Coalescent inference of HIV transmission history

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T-6: Theoretical Biology and Biophysics
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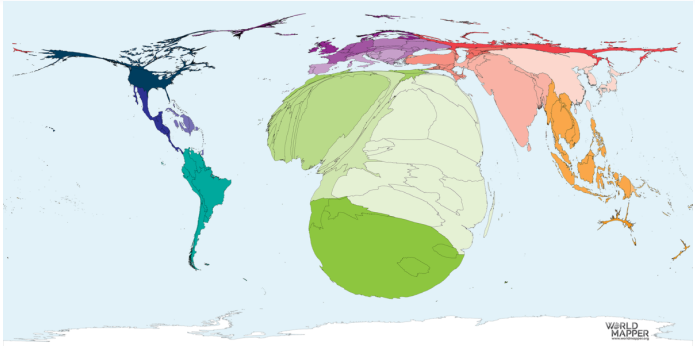
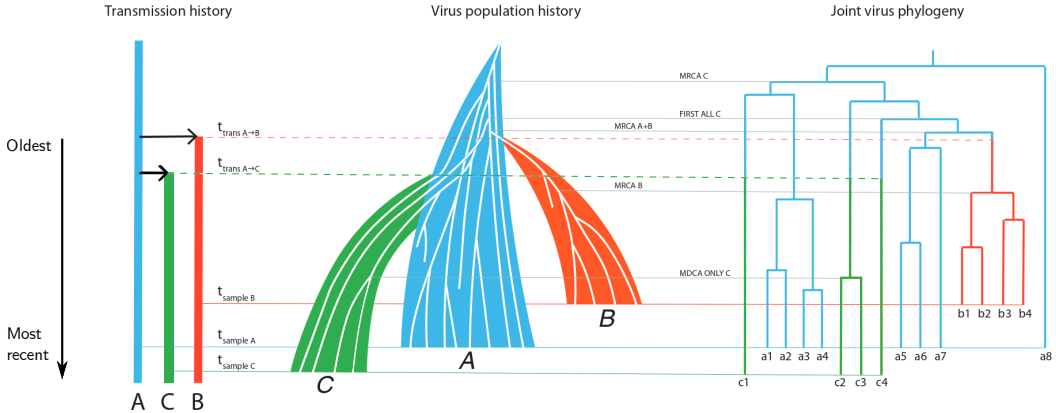
Why this project?



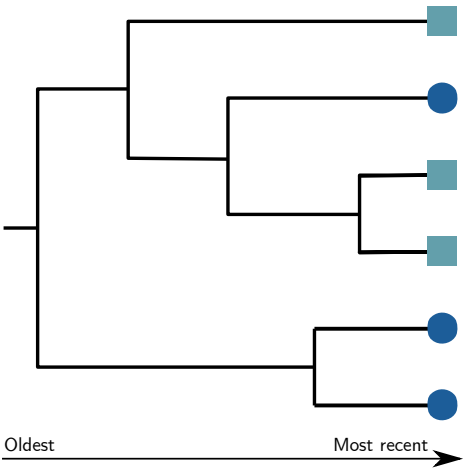
- Prevalence of HIV
- Transmission pairs
- Using genetics to find transmission time

Image: World Mapper, data from WHO Human Development Report (2013)

What can we expect to see?

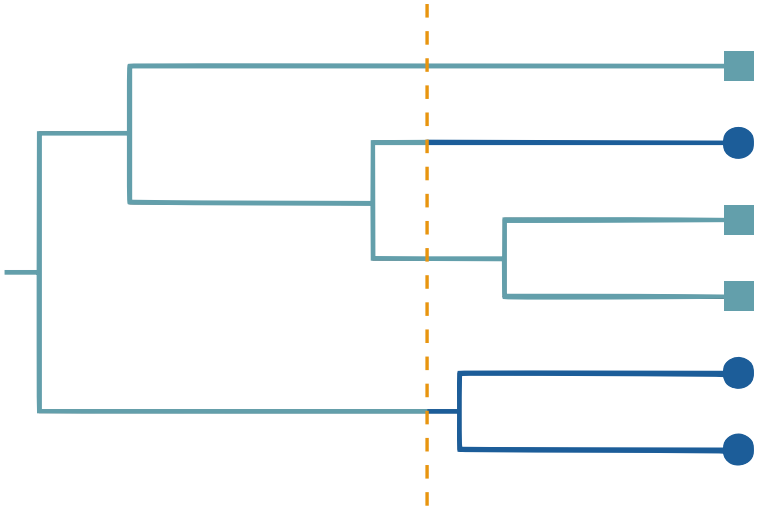


Inferring information from a tree



- 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



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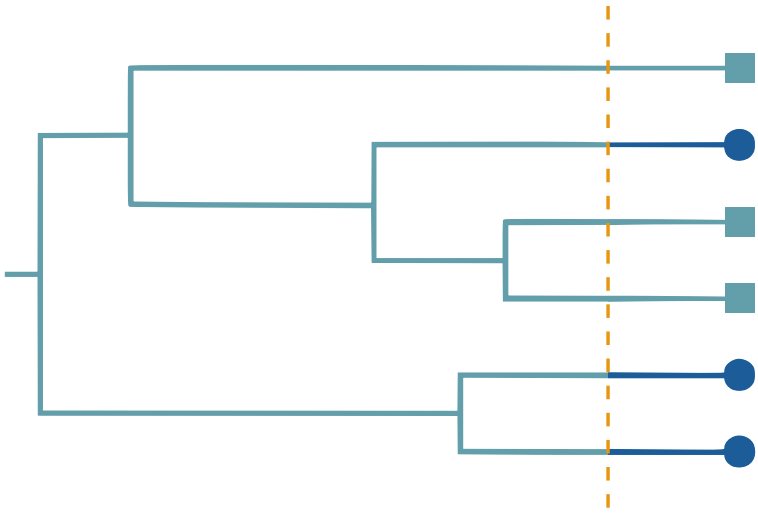

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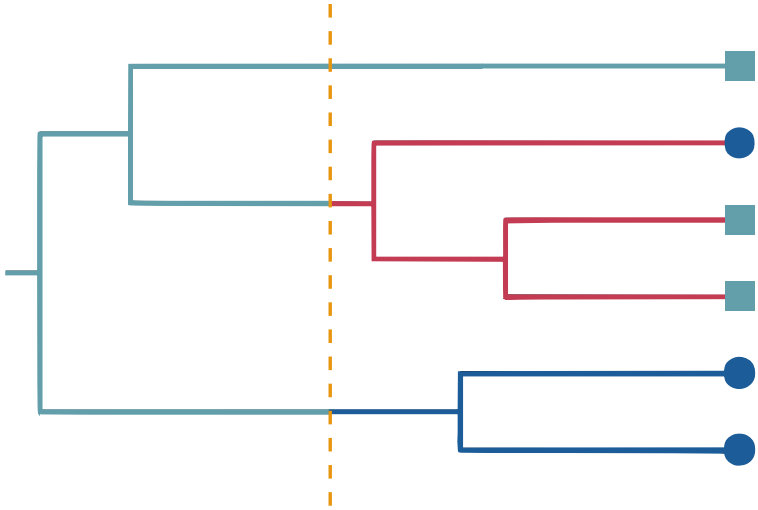
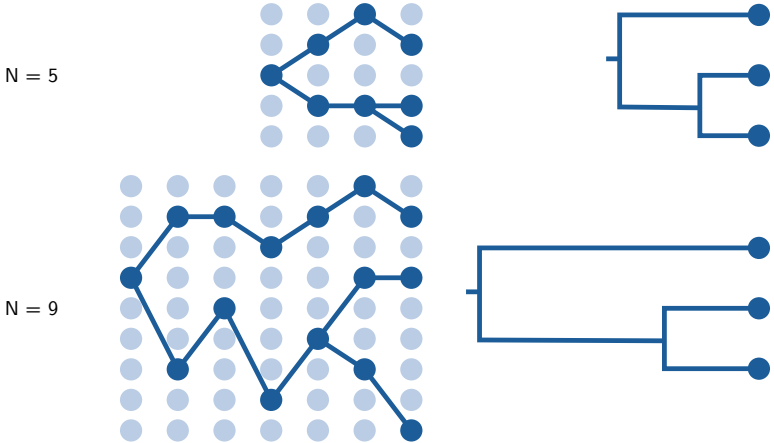


Coalescent modeling

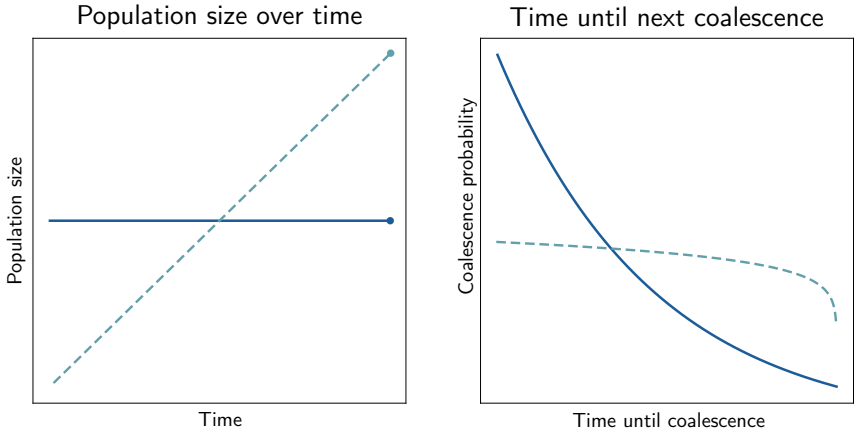
Node times as a function of population size

Relationship between population and samples

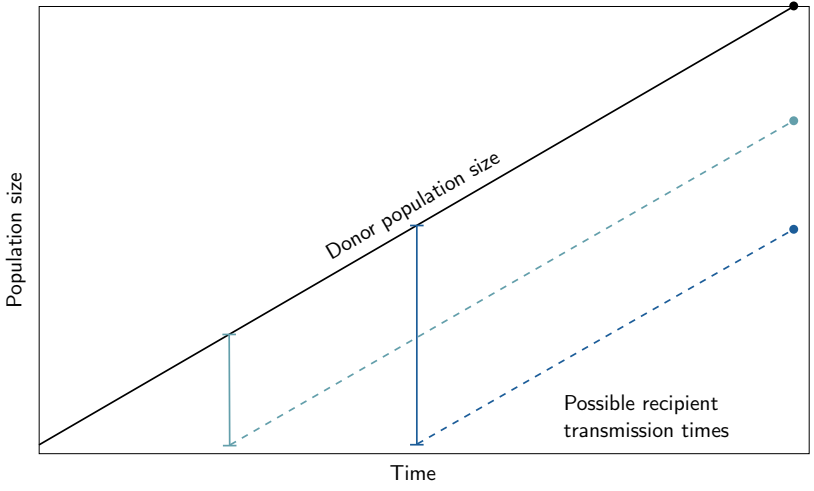
Large N causes node times to be further apart, stretching the tree



Effect of changing population size

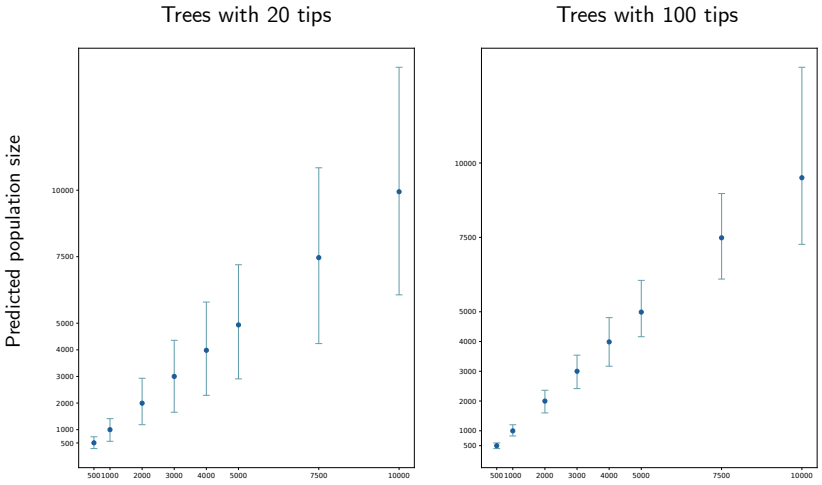


Predicting transmission time on a changing population



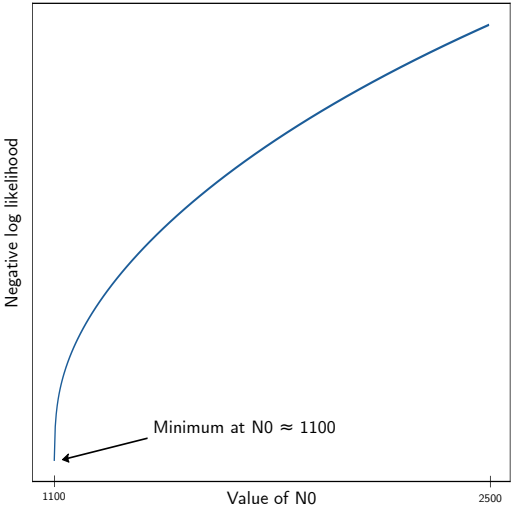
Results

Highest Density Interval of N with Constant Population Trees

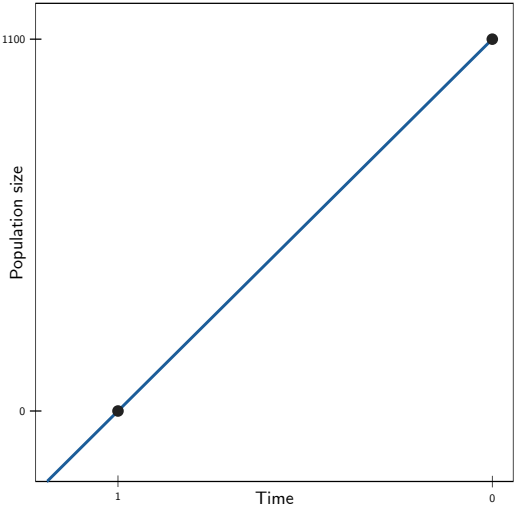


Results

Likelihood surface of N0 with b fixed at 1100



Population size of a tree with b fixed at 1100

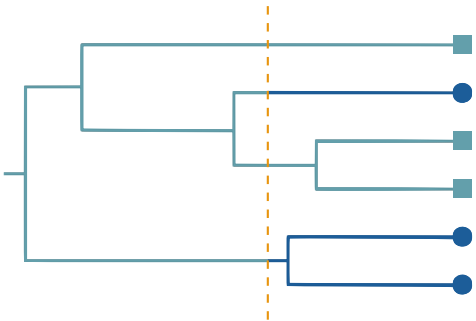


Next steps

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!