

Mathematical Genomics ECL Research Unit (2024)

Unit Leader: Leo Speidel (DPhil)



(1) Research fields

CPR Subcommittee: Biology

Keywords: Evolution, population genetics, statistical inference, genomics, ancestral recombination graphs, ancient DNA

(2) Long-term goal of laboratory and research background

Our lab focuses on the development and application of new mathematical and statistical techniques to reveal the evolutionary forces that have shaped our DNA, from key events in a nation's recent past to the earliest days of our species. Our methods reconstruct past migrations and mixtures, introgression with Neanderthals and other extinct hominids, changes in the molecular machinery generating DNA differences, or map the genetic adaptation that enabled survival against changing environmental exposure. We achieve this by reconstructing "genetic family trees" using genetic data sequenced from thousands of modern-day people as well as genomes sequenced from ancient human bone.

(3) Current research activities (FY2024) and plan

Our lab started in November 2024. We are planning to establish our lab in the coming year, with several new postdoctoral scientists expected to join the lab. Our work will focus on the development of new methods in particular to robustly model natural selection from genetic variation data, including ancient DNA. We will further improve methods to characterise genomic diversity within and across species, focusing particularly on events implicated within ancestral recombination graphs.

(4) Members

(Unit Leader)

Leo Speidel

(4) Representative research achievements

1. Leo Speidel, Marina Silva, Thomas Booth, Ben Raffield, Kyriaki Anastasiadou, Christopher Barrington, Anders Götherström, Peter Heather, Pontus Skoglund. High-resolution genomic history of early medieval Europe. *Nature* 637, 118–126 (2025)

Supplementary

Laboratory Homepage

<https://speidellab.github.io/>