

Example used in manuscript

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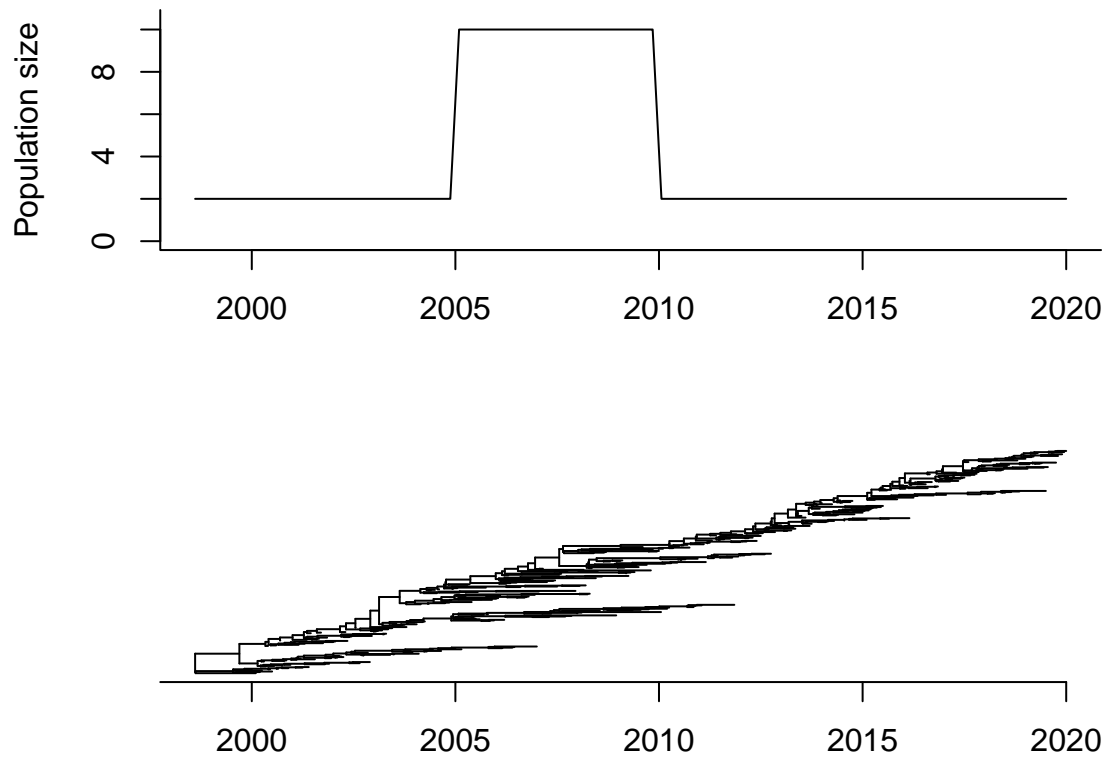
This is the code to reproduce an example shown in the manuscript. The main point is to show that ignoring changes in the local population size leads to false positives.

Initialisation

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

Simulation with no import but varying population size

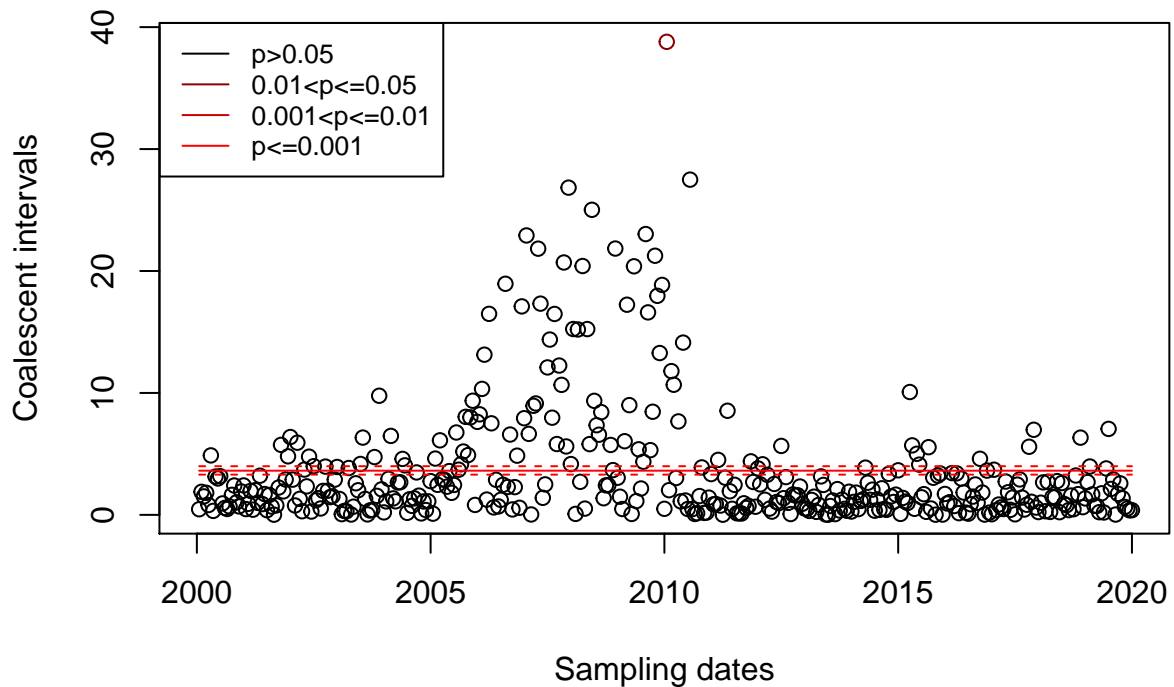
```
set.seed(0)
Ne=function(t){if (t>2010|t<2005) return(2) else return(10)}
tree=simCoal(seq(2000,2020,0.05),Ne)
plotBoth(tree,Ne)
```



Inference assuming constant population size

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

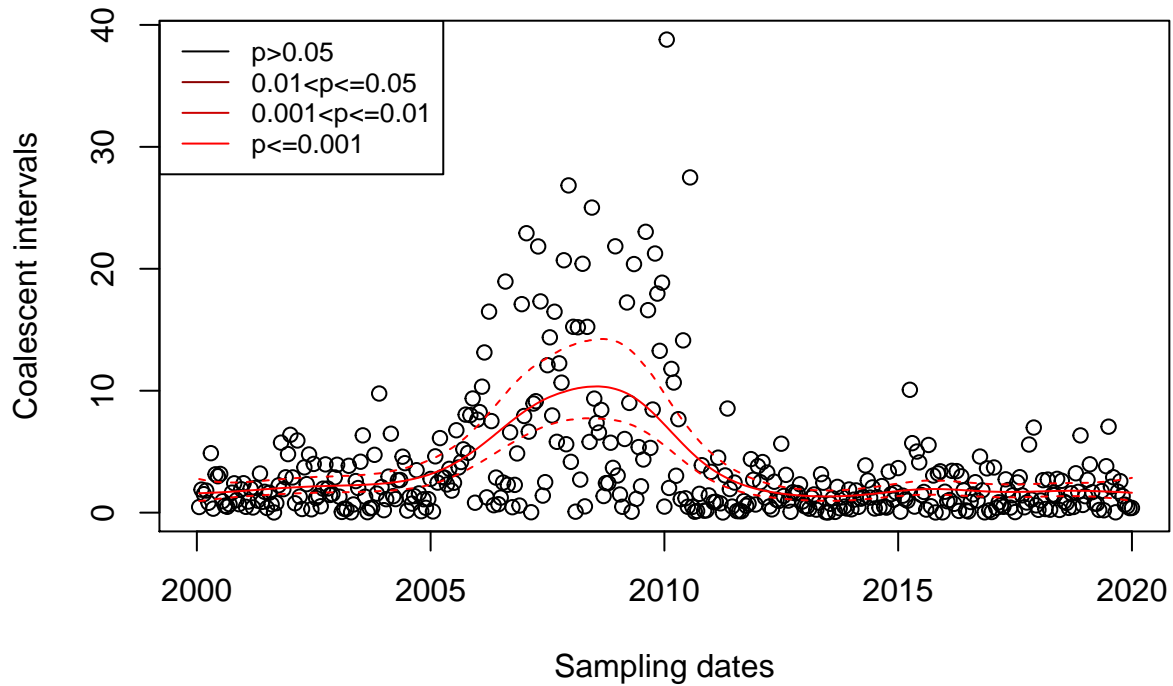
```
res=detectImports(tree,constant=T,verbose=F,seed=0)
plot(res)
```



Inference under full model

Let's detect the imports under the full model:

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



Combine into a figure to include in paper

```
pdf('/tmp/figFalsePos.pdf',5,7)
par(mfrow=c(3,1),mar = c(3,4,3,4),xpd=NA)
plotImports(tree,tree$imports,xaxs='i')
plot(res,bty='l',xlim=c(1998.5,2020),xaxs='i')#,xaxt='n')
#axis(1,2020+seq(0,1,0.2),2020+seq(0,1,0.2))
plot(res2,bty='l',xlim=c(1998.5,2020),xaxs='i')#,xaxt='n')
#axis(1,2020+seq(0,1,0.2),2020+seq(0,1,0.2))
text(1996.5,33*5,'A',cex=2)
text(1996.5,21*5,'B',cex=2)
text(1996.5,8.5*5,'C',cex=2)
dev.off()
```

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

```
system('open /tmp/figFalsePos.pdf')
```