

Coalescent inference of HIV transmission history

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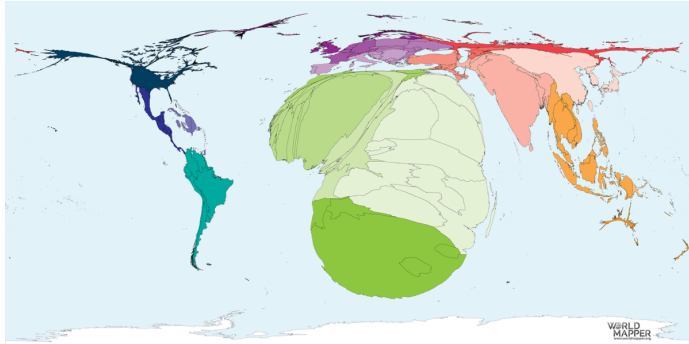
T-6: Theoretical Biology and Biophysics

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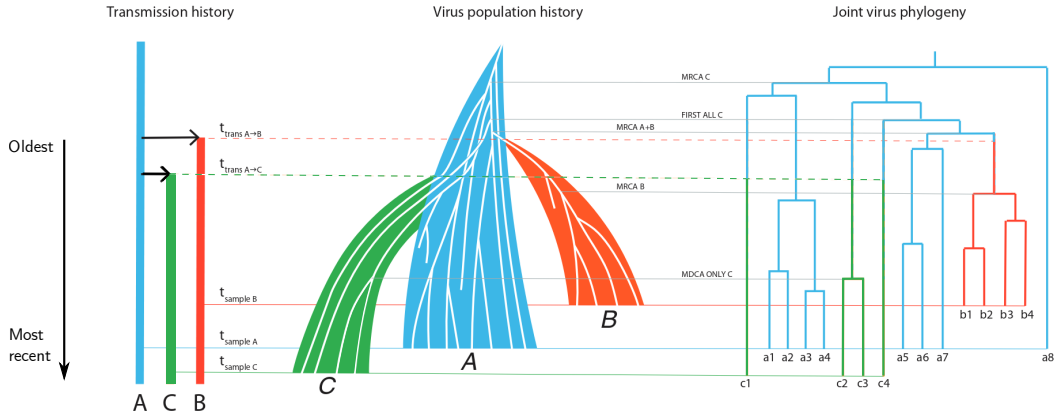


Why this project?

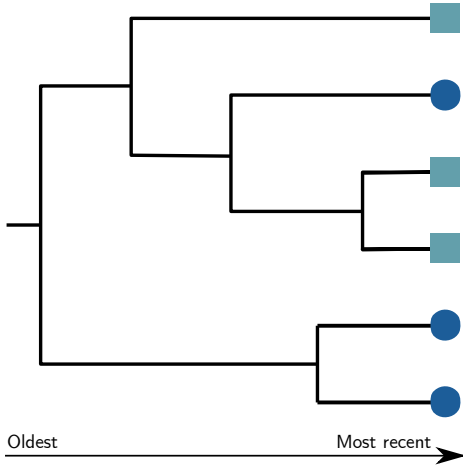


- * Prevalence of HIV
- * Transmission pairs
- * Using genetics to find transmission time

What can we expect to see?

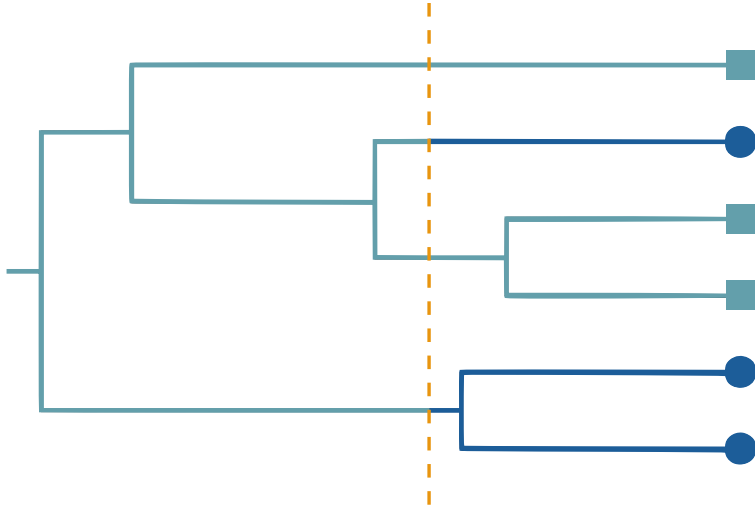


Inferring information from a tree

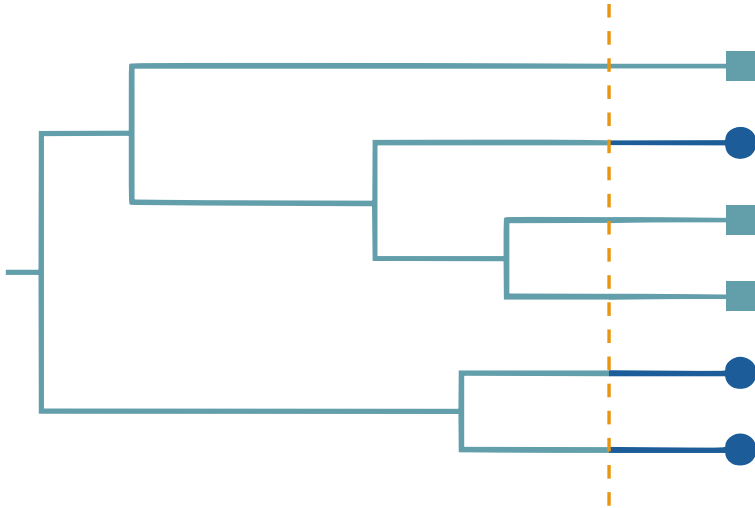


- * Tips represent individual viral sequences
- * Shows the evolutionary distance between individuals
- * What can we infer about a single transmission time?

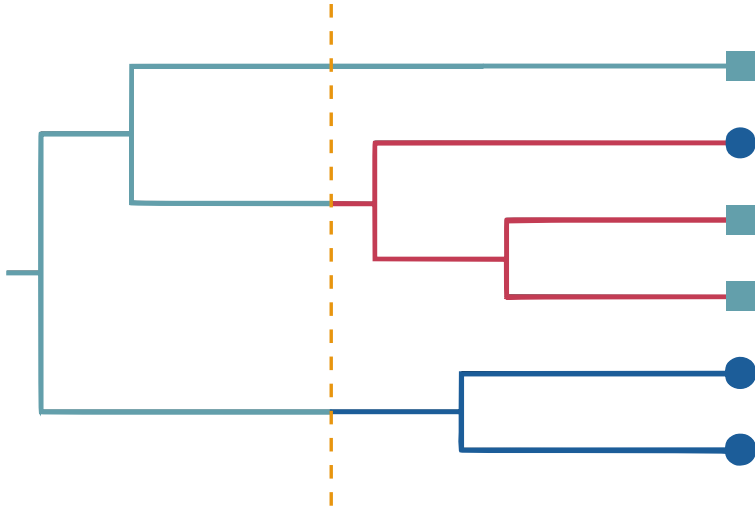
Inferring information from a tree



Inferring information from a tree



Inferring information from a tree



Coalescent modeling

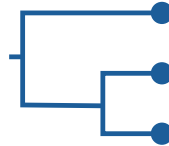
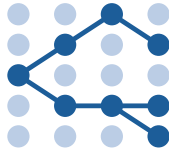
Node times as a function of population size



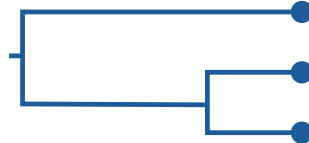
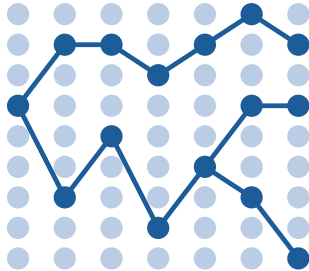
Relationship between population and samples

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

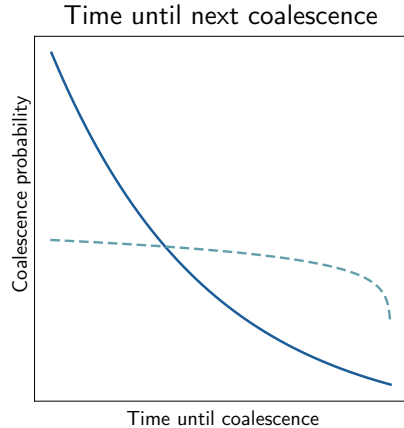
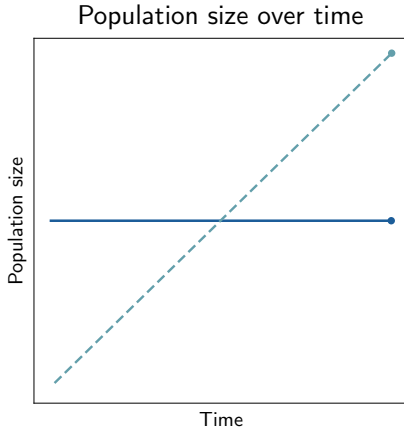
N = 5



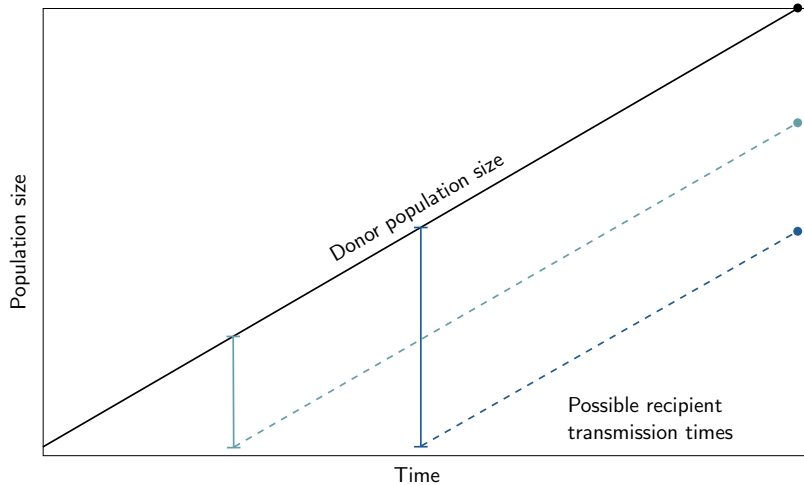
N = 9



Effect of changing population size



Predicting transmission time on a changing population



Results

What I did...

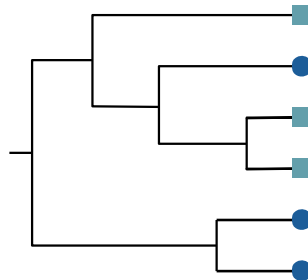
In this, I could show what's going on for my



Next steps: this summer

Extend my current work to trees with multiple hosts

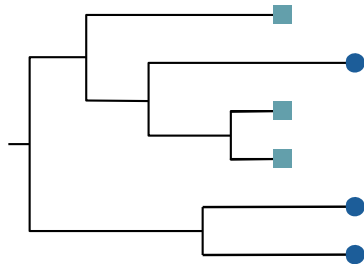
- * Split tree by host
- * Isolate hosts until a transmission occurs
- * Transmit a certain number of lineages



Next steps: this summer

Work with different sampling times for each host

- * Do not allow nodes that don't exist to coalesce
- * Add several nodes to the model when the second sample is taken



Next steps: future years

Next year (and later)...

