

Practical 2:

1 – Create a data set with the following properties:

| Symbol | Description | Truth |
|-----------------------|---|---------------------------|
| Ne₁ | Effective size of Population 1 | 10000 individuals |
| Ne₂ | Effective size of Population 2 | 20000 individuals |
| Ne_A | Effective size of ancestral population | 5000 individuals |
| t | Splitting time between modern populations | 5000 years |
| m₁ | Migration rate entering Population 1 | 0.0001 mig rate per gen |
| m₂ | Migration rate entering Population 2 | 0.0001 mig rate per gen |
| Mutation rate | | 0.001 mut per loc per gen |
| Generation time | | 1 year |

2 – Summarize the created data set with the following summary statistics:

| Symbol | Description | Prior distribution |
|-------------------------|---------------------------------|---------------------------|
| π | Mean of the pairwise difference | Uniform(0, 12500) |
| S | Number of segregating sites | Uniform(0, 40000) |
| k | Number of different haplotypes | Uniform(0, 10000) |

3 – Run 500,000 simulations with the following priors:

| Symbol | Description | Prior distribution |
|-----------------------|---|---------------------------|
| Ne₁ | Effective size of Population 1 | Uniform(0, 12500) |
| Ne₂ | Effective size of Population 2 | Uniform(0, 40000) |
| Ne_A | Effective size of ancestral population | Uniform(0, 10000) |
| T | Splitting time between modern populations | Uniform(0, 10000) |
| m₁ | Migration rate entering Population 1 | Uniform(0, 0.0005) |
| m₂ | Migration rate entering Population 2 | Uniform(0, 0.0005) |

4 – Perform the rejection-step with a tolerance of 0.004

5 – Perform the regression-step with the log transformation.