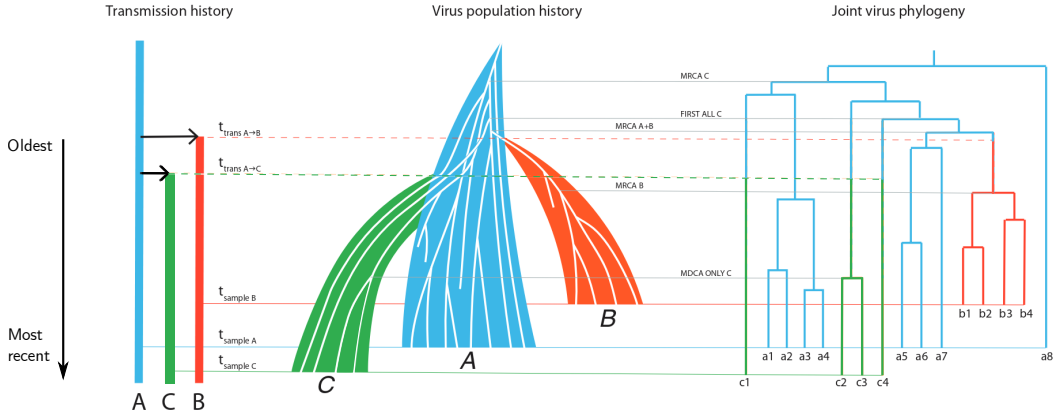


My goal this summer

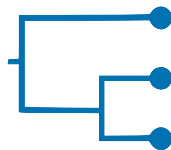
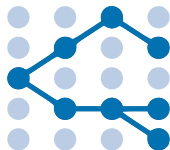


Work from a phylogeny to the original transmission history

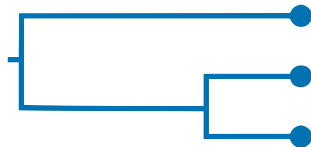
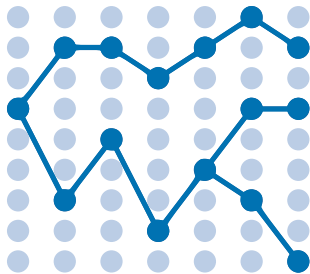
Coalescent modeling

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

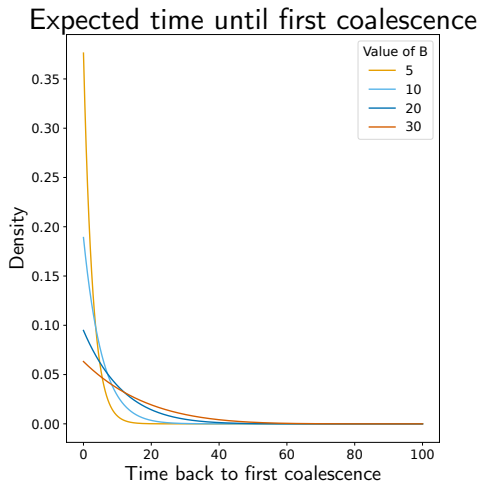
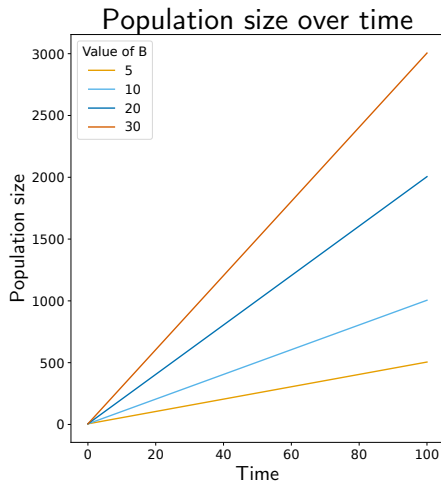
$N = 5$



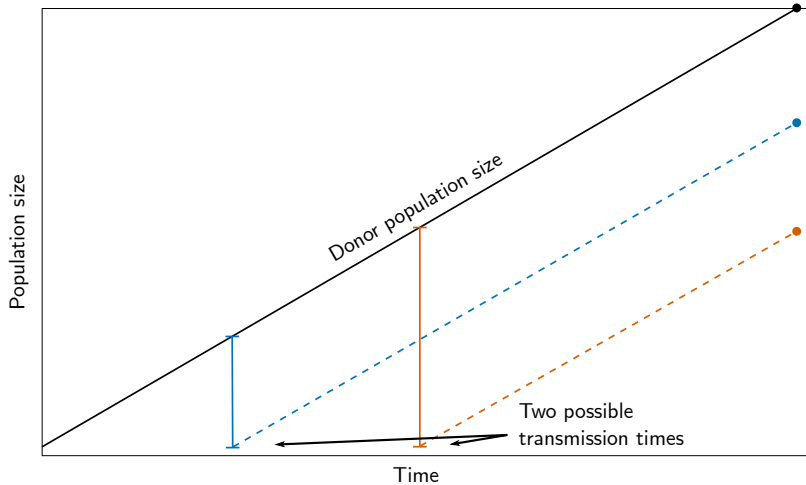
$N = 9$



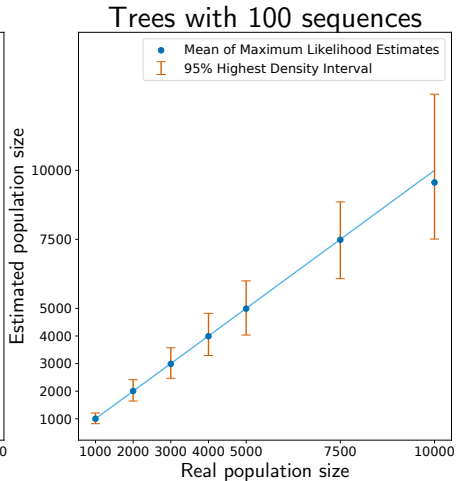
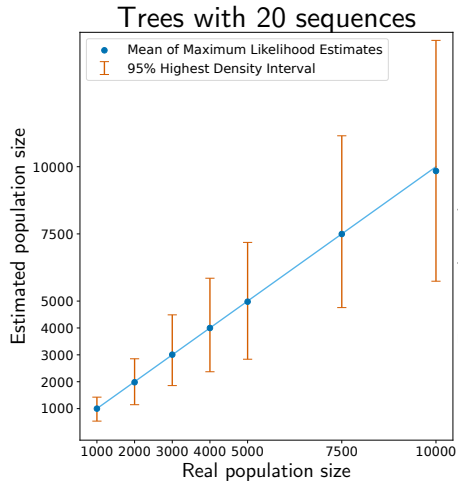
Time until first coalescence with arbitrary B



Expected signal for transmission time with two hosts

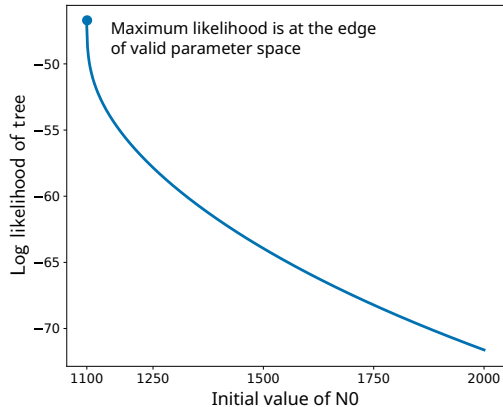


My results so far: Constant population size, single host

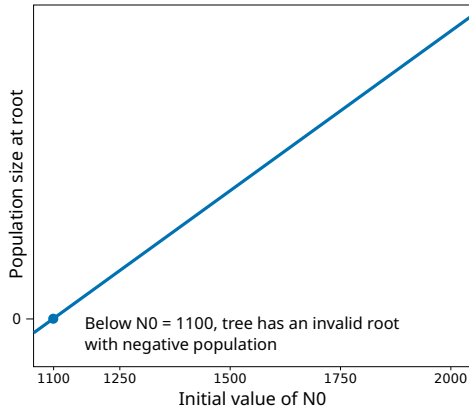


My current progress on linear populations

Likelihood of N_0 values with fixed B



Population dynamics that may cause this



Attempting a grid search revealed scaling mistakes with B

I have the high ground, bananakin!

I can't add this image now because I can't properly git pull, so it will need to be last minute tomorrow morning.



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

