# Documentation of the R package epiphylo

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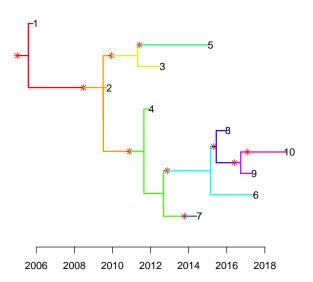
## 1 Simulation

A pathogen has an effective within-host population size of  $N_e = 100$  and a generation time g = 1 day, so that  $N_e g = 100/365$  years. The basic reproduction number is R = 1. To following command simulates an outbreak of this pathogen:

#### > simu <- simulateOutbreak(R=1,neg=100/365)</pre>

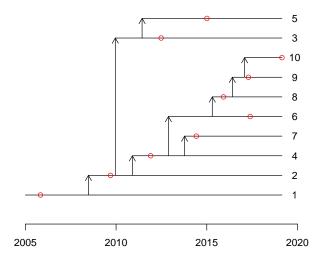
This simulation contains both the transmission tree between infected hosts and the within-host phlogenetic tree of each host. This can be visualised as a colored phlogenetic tree, where each host is represented by a unique color:

#### > plotBothTree(simu)



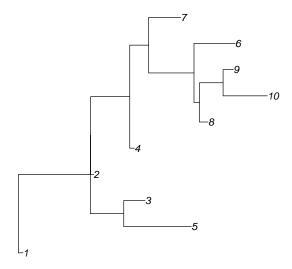
The transmission tree can be extracted and plotted separately from the phylogeny:

- > ttree<-ttreeFromFullTree(simu)
- > plotTTree(ttree)



The phylogenetic tree can be extracted and converted into a phylo object from the ape package:

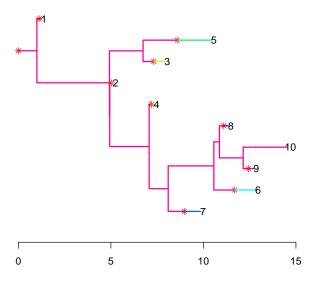
- > library(ape)
- > ptree<-ptreeFromFullTree(simu)</pre>
- > p<-phyloFromPtree(ptree)
- > plot(p)



# 2 Inference of transmission tree given a phylogeny

A phylo object can be turned into a phylogenetic tree and complemented with a wild guess at the transmission tree in order to provide the starting point of the MCMC procedure:

- > ptree<-ptreeFromPhylo(p)</pre>
- > full<-makeFullTreeFromPTree(ptree)</pre>
- > plotBothTree(full)



The MCMC procedure to infer the transmission tree given the phylogenetic tree can be run as follows:

# > record<-inferTTree(ptree,mcmcIterations=100)</pre>

This returns a record of all MCMC iterations. Let's see what the transmission tree looked like at the end of the MCMC:

- > lastIteration<-record[[length(record)]]</pre>
- > plotBothTree(lastIteration\$tree)

