

Tree Likelihood

MULTI-TYPE BIRTH  
DEATH MODEL

Reproductive number,  $R_e$

sampling proportion

Removal probability

Dates at which each  
sequence was sampled

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

Probability of the  
alignment given the tree  
and sequence evolution  
model

Tree Prior

Transmission model  
that describes the tree  
generating process

Average number of second-  
ary 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

**STRICT 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 rela-  
tionships between samples

Stationary frequencies in  
evolutionary equilibrium

Origin

becoming uninf. rate

kappa

nucleotide frequencies

sample dates

Time at which the process started w.r.t most recent sample

Nucleotide transition to transversion ratio

The evolutionary rate in substitution/site/time

clock rate

Branch rate model

substitution model

Alignment

Tree

Re between types

Sample types

type frequencies

Average number of infections of one type caused by a case of a different type

The evolutionary rate in substitution/site/time

Probability of the origin of the process being in each of the type states

Sample trait that defines subpopulations with different epidemic dynamics

**HUMAN - MOOSE**