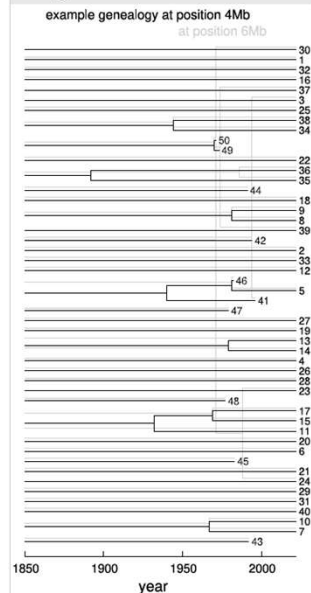
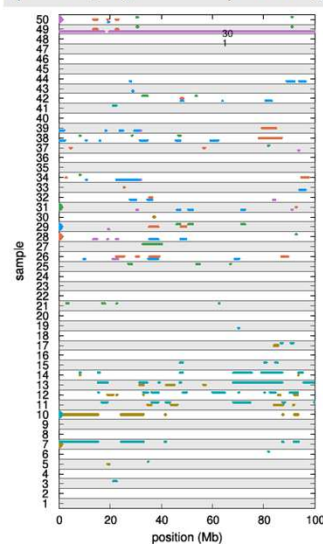


From genetic data to ecology & evolution

Inferred genealogies across the genome...

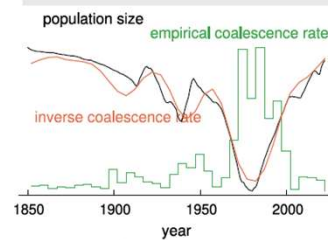


... and patterns of IBD
(identity-by-descent) sharing...

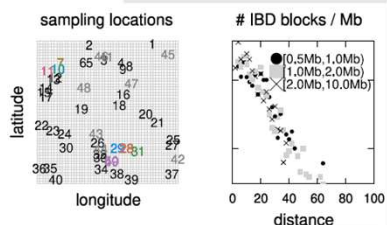


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... can be used to infer demographic history...



... as well as dispersal.



Title: demographic inference from ancestral recombination graphs.

Abstract: Recent developments have made it feasible to conduct approximate statistical inference of genealogical relationships across the entire genome for a population sample (the so-called "ancestral recombination graph" or ARG) using whole-genome sequencing data. Such an inferred ARG contains a wealth of information about the evolutionary history of the sample, and can, in principle, be used to estimate the demographic history of a population, infer patterns of dispersal, and even study the contribution of natural selection to genomic change. In this master thesis project, the aim is to conduct Bayesian ARG inference using state-of-the-art methodologies (e.g. SINGER, Deng et al. 2025) for both simulated and empirical data, and use these inferred ARGs to conduct approximate inference of effective population size changes over time. A possible additional challenge is to infer patterns of dispersal (approximate locations of ancestors) from an inferred ARG (see Osmond & Coop 2024), assuming a given global demographic history.

keywords: population genetics, bioinformatics, (bayesian) statistics

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