

Coalescent inference of HIV transmission history

Raymond Heil

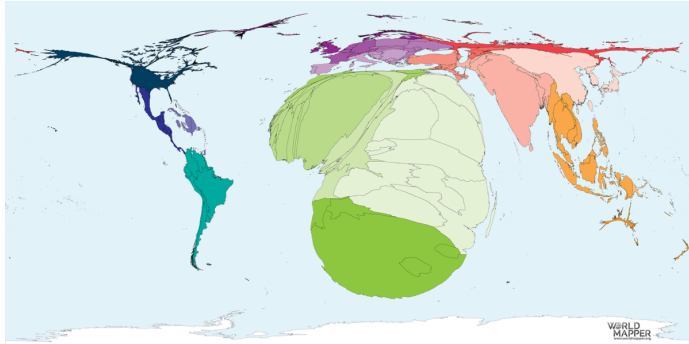
T-6: Theoretical Biology and Biophysics

Emma Goldberg, Thomas Leitner

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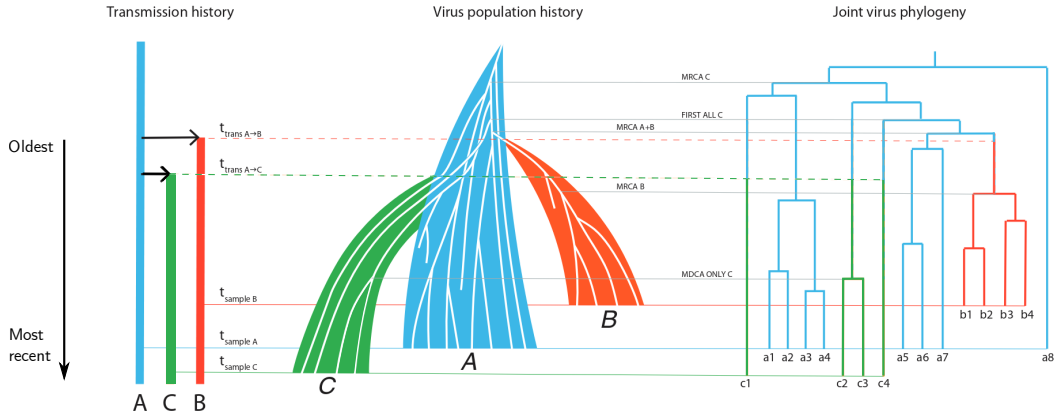


Why this project?

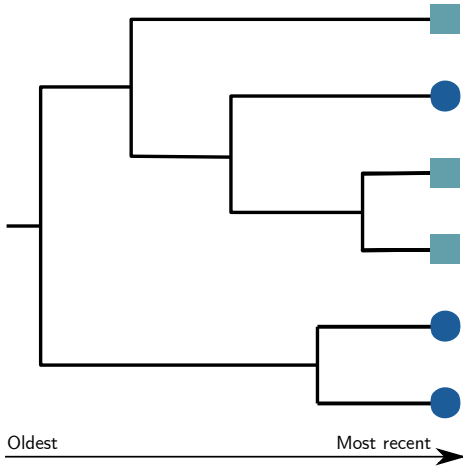


- * Prevalence of HIV
- * Transmission pairs
- * Using genetics to find transmission time

What can we expect to see?

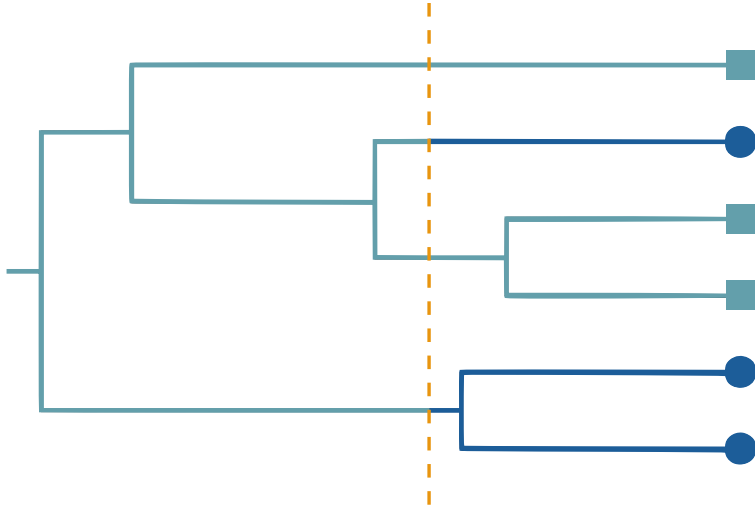


Inferring information from a tree

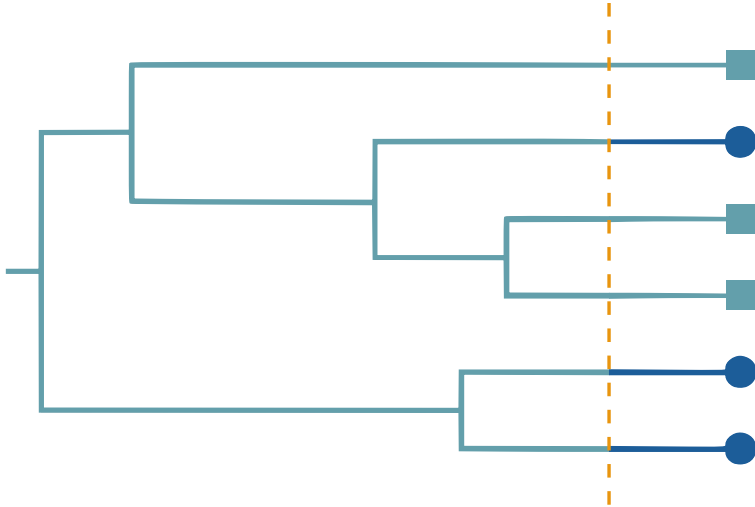


- * Tips represent individual viral sequences
- * Shows the evolutionary distance between individuals
- * What can we infer about a single transmission time?

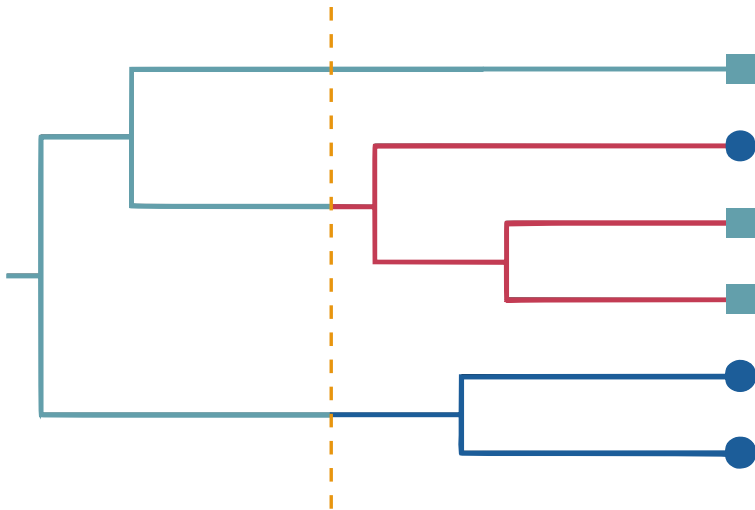
Inferring information from a tree



Inferring information from a tree



Inferring information from a tree



Coalescent modeling

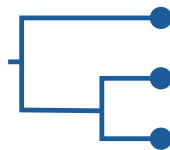
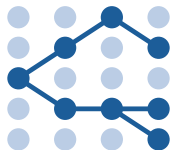
Node times as a function of population size



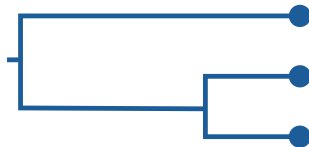
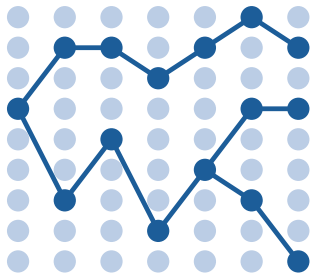
Relationship between population and samples

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

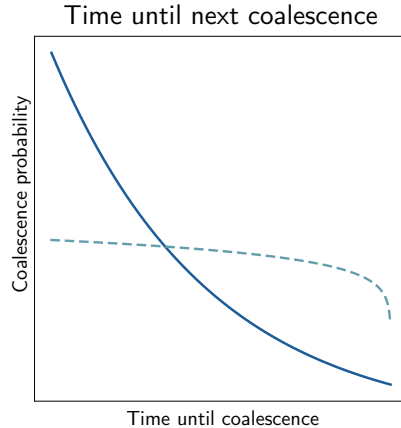
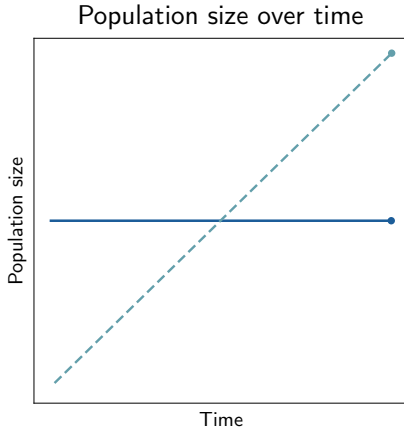
$N = 5$



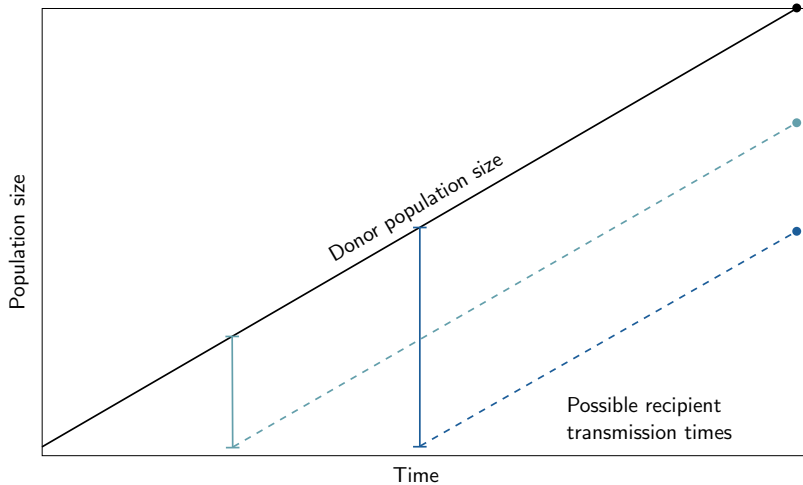
$N = 9$



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

In the coming weeks...

- * Getting linear population to...um, work.
- * What else was I even thinking about lol



Next steps

Next year (and later)...

