```
## Load libraries
library(splines)
library(MASS)

library(doParallel) ##to make cluster (on Windows)

## Warning:  package 'doParallel' was built under R version 3.3.2
## Loading required package:  foreach
## Loading required package:  iterators
## Loading required package:  parallel

library(foreach) ##to use foreach function that does the parallel processing
library(doRNG) ##for reproducible seeds when doing parallel processing

## Loading required package:  rngtools
## Loading required package:  pkgmaker
## Loading required package:  registry
##
## Attaching package:  'pkgmaker'
## The following object is masked from 'package:base':
##
##    isNamespaceLoaded

##Source functions
source("../functions.R")

## Define the number of tests
ntest <- 1000

## Set nuber of simulations
nSims <- 10000

##second shape parameter for beta distribution
shape2 <- 2
```

1 Probability of being a false positive as a linear function of time

```
## Set up the time vector and the probability of being null
tme <- seq(-1,2,length=ntest)
pi0 <- 1/4*tme+1/2

##Simulate data
```

```
cl<-makeCluster(8) ##specify number of cores less than or equal to number of cores on your c
registerDoParallel(cl)

set.seed(1345)

pValuesSims <- foreach(sim=1:nSims) %dorng% {
  genPvalsInd(pi0, shape2)
}

##close the cluster
stopCluster(cl)

##save results
save(file="simResults_1.RData",
     list=c("pValuesSims"))
```

2 Probability of being a false positive as a smooth function of time

```
## Set up the time vector and the probability of being null
tme <- seq(-1,2,length=ntest)
pi0 <- pnorm(tme)

##Simulate data
cl<-makeCluster(8) ##specify number of cores less than or equal to number of cores on your c
registerDoParallel(cl)

set.seed(1345)

pValuesSims <- foreach(sim=1:nSims) %dorng% {
  genPvalsInd(pi0, shape2)
}

##close the cluster
stopCluster(cl)

##save results
save(file="simResults_2.RData",
     list=c("pValuesSims"))
```

3 Probability of being a false positive as a sine + step function

```
## Set up the time vector and the probability of being null
tme1 <- seq(-1*pi,2*pi,length=ntest)
tme2 <- rep(1:0, each=ntest/2)
pi0 <- 1/4*sin(tme1) + tme2/4 + 1/2
range(pi0)

## [1] 0.2500028 0.9999972

##Simulate data
cl<-makeCluster(8) ##specify number of cores less than or equal to number of cores on your c
registerDoParallel(cl)

set.seed(1345)

pValuesSims <- foreach(sim=1:nSims) %dorng% {
  genPvalsInd(pi0, shape2)
}

##close the cluster
stopCluster(cl)

save(file="simResults_3.RData",
     list=c("pValuesSims"))
```

Session info:

```
devtools::session_info()

## Session info -------------------------------------------------

##  setting  value
##  version  R version 3.3.1 (2016-06-21)
##  system   x86_64, mingw32
##  ui       RTerm
##  language (EN)
##  collate  English_United States.1252
##  tz       America/New_York
##  date     2017-01-04

## Packages -----------------------------------------------------

##  package    * version date       source
##  codetools    0.2-14  2015-07-15 CRAN (R 3.3.1)
```

```
##  devtools     1.12.0  2016-06-24 CRAN (R 3.3.1)
##  digest       0.6.9   2016-01-08 CRAN (R 3.3.1)
##  doParallel * 1.0.10  2015-10-14 CRAN (R 3.3.2)
##  doRNG      * 1.6     2014-03-07 CRAN (R 3.3.1)
##  evaluate     0.10    2016-10-11 CRAN (R 3.3.2)
##  foreach    * 1.4.3   2015-10-13 CRAN (R 3.3.1)
##  highr        0.6     2016-05-09 CRAN (R 3.3.1)
##  iterators  * 1.0.8   2015-10-13 CRAN (R 3.3.0)
##  knitr      * 1.15.1  2016-11-22 CRAN (R 3.3.2)
##  magrittr     1.5     2014-11-22 CRAN (R 3.3.1)
##  MASS       * 7.3-45  2016-04-21 CRAN (R 3.3.1)
##  memoise      1.0.0   2016-01-29 CRAN (R 3.3.1)
##  pkgmaker   * 0.22    2014-05-14 CRAN (R 3.3.1)
##  registry   * 0.3     2015-07-08 CRAN (R 3.3.1)
##  rngtools   * 1.2.4   2014-03-06 CRAN (R 3.3.1)
##  stringi      1.1.1   2016-05-27 CRAN (R 3.3.0)
##  stringr      1.0.0   2015-04-30 CRAN (R 3.3.1)
##  withr        1.0.2   2016-06-20 CRAN (R 3.3.1)
##  xtable       1.8-2   2016-02-05 CRAN (R 3.3.1)
```