

Coalescent inference of HIV transmission history

Raymond Heil

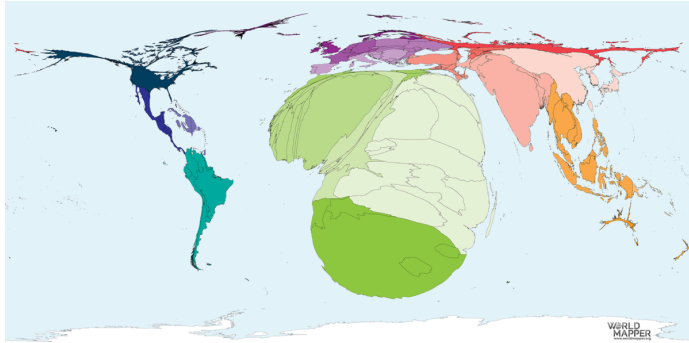
T-6: Theoretical Biology and Biophysics

Emma Goldberg, Thomas Leitner

20 July 2022

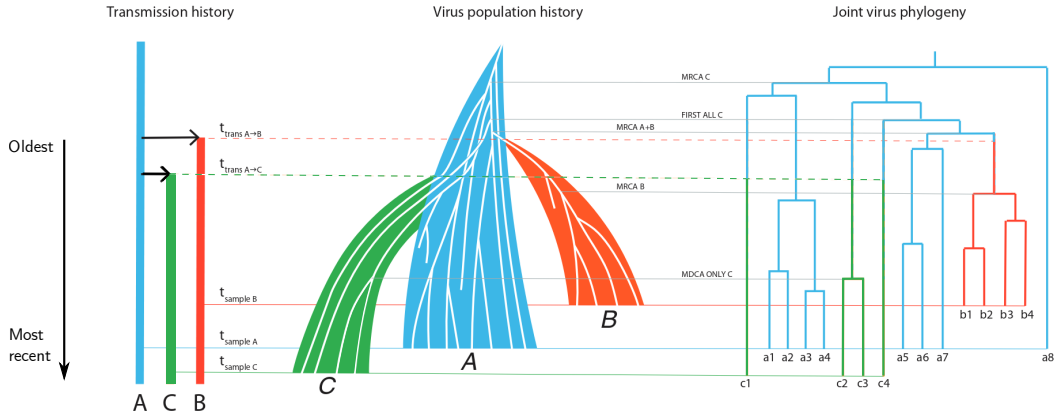


Why this project?

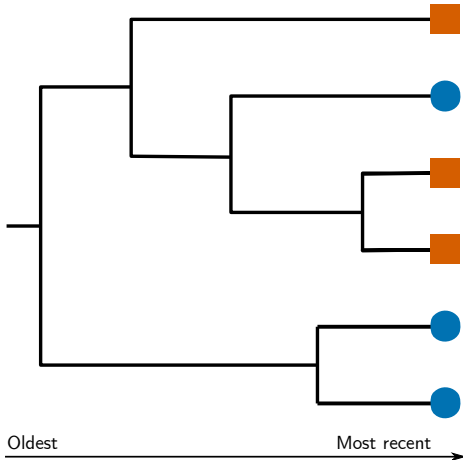


- * Prevalence of HIV
- * Transmission pairs
- * Using genetics to find transmission time

What can we expect to see?

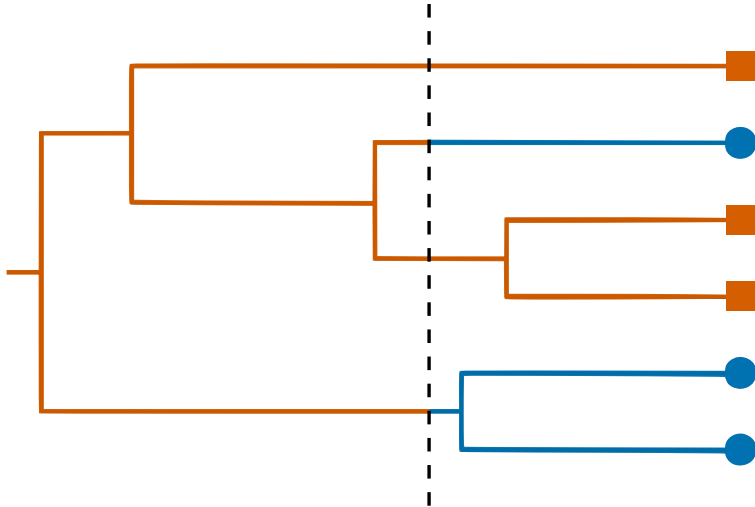


Inferring information from a tree

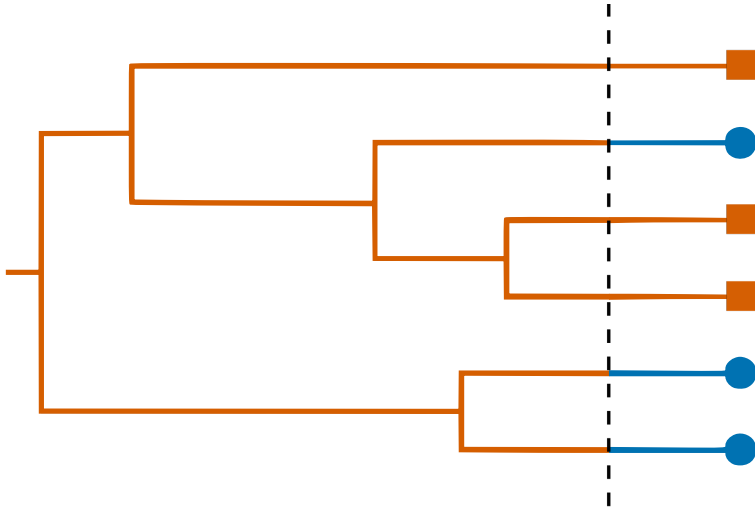


- * Tips represent individual viral sequences
- * Shows the evolutionary distance between individuals
- * What can we infer about a single transmission time?

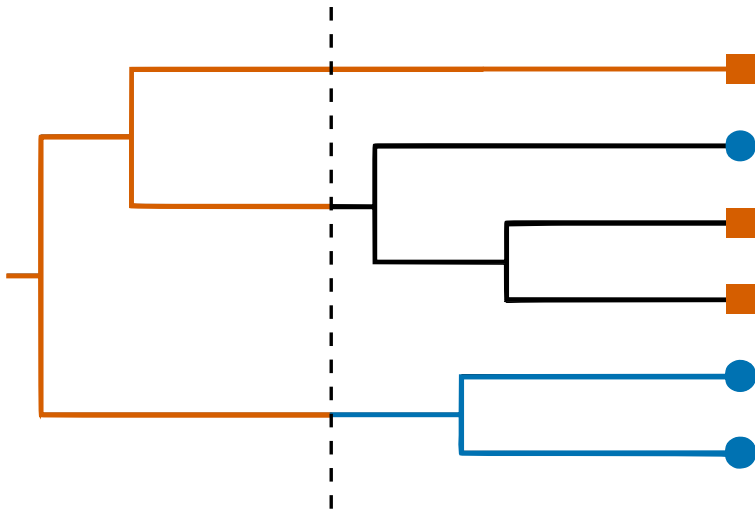
Inferring information from a tree



Inferring information from a tree



Inferring information from a tree



Coalescent modeling

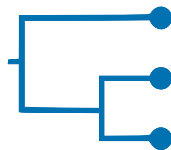
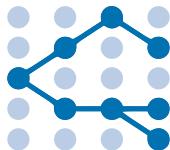
Node times as a function of population size



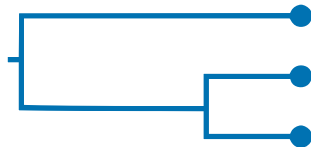
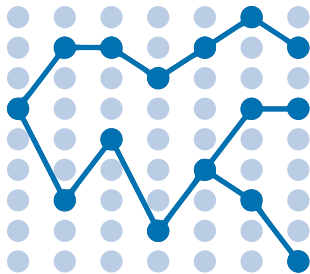
Relationship between population and samples

Large N causes node times to be further apart, stretching the tree

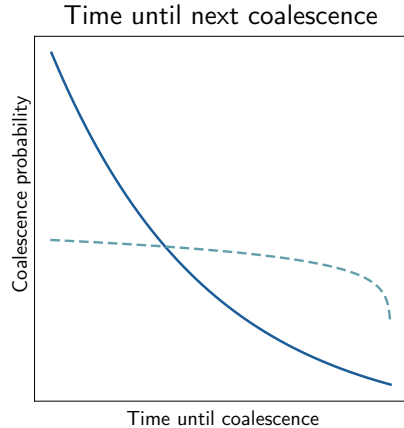
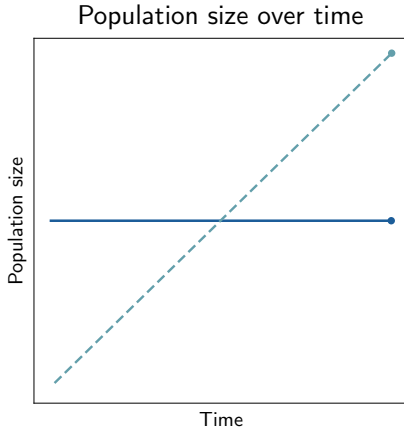
N = 5



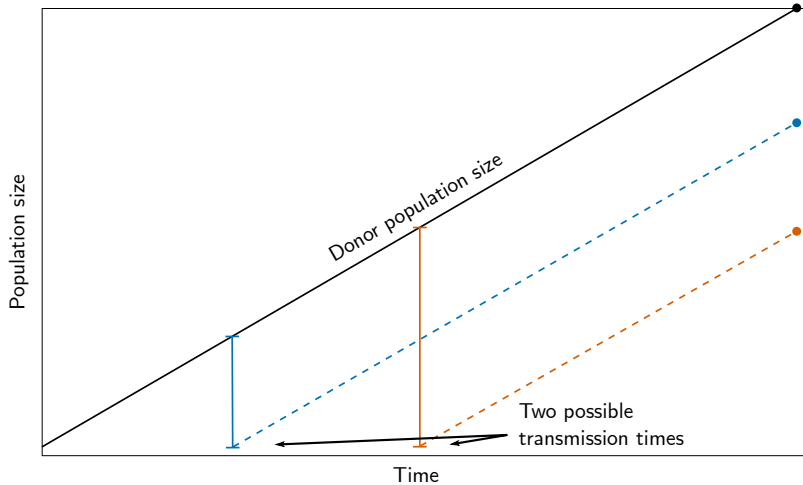
N = 9



Effect of changing population size



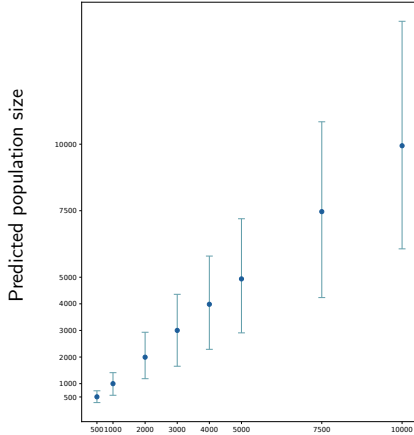
Predicting transmission time on a changing population



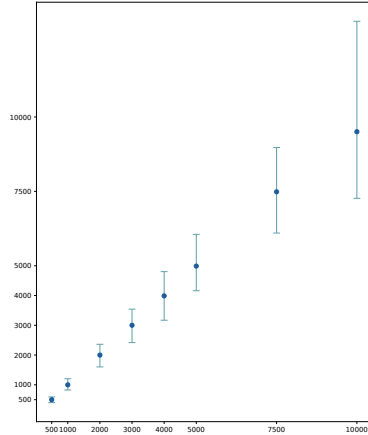
Results

Highest Density Interval of N with Constant Population Trees

Trees with 20 tips



Trees with 100 tips

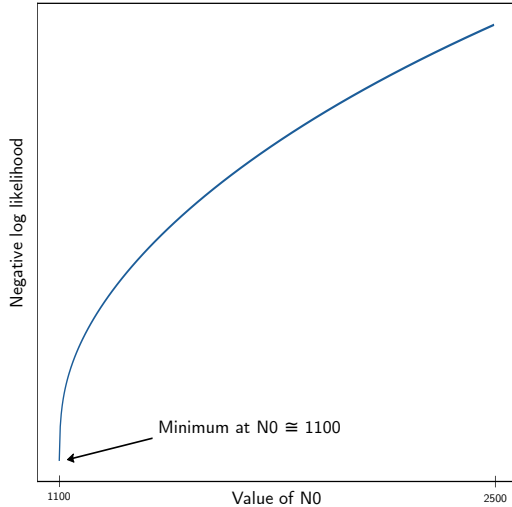


Simulation population size

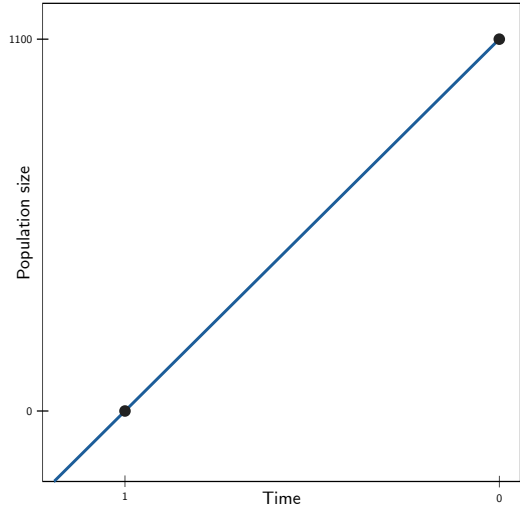


Results

Likelihood surface of N_0 with b fixed at 1100



Population size of a tree with b fixed at 1100

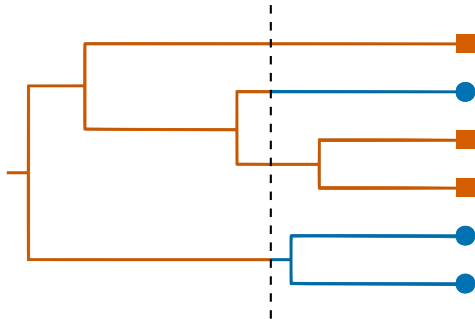


Next steps

Immediately: Solve numerical issues with multi-parameter optimization

Immediately: Extend my current work to trees with multiple hosts

- * Split tree by host
- * Isolate hosts until a transmission occurs



Overall: Find the most likely time of transmission for phylogenetic trees under a range of conditions (number of tips, population growth in each host, sampling times, etc.)

Thank you!

