simTool

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Contents

1 Note

This SweaveFile is part of μToss package. But because some parts of this document are computational intensiv the extension of the Sweavefile is ".actuallyRnw".

2 Introduction

This document will give an introduction to the use of simTool. We will start with a very simple application then raise the degree of complexity in a few steps and in the end reproduce some of the results from Benjamini, Krieger, Yekutieli (2006). Basically for a simulation we need the following things

1. a function that generates the data (for example p-values)
2. some procedures that evaluates the generated data (for example the bonferroni correction)
3. statistics we want to calculate. For example the the false discovery proportion (FDP).

If we are speak for example of 1000 replications, we mean that these 3 steps were repeated 1000 times. That means, after 1000 replications there have been 1000 data sets generated. Every procedure was applied to these 1000 data sets. If we have specified for example 3 procedures then every of these procedures will give us an output, this means 3000 "output objects". And every specified statistic is applied to these 3000 "output objects".

2.1 Motivation

2.1.1 Example 1

Suppose we want to compare some characteristics of the two procedures `BH` and `holm`. Denote by $V_n(BH)$ and $V_n(holm)$ the number of true hypotheses rejected. For example we are interested in the distribution of $V_n(BH)$ and $V_n(holm)$ and also in $E[V_n(BH)]$ and $E[V_n(holm)]$. Lets have a look on the arguments of theses procedures:

```
> args(BH)

function (pValues, alpha, silent = FALSE)
NULL

> args(holm)

function (pValues, alpha, silent = FALSE)
NULL
```

Both have the argument `alpha`, which stands for the niveau of the corresponding error measure. `BH` controls the false discovery rate (FDR) and `holm` controls the family-wise error rate (FWER). One question may be how must `alpha` be set in `holm` such that for fixed `alpha` $= 0.1$ in `BH` we have $E[V_n(BH)] \approx E[V_n(holm)]$? And perhaps we are also interested in how a dependence structure affects the distribution of $V_n(BH)$ and $V_n(holm)$.

2.1.2 Example 2

Suppose you have developed a new procedure controlling some error measure and you want to compare this new procedure with some other already established procedures. Then a simulation study will consist of creating data and gathering statistics for different sample sizes, dependence structures and parameter constellations.

Basically it is always the same story. Data is generated by a specific function, perhaps this depends on some parameters, and we want to apply different procedures, again depending on some paramters, to this generated data. Nearly everyone will say, "don't bother me with the details of programming, just do the simulation with the above information and give me a nice `data.frame` which I can analyze." And this is exactly the purpose of the simTool.

2.2 Data generating function

For now we only want to use the procedures `BH` and `holm`. Again, lets have a look on the arguments of these procedures:

```
> args(BH)

function (pValues, alpha, silent = FALSE)
NULL

> args(holm)

function (pValues, alpha, silent = FALSE)
NULL
```

Not much has to be specified. The parameter `alpha` is the level at which the corresponding error rate should be controlled and `pValues` are the p-values of the hypotheses that should be tested. In general, if we say that we reject a p-value this means that we reject the corresponding hypotheses. The following function generates data and will be used throughout the whole document. The data generating function **must have** an entry $procInput. All in $procInput will be used as input for the specified procedures. In our situation we will generate a list with 2 entries. $procInput will only consist of the generated p-values . And $groundTruth indicates which p-value corresponds to a true or false hypothesis.

```
> pValFromEquiCorrData <- function(sampleSize, rho, mu, pi0) {
+     nmbOfFalseHyp <- round(sampleSize * (1 - pi0))
+     nmbOfTrueHyp <- sampleSize - nmbOfFalseHyp
+     muVec <- c(rep(mu, nmbOfFalseHyp), rep(0, nmbOfTrueHyp))
+     Y <- sqrt(rho) * rnorm(1) + sqrt(1 - rho) * rnorm(sampleSize) +
+         muVec
+     return(list(procInput = list(pValues = 1 - pnorm(Y)), groundTruth = muVec ==
+         0))
+ }
```

2.2.1 Illustration of generated Data

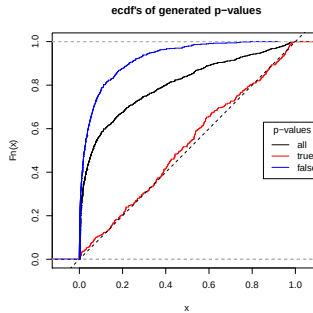
We will now generate 1000 p-Values independently (`rho` $= 0$). `sampleSize *` `(1-pi0)` $= 700$ of them correspond to false hypotheses and 300 to true hypotheses.

```
> set.seed(123)
> data <- pValFromEquiCorrData(sampleSize = 1000, rho = 0, mu = 2,
+     pi0 = 0.3)
```

Lets visualize the different p-values .

```
> local({
+     pValues = data$procInput$pValues
+     groundTruth = data$groundTruth
+     plot(ecdf(pValues), do.points = FALSE, verticals = TRUE,
+         main = "ecdf's of generated p-values")
```

```
+     lines(ecdf(pValues[groundTruth]), do.points = FALSE, verticals = TRUE,
+         col = 2)
+     lines(ecdf(pValues[!groundTruth]), do.points = FALSE, verticals = TRUE,
+         col = 4)
+     abline(0, 1, lty = 2)
+     legend("right", legend = c("all", "true", "false"), col = c(1,
+         2, 4), lty = 1, title = "p-values")
+ })
```



2.3 A very simple example

Lets directly start with the function call and then analysing what happend. Just for now we implement a simple version of the data generating function in section 2.2 and a simple version of the BH.

```
> myGen <- function() {
+     pValFromEquiCorrData(sampleSize = 200, rho = 0, mu = 2, pi0 = 0.5)
+ }
> BH.05 = function(pValues) {
+     BH(pValues = pValues, alpha = 0.05, silent = TRUE)
+ }

> set.seed(123)
> sim <- simulation(replications = 10, list(funName = "myGen",
+     fun = myGen), list(list(funName = "BH.simple", fun = BH.05)))
```

The following happend:

1. Call `myGen`
2. Append generated data set to `sim$data`
3. Call `BH.05` with the generated p-values
4. Add to the results of `BH.05` the parameter constellation used by `myGen` and `BH.05` and also the position of the used data in `sim$data`
5. Append this extended results of `BH.05` to `sim$results`
6. repeat this 9 more times

Since `replications = 10` in `simulation` the object `sim` consists of:

```
> names(sim)

[1] "data"    "results"

> length(sim$data)

[1] 10

> length(sim$results)

[1] 10
```

The structure of one object in `sim$data` coincides with the structure of the return of `myGen`:

```
> names(myGen())

[1] "procInput"   "groundTruth"

> names(sim$data[[1]])

[1] "procInput"   "groundTruth"
```

Lets have a look at the additional information added by `simulation` to the object returned by `BH.05`. First the entries of the pure return value of `BH.05` and then of `sim$results`

```
> names(BH.05(runif(100)))

[1] "adjPValues"     "criticalValues" "rejected"       "errorControl"

> names(sim$results[[1]])

[1] "data.set.number" "parameters"      "adjPValues"      "criticalValues"
[5] "rejected"        "errorControl"
```

`data.set.number` is the number of the used data set in `sim$data`. Since every generated data set is used only once we have

```
> sapply(sim$results, function(x) x$data.set.number)

 [1]  1  2  3  4  5  6  7  8  9 10
```

Thus it is possible to reproduce any result directly. Let us reproduce the results of the 6th replication

```
> idx <- sim$results[[6]]$data.set.number
> pValues <- sim$data[[idx]]$procInput$pValues
> all(BH.05(pValues)$adjPValues == sim$results[[6]]$adjPValues)
```

```
[1] TRUE
```

Since our data generating function and procedure did not really have any parameter, there is not much information in:

```
> sim$results[[1]]$parameters
```

```
$funName
[1] "myGen"

$method
[1] "BH.simple"
```

Note, `BH.05` technically has the parameter `pValues` but since this parameter is the "input channel" for the output data of the data generating function it is not really regarded as parameter that affect the behaviour of the procedure like for example the level α for the error measure.

2.4 A simple example

Indeed, for the simple example above the simTool is not very helpful. Let us increase the complexity of our simulation. As a first step, we want to increase the parameter `rho` of the data generating function gradually and investigate $EV_n(BH)$ and $EV_n^2(BH)$.

```
> set.seed(123)
> sim <- simulation(replications = 10, list(funName = "pVGen",
+     fun = pValFromEquiCorrData, sampleSize = 100, rho = seq(0,
+         1, by = 0.2), mu = 2, pi0 = 0.5), list(list(funName = "BH",
+     fun = BH, alpha = c(0.5, 0.25), silent = TRUE)))
```

The following happend:

1. Call `myGen` with `rho = 0`
2. Append generated data set to `sim$data`
3. Call `BH` with `alpha = 0.5` and the generated p-values
4. Add to the results the parameter constellation used by `myGen` and `BH` and also the position of the used data in `sim$data`
5. Append this extended results to `sim$results`
6. Call `BH` with `alpha = 0.25` and the **same** p-values as in 3.
7. Add to the results the parameter constellation used by `myGen` and `BH` and also the position of the used data in `sim$data`

8. Append this extended results of to `sim$results`
9. repeat this 9 more times
10. Call `myGen` with `rho = 0.2`
11. and so on

So we have now a bunch of data sets and results.

```
> length(sim$data)
```

```
[1] 60
```

```
> length(sim$results)
```

```
[1] 120
```

60 data sets have been generated because we have `rho = 0, 0.2, 0.4, 0.6, 0.8, 1` and for each `rho` we generated 10 data sets. We have applied `BH` with `alpha = 0.5` to all 60 data sets and `BH` with `alpha = 0.25`, yielding 120 objects in `results`. We see from the `data.set.number` that after generating a data set it is used two times in series

```
> sapply(sim$results, function(x) x$data.set.number)
```

```
  [1]  1  1  2  2  3  3  4  4  5  5  6  6  7  7  8  8  9  9 10 10 11 11 12 12 13
 [26] 13 14 14 15 15 16 16 17 17 18 18 19 19 20 20 21 21 22 22 23 23 24 24 25 25
 [51] 26 26 27 27 28 28 29 29 30 30 31 31 32 32 33 33 34 34 35 35 36 36 37 37 38
 [76] 38 39 39 40 40 41 41 42 42 43 43 44 44 45 45 46 46 47 47 48 48 49 49 50 50
[101] 51 51 52 52 53 53 54 54 55 55 56 56 57 57 58 58 59 59 60 60
```

In order to gather how many true hypotheses have been rejected corresponding to the different parameter constellations we need a function that is able to calculate it.

```
> NumberOfType1Error <- function(data, result) sum(data$groundTruth *
+     result$rejected)
> V2 <- function(data, result) NumberOfType1Error(data, result)^2
```

Lets us calculate for the first result object the number of rejected true hypotheses explicitly.

```
> idx = sim$results[[1]]$data.set.number
> data = sim$data[[idx]]
> NumberOfType1Error(data, sim$results[[1]])
```

```
[1] 15
```

This means for the following parameter constellation

```
> sim$results[[1]]$parameters
```

```
$funName
[1] "pVGen"

$sampleSize
[1] 100

$rho
[1] 0

$mu
[1] 2

$pi0
[1] 0.5

$method
[1] "BH"

$alpha
[1] 0.5

$silent
[1] TRUE
```

we one time observed

```
[1] 15
```

rejected true null hypotheses. In order to estimate $EV_n(BH)$ and $EV_n^2(BH)$ we have to search in `sim$results` for the other 9 results using the same parameter constellation. In order to facilitate this task we provide a function.

```
> result <- gatherStatistics(sim, list(V = NumberOfType1Error,
+     V2 = V2), mean)
> result

$statisticDF
   funName sampleSize rho mu pi0 method alpha silent V.mean V2.mean
1    pVGen        100   0  2 0.5     BH   0.5   TRUE   15.1   245.3
2    pVGen        100   0  2 0.5     BH  0.25   TRUE    5.9    40.9
3    pVGen        100 0.2  2 0.5     BH   0.5   TRUE   21.5   591.9
4    pVGen        100 0.2  2 0.5     BH  0.25   TRUE    9.2   163.2
5    pVGen        100 0.4  2 0.5     BH   0.5   TRUE   14.6   401.6
6    pVGen        100 0.4  2 0.5     BH  0.25   TRUE    6.2   126.6
7    pVGen        100 0.6  2 0.5     BH   0.5   TRUE   22.3   860.7
8    pVGen        100 0.6  2 0.5     BH  0.25   TRUE    9.3   265.7
9    pVGen        100 0.8  2 0.5     BH   0.5   TRUE   18.1   711.1
10   pVGen        100 0.8  2 0.5     BH  0.25   TRUE    8.0   328.6
11   pVGen        100   1  2 0.5     BH   0.5   TRUE   20.0  1000.0
12   pVGen        100   1  2 0.5     BH  0.25   TRUE   15.0   750.0
```

```
$name.parameters
[1] "funName"    "sampleSize" "rho"        "mu"         "pi0"
[6] "method"     "alpha"      "silent"

$name.statistics
[1] "V.mean"  "V2.mean"

$name.avgFun
[1] "mean"
```

As you can see every, parameter constellation has its own row in `$statisticDF`. By the way, again, we see that p-values is a parameter of `BH` but since it is contained in `$procInput` it is not considered as "real parameter".
If we are interested in more than one statistics, then we simply provide a list with "average functions"

```
> result <- gatherStatistics(sim, list(V = NumberOfType1Error,
+     V2 = V2), list(mean = mean, sd = function(vec) round(sd(vec),
+     1)))
> result$statisticDF
```

```
   funName sampleSize rho mu pi0 method alpha silent V.mean V2.mean V.sd  V2.sd
1    pVGen        100   0  2 0.5     BH   0.5   TRUE   15.1   245.3  4.4  131.7
2    pVGen        100   0  2 0.5     BH  0.25   TRUE    5.9    40.9  2.6   34.9
3    pVGen        100 0.2  2 0.5     BH   0.5   TRUE   21.5   591.9 12.0  597.3
4    pVGen        100 0.2  2 0.5     BH  0.25   TRUE    9.2   163.2  9.3  329.0
5    pVGen        100 0.4  2 0.5     BH   0.5   TRUE   14.6   401.6 14.5  684.8
6    pVGen        100 0.4  2 0.5     BH  0.25   TRUE    6.2   126.6  9.9  318.5
7    pVGen        100 0.6  2 0.5     BH   0.5   TRUE   22.3   860.7 20.1  981.2
8    pVGen        100 0.6  2 0.5     BH  0.25   TRUE    9.3   265.7 14.1  508.8
9    pVGen        100 0.8  2 0.5     BH   0.5   TRUE   18.1   711.1 20.6 1051.5
10   pVGen        100 0.8  2 0.5     BH  0.25   TRUE    8.0   328.6 17.1  801.7
11   pVGen        100   1  2 0.5     BH   0.5   TRUE   20.0  1000.0 25.8 1291.0
12   pVGen        100   1  2 0.5     BH  0.25   TRUE   15.0   750.0 24.2 1207.6
```

Another possibility is to call `gatherStatistics` without and "average function". Then every result get his own row in `$statisticDF`

```
> result <- gatherStatistics(sim, list(V = NumberOfType1Error,
+     V2 = V2))
> head(result$statisticDF)
```

```
  funName sampleSize rho mu pi0 method alpha silent  V  V2
1   pVGen        100   0  2 0.5     BH   0.5   TRUE 15 225
2   pVGen        100   0  2 0.5     BH   0.5   TRUE 10 100
3   pVGen        100   0  2 0.5     BH   0.5   TRUE 20 400
4   pVGen        100   0  2 0.5     BH   0.5   TRUE 11 121
5   pVGen        100   0  2 0.5     BH   0.5   TRUE 19 361
6   pVGen        100   0  2 0.5     BH   0.5   TRUE 16 256
```

```
> tail(result$statisticDF)
```

```
    funName sampleSize rho mu pi0 method alpha silent  V   V2
115   pVGen        100   1  2 0.5     BH  0.25   TRUE  0    0
116   pVGen        100   1  2 0.5     BH  0.25   TRUE 50 2500
117   pVGen        100   1  2 0.5     BH  0.25   TRUE 50 2500
118   pVGen        100   1  2 0.5     BH  0.25   TRUE 50 2500
119   pVGen        100   1  2 0.5     BH  0.25   TRUE  0    0
120   pVGen        100   1  2 0.5     BH  0.25   TRUE  0    0
```

2.5 Plotting a bit

```
> if (!is.element("sim.plot", ls())) {
+     sim.plot <- simulation(replications = 1000, list(funName = "pVGen",
+         fun = pValFromEquiCorrData, sampleSize = 100, rho = seq(0,
+             1, by = 0.2), mu = 0, pi0 = 1), list(list(funName = "BH",
+         fun = function(pValues, alpha) BH(pValues, alpha, silent = TRUE),
+         alpha = c(0.5, 0.75))))
+ }
> length(sim.plot$data)

[1] 6000

> length(sim.plot$results)

[1] 12000
```

The are already different kind of R functions that take data.frames and generate histograms, boxplots and so on from them. For some plot example we will need the lattice package.

```
> require(lattice)
```

First we calculate V for every MutossSim object and then plot a histogram and a boxplot of V, see Figure 1 (p. 11), Figure 2 (p. 12).

```
> result.all <- gatherStatistics(sim.plot, list(V = NumberOfType1Error))
```

Also after the "average process" we again get an data.frame which can be used to generate plots.

```
> result <- gatherStatistics(sim.plot, list(V = NumberOfType1Error),
+     list(Ml = function(x) mean(x) - 2 * sd(x)/sqrt(length(x)),
+         Mu = function(x) mean(x) + 2 * sd(x)/sqrt(length(x)),
+         M = mean, SD = sd))
> subset(result$statisticDF, alpha == "0.5")[1:3, -1]

  sampleSize rho mu pi0 method alpha      V.Ml      V.Mu     V.M      V.SD
1        100   0  0   1     BH   0.5  1.610993  1.973007  1.792  2.861980
3        100 0.2  0   1     BH   0.5  8.833764 11.544236 10.189 21.428169
5        100 0.4  0   1     BH   0.5 12.131991 15.860009 13.996 29.472574
```

```
> print(histogram(~V | rho, data = subset(result.all$statisticDF,
+      alpha == "0.5")))
```

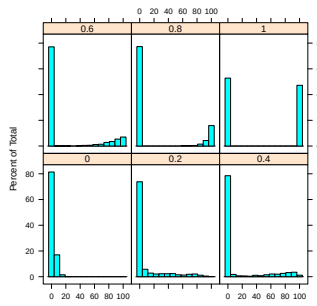


Figure 1: Histogram of the number of rejected true hypotheses for alpha equals 0.5

```
> print(bwplot(V ~ rho | alpha, data = subset(result.all$statisticDF)))
```

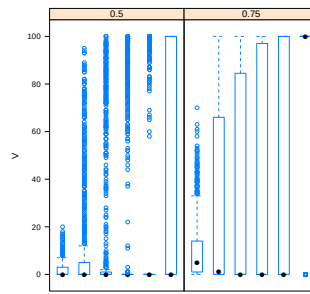


Figure 2: Boxplot of the number of rejected true hypotheses

```
> print(xyplot(V.Ml + V.M + V.Mu ~ rho | alpha, data = result$statisticDF,
+     type = "a", auto.key = list(space = "right", points = FALSE,
+         lines = TRUE)))
```

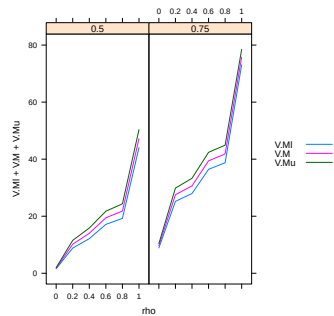


Figure 3: XYPlot of the mean number of rejected true hypotheses with asymptotic 95% confidence intervalls (pointwise)

2.6 Memory considerations

Up to now we have kept any information in memory. Somtimes, it is useful not to discard any generated Information. For example, if some objects in results appear odd, they can directly be reproduced and of course with all information availible we can investigate anything like distribution or any statistic we did not consider before the simulation. The price for this liberty is in general an extensive memory usage which of course restrict the size of our simulation. On the other hand if we exactly know that we are only interested in EV_n the mean number of true rejected hypotheses, why should we keep the generated p-values or the index of the rejected p-values ? Thus it would be enough that an obejct in `$results` contains V_n the number of rejected true hypotheses. We will know show an example were only the information needed is kept in memory. The following is basically the "simple example" from section 2.4 The main issue is to save memory thus we will calculate the V_n right after applying the procedure to the generated data set. If done so, we can also discard the generated data!

```
> V.BH <- function(pValues, groundTruth, alpha) {
+     out <- BH(pValues, alpha, silent = TRUE)
+     V <- sum(out$rejected * groundTruth)
+     return(list(V = V))
+ }
```

As already mentioned anything in `$procInput` will be used as an input for the procedures. Since our procedure now has a parameter `groundTruth` our data generated function has to be adepted. We just move `groundTruth` in `$procInput`.

```
> pValFromEquiCorrData2 <- function(sampleSize, rho, mu, pi0) {
+     nmbOfFalseHyp <- round(sampleSize * (1 - pi0))
+     nmbOfTrueHyp <- sampleSize - nmbOfFalseHyp
+     muVec <- c(rep(mu, nmbOfFalseHyp), rep(0, nmbOfTrueHyp))
+     Y <- sqrt(rho) * rnorm(1) + sqrt(1 - rho) * rnorm(sampleSize) +
+         muVec
+     return(list(procInput = list(pValues = 1 - pnorm(Y), groundTruth = muVec ==
+         0)))
+ }
```

Obviously, it is unnecessary to store this generated data, because the number of Type 1 Errors we are interested in will be directly calculated. Setting `discardProcInput = TRUE` in `simulation` removes `$procInput` from the object generated by the data generating function after `$procInput` has been used by all specified procedures. In our case theses will be the 2 procedures `V.BH` with `alpha = 0.5` and `alpha = 0.25`.

```
> set.seed(123)
> sim <- simulation(replications = 10, list(funName = "pVGen2",
+     fun = pValFromEquiCorrData2, sampleSize = 100, rho = seq(0,
+         1, by = 0.2), mu = 2, pi0 = 0.5), list(list(funName = "V.BH",
+     fun = V.BH, alpha = c(0.5, 0.25))), discardProcInput = TRUE)
> result <- gatherStatistics(sim, list(V = function(data, results) results$V),
+     mean)
> result
```

```
$statisticDF
   funName sampleSize rho mu pi0 method alpha V.mean
1   pVGen2        100   0  2 0.5   V.BH   0.5   15.1
2   pVGen2        100   0  2 0.5   V.BH  0.25    5.9
3   pVGen2        100 0.2  2 0.5   V.BH   0.5   21.5
4   pVGen2        100 0.2  2 0.5   V.BH  0.25    9.2
5   pVGen2        100 0.4  2 0.5   V.BH   0.5   14.6
6   pVGen2        100 0.4  2 0.5   V.BH  0.25    6.2
7   pVGen2        100 0.6  2 0.5   V.BH   0.5   22.3
8   pVGen2        100 0.6  2 0.5   V.BH  0.25    9.3
9   pVGen2        100 0.8  2 0.5   V.BH   0.5   18.1
10  pVGen2        100 0.8  2 0.5   V.BH  0.25    8.0
11  pVGen2        100   1  2 0.5   V.BH   0.5   20.0
12  pVGen2        100   1  2 0.5   V.BH  0.25   15.0

$name.parameters
[1] "funName"    "sampleSize" "rho"        "mu"         "pi0"
[6] "method"     "alpha"

$name.statistics
[1] "V.mean"

$name.avgFun
[1] "mean"
```

Here the corresponding table from section 2.4.

```
> set.seed(123)
> sim.simple <- simulation(replications = 10, list(funName = "pVGen",
+     fun = pValFromEquiCorrData, sampleSize = 100, rho = seq(0,
+         1, by = 0.2), mu = 2, pi0 = 0.5), list(list(funName = "BH",
+     fun = BH, alpha = c(0.5, 0.25), silent = TRUE)))
> result.simple <- gatherStatistics(sim.simple, list(V = NumberOfType1Error),
+     mean)
> print(result.simple)

$statisticDF
   funName sampleSize rho mu pi0 method alpha silent V.mean
1    pVGen        100   0  2 0.5     BH   0.5   TRUE   15.1
2    pVGen        100   0  2 0.5     BH  0.25   TRUE    5.9
3    pVGen        100 0.2  2 0.5     BH   0.5   TRUE   21.5
4    pVGen        100 0.2  2 0.5     BH  0.25   TRUE    9.2
5    pVGen        100 0.4  2 0.5     BH   0.5   TRUE   14.6
6    pVGen        100 0.4  2 0.5     BH  0.25   TRUE    6.2
7    pVGen        100 0.6  2 0.5     BH   0.5   TRUE   22.3
8    pVGen        100 0.6  2 0.5     BH  0.25   TRUE    9.3
9    pVGen        100 0.8  2 0.5     BH   0.5   TRUE   18.1
10   pVGen        100 0.8  2 0.5     BH  0.25   TRUE    8.0
11   pVGen        100   1  2 0.5     BH   0.5   TRUE   20.0
12   pVGen        100   1  2 0.5     BH  0.25   TRUE   15.0
```

```
$name.parameters
[1] "funName"    "sampleSize" "rho"        "mu"         "pi0"
[6] "method"     "alpha"      "silent"

$name.statistics
[1] "V.mean"

$name.avgFun
[1] "mean"
```

The same results but the memory usage differ much:

```
> print(s1 <- object.size(sim))

127192 bytes

> print(s2 <- object.size(sim.simple))

565912 bytes

> unclass(s2/s1)

[1] 4.449274
```

3 Reproducing some results from BKY (2006)

Now, we will reproduce figure 1 from the publication. For this we need to estimate the FDR. This will be done be calculating the FDP for every object in `$results` and then calculating the empirical mean. In this simulation where we exactly know what we want and thus retain only the necessary information. To be able to calculate the FDP right after applying the procedure we need to know which pValue belongs to a true or false hypothesis. Thus, like in the foregoing section, `$groundTruth` will be an element of `$procInput`.

```
> pValFromEquiCorrData2 <- function(sampleSize, rho, mu, pi0) {
+     nmbOfFalseHyp <- round(sampleSize * (1 - pi0))
+     nmbOfTrueHyp <- sampleSize - nmbOfFalseHyp
+     muVec <- c(rep(mu, nmbOfFalseHyp), rep(0, nmbOfTrueHyp))
+     Y <- sqrt(rho) * rnorm(1) + sqrt(1 - rho) * rnorm(sampleSize) +
+         muVec
+     return(list(procInput = list(pValues = 1 - pnorm(Y), groundTruth = muVec ==
+         0)))
+ }
```

We also need a function that calculates the FDP.

```
> FDP <- function(pValues, groundTruth, proc = c("BH", "M-S-HLF")) {
+     if (proc == "BH")
+         out <- BH(pValues, alpha = 0.05, silent = TRUE)
+     else out <- adaptiveSTS(pValues, alpha = 0.05, silent = TRUE)
+     R <- sum(out$rejected)
+     if (R == 0)
```

```
+         return(list(FDP = 0))
+     V <- sum(out$rejected * groundTruth)
+     return(list(FDP = V/R))
+ }
```

Now, the (partial) reproduction of the results can start!

```
> set.seed(123)
> date()

[1] "Thu Dec 01 18:05:29 2011"

> sim <- simulation(replications = 10000, list(funName = "pVGen2",
+     fun = pValFromEquiCorrData2, sampleSize = c(16, 32, 64, 128,
+         256, 512), rho = c(0, 0.1, 0.5), mu = 5, pi0 = c(0.25,
+         0.75)), list(list(funName = "FDP", fun = FDP, proc = c("BH",
+     "M-S-HLF"))), discardProcInput = TRUE)
> date()

[1] "Thu Dec 01 18:39:30 2011"

> result <- gatherStatistics(sim, list(FDP = function(data, results) results$FDP),
+     mean)> result

$statisticDF
   funName sampleSize rho mu  pi0 method    proc   FDP.mean
1   pVGen2         16   0  5 0.25    FDP      BH 0.01243507
2   pVGen2         16   0  5 0.25    FDP M-S-HLF 0.04680482
3   pVGen2         32   0  5 0.25    FDP      BH 0.01254447
4   pVGen2         32   0  5 0.25    FDP M-S-HLF 0.04933171
5   pVGen2         64   0  5 0.25    FDP      BH 0.01245073
6   pVGen2         64   0  5 0.25    FDP M-S-HLF 0.05027779
7   pVGen2        128   0  5 0.25    FDP      BH 0.01250933
8   pVGen2        128   0  5 0.25    FDP M-S-HLF 0.05000333
9   pVGen2        256   0  5 0.25    FDP      BH 0.01259937
10  pVGen2        256   0  5 0.25    FDP M-S-HLF 0.05021692
11  pVGen2        512   0  5 0.25    FDP      BH 0.01246457
12  pVGen2        512   0  5 0.25    FDP M-S-HLF 0.04993815
13  pVGen2         16 0.1  5 0.25    FDP      BH 0.01243852
14  pVGen2         16 0.1  5 0.25    FDP M-S-HLF 0.04929676
15  pVGen2         32 0.1  5 0.25    FDP      BH 0.01290907
16  pVGen2         32 0.1  5 0.25    FDP M-S-HLF 0.05355816
17  pVGen2         64 0.1  5 0.25    FDP      BH 0.01271804
18  pVGen2         64 0.1  5 0.25    FDP M-S-HLF 0.05626510
19  pVGen2        128 0.1  5 0.25    FDP      BH 0.01233749
20  pVGen2        128 0.1  5 0.25    FDP M-S-HLF 0.05637963
21  pVGen2        256 0.1  5 0.25    FDP      BH 0.01231818
22  pVGen2        256 0.1  5 0.25    FDP M-S-HLF 0.05619898
23  pVGen2        512 0.1  5 0.25    FDP      BH 0.01248149
24  pVGen2        512 0.1  5 0.25    FDP M-S-HLF 0.05719747
25  pVGen2         16 0.5  5 0.25    FDP      BH 0.01269308
26  pVGen2         16 0.5  5 0.25    FDP M-S-HLF 0.06255181
```

```
27  pVGen2          32 0.5  5 0.25    FDP       BH 0.01227550
28  pVGen2          32 0.5  5 0.25    FDP M-S-HLF 0.06710637
29  pVGen2          64 0.5  5 0.25    FDP       BH 0.01183768
30  pVGen2          64 0.5  5 0.25    FDP M-S-HLF 0.07187446
31  pVGen2         128 0.5  5 0.25    FDP       BH 0.01200182
32  pVGen2         128 0.5  5 0.25    FDP M-S-HLF 0.07523846
33  pVGen2         256 0.5  5 0.25    FDP       BH 0.01245500
34  pVGen2         256 0.5  5 0.25    FDP M-S-HLF 0.07724869
35  pVGen2         512 0.5  5 0.25    FDP       BH 0.01193485
36  pVGen2         512 0.5  5 0.25    FDP M-S-HLF 0.07817799
37  pVGen2          16   0  5 0.75    FDP       BH 0.03687048
38  pVGen2          16   0  5 0.75    FDP M-S-HLF 0.05066989
39  pVGen2          32   0  5 0.75    FDP       BH 0.03771246
40  pVGen2          32   0  5 0.75    FDP M-S-HLF 0.04999444
41  pVGen2          64   0  5 0.75    FDP       BH 0.03736944
42  pVGen2          64   0  5 0.75    FDP M-S-HLF 0.04979089
43  pVGen2         128   0  5 0.75    FDP       BH 0.03716345
44  pVGen2         128   0  5 0.75    FDP M-S-HLF 0.04963708
45  pVGen2         256   0  5 0.75    FDP       BH 0.03812883
46  pVGen2         256   0  5 0.75    FDP M-S-HLF 0.05079616
47  pVGen2         512   0  5 0.75    FDP       BH 0.03731167
48  pVGen2         512   0  5 0.75    FDP M-S-HLF 0.05002008
49  pVGen2          16 0.1  5 0.75    FDP       BH 0.03624063
50  pVGen2          16 0.1  5 0.75    FDP M-S-HLF 0.06107526
51  pVGen2          32 0.1  5 0.75    FDP       BH 0.03702100
52  pVGen2          32 0.1  5 0.75    FDP M-S-HLF 0.06206310
53  pVGen2          64 0.1  5 0.75    FDP       BH 0.03771594
54  pVGen2          64 0.1  5 0.75    FDP M-S-HLF 0.06404561
55  pVGen2         128 0.1  5 0.75    FDP       BH 0.03677325
56  pVGen2         128 0.1  5 0.75    FDP M-S-HLF 0.06185353
57  pVGen2         256 0.1  5 0.75    FDP       BH 0.03694803
58  pVGen2         256 0.1  5 0.75    FDP M-S-HLF 0.06317781
59  pVGen2         512 0.1  5 0.75    FDP       BH 0.03694764
60  pVGen2         512 0.1  5 0.75    FDP M-S-HLF 0.06267116
61  pVGen2          16 0.5  5 0.75    FDP       BH 0.03533002
62  pVGen2          16 0.5  5 0.75    FDP M-S-HLF 0.11075864
63  pVGen2          32 0.5  5 0.75    FDP       BH 0.03501351
64  pVGen2          32 0.5  5 0.75    FDP M-S-HLF 0.11841870
65  pVGen2          64 0.5  5 0.75    FDP       BH 0.03331830
66  pVGen2          64 0.5  5 0.75    FDP M-S-HLF 0.12028660
67  pVGen2         128 0.5  5 0.75    FDP       BH 0.03413304
68  pVGen2         128 0.5  5 0.75    FDP M-S-HLF 0.12464657
69  pVGen2         256 0.5  5 0.75    FDP       BH 0.03561711
70  pVGen2         256 0.5  5 0.75    FDP M-S-HLF 0.12532959
71  pVGen2         512 0.5  5 0.75    FDP       BH 0.03463151
72  pVGen2         512 0.5  5 0.75    FDP M-S-HLF 0.12510925

$name.parameters
[1] "funName"    "sampleSize" "rho"        "mu"         "pi0"
[6] "method"     "proc"
```

```
$name.statistics
[1] "FDP.mean"

$name.avgFun
[1] "mean"

> print(xyplot(FDP.mean ~ sampleSize | pi0 * rho, data = result$statisticDF,
+     group = proc, type = "a", auto.key = list(space = "right",
+         points = FALSE, lines = TRUE)))
```