Example used in manuscript

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This is the code to reproduce an example shown in the manuscript. The main point is to show that ignoring changes in the local population size leads to false negatives.

Initialisation

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

Simulation with a single import

Let's consider that the local population started in 2020 and a single import occurred in 2020.5. 1000 genomes were sampled between 2020 and 2021.
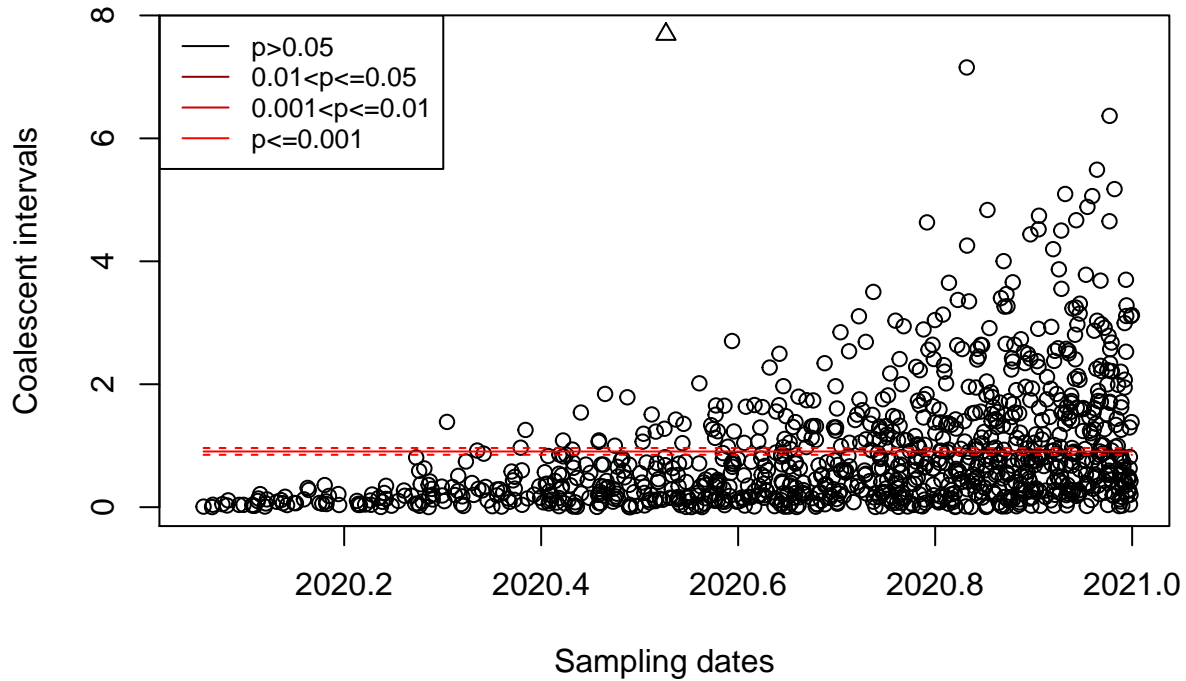
```
tree=simImports(localPopStart=2020,importDates=c(2020.5),
                samplingStartDate=2020,samplingEndDate=2021,samplingNumber=1000)
plot(tree,show.tip.label = F)
axisPhylo(backward = F)
```
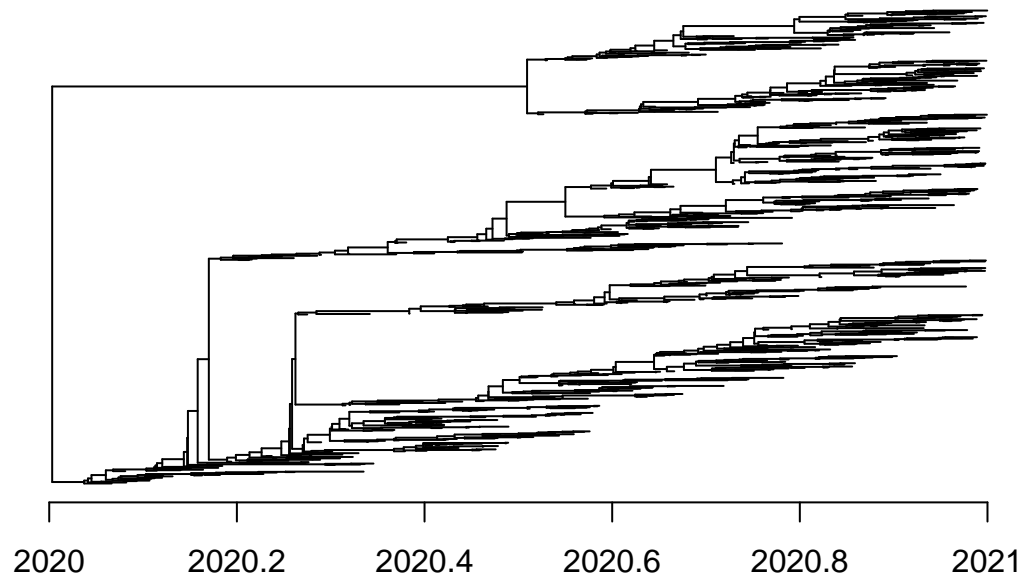
Inference assuming constant population size

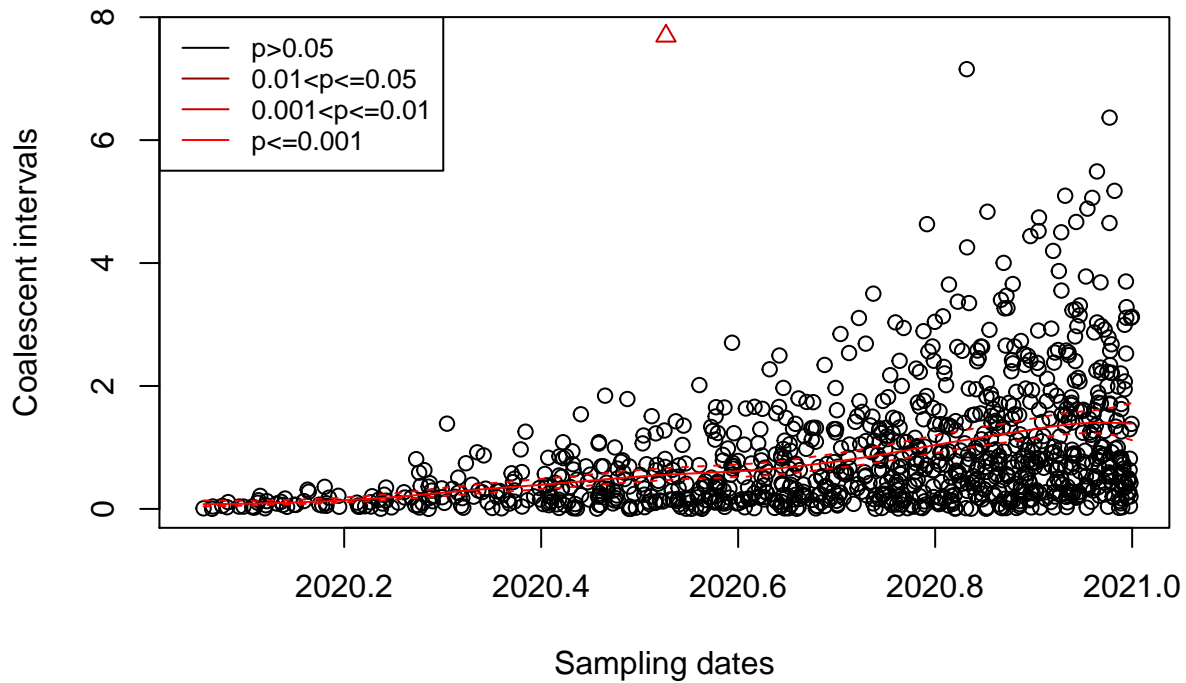Let's detect the imports under the constant population size model:

```r
res=detectImports(tree,constant=T,verbose=F,seed=0)
plot(res)
```


Inference under full model

Let's detect the imports under the full model:

```r
res2=detectImports(tree,verbose=F,seed=0)
plot(res2)
```

p>0.05
0.01<p<=0.05
0.001<p<=0.01
p<=0.001

Coalescent intervals

Sampling dates

2020.2   2020.4   2020.6   2020.8   2021.0

Combine into a figure to include in paper

```r
pdf('/tmp/figFalseNeg.pdf',5,7)
par(mfrow=c(3,1),mar = c(3,4,3,4),xpd=NA)
plotImports(tree,tree$imports,xaxs='i')
plot(res ,xlim=c(2020,2021),bty='l',xaxs='i',xaxt='n')
axis(1,2020+seq(0,1,0.2),2020+seq(0,1,0.2))
plot(res2,xlim=c(2020,2021),bty='l',xaxs='i',xaxt='n')
axis(1,2020+seq(0,1,0.2),2020+seq(0,1,0.2))
text(2020-0.1,33,'A',cex=2)
text(2020-0.1,21,'B',cex=2)
text(2020-0.1,8.5,'C',cex=2)
dev.off()
```

```
## pdf
##   2
```

```r
system('open /tmp/figFalseNeg.pdf')
```