

Coalescent inference of HIV transmission history

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T-6: Theoretical Biology and Biophysics

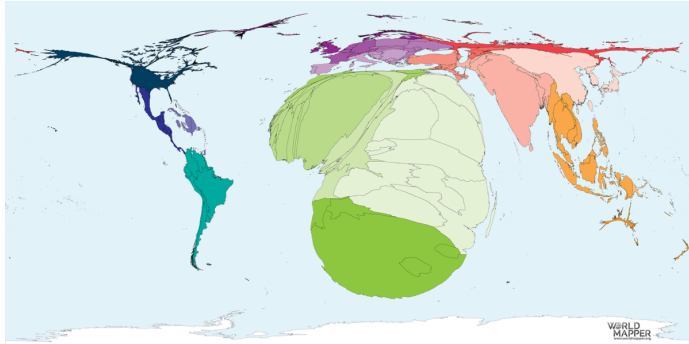
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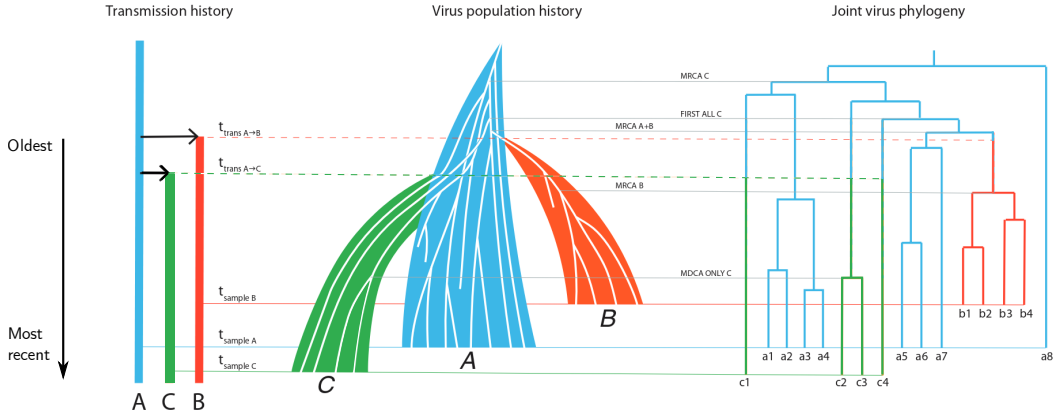


Why this project?

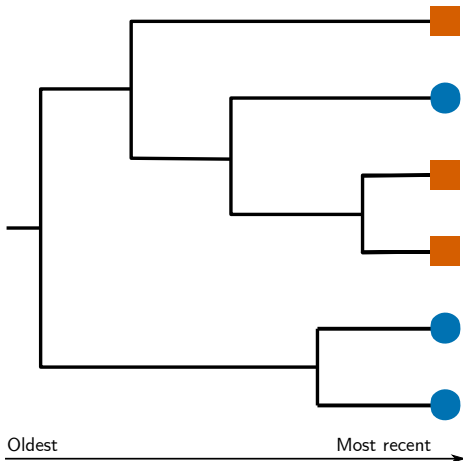


- * HIV is globally widespread
- * Despite effective therapy, it is still spreading
- * How can we understand the way it spreads?

Setting up the problem

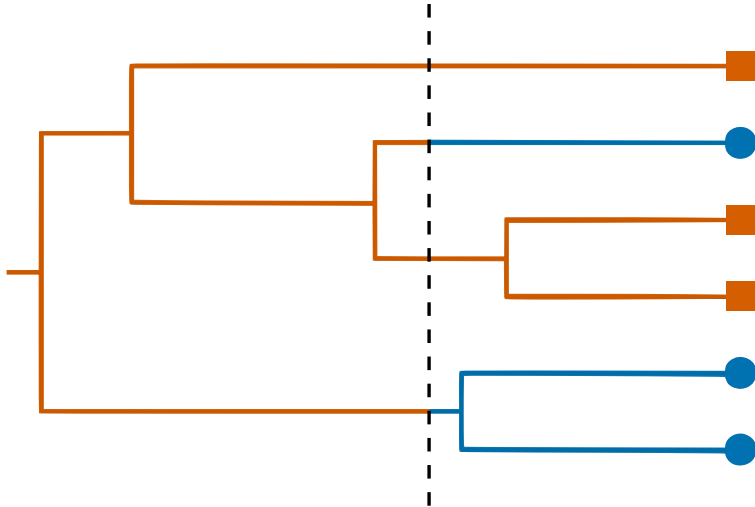


Inferring information from a tree

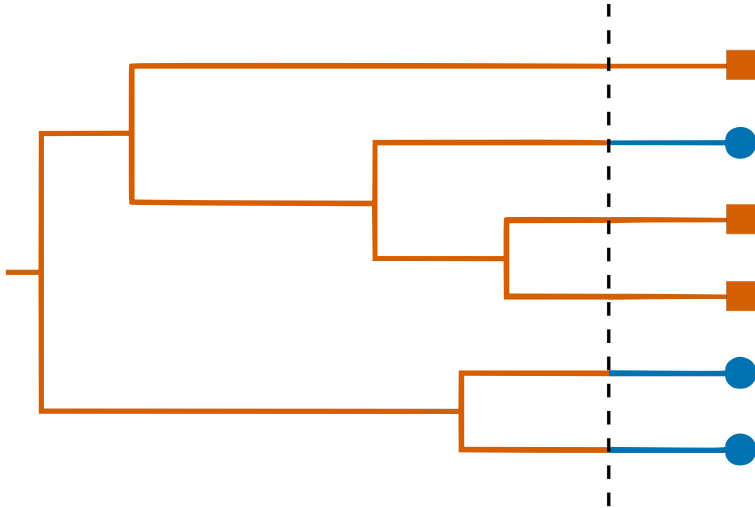


- * Tree tips represent **individual viral sequences**
- * Three samples from each individual
- * If one infected the other, when?

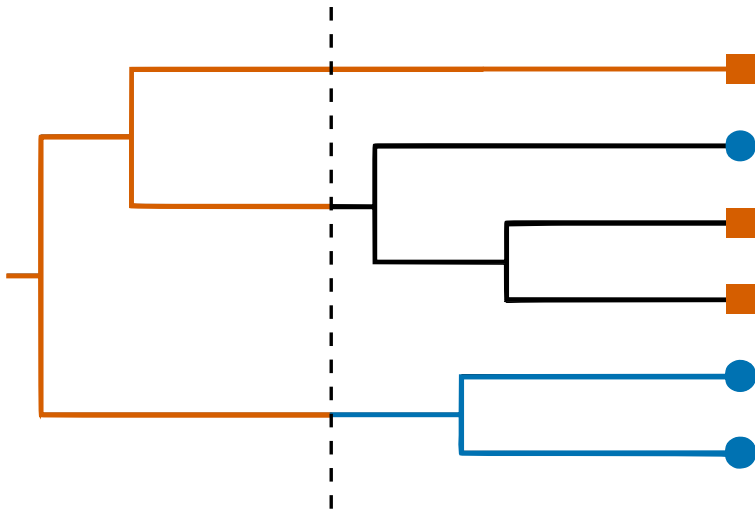
Inferring information from a tree



Inferring information from a tree



Inferring information from a tree



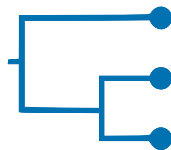
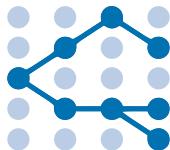
Coalescent theory

Node times as a function of population size

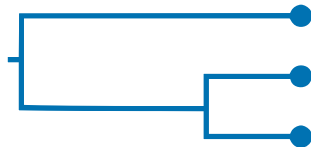
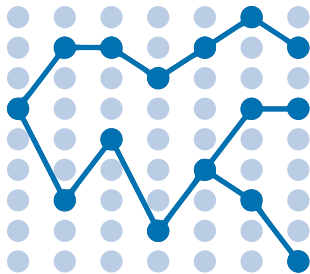
Relationship between population and samples

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

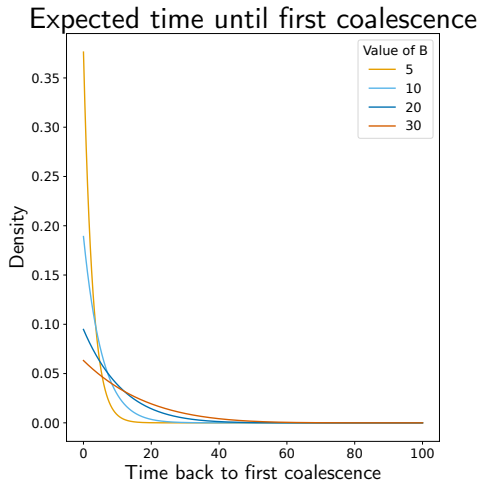
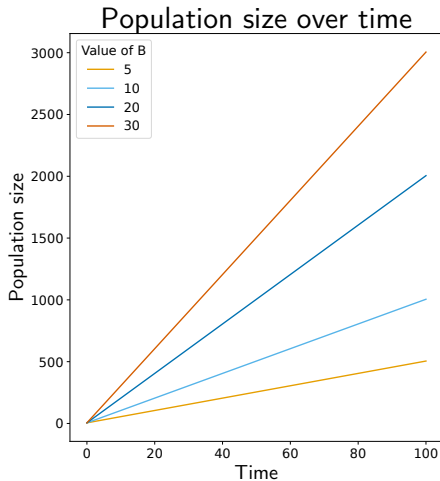
$N = 5$



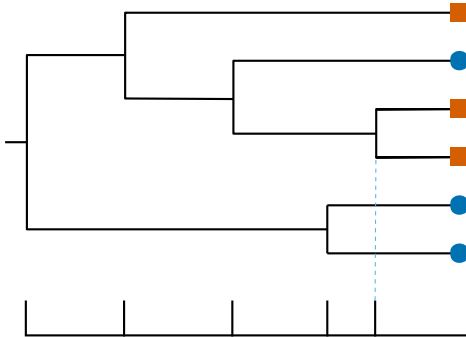
$N = 9$



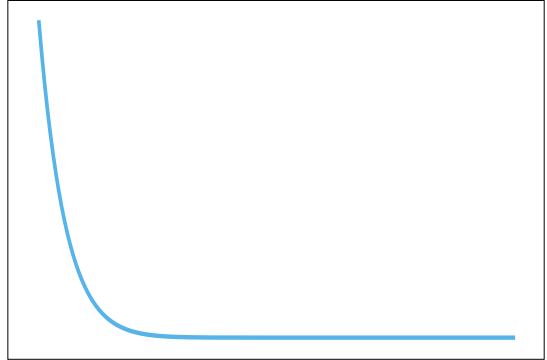
Effect of different linear populations



Finding the likelihood of a whole tree

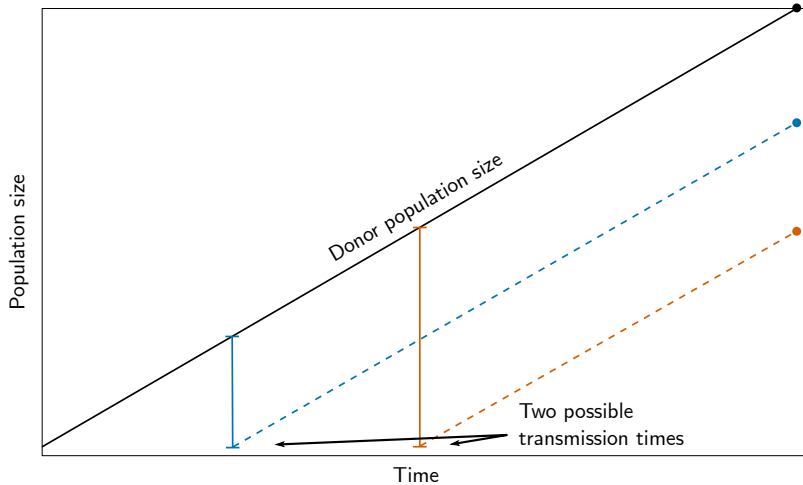


Divide tree into segments where coalescence events occur

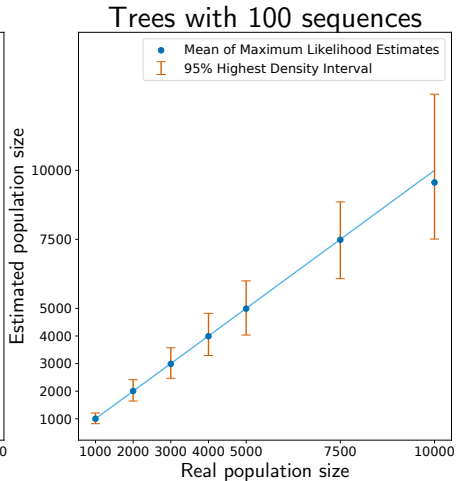
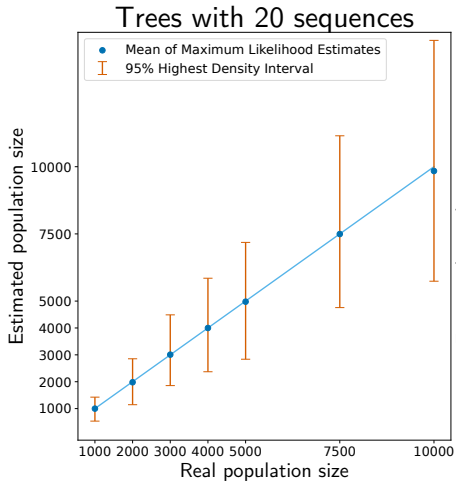


The likelihood of each event contributes to the tree likelihood

Predicting transmission time on a changing population

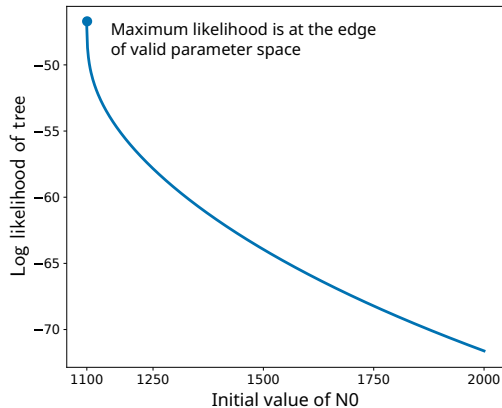


Results: Single host with constant population

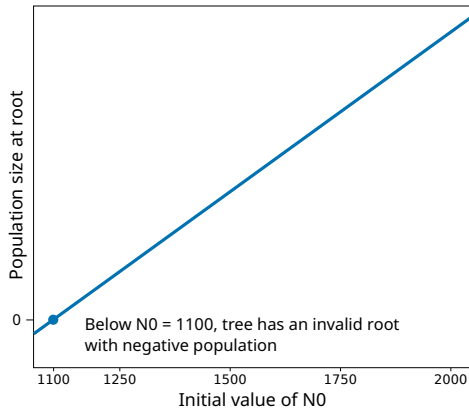


Current progress on linear populations

Likelihood of N_0 values with fixed B



Population dynamics that may cause this

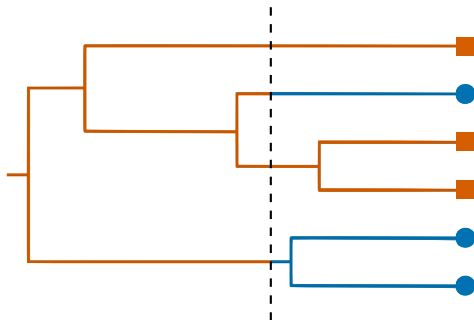


Next steps: Two hosts with linear population

Immediately: Solve numerical issues with linear 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!

