Documentation of the R package epiphylo

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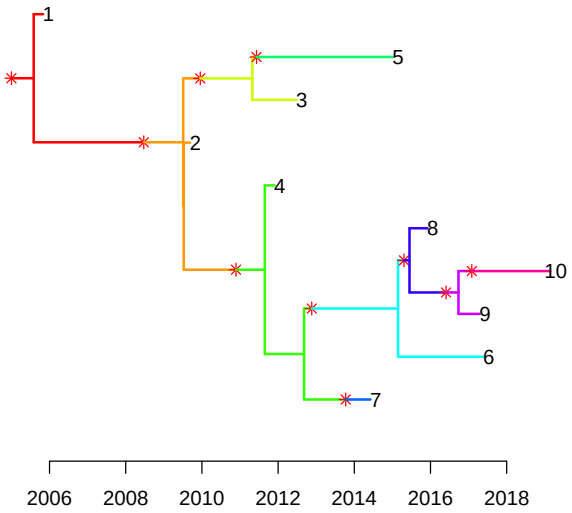
A pathogen has an effective within-host population size of $N_e = 100$ and a generation time $g = 1$ day, so that $N_e g = 100/365$ years. The basic reproduction number is $R = 1$. To following command simulates an outbreak of this pathogen:

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

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:

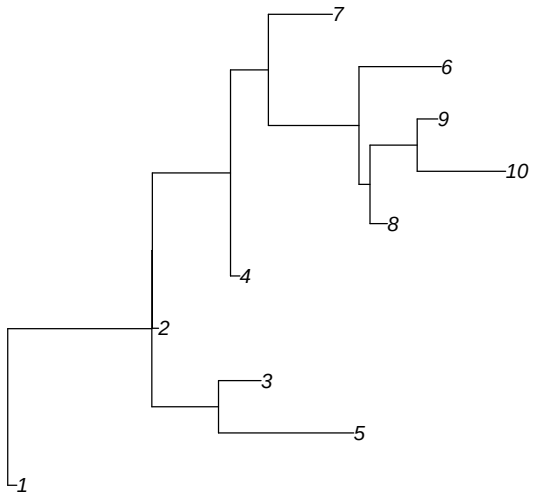
```
> plotBothTree(simu)
```



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

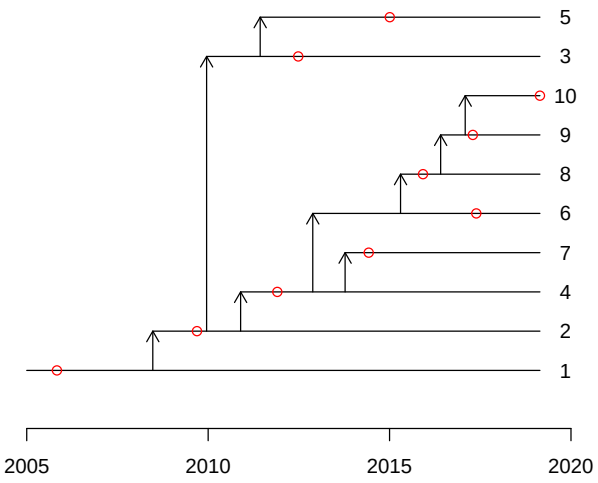
```
> library(ape)
> ptree<-ptreeFromFullTree(simu)
```

```
> p<-phyloFromPtree(ptree)
> plot(p)
```



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

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


5
3
10
9
8
6
7
4
2
1
2005
2010
2015
2020