Probability of the alignment given the tree and sequence evolution model

sequence

was sample

Dates at which each

## Tree Prior

Transmission model that describes the tree generating process

Average number of secondary infections caused by one case within the same type

Proportion of infections sequenced and included in the analysis

Probability that an infected case is removed from the population after sampling

Model describing the rate of evolution along the branches of the tree

## **RELAXED CLOCK**

Model describing the rates of substitution between nucleotides

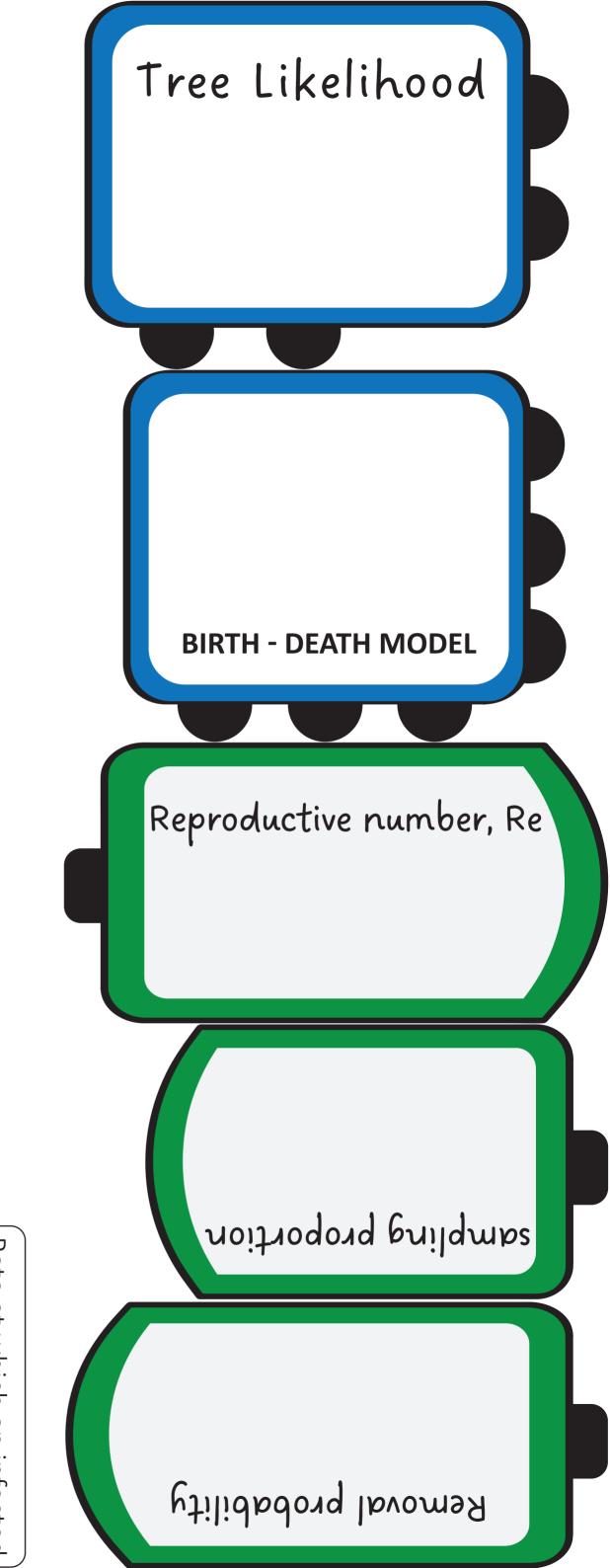
## **HKY**

A set of aligned sequences representing the genetic data for each sample

Graphical representation of the evolutionary relationships between samples

Stationary frequencies in evolutionary equilibrium

Rate at which an infected case becomes non-infections/dies/recovers



Origin clock rates Branch rate model becoming uninf. rate kappa labom noitutitedus nucleotide frequencies Alignment evolutionary rates per branch n substitution/site/time sample dates Time at which the process started w.r.t most recent sample 1166 Nucleotide transition to transversion ratio

## ne evolutional IN SUBSTITUTION / SILE/ rates per r branct