Probability of the alignment given the tree and sequence evolution model

Dates at which each sequence was sampled

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
STRICT CLOCK

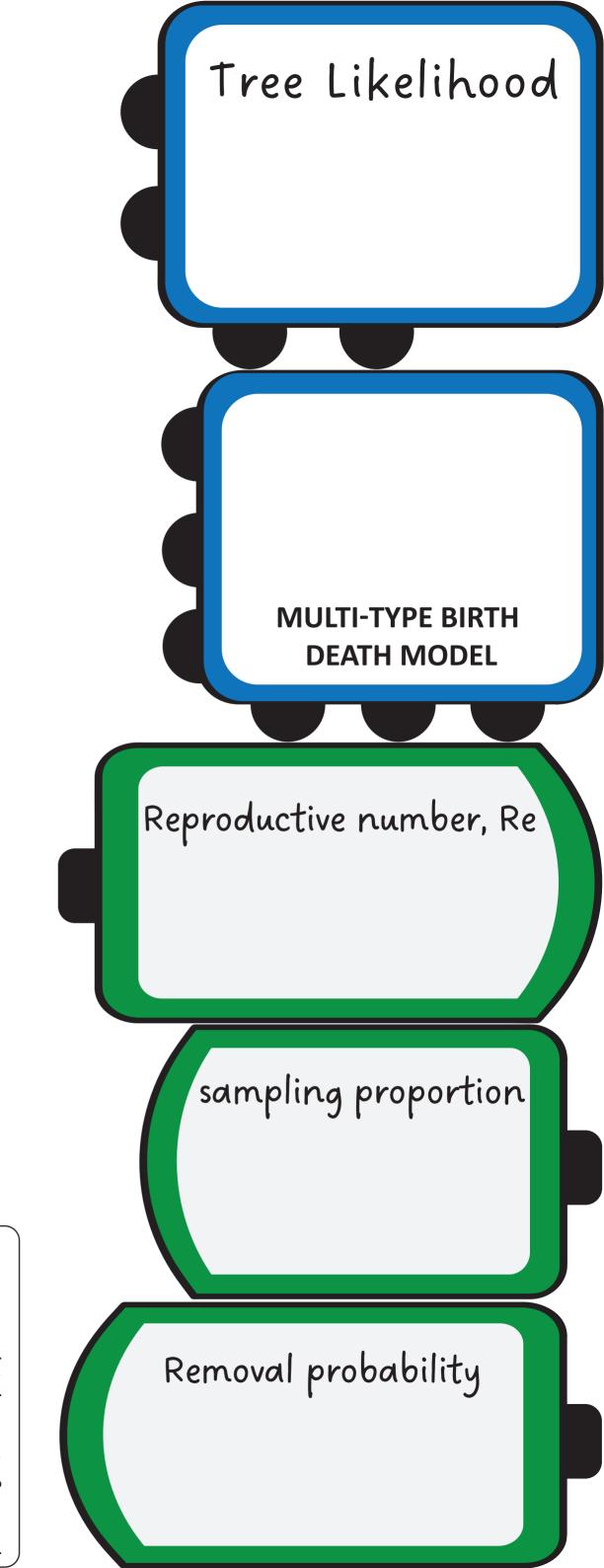Model describing the rates of substitution between nucleotides
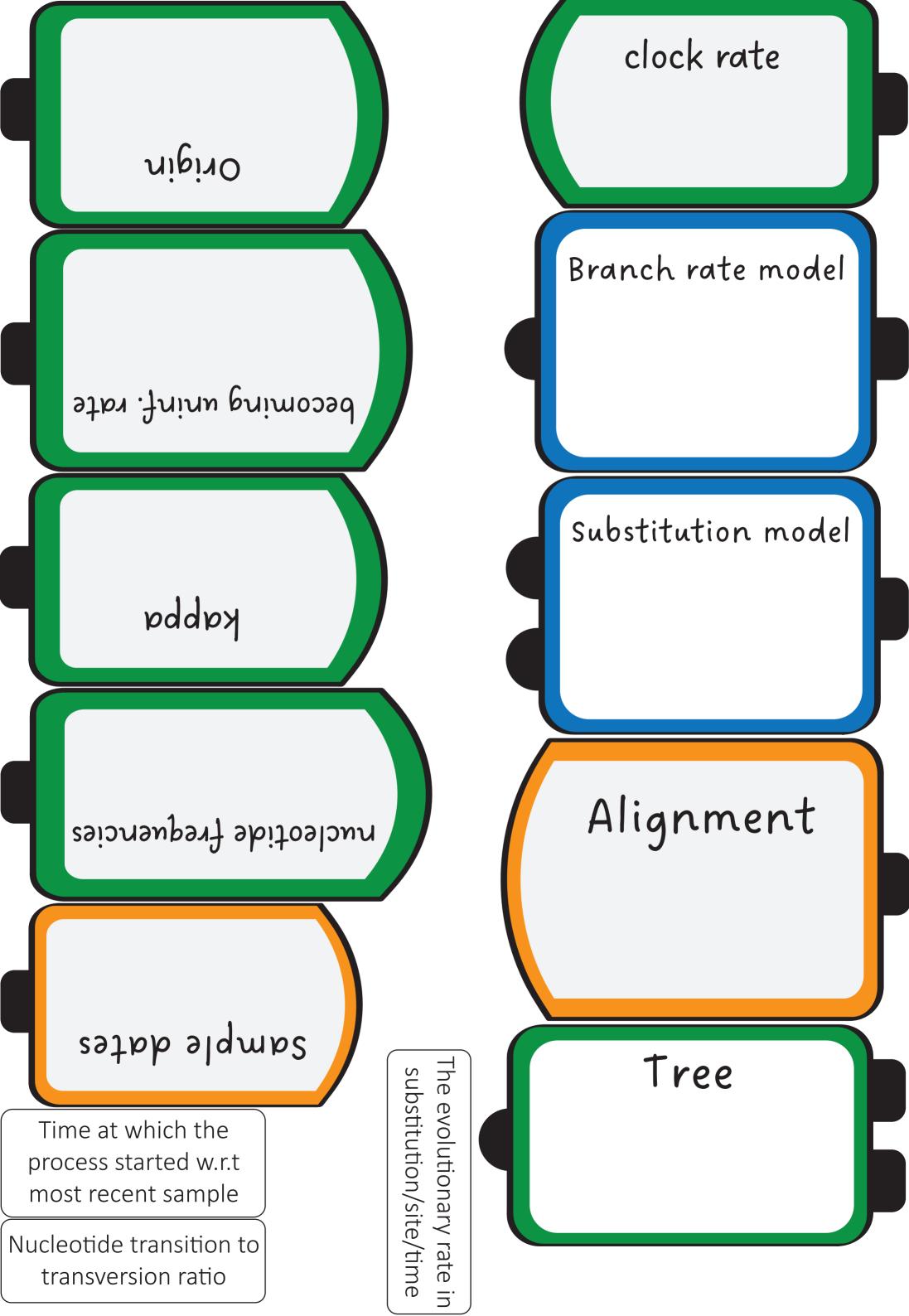**HKY**

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

Graphical representation of the evolutionary relationships between samples

Stationary frequencies in evolutionary equilibrium

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

Tree Likelihood

MULTI-TYPE BIRTH DEATH MODEL

Reproductive number, Re

sampling proportion

Removal probability

clock rate

Branch rate model

Substitution model

Alignment

Tree

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

Re between types

Sample types

type frequencies

clock rate

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