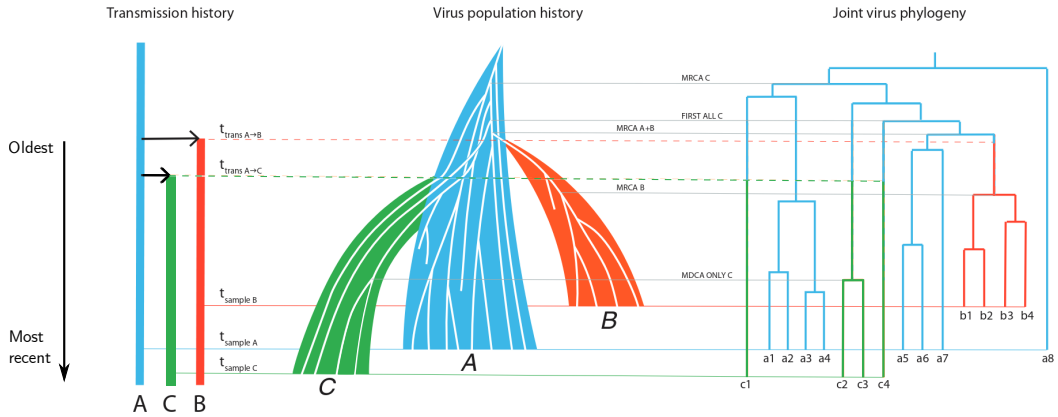
My goal this summer

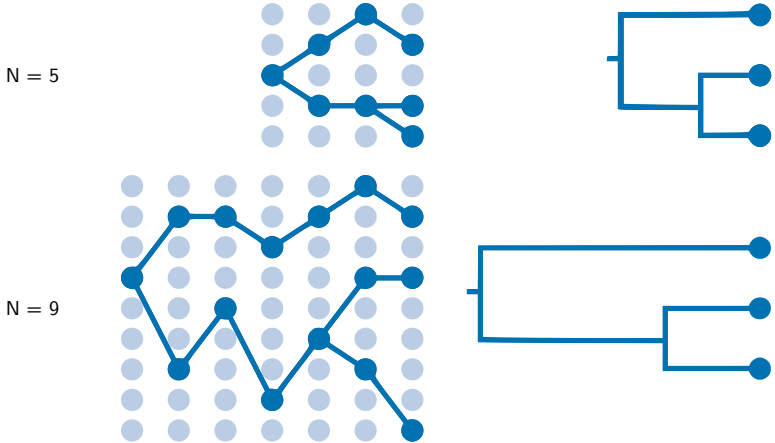


Work from a phylogeny to the original transmission history

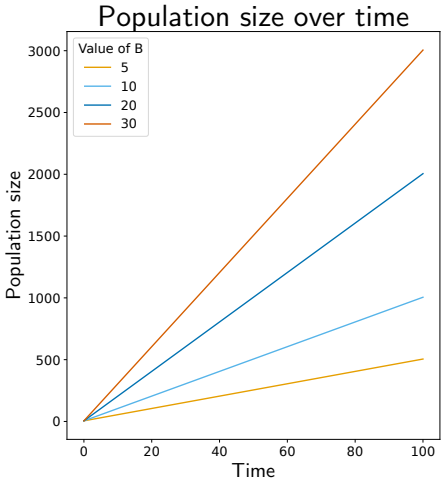
Modified from Leitner et al., Curr. Opin. HIV AIDS (2019)

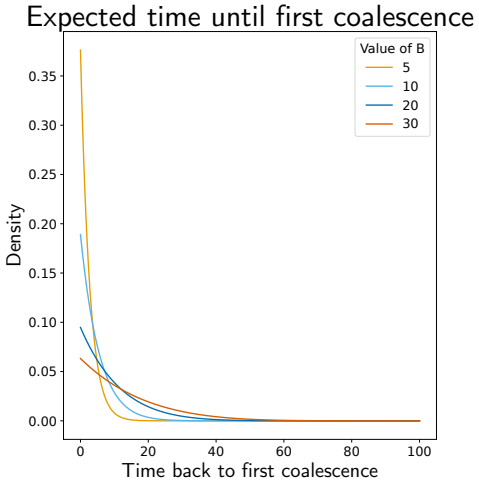
Coalescent modeling

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

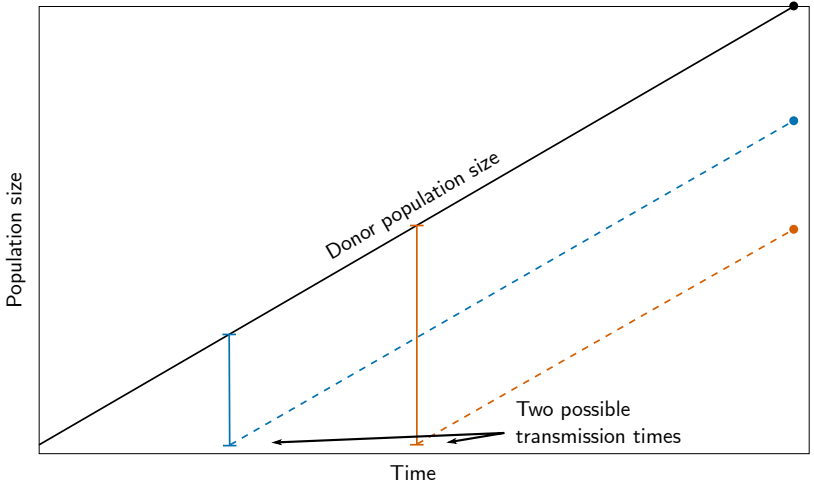


Time until first coalescence with arbitrary B

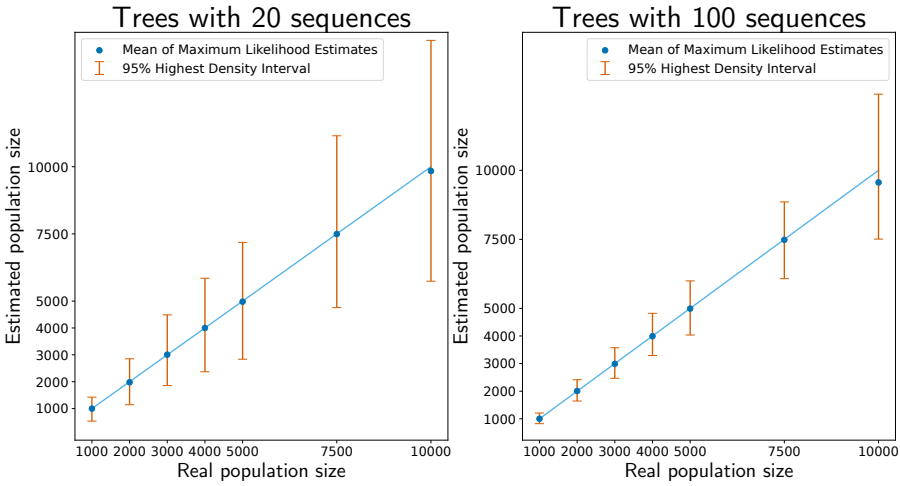




Expected signal for transmission time with two hosts

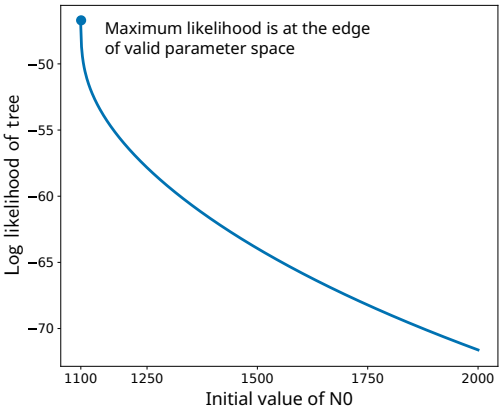


My results so far: Constant population size, single host

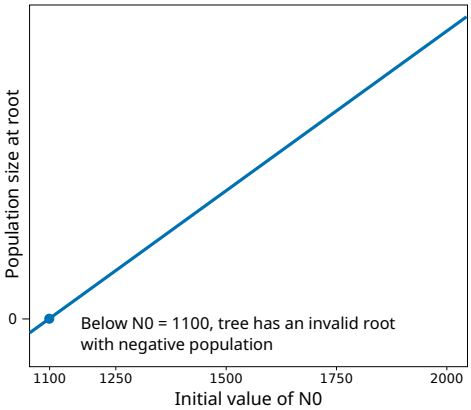


My current progress on linear populations

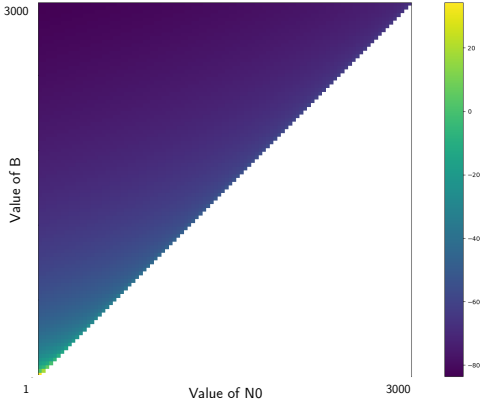
Likelihood of N0 values with fixed B

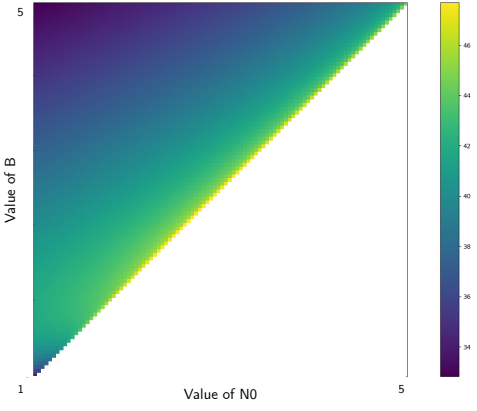


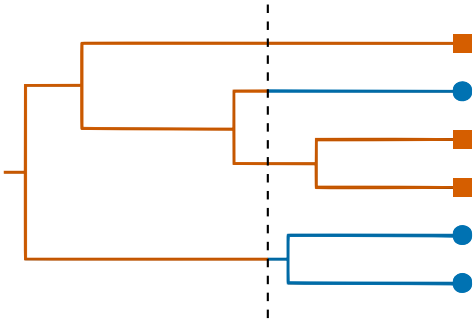
Population dynamics that may cause this



Attempting a grid search revealed scaling mistakes with B





Next steps: Moving towards two hosts and linear population

- Look into incorrect population growth scaling across the project
- Instead of a grid search, explore more serious optimization methods
- Expand to a two-host problem so I can examine transmission time
  - Split tree by host
  - Isolate hosts until a transmission occurs