

Coalescent inference of HIV transmission history

Raymond Heil

T-6: Theoretical Biology and Biophysics

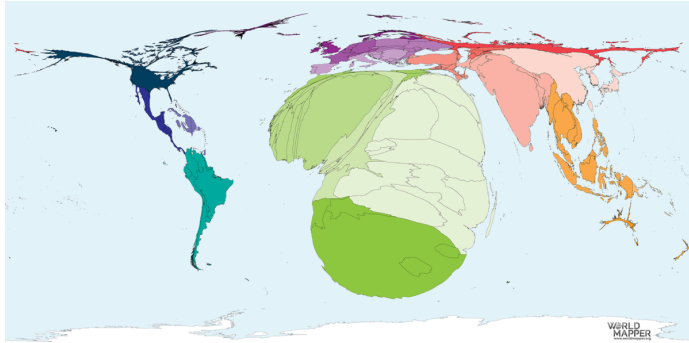
Mentors

Emma Goldberg, Thomas Leitner, Ethan Romero-Severson

20 July 2022

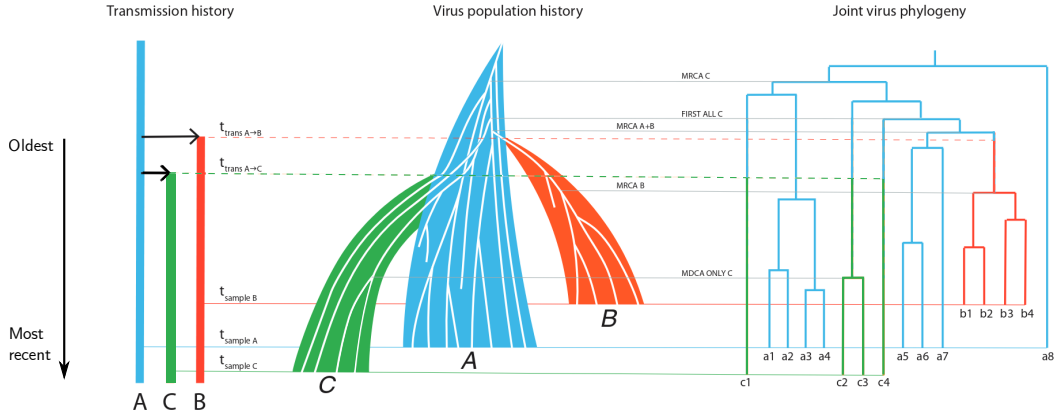


Why this project?

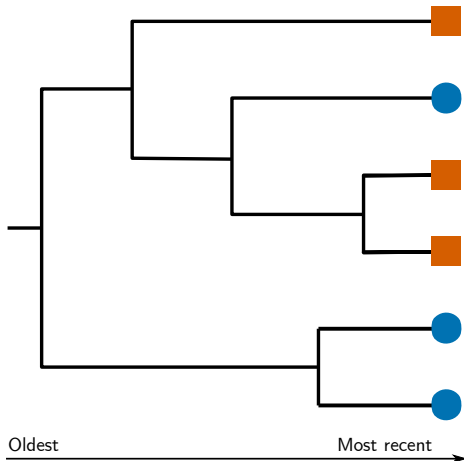


- * HIV is globally widespread
- * Despite effective therapy, it is still spreading
- * How can we understand the way it spreads?

Setting up the problem

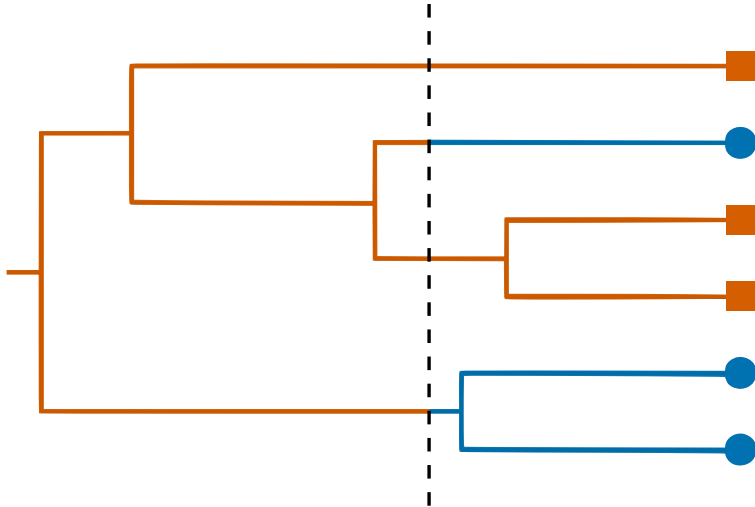


Inferring information from a tree

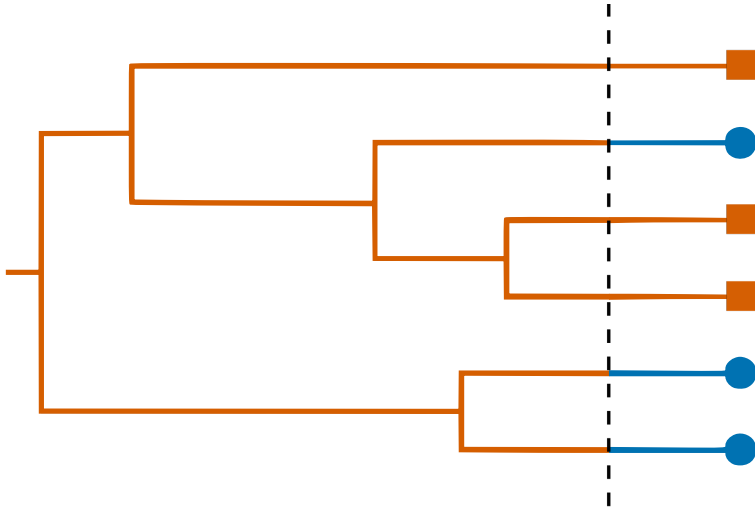


- * Tree tips represent **individual viral sequences**
- * Three samples from each individual
- * If one infected the other, when?

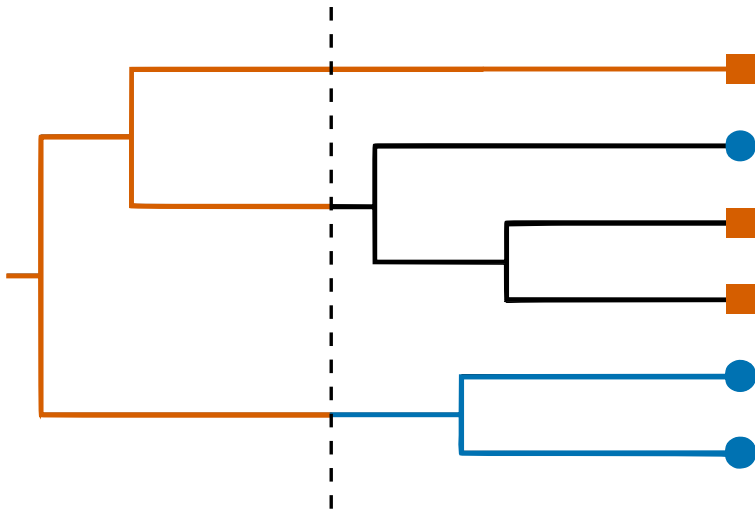
Inferring information from a tree



Inferring information from a tree



Inferring information from a tree

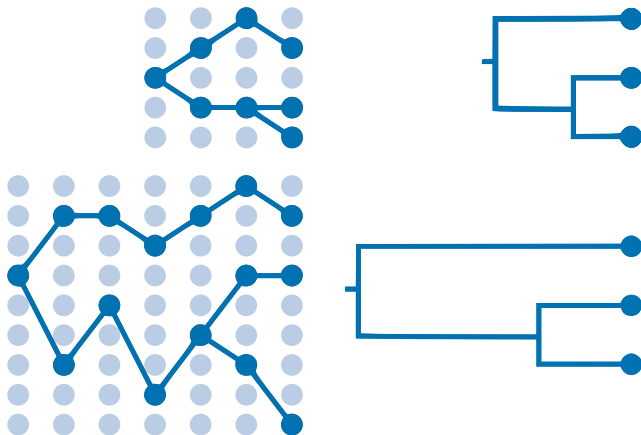


Coalescent theory

Node times as a function of population size

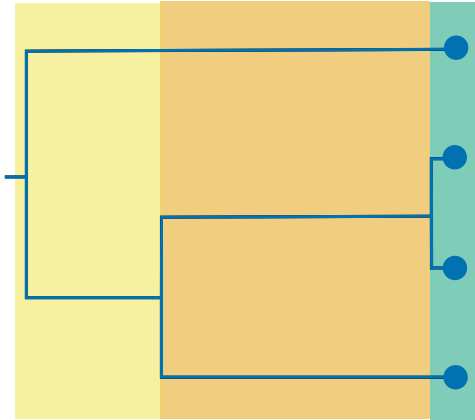
Relationship between population and samples

Larger effective population results in longer expected coalescence times

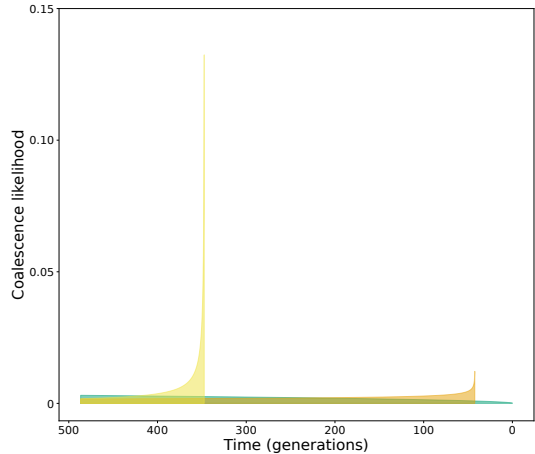


Finding the likelihood of a whole tree

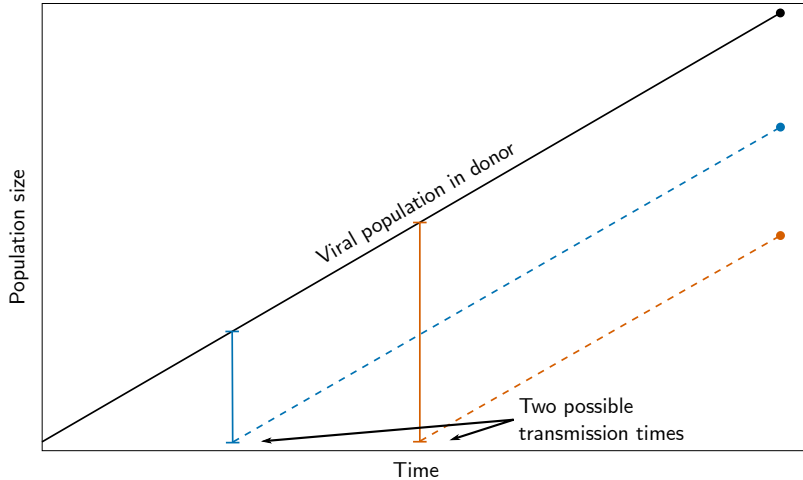
Divide tree into segments
where coalescences occur



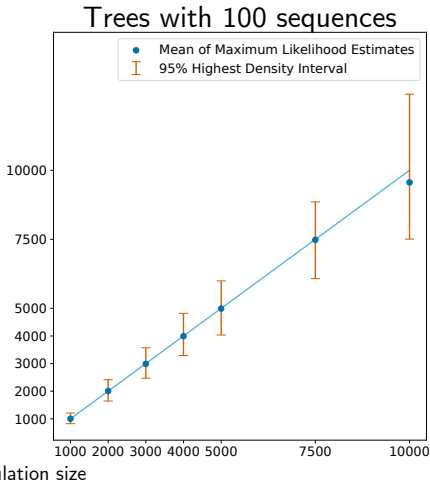
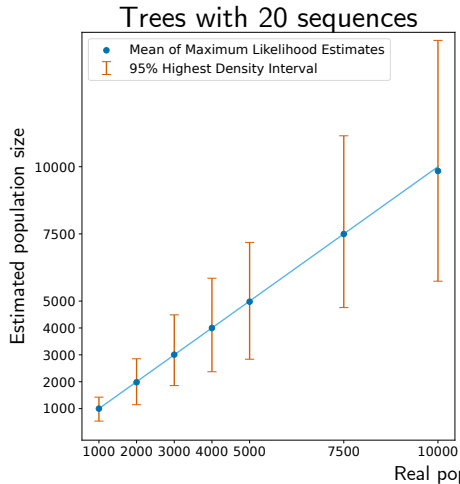
Each segment contributes
to the likelihood of the tree



Predicting transmission time on a changing population

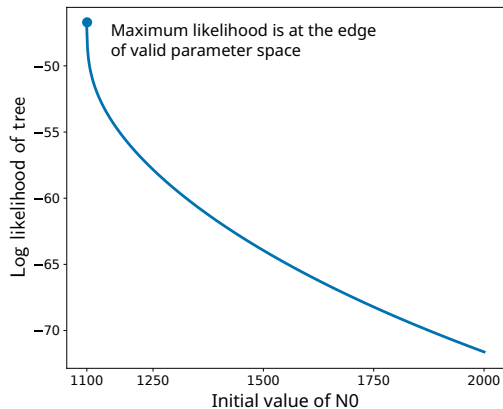


Results: Single host with constant population

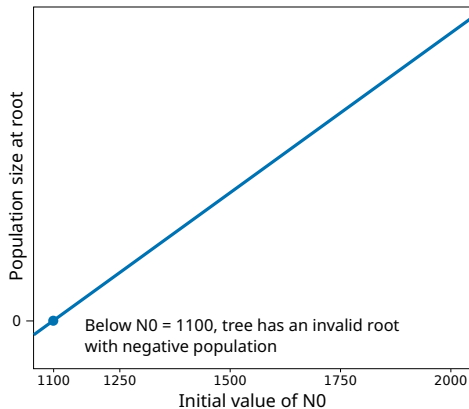


Current progress on linear populations

Likelihood of N_0 values with fixed B



Population dynamics that may cause this



Current progress on trees with multiple hosts

Hello, world!

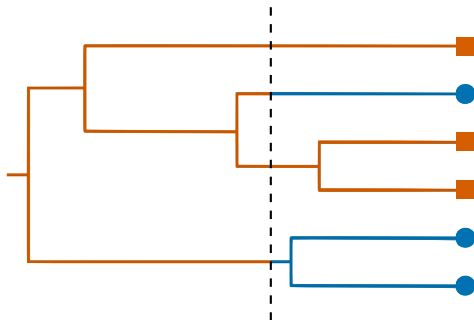


Next steps: Two hosts with linear population

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!

