

Analysis of data from aCGH experiments using parallel computing and ff objects: long list of examples

Ramón Díaz-Uriarte¹

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1. Department of Biochemistry, Universidad Autonoma de Madrid Instituto de Investigaciones Biomedicas “Alberto Sols” (UAM-CSIC), Madrid (SPAIN).
rdiaz02@gmail.com

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1 This vignette

We provide here example calls of all segmentation methods, with different options for methods, as well as different options for type of input object and clustering. This is provided here as both extended help and as a simple way of checking that all the functions can be run and yield the same results regardless of type of input and clustering.

2 Creating objects

We must ensure that we can run this vignette as stand alone. Thus, we load the package and create all necessary objects. This repeats work done in the main vignette.

We first try to move to the “/tmp” directory, if it exists. If it does not, the code will be executed in your current directory.

```
> try(setwd("~/tmp"))  
  
> library(ADaCGH2)  
> ## loading in-RAM objects  
> data(inputEx)  
> summary(inputEx)
```

ID	chromosome	position	L.1
Hs.101850: 1	Min. :1.00	Min. :1.18e+06	Min. : -1.078
Hs.1019 : 1	1st Qu.:1.00	1st Qu.:3.60e+07	1st Qu.: -0.226
Hs.105460: 1	Median :2.00	Median :7.08e+07	Median : -0.016
Hs.105656: 1	Mean :2.28	Mean :9.26e+07	Mean : -0.035
Hs.105941: 1	3rd Qu.:3.00	3rd Qu.:1.50e+08	3rd Qu.: 0.160
Hs.106674: 1	Max. :5.00	Max. :2.44e+08	Max. : 0.883
(Other) :494			NA's :5

L.2	m4	m5	L3
Min. : -0.795	Min. : -0.187	Min. : -4.67	Min. : -13.27
1st Qu.: -0.139	1st Qu.: 1.979	1st Qu.: -0.02	1st Qu.: 3.63
Median : -0.006	Median : 2.281	Median : 0.44	Median : 3.92
Mean : 0.008	Mean : 3.450	Mean : 1.60	Mean : 1.98
3rd Qu.: 0.134	3rd Qu.: 5.824	3rd Qu.: 3.04	3rd Qu.: 4.11
Max. : 1.076	Max. : 6.604	Max. : 9.60	Max. : 6.37
NA's :15		NA's :41	NA's :9

m6
Min. : -0.77
1st Qu.: -0.23
Median : -0.04
Mean : -0.04
3rd Qu.: 0.16
Max. : 0.78
NA's :203

```

> head(inputEx)

```

ID	chromosome	position	L.1	L.2	m4	m5
1*1180411*Hs.212680	Hs.212680	1 1180411	NA	0.038	6.226	3.226
1*1188041.5*Hs.129780	Hs.129780	1 1188042	NA	0.028	6.174	3.174
1*1194444*Hs.42806	Hs.42806	1 1194444	NA	0.042	6.174	3.174
1*1332537*Hs.76239	Hs.76239	1 1332537	NA	0.285	5.624	2.624
1*2362211*Hs.40500	Hs.40500	1 2362211	NA	0.058	5.851	2.851
1*2372287*Hs.449936	Hs.449936	1 2372287	0.294	-0.006	5.685	2.685

L3	m6
1*1180411*Hs.212680	6.038 NA
1*1188041.5*Hs.129780	6.028 NA
1*1194444*Hs.42806	6.042 NA
1*1332537*Hs.76239	NA NA
1*2362211*Hs.40500	NA NA
1*2372287*Hs.449936	NA NA

```

> cgh.dat <- inputEx[, -c(1, 2, 3)]
> chrom.dat <- as.integer(inputEx[, 2])
> pos.dat <- inputEx[, 3]
> ## choosing working dir for cluster
> originalDir <- getwd()
> if(!file.exists("ADaCGH2_vignette_tmp_dir"))
+   dir.create("ADaCGH2_vignette_tmp_dir")
> setwd("ADaCGH2_vignette_tmp_dir")
> ## creating ff objects
> fnameRdata <- list.files(path = system.file("data", package = "ADaCGH2"),
+                           full.names = TRUE, pattern = "inputEx.RData")

```

```
> inputToADaCGH(ff.or.RAM = "ff",
+               RDatafilename = fnameRdata)

... done reading; starting checks

... checking identical MidPos

... checking need to reorder inputData, data.frame version

... done with checks; starting writing

... done writing/saving probeNames

... done writing/saving chromData

... done writing/saving posData

... done writing/saving cghData
```

Calling gc at end

```
          used (Mb) gc trigger   (Mb) max used (Mb)
Ncells 1557642 83.2    2403845 128.4  1835812 98.1
Vcells 1528388 11.7    2481603  19.0   2001668 15.3
```

Files saved in current directory
/home/ramon/tmp/ADaCGH2_vignette_tmp_dir
with names :
chromData.RData, posData.RData, cghData.RData, probeNames.RData.

```
> ## setting random number generator for forking
> RNGkind("L'Ecuyer-CMRG")
> ## initializing cluster and setting up random number generator
> number.of.nodes <- detectCores()
> cl2 <- parallel::makeCluster(number.of.nodes,"PSOCK")
> parallel::clusterSetRNGStream(cl2)
> parallel::setDefaultCluster(cl2)
> parallel::clusterEvalQ(NULL, library("ADaCGH2"))
```

```
[[1]]
[1] "ADaCGH2"    "ff"         "bit"         "tools"       "parallel"    "methods"
[7] "stats"      "graphics"   "grDevices"   "utils"       "datasets"    "base"
```

```
[[2]]
[1] "ADaCGH2"    "ff"         "bit"         "tools"       "parallel"    "methods"
[7] "stats"      "graphics"   "grDevices"   "utils"       "datasets"    "base"
```

```
[[3]]
[1] "ADaCGH2"    "ff"         "bit"         "tools"       "parallel"    "methods"
[7] "stats"      "graphics"   "grDevices"   "utils"       "datasets"    "base"
```

```
[[4]]
```

```

[1] "ADaCGH2"      "ff"          "bit"          "tools"        "parallel"     "methods"
[7] "stats"        "graphics"    "grDevices"    "utils"        "datasets"     "base"

> ## verify we are using the right version of ADaCGH2
> parallel::clusterEvalQ(NULL,
+                           library(help = ADaCGH2)$info[[1]][[2]])

[[1]]
[1] "Version:      2.3.6"

[[2]]
[1] "Version:      2.3.6"

[[3]]
[1] "Version:      2.3.6"

[[4]]
[1] "Version:      2.3.6"

> wdir <- getwd()
> parallel::clusterExport(NULL, "wdir")
> parallel::clusterEvalQ(NULL, setwd(wdir))

[[1]]
[1] "/home/ramon/tmp/ADaCGH2_vignette_tmp_dir"

[[2]]
[1] "/home/ramon/tmp/ADaCGH2_vignette_tmp_dir"

[[3]]
[1] "/home/ramon/tmp/ADaCGH2_vignette_tmp_dir"

[[4]]
[1] "/home/ramon/tmp/ADaCGH2_vignette_tmp_dir"

>

```

3 The examples

3.1 RAM objects and forking

```

> cbs.mergel.RAM.fork <- pSegmentDNACopy(cgh.dat, chrom.dat,
+                                       merging = "mergeLevels")
> cbs.mad.RAM.fork <- pSegmentDNACopy(cgh.dat, chrom.dat, merging = "MAD")
> cbs.none.RAM.fork <- pSegmentDNACopy(cgh.dat, chrom.dat, merging = "none")
> hmm.mergel.RAM.fork <- pSegmentHMM(cgh.dat, chrom.dat, merging = "mergeLevels")
> hmm.mad.RAM.fork <- pSegmentHMM(cgh.dat, chrom.dat, merging = "MAD")
> hs.mergel.RAM.fork <- pSegmentHaarSeg(cgh.dat, chrom.dat,
+                                       merging = "mergeLevels")
> hs.mad.RAM.fork <- pSegmentHaarSeg(cgh.dat, chrom.dat,
+                                       merging = "MAD")
> hs.none.RAM.fork <- pSegmentHaarSeg(cgh.dat, chrom.dat,
+                                       merging = "none")

```

```

> glad.RAM.fork <- pSegmentGLAD(cgh.dat, chrom.dat)
> biohmm.mergel.RAM.fork <- pSegmentBioHMM(cgh.dat,
+                                           chrom.dat,
+                                           pos.dat,
+                                           merging = "mergeLevels")
> biohmm.mad.RAM.fork <- pSegmentBioHMM(cgh.dat,
+                                           chrom.dat,
+                                           pos.dat,
+                                           merging = "MAD")
> biohmm.mad.bic.RAM.fork <- pSegmentBioHMM(cgh.dat,
+                                           chrom.dat,
+                                           pos.dat,
+                                           merging = "MAD",
+                                           aic.or.bic = "BIC")
> cghseg.mergel.RAM.fork <- pSegmentCGHseg(cgh.dat,
+                                           chrom.dat,
+                                           merging = "mergeLevels")
> cghseg.mad.RAM.fork <- pSegmentCGHseg(cgh.dat,
+                                           chrom.dat,
+                                           merging = "MAD")
> cghseg.none.RAM.fork <- pSegmentCGHseg(cgh.dat,
+                                           chrom.dat,
+                                           merging = "none")
> waves.mergel.RAM.fork <- pSegmentWavelets(cgh.dat,
+                                           chrom.dat, merging = "mergeLevels")
> waves.mad.RAM.fork <- pSegmentWavelets(cgh.dat,
+                                           chrom.dat, merging = "MAD")
> waves.none.RAM.fork <- pSegmentWavelets(cgh.dat,
+                                           chrom.dat, merging = "none")
>

```

3.2 *ff* objects and cluster

Compared to the section 3.1, the main differences are that we explicitly set the `typeParall` argument to "cluster" (the default is "fork") and the change in the names of the input data (which now refer to the names of the RData objects that contain the *ff* objects).

```

> cbs.mergel.ff.cluster <- pSegmentDNAcopy("cghData.RData", "chromData.RData",
+                                           merging = "mergeLevels",
+                                           typeParall = "cluster")
> cbs.mad.ff.cluster <- pSegmentDNAcopy("cghData.RData", "chromData.RData",
+                                           merging = "MAD",
+                                           typeParall = "cluster")
> cbs.none.ff.cluster <- pSegmentDNAcopy("cghData.RData", "chromData.RData",
+                                           merging = "none",
+                                           typeParall = "cluster")
> hmm.mergel.ff.cluster <- pSegmentHMM("cghData.RData", "chromData.RData",
+                                           merging = "mergeLevels",
+                                           typeParall = "cluster")
> hmm.mad.ff.cluster <- pSegmentHMM("cghData.RData", "chromData.RData",
+                                           merging = "MAD",
+                                           typeParall = "cluster")

```

```

> hs.mergel.ff.cluster <- pSegmentHaarSeg("cghData.RData", "chromData.RData",
+                                         merging = "mergeLevels",
+                                         typeParall = "cluster")
> hs.mad.ff.cluster <- pSegmentHaarSeg("cghData.RData", "chromData.RData",
+                                       merging = "MAD", typeParall = "cluster")
> hs.none.ff.cluster <- pSegmentHaarSeg("cghData.RData", "chromData.RData",
+                                       merging = "none", typeParall = "cluster")
> glad.ff.cluster <- pSegmentGLAD("cghData.RData", "chromData.RData",
+                                  typeParall = "cluster")
> biohmm.mergel.ff.cluster <- pSegmentBioHMM("cghData.RData",
+                                             "chromData.RData",
+                                             "posData.RData",
+                                             merging = "mergeLevels",
+                                             typeParall = "cluster")
> biohmm.mad.ff.cluster <- pSegmentBioHMM("cghData.RData",
+                                          "chromData.RData",
+                                          "posData.RData",
+                                          merging = "MAD",
+                                          typeParall = "cluster")
> biohmm.mad.bic.ff.cluster <- pSegmentBioHMM("cghData.RData",
+                                              "chromData.RData",
+                                              "posData.RData",
+                                              merging = "MAD",
+                                              aic.or.bic = "BIC",
+                                              typeParall = "cluster")
> cghseg.mergel.ff.cluster <- pSegmentCGHseg("cghData.RData",
+                                             "chromData.RData",
+                                             merging = "mergeLevels",
+                                             typeParall = "cluster")
> cghseg.mad.ff.cluster <- pSegmentCGHseg("cghData.RData",
+                                          "chromData.RData",
+                                          merging = "MAD",
+                                          typeParall = "cluster")
> cghseg.none.ff.cluster <- pSegmentCGHseg("cghData.RData",
+                                           "chromData.RData",
+                                           merging = "none",
+                                           typeParall = "cluster")
> waves.mergel.ff.cluster <- pSegmentWavelets("cghData.RData",
+                                              "chromData.RData",
+                                              merging = "mergeLevels",
+                                              typeParall = "cluster")
> waves.mad.ff.cluster <- pSegmentWavelets("cghData.RData",
+                                           "chromData.RData",
+                                           merging = "MAD",
+                                           typeParall = "cluster")
> waves.none.ff.cluster <- pSegmentWavelets("cghData.RData",
+                                             "chromData.RData",
+                                             merging = "none",
+                                             typeParall = "cluster")
>

```

3.3 *ff* objects and forking

The main difference with section 3.2 is the argument `typeParall`; we did not need to pass it explicitly (since the default is `fork`), but we will do for clarity.

```
> cbs.mergel.ff.fork <- pSegmentDNACopy("cghData.RData", "chromData.RData",
+                                     merging = "mergeLevels",
+                                     typeParall = "fork")
> cbs.mad.ff.fork <- pSegmentDNACopy("cghData.RData", "chromData.RData",
+                                   merging = "MAD",
+                                   typeParall = "fork")
> cbs.none.ff.fork <- pSegmentDNACopy("cghData.RData", "chromData.RData",
+                                    merging = "none", typeParall = "fork")
> hmm.mergel.ff.fork <- pSegmentHMM("cghData.RData", "chromData.RData",
+                                  merging = "mergeLevels", typeParall = "fork")
> hmm.mad.ff.fork <- pSegmentHMM("cghData.RData", "chromData.RData",
+                                merging = "MAD", typeParall = "fork")
> hs.mergel.ff.fork <- pSegmentHaarSeg("cghData.RData", "chromData.RData",
+                                     merging = "mergeLevels", typeParall = "fork")
> hs.mad.ff.fork <- pSegmentHaarSeg("cghData.RData", "chromData.RData",
+                                   merging = "MAD", typeParall = "fork")
> hs.none.ff.fork <- pSegmentHaarSeg("cghData.RData", "chromData.RData",
+                                    merging = "none", typeParall = "fork")
> glad.ff.fork <- pSegmentGLAD("cghData.RData", "chromData.RData",
+                              typeParall = "fork")
> biohmm.mergel.ff.fork <- pSegmentBioHMM("cghData.RData",
+                                         "chromData.RData",
+                                         "posData.RData",
+                                         merging = "mergeLevels",
+                                         typeParall = "fork")
> biohmm.mad.ff.fork <- pSegmentBioHMM("cghData.RData",
+                                       "chromData.RData",
+                                       "posData.RData",
+                                       merging = "MAD",
+                                       typeParall = "fork")
> biohmm.mad.bic.ff.fork <- pSegmentBioHMM("cghData.RData",
+                                          "chromData.RData",
+                                          "posData.RData",
+                                          merging = "MAD",
+                                          aic.or.bic = "BIC",
+                                          typeParall = "fork")
> cghseg.mergel.ff.fork <- pSegmentCGHseg("cghData.RData",
+                                         "chromData.RData",
+                                         merging = "mergeLevels",
+                                         typeParall = "fork")
> cghseg.mad.ff.fork <- pSegmentCGHseg("cghData.RData",
+                                       "chromData.RData",
+                                       merging = "MAD", typeParall = "fork")
> cghseg.none.ff.fork <- pSegmentCGHseg("cghData.RData",
+                                       "chromData.RData",
+                                       merging = "none", typeParall = "fork")
> waves.merge.ff.fork <- pSegmentWavelets("cghData.RData",
+                                          "chromData.RData",
```

```

+             merging = "mergeLevels",
+             typeParall = "fork")
> waves.mad.ff.fork <- pSegmentWavelets("cghData.RData",
+             "chromData.RData",
+             merging = "MAD",
+             typeParall = "fork")
> waves.none.ff.fork <- pSegmentWavelets("cghData.RData",
+             "chromData.RData",
+             merging = "none",
+             typeParall = "fork")
>
>

```

3.4 Comparing output

Here we verify that using different input and clustering methods does not change the results. Before carrying out the comparisons, however, we open the *ff* objects gently.

First, we will open the objects created above (same objects as were also created in the main vignette, in section "Carrying out segmentation and calling"). Instead of inserting many calls to each individual object, we open all available objects that match *ff.cluster*. To do that quickly we store the names of the objects

```
> ff.cluster.obj <- ls(pattern = "*.ff.cluster")
```

pages with the string "TRUE")

```

> tmpout <-
+   capture.output(
+     lapply(ff.cluster.obj, function(x) lapply(get(x), open))
+   )

```

We repeat that operation with the output from section 3.3:

```

> ff.fork.obj <- ls(pattern = "*.ff.fork")
> tmpout <-
+   capture.output(
+     lapply(ff.fork.obj, function(x) lapply(get(x), open))
+   )
>

```

And we create the list of results from the RAM and forking runs (no need for special opening here, since these are not *ff* objects)

```
> RAM.fork.obj <- ls(pattern = "*.RAM.fork")
```

We can now compare the output. We want to compare the output from three different methods, so we need to run three comparisons (this is what we did explicitly in the help for *pSegment*). Since this is a very repetitive operation, we define a small utility function that will return TRUE if both components (*outSmoothed* and *outState*) of all three objects are identical. (Since the function will take as input not an actual object, but a name, we use *get* inside the function.)

We use *all.equal* to compare the output from the smoothing, to allow for possible numerical fuzz (that could result from differences in storage). When comparing the assigned state, however, we check for exact identity.


```

> identical3 <- function(x, y, z) {
+   comp1 <- all.equal(get(x)$outSmoothed[ , ], get(y)$outSmoothed[ , ])
+   comp2 <- all.equal(get(y)$outSmoothed[ , ], get(z)$outSmoothed[ , ])
+   comp3 <- identical(get(x)$outState[ , ], get(y)$outState[ , ])
+   comp4 <- identical(get(y)$outState[ , ], get(z)$outState[ , ])
+   if (!all(isTRUE(comp1), isTRUE(comp2), comp3, comp4)) {
+     cat(paste("Comparing ", x, y, z, "\n",
+       "not equal: some info from comparisons.\n",
+       "\n comp1 = ", paste(comp1, sep = " ", collapse = "\n  "),
+       "\n comp2 = ", paste(comp2, sep = " ", collapse = "\n  "),
+       "\n comp3 = ", paste(comp3, sep = " ", collapse = "\n  "),
+       "\n comp4 = ", paste(comp4, sep = " ", collapse = "\n  "),
+       "\n\n"))
+     return(FALSE)
+   } else {
+     TRUE
+   }
+ }

```

You should expect most (though not necessarily all) the comparisons to yield a TRUE. In some cases, however, different runs of the same method might not yield the same results (e.g., CBS, HMM, etc). If you get non-identical results, you can try running those methods a few times, to check for differences. You can also disable load balancing, and try using reproducible streams for the random number generators (see the vignette of package **parallel**).

Let's check those results then:

```

> mapply(identical3, RAM.fork.obj,
+         ff.fork.obj, ff.cluster.obj)

```

```

Comparing  cbs.mad.RAM.fork cbs.mad.ff.fork cbs.mad.ff.cluster
not equal: some info from comparisons.

```

```

comp1 = TRUE
comp2 = Component 4: Mean relative difference: 0.0334
comp3 = TRUE
comp4 = TRUE

```

```

Comparing  glad.RAM.fork glad.ff.fork glad.ff.cluster
not equal: some info from comparisons.

```

```

comp1 = TRUE
comp2 = Component 4: Mean relative difference: 4.221
comp3 = TRUE
comp4 = FALSE

```

```

Comparing  hmm.mad.RAM.fork hmm.mad.ff.fork hmm.mad.ff.cluster
not equal: some info from comparisons.

```

```

comp1 = TRUE
comp2 = Component 3: Mean relative difference: 0.02516
comp3 = TRUE
comp4 = TRUE

```

Comparing `hmm.mergel.RAM.fork` `hmm.mergel.ff.fork` `hmm.mergel.ff.cluster`
not equal: some info from comparisons.

```
comp1 = TRUE
comp2 = Component 3: Mean relative difference: 0.024
comp3 = TRUE
comp4 = TRUE
```

<code>biohmm.mad.bic.RAM.fork</code>	<code>biohmm.mad.RAM.fork</code>	<code>biohmm.mergel.RAM.fork</code>
TRUE	TRUE	TRUE
<code>cbs.mad.RAM.fork</code>	<code>cbs.mergel.RAM.fork</code>	<code>cbs.none.RAM.fork</code>
FALSE	TRUE	TRUE
<code>cghseg.mad.RAM.fork</code>	<code>cghseg.mergel.RAM.fork</code>	<code>cghseg.none.RAM.fork</code>
TRUE	TRUE	TRUE
<code>glad.RAM.fork</code>	<code>hmm.mad.RAM.fork</code>	<code>hmm.mergel.RAM.fork</code>
FALSE	FALSE	FALSE
<code>hs.mad.RAM.fork</code>	<code>hs.mergel.RAM.fork</code>	<code>hs.none.RAM.fork</code>
TRUE	TRUE	TRUE
<code>waves.mad.RAM.fork</code>	<code>waves.mergel.RAM.fork</code>	<code>waves.none.RAM.fork</code>
TRUE	TRUE	TRUE

>

(Of course, we depend on the lists of names of objects having the output from the same method and option in the same position, which is the case in these examples).

4 Exercising the code for the load balancing options

This section simply exercises the load balancing options. We use Haar as it is the fastest method, and one unlikely to be affected by the order in which different columns are run (in contrast to, say, HMM), so we need not worry about random numbers here.

```
> hs.none.RAM.fork <- pSegmentHaarSeg(cgh.dat, chrom.dat,
+                                   merging = "none")
> hs.none.RAM.fork.lb <- pSegmentHaarSeg(cgh.dat, chrom.dat,
+                                       merging = "none", loadBalance = TRUE)
> hs.none.RAM.fork.nlb <- pSegmentHaarSeg(cgh.dat, chrom.dat,
+                                       merging = "none", loadBalance = FALSE)
> identical3("hs.none.RAM.fork", "hs.none.RAM.fork.lb", "hs.none.RAM.fork.nlb")

[1] TRUE

> hs.none.ff.cluster <- pSegmentHaarSeg("cghData.RData", "chromData.RData",
+                                       merging = "none", typeParall = "cluster")
> hs.none.ff.cluster.lb <- pSegmentHaarSeg("cghData.RData", "chromData.RData",
+                                       merging = "none", typeParall = "cluster",
+                                       loadBalance = TRUE)
> hs.none.ff.cluster.nlb <- pSegmentHaarSeg("cghData.RData", "chromData.RData",
+                                       merging = "none", typeParall = "cluster",
+                                       loadBalance = FALSE)
> ## do not show all the opening ... messages
```

```

> tmpout <-
+   capture.output(
+     lapply("hs.none.ff.cluster", function(x) lapply(get(x), open))
+   )
> tmpout <-
+   capture.output(
+     lapply("hs.none.ff.cluster.lb", function(x) lapply(get(x), open))
+   )
> tmpout <-
+   capture.output(
+     lapply("hs.none.ff.cluster.nlb", function(x) lapply(get(x), open))
+   )
> identical3("hs.none.ff.cluster", "hs.none.ff.cluster.lb",
+            "hs.none.ff.cluster.nlb")

[1] TRUE

> hs.none.ff.fork <- pSegmentHaarSeg("cghData.RData", "chromData.RData",
+                                   merging = "none", typeParall = "fork")
> hs.none.ff.fork.lb <- pSegmentHaarSeg("cghData.RData", "chromData.RData",
+                                       merging = "none", typeParall = "fork",
+                                       loadBalance = TRUE)
> hs.none.ff.fork.nlb <- pSegmentHaarSeg("cghData.RData", "chromData.RData",
+                                       merging = "none", typeParall = "fork",
+                                       loadBalance = FALSE)
> tmpout <-
+   capture.output(
+     lapply("hs.none.ff.fork", function(x) lapply(get(x), open))
+   )
> tmpout <-
+   capture.output(
+     lapply("hs.none.ff.fork.lb", function(x) lapply(get(x), open))
+   )
> tmpout <-
+   capture.output(
+     lapply("hs.none.ff.fork.nlb", function(x) lapply(get(x), open))
+   )
> identical3("hs.none.ff.fork", "hs.none.ff.fork.lb", "hs.none.ff.fork.nlb")

[1] TRUE

>

```

(There is no need to compare between ff.fork, ff.cluster, RAM.fork, as those were already shown to be identical.)

5 Clean up actions

These are not strictly necessary, but we will explicitly stop the cluster. In this vignette, we will not execute the code below to remove the directory we created or the objects, in case you want to check them out or play around with them, but the code is below.

To make sure there are no file permission problems, we add code below to explicitly delete some of the "ff" files and objects (and we wait a few seconds to allow pending I/O operations to happen before we delete the directory).

```

> parallel::stopCluster(cl2)

> ## This is the code to remove all the files we created
> ## and the temporary directory.
> ## We are not executing it!
>
> load("chromData.RData")
> load("posData.RData")
> load("cghData.RData")
> delete(cghData); rm(cghData)
> delete(posData); rm(posData)
> delete(chromData); rm(chromData)
> tmpout <-
+   capture.output(
+     lapply(ff.fork.obj, function(x) {
+       lapply(get(x), delete)}))
> rm(list = ff.fork.obj)
> tmpout <-
+   capture.output(
+     lapply(ff.cluster.obj, function(x) {
+       lapply(get(x), delete)}))
> rm(list = ff.cluster.obj)
> setwd(originalDir)
> print(getwd())
> Sys.sleep(3)
> unlink("ADaCGH2_vignette_tmp_dir", recursive = TRUE)
> Sys.sleep(3)

```