

Example of using CreDating after recombination analysis

Xavier Didelot

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Initialisation

```
library(CreDating)
library(ape)
set.seed(0)
```

Data

A ClonalFrameML output can be read using:

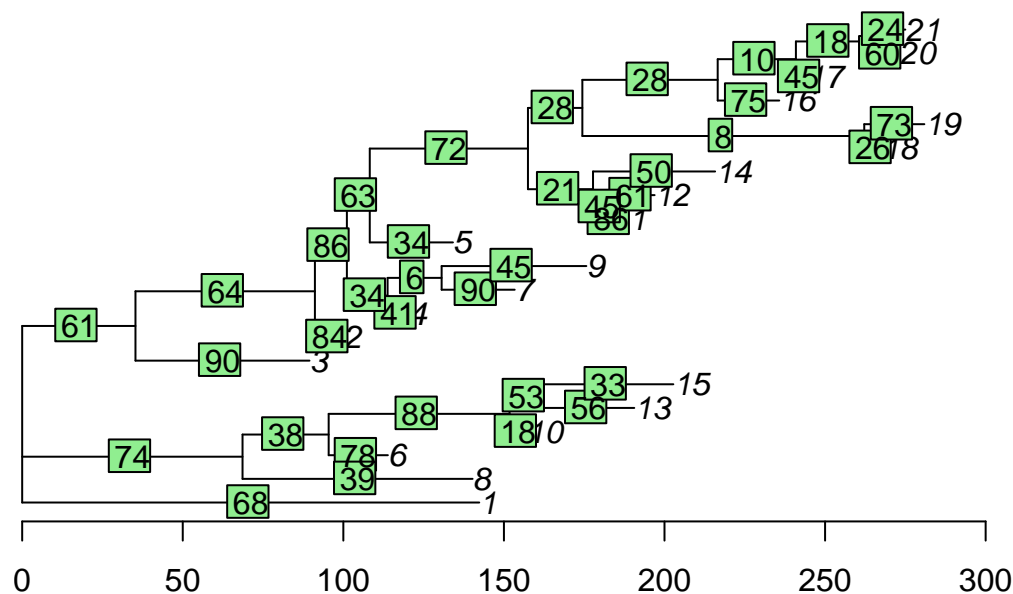
```
t=loadCFML(prefix='cfml-output')
```

A Gubbins output can be read using:

```
t=loadGubbins(prefix='gubbins-output')
```

Instead, for the purpose of making this vignette self-contained, we will simulate an output from a recombination analysis. This is just an object of class `phylo`, unrooted and with the added field `unrec` representing the proportion that is unrecombined for each branch.

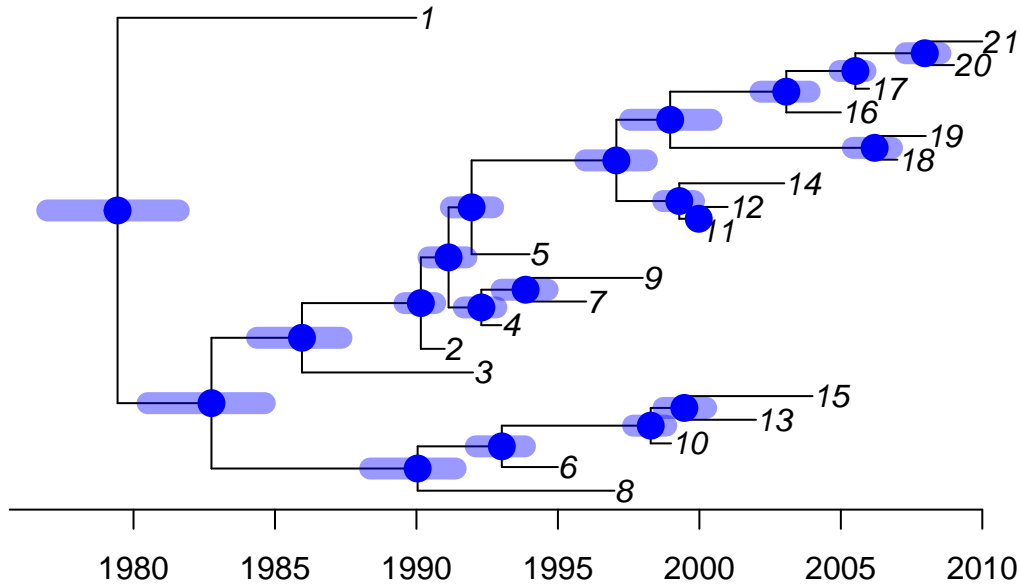
```
dates=1990:2010
t=unroot(simobsphy(simcoaltree(dates)))
t$unrec=runeif(length(t$edge.length))
plot(t)
axisPhylo(backward = F)
edgelabels(round(100*t$unrec))
```



Analysis

We run CreDating as follows:

```
res=credatate(t,dates,useRec=T)
plot(res,'treeCI')
```



We can see what the MCMC traces look like:

```
plot(res,'trace')
```

