

COMPUTATIONAL POPULATION GENETICS — EXERCISE SHEET 4

---

1. Simulate datasets of sequence data sampled from two populations that stem from a recent joint ancestral population and compute the JSFS of the data. Explore (e.g. by averaging over many simulations) how the expectation values of the entries of the JSFS depend on parameters like the time since the split, rates of gene-flow between the population, population size ratios and population growth rates.
2. Implement ABC-PMC in R for a demographic model like in the above exercise and explore the performance of this approach. (For the actual ABC steps you can use the `abc` command from the `abc` package.)
3. Two populations emerged from a recent split of an ancestral population. There may still be a little amount of gene-flow between the populations.
  - (a) Explore for different sizes of datasets (start with 10 independent gene loci) how accurate ABC, IM/IMa, Lamarc and Jaatha can estimate the model parameters  $\theta$  for the ancestral and the two descendant populations, time of populations split, migration rates and population growth rates.
  - (b) How can we deal with recombination within loci? Does recombination within loci increase or decrease the accuracy of parameter estimations?