Coalescent inference of HIV transmission history

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T-6: Theoretical Biology and Biophysics

Mentors
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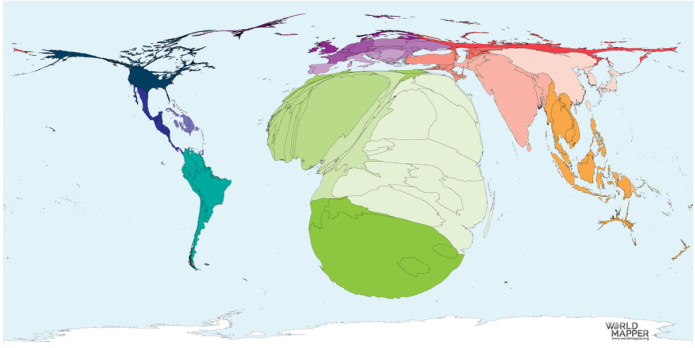
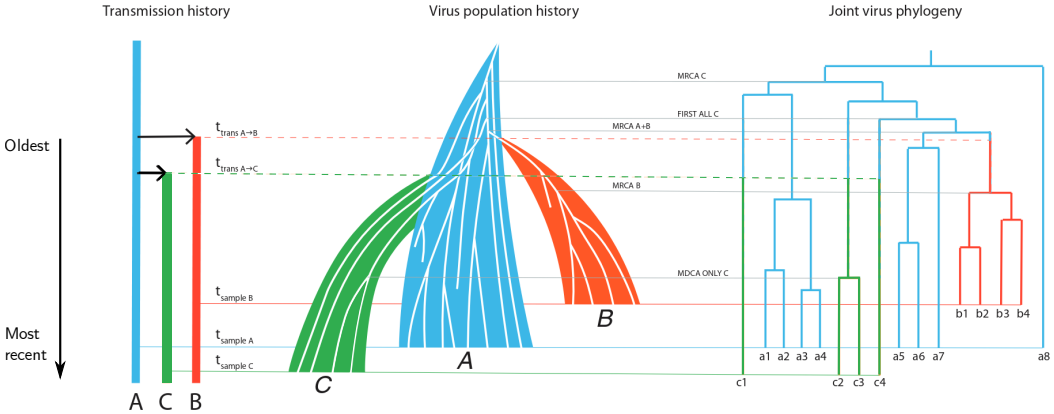
Why this project?



- HIV is globally widespread
- Despite effective therapy, it is still spreading
- How can we understand the way it spreads?

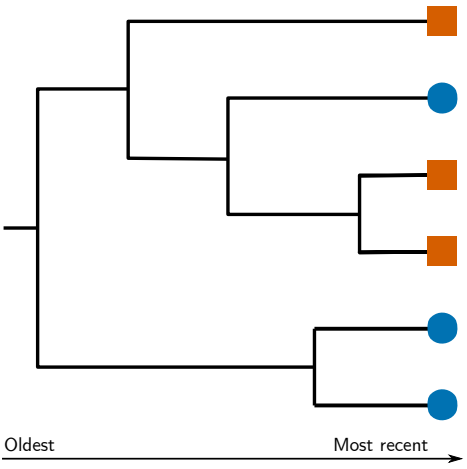
Image from World Mapper, data from WHO Human Development Report (2013)

Setting up the problem



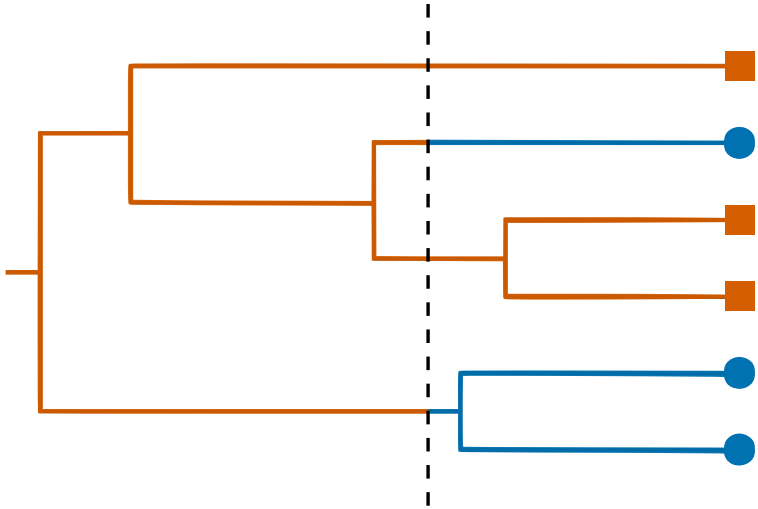
Modified from Leitner et al., Curr. Opin. HIV AIDS (2019)

Inferring information from a tree

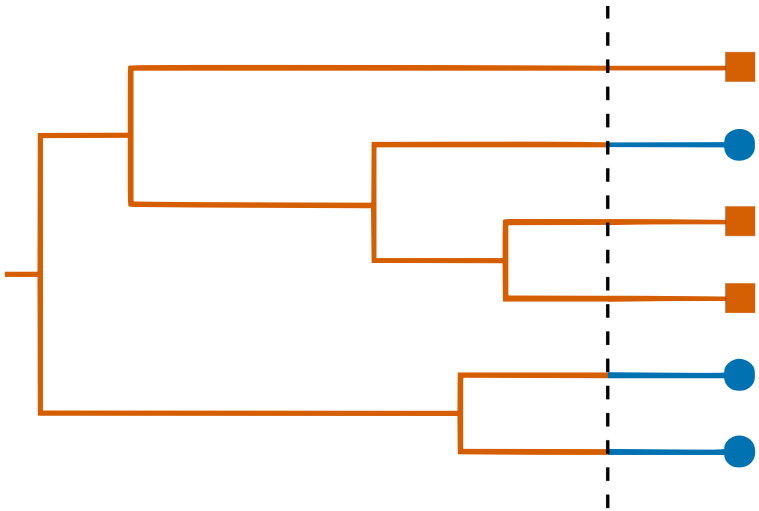


* Tree tips represent **invividual viral sequences**
* Three samples from each invididual
* If one infected the other, when?

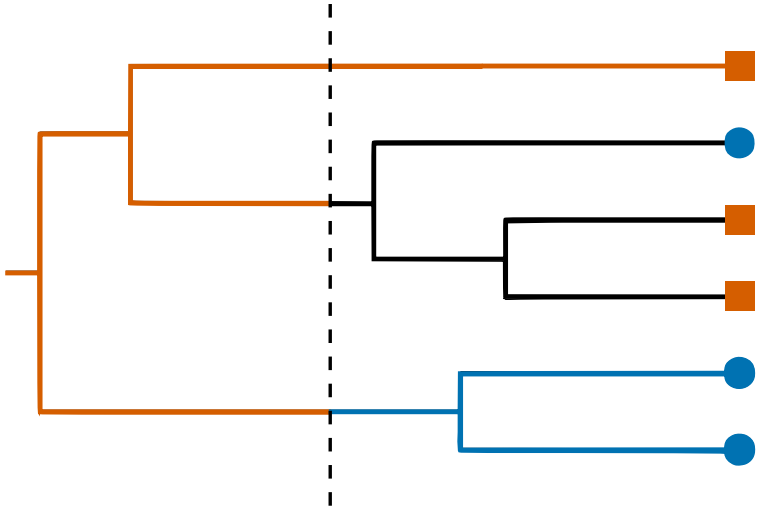
Inferring information from a tree



Inferring information from a tree



Inferring information from a tree

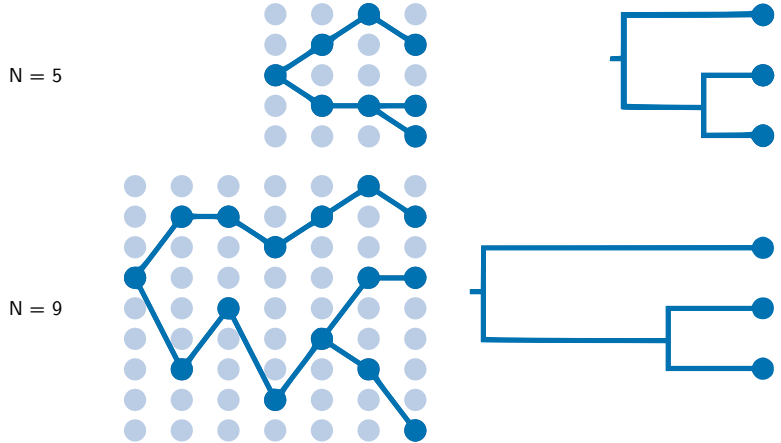


Coalescent modeling

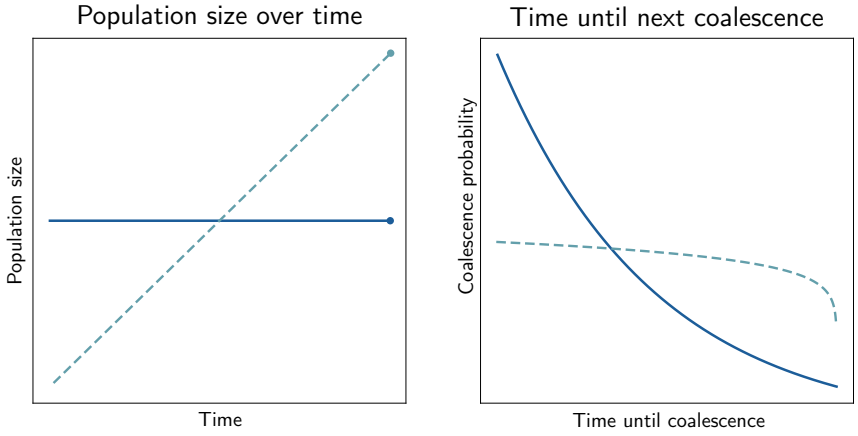
Node times as a function of population size

Relationship between population and samples

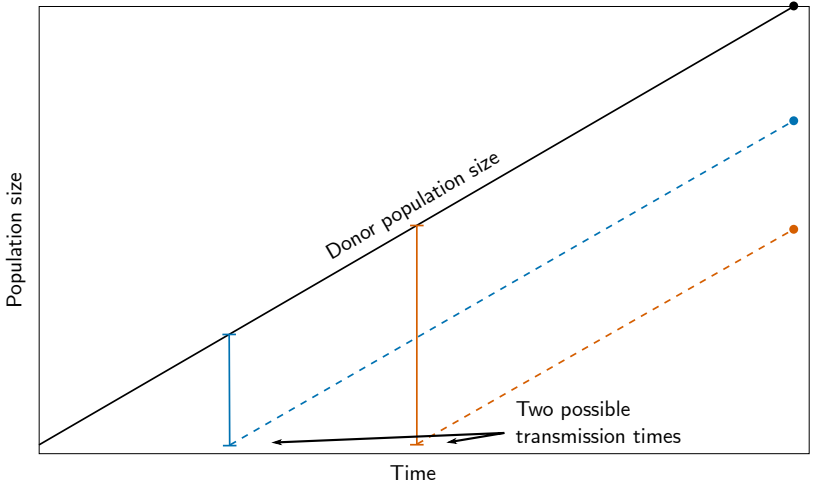
Large N causes node times to be further apart, stretching the tree



Effect of changing population size

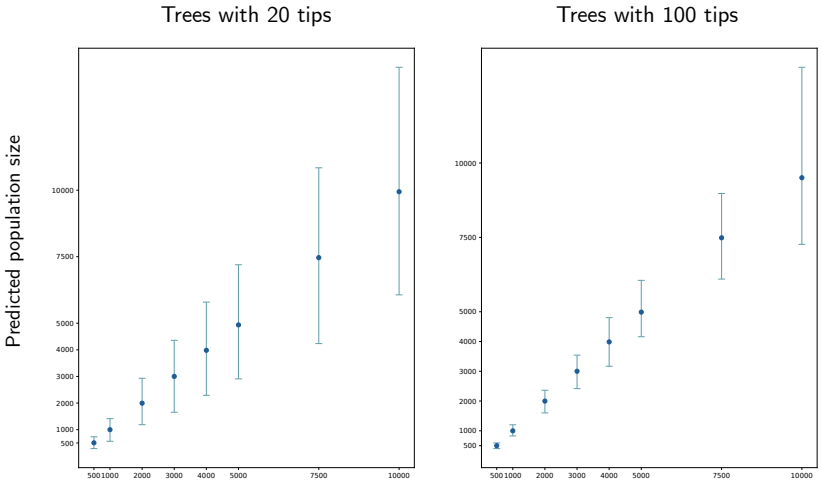


Predicting transmission time on a changing population



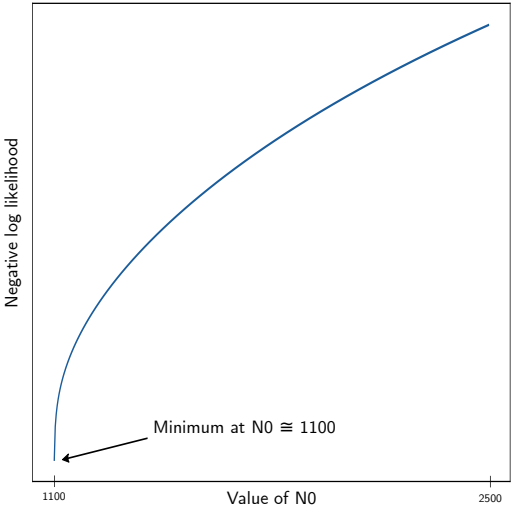
Results

Highest Density Interval of N with Constant Population Trees

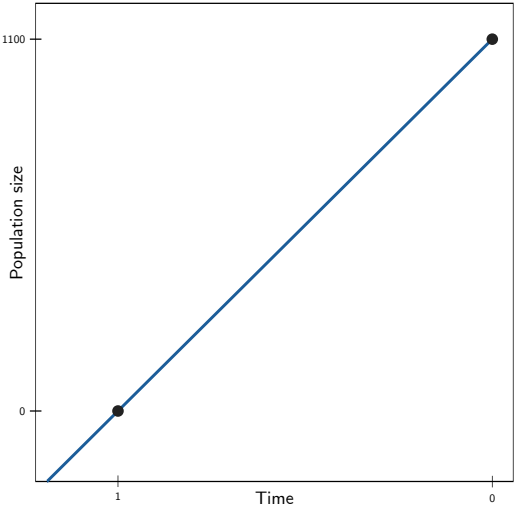


Results

Likelihood surface of N0 with b fixed at 1100



Population size of a tree with b fixed at 1100

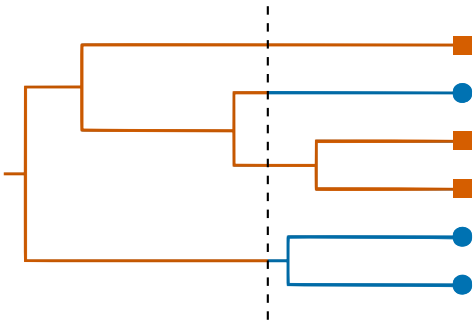


Next steps

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

Thank you!