

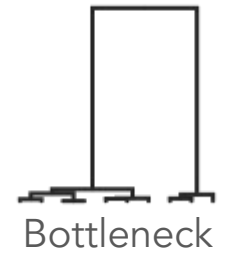
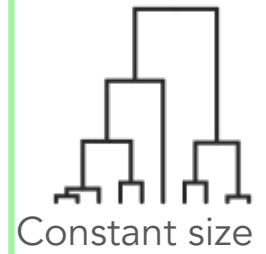
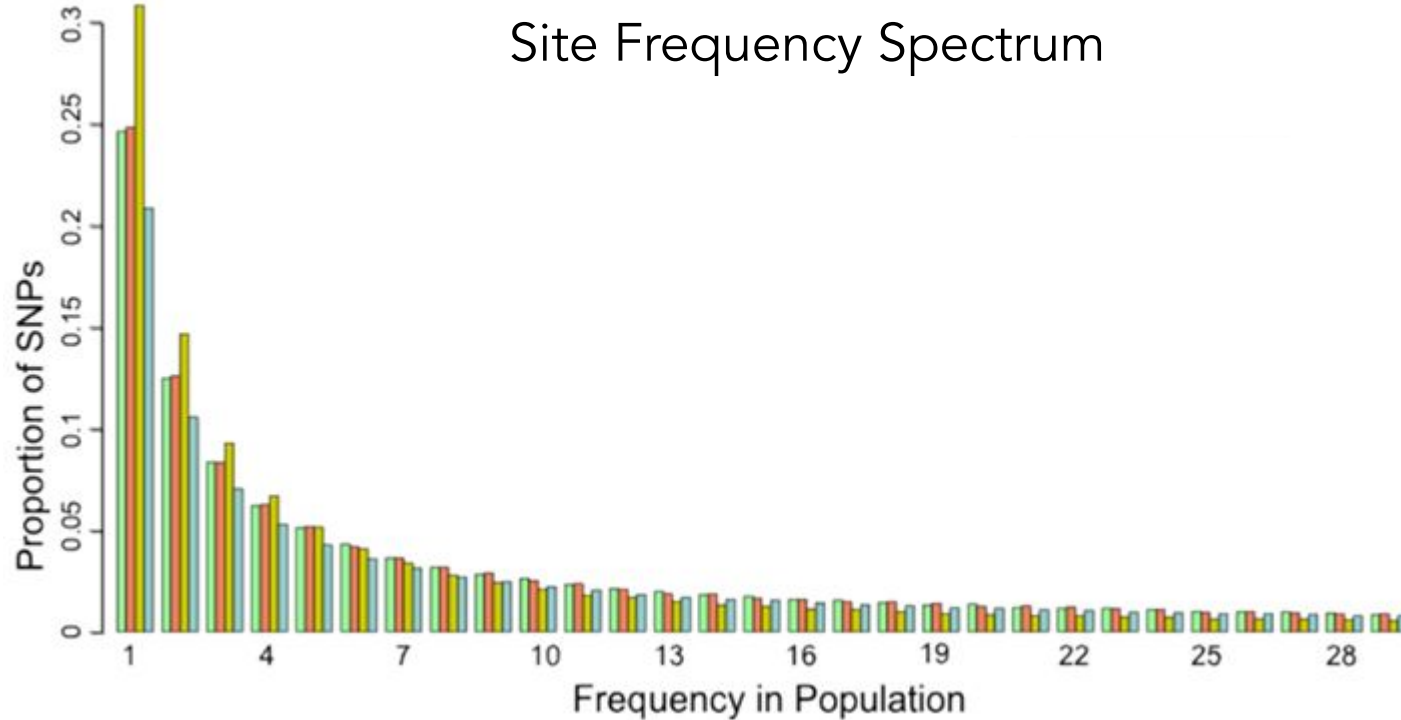
Introduction to demographic inference with the SFS in momi2

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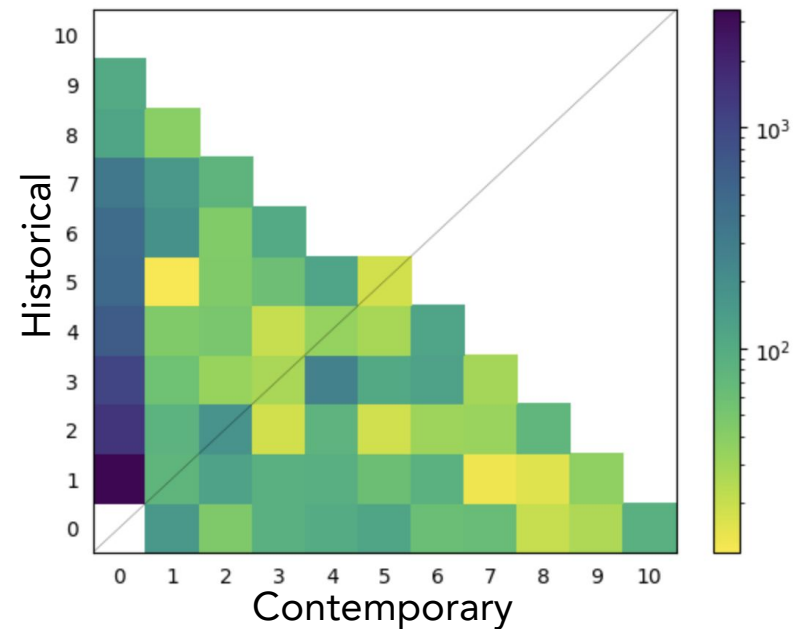
Different demographic scenarios leave different signatures in genetic data

Site Frequency Spectrum

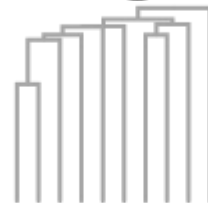
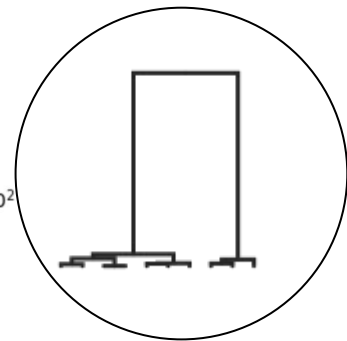
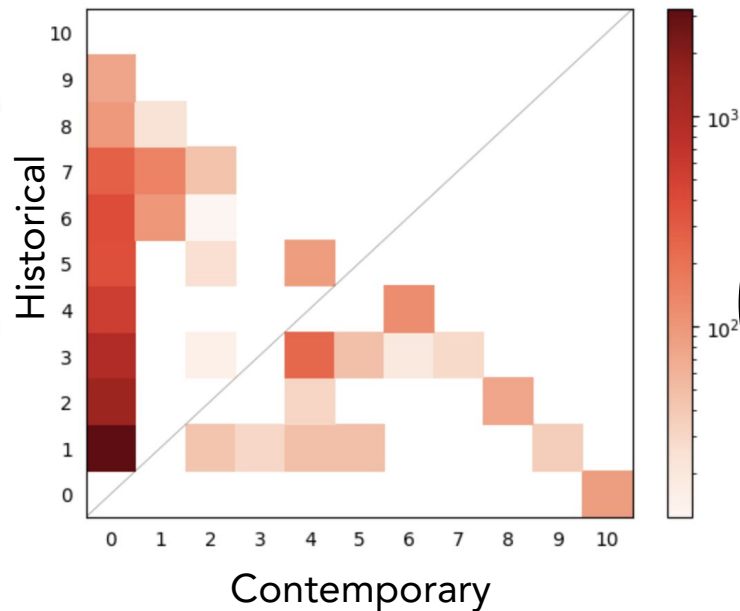


Leveraging temporal genomic samples for comparative phylogeographic inference

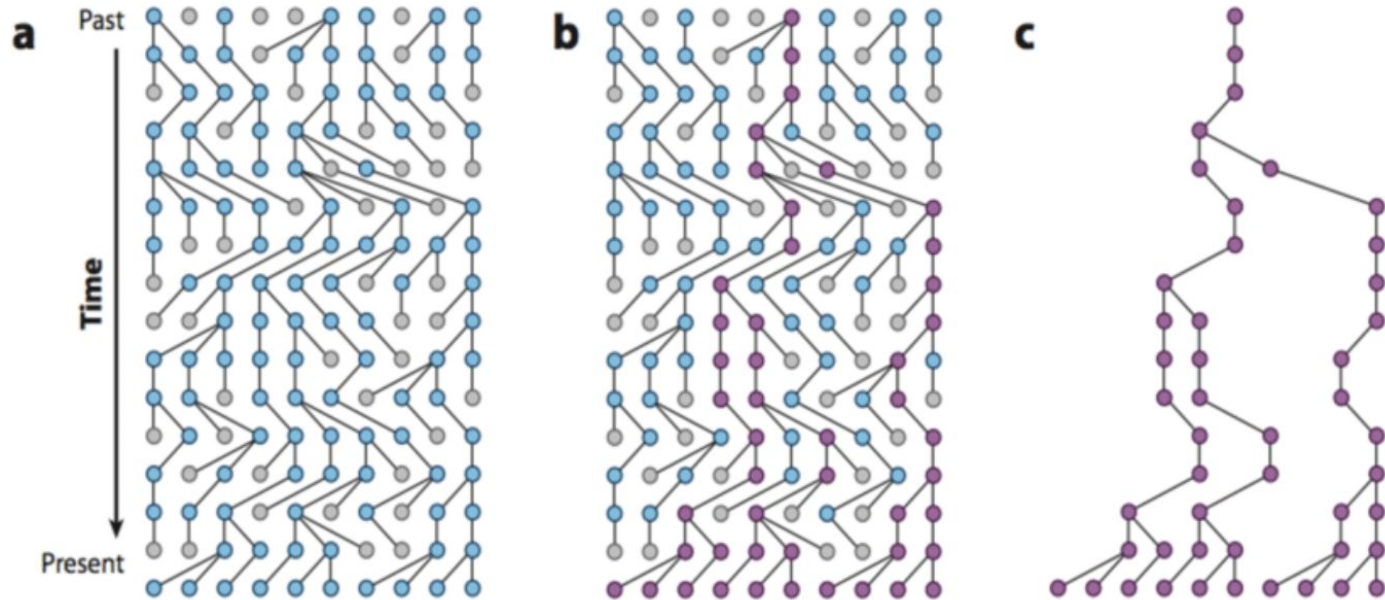
Joint SFS



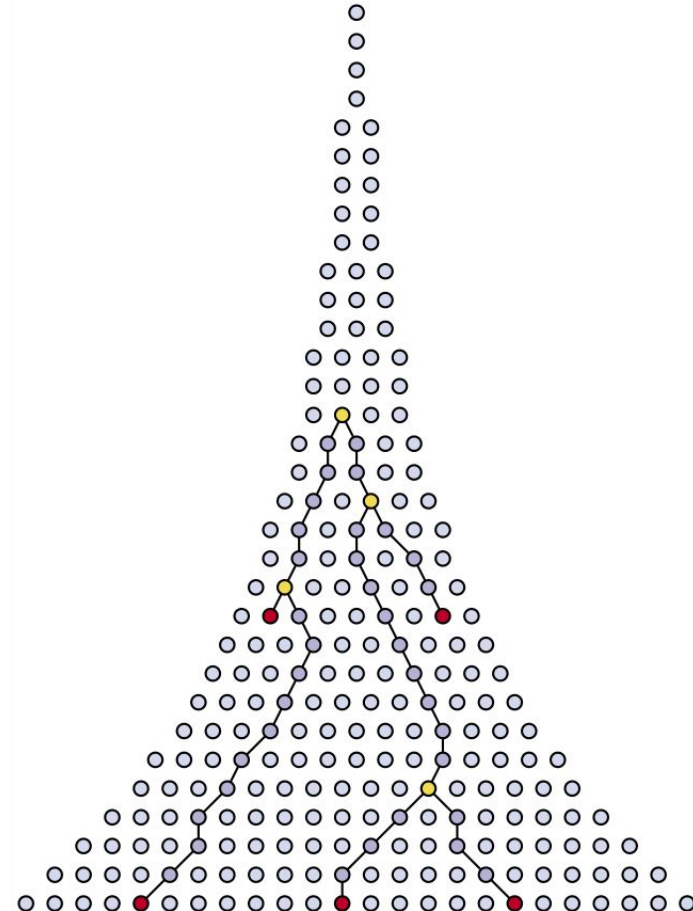
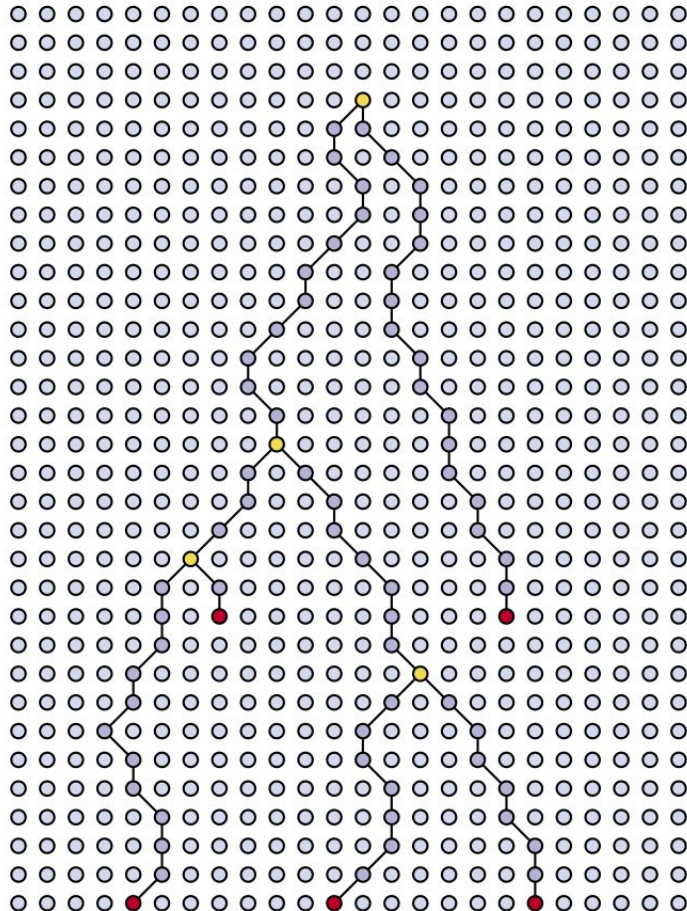
Net difference



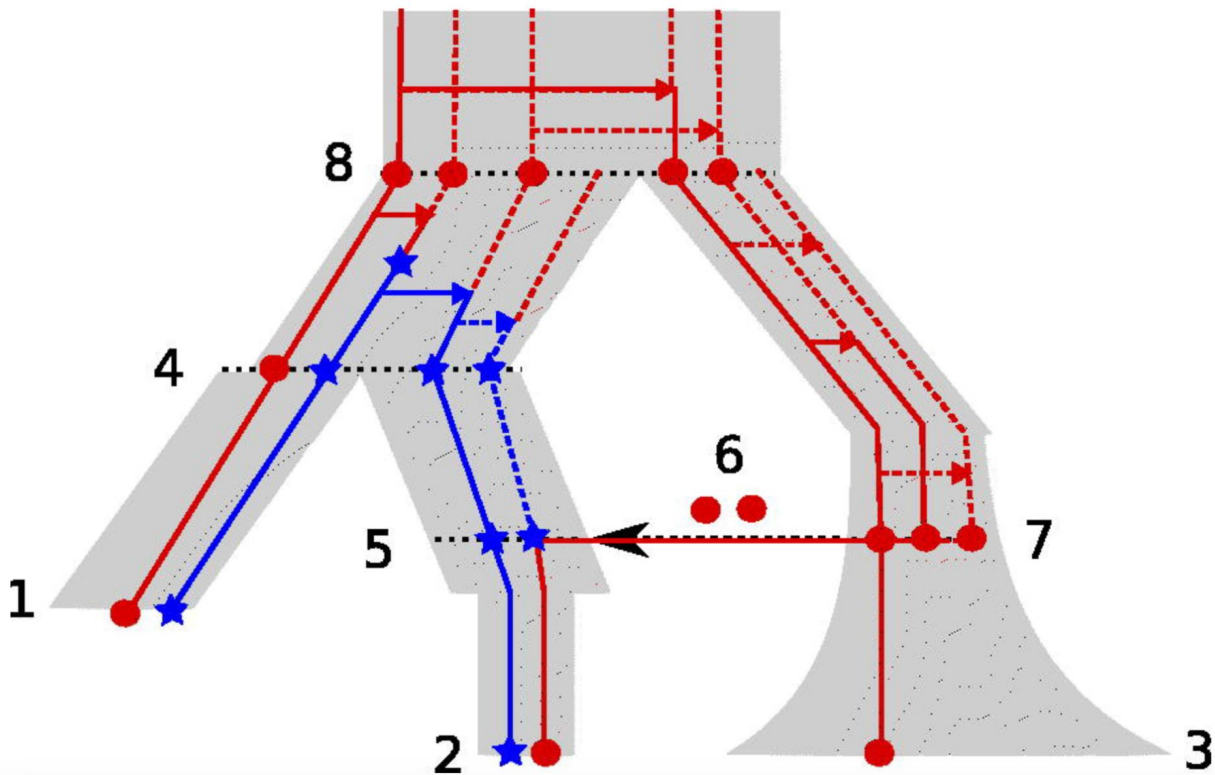
The coalescent as a tool for modeling lineages over time



Coalescence and population size



momi: MOran Models for Inference

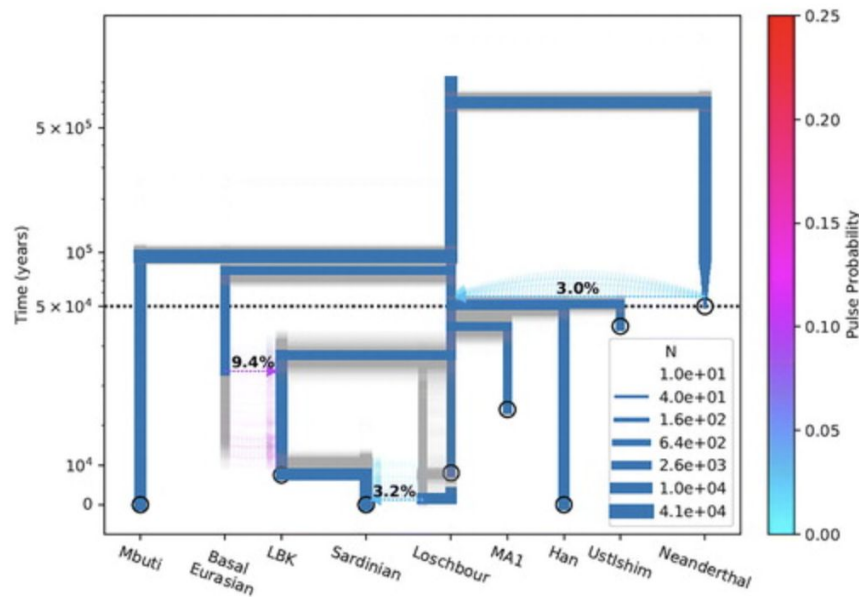


The importance of model structure and model testing

Models can be as simple or as complex (to a point) as you want

Inference relies on how closely your model matches “reality”

Identifying population structure, migration, and fitting different models (rank with AIC) can be hugely useful



Data considerations

For historical N_e , lots of loci can be just as good as lots of individuals (because we can sample many different demographic histories)

For contemporary N_e , sampling lots of individuals can help (because rare alleles tell us a lot about recent size changes)

Data considerations

Best to use the “full” SFS

Filtering is important - ideally, don't filter your data by allele frequency!

Knowing the ‘length’ of the SFS is important

Mutation rate is important!

momi exercise