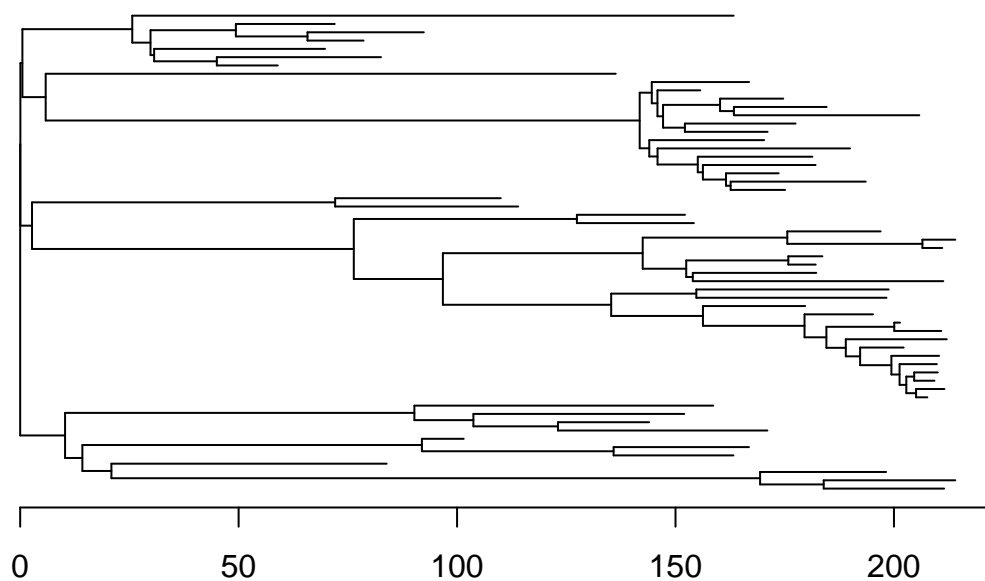# Example of using CreDating on the data of Harris et al (2010)

Xavier Didelot

2017-11-22

Initialisation

```
library(CreDating)
library(ape)
set.seed(0)
data(harris2010)
plot(harris2010$tree, show.tip.label = F)
axisPhylo(backward = F)
```
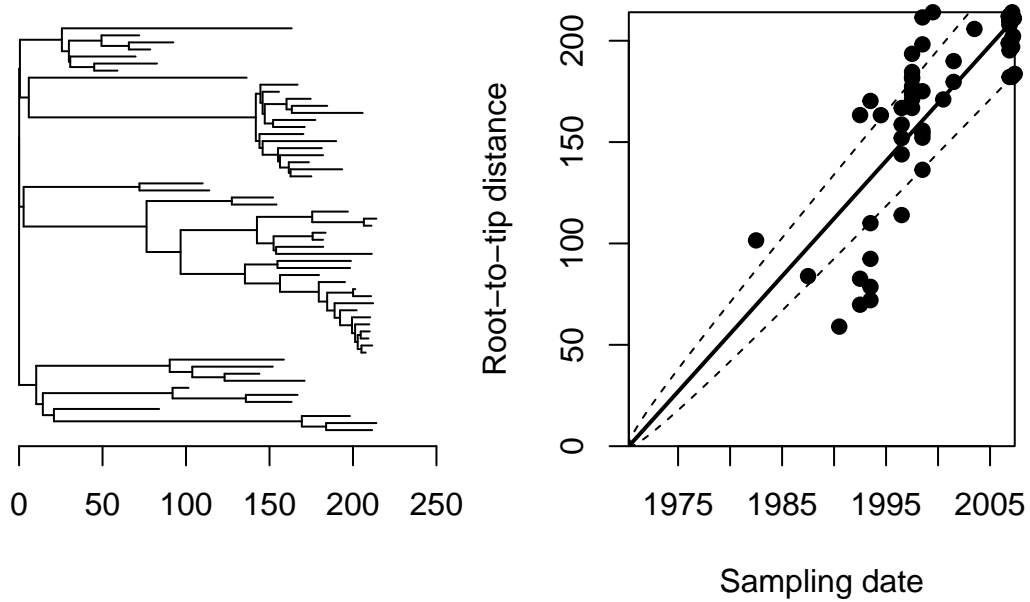

Root-to-tip analysis

Let's do a root-to-tip regression analysis:

```
res=roottotip(harris2010$tree,harris2010$dates)
```
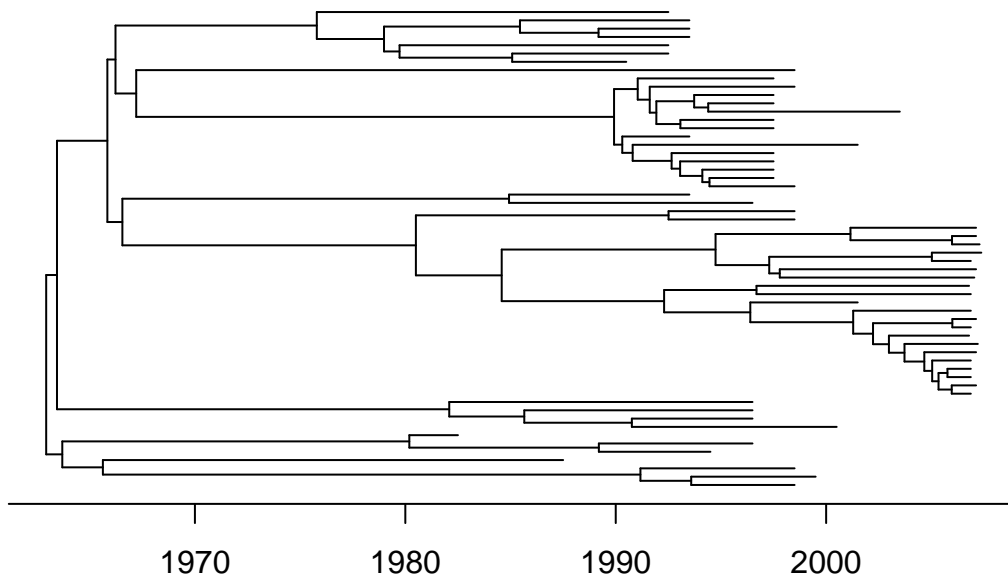
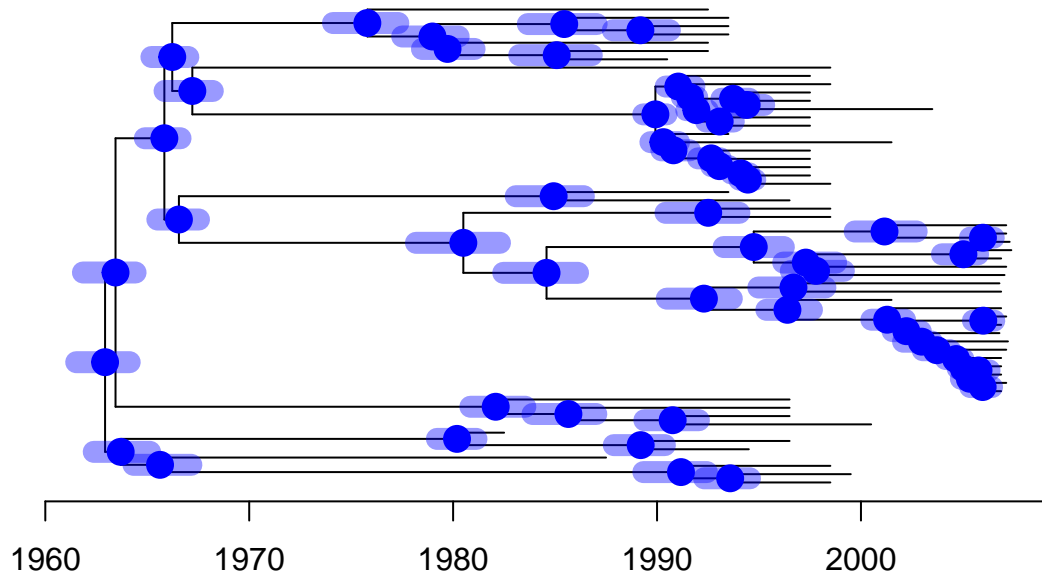# Rate=5.69e+00,MRCA=1970.26,R2=0.63,p<1.00e−04

Analysis

We run CreDating as follows:

```
res=credate(harris2010$tree,harris2010$dates, nbIts = 1000)
plot(res,show.tip.label = F)
```
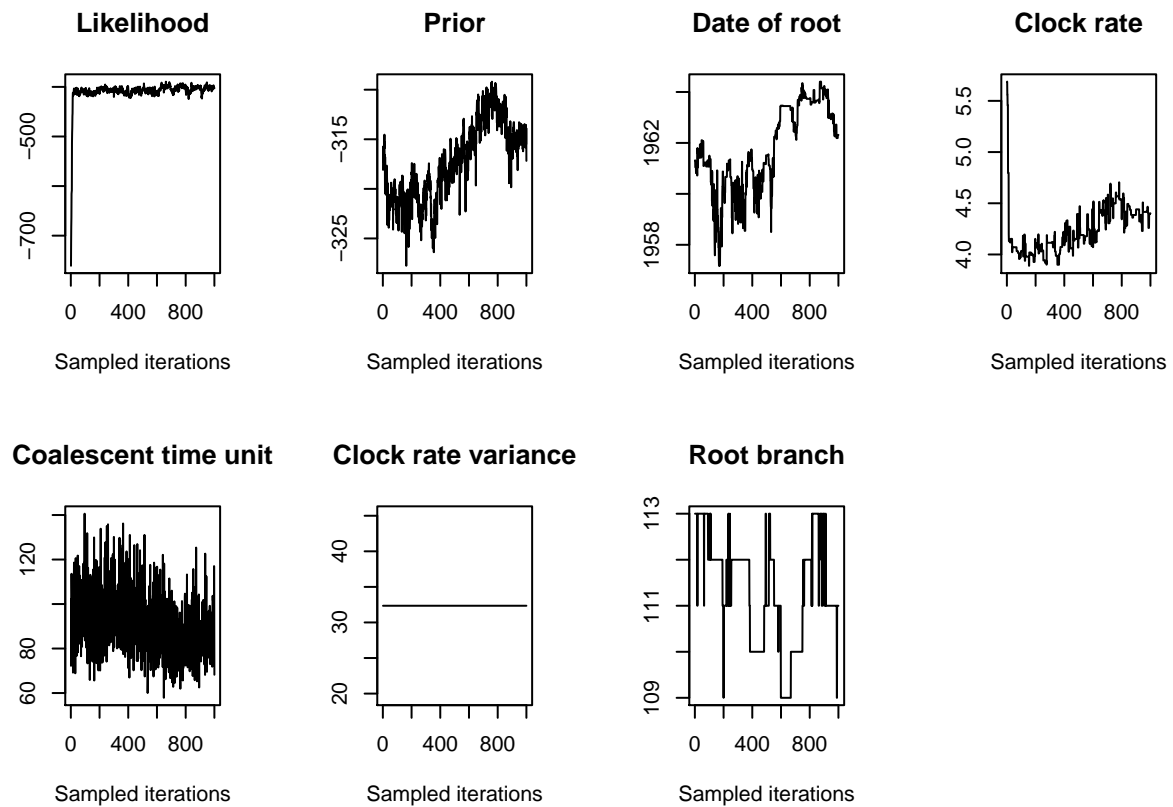

Plot with credibility bars:

2

```
plot(res,'treeCI',show.tip.label = F)
```


1960   1970   1980   1990   2000

We can see what the MCMC traces look like:

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


Let's see where the root is likely to be:

```
plot(res,'treeRoot',show.tip.label=F)
```