clock rate
The evolutionary rate in substitution/site/time

Branch rate model
Model describing the rate of evolution along the branches of the tree
STRICT CLOCK

Tree Likelihood
Probability of the alignment given the tree and sequence evolution model

kappa
Nucleotide transition to transversion ratio

Substitution model
Model describing the rates of substitution between nucleotides
HKY

nucleotide frequencies
Stationary frequencies in evolutionary equilibrium

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

Sample dates
Dates at which each sequence was sampled

Tree
Graphical representation of the evolutionary relationships between samples

Sample types
Sample trait that defines subpopulations with different epidemic dynamics
HUMAN - MOOSE

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

Tree Prior
Transmission model that describes the tree generating process
MULTI-TYPE BIRTH DEATH MODEL

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

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

sampling proportion
Proportion of infections sequenced and included in the analysis

becoming uninf. rate
Rate at which an infected case becomes non-infectious/dies/recovers

Re between types
Average number of infections of one type caused by a case of a different type

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