

Coalescent inference of HIV transmission history

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T-6: Theoretical Biology and Biophysics

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Why this project?

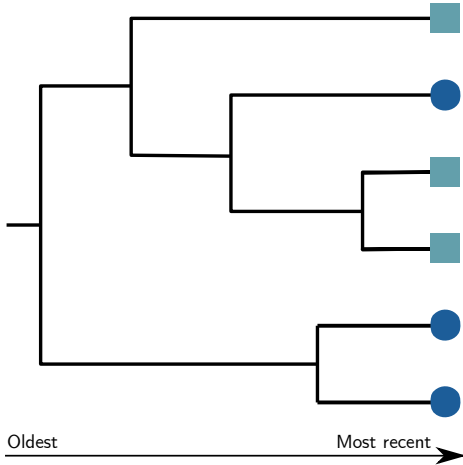
Wowie!

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

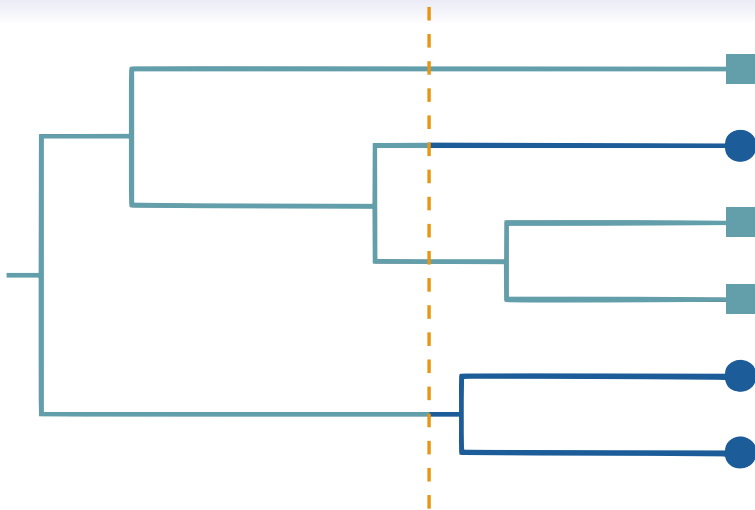
This text sure
does exist...

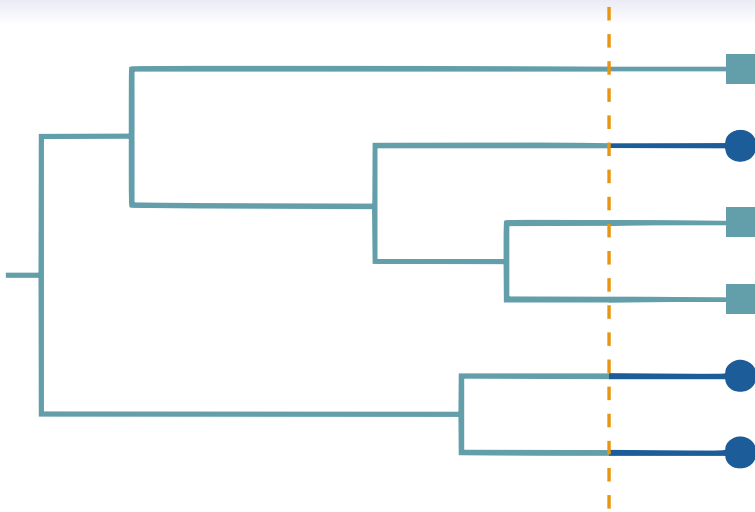


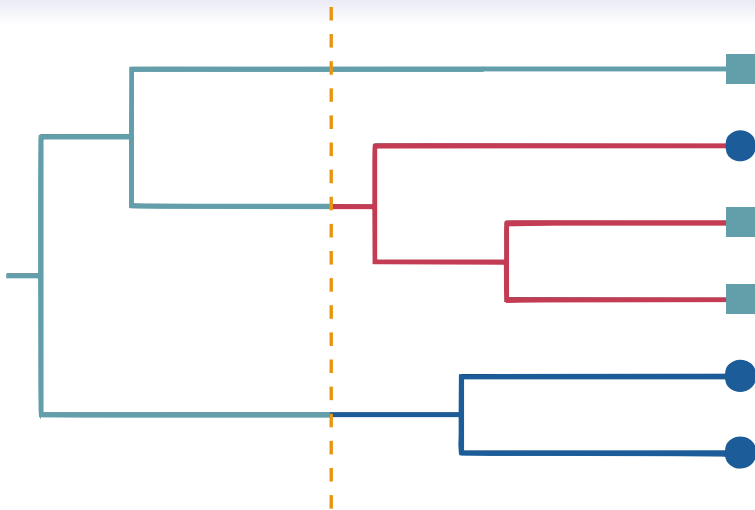
Inferring information from a tree



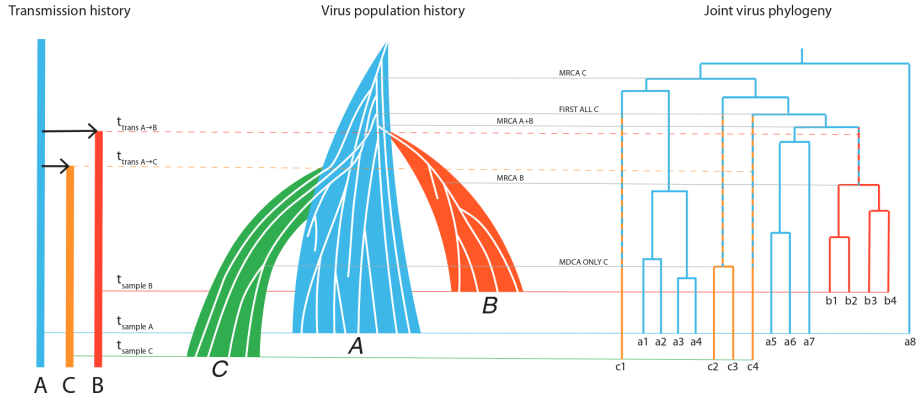
- * Tips represent individual viral sequences
- * Shows the evolutionary distance between individuals
- * What can we infer about a single transmission time?





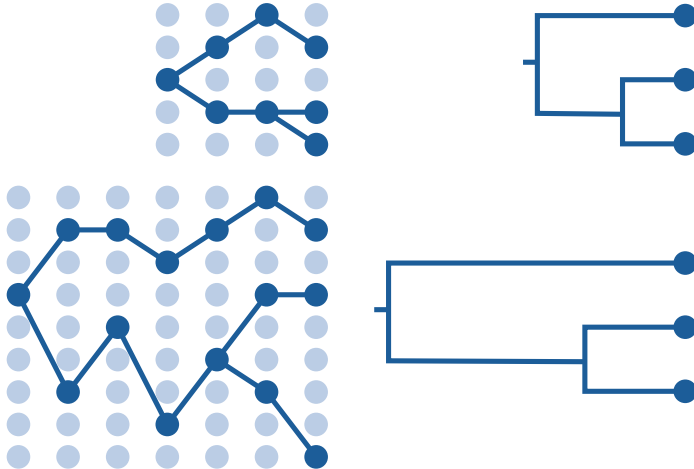


Linear population growth (IDK where this should go)



Coalescent modeling

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



Coalescent modeling

Main findings:

- * First
- * Second



Coalescent modeling

Need a good example of text on here...

Predictions on a changing population

This is where I plan to put my stuff about expanding everything up to a linear model, and how it should allow us to make inferences based on how the times are changing.



Results

What I did...



Conclusion

Parting thoughts...

