



Spherical cows and bipedal goats

Perspectives on mathematical models in biology

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Les 13 et 14 novembre 2025, 9h30-19h et 10h-19h

Salle Jaurès, École normale supérieure, 29 rue d'Ulm, 75005 Paris

Workshop organization:
Ruán Batista, Maël Montévil, Anton Robert



Spherical cows and bipedal goats: perspectives on mathematical models in biology – 13-14/11/2025

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Abstract

The National Research Council of the National Academies (USA) published a report in 2009 arguing for “a New Biology for the XXIst century”, based on the integration “through the unifying languages of mathematics, modeling, and computational science”. This perspective is well represented and illustrated in CNRS¹ by the committee labeled “Mathematical modeling, informatics, and physics for the life sciences”².

However, long-lasting problems in the relationship between mathematics are not addressed by this strategy. They are illustrated by the famous joke whereby a farmer asks for help from the university. After some time, the chief of the interdisciplinary committee comes to him and declares: We have found an exact solution to your problem, but it only holds for spherical cows in the vacuum. The issue here is not just one of approximation or idealization; it is also that cows, according to evolutionary theory, have a history and continue to evolve, and this historicity defines the cows we observe today. Notably, the plasticity of living beings collides with the invariance of underlying mathematical structures. For example, in the context of the emerging field of evo-devo, West-Eberhardt discussed the dramatic changes displayed in a goat with paralysis of its forelegs. This paralysis and its subsequent activities led to a major restructuring of bones, muscles, and tendons, resulting in a bipedal goat that became a banner for the magnitude and theoretical significance of developmental plasticity.

This event aims to take a step back and reflect on everyday mathematical modeling. We aim to organize a discussion on the diversity of this practice in biology and the homologies in current models. We wish to center those discussions around two related problems. First, given that the general reference system of biology builds on a notion of novelty to classify living beings, how can we use mathematical structures (using predefined spaces of possibilities) to describe living beings while avoiding contradiction? Is it reasonable that many of these practices do not even consider the organization of the organisms? Second, if models can be considered as instruments that contribute to shaping scientific reasoning, is their inscription within broader theoretical frameworks (not) necessary? Are data-based approaches sufficient to understand the living, or should theoretical and methodological jumps be performed? Is the perspective of the National Research Council sound when it states that not all New Biologists are now, or will in the future be, biologists? How to take mathematics and modelling seriously and, at the same time, avoid the disruption of biological knowledge by the fetishization of those tools?

Program

Day 1

9:30 Introduction

Session 1: Measuring what? Models and the general reference system of biology (chair: Maël Montévil)

9:45 Ruãn Batista (Federal University of Bahia, Brazil)
Hennigian metaphysics and the general reference system of biology

10:25 Valentin Rineau (Centre de Recherche en Paléontologie, MNHN CNRS Sorbonne Université)
Phylogenetics and classifications: another perspective on change and evolution.

11:05 **Coffee Break**

¹The *Centre national de la recherche scientifique* is the largest French institution for scientific research.

²Modélisation mathématique, informatique et physique pour les sciences du vivant.

11:20 Ignacio Quintero (Institut de Biologie de l'École Normale Supérieure (IBENS), ENS)
Environmental controls on evolutionary dynamics using interdependent models

12:00 **Round table**

12:45 **Lunch**

Session 2: The tension between historicity and mathematics (chair: Giuseppe Longo)

14:30 Aleksandra Walczak (Laboratoire de physique de l'ENS)
Randomness and organization of immune repertoires

15:10 Guillaume Achaz (Collège de France, MNHN, U.P.-Cité)
What process(es) explain(s) (genetic) diversity?

15:50 **Coffee break**

16:20 Katja Heuer and Roberto Toro (Institut Pasteur, Unité de Neuroanatomie Appliquée et Théorique)
Role of mechanical morphogenesis in the development and evolution of the brain

17:00 Maël Montévil (Centre Cavallès, RdS, CNRS - ENS)
Biology lies between historical and relational frameworks

17:40 **Round table**

19:00 **Cocktail party**

Day 2

Session 3: Data, models, and theory (chair: Anton Robert)

10:00 Paul Villoutreix (Aix-Marseille Université, MMG, Inserm U1251, Turing Centre for Living systems)
From high-dimensional measurements to the manifold hypothesis: how we are trying to make sense of very large datasets in biology

10:40 Barbara Bravi (Department of Mathematics, Imperial College London)
Machine learning representation manipulability and its relevance to scientific modelling

11:20 **Coffee break**

11:35 Cyril Rauch (University of Nottingham)
Find the mistake : From the genotype-phenotype cartography to the phenotype-genotype cartography

12:15 **Round table**

12:50 **Lunch**

Session 4: The challenge of theory-based model in biology (chair: Ruán Batista)

14:30 Giuseppe Longo (Centre Cavallès, RdS, CNRS - ENS)
The primary motor of morphogenesis: a heterogenetic cell reproduction

15:10 Anton Robert (Centre Cavallès, RdS, ENS)
How can mathematical models possibly be useful in biology?

15:50 **Coffee break**

16:20 Charbel El-Hani (Institute of Biology, Federal University of Bahia, Brazil)
A pragmatist, radically naturalista view on modeling

17:00 Ana Soto (Tufts University School of Medicine)
Modeling mammary gland morphogenesis from first principles

17:40 **Round table**

18:30 **Synthesis**