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

STRICT CLOCK

Model describing the rates of substitution between nucleotides

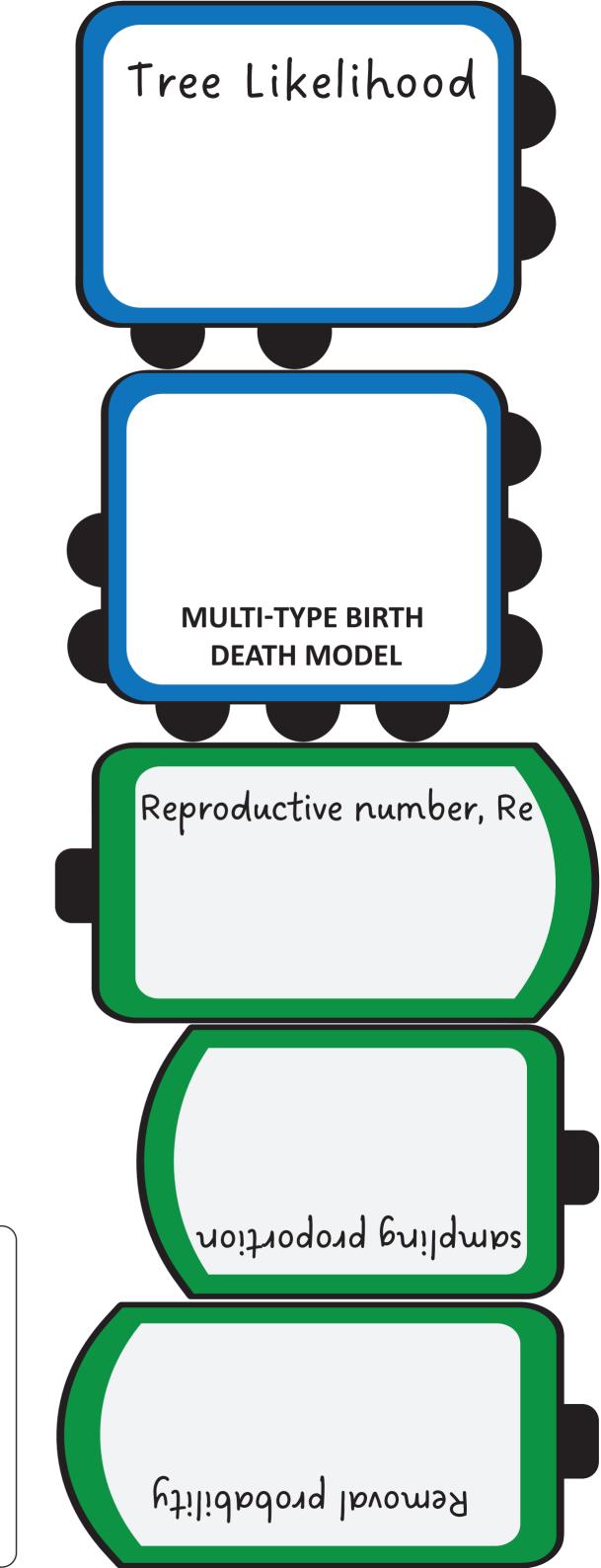
HKY

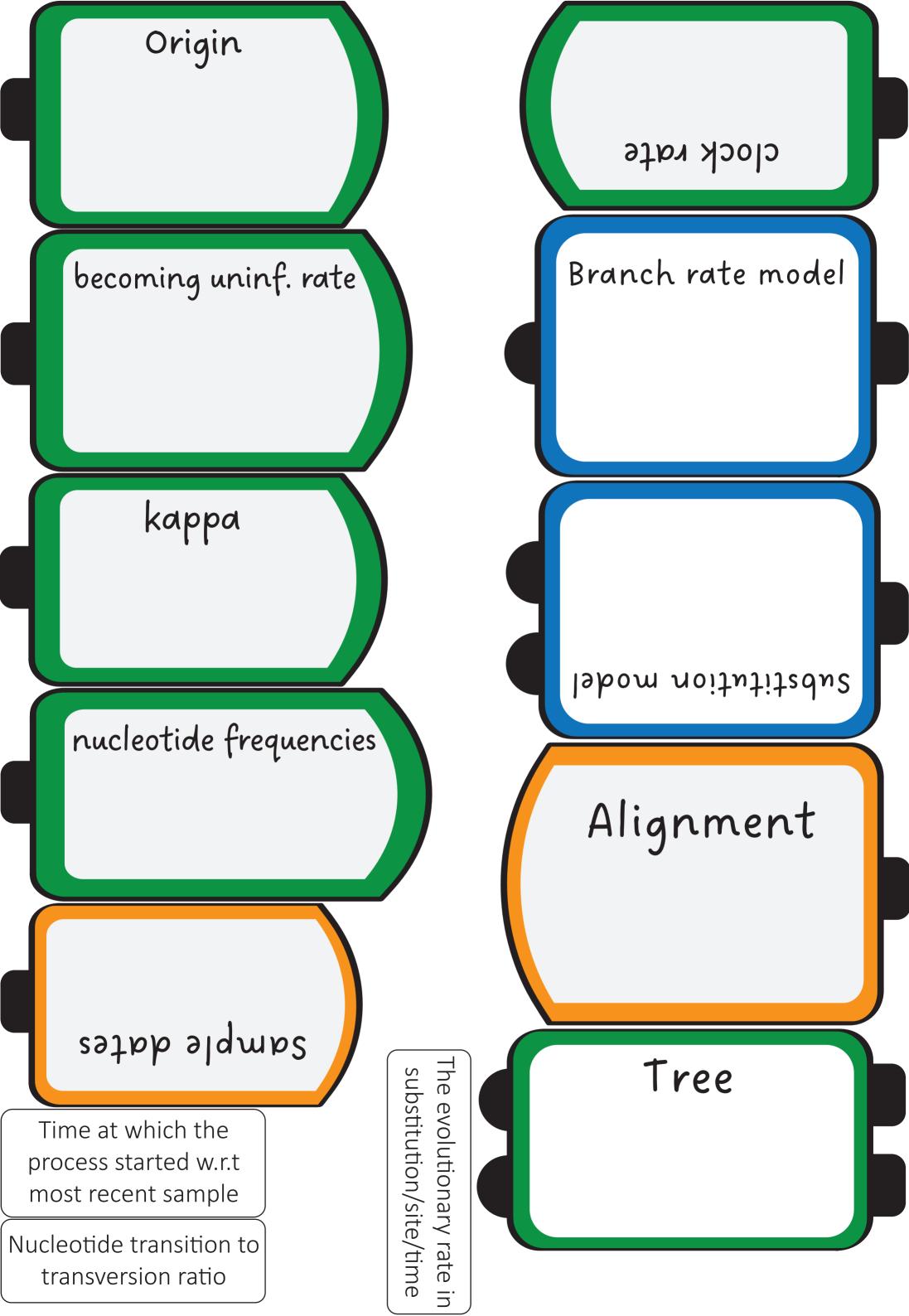
A set of aligned sequences representing the genetic data for each sample

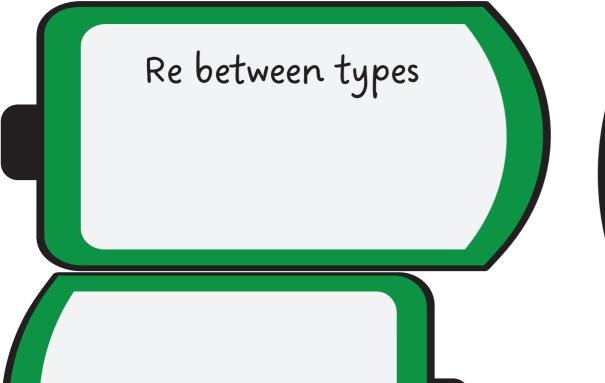
Graphical representation of the evolutionary relationships between samples

Stationary frequencies in evolutionary equilibrium

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







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