

# 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?

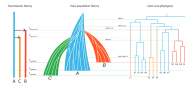
Wowie!

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

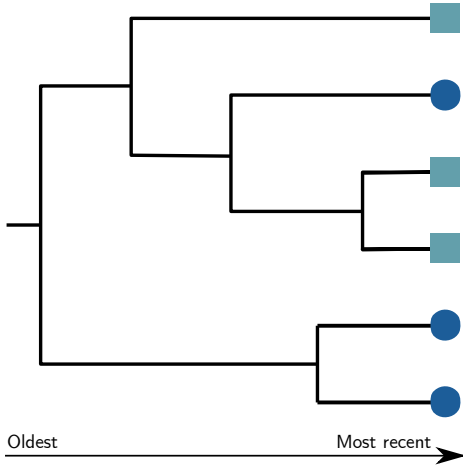
This text sure  
does exist...



# How can we know what we're looking for?

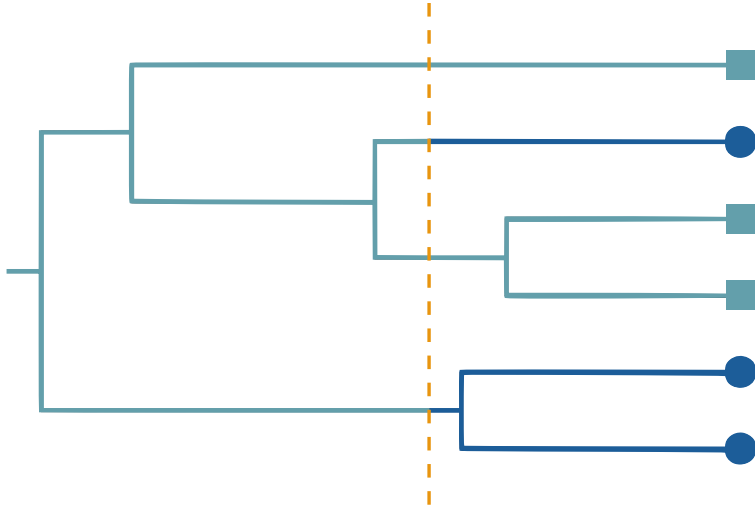


## Inferring information from a tree

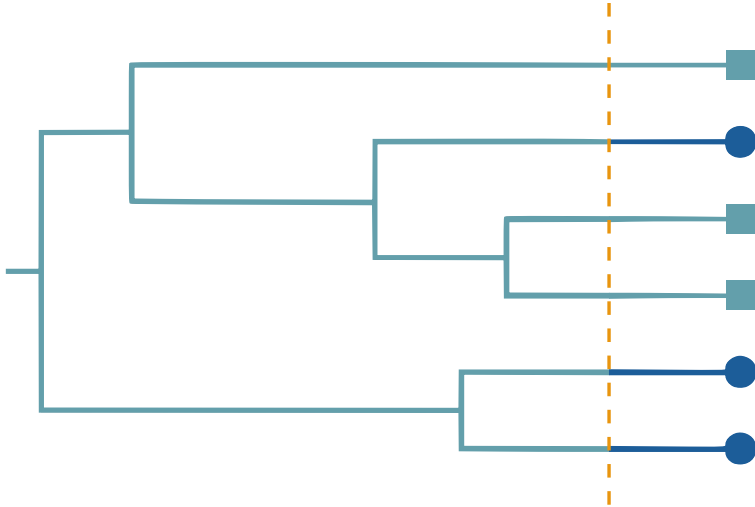


- \* Tips represent individual viral sequences
- \* Shows the evolutionary distance between individuals
- \* What can we infer about a single transmission time?

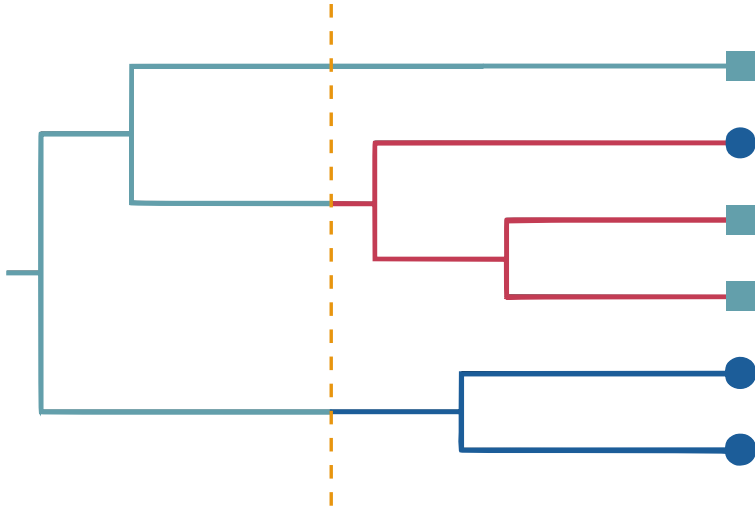
## Inferring information from a tree



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## Inferring information from a tree



# Coalescent modeling

Node times as a function of population

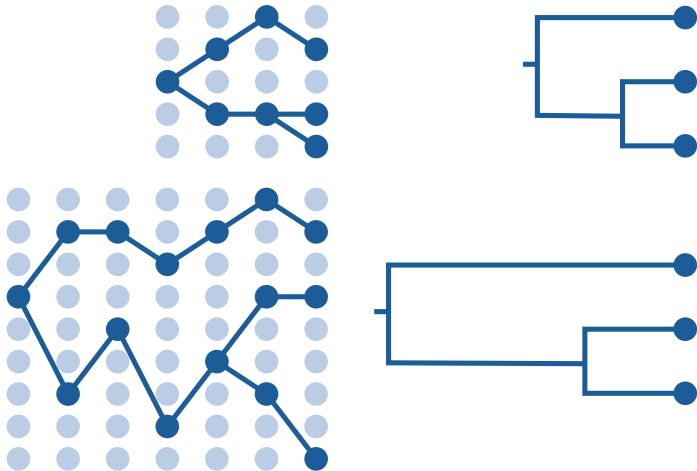
- \* Constant, linear, and exponential population change
- \* Neutral evolution





## 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...

