earth is an organism (e.g., Doolittle 1981; Dawkins 1999, 234-7). Central to this critique was the observation that Gaia was alone and, relatedly, Gaia does not reproduce. Without reproduction and a population, critics maintained, there was no viable way to explain how Earth could possibly have been shaped by natural selection, which was, not unreasonably, taken to be characteristic of organisms. The Gaia hypothesis is currently undergoing something of a revival. In this presentation, I will address a particular thread in the discussion—the effort to bring Gaia into a robust evolutionary framework, exemplified by Ford Doolittle’s effort to “Darwinize Gaia” (2017). Doolittle, originally an ardent critic of the Gaia hypothesis, has recently argued that, with a few tweaks to Lewontin’s recipe, an account of Gaia as a product of natural selection can be articulated. While this has been criticized as straining the theory, perhaps to the point of breaking, another possible approach is available. While the Gaia hypothesis postulates that the Earth is an organism, this need not entail that the Earth is a Darwinian individual. This would mean that Gaia is a product of natural selection but not a unit of selection, thus undermining the key lines of argument against the Gaia hypothesis—lack of a population and failure to reproduce. Recent work by Subrena Smith (2017) (following Godfrey-Smith 2013) usefully articulates the distinction between organism and Darwinian individual, drawing on recent work on the ontology of holobionts. According to Smith, organismality does not depend on being a member of a population and organisms are characterized as being fundamentally persisters rather than reproducers. Smith thus provides a compelling approach to defending a scientifically robust account of Gaia as an organism. Whether such a claim is ultimately trivial will be considered as the most serious objection to the view.

The selected effect account of function: Problems, extension, reconciliation and applications – Session 1

Subrena Smith¹, Paul Griffiths², Justin Garson³, Peter Takacs², Pierrick Bourrat^{4,2}

¹University of New Hampshire, Philosophy, Durham, NH, ²University of Sydney, Philosophy & Charles Perkins Centre, Sydney, Australia, ³City University of New York, Hunter College & the Graduate Center, New York, NY, ⁴Macquarie University, Philosophy, Sydney, Australia

According to the selected effect (SE) account of function, traits are *selected* because of their positive *effects* on the fitness of the organisms that have them. While immensely popular, the SE account is built on a very simplified view of natural selection. Recently this account has been extended for situations where selection does not involve differential reproductive success of organisms into a generalised selected effects (GSE) account by Justin Garson.

This non-traditional session will consist of two roundtables. In each half session, 3/4 people will state the essence of some viewpoint they want to advocate in 10m and commentators will respond, before a discussion and question period. The participants advocating viewpoints will pre-circulate their papers to the group.

Session 1

Paul Griffiths will present some collaborative results from the Theory and Method in Biosciences at the University of Sydney that challenge the idea that SE functions explain the existence of the traits that bear them whenever we depart from the simplest models of natural selection (e.g., frequency-independent selection).

Pierrick Bourrat will challenge some aspects of the version of the GSE account. Garson's account seems to be ascribing functions to entities undergoing mere sorting processes (rock on the beach resisting erosion by waves). Garson argues that one should not ascribe functions to such processes. It will be argued instead that one can ascribe functions in such situations.

Peter Takacs will examine the phenomenon of negative frequency-dependent selection that many (e.g., Birch 2016; Okasha 2019; Griffiths et al. forthcoming) point to when questioning the efficacy of natural selection's power to forge adaptation. A mechanistic or dynamic understanding of this phenomenon may provide the means for interpreting it in a manner that is not necessarily at odds with recent SE accounts of function.

Justin Garson and Subrena Smith will comment on the issues raised and prospects for the SE approach.

Must genetics education start with Mendel? Two attempts to do otherwise in the 1970s and 80s

Hannah Bapty^{1,2}

¹University of Leeds, School of Philosophy, Religion and History of Science, Leeds, United Kingdom, ²University of Oxford, Department of Education, Oxford, United Kingdom

It is 156 years since Mendel's presentation of his results on hybridization in peas to the Brünn Society for Natural Science. Yet even now, when multifactorial causation and trait variability are mainstays of research, teaching in genetics typically starts with Mendel and his peas, where seemingly none of that complexity matters. Must genetics always start from such a simplistic, determinist beginning? A number of recent studies (e.g., Dougherty 2010; Jamieson & Radick 2013; Jamieson & Radick 2017) have made the case for emphasizing the complexity of genetics from the beginning and throughout. In this talk I'll examine the origins and fate of two earlier attempts at reform, from the 1970s and 80s. One was from Steven Rose, a biochemist in London and founder of the British Society for Social Responsibility in Science, who developed a genetics course for distant teaching at the Open University. The other was from Garland Allen, a historian of science and influential writer of biology textbooks, including four editions of *Study of Biology*. Both tried to depart from the standard start-with-Mendel script, and in ways that aimed to help students better appreciate not only the complexities of genetics but the embeddedness of genetics – and genetic knowledge – in the social world. And both met significant resistance, touching on everything from concerns about placing unrealistic demands on students to the impossibility of making large-scale changes given previous investment in materials.

In closing I'll suggest that the experiences of Rose and Allen hold valuable lessons for would-be reformers of the genetics curriculum today.

Undergraduate genetics assessments: What are we assessing and how?

Kelly M Schmid¹, Dennis Lee², Monica Weindling², Awais Syed², Stephanie-Louise Yacoba Agyemang¹, Michelle K Smith¹

¹Cornell University, Ecology and Evolutionary Biology, Ithaca, NY, ²Biological Sciences Curriculum Study, Colorado Springs, CO

The field of genetics has recently experienced rapid growth. New technologies have aided in research that has expanded our knowledge about the complex nature of genetics, with genes and environments both playing important roles. As our knowledge of genetics continues to expand, so does our students', with increased access to genetic information, data, and resources leading to increased student interest in complex genetics concepts. Here, we aim to determine if current undergraduate genetics assessments match these changes. We address the following questions: (1) In validated assessments developed to investigate students' learning in genetics, what proportion of questions address the effect of the following on phenotypes: single gene, many genes, genes and the environment (G+E), gene-by-environment interactions (GxE)? (2) Are there categories that are underrepresented? (3) How can they be better represented? To investigate these questions, we employed qualitative content analyses to categorize questions published in genetics concepts assessments and CourseSource genetics lessons. Our analyses reveal that the majority of genetics questions about the inheritance of at least one allele do not ask students about the role of the environment on phenotypic outcomes. We also investigated the intersection of these outcomes and question features such as the question style, level of cognitive demand needed, and organism featured. The results suggest that available undergraduate genetics curricula focus on the effect of genes only. Therefore, while our knowledge of genetics has greatly expanded and our students' interests have evolved, our genetics curricula continue to focus on simple models, rather than including more multifactorial concepts and meeting our students where their interests lie. We suggest the introduction of more multifactorial genetics concepts into the undergraduate genetics curriculum, including the development of assessment questions that incorporate the effect of the environment. Ultimately, this is especially important as it will help students develop a more accurate understanding of genetics and, in turn, reduce deterministic thinking.

Fostering complex genetics literacy: Effects of a Weldonian curriculum on Year Ten students' genetics knowledge and social views

Oliver S Brown¹

¹ACG Parnell College, Science, Auckland, New Zealand

Genetic literacy, the capacity of the non-scientist citizen to make well-informed decisions regarding genetics issues, such as genetic testing, is a key tenet of science education. It requires an understanding that human characteristics are the product of a developmental process that involves multiple interacting genetic and environmental factors. This Weldonian perspective, named for the early 20th century biologist Walter Weldon, differs markedly from that of Mendel, whose work on the transmission patterns of monogenic traits dominates much of genetics education in high schools. Over the course of 2019, I developed a Year Ten genetics curriculum that addressed the key components of genetic literacy and which drew on the emphases and learning outline utilised by Jamieson and Radick (2017) in their novel Weldonian curriculum. My genetics unit emphasised a molecular approach to the gene concept, aimed to present multifactorial or complex traits as the norm and sought to inculcate a developmentalist perspective, instead of a transmission-focused view, on genetics within students. Taking an action research approach, I sought to explore the impact of this unit on Year Ten students' social views regarding genetics-related issues and identify difficulties hampering their development of genetic literacy. Pre- and Post-tests were carried out with 56 students and data was collected from end-of-lesson minute papers and focus groups. The research showed that the concept of multifactorial traits was congruent with students' prior conceptions of human characteristics, highlighting the potential for this learning approach to work with students. With respect to students' social views, the data collected showed that students' degree of belief in genetic determinism prior to the unit was reasonably acceptable and the unit did not significantly shift these views. The research also highlighted some of the challenges faced in introducing these ideas to the classroom. For example, students struggled to progress beyond a surface-level understanding of multifactorial traits and remained more likely to utilise a transmission inheritance rather than a developmentalist lens when explaining genetic phenomena. These key findings will be discussed more fully in my presentation.

Probing the “grey area”: Natural kinds and extraterrestrial life

Aleksandar V Božić¹

¹University of Rijeka, Department of Philosophy, Rijeka, Croatia

In this paper I deal with the so-called “grey area”, which refers to entities that lie between life and nonlife and whose aliveness is vaguely established. These entities are either subcellular (e.g., organelles, proteins) or noncellular (e.g., viruses, prions). Accounts such as the ones put forward by Forterre (2016, 2017) and Dupré & O'Malley (2009) establish the aliveness of such entities on the basis of their involvement with what is already considered to be alive on Earth. Accordingly, entities such as viruses and proteins are alive in virtue of their participation in processes within living beings. One undesirable consequence of such accounts is that the aliveness of a possible extraterrestrial “grey area” entity, belonging to the same natural kind as a terrestrial one, depends on its performance within terrestrial living beings. I will argue that the aliveness of such a “grey area” entity should be determined in a manner not constrained by terrestrial scenarios. By proceeding from the property-cluster kind (PCK*) approach to living entities proposed by Ferreira Ruiz & Umerez (2018) I will argue that the natural kinds of the “grey area” entities are best understood as borderline or tentative subkinds of the natural kind “life”. In this case, the putative aliveness of a subkind applies to all its instances, whether familiar terrestrial or unfamiliar extraterrestrial ones. For example, if we discover an extraterrestrial protein composed of dextro amino acids, its aliveness is determined notwithstanding its nonfunctionality within terrestrial living beings. I will conclude by claiming that the PCK* account of natural kindhood of life is appropriate for astrobiological research since it can provide a framework for assessing the aliveness of various phenomena in a manner not constrained by terrestrial scenarios. This includes possible novel forms of life and possible new examples of the „grey area“ entities.

The new N=1 problem

Carlos Mariscal¹

¹University of Nevada, Reno, Philosophy, Reno, NV

Due to its shared origin, all life on Earth is regarded as a single phenomenon, meaning our sample size (N) of the category ‘life’ is 1, or N=1. This raises a problem, called the N=1 Problem, about whether any features of Life on Earth can be justifiably said to hold among other instances of life in the Universe. The N=1 Problem is a serious issue for anyone interested in discovering new examples of life or contemplating its nature. Implicit in the N=1 Problem is the notion that life is a natural kind and scientists can discover its properties. In this presentation, following on the conceptual move of Goodman’s paradox, I present the New N=1 Problem. This riddle holds that there are an indefinite number of broader categories to which any single example belongs. Some of these categories may be natural kinds, but none are non-controversially equivalent to the life category itself. Thus, properties of life on Earth provide equivalent evidence for categories such as evolving systems, far-from-equilibrium systems, squishy things, etc. The logic of this problem also applies to any *sui generis* phenomenon that is (or is thought to be) an instance of a broader category, including the Universe and history itself. Privileging any category must rely on other explanatory considerations, which are shaped by the epistemic values and philosophical commitments favored by a disciplinary background. No creation nor discovery of a lifelike phenomenon is likely to resolve this riddle, so negotiation between competing values is essential.

Are viruses alive and should we care?Gregory J Morgan¹¹Stevens Institute of Technology, Philosophy, Hoboken, NJ

I assess arguments, pro and con, regarding whether viruses should be considered living agents. I also assess related second-order arguments for why we should abandon the living/non-living distinction itself. Among others, I consider the arguments of the philosopher Edouard Machery and the science writer Carl Zimmer.

Interface pedagogy-biology-medicine in home education in the GDR: Transdisciplinary logics of action in the mirror of biographical interviews

Felicitas P Söhner¹

¹Heinrich-Heine-Universität, History, Philosophy and Ethics of Medicine, Düsseldorf, Germany

The contribution focuses on the life situation of the former residents of the Combined Special Homes for Psychodiagnostics and Pedagogical-Psychological Therapy. In this institution, actors worked together whose actions followed different value systems and rules, who understood different aspects as goals and risks, and who did not apply the same strategies in dealing with difficult situations. The focus is on the perception of different professional cultures and their analysis from the perspective of professional actors as they present themselves in biographical interviews.

Assuming that the human brain is the biological basis for learning processes, the question arises to what extent the connection between biology and cognition has been discussed and theoretically formulated.

The contribution provides a system-theoretical framework in which the interlocutors under consideration are understood as members of different professional cultures. Exemplary examples are used to examine whether and to what extent actors could belong to several subsystems. The conference contribution proposed here aims to empirically record the logics of action of the subjects in concrete situations and to relate them to social developments. Based on the collected experiences, it will be discussed what the encounter of different subject cultures and thought patterns meant for everyday actions and experiences in a children's home of the Combined Special Homes and to what extent the relation of the nature and functioning of physical materiality was included in the explanation of cognitive phenomena.

For this purpose, a historical document analysis is combined with the qualitative content evaluation of expert interviews. The research approach, which starts from the perspective of formerly acting actors, makes it possible to analyze frames of action and strategies of the interviewees and to clarify according to which structures of meaning the included interviewees interpret their reality.

An animal history of biology: Questioning the place of biologists and historians

Quentin Lade¹

¹Centre Léon Bérard, Social Science department, Lyon, France

This talk is a methodological and historiographical discussion on the animal biographical narratives for historical account of biology. This reflection is based on a doctoral thesis which retraces the long-term trajectory of a scientific animal, the marine mollusk *Aplysia*.

The choice of such an animal was motivated by the peculiar importance attached to *Aplysia* by many neurobiologists during the second half of the 20th century. The sea slug became famous to biologists and beyond the scientific world, when the neuroscientist Eric Kandel chose it as the flagship model for his researches on memory at the neural and molecular scale, during half a century. The great success of his work, rarely equaled in his field of research, was rewarded by the Nobel Prize in 2000.

Nevertheless, our narrative begins in the sixteenth century. We describe how *Aplysia* became an object of study for natural history, then a scientific animal for nascent biology. Finally, we focus on the transformation of *Aplysia* into a model organism for neurobiology.

Beyond this particular animal trajectory, we discuss the general interest of this historiographical choice for the History of Biology. Thus, by retracing the course of the domestication of *Aplysia*, we shed light on the process of domestication of nature by life science anchored in industrial modernity. This way, our historical account shows the particular material arrangements on which relies the domestication of the animal and the contingency of those processes.

By giving a central place to non-humans, this historiographical choice questions the place of scientists in History: far from the figure of heroes participating in progress, they appear constantly dealing with unexpected events and difficulties that arise from living matter. Finally, this also questions the place of the historian who, by retracing Biology through the animal trajectory, is himself subject to the contingency and the unexpected in History.

Once upon a time the construction of molecular genetics of bacteria in Mexico: Interviews from the past

Marco Ornelas-Cruces¹

¹National Autonomous University of Mexico, Evolutionary Biology Department, School of Sciences, Mexico City, Mexico

Science, understood as a social and cultural system, cannot be studied in isolation and out of context. In this paper I performed a historical analysis of the emergence of molecular genetics of bacteria in Mexico during the last years of the Cold War. The aim is to answer the question of how this scientific practice was constructed. Knowing that neither the original laboratory nor the historical archives or physical libraries were accessible due to the COVID-19, I conducted qualitative interviews with key informants who were present at the historical moment studied in this work. I also aim to establish a theoretical justification to show the importance of these oral records for a history of science that does not involve an exhaustive search of traditional archives. Consequently, my intention is to explain the case of scientific innovation in terms of laboratory practices, in the sense of epistemic cultures, and then to situate them in the context of the then novel techniques of molecular biology and the standardisation of the techniques that would later become part of everyday laboratory practice.

Roles of scientific generalizations beyond explanation: The case of collective cell migrationYoshinari Yoshida¹¹University of Minnesota, Department of Philosophy, Minneapolis, MN

Philosophical discussions of scientific generalizations have been dominated by an interest in scientific explanation; it has been assumed that if generalizations are valuable in science, that is because of the role they play in explanations. In this presentation, I challenge this image and provide a picture of generalization that is more sensitive to details of scientific practices. Generalizations (including their pursuit and development) play several different roles in scientific research. In particular, I analyze ways that generalizations promote interactions and “mutual informing” between subcommunities within an area of research and thereby facilitate investigations. As a case study, I explore the advancement of research into collective cell migration in developmental biology in the last few decades. In this area, a number of biological systems have been studied as “model systems” of the phenomenon of collective cell migration, which have revealed diversity of underlying cellular and molecular mechanisms, as well as interesting similarities. I discuss how pursuits and development of generalizations concerning particular features of those mechanisms have both facilitated studies of individual biological systems and shaped the way that the phenomenon is conceptualized and investigated.

Monads and cells: Investigating on simplicity and complexity in simple biological entities

Caroline Angleraux¹

¹IHPST, Paris 1 Panthéon Sorbonne, Paris, France

In 1827, the French naturalist Pierre Jean François Turpin published a paper on microscopic plants and the part of their analogues in the development of the cellular tissue. He put as an epigraph “Variety into unity, Leibniz”. This mention made a connection between the globulist cell theory of Turpin and the monadological thesis of Leibniz. Even though it is quite surprising first, this epigraph emphasizes the epistemic context in which the cell theory developed and it reminds us that the cell resulted from empirical observations under the microscope, but it also resulted from a speculative tradition that impacted on the background.

After Leibniz’s death, some biologists and philosophers understood the monad as a simple entity endowed with an intrinsic activity that characterized living beings. For C. Wolff, Kant or Schelling, the monad meant (1) the simple living unity characterized by an intrinsic complexity. In parallel with this (1) “intensive approach” of monadic simplicity, the monad was also understood in (2) a “compositional approach” in which naturalists like Bonnet, O. F. Müller or Oken considered the monad as (2) an active simple entity that combined with others, similar, to make more complex living structures. Since it combined (1) an intensive and (2) a compositional conception of simplicity, the monad developed a lexicon of the simple biological entity that enhanced and troubled the reception of the cell concept. Then, this talk aims to present conceptions 1 and 2 of the monadic simplicity in order to outline how the naturalization of the Leibnizian monad shifted its conceptual content as a simple entity. Then, focusing on the naturalized meaning of the monad and the cell, my goal is to study what simplicity and complexity meant for a simple biological entity in this context.

DuBois-Reymond, E. (2004). Leibnizische gedanken in der neueren naturwissenschaft. In *The Origin of Life Debate*, J. E. Strick (ed.), Thoemmes, pp. 835–854.

Duchesneau, F. (2018). *Organisme et corps organique de Leibniz à Kant*, Vrin.

Nicholson, D. (2010). Biological atomism and cell theory. *Stud Hist Philos Biol Biomed Sci* 41, pp. 202–211.

Richards, R. (2002). *The Romantic Conception of Life*, Univ. of Chicago Press.

Schmitt, S. (2004). *Histoire d’une question anatomique: la répétition des parties*, MNHN.

Zammito, J.H. (2017). *The Gestation of German Biology*, Univ. of Chicago Press.

The selected effect account of function: Problems, extension, reconciliation and applications -- Session 2

Daniel J Nicholson¹, Carl Brusse², John Matthewson³, Justine Kingsbury⁴

¹George Mason University, Philosophy, Fairfax, VA, ²University of Sydney, Philosophy & Charles Perkins Centre, Sydney, Australia,

³Massey University, Philosophy, Auckland, New Zealand, ⁴University of Waikato, Philosophy, Hamilton, New Zealand

Session 2

John Matthewson will consider what modifications might be required to accommodate recent concerns regarding the selected effects account. Can there be an account of function based on selective history that truly accommodates the details of natural selection and still discharges the role this account plays in philosophical theories?

Carl Brusse will consider the SE account in the philosophy of medicine. Most naturalistic accounts of pathology see it as a breakdown in biological function. If SE function fits well here, it would bolster the appeal of both itself and naturalism. However, Carl will argue that the fit seems to be an awkward one, especially outside of standardly considered cases.

Dan Nicholson will present collaborative work on the relationship between the SE account and the organisational account of function. He will argue that neither account, taken on its own, is sufficient to capture the wide range of contexts in which function-talk is used in the life sciences. Because each account has different explanatory targets both are likely to remain necessary to make philosophical sense of functional attributions in biology.

Justine Kingsbury will provide a commentary on the issues raised in the session.

Is global biodiversity loss bad?

Katie Morrow¹

¹University of Pittsburgh, History and Philosophy of Science, Pittsburgh, PA

We may be at the beginning of a mass extinction event, with around a quarter of species currently threatened with extinction in many of the best-studied taxa. Environmental philosophers often take it for granted that we should try to prevent global biodiversity losses, but there have been difficulties with the main arguments which are supposed to support this position. A popular instrumental argument is the Ecosystem Services Argument, which claims that species diversity is needed to support ecosystem functions and services. I develop an overlooked objection to the Ecosystem Services Argument by identifying a false implicit premise in the argument.

My objection starts by pointing to a scale mismatch between ecosystem services and the intended target of the argument, which is to support global biodiversity preservation. The argument claims that local ecosystem services are supported by local diversity levels. This argument can only support protecting global diversity if it includes a “scale change” step stating that global species losses contribute to local diversity losses. But this (usually missing) step in the argument cannot be justified. I present both an empirical problem and a conceptual problem for this implicit scale change premise. Without a scale change premise, the argument fails on a formal level. I conclude that the Ecosystem Services Argument is unsuccessful, and will remain unsuccessful even if some relevant empirical evidence were to change. An upshot is that global species diversity may not have any conventional type of instrumental value to humans, at least none recognized by existing arguments or scientific evidence.

Remaining arguments which may avoid the scale problem include arguments from aesthetic, cultural, scientific, or intrinsic value. Arguments based on these types of value may support the value of biological diversity at the global scale, but they do not clearly explain why moderate diversity losses are bad or why we should spend significant resources preventing arbitrary species losses. I conclude that continuing work is urgently needed on the value of biological diversity, with more attention paid to the scale-dependence of relevant ecological phenomena as well as realistic projections for the extent of species losses we are facing over a timeframe relevant to humans.

Aldo Leopold and the biodiversity-stability connection

Roberta L. Millstein¹

¹University of California, Davis, Philosophy, Davis, CA

In an unpublished essay written around 1942 (“Biotic Land-Use”), ecologist and conservationist Aldo Leopold states that, aside from soil fertility, “diversity of fauna and flora” is the factor “most closely associated with stability.” To today’s ears, this resembles an assertion of the controversial and oft-criticized (if not defeated) “biodiversity-stability hypothesis” — roughly, the proposition that the more biodiverse an ecosystem is, the more stable it tends to be. But as I have argued elsewhere (e.g., Millstein 2018ab), Leopold was an independent thinker, and we have to be extremely careful in assuming that meanings of his contemporaries or our contemporaries can be mapped on to Leopold’s meanings. Often they cannot be. Thus, I seek to further examine Leopold’s understanding of “diversity” and “stability”. I argue, in line with other scholars (especially Warren 2013), that Leopold equated “stability” with “land health,” which Leopold characterized as “the capacity of the land for self-renewal.” Leopold further argued that long and diverse food chains – and importantly, the interactions represented by those food chains – were generally required for stability/land health. But the nature of this claim was in the realm of an educated, defeasible guess. My goal in this presentation is to further elaborate on these two Leopoldian concepts and the connection that he saw between them in order to see if they offer anything new for contemporary debates to consider – that is, do they offer a new conception of biodiversity or a new conception of stability? Do they offer a new understanding of biodiversity in relationship to stability? In addition to potentially shedding light on the biodiversity-stability debate within ecology, answering these questions will help to enlarge our understanding of the ideas of this important and influential thinker.

Research biodiversity and the presumption of generality in the life sciences

Michael R Dietrich¹

¹University of Pittsburgh, History and Philosophy of Science, Pittsburgh, PA

When the NIH decided that a small set of organisms would be designated model organisms in 1990, some biologists feared that this designation would cause a drop in the diversity of organisms used in biological research. Such a change in research biodiversity could have a major impact on the kinds of questions posed, the methods used, the data collected, and the knowledge generated in the life sciences. Using publications from 1970 to the present in major journals associated with specific fields, we have created a record of organism use in genetics, evolutionary biology, ecology, cell biology, developmental biology, neurobiology, and physiology. Using two measures of phylogenetic biodiversity, species abundance, and species richness, we compare the research organisms used in each of these biological fields. Our expectation is that the designation of model organisms will have had little impact in fields such as ecology and evolution, but more significant impact in fields such as cell biology. Comparison of changes in research biodiversity across these different fields reveals the extent to which some areas of biology are willing to assume, often without much justification, that research on a single species is sufficient grounds for generalized conclusions. We will use this new data on research biodiversity to understand the different circumstances that inform generalizations from organismal results in different biological fields.

A novel argument for a progenerative view of kinship

Rob Wilson¹

¹University of Western Australia, Philosophy, Perth, Australia

Performativist or constructivist perspectives have come to occupy a central place in the study of kinship within cultural anthropology over the past 50 years. This paper draws on contemporary psychology, cognitive science, and the philosophy of science to argue for the contrasting, old-school view of kinship as *progeneratively constrained*. I hypothesize that kinship involves a form of extended cognition and show how an influential conception of kinds, the homeostatic property cluster view, can be developed to specify kinship's progenerative nature. Drawing on these conceptual resources from beyond anthropology highlights the distinctive roles that our cognitive access to progenerative facts plays in kinship while avoiding the standard traps of reductionism and ethnocentrism.

As cognitive anthropologists have long recognised (D'Andrade 1995, ch.3), articulating an appropriate role for cognitive mechanisms in an account of kinship is a key part of the integrative bridge to be built between biological and sociocultural dimensions to kinship. This recognition drives the novel pairing of ideas at the heart of the present paper: (i) human kinship is generated and regulated by externally-mediated forms of cognition, and (ii) there is an asymmetry between certain kinds of facts, progenerative facts, and other kinds of fact important to the performance of kinship and to the grip that kinship has on us. (i) in effect treats kinship systems as constituted by both internal and external cognitive resources, the latter of which lie beyond the boundary of the individual. So conceived, kinship involves a form of extended cognition. (ii) justifies the view that kinship is progeneratively constrained and suggests a way to articulate a view of kinship as distinctively progenerative.

Pathological complexity and the evolution of consciousness

Walter Veit¹

¹University of Sydney, School of History and Philosophy of Science, Sydney, Australia

This paper is a contribution to the emerging science of animal sentience. I am motivated by a set of questions that have for a long time puzzled both scientists and philosophers, yet been deemed exceedingly difficult if not impossible to answer: What is consciousness and why does it exist at all? Are humans the only sentience creatures on our planet? Which non-human animals (hereafter animals) are conscious and do they differ in their subjective experiences? Could consciousness come in degrees and different kinds or is it like a light-switch that is either either 'on' or 'off'?

I want to make progress on these questions, complex as they may be, by largely defending a single idea:

Pathological Complexity Thesis (PCT):

The function of consciousness is to enable the agent to respond to pathological complexity.

The PCT is a complexity thesis about the relationship between life and mind (see Godfrey-Smith 1996). When I speak of mind here, I am not only referring to the peculiarities of human minds, but rather of minds as a phenomenon in nature. The point is not to anthropomorphize other animals but to naturalize the mind by placing it in its phylogenetic history. I want to ask, not only, what it is doing now, but what it is for. It is a question regarding the place of mind in nature both in the sense of where minds are found and what role they play(ed). The pathological complexity thesis is an attempt to develop such a theory. In order to understand consciousness as a complex natural rather than a human phenomenon, we will inevitably have to address its nebulous evolutionary origins and distribution across the entire tree of life.

References

Godfrey-Smith, Peter. Complexity and the Function of Mind in Nature. Cambridge University Press, 1998.

Issues when applying structuralism to biology

Angella Yamamoto¹

¹University of Waterloo, Philosophy, Waterloo, Canada

This paper discusses some issues that arise when applying structural realism to biology. I begin by reviewing Katherine Brading's version of structural realism with a hierarchy with proliferation of models.² I then attempt to apply Brading's structural realism to a biological example. This biological example suggests an issue with the use of shared structure. In response, I suggest the use of relevant relations instead of shared structure. I then discuss Steven French's use of eliminativist ontic structural realism in biology. Additionally, I consider John Dupré and Maureen A. O'Malley's discussion of metagenomics and claim that biological entities are better described as self-sustaining biological processes.³ These metagenomic insights suggest an eliminativist view is preferable in biology. I conclude with an attempt to combine Brading's and French's approaches into an eliminativist relevant relationalism that retains the structuralist favor and is applicable to the fluid, constantly changing entities found in biology.

2. Katherine Brading, "Structuralist Approaches to Physics: Objects, Models and Modality," chap. 3 in *Scientific Structuralism*, ed. Alisa Bokulich and Peter Bokulich, vol. 281, Boston Studies in the Philosophy of Science (Dordrecht: Springer Netherlands, 2011), 43-65, isbn: 9789048195978, doi:10.1007/978-90-481-9597-8_3.

3. John Dupré and Maureen A. O'Malley, "Metagenomics and biological ontology," *Studies in History and Philosophy of Biological and Biomedical Sciences* 38 (2007): 842.

Lessons from history: what Schelling might add to the New Mechanistic approach and contemporary biological science

Sarah M Roe¹, Steven M Brown²

¹Southern Connecticut State University, History, New Haven, CT, ²Southern Connecticut State University, History, New Haven, CT

Perhaps shockingly, we argue that the overall projects of F.W.J. Schelling and the New Mechanists have many similarities once we take seriously Schelling's work, particularly his early work regarding the biological sciences. After illuminating the salient similarities between these two projects, we hope to offer some possible refinement regarding mechanistic explanations. Utilizing Schelling's insights, we explore a more nuanced understanding of "activity" and the importance of both inhibition and ephemeral mechanisms to scientific practice and explanation.

'Principled mechanistic' explanations in biology: A case study of Alzheimer's disease

Sepehr Ehsani^{1,2}

¹University College London, Department of Philosophy, London, United Kingdom, ²Ronin Institute for Independent Scholarship, Montclair, NJ

Following an analysis of the state of investigations and clinical outcomes in the Alzheimer's research field, I argue that the widely-accepted 'amyloid cascade' mechanistic explanation of Alzheimer's disease appears to be fundamentally incomplete. In this context, I propose that a framework termed 'principled mechanism' (PM) can help with remedying this problem. First, using a series of five 'tests', PM systematically compares different components of a given mechanistic explanation against a paradigmatic set of criteria, and hints at various ways of making the mechanistic explanation more 'complete'. These steps will be demonstrated using the amyloid explanation, and its missing or problematic mechanistic elements will be highlighted. Second, PM makes an appeal for the discovery and application of 'biological principles' (BPs), which approximate *ceteris paribus* laws and are operative at the level of a biological cell. As such, although thermodynamic, evolutionary, ecological and other laws or principles from chemistry and the broader life sciences could inform them, BPs should be considered ontologically unique. BPs could augment different facets of the mechanistic explanation but also allow further *independent* nomological explanation of the phenomenon. While this overall strategy can be complementary to certain 'New Mechanist' approaches, an important distinction of the PM framework is its equal attention to the explanatory utility of biological principles. Lastly, I detail two hypothetical BPs, and show how they could each inform and improve the potentially incomplete mechanistic aspects of the amyloid explanation and also how they could provide independent explanations of the cellular features associated with Alzheimer's disease.

Epistemic progress in animal models of mental disorders: From the depressed mouse to the mouse with aspects of depression

Derek W Braverman¹

¹Washington University in St. Louis, Department of Philosophy, St. Louis, MO

The practice of modeling mental disorders in animals has evolved in tandem with the medical understanding of those disorders themselves. Here, I clarify the importance of this iterative process by describing the characteristic case of animal models of depression, detailing key changes over five decades. Then, I elucidate the epistemic significance of these changes by bringing work on modeling and mechanisms from the philosophy of science to bear on this historical development: I argue that the shift in practice both constitutes epistemic progress and provides reasons to temper enthusiasm regarding the translation of results from animal models to people with depression.

Initial attempts in the 1970s to produce animal models explicitly aimed to simulate human depression in its entirety to the greatest extent possible. But this practice has matured in line with the increasing, though contentious, recognition that mental disorders as currently categorized have heterogeneous symptoms and diverse, interacting causes. Accordingly, efforts to fully simulate depression in animals have given way to the creation of models for particular aspects of depression. This shift in the methodology and conception of animal models of depression is mirrored in developing standards for their validity.

I argue that this change is epistemically positive as the approach of decomposing depression into aspects and investigating such aspects individually better coheres with our current understanding of the complexity of the model's representational target. Furthermore, I suggest that the aspects of depression that researchers now seek to model are entities and activities that comprise mechanisms that are putatively responsible for depression.

However, enthusiasm about such epistemic progress should be tempered by the implications of these advances in practice and understanding. First, simulating aspects of depression rather than depression in its entirety requires a proportionate narrowing of the representational scope of the model, indicating reduced generalizability. Second, the more complex the mechanisms responsible for a mental disorder are, the less likely we are to identify biological loci that are both intervenable and clinically significant.

Corroborative and anticipatory predictions

Solange Haas¹, Philippe Huneman¹, Philippe Jarne², Virginie Maris³, Sonia Kéfi⁴

¹IHPST/CNRS, Philosophy of Biology, Paris, France, ²CEFE/CNRS, Evolutionary Ecology, Montpellier, France, ³CEFE/CNRS, Philosophy of Environment, Montpellier, France, ⁴ISEM/CNRS, Ecology, Montpellier, France

Based on the 2018 article in *Oikos* Prediction in ecology: promises, obstacles and clarifications, we would like to present the distinction between anticipatory and corroborative predictions. These predictions differ in the first place in their purpose: informing a decision for the former and validating or invalidating a scientific hypothesis for the latter. From this distinction stems a difference in their nature. Indeed, their relationship with time, scientific theories and verification by experiment is not the same. Anticipatory predictions in particular do not have to be verified by any observation or experiment; this means that its underlying theory does not necessarily have to be questioned if the prediction has not come true. This result seems to us to be particularly interesting for thinking about the use of predictions in a policy-making context.

We would then like to discuss the application of these concepts of anticipatory and corroborative predictions to some examples of ecological models. The models of demographic projection matrices seem to us to be a good illustration of the production of anticipatory predictions.

Finally, in addition to these differences of nature, the predictions do not face the same obstacles in their development. In the particular case of ecology, these obstacles may be that ecosystems are historical entities, that many interactions between scales take place, that there are stochastic and chaotic phenomena, and finally that the human component plays a role in their evolution. Each of these obstacles affects each prediction in its own way and in a different way depending on whether it is anticipatory or corroborative. Therefor we will try to propose examples of situations where one type of prediction is prevented while the other is not, in order to better reveal the difference in the elaboration of anticipatory and corroborative predictions.

The origins of Muller's mutation concept

Sander Gliboff¹

¹Indiana University, History and Philosophy of Science and Medicine, Bloomington, IN

The modern conception of the “random” genetic mutation as unpredictable and undirected, yet explicable in terms of molecular- or even quantum-level events, grew out of Herman J. Muller's 1927 paper on “The Artificial Transmutation of the Gene,” and helped solidify the modern evolutionary synthesis by ruling out teleological, Lamarckian, and saltational explanations of variation. The paper also marks a transition in Muller's career from the classical transmission genetics of the Morgan school with which he began, to a research program of his own using X-rays to reveal the nature of genes and mutations, and to strive for a molecular-level understanding of heredity. The X-ray work won him the Nobel Prize in 1946, which then gave him a platform for his postwar campaign for radiation safety standards.

For the past decade or more, concerted efforts to weaken radiation-safety standards have relied in large part on disseminating a “fake history” of radiation biology that would discredit Muller's contributions, particularly his case for a linear relationship between X-ray dose and mutation rate and against the idea that there could be a safe threshold dose. It was all supposedly overhyped and undersupported, and promoted by underhanded means.

The story has been shot down by several authors, but we still lack a full account to put in its place. By what steps did Muller really arrive at his conception of the random, X-ray-induced mutation? What made him try X-raying his flies at all? What were his exact claims about linearity and threshold doses, and how did he support them?

This paper reconstructs Muller's path to discovery from the beginning of his career in the 1910s to his Nobel Award of 1946, and shows how he evaluated and rejected alternative gene- and mutation concepts, adopted the idea of quantum hits by X-ray photons, and analyzed the mutation process and the dose-response curve.

The vexed question of human genetic load

Evan Arnet¹

¹Indiana University, History and Philosophy of Science, Bloomington, IN

On December 29th, 1949 Hermann Muller, perhaps the world's foremost expert in mutation genetics, gave his presidential address to the American Society for Human Genetics. In the talk, later published as "Our Load of Mutations", he made a deceptively simple argument: Relaxed natural selection in modern society together with incautious use of radiation was leading to the accumulation of mildly deleterious mutations which would represent a long term health concern for humanity. For Muller, the argument was an ethical imperative. A committed socialist and humanist, he was deeply concerned about mutation accumulation and wanted scientists and policy makers to begin to take the genetic health of humanity seriously. For others, the argument is nothing more than a Trojan horse for the worst sort of eugenics. Nonetheless, despite such concerns, the argument has found purchase in modern science. Mullerian genetic load arguments have been used by scientists to (partly) explain increasing cancer incidence among humans, increasing global obesity, and even alleged dysgenic IQ loss in humans. Given this, it bears looking at in more detail. As originally developed by Muller, the argument did not problematize race, immigration, poverty, or any of the stereotypical bugbears of eugenics, but rather targeted modern society and ordinary reproduction itself such that, he contended, humans had no choice except to think genetically if they cared about the long-term health of humanity. It is this aspect of the argument in particular I wish to draw out and critically evaluate. I do so by analyzing the specific argument of Muller, developing a family of arguments to capture the use of human genetic load in modern science, and then evaluating these arguments conceptually, empirically, and ethically.

Gradualism, natural selection, and randomness of mutation: Darwin, Fisher, and connecting the dots

Matthew J Maxwell¹, Elliott Sober¹

¹University of Wisconsin - Madison, Philosophy, Madison, WI

Evolutionary gradualism, the randomness of mutations, and the hypothesis that natural selection exerts a pervasive influence on evolutionary outcomes are pair-wise logically independent. Darwin treated them as separate elements in his theory of evolution, but Fisher, in his "geometric argument," showed that small random mutations are more apt to be adaptive than large random mutations are, thus connecting these three ideas. After analyzing Fisher's argument and connecting it to questions about the impact of variance on fitness and the probability of stochastic loss, we explore this three-way connection further, distinguishing likelihoodist from Bayesian formulations of gradualism. As a first approximation, "evolutionary gradualism" means that a species (or a population) that evolves from one state to another does so by a large number of small changes rather than by a small number of large changes. Thus formulated, "gradualism" is vague, owing to the vagueness of "small" and "large," but that does not mean that this *ism* is suspect or that it has no place in real science. Gradualism was central to Darwin's theory of evolution and to much of the evolutionary theorizing that followed. In due course, we reformulate what we mean by gradualism in a way that avoids vagueness. Gradualism need not be a thesis just about selection. For example, it could be advanced as a claim about the influence of random genetic drift on the evolution of quantitative phenotypes. Historically, however, gradualism has been important as a thesis about adaptive evolution, and that's the version of gradualism that we discuss in what follows. When a phenotype evolves because it is adaptive, does it evolve because a large number of small adaptive mutations evolved, or does it evolve because a smaller number of big adaptive mutations evolved? In what follows, we briefly describe Darwin's (1859, 1868) views about gradualism and then move on to Fisher's (1930) geometric argument concerning the size of mutation. We then consider how Fisher's result is connected to the idea that the expected number of offspring is not a fully adequate definition of fitness; variance needs to be considered as well. After that we consider how Fisher's result is affected by "stochastic loss" and how the result changes when a gene affects two, three, or n quantitative phenotypes. Finally, we take up the question of how these results bear on the status of adaptive gradualism.

Teleonomy and teleology revisited: The continental critique of cybernetics

Auguste A Nahas¹

¹University of Toronto, IHSPT, Toronto, Canada

Recent years have seen resurgent interest in the idea of biological purposiveness and the so-called ‘naturalization’ of teleology, along with a flurry of debate regarding the prospects for such a project. The aim of this paper is to bring some clarity to these contemporary debates by retracing them to the conceptual bifurcation which teleology underwent during the middle of the 20th century. The ‘origin’ of this shift can be traced back to Rosenblueth et al.’s landmark 1943 paper, *Behavior, Purpose, and Teleology*, which proposed a new, scientifically legitimate conception of teleology. This new conception of teleology was popularised by Colin Pittendrigh, who first named it ‘teleonomy’, and Ernst Mayr who connected it to the idea of the genetic ‘program’. Though little discussed, this attempt to naturalise teleology was extensively critiqued by continental philosophers such as Georges Canguilhem, Gilbert Simondon, Raymond Ruyer, and Hans Jonas, who unanimously saw teleonomy as a way of eliminating teleology rather than naturalising it.

The aim of this paper is to revisit this episode with an emphasis on its place in the historical debates over teleology’s place in biology, and with special attention to the various critiques which were leveled at the concept of teleonomy by the continental philosophers previously mentioned. Beyond the need for a historical reconstruction of this episode which emphasises the centrality of teleology as an area of inter-disciplinary and inter-continental debate, it is my contention that a better understanding of this period can lead to crucial insights into current debates on teleology in the context of an agentic conception of the organism. More specifically, I argue that it provides two possibilities for understanding the relationship between teleology (or purposiveness) and similarly controversial debates over biological individuality and normativity. The teleonomic approach, for its part, seeks to naturalize teleology in a way that does not have recourse to notions of the biological self or individual. The approach to teleology championed by the Continental critics, on the other hand, is one which sees the notion of the individual or beneficiary as crucial to a proper understanding of biological teleology. I suggest that both of these options are currently at play, and that each comes with distinct strengths and weaknesses.

Understanding teleology. A strategy for the study of value on biological systems

David Suárez Pascal¹

¹Universidad Nacional Autónoma de México, Facultad de Ciencias, Mexico City, Mexico

Teleology has been a recurrent topic in the philosophy of biology (Ayala, 1998; Cummins, 2010; Nagel, 1979), and several scientific and philosophical proposals have been advanced to explicate, or to explain away, this issue by recourse to a vast array of mechanistic, cybernetic, selectionist, autopoietic, or other varieties of resources (Cummins, 1975; Garson, 2016; Saborido et al., 2010; Wright, 1976). While those approaches have had differential success in terms of accounting for (or dispensing with) teleological aspects of living systems, each one of them has provided us with distinct understandings of what teleology means which are interesting in themselves. Nonetheless, alternative accounts show that a common pitfall in attempts at analyzing teleology is connected with the relationship that exists between teleological notions and value (Bedau, 1992, 1993; McLaughlin, 2001; Nguyen, 2018). Even when this position could be interpreted as supporting non-reductionistic or non-naturalistic views on teleology, I suggest that it is possible (and advisable) to pursue at the same time both better descriptions and a deeper understanding of teleology in biological systems.

Generations and heredity: The social and biological careers of ‘intergenerational’ and ‘transgenerational’ inheritance

Tatjana Buklijas¹

¹The University of Auckland, Koi Tu: The Centre of Informed Futures, Auckland, New Zealand

The concept of generation had once stood for procreation but by the late 1700s it came to be replaced with reproduction in which ancestral traits were faithfully transferred, akin to the inheritance of material property. By the early twentieth century, the new science of genetics asserted its monopoly over biological inheritance. Only the transmission of genetic material was conceptualized as true heredity while phenomena that reoccurred across generations yet without a genetic basis were excluded from biological disciplines and left to social sciences, public health and psychology. Sociologists, social workers, psychologists talked about intergenerational cycles of violence and poverty; psychiatrists studied the "second generation" trauma of the children of Holocaust survivors. When biologists addressed non-genetic phenomena that persisted across two or three generations, they called it transgenerational. But around 1990 these unstable forms of heredity came to be reinstated into life sciences through disciplines such as developmental origins of health and disease (DOHaD) and epigenetics.

In this paper I investigate how this return created a problem of definition. The terminology of intergenerational inheritance (also known as parental and grandparental effects) now came to be understood as biological – but not genetic. Genetics still dictates the terms of debate: the stability of inheritance across multiple generations remains the key criterion to distinguish “true heredity” from lesser forms, and the term transgenerational has been co-opted to designate stable yet non-genetic inheritance. In this presentation I will investigate how this terminology travelled – through which scholars, disciplines and projects– from social sciences and psychology into biomedical sciences. I will then discuss how it was used as it travelled back from biological disciplines into social sciences. Finally, I want to ask whether the apparent dominance of genetics still holds, or whether for other groups – e.g., policymakers and clinicians - the "less stable" inheritance may be of more interest and value than “true heredity”.

The good species

John S Wilkins¹

¹The University of Melbourne, School of Historical and Philosophical Studies, Melbourne, Australia

Much of the species problem lies in trying to find necessary and sufficient theoretical criteria for both their explanation and delimitation. I argue in this paper that species are instead “operative concepts”, built up by the collective experience and context of subdisciplines of systematics as the field develops, relying on assays and criteria that make a putative taxon a “good species”. I reiterate my view that species are phenomena that stand in need of explanation, and that the category itself is so polysemic, because of the haphazard way the concept develops in the various specialties’ history, that it is merely an epistemic notion.

Ornithology and the “empire of nature”: The classification of birds in eighteenth-century France

Yotam A Tsal¹

¹University of California, Berkeley, History, Berkeley, CA

Today biologists are preoccupied with the extinction of species. However, in the second half of the eighteenth century, French naturalists were more concerned about nature’s plentitude. They commented on the vastness of the “empire of nature,” and obsessively tried to estimate the number of mammals, birds, and insects in nature. They also carefully amassed animal specimens in growing collections of natural history. In this paper I argue that ornithology, as a defined field of knowledge, emerged out of this obsession with nature’s expansiveness in the period.

The universe of birds seemed to contemporaries particularly overwhelming and hard to manage, because of the number of species and the confusing differentiations in color between species, varieties, sexes, age groups, and between same species in different seasons. Naturalists argued against and in favor of their peers’ naming of new species. In some cases, the question revolved around the extent to which the specimen was reliable enough to serve as a representation of the animal in nature. In other cases, the question concerned whether two individuals were different enough from each other in order to determine that they were indeed separate species. In yet other cases naturalists criticized each other for mistaking two individuals of the same species but of different ages, sexes, or seasons for separate species. Because of the instability of both live and dead bird specimens, the space for naturalists’ discretion in naming new species was quite wide. The inclination of many ornithologists was to add more and more names to lists of new species.

The paper ties this fascination with the number and differentiations between bird species to a moment of search in French imperial history, after the Seven Years War, and before the collapse of the first colonial empire in 1815. In this period of global transformation, a firm apprehension of nature in both totality and minutiae seemed a pressing question of great consequence.

The anomaly of a basic population-genetic cause missing from the Modern Synthesis

Arlin B Stoltzfus¹

¹National Institute of Standards and Technology, Office of Data and Informatics, Gaithersburg, MD

A process of evolutionary change dependent on events of mutation that introduce new alleles (or events of mutation-and-altered-development that introduce new phenotypes) is subject to biases in the introduction process, via a simple "first come, first served" mechanism. The implications of this kind of causation, formally demonstrated in 2001 and elaborated in subsequent theoretical work, include a novel prediction of mutation-biased adaptation that is now verified empirically. My focus here is not on explaining the theory or assessing the evidence, but on problematizing the conspicuous absence of this theory from key debates of the 20th century. The theory was not invoked to rebut a highly influential Haldane-Fisher argument that, because mutation rates are too small for mutation to be an important force, theories of evolutionary tendencies due to internal biases (orthogenesis) may be rejected. The theory was not leveraged to subvert neutralist claims that effects of mutation bias on molecular evolution are evidence of neutrality. Finally, the theory was not used to map controversial notions of "developmental constraints" and "self-organization" onto a population-genetic mode of causation that would have added to their perceived legitimacy. Why was a theory of biases in the introduction process not proposed 70 years earlier? I argue that this theory exists in a conceptual blind-spot fostered by specific aspects of mid-20th-century thinking. One key aspect is the way that theory-based arguments about the nature of evolutionary causation, aggressively promoted by the architects of the Modern Synthesis, equated evolution with shifting the frequencies of alleles already available in an abundant gene pool, with formal causes defined (by analogy with statistical physics) as mass-action forces, a conception that does not cover a point process of introduction. This position originally emerged as a way to exclude mutationist thinking (mutation proposes, selection disposes) and harvest the methodological power and conceptual simplification that came with a shifting-gene-frequencies paradigm.

The role of theoretical population genetics in mutation-biased adaptation

Kevin Gomez¹, Jason Bertram², [Joanna Masel](#)³

¹University of Arizona, Applied Mathematics, Tucson, AZ, ²Indiana University, Biology, Bloomington, IN, ³University of Arizona, Ecology & Evolutionary Biology, Tucson, AZ

A key role for development in shaping adaptive evolution has typically been proposed by developmental biologists critical of theoretical population genetics, sometimes under in terms of the need for an “extended evolutionary synthesis”. But population genetic models can incorporate this role through quantitative biases in mutational terms, with those biases having developmental causes. “Mutation-biased adaptation” occurs when relative mutational rates, not just relative selective strengths, direct the course of adaptive evolution. Some have previously claimed that mutation-biased adaptation is restricted to regimes in which adaptive mutations are rare and/or recombination is common. This is because clonal interference is a powerful force favoring whichever adaptive mutation has the largest selection coefficient. To address this claim, we model the adaptation of an asexual population with high adaptive mutation rates, and find that mutation-biased adaptation can continue to play a role. Instead of adaptation being dominated by the trait whose adaptive mutations have the largest selection coefficients, we find that it is dominated by the trait that would, if evolving in isolation, evolve the fastest, with “evolutionary stalling” seen for other traits. More complex population genetic models of fitness landscapes are also helpful for understanding questions about higher-level evolutionary accessibility.

Do mutational biases influence adaptive evolution?

David M McCandlish¹

¹Cold Spring Harbor Laboratory, Simons Center for Quantitative Biology, Cold Spring Harbor, NY

Whether and how internal influences on the production of phenotypic variation affect the dynamics and direction of adaptive evolution remains an open question. Arguments in favor of a strong role for internal influences from the evo-devo and process structuralist traditions have often been couched in terms of "developmental constraints" or, alternatively, statistical explanations based in the generic behaviors exhibited by physico-chemical and developmental systems. These arguments have by and large not convinced evolutionary and population geneticists, due in part to a strong preference among evolutionary and population geneticists for causal arguments and/or arguments couched in terms of population-genetic quantities such as selection coefficients, mutation rates, and effective population sizes. Here I will discuss an emerging form of evidence that bridges this gap between communities. This evidence consists of the combination of (1) our expanding knowledge of the specific single nucleotide mutations responsible for adaptive phenotypic changes in natural populations, experimental evolution, and human cancers, and (2) our knowledge concerning the spectrum of mutational variants characteristic of each of these systems. In particular, we can ask to what extent the spectrum of these known adaptive substitutions can be predicted from either broad-scale patterns of mutational bias (e.g. the elevated rate of transitions relative to transversions, or elevated mutation rates at CpG dinucleotides in many species) or finer-scale data on mutational propensities for particular systems obtained directly via mutation accumulation experiments, as well as the extent to which the spectrum of adaptive substitutions reflects the biases inherent in simple genotype-phenotype maps such as the genetic code. Here I will discuss the current state of this evidence, drawing from both the published literature and new results from ongoing work. More generally, as a simple and quantifiable case of biases in the introduction of variation, investigating the role of mutational biases on adaptive molecular evolution provides an important test case for more expansive theories of the role of internal variational biases in the evolutionary process.

When did we first talk about "primatology" ?

Marie L Lacomme¹

¹Sphère, Université de Paris, Paris, France

In the few accounts of the history of primatology that exist, often written by primatologists themselves, the origin of the name of the discipline is invariably said to date back to the 1930s or 1940s (Bernstein 1983, Fridman and Nadler 2002, Ankel-Simons 2007, Leblan and Narat 2017), with the date 1941 being often mentioned as the first occurrence of the word “primatology” in a scientific publication. It is believed that it was during this period that Theodore C. Ruch coined this neologism in the title of his compilation of scientific studies on primates. I will show in this paper that the word "primatology" in fact appears in several sources at the end of the 19th century. It can be found for example in an article of 1874 written in English by Louis Elsberg, laryngologist at the NYU School of Medicine and in an article of 1897 written in Italian by Raffaele Schiattarella, professor of law at the University of Palermo. I will highlight that these two authors, despite the apparent remoteness of their backgrounds, both discussed the place that a science named primatology should have in relation to anthropology and that they did so by referring more or less directly to the writings of Auguste Comte.

The purpose of this paper is not only to find the first occurrence of a word. Through this study, my goal is above all to better understand the emergence and constitution of primatology as a scientific discipline. In this perspective, the meaning the actors attribute to the term "primatology" and the context in which they propose it will be examined. Returning to the historical roots of the term "primatology", this article challenges the classical thesis that a discipline devoted to all primates, human and non-human could not be envisaged until the end of the 1930s. It suggests that this idea is in fact already germinating in the context of a positivist and Darwinian tradition of the late 19th century.

Out of Africa: Yerkes and Nissen's primate field studies in French Guinea (1920s-1930s)

Marion C Thomas¹

¹University of Strasbourg, Faculty of Medicine, Strasbourg, France

In 1922, in French Guinea, the bacteriologist Albert Calmette launched an overseas Pasteur Institute (commonly known as “Pastoria”), which used apes as its central research model (Rossianov, Leblan). Abundant and accessible in the Africa, apes reinforced the attractiveness of the French colonies, becoming a raw material to be exploited. Calmette was well aware that apes could be a bargain chip when he offered to host prestigious foreign scientists. Among them were the American psychologists Robert Yerkes and Henry Nissen, who played a major role in the emergence of primatology as a discipline in the first part of the XXth century in the United States. A correspondence disclosed Calmette's concern to entice American funding bodies, like the Carnegie Institution, or the Rockefeller Foundation, making Yerkes a leverage between France and the United States, insofar as he enjoyed special relations with these rich patrons. I first want to examine the socio-political and scientific connections between the Pastorians and the Americans. Those connections, which initially showed signs of a fruitful collaboration, finally fizzled out, and I provide hypotheses to explain this failure. Yerkes, however, made the best of his bonds with the colonial Pastorians. He used Pastoria not only as a supplier for his own laboratories, but also as a platform to venture into the wild to study chimpanzees. In the late-1920s, Yerkes strove to develop the fledgling science of primatology beyond the laboratory walls and he notably sent his co-worker Nissen on assignment to the Guinean bush (Dewsbury, Montgomery, Rees). Drawing on Nissen's field notebooks, as well as related correspondence and administrative notes, I cast a light on Nissen's practices in the field and explore the ways in which Nissen appropriated indigenous people's observations of primates and drew the line between local knowledge and expert observation. While retrieving the relations between Nissen and the French colonists, I finally want to assess to what extent colonial stereotypes informed Nissen's scientific discourses and practices and also to document the paradox inherent in relying on indigenous knowledge while asserting the intellectual superiority of the white man.

Vector Biology Network: Bringing innovations in modern biology to the field of vector borne diseases

Kulash Zhumadilova¹

¹Virginia Tech, Science, Technology and Society, Blacksburg, VA

In this work I will focus on the history of Vector Biology Network (VBN), an organization that was aimed to bring innovations in modern biology (mainly DNA editing tools) to the field of vector borne diseases. The history behind this organization is a good example of how historical and social factors like colonialism, philanthro-capitalism, policies and ideology influence production of scientific knowledge. Through this example I will illustrate how private philanthropies like the Rockefeller and the MacArthur foundations got involved in global health and how this model is still being practiced today by the Gates Foundation. I will argue that processes which led to the formation of the VBN and similar interests groups helped to cement the narrative of emerging diseases coming out of the "jungles" of the Global South, be it Uganda or China. In the light of current pandemic, I will attempt to show how colonial history of the field of vector borne diseases informed current state of vaccine development.

Cognitive norms in autonomous systems: Rooting teleosemantics within organicism

Tiago Rama¹, Xabier Barandiaran²

¹Autonomous University of Barcelona (UAB), Center of Theoretical Linguistics, Barcelona, Spain, ²University of Basque Country (UPV/EHU), Departament of Philosophy, San Sebastián, Spain

While the most widespread attempt to explain cognitive norms in naturalistic terms is etiological teleosemantics (e.g. Ruth Millikan and Karen Neander), there is an increasing alternative anchored in Organismic Biology (e.g., in the work of William Ashby, Patrick Bateson, Scott Camazine, Gerald Edelman, Scott Gilbert, Brian Goodwin, Stuart Kauffman, Christopher Langton, Robert Rosen, Esther Thelen y Linda Smith, Francisco Varela y Humberto Maturana, o Denis Walsh). A prominent area to approach natural normativity within organismal biology is Autonomous System Theory (cf. the work of Xabier Barandiaran, William Bechtel, Mark Bickhard, Alvaro Moreno, Mateo Mossio, and Kepa Ruiz-Mirazo). Within this approach, normativity has been naturalized as self-established viability conditions by the organism. Departing from different works on sensorimotor theory and the autonomy of cognition (especially in the work of Ezequiel Di Paolo, Xabier Barandiaran, Matthew Egbert, and Wayne Christensen) we extend and discuss the notion of cognitive normativity from an organismic perspective that understands cognitive norms as emerging from interdependencies between sensorimotor habits. First, we attempt to refine the different sensorimotor layers that build cognitive norms, by empathizing both the role of development in norm-establishing and the scaffolding role of social dynamics. Secondly, we will put our theory in dialogue with the issue of cognitive normativity in the philosophy of mind and life. In particular we argue that an organismic perspective on cognitive normativity is capable of addressing the following issues: a) the relation between normal traits and pathologies; b) the capacity to move forward statistical notions of normativity; c) the plasticity of cognitive norms and their importance for phenotypic variation and ontogenetic transformation; d) the central role of sensorimotor development and the continuities and discontinuities between life and mind.

Emotional appraisal is not memory

Isaac Wiegman¹

¹Texas State University, Philosophy, San Marcos, TX

Many have argued or assumed that there is an important discontinuity between basic and higher cognitive emotions. Among the most influential of these is Paul Griffiths (1997). Griffiths followed Ekman (2005) in arguing that basic emotions are a restricted class of emotional responses that have some overlap with folk emotion categories such as anger, fear, joy, sadness, surprise, and disgust. Affect programs were posited to explain the coordination of various dimensions of these responses including brief, stereotyped facial expressions, changes in posture, and activation of the autonomic nervous system (Ekman, 1971; Ekman & Cordaro, 2011). Moreover, they can be triggered without the mediation of higher cognitive processes like beliefs and desires. By contrast, higher cognitive emotions are thought to be highly culturally variable and thought to lack stereotyped physiological responses. Finally, some claim that the occurrence of higher cognitive emotions requires phylogenetically recent cognitive inputs (e.g., causal reasoning, self-awareness, theory of mind). Higher cognitive emotions include not only emotions like shame, guilt, embarrassments and pride (e.g., Clark, 2013), but also some instances of folk emotion categories like instances of anger or disgust that are elicited by moral offenses (Griffiths & Scarantino, 2009). Importantly, the features of higher cognitive emotions and basic emotions are not definitions but a posteriori identities. Accordingly, these characterizations are subject to revision as we learn more about basic and higher cognitive emotions.

I challenge this distinction between basic and higher cognitive emotions, arguing that at least part of its basis is flawed. Proponents of this distinction assume that the input/appraisal processes of higher cognitive emotions are integrated with beliefs and desires and long term planning (etc.), whereas the input/appraisal processes of basic emotions are realized by a proprietary, modular memory system, sometimes described as a kind of database of emotion elicitors. I present a new model of emotion learning and appraisal, which accounts for the evidence of modularity just as well. Yet this model allows for the resolution of two key problems for the database model: evolutionarily novel emotions, and the effectiveness of cognitive therapies for PTSD.

The evolution of imaginative consciousness

Oryan Zacks¹

¹Tel Aviv University, Philosophy Linguistics and Science Studies, Tel Aviv, Israel

Human imagination is a unique, rich and highly developed cognitive ability, constituting an important part of human consciousness. With my colleagues, I characterize imaginative consciousness as a system of relationships among partially overlapping capacities such as event memory, causal reasoning and emotional control. Focusing on the hippocampus and its connectivity to other brain regions we show how a version of this system is realized in the rhesus monkey brain. We employ an evolutionary approach to trace the phylogeny of imaginative consciousness in the vertebrate lineage and attempt to characterize minimal versions of this type of consciousness by following its evolutionary dynamics in mammals, birds and fish.

Epigenetics and the biology of race: Naturalism, environmentalism, constructivism

Gaëlle Pontarotti¹

¹IHPST, Philosophy, Paris, France

The concept of race has been oscillating, since its introduction in the history of ideas, between politico-social and biological areas (Gayon, 1997). While the social perspectives have been dominant in the second half of the 20th century (Gravlee, 2009), “race” seems to be subject to a new kind of biologisation in the time of Epigenetics. In this paper, I examine this new biologisation and I highlight some of its paradoxes. I show that in the considered theoretical context, biological race does not refer to a genetic profile but to a set of hereditary somatic marks resulting from social-environmental exposures (Kuzawa & Sweet, 2009; Gravlee, 2009). I therefore argue that the new naturalisation of race paradoxically supports and strengthens social perspectives. I claim that this approach, which allows a synthesis between biological and social accounts (Meloni, 2017), echoes earlier externalist conceptions and leads to the articulation of naturalism, environmentalism and (socio-biological) constructivism as far as race is concerned. Finally, I insist on the fact that the new biologisation of race surprisingly invites considering that racial categories are biologically underdetermined.

Race eliminatedTarik D LaCour¹¹Texas A&M, Philosophy, College Station, TX

Eliminative materialism is the thesis that folk psychology is an empirical failure and as such will be and ought to be eliminated from our philosophical and scientific discourse. Typically, this is seen as a thesis applying only to the philosophy of mind and cognitive science, with things such as phenomenal consciousness, beliefs, intentionality, personal identity, and theory of mind being the things that must go. In this paper, I will propose that the concept of race is dependent upon the theory of mind, therefore if it goes by the wayside then race should go along with it. The concept of race has been used and is still used as a way of predicting attitudes, behaviors, and dispositions of a group of people; this is the theory of mind in practice. But as the theory of mind is false and our concept of race is dependent on it, it follows that race ought to be eliminated from our philosophical and scientific discourse because the theory on which it depends is false.

Liberal eugenics and the enhancement technologies

Tomás M Hernández Mora¹

¹Universidad de La Laguna, Philosophy of Science, Education and Language, La Laguna, Spain

The notion of eugenics refers to a social movement whose purpose was the improvement of the human species through the intervention in genetic heritage and reproduction. This social movement was created by the British anthropologist, Francis Galton, who was Darwin's cousin. After World War II, and the nazi Holocaust, the concept of eugenics fell into discredit and social rejection. Nevertheless, at the end of the nineties, a new form of eugenics started to emerge. It was liberal eugenics. This notion refers to a new kind of eugenics in which future parents have the freedom to decide if they want to genetically modify their future offspring or not.

This presentation aims to analyze the philosophy of liberal eugenics. For this purpose, I will examine the meaning of this concept, its origins, basic features, main purposes, and what are the differences between liberal eugenics and its predecessor. Moreover, in order to have a deep contact with this bioethical thought, I will study the tools that are used in this scope, this is, the enhancement technologies.

These are the future technologies that will become the means to have improved children, who will obtain the desired physical and psychological features. During this exposición, I will focus on some of them, such as Cloning or Preimplantation Genetic Diagnosis, among others. I will also show experiments of these technologies, like Dolly the sheep, or Doogy mice.

At the end of the talk, I will explore some ethical controversies that surround the notion of liberal eugenics, for example, the issue of identity and autonomy that these new modified humans can develop. Finally, I will give some conclusions.

Taphonomy as planetary science

Ana María Gómez López¹

¹University of Amsterdam, ASCA, Amsterdam, Netherlands

How did taphonomy, or the analysis of evidence related to time and place of death of a biological organism, become a field of inquiry in paleontology, physical anthropology, and archaeology? This paper is a contribution to the overlooked events by which taphonomic evidence—stages of decomposition, environmental influences, or geo-physical processes affecting a body's deposition—became integrated into the study of osteological and fossilized remains. Focusing primarily on the period between 1925 and 1975, specific instances of knowledge transfer that led to the transnational consolidation of taphonomy as a field are identified and analyzed. These "hinge moments" range from taphonomy's origins by paleontologists from Germany and Soviet Union in the first half of the 20th century, to the seminal formation of the first "body farm" or taphonomic research center in the United States. A special focus of attention are the modes of representation that arose for understanding problems in taphonomic research, such as analogue photography, mapping, and diagrammatic depictions of in-situ information. Examining taphonomy's development through these visual and archival records, this historical overview of taphonomy offers a hitherto unexplored framework from which to critically assess post-mortem processes at a planetary level, both in the present and across the geological record.

Analogue models in paleontology

Aja Watkins¹

¹Boston University, Philosophy Department, Boston, MA

Philosophers of science have recently analyzed the use of models, primarily simulations, in paleontology, and concrete models in the geosciences, but a philosophical analysis of concrete models in paleontology is missing. In this talk, I will begin to fill this gap by discussing three examples of concrete models in paleontology, as well as their implications for model ontology and epistemology.

The first example is the use of biorobotics. Like simulations, robots are constructed to resemble target systems, in this case extinct organisms. However, some scientists have preferred to study concrete model systems instead of simulated ones, for example to study the motion of extinct organisms. An advantage of concrete models is that we do not have to have a mathematical/computational understanding of the target system to build a model of it. Biorobotic examples enable us to extend the philosophical conclusions about simulations in paleontology to concrete models. Biorobotic examples also extend analyses of concrete models in the geosciences, including regarding dynamical scaling.

The second example is the use of extant organisms as models of extinct organisms. Unlike robots, extant organisms are not made by us, but we can choose appropriate extant organisms to serve as models of the extinct organisms under consideration. Scientists often use homology (similarity due to common descent) or analogy to select extant organisms to use as models; their selection depends on their research purpose. The use of extant organisms in paleontology is similar to the use of model organisms in other biological fields, insofar as both involve the use of an easily manipulable system to stand in for a less accessible one. The use of extant organisms as models shows that models need not be constructed to be useful.

The third example is more unusual: prepared fossils can serve as concrete data models. Data models are processed versions of “raw” data. Prepared fossils represent the organisms from which they formed. Not only is the physical material of the fossil different from that of the original organism, due to mineralization processes, but the prepared fossil also incorporates theory-laden decisions on the part of taphonomists who have this representational purpose in mind. This example even further complicates the extent to which concrete models need not be constructed by us, given an instance where both natural and scientific processes combine to produce the ultimate model.

Proximate and distant ancestry in forensic genetics

Vivette Garcia-Deister¹

¹UNAM, School of Sciences, Mexico City, Mexico

Over the past couple of decades, forensic science has seen a new and ever-growing use of DNA as an investigative tool distinct from the more common use of DNA profiling first developed in the 1980s and now widely acceptable. The technical possibility to infer visible traits from coding DNA—as in DNA phenotyping—has attracted attention from scholars examining population-making practices, racial classification, and ethnicity inference in forensics. These works have duly scrutinized the presuppositions and inferences that go into expanding the forensic uses of DNA. Here I focus on the data infrastructures that have made the expansion of forensic uses of DNA possible. More specifically, I examine the contingent use of genealogical direct to consumer genetics databases in criminal investigation (e.g., the case of the Golden State Killer) and of forensic genealogy, a methodology which allows investigators to arrive at a suspect based on inferences about their recent ancestry, as an investigative tool. I contrast these with the methods and databases available for inferring visible traits from ancestry informative markers. This comparison brings to the fore the emergent uses of both proximate and distant notions of ancestry in forensics. It also allows me to show what infrastructures and inference routes are becoming increasingly shared by forensic researchers and other audiences.

Making sense of the relationship between adaptive thinking and heuristics in evolutionary psychology

Shunkichi Matsumoto¹

¹Tokai University, Student Achievement Center, Kanagawa, Japan

In recent years, quite a few evolutionary psychologists have come to embrace a heuristic interpretation of the discipline. They claim that, no matter how methodologically incomplete, adaptive thinking works fine as a good heuristic for effectively reducing the hypothesis space by generating novel and promising hypotheses that can eventually be empirically tested. In this talk, I will elucidate the use of heuristics in evolutionary psychology, thereby clarifying the role adaptive thinking has to play. To that end, two typical heuristic interpretations—Machery's "bootstrap strategy" and Goldfinch's heuristically streamlined evolutionary psychology—are examined, focusing on the relationship between adaptive thinking and heuristics.

Two primary conclusions are drawn. The first is that the reliability of the heuristic hypothesis generation procedure (in the context of discovery) should count no less than the conclusiveness of the final testing procedure (in the context of justification) in establishing scientific facts; nature does not always get the last word. Philosophy also counts. The second is that adaptive thinking constitutes a core heuristic in evolutionary psychology that provides the discipline with its *raison d'être*, but this is only possible when adaptive thinking is substantiated with sufficient historical underpinnings.

Intelligence is not reason: Adaptationist biology and the psychology of the in-between

David I. Delano¹

¹University of California-Berkeley, History, Berkeley, CA

The concept of intelligence is part of the basic vocabulary of our time for making sense of such disparate problems as the sources of individual difference, the status of non-human minds, and the repercussions of technological change. From animal intelligence to intelligence testing, from artificial intelligence to intelligent extraterrestrial life, intelligence supplies our tacitly accepted framework for understanding the nature of cognition and its role in the universe. Prior to the late nineteenth century, however, intelligence was virtually absent from scientific and philosophical discussions of mind. While intelligence would become enduringly tied to the psychometric indexing of human difference, its earliest formulations took place amid studies of animal cognition meant to clarify the impact of evolutionary theory on questions of what mind is, what it does, and the specificity of human thinking. This presentation traces the late nineteenth-century migration of intelligence from adaptationist biology to psychology in Britain and the United States. Before the spread of psychometric intelligence testing in the first decade of the twentieth century, intelligence designated a vision of behavioral plasticity and instrumental problem solving derived from a Darwinian rendering of the interface between animal and environment. Not merely a technology of measurement intelligible within the broad trajectory of quantification in science, that is to say, intelligence announced the recasting of mind itself as an instrument for solving problems: before mind could be quantified, it had to be *reinvented* in such a way that its measurement became at once plausible and desirable. In this talk, I'll show how intelligence was for the first time widely embraced in scientific discourse in the 1880s to meet the epistemic demands of Darwinian comparative psychology. Faced with the problem of rendering animal thought intelligible, and in search of a technical vocabulary amenable to the comparison of heterogeneous minds, the discipline's founders realized that traditional philosophical discussions of consciousness and the mental faculties were hardly adaptable to the "genealogical" work of biological classification. By linking cognition to behavior in general and to environmental problem solving in particular, intelligence transformed mind into something visible, transparent to the scientific observer, and measurable in terms of behavioral success.

Adaptationism and its limitations in biology and machine learning

Richard Ngo¹

¹University of Cambridge, Department of History and Philosophy of Science, Cambridge, United Kingdom

The view that selective pressures can explain most traits of biological organisms is known as adaptationism. Discussions of adaptationism often highlight its uniqueness compared with the types of explanation used in other sciences. However, the evolution of complex traits in biological organisms bears striking similarities to the development of sophisticated machine learning models using optimisation algorithms. In this paper I argue that the default explanatory paradigm in modern machine learning is closely analogous to adaptationism. This similarity allows us to draw on the extensive literature on adaptationism to address core issues in the nascent field of philosophy of machine learning.

I first present an account of how the use of optimisation in machine learning gives rise to “adaptationist” explanations for model traits, using examples of models trained for image classification (Olah et al., 2020) and robotic manipulation (Popov et al., 2017). Key to this account is a distinction between the process of optimisation and the process of intentional (human) design, which mirrors Lewens’ (2004) account of artificial selection. This approach is particularly relevant given recent rapid increases in the scale of optimisation used in machine learning.

Yet the example of biology also points to the limitations of adaptationism in machine learning. I discuss two major criticisms of adaptationism as practiced by biologists in the mid-to-late 20th century: the “historical turn” towards adaptive historicism (Griffiths, 1996), and the longstanding debate over structuralism. These criticisms purported to identify types of explanation unjustly overlooked by biological adaptationists. I argue that these correspond to ways in which the best explanations for some traits of machine learning models may also be non-adaptationist.

References:

- Griffiths, P.E., 1996. The historical turn in the study of adaptation. *The British journal for the philosophy of science*, 47(4), pp.511-532.
- Lewens, T., 2004. *Organisms and artifacts: Design in nature and elsewhere*. MIT Press.
- Olah, C., Cammarata, ... & Carter, S., 2020. Zoom in: An introduction to circuits. *Distill*.
- Popov, I., Heess, N., ... & Riedmiller, M., 2017. Data-efficient deep reinforcement learning for dexterous manipulation. *arXiv preprint*.

Reference and ignorance

Aaron Novick¹

¹University of Washington, Philosophy, Seattle, WA

This paper considers how reference is fixed under conditions of ignorance, focusing on Richard Owen's attempt to delineate a workable 'homology' concept at a time when the nature of homology was unknown.

There are two traditional accounts of reference fixation: descriptive and causal. According to descriptive theories, a term refers to whatever meets some appropriate description. Under conditions of ignorance, such theories predict that terms fail to refer, as nothing in the world will meet the descriptions given. Nevertheless, Owen developed a workable notion of 'homology'.

Causal theories, by contrast, make successful reference under conditions of ignorance too easy. They allow for reference to be fixed by an initial baptism, in which the baptizer stands in the appropriate sort of causal contact with the referent. I argue, however, that the bit of the world that Owen was in contact with is too complex for reference to fix on any particular relation.

I investigate Owen's strategies for securing the reference of the term and enabling its use by a community of researchers who disagreed over fundamental theoretical issues (how to interpret the natural system, the nature of the relations the natural system was supposed to capture, the reality and nature of transmutation, the relative priority of form and function, etc.). 'Homology' played a role in all of these debates, yet Owen was able to make the concept a shared resource that all parties could use to communicate effectively.

Owen achieved this by balancing a diverse set of conceptual pressures. He developed an open-ended, flexible definition of 'homology' that could be preserved under various different background theories (and that still surfaces in contemporary discussions). Further, he developed criteria for homologizing parts of organisms that were acceptable across theoretical divides. Thus, the term could be applied despite disagreement over the nature of the relation to which it referred.

The best way to understand Owen's accomplishment here requires recognizing that, while particular homologous parts could be clearly identified, the reference of 'homology' itself was importantly indeterminate—the term gestured, in a somewhat indefinite way, at a complicated, messy region of the world, and this very indefiniteness is crucial to Owen's success, as well as illuminating of the subsequent convoluted history of the term.

Approaching avian digit homology

Devin Gouvêa¹

¹College of the Holy Cross, Philosophy, Worcester, MA

This paper analyzes the ongoing effort to homologize the three fingers of modern birds, and of some dinosaurian ancestors, to the five fingers of ancestral (and most modern) tetrapods. This problem dates back at least to Richard Owen (1836) and has resisted an easy solution, in part because paleontological and embryological bodies of evidence suggest different answers. On the surface this case seems to exemplify a dichotomy (now standard in philosophical analyses of homology) between *genealogical* and *developmental* approaches. The former explicate homological sameness by appeal to shared ancestry (which in this case is assessed through fossil analysis) while the latter rely on shared features of development.

Here I show that the reality is much more complicated upon closer inspection. Neither approach to avian digit homology is historically stable or ideologically uniform, and the problem has recently become fundamentally interdisciplinary. Researchers with different kinds of expertise have teamed up to explore different evolutionary scenarios that entail different judgments of homology. The basic premise that each digit should count as a separate body part is increasingly being challenged. Though there is conflict between different groups of researchers, that conflict is not actually caused by the differences that philosophers commonly identify as root causes of tension between the genealogical and developmental approaches.

This case suggests several cautions for ongoing philosophical work on homology. First, the familiar dichotomy between genealogical and developmental approaches currently runs the risk of mistakenly essentializing what are actually highly dynamic lines of research. Second, by focusing too much on theoretical definitions of sameness, it also runs the risk of obscuring other important (and philosophically interesting) causes of conceptual change and variation. These include concrete practices of collecting and interpreting data, as well as more abstract commitments of individual researchers that transcend their work on homology. I propose the notion of a conceptual environment to capture this heterogeneous collection of factors, which are united by their ability to influence multiple concepts at the same time.

The link between historical continuity and molecular mechanisms: Traceability and individuation

Gunter P Wagner¹

¹Yale University, Ecology and Evolutionary Biology, New Haven, CT

Homology, long a core concept of comparative biology, had for most of its history a tenuous relationship to mechanistic explanations. In this paper I will present a perspective that aims at conceptual continuity between historical narratives of character evolution and their mechanistic underpinnings. The core problem results from the question what is meant by “the same organ [...] regardless of form or function” in Richard Owen’s influential definition of homology. The first step is to replace “sameness” with “traceability”: two organs/body parts are homologous if their existence can be traced back to a common ancestor. The basic idea is not radical and consistent how biologists have thought of homology since Ray Lancaster, 1870, but makes homology a problem of epistemology [how do we know...] rather than metaphysics [what is...]. Traceability as the starting point to talk about homology is applicable to all levels of organization from genes to behavioral patterns. The move is enabled by the fact that phylogenetic relationships are now reconstructed by molecular genomic means rather than by the phenotypic characters themselves, avoiding circularity. The second step consists in the realization that for an entity to be traceable it needs to be individuated from other entities of the same kind, i.e. need to be able to have its own quasi-independent evolutionary history. Individuation implies molecular mechanisms that enable independent evolutionary change, for instance by differential regulation of genes and others more. How this is achieved is subject of ongoing research but conceptually boils down to the hypothesis that homology is underpinned by “character identity mechanisms” that are of different kind at different levels of organization. I will discuss models of different kinds of character identity mechanisms.

Revisiting H.J. Muller and N. Vavilov in Russian Genetics

Garland E. Allen, Professor Emeritus, Washington U. and Chair of Diverse Format Session

Victor E. Spangenberg, Senior Researcher, Vavilov Institute of Genetics, Moscow

Helen J. Muller, Sydney Brenner Scholar, CSHL and Professor Emerita, U. of NM

We focus on the dramatic relationship of American Hermann J. Muller and Russian geneticist Nicolai Vavilov. Muller received his PhD under Thomas H. Morgan where he worked in the historic “Fly Lab” in the 1910s which established the foundation of genetics research uniting breeding experiments with the cytology of chromosomes. Muller won the Nobel Prize in 1946. He believed science was an international endeavor and results shared worldwide. He advocated social and economic equality. He went to Europe in summer 1922 and at Vavilov’s invitation, flew from Berlin to Leningrad with stocks of *Drosophila Melanogaster*. Then Russian genetics used other biological objects and Muller’s visit with fly stocks gave a boost. Muller was interested in the application of eugenic ideas in a socialist society and thus began a decade of long distance collaboration.

In 1930, Israel Agol and Solomon Levit, Russian geneticists, won Rockefeller Fellowships to work with Muller. Vavilov travelled to the Americas that year to collect seeds for his renowned bank in Leningrad. He visited Muller’s lab in Texas and invited him to be chief USSR geneticist. The Cytogenetics laboratory where Spangenberg is Senior Researcher is in the Vavilov Institute of Genetics. He met Muller’s daughter on her visit to Moscow in 2018 and 2019 to inquire more deeply into Vavilov and her father’s relationship and the fate of their Russian colleagues.

Alexandra Prokofieva, a cytologist, was a brilliant scientific collaborator of Muller in Moscow 1934-37. They published several articles. Her student Yuri Bogdanov reorganized her lab and became Professor, Vavilov Institute of General Genetics in 1982. He was head of the laboratory where Spangenberg got his Ph.D.

Vavilov and Muller became involved in a fiery debate with Trofim Lysenko over genetics: Lamarckism vs. Mendelism. Joseph Stalin supported Lysenko partly because he thought Mendelism was of the bourgeoisie. Vavilov and Muller got caught in the public controversy fueling scientific debate at the 1936 Academy Of Agricultural Sciences. Vavilov warned Muller to leave Russia as their colleagues (Agol, Levit, Karpenchenko, etc) were shot! Vavilov was sent to prison where he starved to death in 1943. Russian genetics was set back but is now actively developing. We expand on Vavilov’s rehabilitation as a heroic figure along with implications of Spangenberg’s work with parthenogenic reptiles.

Muller visited Russia some seventy five years later to research her father’s history. She met two sons of her father’s colleagues, Agol and Medvedev. Unexpectedly, she connected with Vavilov’s ailing younger son Yuri who treated her like a long lost sister. Agol, told of his father’s execution by Stalin’s thugs at Lubyanka Prison. Spangenberg took Muller to two gruesome *Killing Fields* near Moscow where colleagues were shot. Muller owes his life to Vavilov. He became world-renowned in fighting for radiation protection but cried at home when he spoke of Vavilov, a horrific tragedy haunting him till death.

Gaia: controversial hypothesis, research programme or philosophy of nature?

Sébastien Dutreuil¹

¹CNRS, Centre Gilles Gaston Granger, Aix en provence, France

The Gaia hypothesis (GH) proposed by Lovelock and Margulis in the 1970's has long been ridiculed by (evolutionary) biologists: after Doolittle (1981) and Dawkins (1982) criticisms, evolutionary biology took for granted a standard narrative about GH: (i) if there was a scientific controversy, the controversy hold within evolutionary biology, (ii) GH has been abandoned by the scientific community after the early 1980's criticisms, (iii) GH is of interest only for new agers/ Lovelock is a Guru of environmentalism. Not surprisingly, philosophy of biology (dominated by evolutionary biology) endorsed this narrative (Ruse 2013).

The first argument of the paper will be that this narrative does not resist a historical analysis: I'll show that there was no scientific controversy within evolutionary biology: evolutionary biologists simply did not care about GH. But GH has received a very rich scientific reception and discussion, mostly in the Earth sciences (climatology, geochemistry, etc.), and, to a lesser extent, in various other fields (exobiology, ecology, complexity sciences).

Within the Earth sciences, a critical stance led to a second narrative (Kirchner 1989, 2002): GH is an ill-formulated hypothesis which is either not testable or false. The second argument of the paper will be to show, through a historical analysis of the way GH has been discussed in various contexts (by Lovelock and Margulis, within the scientific literature, large audience books and press articles, the environmental literature, etc.), that the Popperian category of "testable hypothesis" is not suited to understand Gaia's rich reception. One need to mobilize at least three philosophical category: a theory elaborated with abstract models; a research program with ontological and methodological revendications; a philosophy of nature changing our understanding of life, nature, and the Earth associated with concrete political prescriptions.

The third narrative about Gaia has been elaborated by Lovelock himself: Gaia is an abstract reflection about life on Earth elaborated by an independent scientist working at a time for NASA. The third argument of the paper will nuance and complexify Lovelock's narrative as much as it will put into question the idea that Lovelock is a hero of the environmental movement: hinging on works on Lovelock's archives (Aronowsky 2021, Dutreuil 2016, 2017) I'll show that Gaia can be read as an anthropological reflexion on pollution elaborated by a scientific entrepreneur.

Gaia in the mud

Leah Aronowsky¹

¹Columbia University, Society of Fellows, New York, NY

Every summer from 1977 to 1992, American microbiologist Lynn Margulis and members of her Boston University lab traveled to Laguna Figueroa, a salt flat on the Pacific coast of Baja California, Mexico. Here they studied and collected microbial mats: communities of extremophilic bacteria that were among the oldest life forms on Earth. It was at Laguna Figueroa that Margulis observed the techniques by which microbial communities literally controlled their surrounding environments, by cycling elements through the atmosphere, dissolving and precipitating metals, weathering rocks, and decomposing organic matter. Margulis believed that these processes constituted, at the microscale, evidence of the earliest mechanisms of Gaia—the theory that the Earth is a planetary-scale, biological cybernetic system.

This talk focuses on Margulis's Baja field work to explore the relationship between microbiology, the earth and environmental sciences, and the Gaia hypothesis. In searching for ecological evidence of the theory's validity in places like Baja, Margulis and her collaborators came to focus on the special role of microbes in regulating the planetary environment. They postulated that extremophilic microbes played a role in a wide range of planetary-scale chemical processes. The theory hinged on the notion of metabolic novelty. Biochemically speaking, microbes could do things no other life forms could do, producing gases like sulfur dioxide, hydrogen sulfide, and nitrogen—crucial pathways in the global cycling of chemicals.

Margulis's Gaian field research reflected a broader shift in the earth and environmental sciences to consider the extent to which the planetary environment could be said to be the product of the forces of the microbial. And while Gaia was rejected by evolutionary biologists committed to a new-Darwinian view of the relationship between life and its environments, the theory proved influential in the emerging field of “planetary biology.” Especially notable, as this talk will explain, was the emergence of the notion of microbes as modulator of planetary processes as a prominent area of research in the 1980s institutional context of the National Aeronautics and Space Administration (NASA).

On the contribution of earth system science to the thermodynamic account of life

Alejandro Merlo¹, Xabier E Barandiaran²

¹University of the Basque Country (UPV/EHU), IAS-Research Centre for Life, Mind and Society, Department of Philosophy, Faculty of Education, Philosophy & Antropology, Donostia - San Sebastián, Spain, ²University of the Basque Country (UPV/EHU), IAS-Research Centre for Life, Mind and Society, Department of Philosophy, Faculty of Labour Relations and Social Work, Vitoria-Gasteiz, Spain

The classic thermodynamic account of life describes organisms as open systems, which compensate their internal low entropy by an increased dissipation in their surroundings. A consequence of this account is that complex living systems would seem to necessarily decrease the potential for life in their environment by their increased entropy production.

Within this framework, some accounts have attempted to explain biological organisation as a manifestation of the second law and the tendency to increase entropy; others have rejected this position as reductionist and moved to an account of biological organisation in non-thermodynamic terms. However, even if thermodynamics can not give a full account of biological organisation, there is in all cases a thermodynamic background to biological phenomena which needs to be accounted for in an understanding of the materiality of life.

In this context, James Lovelock's idea, according to which a planet with life could be distinguished because of a thermodynamic disequilibrium in its atmospheric composition, moves the discussion to the planetary scale, where the presence of Life becomes the explanans of a certain thermodynamic configuration. This observation, which corresponds to the Gaian principle according to which Life modifies its physical environment to improve and maintain its own conditions of existence, has been recently developed in a systematic way by German physicist Axel Kleidon.

From this planetary standpoint, it is Life together with its physical environment that has to be considered as the primordial open, far from equilibrium dissipative system. So, while individual organisms or complex organisations within the Earth can be described as dissipative systems if considered separately from the whole, a full thermodynamic account needs to integrate them in the planetary scale, where they might (or might not) function as part of the global material organisation that sustains a low entropy environment.

The dynamics of modeling and empirical techniques in the history of protein crystallography

Dana Matthiessen¹

¹University of Pittsburgh, History and Philosophy of Science, Pittsburgh, PA

Over recent decades science scholars have produced a variety of studies of representational practices in science. While detailed investigations can be found in earlier work across these fields (Cf. Lynch and Woolgar 1990), philosophers of science have lately argued more forcefully that a scientific model's historical construction, reception, and communal use play a constitutive role in the model's ability to function as a representation (Knuuttila 2011; Boesch 2017). This is a welcome invitation for philosophers delve further into relevant historical practices. So far, however, these views have tended to focus on model construction as a relatively autonomous or isolated activity taking place over a relatively short span of time. By contrast, this paper will present model construction within an expanded historical frame, in the interest of showing how this activity may often be interwoven with the simultaneous development of empirical techniques.

I draw on an illustrative historical case: the study and modeling of the protein components of blood, with an emphasis on crystallographic techniques as they evolved from the mid-19th into the 20th century. This case will be used to support a view of modeling and empirical techniques as working in reciprocal interaction: as methods for the preparation of a system of interest are refined, they enable the production of data that can reliably discriminate between competing conceptions of this system, in turn hewing the hypothesis space into assumptions that can be built into more detailed models, the investigation of which then calls for further refinements of technique. As a method of preparing a system is integrated with diverse forms of experimentation, a body of concordant evidence is produced that stabilizes the representational utility of a particular model.

Through this process, conceptions of blood protein evolved from a primarily empirical notion of “coloring matter” or Blutroth into an oxygen-carrying polypeptide chain containing four heme groups and a specific structural arrangement. That said, time constraints require that I focus on several key episodes that I believe demonstrate the general dynamic described above. With that in mind, I will show how the refinement of blood crystallization techniques and its integration with microscopy, chemical analysis, spectroscopy, and X-ray analysis progressively altered the blood protein hypothesis and stabilized a particular form of representation.

Integrating-for-purposes: The aims-based approach to scientific integration in biology

Alican Basdemir¹

¹University of Calgary, Department of Philosophy, Calgary, Canada

Scientific integration is a practice of combining various scientific activities including modelling, explaining, and data-analysis. It is fundamental to the joint scientific work that allows scientists from different disciplines, fields, and sub-fields to coordinate and communicate their activities. Integrative pluralism maintains that scientists use multiple explanations to represent complex phenomena, but scientists intend to integrate different representations to make them compatible with each other (Mitchell, 2002). Against this view, I claim that integration is not always desired or achieved in all contexts so that there is a need to examine how integrative activities succeed or fail in relation to the aims that scientists pursue. Drawing upon Brigandt (2010), I propose the *integrating-for-purposes* view stating that integration is not an overarching aim of science, but it is an activity that is associated with the achievement of various purposes in specific scientific contexts. I claim that integrative activities involve the use of multiple scientific activities that are associated with certain aims that cannot be achieved by individual activities. The literature falls short of emphasizing the different aims allowing, constraining, or precluding integrative activities. To fill this gap, I will provide the conditions of success and failure by examining different aims that are associated with integrative activities in structural biology. I will articulate some cases of failure in which (i) scientists prioritize aims that are not associated with integrative activities, and/or (ii) the presence of some constraints prevents integrative activities. This aim-based framework is intended to capture the practice of integrative better by examining the aims underpinning the integrative research in biology.

What (and how) can we learn from divergent experimental results?

Sandra D Mitchell¹

¹University of Pittsburgh, History and Philosophy of Science, Pittsburgh, PA

Many agree that the convergence of scientific experimental results or model robustness provides strong epistemic support to a hypothesis. There is less agreement about how to understand the epistemic role of divergence. Duhem-Quine underdetermination arguments provide reasons why divergence between model and data, or model and model is not sufficient for disproof or rejection. Stegenga (2009) argues that the ubiquity of divergence casts suspicion on the epistemic value of convergence. Kuorikoski and Marchionni (2016) argue that triangulation of diverse evidence can be used to reduce bias and error by appeal to the causal independence of diverse approaches. While I agree with Kuorikoski and Marchionni's conclusion, I will explore the epistemic benefits of divergence by appeal to what assumptions the diverse sources of inference must share. I will explore these issues in examples of predictions of protein structure.

Darwin's discussion of the origin of electric fish: A teaching and learning sequence in Brazilian youth and adult education

Gerda Jensen¹, Maria Elice Prestes¹

¹History of Biology and Education Lab.(LaHBE), Biosciences Institute, São Paulo, Brazil, ²University of São Paulo, Biosciences Institute, São Paulo, Brazil

This communication presents a performed qualitative empirical science education research of a Teaching-Learning-Sequence (TLS) based on the history of science and on an inquiry approach for youth and adults students in São Paulo city, Brazil. The research question was whether students' religious affiliations would cause restrictions or resistance for them to understand and explain the origin of the electric organs in different groups of fish through evolutionary theory. The inquiry question was: how can we explain the origin of the electric organs of fish belonging to different biological families? The aim was to teach two main aspects of the evolutionary theory: that species descend from a common ancestor and that they undergo modifications by means of natural selection. The activities used primary sources texts translated to Portuguese, validated by researchers and teachers and was implemented in a class of middle school students of the Youth and Adult Education – a Brazilian state modality of education devoted to those who did not have access to elementary and secondary education in the proper age. The group of 9 to 11 students that participated in this research varied from 15 to 70 years old. The diverse historical explanations for the origin of the electric organs of different fish groups motivated students to propose and debate their hypotheses. Students with life experience in rural or small-town settings had easy access to the understanding of evolutionary theory approached according to Darwin's "long argument" in *The Origin of Species*. So it was productive the adoption of the sequence of the four initial chapters of *The Origin*, namely, beginning with the discussion of the variation of species under domestication, then going to variation in nature, then to the concepts of the struggle for existence and natural selection. The historical approach also created an inviting environment for them to express their positions and at least partially attempt to incorporate scientific explanations for the phenomenon studied.

Fritz Müller 200 years and the teaching of Brazilian biodiversity and evolution

Leonardo Augusto L Araújo¹, Nelio Bizzo^{1,2}

¹São Paulo University, School of Education, São Paulo, Brazil, ²Federal University of São Paulo, Institute of Environmental, Chemical and Pharmaceutical Sciences, Diadema, Brazil

Fritz Müller (1822–1897) emigrated from Germany to Brazil in 1852 and studied the biodiversity of Atlantic rainforest for 45 years, publishing around 250 papers. Müller's life in Santa Catarina province gave him extraordinary access to the diverse tropical fauna and flora, as well as the many marine plants and animals. Müller also was appointed to the position of a Traveling Naturalist to the Museum of Natural History in Rio de Janeiro. In the process, Müller gained deep insights into the natural processes that other nineteenth-century thinkers were seeking to understand, such as Ernst Haeckel and August Weissmann. However, the closest naturalist to Müller was undoubtedly Charles Darwin. Müller and Darwin maintained an intense correspondence from 1865 until Darwin's death in 1882, with a registry of 106 letters. From this intimacy with the natural history of Brazil and original observations of morphology and development, Müller putting to test Darwin's theory of natural selection and sexual selection. To Darwin, Müller became a main source for biological information and his name became the most cited reference from the fourth edition of the *Origin of Species*. Thus, Müller has a unique importance to the development of nineteenth-century evolutionary theory, including the evidence used to support natural selection, sexual selection, and interpretations on mimicry - Müllerian mimicry as it is known since. Despite its importance, his legacy might have been neglected and the bicentenary of his birth in the next year is an opportunity to divulge the impact of Müller's work on evolution and biodiversity. Considering the relevance of Müller's studies in the history of biology, this communication has two goals. The first is to present a recontextualized analysis of Fritz Müller importance to the development of nineteenth-century evolutionary theory and to the knowledge about Brazilian biodiversity. The second goal is to show possibilities of use of Müller's studies as historical episodes to make discussions about aspects of the nature of science and to incorporate the history of science into the biology curriculum.

Bungtown style: Scientific thought and practice at Cold Spring Harbor

Nathaniel Comfort¹, Vassiliki B Smocovitis², Robin Scheffler³

¹Johns Hopkins University, History of Medicine, Baltimore, MD, ²University of Florida, History, Gainesville, FL, ³Mass. Institute of Tech., Science & Technology Studies, Cambridge, MA

Is a sand spit a scientific space? Are wine and cheese dialectical? How is a pub a site of knowledge production?

Expanding on Jonathan Harwood's classic 1993 treatise on styles of scientific thought, we will discuss how geography, landscape, architecture, traditions, and culture of Cold Spring Harbor have shaped, and continue to shape, the practice and discourse of science there.

Our format will be an open-ended round-table. Several experts on diverse aspects of Cold Spring Harbor science will give brief presentations, posing themes and frames for thinking about the power of place, resources, and traditions of this unique institution. We will then open the floor to group discussion. Scientists, philosophers, social scientists, and historians all are encouraged to become participants: to bring experiences, interpretations, theories, anecdotes, and reminiscences, as we explore the "Cold Spring Harbor style."

Clonal evolution: toward a new view of clonesLucie Laplane¹¹CNRS, University Paris I, IHPST, Paris, France

Tumors are made up of heterogeneous cells. This heterogeneity makes cancer cells difficult to target and contributes to therapeutic avoidance and relapses. The clonal evolution model describes the dynamical processes of emergence, growth, decline or disappearance of clones constituting a tumor in space and time. Understanding these dynamics helps avoiding certain pitfalls (such as the selection of resistant clones) and lead to innovative therapeutic strategies taking these dynamics into account, such as adaptive therapies. However, the concept of clone, central to the clonal evolution model, is ambiguous and yet seldom questioned. This talk will first highlight the current pitfalls of the notion of clone, leading to the conclusion that the concept is no longer in adequacy with knowledge. Moreover, the concept of clone is late on technological innovations, constraining the interpretation of single-cell multi-omics. More information is available in these data than currently explored and a revision of the concept of clone is also required to leverage these new sources of knowledge. I will thus (1) suggest a conceptual turn, abandoning the current typological view—in which cells of a clone are seen as exemplar of a same type—in favor of a similarity view—where clones are conceived as composed of cells with the highest degree of similarity with respect to different traits, and (2) propose a new definition of clones.

Going big by going small: Tradeoffs in microbiome explanations of cancer

Anya Plutynski¹, Emily Parke¹

¹Washington University in St. Louis, Philosophy, St. Louis, MO, ²University of Auckland, Philosophy, Auckland, New Zealand

Much of cancer research involves simplification: decomposing complex interactions involving many parts and processes in the body into just a few parts and processes, typically zooming in on single aspects or mechanisms. This reductive strategy has been fruitful, but it also has limitations. For example, focus on genetic and genomic factors in cancer has narrowed research attention so much that factors outside of the cancer cell have received inadequate attention. One area of research into extra-genomic factors in cancer that has recently gained a great deal of attention is microbial factors.

Microbial factors have been implicated in everything from cancer risk to treatment and prevention (McQuade, et al. 2019; Xavier, et. al. 2020). The key word here, however, is “implicated.” Much of this research is able to establish correlations between, e.g., a particular microbiota profile and cancer risk, or a particular microbial species and effective or ineffective treatments. Yet, as in many causal explanations in microbiome research, there is a tension between appeal to more fine-grained (e.g., causal core) or coarse-grained (e.g., whole microbiome) explanatory variables (Lynch et al. 2019). Our aim in this talk is to map out some of the tensions between competing methods, goals, and standards of evidence in cancer research. We will explore the pragmatic and epistemic factors at play in prioritizing coarse-grained or black-boxed versus fine-grained microbiome explanations in cancer; explaining general versus particular patterns; the strategy of focusing on the human body, versus model systems; and the goals of understanding and explaining cancer versus clinical intervention. We see these as an array of dimensions in such research, along which there are various trade-offs.

What does ‘aging causes cancer’ mean?

Mael Lemoine¹

¹University of Bordeaux, ImmunoConcept, Bordeaux, France

In this paper, the question is raised of which causal model fits with the facts about “aging causes cancer.” Two obstacles lie in the way of a fruitful conceptualization.

First, if aging is explained by mutations that accumulate with time and lead to dysfunction, and cancer only by a subset of them, then ‘aging explains cancer’ is an empty proposition, as all the relevant mutations to explain cancer are contained in ‘cancer’ and none of the others contained in ‘aging’ is relevant to explain cancer.

Second, cancer has been defined as the breakdown of the “central features of cooperation” in a multicellular organism. However, this definition postulates that cases like gale in trees, are bona fide cases of cancer, although they resemble warts rather than cancer in humans.

The first step to avoid this conceptual dead-ends is to compare the evolution of the hallmarks of ageing with the evolution of the hallmarks of cancer. The second conceptual step is to consider the possibility that cancer is not a specific form that the breakdown of collaboration in a multicellular organism may take, but rather, that it may be a reaction of a group of cells that occurs in the context of a breakdown of collaboration. In other terms, aging does not facilitate cancer, but cancer would be a process of resistance to aging – what some cells do to survive in an aging organism.

Generalized Darwinism and the causal structure of natural selection

Adam Krashniak¹

¹Tel Aviv University, The Cohn Institute for the History and Philosophy of Science and Ideas, Tel Aviv, Israel

Generalized Darwinism is the idea that the process of natural selection is not restricted to the biological domain (Godfrey-Smith 2014; Hull et al. 2001). Adaptations in some non-biological domains evolve due to processes analogous to natural selection. Generalized Darwinism stimulates ongoing debates over whether the processes of change that take place in some non-biological domains, for instance human culture, are indeed analogous to selection. This paper offers a novel criterion for determining whether processes that take place in non-biological domains are analogous to natural selection, based on a causal analysis of selection. This criterion distinguishes selection from similar processes based on the way in which better adapted variants are selected. I argue that in natural selection, the same causes that determine the relative adaptedness of variants are also the ones that select those variants that are better adapted, or cause them to proliferate at the expense of less adapted variants. In contrast, some processes which were argued to be analogous to selection involve causes that determine the adaptedness of variants, and an additional causal factor that "detects" those variants that are better adapted and selects them. As such, these processes cause adaptation in virtue of their ability to detect the adaptedness of variants, in contrast with selection, which does not rely on such an ability. Hence, these processes are not genuinely analogous to natural selection.

The causal decomposition of evolutionary change revisited

Samir Okasha¹

¹University of Bristol, Philosophy, Bristol, United Kingdom

It is a commonplace that the evolutionary change experienced by a biological population may arise from a number of different sources, or factors. These include: natural selection of various sorts (e.g. viability selection, sexual selection); genetic mutation or imperfect phenotypic transmission; gene flow from other populations; and random factors. A natural question is then whether it is possible, in principle, to “decompose” the total evolutionary change into its distinct causal components. That such a decomposition is possible seems to be presumed if we want to compare the strength of the different factors, or to quantify their contributions in any given case, or in general. I address this question by focusing on a special case of it. Many biologists claim that the Price equation yields a simple, unambiguous partition of the one-generational evolutionary change into components due to natural selection and transmission bias respectively. I re-analyze this claim in the light of contemporary ideas about causation and hypothetical intervention and show that it is not tenable without further assumptions.

Disambiguating proximate and ultimate “causes”

Yafeng Shan¹

¹University of Kent, Philosophy, Canterbury, United Kingdom

Mayr (1961) famously makes a distinction between proximate and ultimate causes. Though he does not define them explicitly, Mayr illustrates the distinction with a case of the migration of the warbler, where proximate causes refer to “immediate causes of the migration, consisting of the physiological condition of the bird interacting with photoperiodicity and drop in temperature” and ultimate causes are what “have a history and that have been incorporated into the system through many thousands of generations of natural selection.” In the past decade, there was a renewed interest in this distinction. Some (e.g. Laland et al. 2013; Calcott 2013) questioned the legitimacy and utility of the distinction, while others (e.g. Dickins and Barton 2013; Scholl and Pigliucci 2015) attempt to defend its significance. In this paper, I revisit the proximate-ultimate distinction and argue that it is multiply ambiguous. I argue that there are at least four senses of the distinction: proximate-ultimate explanations, proximate-ultimate (conceptual) causation, proximate-ultimate (metaphysical) causation, and proximate (developmental) - ultimate (evolutionary) approach to causation. The disambiguation of proximate and ultimate causes, I argue, sheds light on the issue of causation in biology in general.

Enzymes and substrates: Practices of relational modeling before and after the introduction of quantum chemical methods

Rebecca Mertens¹

¹Bielefeld University, History, Bielefeld, Germany

Until the isolation of enzymes was possible, chemists studied enzymatic structure and behaviour by investigating the structure of their substrates, most prominently carbohydrates. As a result, enzyme classification and representation systems were often based on the hypothesis that the chemical relation between enzymes and their substrates accounted for most of their biological functions (Mertens 2019). Hence, a substantial part of knowledge about enzyme structure and activity was relational knowledge about the reaction of enzymes towards different kinds of substrates. This changed only after details of enzyme structure became empirically accessible due to new physical methods and new experimental techniques (Reinhardt 2006). By the 1950s, when x-ray diffraction patterns of proteins could be systematically compared, a new set of practices towards enzyme analysis and synthesis emerged. Yet despite the new possibilities to access the structure of enzymes directly, the idea that the core biological functions of enzymes can be ascribed to their relation and selective reaction to substrates remained unquestioned and has been challenged only recently by research on the evolutionary adaptation of enzymes (Ganai 2019; Peracci 2018).

In my talk, I will analyze the representation of enzyme-substrate relations before and after the introduction of quantum chemical methods. I will specifically look at modeling practices that encouraged the comparison between enzymes and their substrates in 20th century enzymology and beyond.

A historical approach to enzymes and their functions: Genetics, biochemistry and infection

Maria J Santesmases¹

¹Consejo Superior de Investigaciones Científicas, CSIC, Instituto de Filosofía, Madrid, Spain

This is a historiographical reflection on how intertwined biochemistry and genetics developed in some 20th century research on microorganisms. From E coli and yeast to viruses, microorganisms worked in the research laboratory as experimental systems, cheap sources for experiments and easy to handle pieces of life. Although it has been the historiography of molecular biology - nucleic acids fully on focus- what has included insightful histories of laboratory work on microbes, it was enzymes, however, what remained in “the damned test tubes”, as Sydney Brenner put it, so as to provide evidences of how genetics works. As happened in many other molecules of life, enzymes’ structure and function turned out to provide explanations of life cycles and pathways. In the clinic and the consulting room, at the bedside, microbials were better known as infective agents and had since the early circulation of germ theory well known as causes of diseases: deadly, dreadful diseases. The mechanism of infection in life beings became comprehensively approached through the understanding of enzymes’ structure and activity – in addition to other types of substances, of course. I will reflect on the historiographical basis of current biomedicine, and the present pandemic, by approaching enzymes -main biochemical characters- and their functions in genetics and infection.

Enzyme establishments: Examples from three centers of research in the United States, 1940–1955Gina Surita^{1,2}¹Princeton University, History of Science, Princeton, NJ, ²Max Planck Institute for the History of Science, Dept. III, Berlin, Germany

This talk uses an institutional approach to understand how enzymes came to be at the forefront of biochemical research in the United States during World War II and the postwar period. By focusing on three geographical centers of enzymology that emerged during this time—1) New York, New York, 2) St. Louis, Missouri, and 3) Madison, Wisconsin—this talk demonstrates that in each of these cities, formal and informal enzyme establishments were founded throughout the 1940s. Coinciding with the recent displacement of many European biochemists as a result of geopolitical crisis, the creation of these enzyme establishments—encompassing organized symposia, departmental seminars, clubs, laboratories, and research institutes—played a large role in shifting much of the momentum in the field of enzymology from Europe to the United States. By tracing the constant movement of people, money, and resources between New York, St. Louis, and Madison, this talk reconstructs how a social and academic network of enzyme researchers was built in the United States around midcentury. It also suggests that the interconnectedness of this network contributed to similar patterns of enzymological research in these three cities throughout the 1940s and early 1950s.

Author Index

Abir-Am, Pnina G, 21
Abrams, Marshall, 105
Alassia, Fiorela R, 113
Allen, Garland E, 259
Almeida, Maria S, 39
Angleraux, Caroline, 218
Ankeny, Rachel A, 61
Antiochou, Konstantina, 81
Arantza, Etxeberria, 62
Araujo, Aldo M, 65
Araújo, Leonardo Augusto L, 267
Arnet, Evan, 231
Aronowsky, Leah, 261
Au, Yin Chung, 142
Aylward, Alex, 166

Badgley, Brian, 115
Baedke, Jan, 63
Balorda, Vito, 22
Bangham, Jenny, 1
Bapty, Hannah, 208
Barahona, Ana, 101
Barandiaran, Xabier E, 8, 244, 262
Barker, Matthew J, 84
Barney, Jacob, 115
Barragán, Carlos Andrés, 6
Barrow, Mark V, 135
Basdemir, Alican, 264
Bausman, William C, 118
Bayir, Saliha, 19
Beasley, Charles A, 54
Bellon, Richard, 50
Bertolaso, Marta, 175
Bertoldi, Nicola, 197

Bertram, Jason, 239
Bickle, John, 33
Bissell, Mina J, 32
Bizzo, Nelio, 267
Blecic, Martina, 149
Bloch-Mullins, Corinne, 185
Blute, Marion, 72
Bolduc, Ghyslain, 94
Bondarenko, Olesya, 4
Bonnin, Thomas, 165
Borck, Cornelius, 186
Bosch, Irene, 164
Botes, Marietjie M, 121
Boulicault, Marion, 122
Bourrat, Pierrick, 207
Božić, Aleksandar V, 211
Braverman, Derek W, 228
Brembs, Björn, 59
Brigandt, Ingo, 154
Brito, Ana Paula Oliveira Pereira M, 66
Brown, Bryan, 115
Brown, Oliver S, 210
Brown, Steven M, 226
Brun-Usan, Miguel, 64
Brusse, Carl, 219
Brzovic, Zdenka, 7
Buklijas, Tatjana, 235
Buskell, Andrew, 120

C. Neco, Lucia, 111
Caianiello, Silvia, 175
Calvert, Jane, 173
Carandell Baruzzi, Miquel, 180
Casali, Marco, 9

Cassidy, Angela, 126
Ceccarelli, David, 132
Chacko, Xan S, 1
Charbonneau, Mathieu, 146
Chaudhury, Aadita, 137, 158
Chaves, Willandia, 115
Chellappoo, Azita, 63
Chiu, Lynn, 64
Clatterbuck, Hayley, 152
Colaço, Davd, 33
Comfort, Nathaniel, 268
Conley, Brandon A, 40
Corris, Amanda B, 26
Cortés-García, David, 140
Cowie, Helen L, 178
Culak, Christian, 56
Currie, Adrian, 203
Curry, Helen, 61

Dam, Mie S, 30
De Cesare, Silvia, 199
De Sio, Fabio, 11
Deaven, Katie, 125
Delano, David I, 254
Dhein, Kelle, 143
Dietrich, Michael R, 222
DiFrisco, James, 138
DiMarco, Marina, 188
Doolittle, W. Ford, 83
Downes, Stephen M, 35
Dresow, Max, 169
Dror, Otniel E, 55
Dubois, Michel, 82
Dupré, John, 13
Dutreuil, Sébastien, 260

Ehsani, Sepehr, 227
El-Hani, Charbel N, 192

Elliott, Steve, 29
Esposito, Maurizio Esposito M, 131
Esquivel-Sada, Daphne, 174

Fábregas-Tejeda, Alejandro, 16
Fangerau, Heiner M, 77
Feest, Uljana, 185
Fitzpatrick, Susan, 49
Formosinho, Joana, 128
Frank, David M, 114
Friedman, Yael, 130

Garbayo, Luciana, 108
Garcia-Deister, Vivette, 252
Garson, Justin, 207
Gaudillière, Jean-Paul, 183
Gefaell, Juan, 71
Gerson, Elihu M, 170
Gibson, Abraham H, 41
Ginefra Toni, João Felipe, 91
Girija, Vivek B, 90
Gissis, Snait B, 186
Glackin, Shane N, 163
Gliboff, Sander, 230
Godfrey-Smith, Peter, 83
Gómez López, Ana María, 250
Gomez, Kevin, 239
Gordillo Garcia, Alejandro, 148
Gouvêa, Devin, 257
Green, Sara, 30
Greslehner, Gregor, 70, 151
Griesemer, James R, 6
Griffiths, Paul, 207
Guttinger, Stephan, 42

Haas, Solange, 229
Haber, Matt, 43
Haddad, Yasmin, 36

Haddal, Natasha M, 123
Halm, Derek, 89
Halperin, Topaz, 127
Haueis, Philipp, 185
Hernández Mora, Tomás M, 249
Hoburg, Patrick, 133
Hochadel, Oliver, 179
Hodge, Jonathan, 152
Holmes, Matthew, 34
Hoquet, Thierry, 145
Hossom, Denise R, 76
Howland, Hannah, 98
Huitzil, Saul, 14
Huneman, Philippe, 141, 229
Hutcheson, Emily S, 194

Imperadore, Pamela, 11
Inkpen, S. Andrew, 49
Ioannidis, Stavros, 80

Jablonka, Eva, 60, 186
Jackson, Rebecca, 184
Jarne, Philippe, 229
Jas, Nathalie, 183
Jensen, Gerda, 266
Jones, Elis, 38
Jourdain, Antoine, 37
Jun, Jinkwon, 107

Kaiser, Kevin, 44
Karimasari, Nadya, 137, 158
Kéfi, Sonia, 229
Kelley, David, 112
Killin, Anton, 203
Kingsbury, Justine, 219
Kirchhelle, Claas, 172
Kok, Robert, 73
Kollmer, Charles A, 195

Kolodny, Oren, 147
Kovaka, Karen, 115
Kowal, Emma, 82
Krashniak, Adam, 272
Krimsky, Sheldon, 136
Kulesa, Ryan, 106

Lacomme, Marie L, 241
LaCour, Tarik D, 248
Lade, Quentin, 215
Lamm, Ehud, 147
Laplane, Lucie, 269
Laubichler, Manfred, 49
Lawson-Boyd, Elsher, 82
Lazo, Robert S, 28
Lean, Christopher H, 103
Lee, Dennis, 209
Lee, Victoria, 172
Lefkaditou, Ageliki, 167
Lemoine, Mael, 271
Lenton, Tim M, 83
Leonelli, Sabina, 61
Levin, Michael, 186
Liu, Daniel, 17, 159
Lloyd, Elisabeth A, 15
Loginov, Ivan, 87
Love, Alan, 25, 155
Lowe, James, 57
Ludwig, David, 137, 158

MacCord, Kate, 49
Maclean, Duncan C, 75
Maienschein, Jane, 49
Maris, Virginie, 229
Mariscal, Carlos, 212
Martins, Lilian Al-Chueyr P, 66
Masel, Joanna, 239
Matsumoto, Shunkichi, 253

Matthewson, John, 219
Matthiessen, Dana, 263
Maxson Jones, Kathryn G, 12
Maxwell, Matthew J, 232
McArthur, Cole C, 45
McCandlish, David M, 240
McCloughlin, Thomas J, 92
McConwell, Alison K, 171
McShea, Dan, 198
Meincke, Anne Sophie, 58
Meiring, Henry-James, 95
Meneganzin, Andra, 203
Merlin, Francesca, 9
Merlo, Alejandro, 262
Mertens, Rebecca, 275
Metcalf, Kathryne, 202
Meunier, Robert, 156
Meynell, Letitia, 206
Millstein, Roberta L, 221
Mitchell, Sandra D, 265
Mncube, Zinhle, 137, 158
Montévil, Maël, 182
Montminy, David, 161
Morgan, Gregory J, 213
Morgan, Jennifer R, 12
Morrow, Katie, 220
Muller, Helen, 259
Mundy, Rachel, 74
Munns, David, 93

Nahas, Auguste A, 233
Navarro, Pedro L, 176
Neal, Jacob P, 23
Neto, Celso, 85
Ngo, Richard, 255
Nicholson, Daniel J, 219
Nickelsen, Kärin, 184
Nieves Delgado, Abigail, 137, 158

Novick, Aaron, 256
Nuño de la Rosa, Laura, 153

Odenbaugh, Jay P, 116
Okasha, Samir, 273
Opitz, Don, 3
Ornelas-Cruces, Marco, 216

Pain, Ross, 203
Pancaldi, Giuliano, 88
Papale, François, 86
Parke, Emily C, 104, 270
Pearce, Trevor, 177
Pence, Charles H, 189
Perkins, TJ, 46
Piaia Mendonca Junior, Jorge, 119
Plutynski, Anya, 270
Pollock, Ludmila, 159
Pontarotti, Gaëlle, 247
Potiron, Aline, 201
Pradeu, Thomas, 31
Prestes, Maria Elice, 67, 266
Priest, Greg, 51
Prieto, Guido I, 18

Quinn, Aleta, 47

Radick, Gregory, 152
Rama, Tiago, 8, 244
Reiß, Christian, 10
Rheinberger, Hans-Joerg, 157
Rich, Miriam, 159
Richardson, Sarah S, 122
Richmond, Marsha L, 134
Robles-Piñeros, Jairo, 137, 158
Rodriguez-Caso, Juan M, 52
Roe, Sarah M, 226
Russell, James, 102

Saborido, Cristian, 71
Samaras, Georgia, 82
Sankaran, Neeraja, 172
Santesmases, Maria J, 276
Sarafraz, Lida, 124
Satalino, Stephanie, 159
Scheffler, Robin, 172, 268
Schenk, Todd, 115
Schickore, Jutta, 184
Schmid, Kelly M, 209
Schmidt, Markus, 193
Schneider, Tamar, 129
Schuerch, Caterina, 184
Seyfried, Günter, 193
Shan, Yafeng, 274
Shavit, Ayelet, 204
Sião, José F, 67
Silvestros, Pavlos, 79
Simana, Shelly, 5
Smith, Adam C, 96
Smith, Anthony P, 97
Smith, Michelle K, 209
Smith, Subrena, 207
Smocovitis, Vassiliki B, 268
Sober, Elliott, 232
Söhner, Felicitas P, 214
Sonnenschein, Carlos, 181, 190
Soto, Ana M, 181
Spangenberg, Victor E, 259
Sponsel, Alistair, 159
Srivastava, Alok K, 100
Stahnisch, Frank W, 78
Stencel, Adrian, 69
Stern, Beckett, 29
Stingl, Michael, 109
Stoltzfus, Arlin B, 238
Suárez Pascal, David, 234
Suárez, Javier, 14, 69

Subramaniam, Banu, 3
Sullivan-Clarke, Andrea, 152
Surita, Gina, 277
Šustar, Predrag, 7
Sutto, Antoinette, 159
Svendsen, Mette N, 30
Syed, Awais, 209
Szymanski, Erika A, 173

Takacs, Peter, 207
Thomas, Marion C, 242
Thompson, Morgan, 53
Thompson, Paul, 61
Trappes, Rose, 139
Tsal, Yotam A, 237
Turska, Julia J, 191
Tybjerg, Karin, 2

Valde, Katherine, 99
Vallejo, Arturo, 137, 158
Vandervoort, Arthur, 162
Veigl, Sophie Juliane, 68
Veit, Walter, 224
Ventura, Rafael, 150
Vergara-Silva, Francisco, 205
Vianelli, Alberto, 9
Vilanova, Manuel, 39
Villagómez-Reséndiz, Radamés R, 20
Villegas, Cristina, 155
Villela, Ma-Alicia, 168

Wade, Michael J, 15
Wagner, Gunter P, 258
Wagner, Günter, 25, 258
Wallis, Jacqueline M, 187
Walsh, Patrick M, 196
Walters, Bradley, 33
Wassermann, Merlin, 184

Watkins, Aja, 251
Weindling, Monica, 209
Wiegman, Isaac, 245
Wilkins, John S, 236
Williams, Nicola, 144
Williamson, Hugh, 61
Wilson, Lauren H, 24
Wilson, Rob, 223
Winsor, Mary P, 48
Witteveen, Joeri, 27
Woolley, Sam J, 110
Worliczek, Hanna L, 200

Yacoba Agyemang, Stephanie-Louise, 209
Yamamoto, Angella, 225
Yilmaz, Özlem, 160
Yoshida, Yoshinari, 217
Youssef, Sandra, 193

Zach, Martin, 151
Zacks, Oryan, 246
Zhumadilova, Kulash, 243
Zinser, Jason M, 117

Financial support provided by our sponsors



Department of History

Department of Philosophy



PIEC USP
Programa de Pós-Graduação Interunidades de
Ensino de Ciências
Universidade de São Paulo



