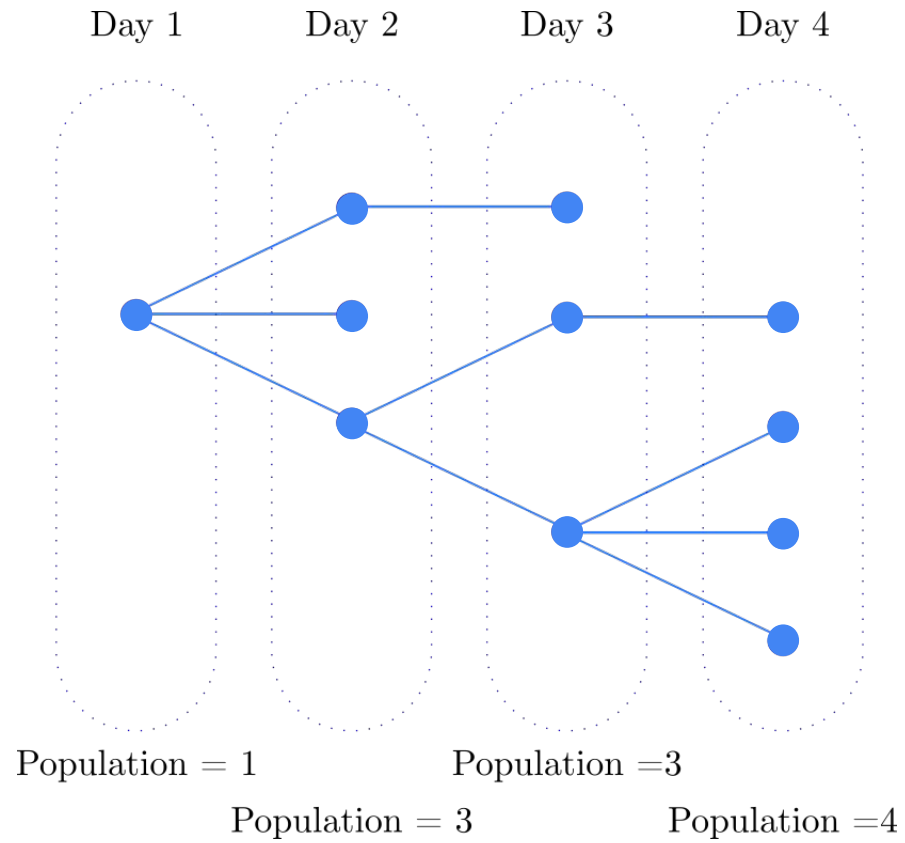
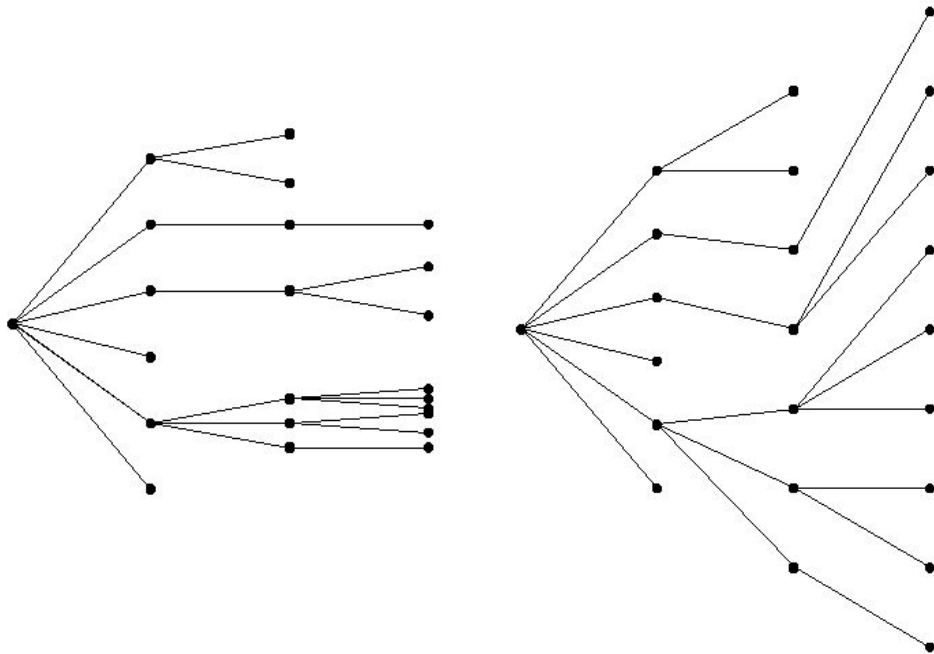


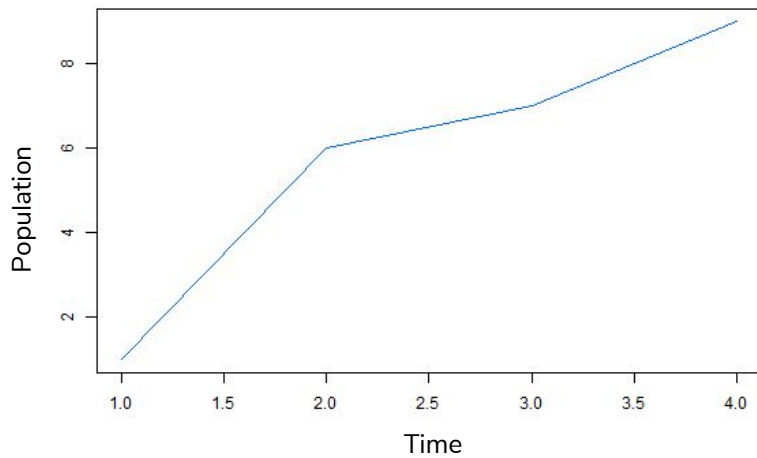
Simulating Branching Processes in R

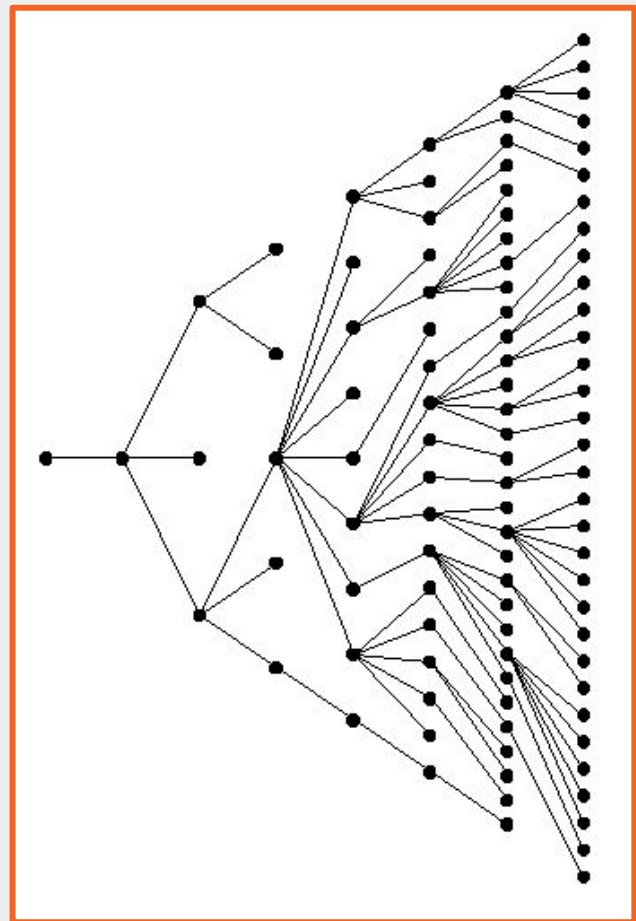
Alice Hankin - Summer Research Scholarship 2020/21



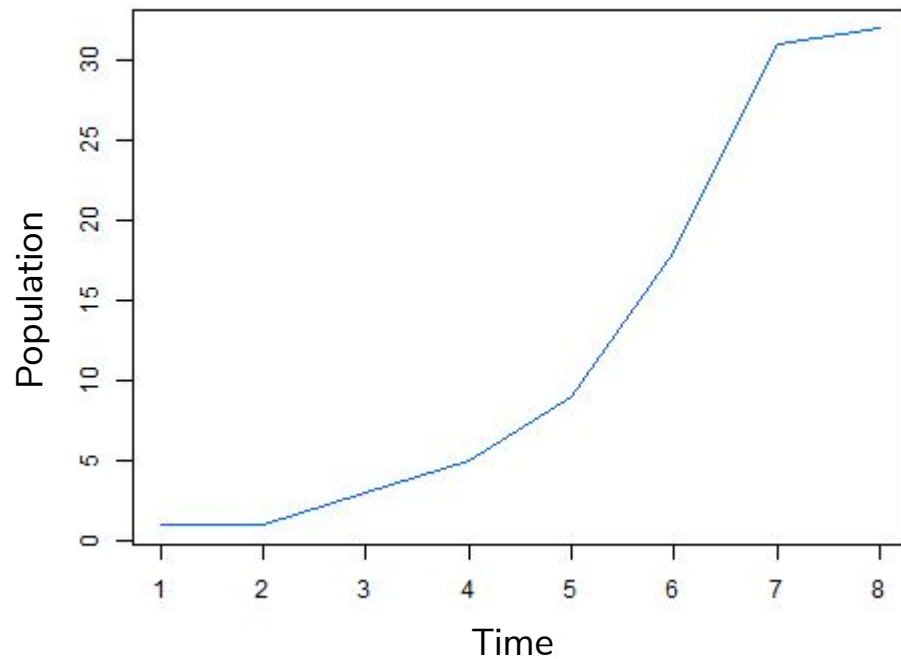


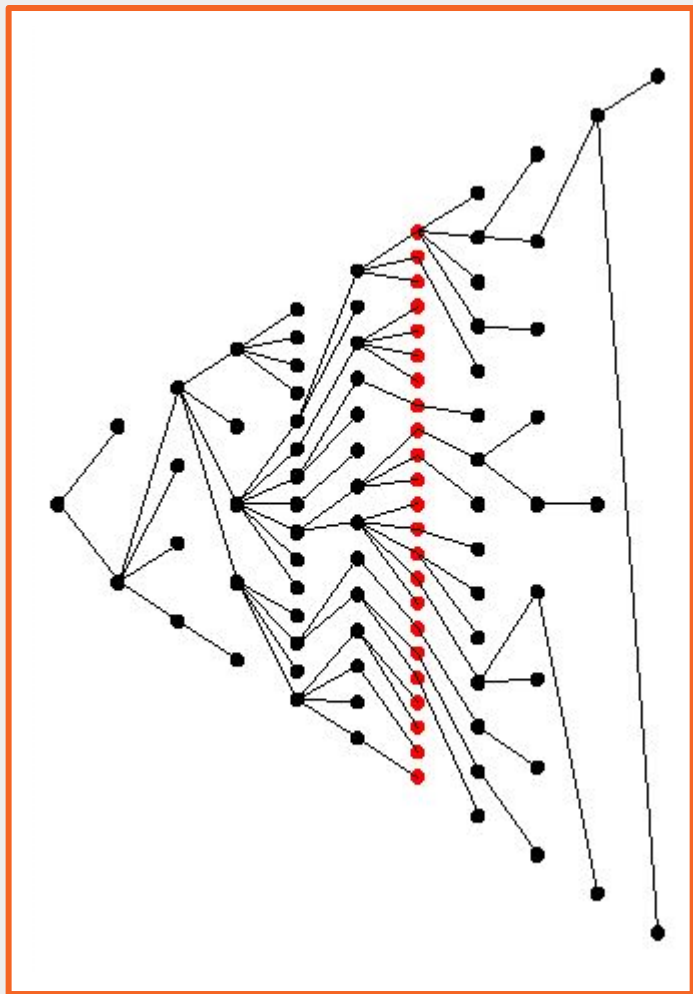
Offspring distribution has a geometric distribution with a **mean of 1.5**





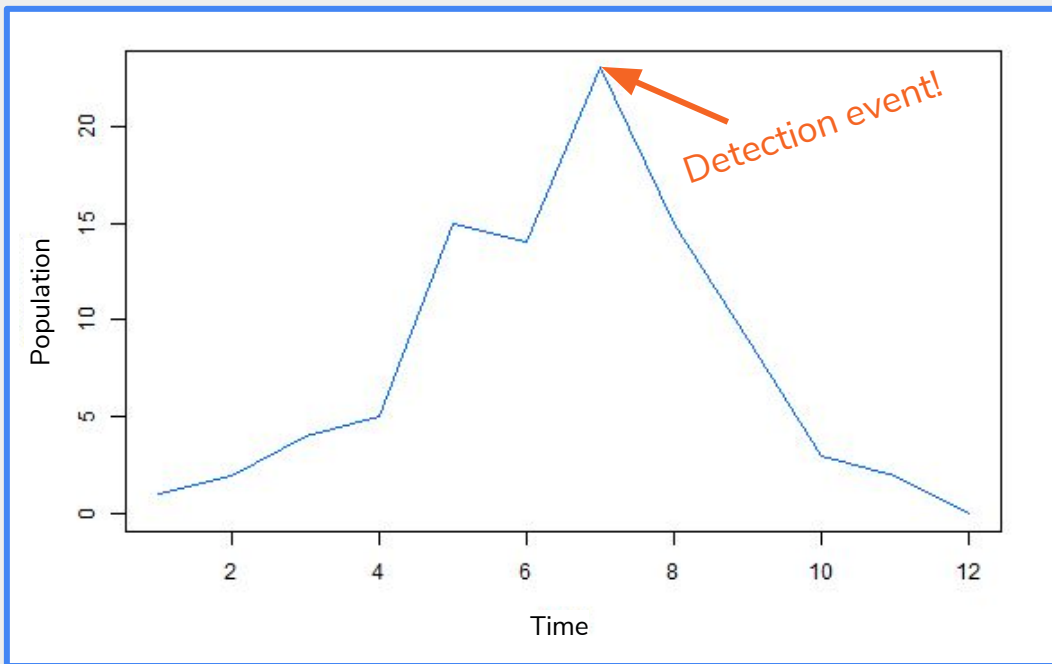
Offspring distribution \sim geometric with
a mean of 1.5

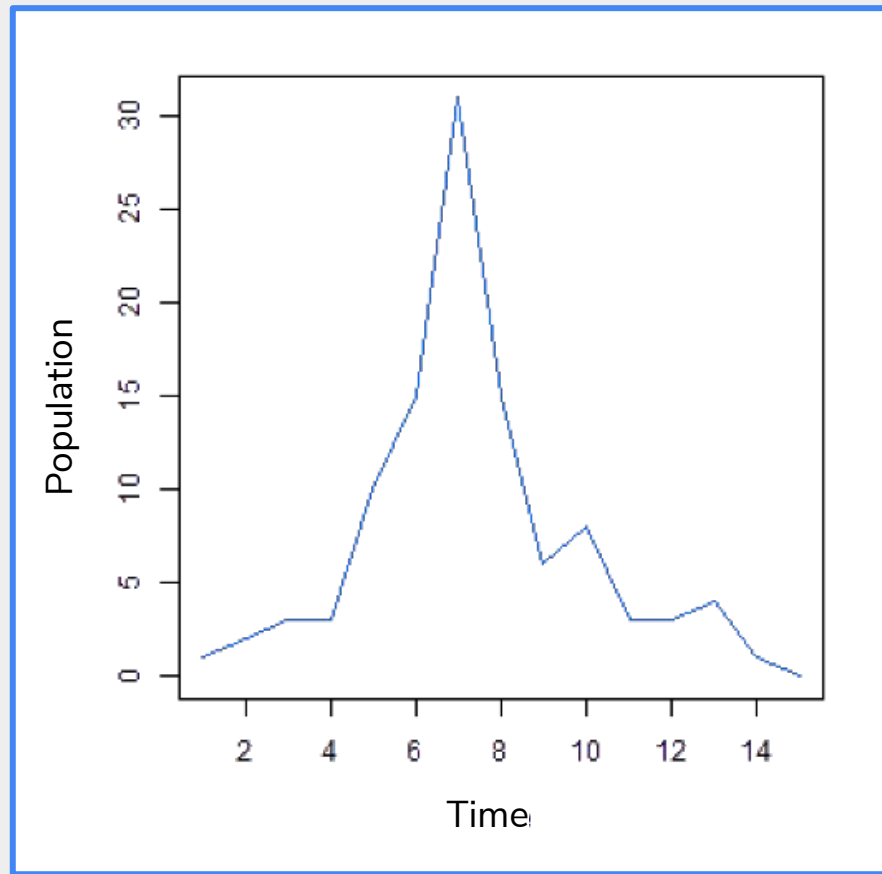
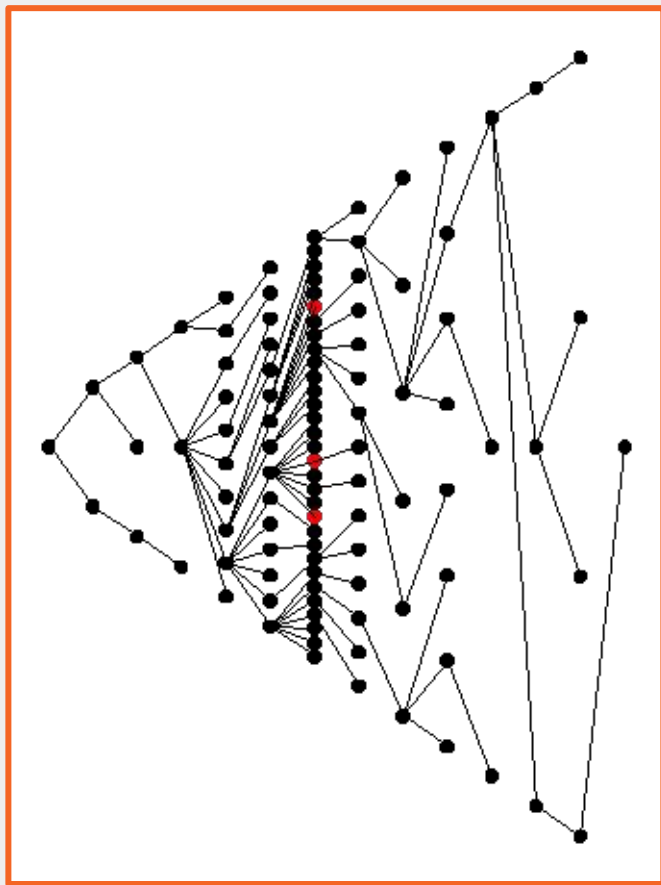




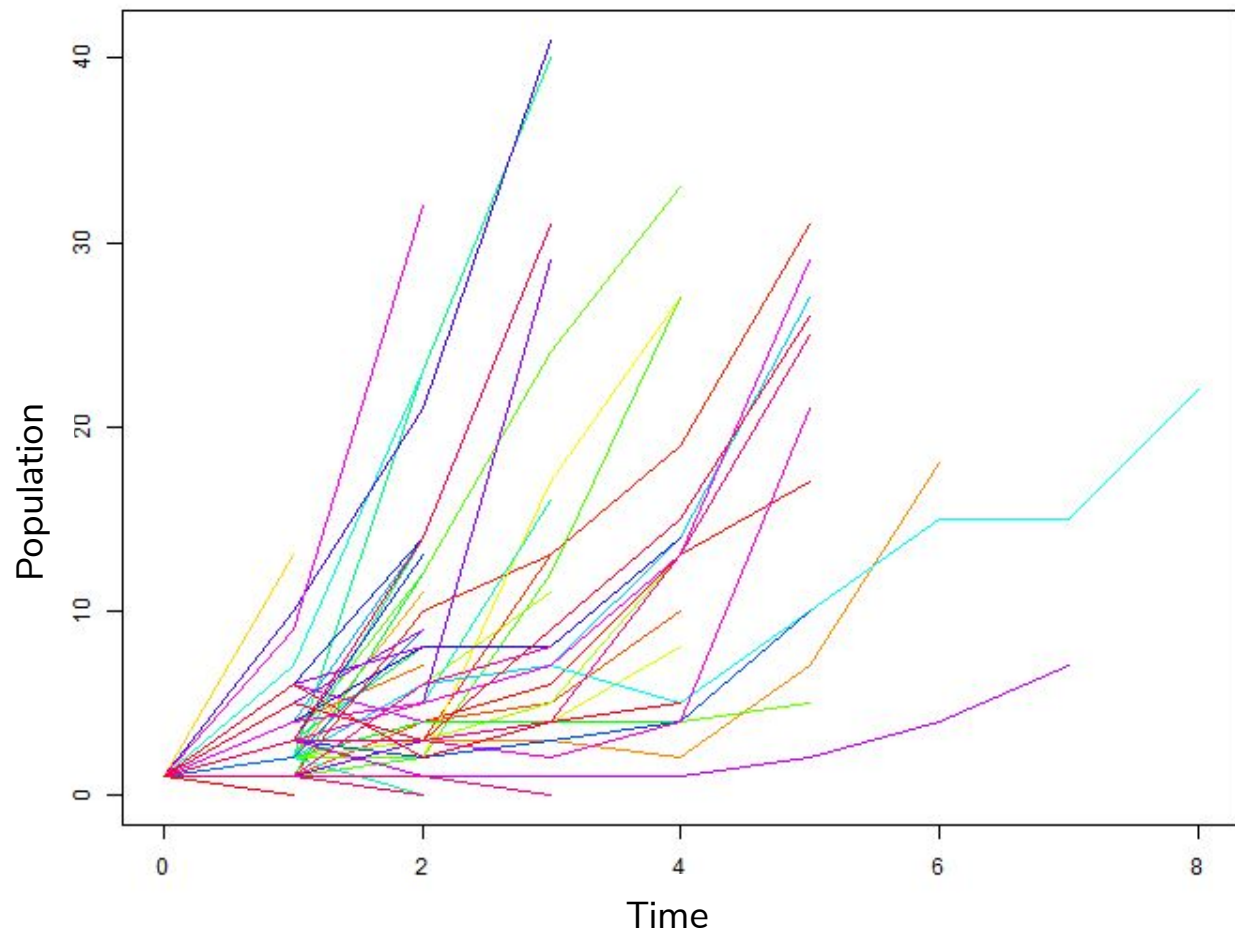
Initial distribution \sim geometric with mean 1.4

Distribution after detection (at generation 7) \sim geometric with mean 0.8





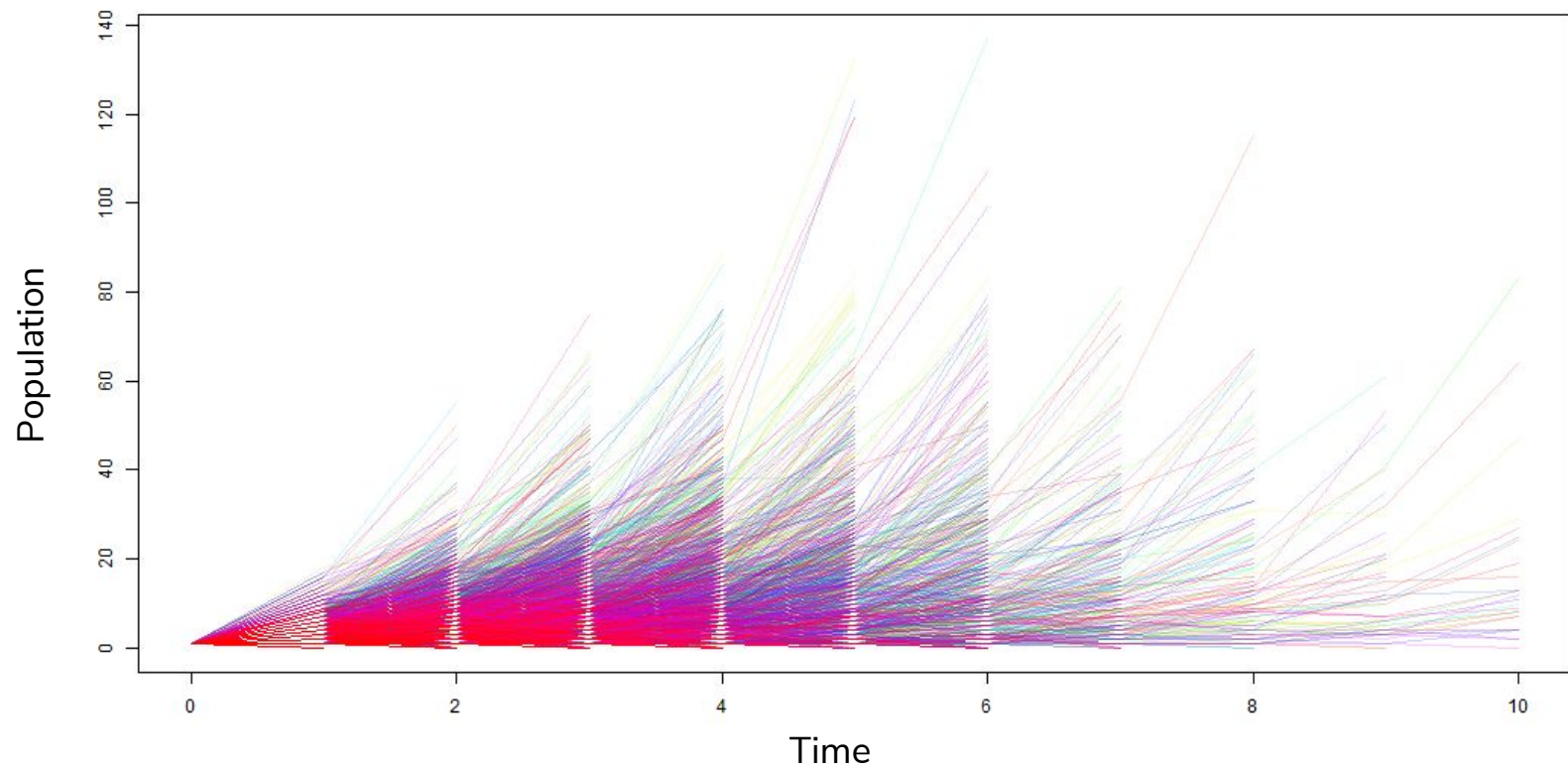
<https://alicemh.shinyapps.io/tree/>



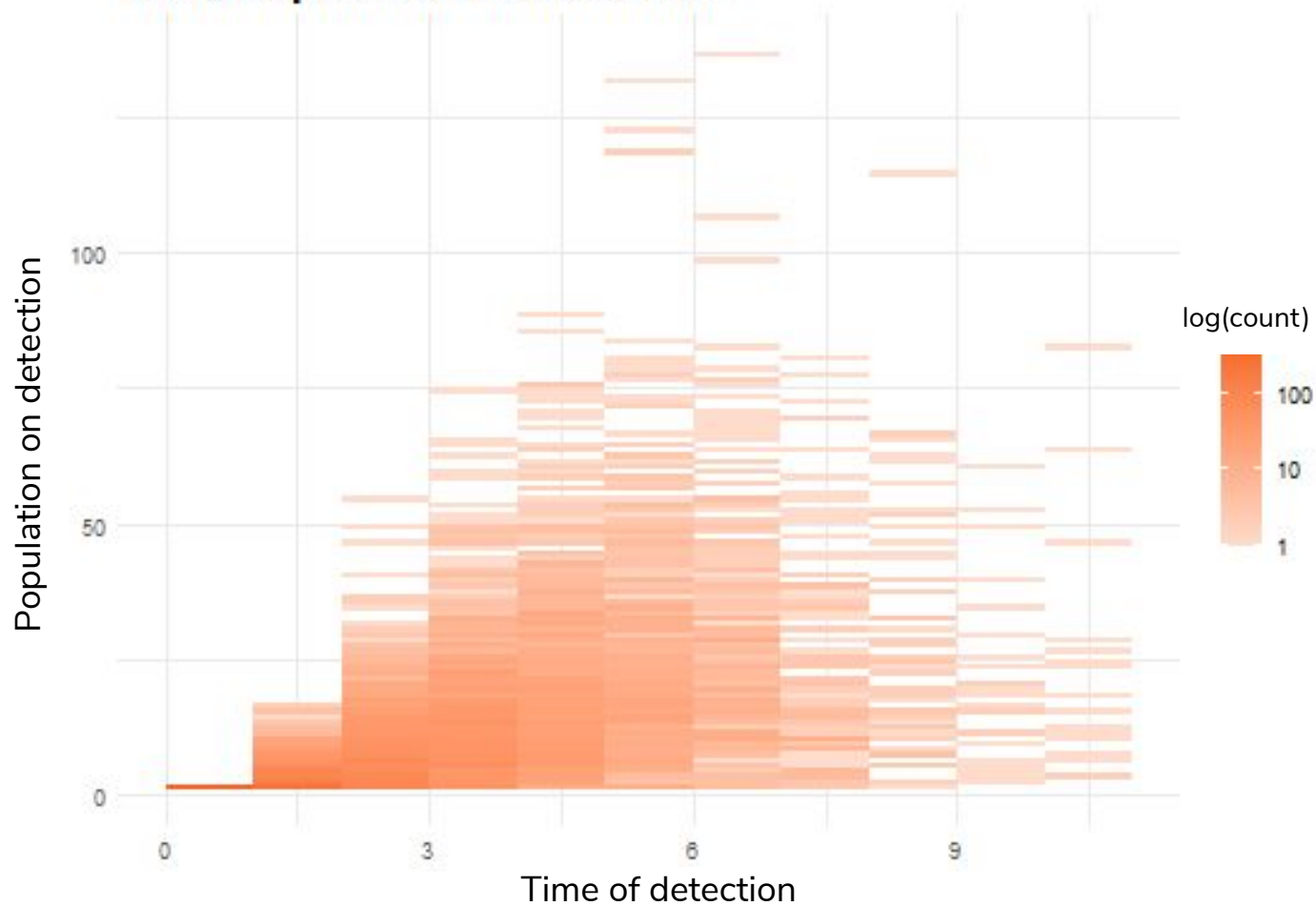
The offspring distribution has a geometric parameter of 0.35 (mean of ~ 1.86)

We sample 100 trees

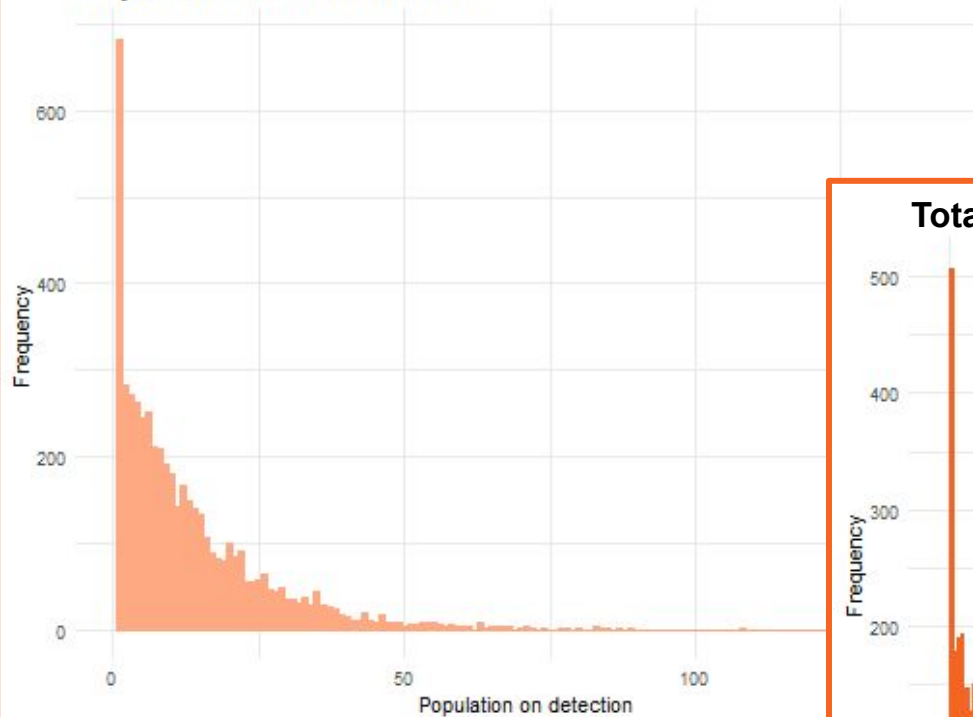
The detection probability is 0.05



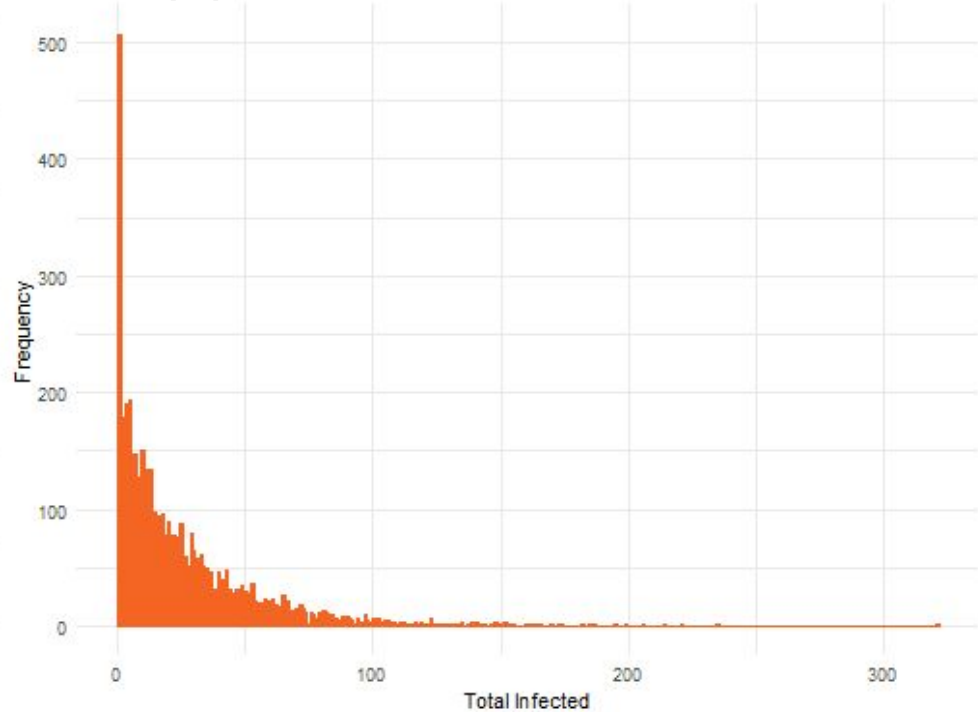
Time/Population at detection



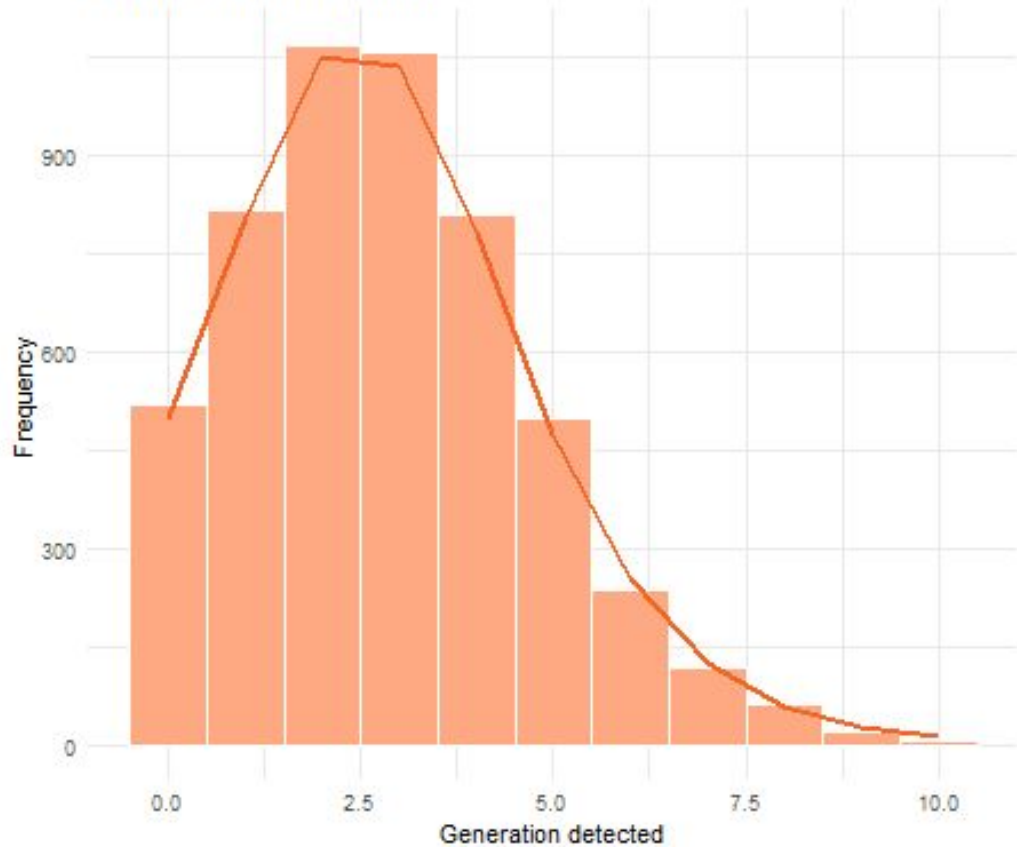
Population on detection



Total population infected



Time of detection



The probability of being detected at generation n is:

$$g^n(0) - g^{n-1}(0)$$

Where $g^n(x)$ is the n^{th} iteration of the probability generating function of the offspring distribution

<https://alicemh.shinyapps.io/hist/>

Multitype model

Two types of node:

- **Infectious** nodes
- **Non-infectious** nodes

Infectious nodes:

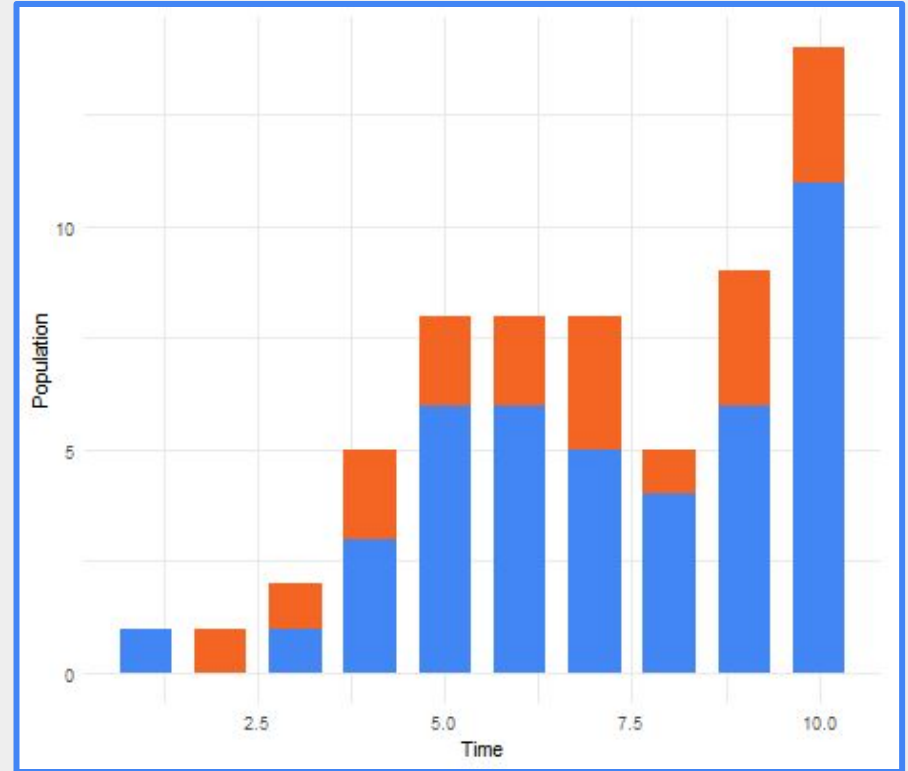
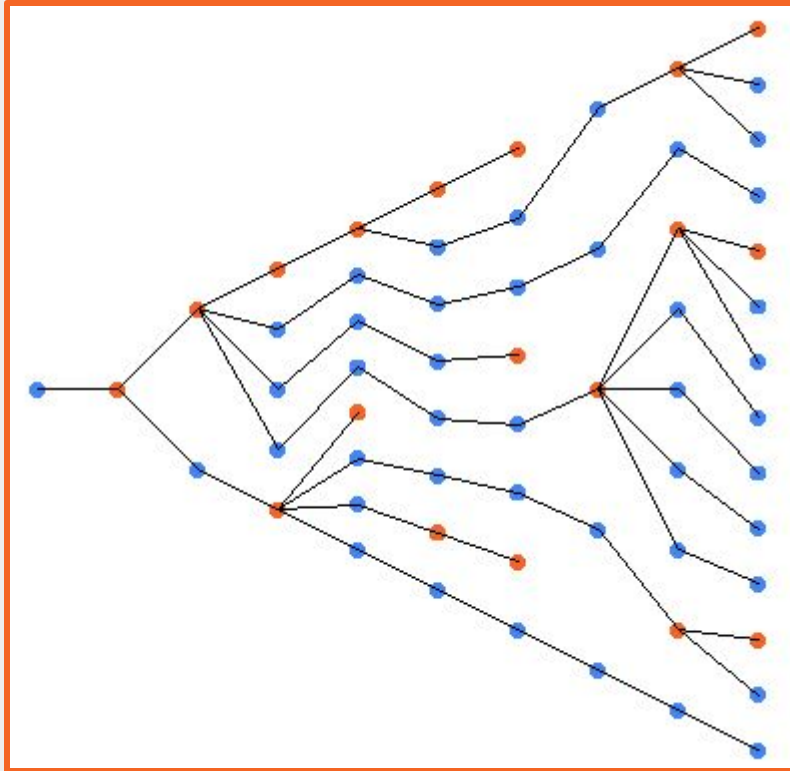
- Die with probability P
- Otherwise remain infectious and spread to a random number of non-infectious people

Non-infectious nodes:

- Turn infectious with probability Q
- Otherwise remain non-infectious

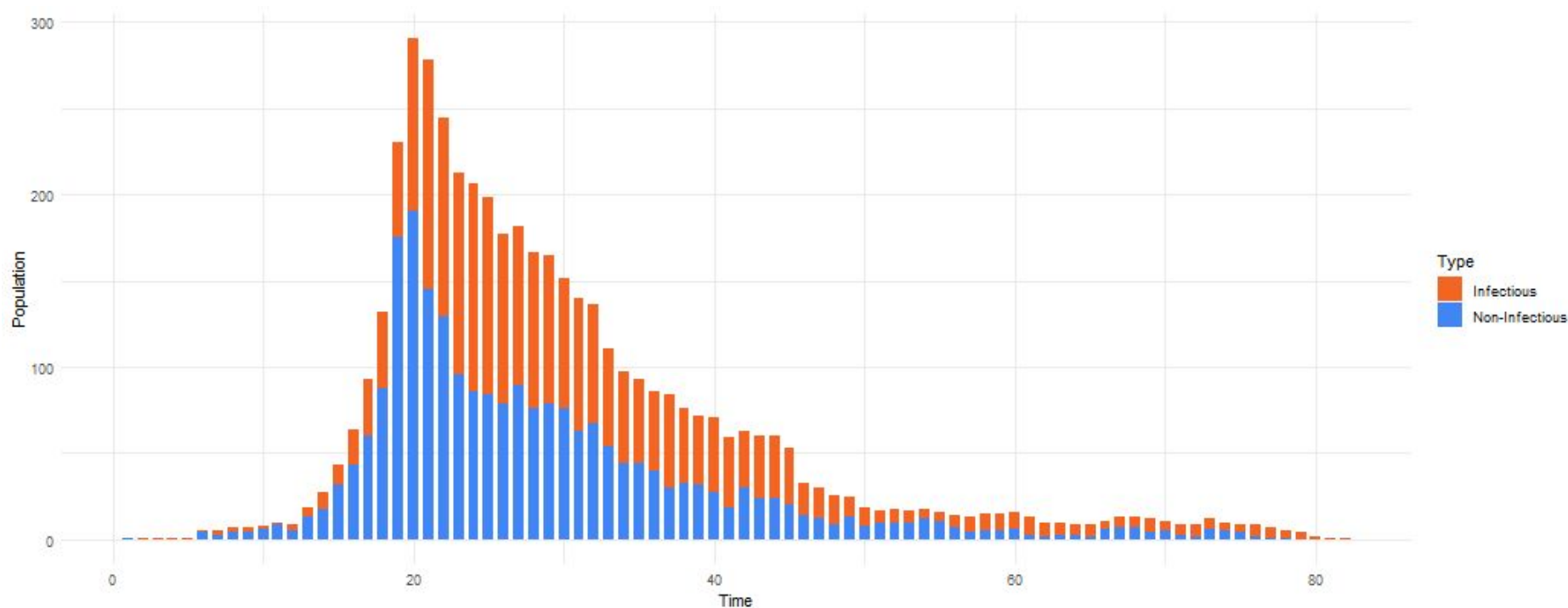
Orange nodes are infectious
Blue nodes are non-infectious

- On average, infectious nodes spread to 1.8 non-infectious nodes (geometrically distributed)
- The probability of infectious dying is $1/3$
- The probability of non-infectious becoming infectious is $1/3$

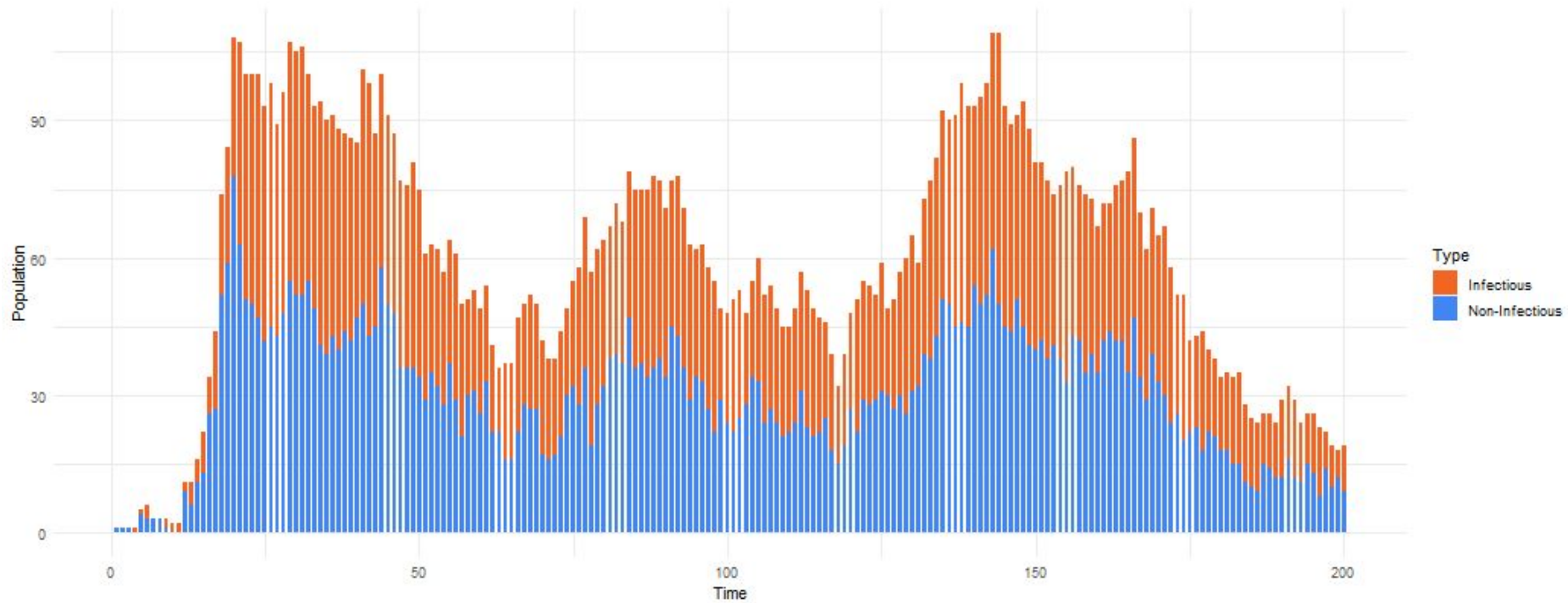


The average spread changes from 2.5 to 0.3 in generation 20

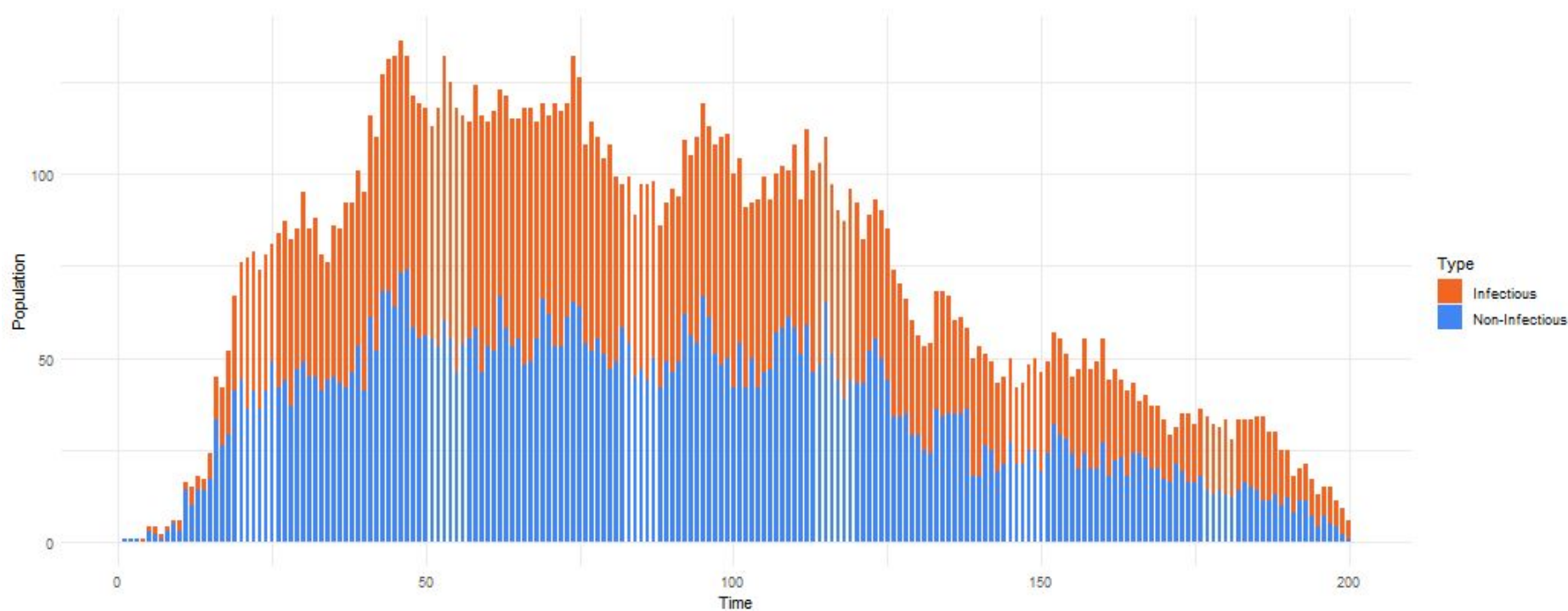
The probability of infectious dying and the probability of non-infectious becoming infectious remain at $1/3$



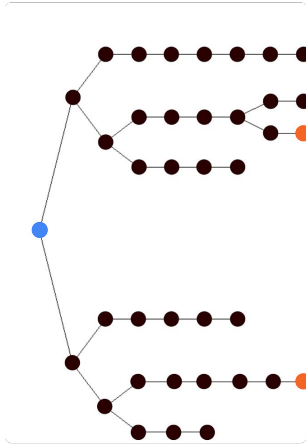
The average spread changes from 1.8 to 0.5 in generation 20



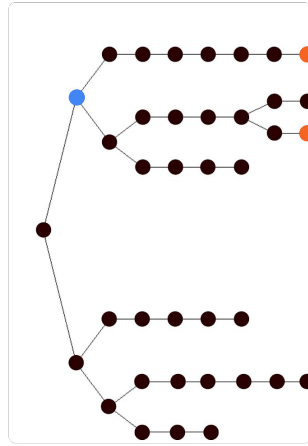
Average spread changes from 1.2 to 0.48 in generation 20



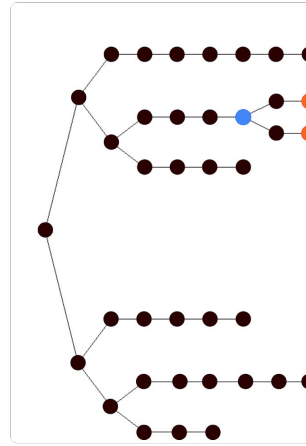
Most recent common ancestor of the orange points is in:



Generation 0



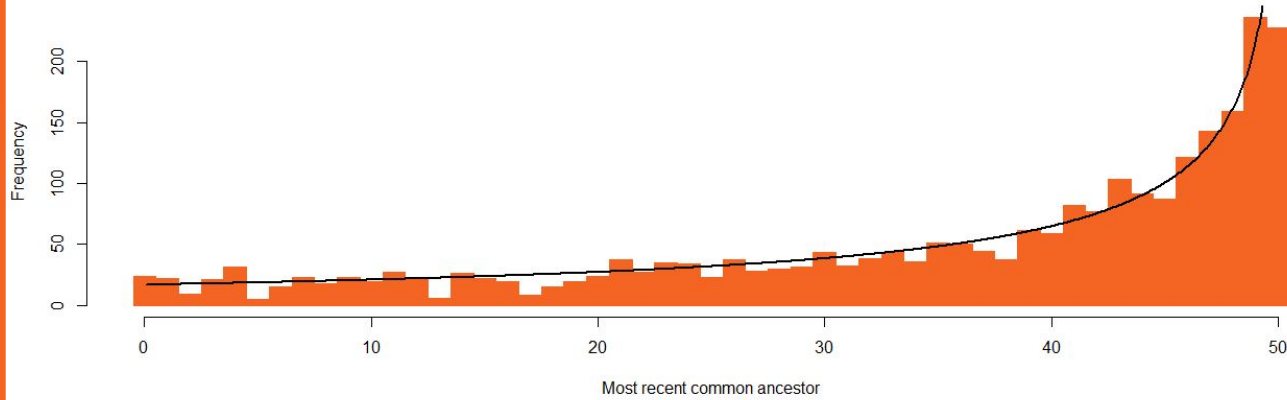
Generation 1



Generation 6

$$\frac{-4x - 2(x - 2) \ln \left(\frac{1}{1-x} \right)}{x^3}$$

simulated vs theoretical frequency of most recent
common ancestor for two points in generation 50



500 trees
5 samples per tree

Sampling at
generation 50

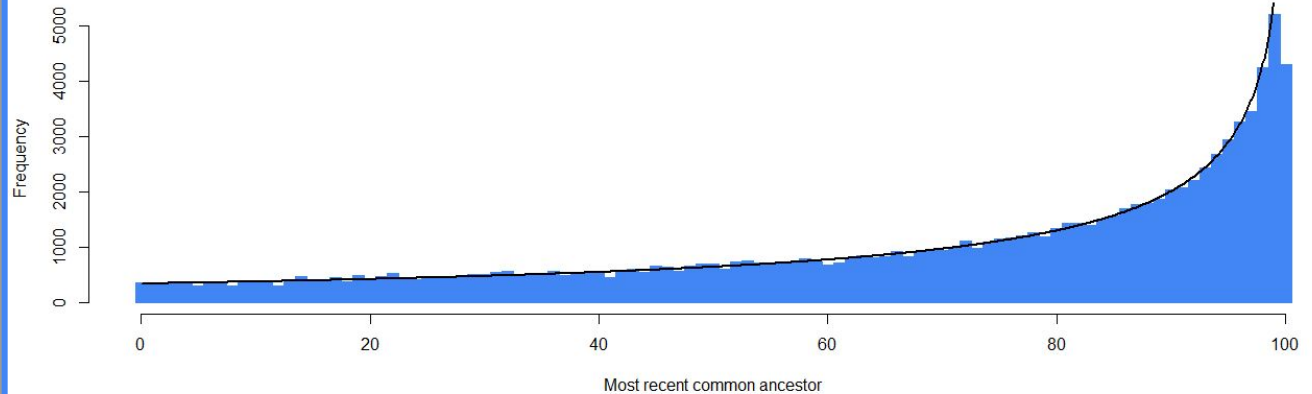


10,000 trees
10 samples per tree

Sampling at
generation 100



simulated vs theoretical frequency of most recent
common ancestor for two points in generation 100



Thank you :)