

# Documentation of the R package epiphylo

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February 19, 2014

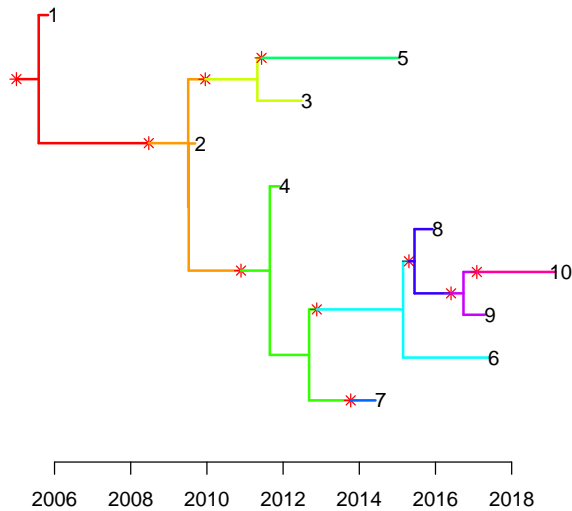
## 1 Simulation

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  $R = 1$ . The following command simulates an outbreak of this pathogen:

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

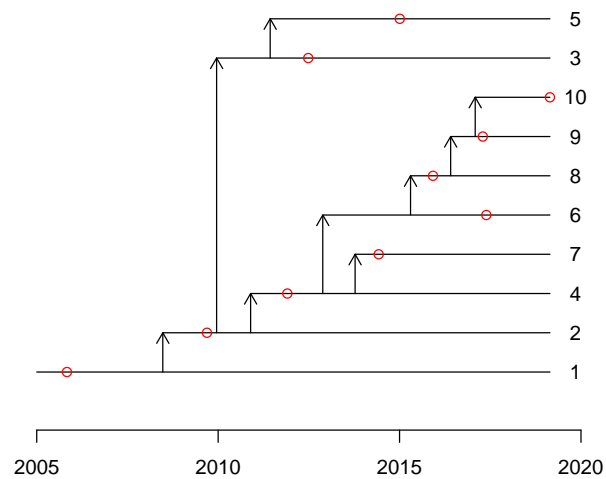
This simulation contains both the transmission tree between infected hosts and the within-host phlogenetic tree of each host. This can be visualised as a colored phlogenetic tree, where each host is represented by a unique color:

```
> plotBothTree(simu)
```



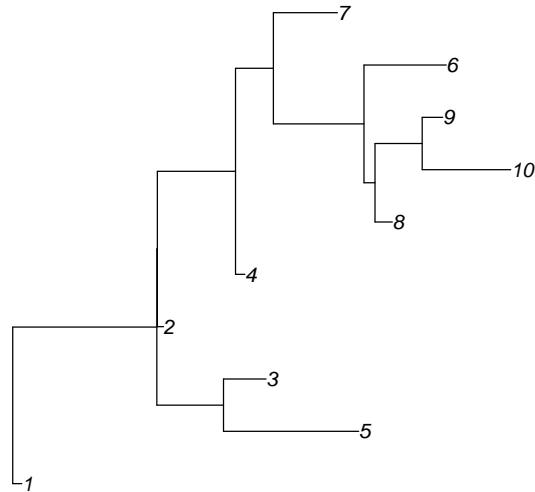
The transmission tree can be extracted and plotted separately from the phylogeny:

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



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

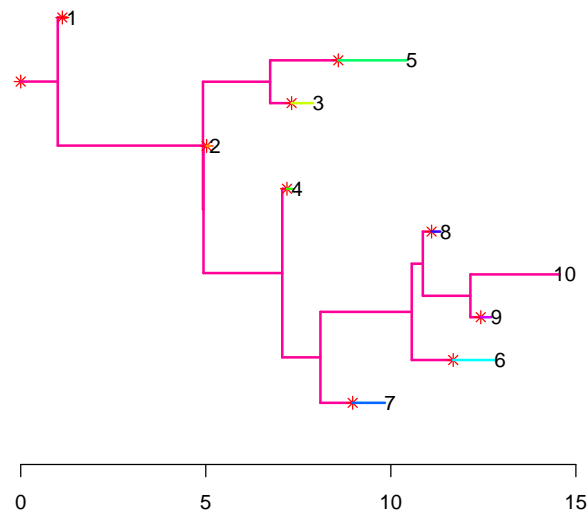
```
> library(ape)
> ptree<-ptreeFromFullTree(simu)
> p<-phyloFromPtree(ptree)
> plot(p)
```



## 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)
> full<-makeFullTreeFromPTree(ptree)
> plotBothTree(full)
```



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

```
> record<-inferTTree(ptree,mcmcIterations=100)
```

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)]]
> plotBothTree(lastIteration$tree)
```

