

# Coalescent inference of HIV transmission history

Raymond Heil

T-6: Theoretical Biology and Biophysics

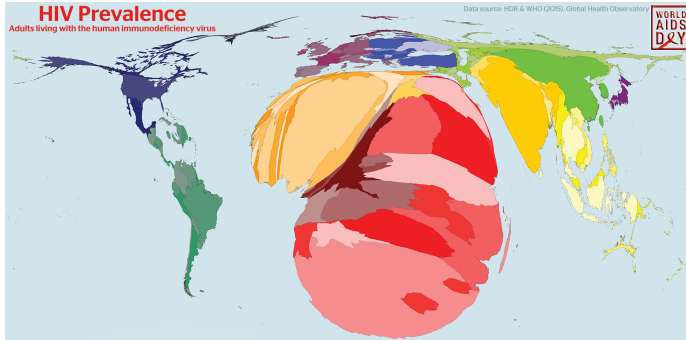
Emma Goldberg, Thomas Leitner

20 July 2022



## Why this project?

- \* Supplementing existing tracing methods
  - o Interviews
  - o Tracing contact pairs
- \* Finding signal in genome sequences

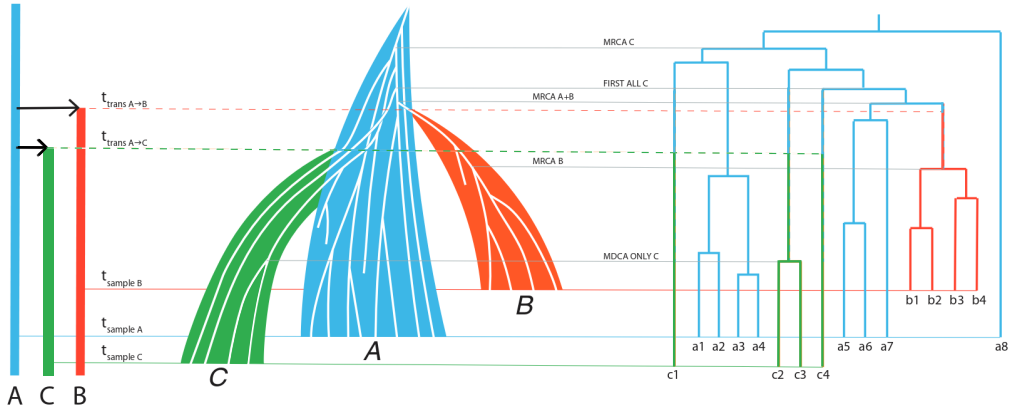


# What are we looking for?

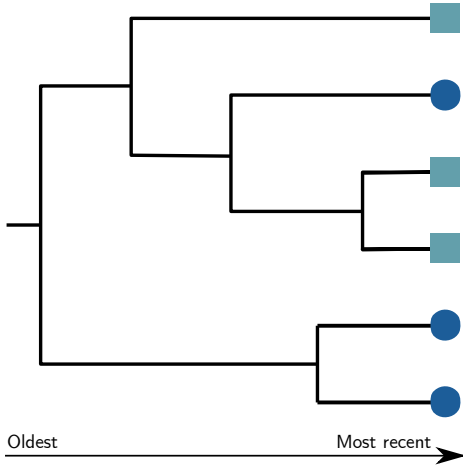
Transmission history

Virus population history

Joint virus phylogeny

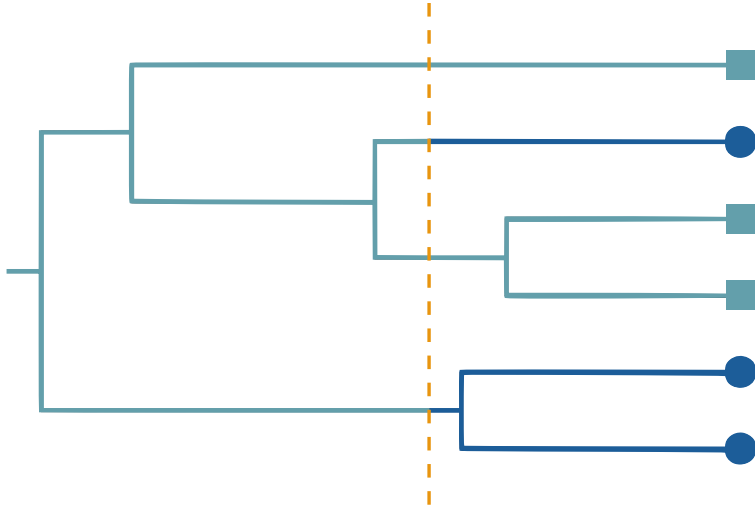


## Inferring information from a tree

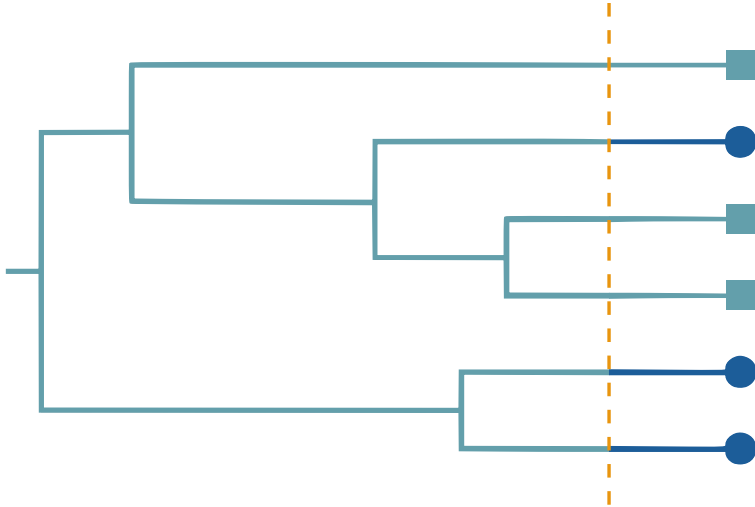


- \* Tips represent individual viral sequences
- \* Shows the evolutionary distance between individuals
- \* What can we infer about a single transmission time?

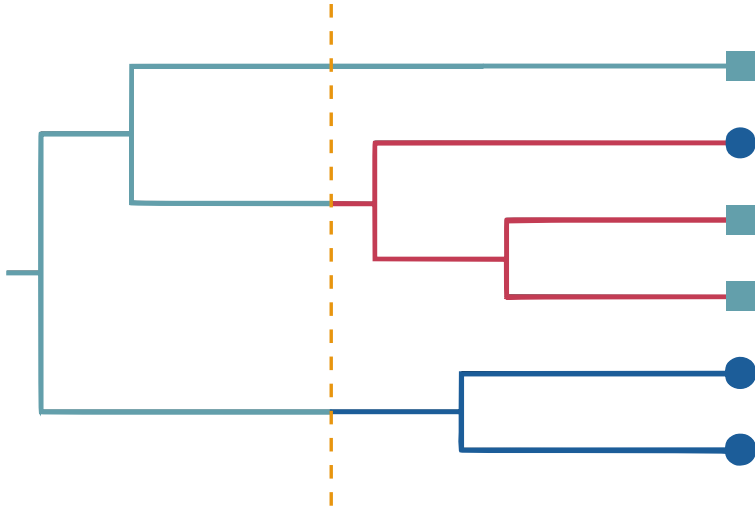
## Inferring information from a tree



## Inferring information from a tree



## Inferring information from a tree



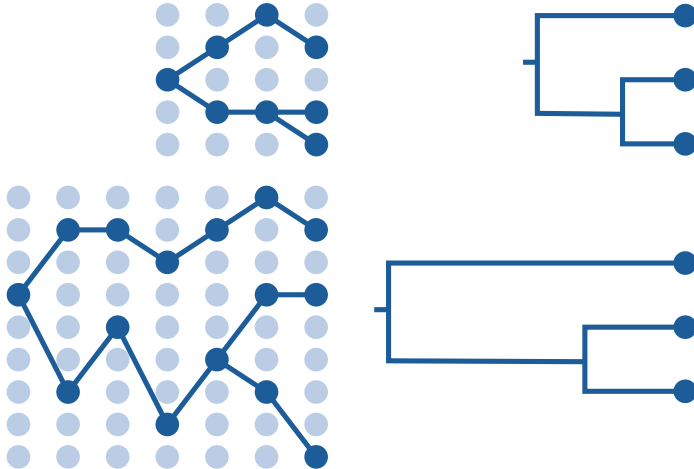
# **Coalescent modeling:**

## Node times as a function of population

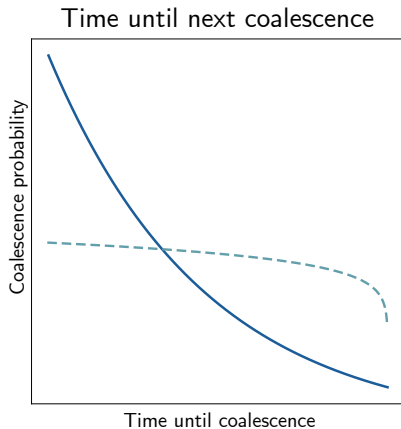
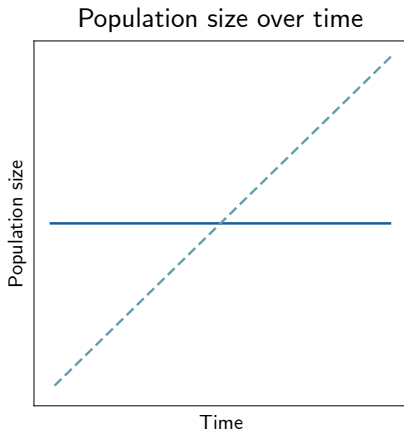


## Relationship between population and samples

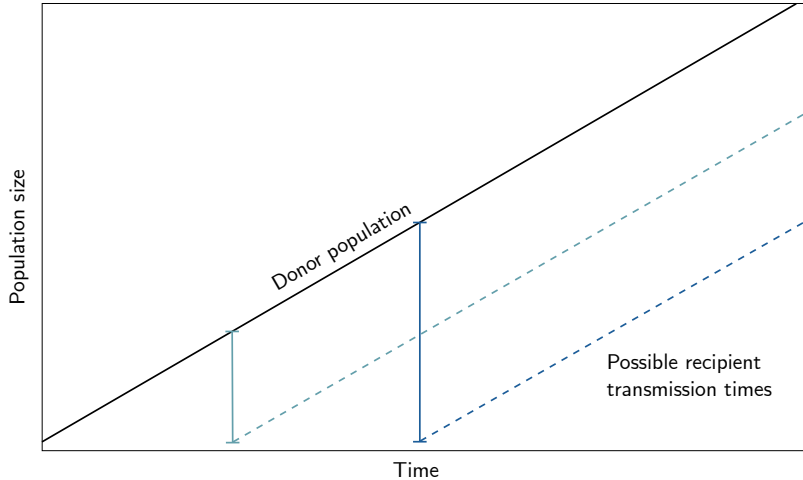
Large N causes node times to be further apart, stretching the tree



## Effect of changing population size



## 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)...

