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,pi=0.5)
```

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)
```
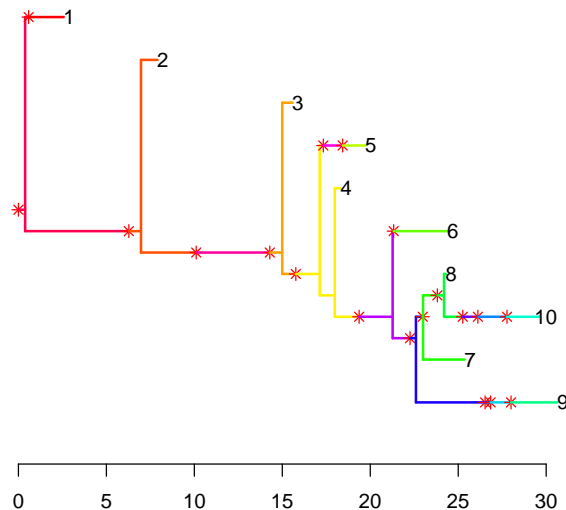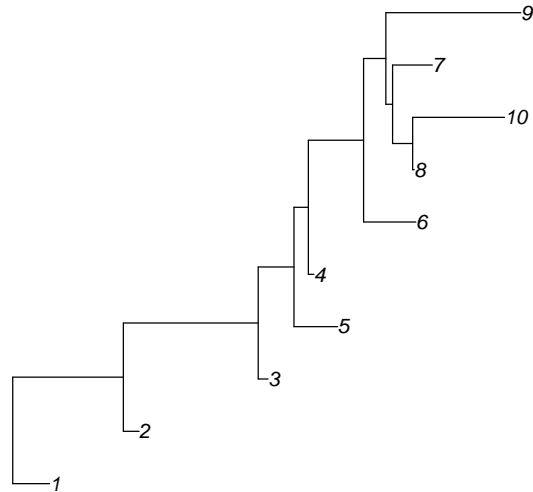

The transmission tree can be extracted and plotted separately from the phylogeny:

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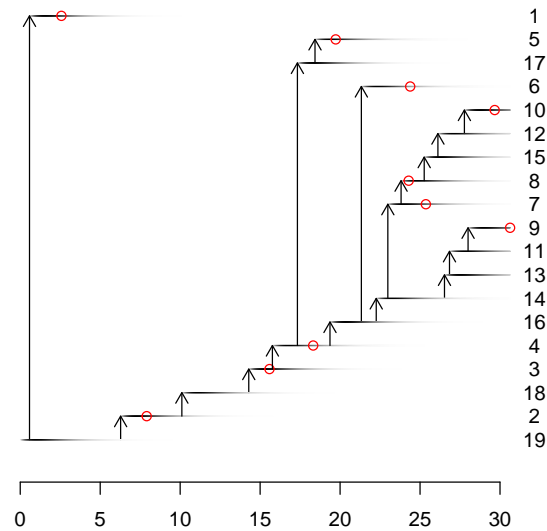

The phylogenetic tree can be extracted and converted into a phylo object
from the ape package:

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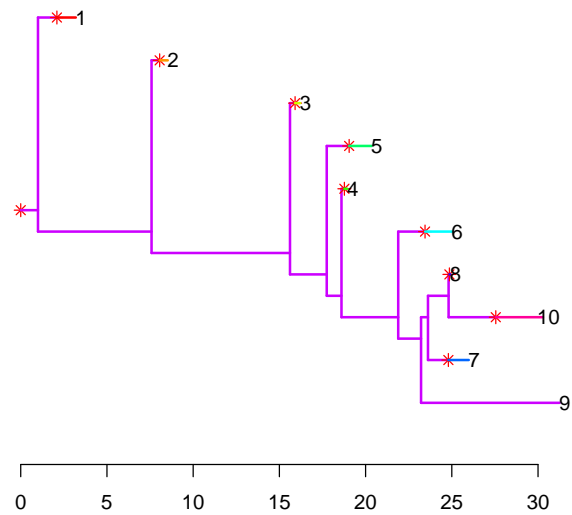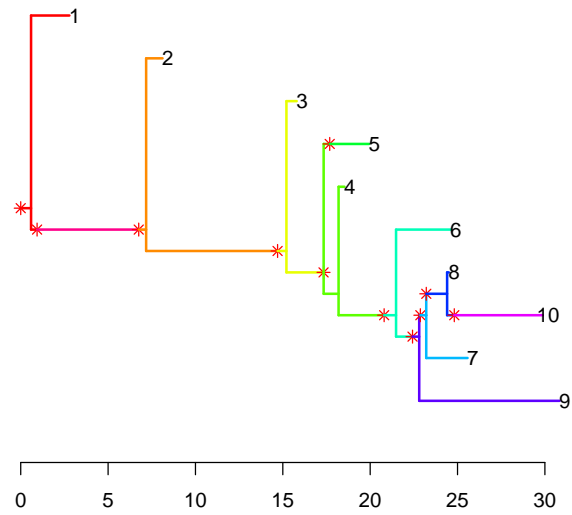
The MCMC procedure to infer the transmission tree given the phylogenetic tree can be run as follows:

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

This returns a record of all MCMC iterations. This is what the transmission tree looks like at the end of the MCMC:

```
> lastIteration<-record[[length(record)]]
> plotBothTree(lastIteration$tree)
```

Traces of the MCMC: