



# Computational Approaches to Early Evolution

A compact, discussion-driven workshop on methods for early life.

Computational Approaches to Early Evolution brings together people who work with messy, real-world data on early life. The aim is simple: connect cutting-edge phylogenetics, genome-resolved metagenomics, and molecular evolution to say something concrete about how cells, metabolisms, and communities emerged and diversified. We'll focus on methods that scale to the current deluge of genomes, handle horizontal gene transfer and link evolutionary inferences to physiology, ecology, and the rock record.

The format is deliberately compact: a small group, plenty of time for discussion, and space to break open half-baked ideas, not just polished stories. The goal is to come away with new collaborations and, ideally, a clearer sense of what it would take to actually test our favourite scenarios for early evolution.

**Please register before January 2nd to be included in the first round of selection!**

Registration link:

<https://forms.oist.jp/form/computational-approaches-to-early-evolution>



## Invited speakers

- Prof. Phil Hugenholtz - University of Queensland, Australia
- Prof. Anja Spang - NIOZ & University of Amsterdam, The Netherlands
- Dr. Masaru K. Nobu - AIST Bioproduction Research Institute, Japan
- Prof. Anne-Florence Bitbol - EPFL Institute of Bioengineering, Switzerland
- Prof. Tom A. Williams - University of Bath, Dept. of Life Sciences, UK
- Dr. Arisa Nishihara - RIKEN BioResource Research Center, Japan
- Prof. Robert Lanfear - Australian National University, Australia
- Dr. Sandra Álvarez-Carretero - University College London, UK
- Prof. Shawn E. McGlynn - Earth-Life Science Institute, Japan
- Prof. Ben J. Woodcroft - Queensland University of Technology, Australia

*Questions, ideas and methods welcome - bring them.*