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
* Supplementing existing tracing methods
  - Interviews
  - Contact tracing
* Finding signal in genome sequences

Just a test for now.
Some sort of image...of HIV? Just to keep them from getting too bored on the FIRST slide.

Looking for a signal in trees

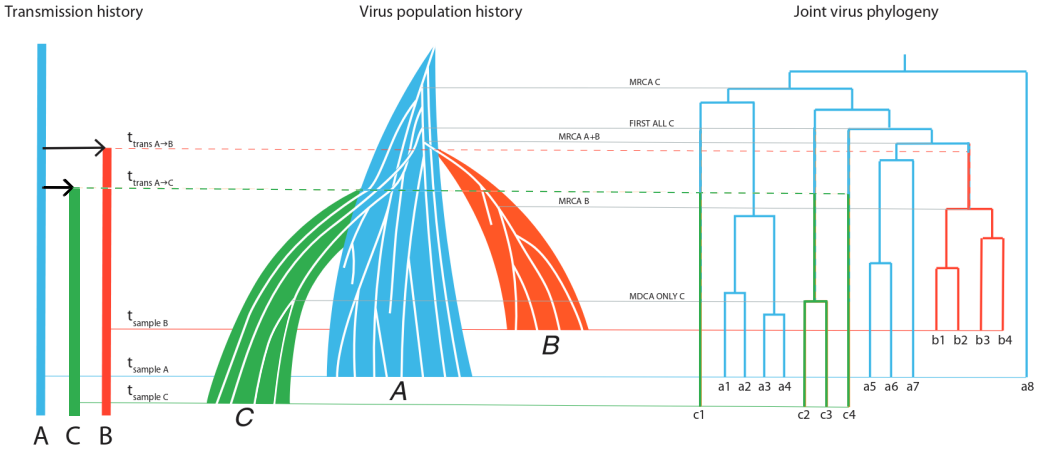
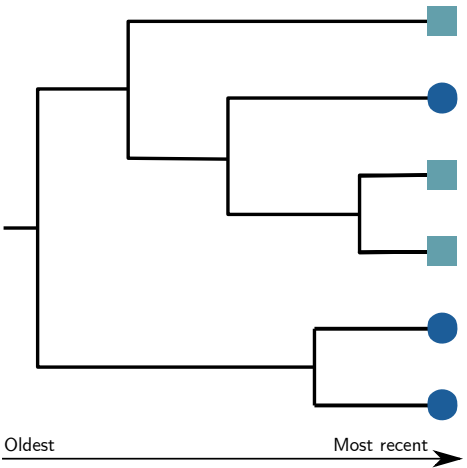


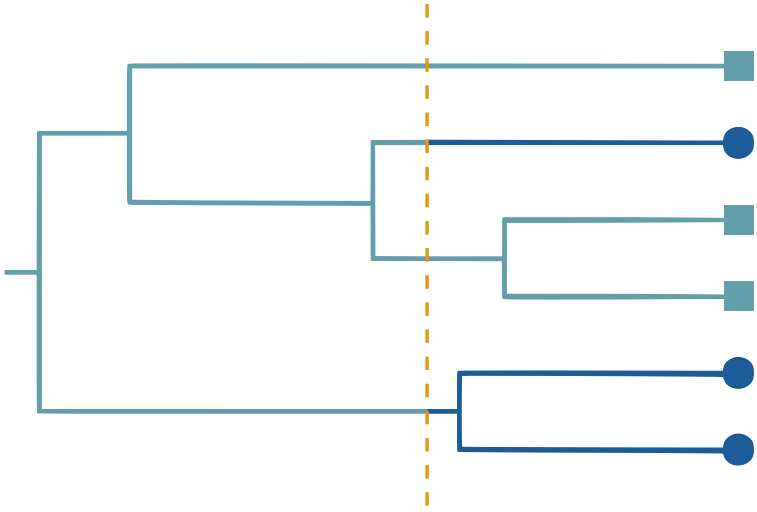
Image: Leitner et al. GET FULL CITATION

Inferring information from a tree

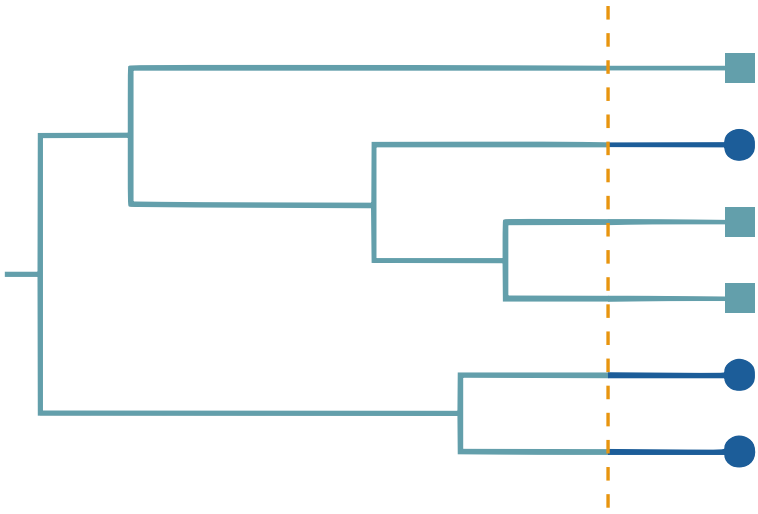


- Tips represent individual viral sequences
- Shows the evolutionary distance between individuals
- What can we infer about a single transmission time?

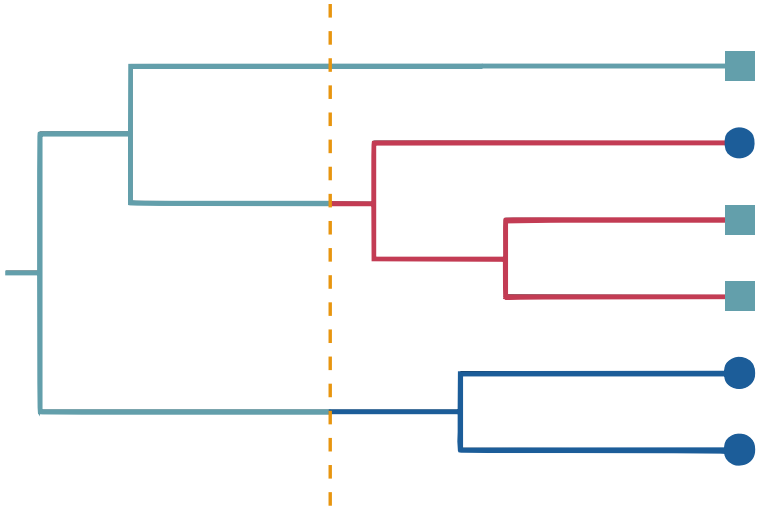
Inferring information from a tree



Inferring information from a tree



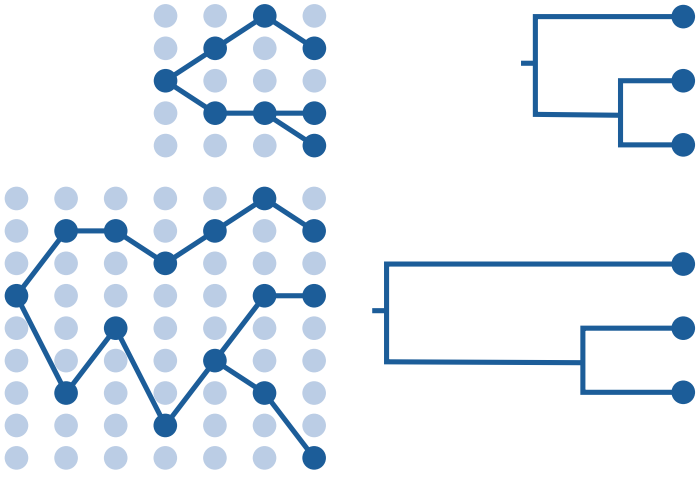
Inferring information from a tree



Coalescent modeling:
Node times as a function of population

Relationship between population and samples

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



Effect of changing population size

This is where I'd have these sort of things:
The comparison between the coalescence PDF of a constant model and of a linear model with some meaningful b
Maybe also a comparison between the kind of trees that we'd see? A cartoon of them?
Should I also show what an exponential population does? Maybe just as an example, and explain that HIV most closely follows a linear model (according to some citation)

Predicting transmission time on a changing population

This is where I wanna have my graph showing what happens with different possible transmission times. I'd connect this back to what we saw happening on the previous slide with coalescence happening more often at the early stages of infection when population size is relatively small.

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)...