

COMPUTATIONAL POPULATION GENETICS — EXERCISE SHEET 1

1. Use the R package `scrm` to simulate trees under three different scenarios:

- (a) The standard case of a panmictic population of constant size
- (b) An exponentially growing population
- (c) A population that consists of two subpopulations with migration.

Visualize the genealogies. For which growth rates and migration rates do the trees begin to look different than the standard coalescent?

2. Assume a haploid Wright-Fisher population of N individuals. Thus, we assume discrete generations and each individual in generation 0 selects purely randomly and independent of all other individuals one parent in generation -1.

- (a) Let a be an individual in generation -1 and let X be the number of his kids in generation 0. Compute $\Pr(X = 2)$.
- (b) Compute $\Pr(X = k)$ for general $k \in \mathbb{N}$.
- (c) Which fraction the individuals of a generation do not have offspring?
- (d) Assume that the population size N is very large. Then, $\Pr(X = k)$ can be approximated by a term of the form

$$b^c \cdot e^d / f!$$

Which are the appropriate values for b , c , d and f ?

- (e) Make a rough calculation: Which fraction of the individuals of a generation will have offspring
 - i. after 10 generations?
 - ii. after 100 generations?
 - iii. after N generations?

3. FOR BIOINFORMATICIANS: Develop a program that reads a sample size and outputs a random standard coalescent for this sample size in Newick format.