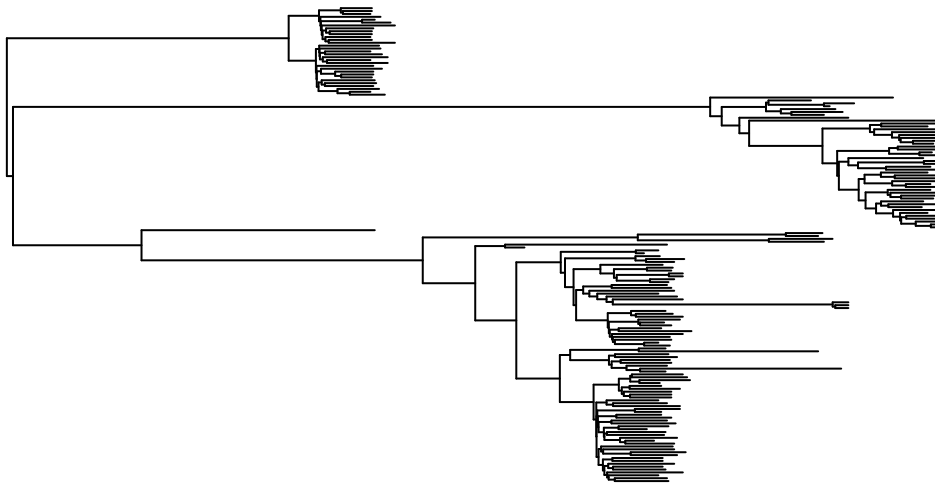


BNPR and BNPR_PS

Influenza A H3N2 Virus in New York

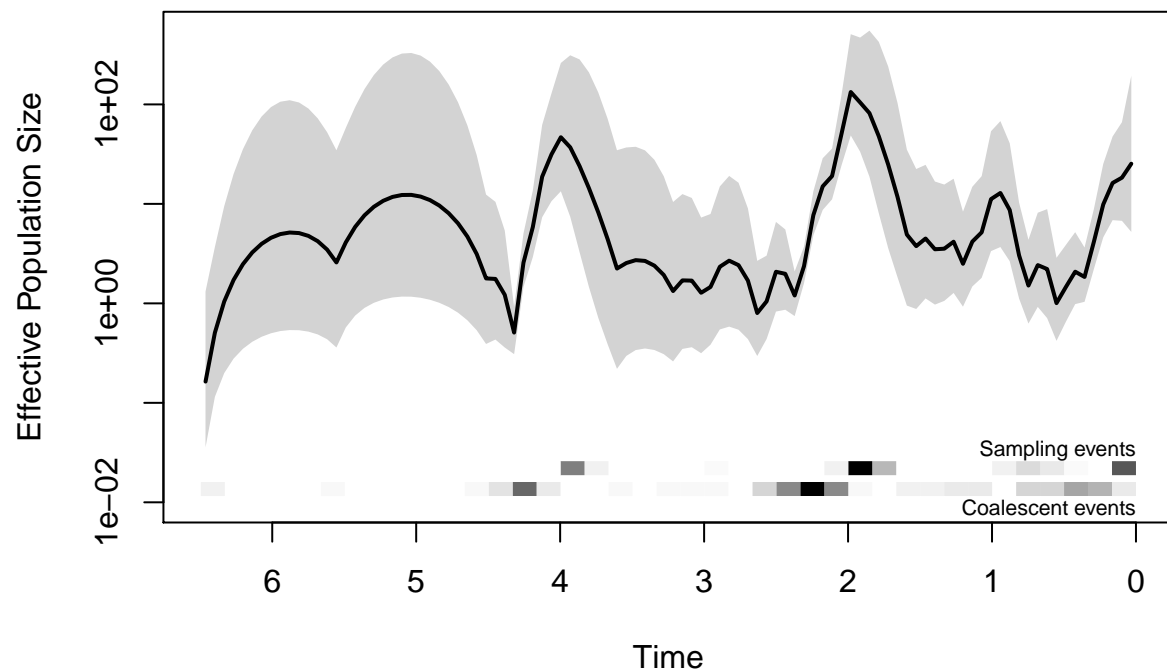
We can visualize the MCCT as follows:

```
library("ape")
mcct<-"~/Documents/sismid/SISMID/Tutorials/Ne_estimation/precooked_runs/NewYork_mcct"
tree<-read.nexus(mcct)
plot(ladderize(tree),show.tip.label = FALSE)
```

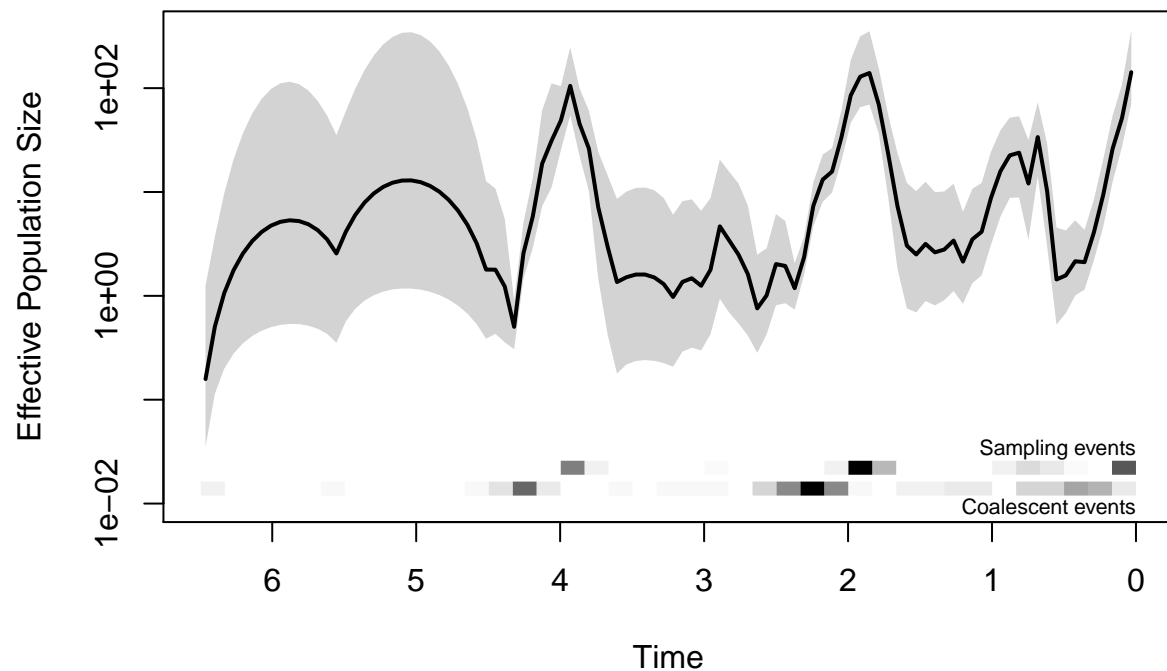


You can estimate the effective population size from a fixed tree as follows:

```
#install.packages("INLA", repos=c(getOption("repos"), INLA="https://inla.r-inla-download.org/R/stable")
#library(devtools)
#install_github("mdkarcher/phyloodyn")
library("phyloodyn")
bnpr_estimate<-BNPR(tree)
plot_BNPR(bnpr_estimate)
```



```
#install.packages("INLA", repos=c(getOption("repos"), INLA="https://inla.r-inla-download.org/R/stable")
#library(devtools)
#install_github("mdkarcher/phyloodyn")
library("phyloodyn")
bnpr_ps<-BNPR_PS(tree)
plot_BNPR(bnpr_ps)
```



More tutorials: [phyloodyn](#)

Reference:

Karcher, MD, Palacios JA, Lan S, and Minin, VN. [phyloodyn](#): an R package for phylodynamic simulation and

inference. *Molecular Ecology Resources* 2017.

Karcher, MD, Palacios JA, Bedford T, Suchard MA and Minin, VN Quantifying and mitigating the effect of preferential sampling on phylodynamic inference. *PLOS Computational Biology* 2016.