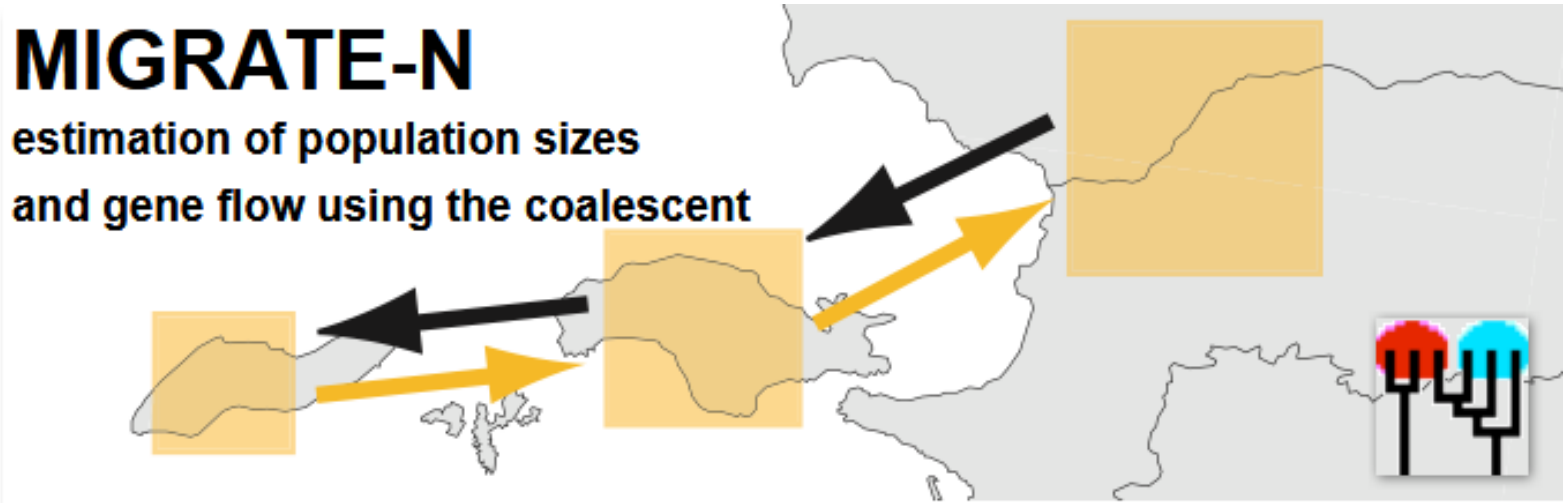

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Migrate-N

Migrate-N is a program written by Peter Beerli

- It estimates effective population sizes and past migration rates between populations
- Jointly estimates all parameters
- ML or Bayesian inference
- Can take in sequence data, SNP data, microsats, electrophoretic data

Migrate-N

We can run models with different parameters (based on biologically plausible scenarios) and compare them using **Bayes Factors**

Bayes Factors

Bayes Factors are ratios of marginal likelihoods

$$logBF = 2[ln(mL(model1)) - ln(mL(model2))]$$

$logBF < -2$ suggests preference for model 2
$logBF > 2$ suggests preference for model 1

Model Probability

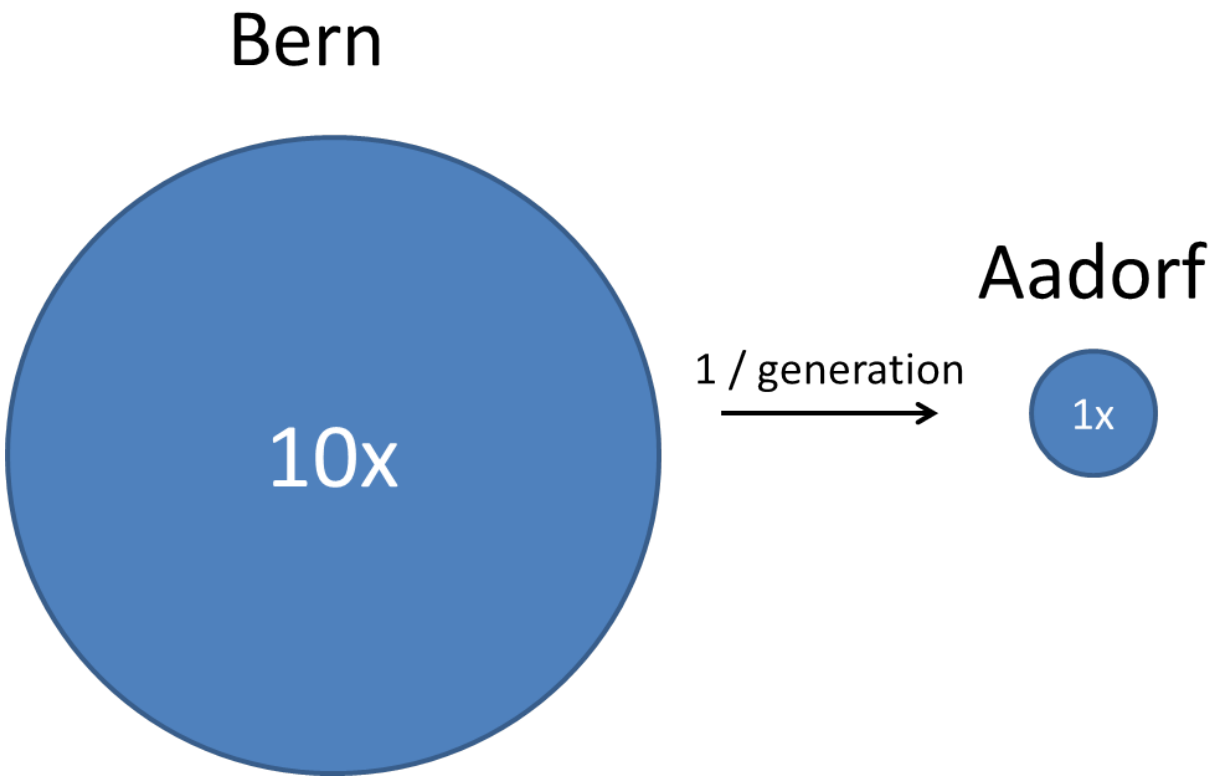
$$Prob(model_i) = \frac{mL_{model_i}}{\sum_j^n mL_{model_i}}$$

Overview

- Decide what models are interesting for comparison.
  - Biologically informed, don't do "all" models!
  - Limist the number of parameters to estimate
- Run each model
  - Use same prior settings for each
  - Use at least four heated chains
- Compare marginal likelihood for the different runs
  - Calculate Bayes Factors
  - Calculate probability for each model

Simulated dataset

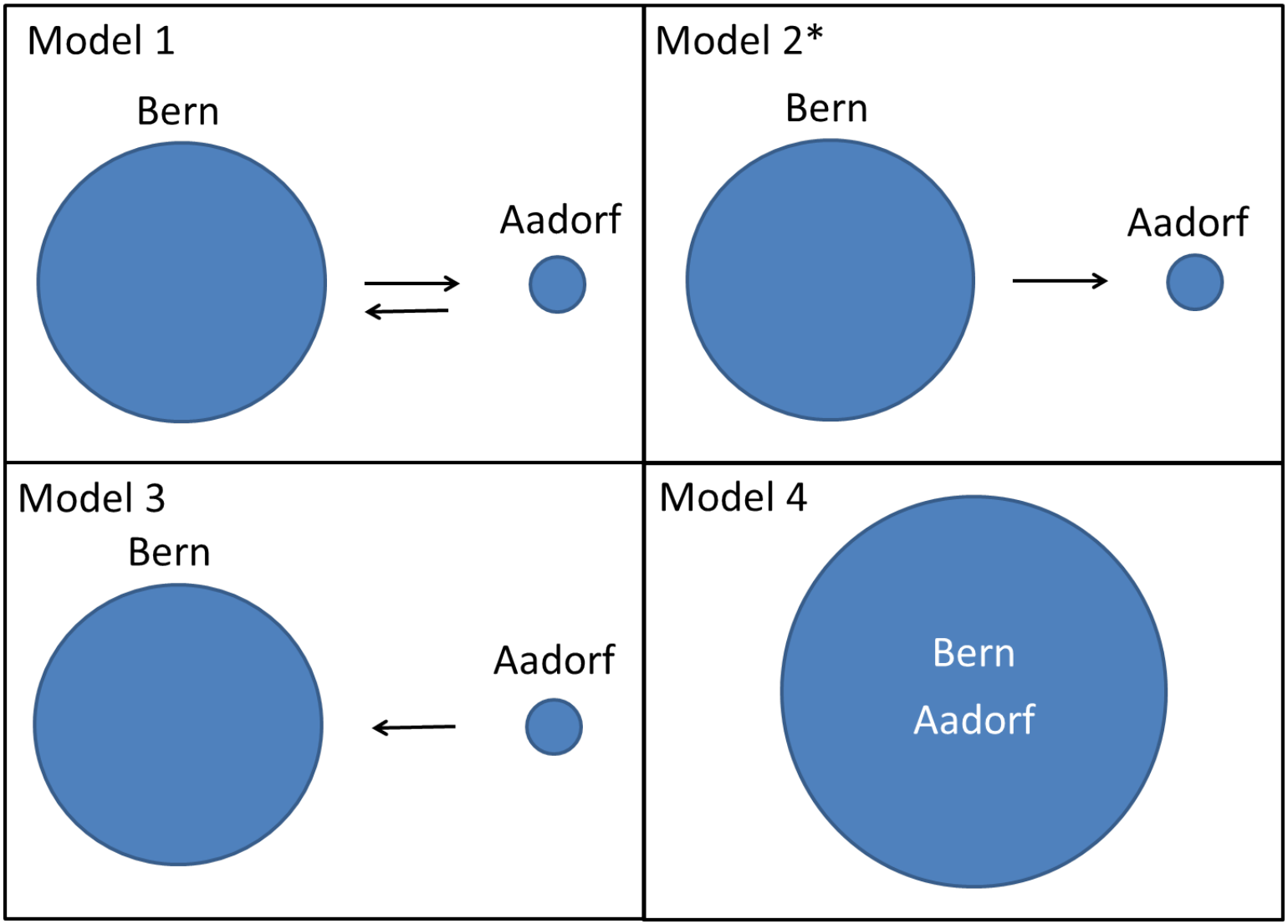
Simulated data based on:



Models to test

1. full model: two population sizes, two migration rates
2. two population sizes, one migration rate to Bern
3. two population sizes, one migration rate to Aadorf
4. Bern and Aadorf part of same panmictic population

Models to test



Running Migrate-N

- Migrate-N is run from the command line
- You will need to download the program and the tutorial example file into the same directory (folder)
- To change settings, you type the letter or number of the setting you wish to change

Instructions

- Download Migrate-N (link on course website)
- Download tutorial file
- Follow tutorial closely, note when to change settings, when to rename files, etc.
- Make sure you record your marginal likelihood values!
- Which model has the highest support? Which would you expect?
- Why may your values differ from those found in the tutorial?

References

- Beerli and Palczewski 2010: Unified Framework to Evaluate Panmixia and Migration Direction Among Multiple Sampling Locations. Genetics (2010) vol. 185 pp. 313–326