

Introduction

Week 1

Kasper Munch

**Welcome to
Genomic Thinking :)**

Agenda

Lecture / Exercise swap

Today

- Course introduction
- Getting set up on the compute cluster

Thursday

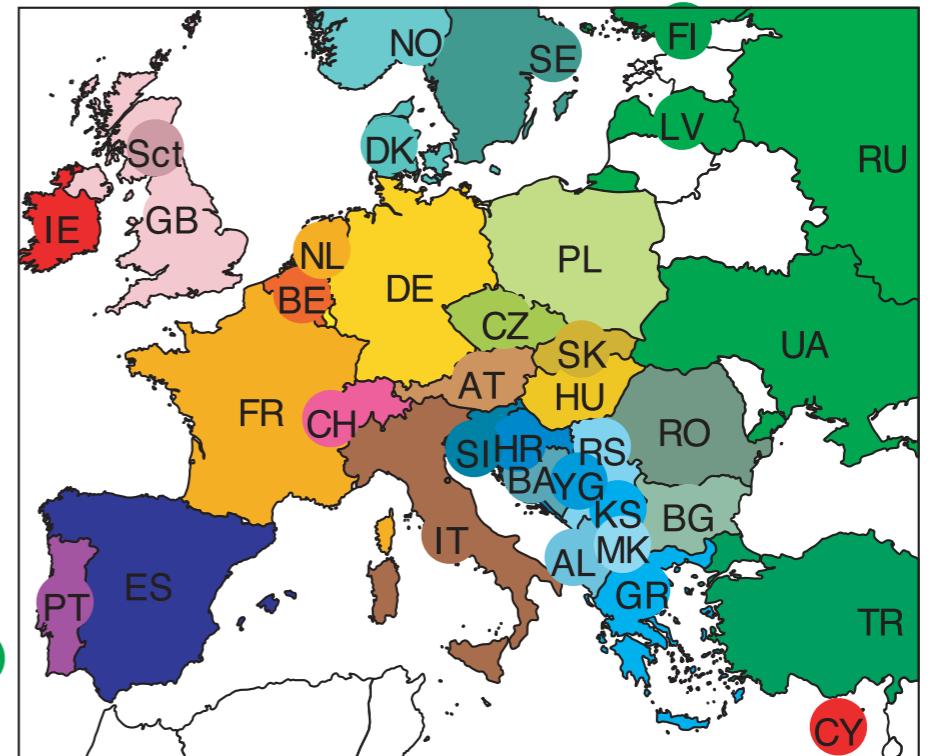
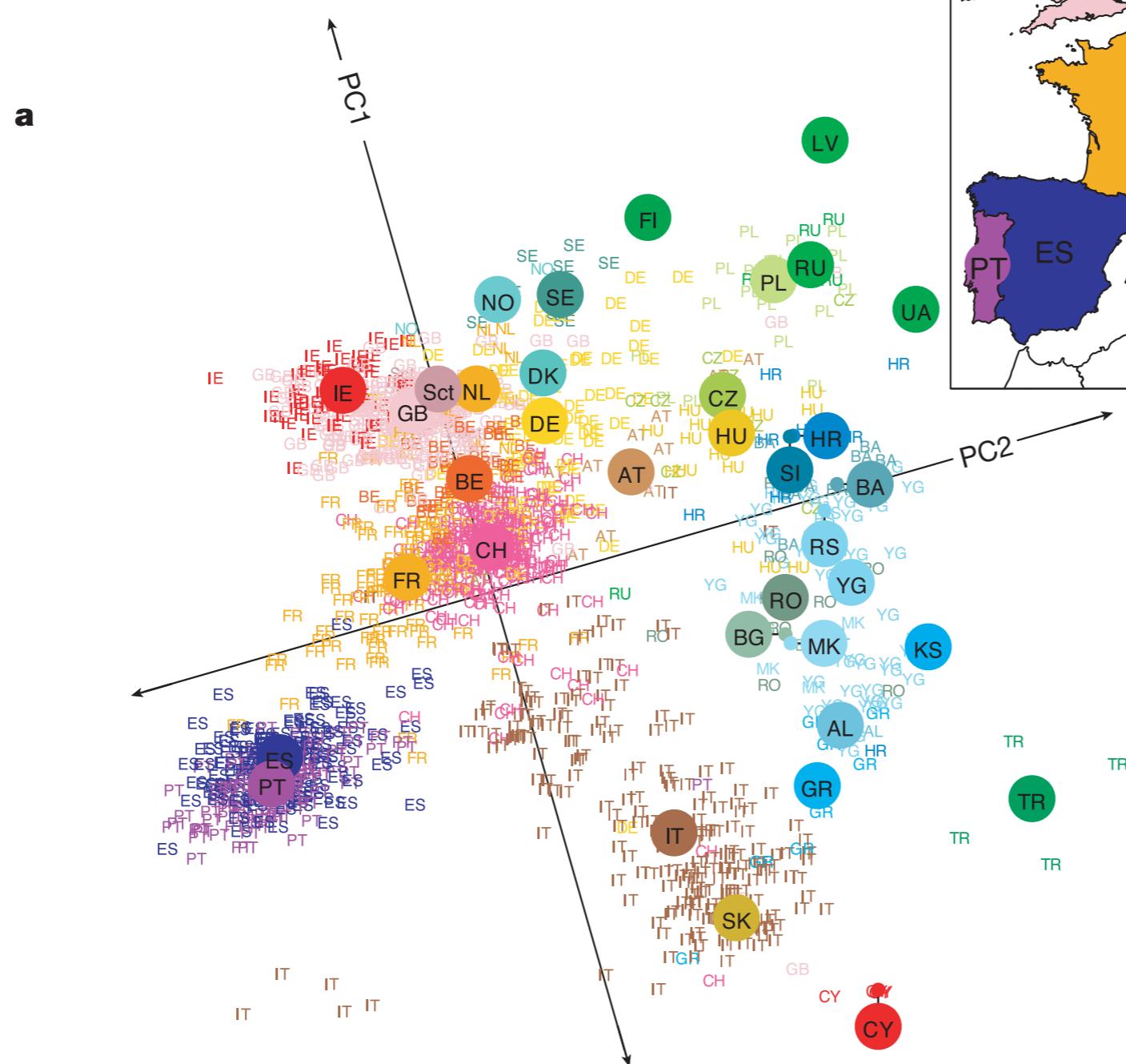
- A bit on generating sequence data
- First look at the coalescent
- Discussion the paper on human genetic diversity
- Discussion of the textbook material

Course introduction

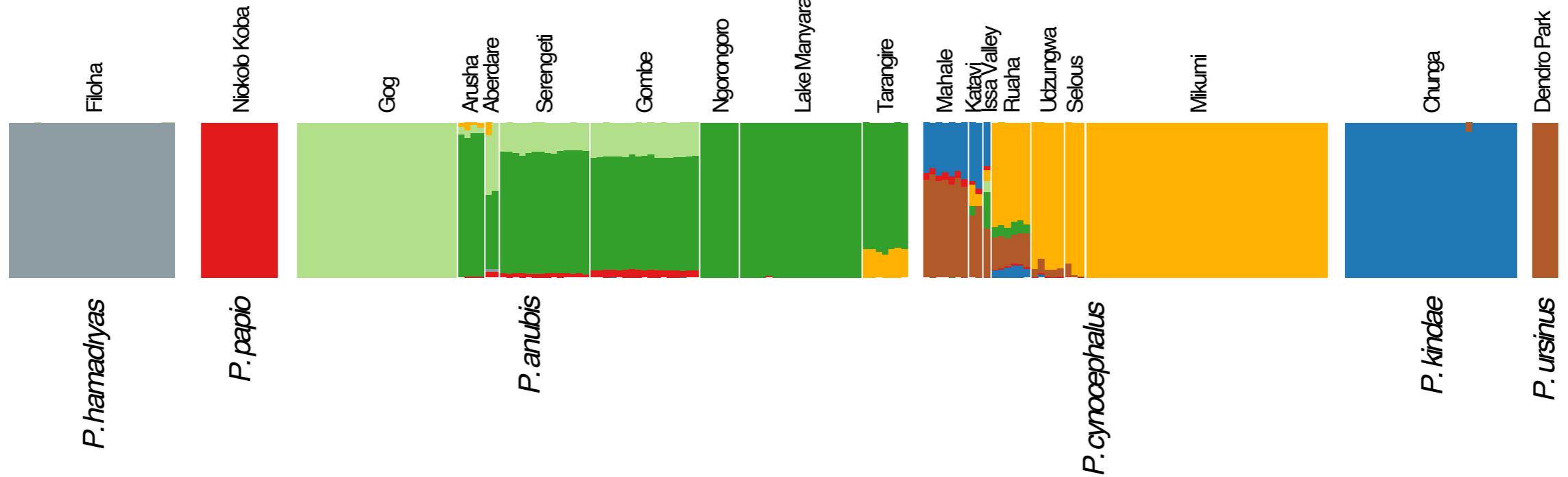
People

- Course responsible: Kasper Munch
- Lecturer: Kasper Munch
- TA: Kasper Munch

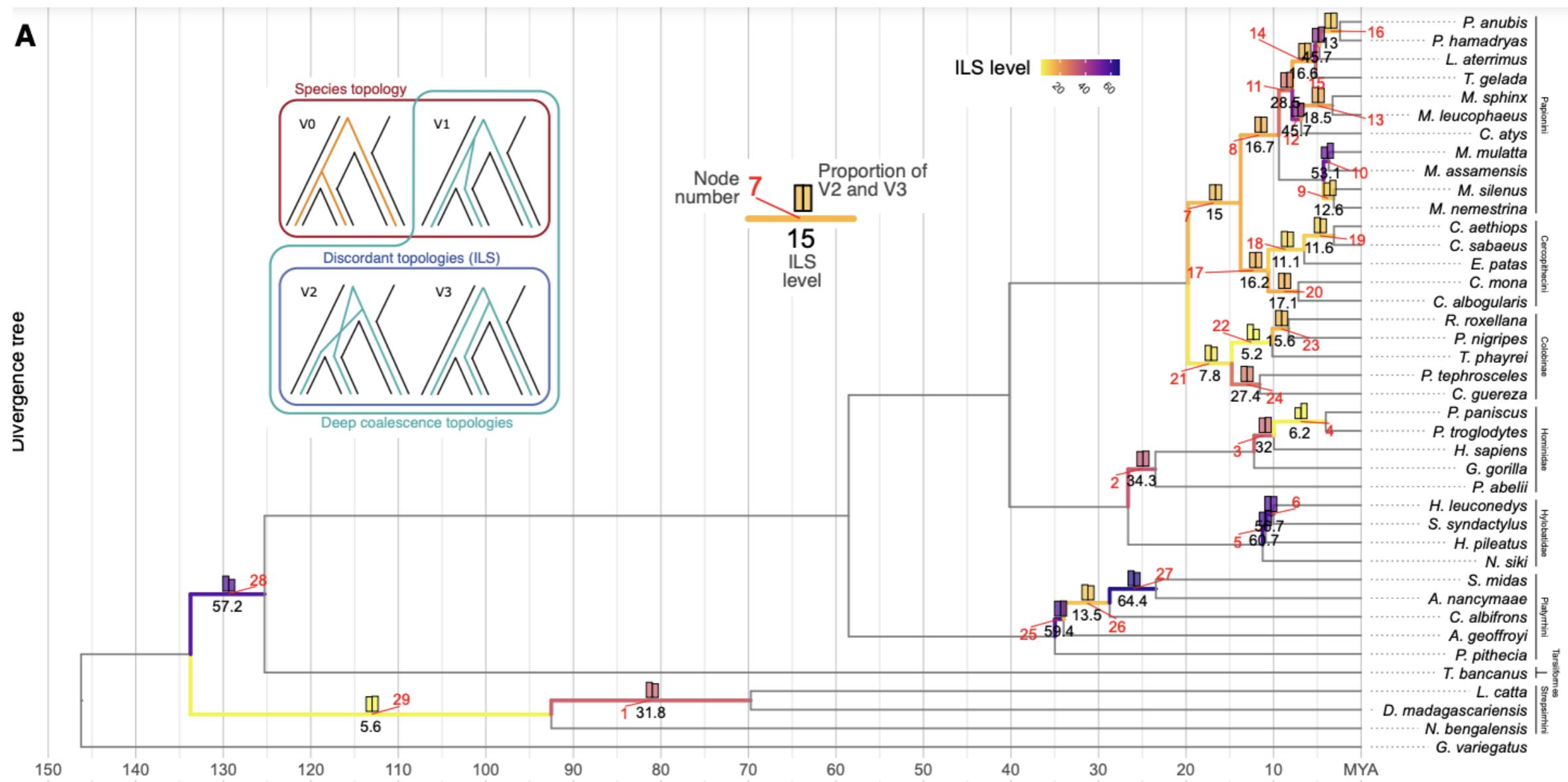
Population structure



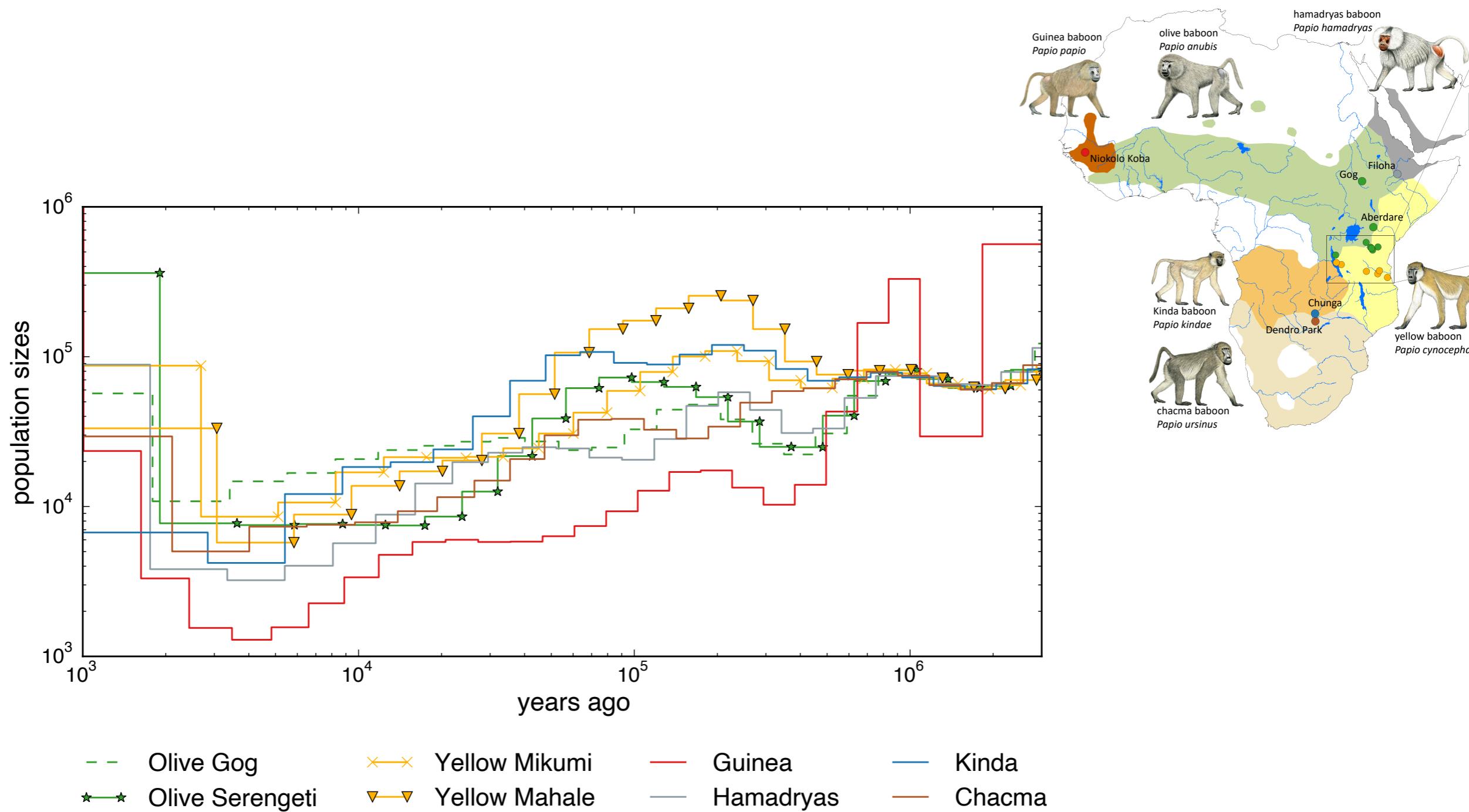
Admixture



Gene and species divergence

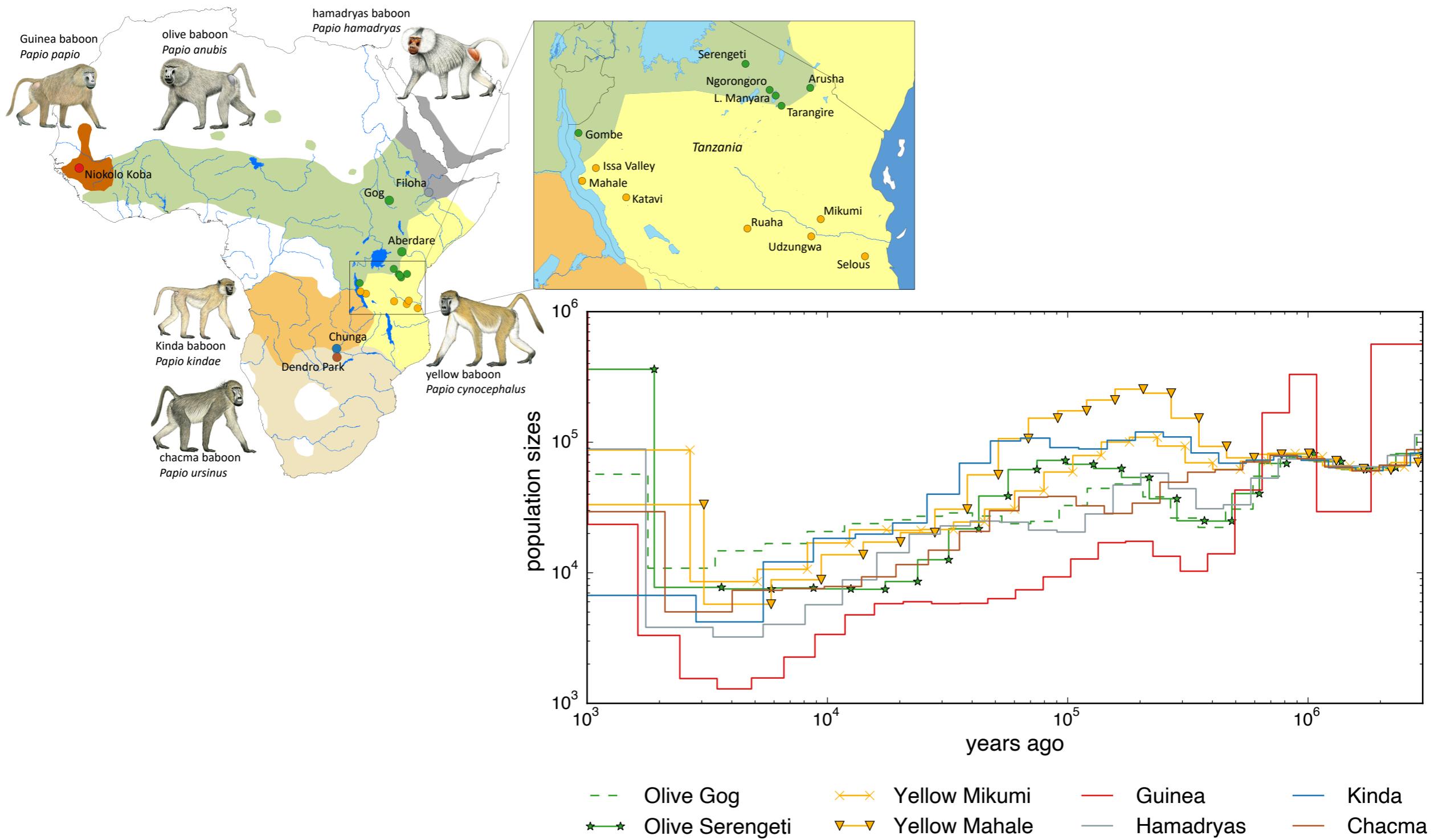


Historical population sizes

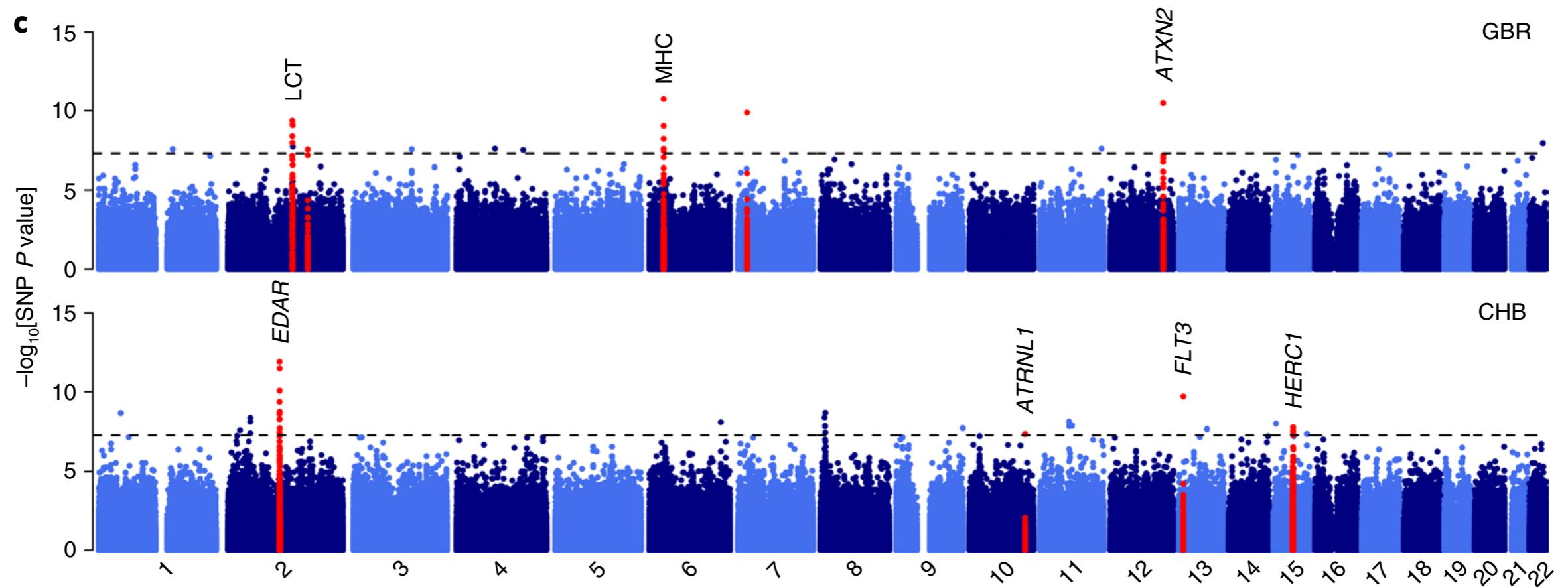


Course introduction

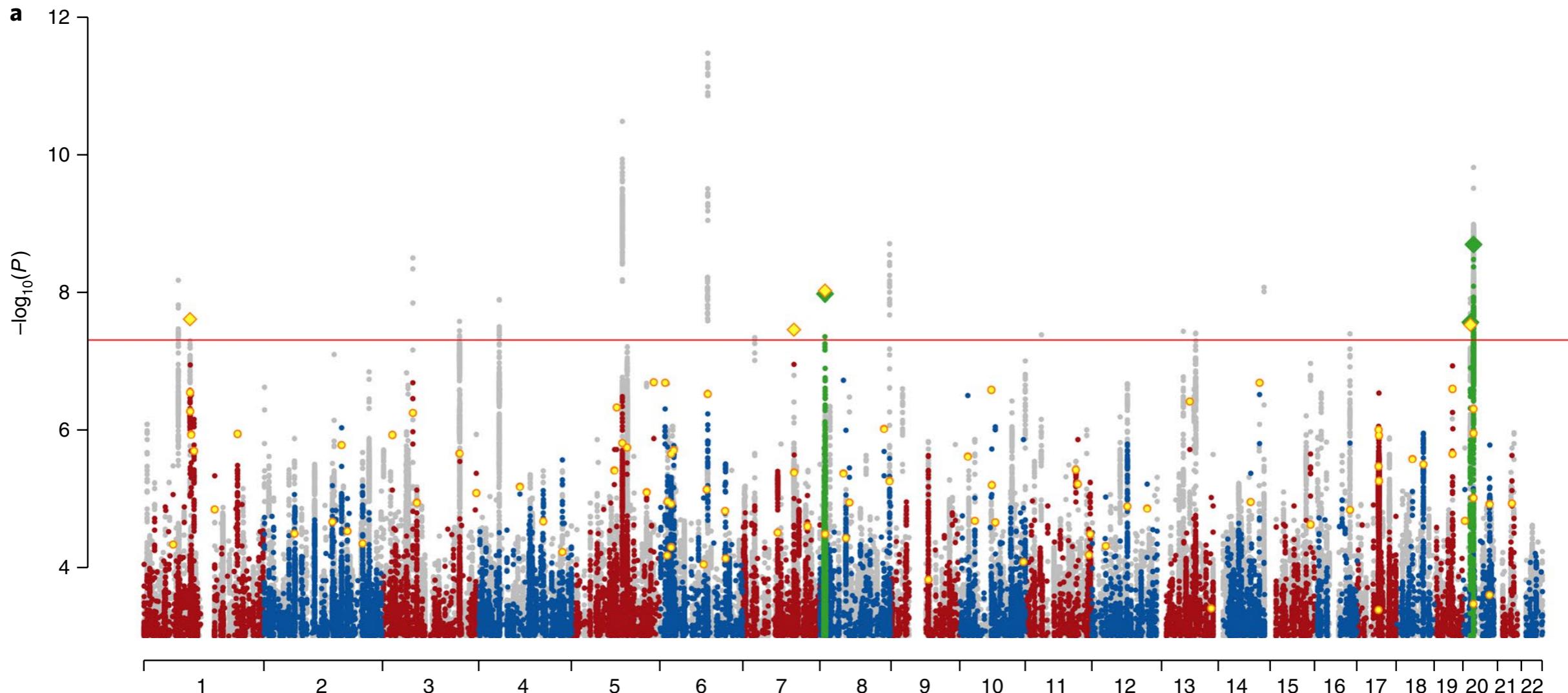
Historical population sizes



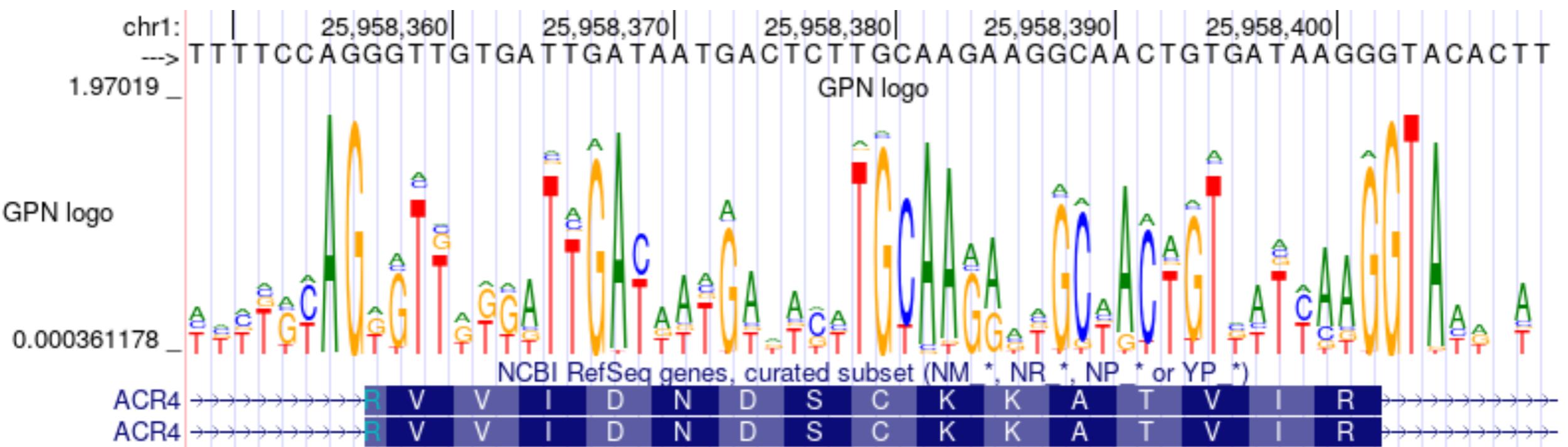
Positive selection



Genetic association and heritability

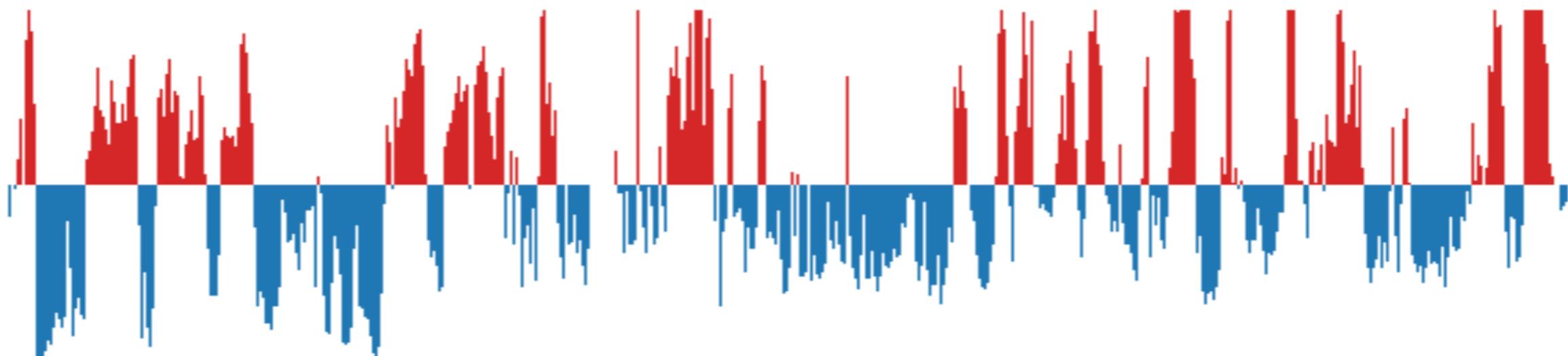
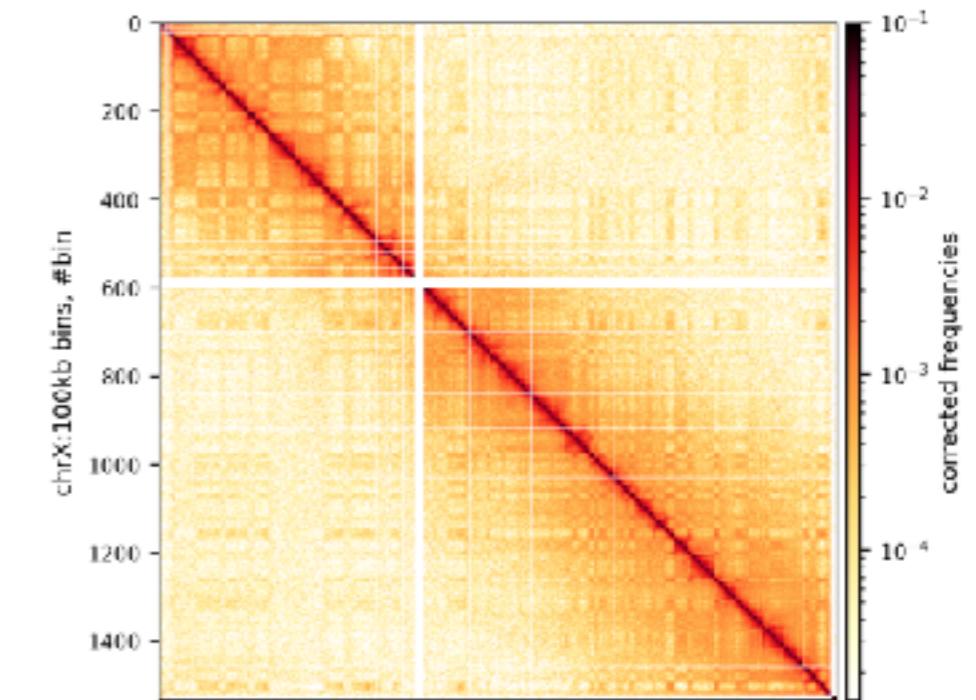
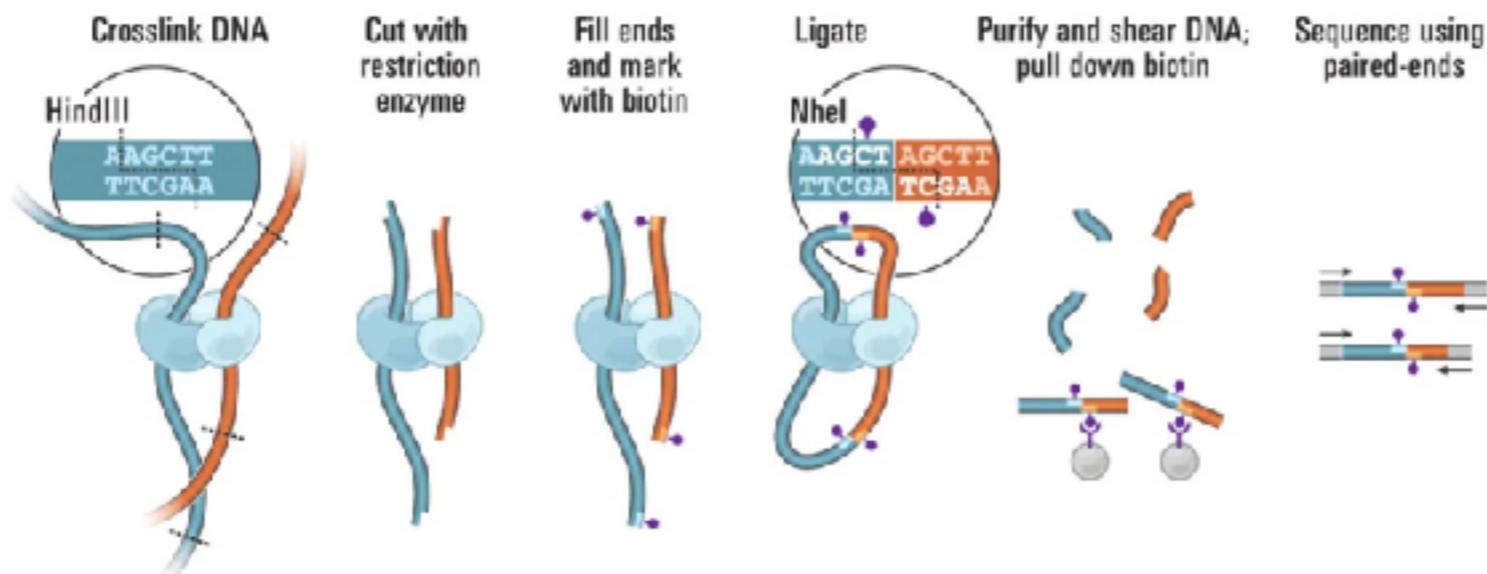


DNA language models



Epigenetic chromosome organisation

Hi-C Sequencing



Curriculum

- Reading material for each week is found the course page:
<https://munch-group.org/docs/genomic-thinking>

GRAHAM COOP

POPULATION AND QUANTITATIVE GENETICS

PLOS GENETICS

ARTICLE doi:10.1371/journal.pgen.1004

The Simons Genome Diversity Project: 300 genomes from 142 diverse populations

Thomas Mailund,¹ Kasper Maack,¹ and Mikkel Heide Schierup^{1,2*}

¹Bioinformatics Research Centre, Aarhus University, DK-8000 Aarhus C, Denmark
email: mailund@bioinfo.au.dk, kaspermaack@bioinfo.au.dk, mheide@bioinfo.au.dk

²Department of BioScience, Aarhus University, DK-8000 Aarhus C, Denmark

Lineage Sorting in Apes

nature genetics

ARTICLES doi:10.1038/ng.4764

A method for genome-wide genealogy estimation for thousands of samples

Lao Saadat¹, Marie Forest¹, Sinen Shi¹ and Simon R. Myers^{1,2*}

PLOS GENETICS

Software | Open access | Published: 15 March 2006

Fast "coalescent" simulation

Paul Marjoram¹ & Jeff D. Wall¹

BMC Genetics 7, Article number: 16 (2006) | [Cite this article](#)

11K Accesses | 143 Citations | 14 Altmetric | [Metrics](#)

RESEARCH ARTICLE

Detecting archaic introgression using an unadmixed outgroup

Laurits Skov^{1,2*}, Ruoyun Hu², Vladimir Shchur², Ágoston Hobolth¹, Aylwyn Scally¹, Mikkel Heide Schierup¹, Richard Durbin^{2,3}

¹Bioinformatics Research Centre, Aarhus University, Aarhus C, Denmark, ²Department of Genetics, University of Cambridge, Cambridge United Kingdom, ³Wellcome Sanger Institute, Hinxton, Cambridge, United Kingdom

Lectures

+ student presentations / discussions

- ~15 min student presentation on a topic related to the *past week's week's* curriculum.
- ~30 min lecture
- 45 min lecture / discussion
- 45 min lecture / discussion