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Department of Philosophy

Inhabiting Data: Objects, Tools, and Frameworks in Post-Genomic Biology

May 22, 2026

Department of Philosophy – University of Vienna,

Room 3a (Room D0312, 3rd floor) Universitätsstraße 7, 1010 Vienna

Organized by: Univ.-Prof. Tarja Knuuttila and Dr. Gregor Paul Greslehner
(Department of Philosophy – University of Vienna)

	Friday| May 22, 2026
13:15 – 14:15	**Robert Meunier (ICI Berlin)** “Towards a historical epistemology of post-genomics: Epistemic and technical objects in data-intensive research”
14:15 – 14:30	Break
14:30 – 15:30	**Gregor Paul Greslehner (University of Vienna)** “AI as a tool for solving scientific problems? The case of AlphaFold and the protein folding problem”
15:30 – 16:00	Break
16:00 – 17:00	**Patrick Ferree (University of Copenhagen)** “What is a good cell atlas? Fitness-for-purpose across big and small biology”
17:00 - 17:15	Break
17:15 – 18:15	**Kevin Purkhauser (University of Vienna)** “Touching Honey: A Philosophical Analysis of Scientific Regress”
19:00	Dinner at: Stuwer - Am Schottentor, Rockhgasse 1, 1010 Wien (only for speakers and the organizing team)

45-minute presentation followed by 15 minutes for questions on topics related to the talk.

Abstracts

Robert Meunier (ICI Berlin)

“Towards a historical epistemology of post-genomics: Epistemic and technical objects in data-intensive research”

Abstract:

Rather than hypothesis-testing, for Rheinberger (1997) twentieth-century biology research aims for grasping objects taking shape in experimental systems, determining their properties and relations, and becoming familiar with working with them. Research does not merely deliver knowledge on objects, but familiarity with objects supports further research, as they embody what is not yet known about them, function as stepping stones to related objects, and serve as tools for further intervention. Hypothesis-testing is not characteristic for post-genomic, data-intensive research either. What then are epistemic objects in high-throughput experimentation, how does becoming familiar with them support further research, or do we need another model of research altogether?

Gregor Paul Greslehner (University of Vienna)

“AI as a tool for solving scientific problems? The case of AlphaFold and the protein folding problem”

Abstract:

The protein folding problem has been receiving a lot of attention, especially since the predictive success of the AI tool AlphaFold and the 2024 Nobel Prize in chemistry. By developing an account of what “solving the protein folding problem” means, I assess what AI can and cannot achieve regarding the protein folding problem. Building on the scientific literature, I investigate three different aspects of the protein folding problem: (a) the physico-chemical principles behind protein folding (b) the kinetics of the folding process, and (c) algorithmically being able to predict the three-dimensional structures of

proteins from their amino acid sequence. While arguably a proper solution to the protein folding problem should cover all three aspects, AlphaFold so far has only contributed to one of them, namely (c). The case of AlphaFold raises some further questions regarding the potential and limitations of AI for addressing scientific problems in general.

Patrick Ferree (University of Copenhagen)

“What is a good cell atlas? Fitness-for-purpose across big and small biology”

Abstract:

Single-cell technologies allow scientists to measure and map the cellular diversity in tissues, organs, and even whole organisms. The annotated products are often called cell atlases. Although large-scale consortia are constructing comprehensive atlases for broad foundational purposes (e.g., the Human Cell Atlas), many smaller-scale research groups continue building and using their own localized reference atlases. How come? What is a good cell atlas? And who should construct them? Drawing on ethnographic fieldwork, this paper argues that cell atlases are best evaluated in terms of their fitness for specific purposes and that local practices are often better suited for their production.

Kevin Purkhauser (University of Vienna)

“Touching Honey: A Philosophical Analysis of Scientific Regress”

Abstract:

In this paper, we examine scientific regress as complementary to scientific progress. While progressive developments have been extensively discussed in the philosophy of science, it can be argued that in relation to some problems and some goals, the state of knowledge may also “worsen” in time e.g. through conceptual, methodological, and institutional entrenchment of what could be called false rigidities. This may occur, for instance, when a theoretical innovation migrates to other problem domains, and meanwhile its underlying assumptions become gradually forgotten – that is, when something that started as a domain-specific hypothesis comes to be applied as a general (and generally constraining) principle. We discuss the Central Dogma of molecular biology and the concept of the Weismann barrier as examples of this kind; namely, as theoretical innovations that have certainly promoted progress in some domains, while having significant and widespread, but not easily tractable, constraining effects in others. We also suggest that for a philosopher of science, an analysis of regress may function as a way of engaging more participatively with the critical development of scientific thought itself.