

The mammaPrintData package: annotated gene expression data from the Glas and Buyse breast cancer cohorts

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1 Overview

This vignette documents the R code used to retrieve from the original sources, annotate, and then assemble into separate `RGList` instances the gene expression data of the Glas and Buyse cohorts [3, 2]. Such data was used to translate the 70-gene breast cancer prognostic signature [7, 6] into the MammaPrint assays [3], and to independently validate it [2]. While the original studies by van't Veer and Van de Vijver and colleagues used the two-colors Agilent/Rosetta 24k array, the redeveloped assays is based on the 1.9k MammaPrint array. For a complete review of these breast cancer studies see Marchionni et al [4, 5].

Briefly, this document contains the complete R code used to:

1. Download the following gene expression data from ArrayExpress [1]:
 - (a) The Glas data set (ArrayExpress E-TABM-115 series), which combined a large proportion of cases from the original van't Veer and Van de Vijver cohorts, and was used as training set;
 - (b) The Buyse data set (ArrayExpress E-TABM-77), which analyzed a European multicenter cohort, and was used as validation set;
2. Pre-process and normalize all gene expression data;
3. Cross-reference the 70-gene list to the new MammaPrint microarray;
4. Create the corresponding `limma` package `RGList` instances.

All the files, among those mentioned above, needed to compile this vignette and create the `mammaPrintData` Rpackage are included inside the `inst/extdata` directory of the source package.

Finally, the R code chunk below was used to download and install from Bioconductor the packages required to prepared the present vignette. if the are not available (e.g `gdata`).

```
> ###Get the list of available packages
> installedPckgs <- installed.packages()[,"Package"]
> ###Define the list of desired libraries
> pckgListBIOC <- c("Biobase", "limma", "gdata")
> ###Source the biocLite.R script from Bioconductor
> source("http://bioconductor.org/biocLite.R")
> ###Load the packages, install them from Bioconductor if needed
> for (pckg in pckgListBIOC) {
  if (! pckg %in% installedPckgs) biocLite(pckg)
  require(pckg, character.only=TRUE)
}
```

2 The 70-gene signature

The list of genes originally identified in the van't Veer study [7] can be obtained from the supplementary data section of the original publication, at the following URL:

- <http://www.nature.com/nature/journal/v415/n6871/extref/415530a-s9.xls>

The Excel spreadsheet named `415530a-s9.xls` corresponds to Table S2, and contains the identifiers and annotation for the 231 genes othat proved to be associated with metastatic recurrence at 5 years. According


```

        gns70any = unique(c(gns70$accession, gns70$gene.name)) )
> ###Remove empty elements
> progSig <- lapply(progSig, function(x) x[x!=""])
> ###Create a data.frame of correlations with combined accession
> ###and gene symbols as identifiers
> gns231Cors <- data.frame(stringsAsFactors=FALSE,
                           ID=c(gns231$gene.name[ gns231$gene.name %in% progSig$gns231any ],
                                gns231$accession),
                           gns231Cors=c(gns231$correlation[ gns231$gene.name %in% progSig$gns231any ],
                                         gns231$correlation) )
> #####Keep unique only
> progSig$gns231Cors <- gns231Cors[!duplicated(gns231Cors$ID), ]
> progSig$gns231Cors <- gns231Cors[gns231Cors$ID != "", ]
> ###Check the structure of the list just created
> str(progSig)

List of 7
 $ gns231acc : chr [1:231] "AL080059" "Contig63649_RC" "Contig46218_RC" "NM_016359" ...
 $ gns231name: chr [1:161] "LOC51203" "ALDH4" "FGF18" "BBC3" ...
 $ gns231any : chr [1:392] "AL080059" "Contig63649_RC" "Contig46218_RC" "NM_016359" ...
 $ gns70acc  : chr [1:70] "AL080059" "Contig63649_RC" "Contig46218_RC" "NM_016359" ...
 $ gns70name: chr [1:50] "LOC51203" "ALDH4" "FGF18" "BBC3" ...
 $ gns70any  : chr [1:120] "AL080059" "Contig63649_RC" "Contig46218_RC" "NM_016359" ...
 $ gns231Cors:'data.frame':      394 obs. of  2 variables:
  ..$ ID          : chr [1:394] "LOC51203" "ALDH4" "FGF18" "BBC3" ...
  ..$ gns231Cors: num [1:394] -0.425 0.421 0.411 0.407 0.402 ...

```

3 Glas and Buyse cohorts: RGList preparation

The original data sets used to redevelop [3] and validate [2] the MammaPrint assays can be obtained from the ArrayExpress database [1]:

- <http://www.ebi.ac.uk/arrayexpress/experiments/E-TABM-77>
- <http://www.ebi.ac.uk/arrayexpress/experiments/E-TABM-115>

These gene expression series account for clinical information, microarray feature annotation, and complete unprocessed raw gene expression data. In both studies a two-color design with dye-swap replication was applied, therefore two distinct RGList objects were prepared for each data set, and included in the `mammaPrintData` R-Bioconductor package, as detailed below. The pre-processed, normalized, and summarized values used by the authors in their original analyses were not included in the submission to ArrayExpress, hence data pre-processing and normalization of the RGList contained in this package is required prior any analysis.

3.1 Glas cohort - ArrayExpress E-TABM-115 Series

The Glas data set combines a large proportion of cases from the original van't Veer and Van de Vijver cohorts, and was used for the implementation of the original 70-gene signature into the MammaPrint assay

[3].

The following chunk of R code was used to download the all the files of the ArrayExpress the E-TABM-115 series. The files needed to compile this vignette and create the `mammaPrintData` Rpackage are included inside the `inst/extdata` directory.

```
> ###Chunk nor executed: files are already included in the package
> ###This chunk is just to show the source of the data
> ###Load the ArrayExpress library
> require(ArrayExpress)
> ###Create a working directory
> dir.create("../extdata/ETABM115", showWarnings = FALSE)
> ###Obtain the data package E-TABM-115 from ArrayExpress
> etabm115 <- getAE("E-TABM-115", type = "full", path="../extdata/ETABM115", extract=FALSE)
> ###Save
> save(etabm115, file="../extdata/ETABM115/etabm115.rda")
```

Below is the R code chunk used to process the phenotypic information retrieved form ArrayExpress and associated with the E-TABM-115 series on Apr 06, 2018

```
> ###Load the Biobase library
> require(Biobase)
> ###List the files obtained from ArrayExpress
> etabm155filesLoc <- system.file("extdata/ETABM115", package = "mammaPrintData")
> head(dir(etabm155filesLoc))

[1] "A-MEXP-318.adf.txt.gz"
[2] "E-TABM-115.sdrf.txt.gz"
[3] "US22502555_16011886011186_S01_1_1.txt.gz"
[4] "US22502555_16011886011186_S01_1_2.txt.gz"
[5] "US22502555_16011886011186_S01_1_3.txt.gz"
[6] "US22502555_16011886011186_S01_1_4.txt.gz"

> ###Read the phenotypic information from "E-TABM-115.sdrf.txt"
> targets <- read.table(dir(etabm155filesLoc, full.names=TRUE, pattern="E-TABM-115.sdrf.txt.gz"),
                        comment.char="", sep="\t", header=TRUE, stringsAsFactors=FALSE)
> ###Check and process the phenotypic information: keep non-redundant information
> targets <- targets[, apply(targets, 2, function(x) length(unique(x)) != 1)]
> ###Reorder by file name
> targets <- targets[order(targets$Array.Data.File, decreasing=TRUE),]
> ###Remove points in colnames
> colnames(targets) <- gsub("\\.$", "", gsub("\\\\.\\.\\.\"", ".", colnames(targets)))
> ###Show the available phenotypic information
> str(targets)

'data.frame':      324 obs. of  16 variables:
 $ Source.Name                : chr  "MRP" "9671397" "MRP" "9
 $ Characteristics.EventDistantMetastases : int  NA 1 NA 0 NA 0 NA NA 0 C
 $ Characteristics.EventDeath           : int  NA 1 NA 0 NA 0 NA NA 0 C
 $ Characteristics.PeriodTillDevelopmentOfDistantMetastases.years: num  NA 4.77 NA NaN NA NaN NA
 $ Characteristics.OverallSurvival      : chr  " " "8.77 years" " " "
```

```

$ Sample.Name           : chr "MRP" "9671397" "MRP" "9
$ Extract.Name          : chr "MRP_e1" "9671397_e1" "M
$ Labeled.Extract.Name  : chr "MRP_e1_l1" "9671397_e1
$ Label                 : chr "Cy3" "Cy5" "Cy3" "Cy5"
$ Hybridization.Name    : chr "agendia.com; ebi.co.uk:
$ Factor.Value.overall_survival : chr "reference pool" "8.77 y
$ Factor.Value.Event_Death : chr "reference pool" "1" "re
$ Factor.Value.Event_distant_metastases : chr "reference pool" "1" "re
$ Factor.Value.Time_to_development_of_distant_metastases : chr "reference pool" "4.77 y
$ Scan.Name             : chr "US22502555_967_2_397"
$ Array.Data.File       : chr "US22502555_967_2_397.tx

```

The Glas cohort accounts for 162 unique cases, which were analyzed using a dye-swap two-colors design, comparing each sample against the same reference RNA. According to ArrayEspress instruction for SDRF files (available at http://tab2mage.sourceforge.net/docs/magetab_docs.html), a complete SDRF annotation file consists of a table in which each hybridization channel is represented by an individual row. Therefore the complete SDRF annotation files for all hybridizations of the Glas cohort should for 648 total rows: 162 samples for 2 channels (cy5 and Cy3) for 2 replicated hybridizations (dye-swap). As shown below, the E-TABM-115.sdrf.txt file currently available from ArrayExpress (Apr 06, 2018) is incomplete, since it contains only 324 rows. An inspection of the information contained in the downloaded SDRF file reveals that it contains a row for each hybridization (n=324), rather than a row for each channel (n=648).

```

> ###Check targets data.frame dimentions
> dim(targets)

[1] 324 16

> ###Count the unique file names
> length(unique(targets$Array.Data.File))

[1] 324

> ###Count the number of rows associated with each channel
> table(CHANNEL=targets$Label)

CHANNEL
Cy3 Cy5
162 162

> ###Count the number of rows for the reference RNA (named "MRP") in each channel
> table(CHANNEL=targets$Label, REFERENCE=targets$Sample.Name == "MRP")

      REFERENCE
CHANNEL FALSE TRUE
Cy3      0    162
Cy5     162     0

> ###Count the number of distinct RNA analyzed (excluding the refernce RNA)
> sum(REFERENCE=targets$Sample.Name!="MRP")

[1] 162

```

```

> ###Count the number of metastatic events
> table(METASTASES=targets$Characteristics.EventDistantMetastases)

METASTASES
  0  1
106 56

> ###Count the number of rown for which metastatic events is missing
> table(MISSING=is.na(targets$Characteristics.EventDistantMetastases))

MISSING
FALSE TRUE
 162  162

> ###Check if missing clinical information is exactly associated with
> ###hybridizations where the "MRP" reference RNA was used in the Cy5 channel
> table(MISSING=is.na(targets$Characteristics.EventDistantMetastases),
        REFERENCE=targets$Sample.Name!="MRP")

        REFERENCE
MISSING FALSE TRUE
  FALSE     0 162
  TRUE     162   0

```

Therefore the following conclusions can be drawn from the evaluation of the information contained in E-TABM-115.sdrf.txt file shown above:

- All hybridizations that were performed have a corresponding row in the SDRF table;
- Half of the rows of the SDRF table, for which the RNA samples described were associated with the Cy5 channel, contain a complete set of clinical information;
- The other half of the rows, for which the RNA samples described were associated with the Cy3 channel, report the information for the reference RNA, and the clinical information is missing;
- Nevertheless, given the dye swap design of the experiment, the SDRF table contains the complete clinical information associated with all the 162 breast cancer patients analyzed in the Glas study;
- It is possible to use the clinical information provided only with one set of dye-swap hybridizations, since for the other set only the “MRP” reference RNA information was provided.

In conclusion, the complete data set can be analyzed only knowing which hybridizations constitute a dye-swap pair. This information can be obtained upon request from Dr. Glas, the corresponding author of the of the original study.

Below is the R code chunk used to create the RGList objects using the raw gene expression data contained in the compressed archive E-TABM-115.raw.1.zip downloaded from ArrayExpress.

```

> ###List files for E-TABM-115 experiment
> etabm155filesLoc <- system.file("extdata/ETABM115", package = "mammaPrintData")
> etabm155files <- list.files(etabm155filesLoc, pattern="^US")
> ###Check whether all available files correspond to the targets$Array.Data.File
> all(paste(targets$Array.Data.File, ".gz", sep="") %in% etabm155files)

[1] TRUE

```

```

> ###Check whether they are ordered in the same way
> all(paste(targets$Array.Data.File, ".gz", sep="") == etabm155files)

[1] FALSE

> ###Load the required library
> require(limma)
> ###Define the columns which will be read from the raw files selection
> colsList <- list(Rf="Feature Extraction Software:rMedianSignal",
                  Rb="Feature Extraction Software:rBGMedianSignal",
                  Gf="Feature Extraction Software:gMedianSignal",
                  Gb="Feature Extraction Software:gBGMedianSignal",
                  logRatio="Feature Extraction Software:LogRatio",
                  logRatioError="Feature Extraction Software:LogRatioError")
> ###Subset the targets data.frame for the hybridization in which the Reference RNA was labeled
> targetsCy3info <- targets[ targets$Source.Name == "MRP" & targets$Label == "Cy3", ]
> dim(targetsCy3info)

[1] 162  16

> ###Subset the targets data.frame for the hybridization in which the Reference RNA was labeled
> targetsCy5info <- targets[ targets$Source.Name != "MRP" & targets$Label == "Cy5", ]
> dim(targetsCy5info)

[1] 162  16

> ###The two sets of hybridizations above should be mutually exclusive
> all(targetsCy3info$Array.Data.File != targetsCy5info$Array.Data.File)

[1] TRUE

> ###Create an "RGList" using specific columns for the first set of swapped hybridizations:
> RGcy3 <- read.maimages(paste(targetsCy3info$Array.Data.File, ".gz", sep=""),
                       source="generic",
                       columns=colsList, annotation="Reporter identifier",
                       path=etabm155filesLoc, verbose=FALSE)
> ###Add targets information
> RGcy3$targets <- targetsCy3info
> ###Format Reporter identifiers
> RGcy3$genes$ID <- gsub(".+A-MEXP-318\\.", "", RGcy3$genes[, "Reporter identifier"])
> ###Check dimensions
> dim(RGcy3)

[1] 1900 162

> ###Create an "RGList" using specific columns for the second set of swapped hybridizations:
> RGcy5 <- read.maimages(paste(targetsCy3info$Array.Data.File, ".gz", sep=""),
                       source="generic",
                       columns=colsList, annotation="Reporter identifier",
                       path=etabm155filesLoc, verbose=FALSE)
> ###Add targets information
> RGcy5$targets <- targetsCy5info
> ###Format Reporter identifiers

```



```

> RGcy5$genes$ID <- gsub(".+A-MEXP-318\\.\"", "", RGcy5$genes[, "Reporter identifier"])
> ###Check dimensions
> dim(RGcy5)

[1] 1900 162

```

Below is the R code chunk used to check whether all data read is of the correct mode (i.e. numeric values are of mode “numeric”, and so on).

```

> ###Check mode of read data for first set of hybridizations
> sapply(RGcy3, mode)

           R           Rb           G           Gb           logRatio
"numeric"  "numeric"  "numeric"  "numeric"  "character"
logRatioError targets      genes      source
"numeric"  "list"      "list"  "character"

> ###Since RGc3$logRatio is character convert to numeric
> RGcy3$logRatio <- apply(RGcy3$logRatio, 2, as.numeric)
> ###Check mode of read data for second set of hybridizations
> sapply(RGcy5, mode)

           R           Rb           G           Gb           logRatio
"numeric"  "numeric"  "numeric"  "numeric"  "character"
logRatioError targets      genes      source
"numeric"  "list"      "list"  "character"

> ###Since RGc3$logRatio is character convert to numeric
> RGcy5$logRatio <- apply(RGcy5$logRatio, 2, as.numeric)

```

Below is the R code chunk used to process the microarray feature annotation for the 1.9k MammaPrint array, as it is provided in the ArrayExpress database (file A-MEXP-318.adf.txt). We will then map the microarray features from this new array to the 231-gene and the 70-gene prognostic signatures. We will finally add annotation information to the RGList objects created above.

```

> ###Read genes information for MammaPrint array from the A-MEXP-318.adf.txt
> genes <- read.table(dir(etabm155filesLoc, full.names=TRUE, pattern="A-MEXP-318.adf.txt"),
                     skip=21, sep="\t", header=TRUE, stringsAsFactors=FALSE)
> ###Remove special characters like points in the columns header
> colnames(genes) <- gsub("\\.$", "", gsub("\\.\\.\\.\"", ".", colnames(genes)))
> ###Use the annotation information previously processed
> str(progSig)

```

List of 7

```

$ gns231acc : chr [1:231] "AL080059" "Contig63649_RC" "Contig46218_RC" "NM_016359" ...
$ gns231name: chr [1:161] "LOC51203" "ALDH4" "FGF18" "BBC3" ...
$ gns231any : chr [1:392] "AL080059" "Contig63649_RC" "Contig46218_RC" "NM_016359" ...
$ gns70acc  : chr [1:70] "AL080059" "Contig63649_RC" "Contig46218_RC" "NM_016359" ...
$ gns70name : chr [1:50] "LOC51203" "ALDH4" "FGF18" "BBC3" ...
$ gns70any  : chr [1:120] "AL080059" "Contig63649_RC" "Contig46218_RC" "NM_016359" ...
$ gns231Cors:'data.frame':      394 obs. of  2 variables:
..$ ID          : chr [1:394] "LOC51203" "ALDH4" "FGF18" "BBC3" ...
..$ gns231Cors: num [1:394] -0.425 0.421 0.411 0.407 0.402 ...

```

```
> ###Count the features mapped to the 231-gene prognostic signature by accession number
> apply(genes, 2, function(x, y) { sum(unique(x) %in% y) }, y = progSig$gns231acc)
```

```
      Block.Column      Block.Row
      0              0
      Column          Row
      0              0
      Reporter.Name    Comment.AEReporterName
      0              68
      Reporter.Database.Entry.embl Reporter.Database.Entry.unigene
      7              0
      Reporter.Group.role Control.Type
      0              0
```

```
> ###Count the features mapped to the 231-gene prognostic signature by gene symbol
> apply(genes, 2, function(x, y) { sum(unique(x) %in% y) }, y = progSig$gns231name)
```

```
      Block.Column      Block.Row
      0              0
      Column          Row
      0              0
      Reporter.Name    Comment.AEReporterName
      0              161
      Reporter.Database.Entry.embl Reporter.Database.Entry.unigene
      0              0
      Reporter.Group.role Control.Type
      0              0
```

```
> ###Count the features mapped to the 231-gene prognostic signature by gene symbol or accession
> apply(genes, 2, function(x, y) { sum(unique(x) %in% y) }, y = progSig$gns231any)
```

```
      Block.Column      Block.Row
      0              0
      Column          Row
      0              0
      Reporter.Name    Comment.AEReporterName
      0              229
      Reporter.Database.Entry.embl Reporter.Database.Entry.unigene
      7              0
      Reporter.Group.role Control.Type
      0              0
```

```
> ###Add mapping information for 229 features using both gene symbols and accession numbers
> genes$genes231 <- genes$Comment.AEReporterName %in% progSig$gns231any
```

```
> ###Count the features mapped to the 70-gene prognostic signature by accession number
> apply(genes, 2, function(x, y) { sum(unique(x) %in% y) }, y = progSig$gns70acc)
```

```
      Block.Column      Block.Row
      0              0
      Column          Row
      0              0
```

```

Reporter.Name          Comment.AEReporterName
0                      19
Reporter.Database.Entry.embl Reporter.Database.Entry.unigene
1                      0
Reporter.Group.role    Control.Type
0                      0
genes231
0

```

```

> ###Count the features mapped to the 70-gene prognostic signature by gene symbol
> apply(genes, 2, function(x, y) { sum(unique(x) %in% y) }, y = progSig$gns70name)

```

```

Block.Column          Block.Row
0                      0
Column                Row
0                      0
Reporter.Name          Comment.AEReporterName
0                      50
Reporter.Database.Entry.embl Reporter.Database.Entry.unigene
0                      0
Reporter.Group.role    Control.Type
0                      0
genes231
0

```

```

> ###Count the features mapped to the 70-gene prognostic signature by gene symbol or accession number
> apply(genes, 2, function(x, y) { sum(unique(x) %in% y) }, y = progSig$gns70any)

```

```

Block.Column          Block.Row
0                      0
Column                Row
0                      0
Reporter.Name          Comment.AEReporterName
0                      69
Reporter.Database.Entry.embl Reporter.Database.Entry.unigene
1                      0
Reporter.Group.role    Control.Type
0                      0
genes231
0

```

```

> ###Add mapping information for 69 features using both gene symbols and accession numbers
> genes$genes70 <- genes$Comment.AEReporterName %in% progSig$gns70any
> ###The resulting gene annotation file
> str(genes)

```

```

'data.frame':      1900 obs. of  12 variables:
 $ Block.Column    : int  1 1 1 1 1 1 1 1 1 1 1 ...
 $ Block.Row      : int  1 1 1 1 1 1 1 1 1 1 1 ...
 $ Column         : int  1 2 13 20 40 42 48 49 50 1 ...
 $ Row           : int  1 1 1 1 1 1 1 1 1 2 ...

```

```

$ Reporter.Name           : chr  "AGEN000001" "AGEN000002" "AGEN000013" "AGEN000020" ...
$ Comment.AEReporterName  : chr  "Pro25G" "3xSLv1" "eQC" "eQC" ...
$ Reporter.Database.Entry.embl : chr  "" "" "" "" ...
$ Reporter.Database.Entry.unigene: chr  "" "" "" "" ...
$ Reporter.Group.role     : chr  "Control" "Control" "Control" "Control" ...
$ Control.Type           : chr  "control_biosequence" "control_biosequence" "control_bi
$ genes231               : logi  FALSE FALSE FALSE FALSE FALSE FALSE ...
$ genes70                : logi  FALSE FALSE FALSE FALSE FALSE FALSE ...

> ###Add original correlation from the van't Veer study
> gns231Cors <- progSig$gns231Cors
> gns231Cors <- gns231Cors[gns231Cors$ID %in% genes$Comment.AEReporterName,]
> ###Merge and remove duplicates
> genes <- merge(genes, gns231Cors, all.x=TRUE, all.y=FALSE,
                by.x="Comment.AEReporterName", by.y="ID")
> genes <- genes[!duplicated(genes$Reporter.Name),]
> ###Check genes
> str(genes)

'data.frame':      1900 obs. of  13 variables:
 $ Comment.AEReporterName  : chr  "3xSLv1" "3xSLv1" "3xSLv1" "3xSLv1" ...
 $ Block.Column           : int  1 1 1 1 1 1 1 1 1 1 ...
 $ Block.Row             : int  1 1 1 1 1 1 1 1 1 1 ...
 $ Column                : int  2 48 1 2 48 49 50 1 4 7 ...
 $ Row                  : int  1 1 2 2 2 2 2 9 9 9 ...
 $ Reporter.Name         : chr  "AGEN000002" "AGEN000048" "AGEN000051" "AGEN000052" ...
 $ Reporter.Database.Entry.embl : chr  "" "" "" "" ...
 $ Reporter.Database.Entry.unigene: chr  "" "" "" "" ...
 $ Reporter.Group.role   : chr  "Control" "Control" "Control" "Control" ...
 $ Control.Type          : chr  "control_biosequence" "control_biosequence" "control_bi
 $ genes231              : logi  FALSE FALSE FALSE FALSE FALSE FALSE ...
 $ genes70               : logi  FALSE FALSE FALSE FALSE FALSE FALSE ...
 $ gns231Cors            : num  NA NA NA NA NA NA NA NA NA NA ...

```

Below is the R code chunk used to add the feature annotation the RGList objects containing the expression data (first set of hybridizations).

```

> ###Compare genes between platform and RGList instances: first set of hybridizations
> if (nrow(genes)==nrow(RGcy3)) {
  ##Compare the identifiers' order
  if ( !all(genes$Reporter.Name == RGcy3$genes$ID) ) {
    ##Reorder if needed
    RGcy3 <- RGcy3[order(RGcy3$genes$ID),]
    genes <- genes[order(genes$Reporter.Name),]
    ##Check for order AGAIN
    if ( all(genes$Reporter.Name == RGcy3$genes$ID) ) {
      ##Substitute genes or stop
      RGcy3$genes <- genes
    } else {
      stop("Wrong gene order, check objects")
    }
  }
}

```

```

    }
  } else {
    print("Updating gene annotation")
    RGcy3$genes <- genes
  }
} else {
  stop("Wrong number of features, check objects")
}
> ###Rename the object
> glasRGcy3 <- RGcy3

```

Below is the R code chunk used to add the feature annotation the RGList objects containing the expression data (second set of hybridizations).

```

> ###Compare genes between paltform and RGList instances: second set of hybridizations
> if (nrow(genes)==nrow(RGcy5)) {
  ##Compare the identifiers' order
  if ( !all(genes$Reporter.Name == RGcy5$genes$ID) ) {
    ##Reorder if needed
    RGcy5 <- RGcy5[order(RGcy5$genes$ID),]
    genes <- genes[order(genes$Reporter.Name),]
    ##Check for order AGAIN
    if ( all(genes$Reporter.Name == RGcy5$genes$ID) ) {
      ##Substitute genes or stop
      RGcy5$genes <- genes
    } else {
      stop("Wrong gene order, check objects")
    }
  } else {
    print("Updating gene annotation")
    RGcy5$genes <- genes
  }
} else {
  stop("Wrong number of features, check objects")
}
> ###Rename the object
> glasRGcy5 <- RGcy5

```

3.2 Buyse cohort - ArrayExpress E-TABM-77 Series

The Buyse data set (ArrayExpress E-TABM-77) accounts for the large European multicenter breast cancer cohort that was used to validate the MammaPrint assay [2].

The following chunk of R code was used to download the all the files of the ArrayExpress the E-TABM-77 series. The files needed to compile this vignette and create the `mammaPrintData` Rpackage are included inside the `inst/extdata` directory.

```

> ###Chunk not executed: files are already included in the package
> ###This chunk is just to show the source of the data

```

```

> dir.create("../extdata/ETABM77", showWarnings = FALSE)
> #####
> ###Obtain the data package E-TABM-115 from ArrayExpress
> etabm77 <- getAE("E-TABM-77", type = "full", path="../extdata/ETABM77", extract=FALSE)
> #####
> ###Save
> save(etabm77,file="../extdata/ETABM77/etabm77.rda")

```

Below is the R code chunk used to process the phenotypic information retrieved form ArrayExpress and associated with the E-TABM-77 series on Apr 06, 2018.

```

> ###List the files obtained from ArrayExpress
> etabm77filesLoc <- system.file("extdata/ETABM77", package = "mammaPrintData")
> head(dir(etabm77filesLoc))

[1] "A-MEXP-318.adf.txt.gz"
[2] "E-TABM-77.sdrf.txt.gz"
[3] "US22502555_251188611675_S01_1_1_04000344_1_MRP.txt.gz"
[4] "US22502555_251188611675_S01_1_2_MRP_04000344_1.txt.gz"
[5] "US22502555_251188611675_S01_2_1_04000346_1_MRP.txt.gz"
[6] "US22502555_251188611675_S01_2_2_MRP_04000346_1.txt.gz"

> ###Read the phenotypic information from "E-TABM-77.sdrf.txt"
> targets <- read.table(dir(etabm77filesLoc, full.names=TRUE, pattern="E-TABM-77.sdrf.txt.gz"),
                        comment.char="", sep="\t", header=TRUE, stringsAsFactors=FALSE)
> ###Check and process the phenotypic information: keep non-redundant information
> targets <- targets[, apply(targets, 2, function(x) length(unique(x)) != 1 )]
> ###Reorder by file name
> targets <- targets[order(targets$Array.Data.File, decreasing=TRUE),]
> ###Remove points in colnames
> colnames(targets) <- gsub("\\.$", "", gsub("\\.\\.", ".", colnames(targets)))
> ###Show the available phenotypic information
> str(targets)

'data.frame':       1228 obs. of  30 variables:
 $ Source.Name             : chr  "MRP" "513" "513" "MRP" ...
 $ Characteristics.Age     : chr  " " "47 years at diagnosis" "47 years
 $ Characteristics.RiskStatus : chr  " " "MammaPrint result:high risk" "Mam
 $ Characteristics.TumorSize : chr  " " "38 mm diameter" "38 mm diameter"
 $ Characteristics.TumorGrading : chr  " " "2" "2" " " " ...
 $ Characteristics.BioSourceProvider : chr  "Agendia" "JRH" "JRH" "Agendia" ...
 $ Characteristics.SurvivalProbability : chr  " " "64.5%" "64.5%" " " ...
 $ Characteristics.Disease.Free.Survival : chr  " " "3.1 years" "3.1 years" " " ...
 $ Characteristics.TestResult : chr  " " "Estrogen Receptor Negative" "Estr
 $ Characteristics.DistantMetastasis.Free.Survival: chr  " " "5.3 years plus" "5.3 years plus"
 $ Characteristics.SurvivalTime : chr  " " "5.3 years" "5.3 years" " " ...
 $ Characteristics.RiskStatus.1 : chr  " " "Adjuvant online:high clinical ris
 $ Characteristics.RiskStatus.2 : chr  " " "NPI:high clinical risk" "NPI:high
 $ Characteristics.RiskStatus.3 : chr  " " "St Gallen category:high clinical
 $ Protocol.REF            : chr  "P-TABM-213" " " " " " "P-TABM-213" ...

```

```

$ Sample.Name           : chr "MRP" "4000702" "4000702" "MRP" ...
$ Extract.Name          : chr "MRP_e1" "4000702_e1" "4000702_e1" "MRP_e1" ...
$ Labeled.Extract.Name  : chr "MRP_e1_l1Cy5" "4000702_e1_l1Cy3" "4000702_e1_l1Cy5" ...
$ Label                 : chr "Cy5" "Cy3" "Cy5" "Cy3" ...
$ Hybridization.Name    : chr "TABM:Tab2MAGE:E-TABM-77.2517.Hybridiza
$ Factor.Value.NPI.Risk.Status : chr "NPI:high clinical risk" "NPI:high clinical risk" ...
$ Factor.Value.Adjuvant.online.risk.status : chr "Adjuvant online:high clinical risk" "Adjuvant online:high clinical risk" ...
$ Factor.Value.MammaPrint.prediction : chr "MammaPrint result:high risk" "MammaPrint result:high risk" ...
$ Factor.Value.Disease.Free.Survival : chr "3.1 years" "3.1 years" "3.1 years" "3.1 years" ...
$ Factor.Value.DistantMetastasis.Free.Survival : chr "5.3 years plus" "5.3 years plus" "5.3 years plus" "5.3 years plus" ...
$ Factor.Value.St.Gallen.Risk.Status : chr "St Gallen category:high clinical risk" "St Gallen category:high clinical risk" ...
$ Factor.Value.SurvivalTime : chr "5.3 years" "5.3 years" "5.3 years" "5.3 years" ...
$ Factor.Value.ER.status : chr "Estrogen Receptor Negative" "Estrogen Receptor Negative" ...
$ Scan.Name             : chr "US22502555_251188613295_S01_2_4_MRP1_8" "US22502555_251188613295_S01_2_4_MRP1_8" ...
$ Array.Data.File       : chr "US22502555_251188613295_S01_2_4_MRP1_8" "US22502555_251188613295_S01_2_4_MRP1_8" ...

```

The Buyse cohort accounts for 307 unique cases, which were analyzed using a dye-swap two-colors design, comparing each sample against the same reference RNA. According to ArrayEspress instruction for SDRF files (available at http://tab2mage.sourceforge.net/docs/magetab_docs.html), a complete SDRF annotation file consists of a table in which each hybridization channel is represented by an individual row. Therefore the complete SDRF annotation files for all hybridizations of the Buse cohort should for 1228 total rows: 307 samples for 2 channels (cy5 and Cy3) for 2 replicated hybridizations (dye-swap). As shown below, the E-TABM-77.sdrf.txt file currently available from ArrayExpress (Apr 06, 2018) is complete and contains all necessary information.

An inspection of the information contained in the downloaded SDRF file reveals that it contains two row for each hybridization (n=1228) as expected.

```

> ###Check targets data.frame dimentions
> dim(targets)

[1] 1228  30

> ###Count the unique file names
> length(unique(targets$Array.Data.File))

[1] 614

> ###Count the number of rows associated with each channel
> table(CHANNEL=targets$Label)

CHANNEL
Cy3 Cy5
614 614

> ###Count the number of rows for the reference RNA (named "MRP") in each channel
> table(CHANNEL=targets$Label, REFERENCE=targets$Sample.Name == "MRP")

          REFERENCE
CHANNEL FALSE TRUE
Cy3      307  307
Cy5      307  307

```

```
> ###Count the number of distinct RNA analyzed (excluding the refernce RNA)
> sum(REFERENCE=targets$Sample.Name!="MRP")
```

```
[1] 614
```

```
> ###Count the MammaPrint predictions
> table(MAMMAPRINT=targets$Factor.Value.MammaPrint.prediction)
```

```
MAMMAPRINT
```

```
MammaPrint result:high risk MammaPrint result:low risk
                        776                        452
```

The E-TABM-77.sdrf.txt file is therefore valid and can be used to assemble the two RGList objects corresponding to the two sets of dye-swap hybridization that were performed, as shown in the R code below.

```
> ###List files for E-TABM-77 experiment
> etabm77filesLoc <- system.file("extdata/ETABM77", package = "mammaPrintData")
> etabm77files <- list.files(etabm77filesLoc, pattern="^US")
> ###Check whether all available files correspond to the targets$Array.Data.File
> all(paste(targets$Array.Data.File, ".gz", sep="") %in% etabm77files)
```

```
[1] TRUE
```

```
> ###Check whether they are ordered in the same way
> all(paste(targets$Array.Data.File, ".gz", sep="") == etabm77files)
```

```
[1] FALSE
```

```
> #####Subset targets table extracting the rows for CANCER and the separate by channel
> caList <- !targets$Sample.Name=="MRP"
> targetsCa <- targets[caList,]
> ###Cy5 channel
> targetsCa.ch1 <- targetsCa[targetsCa$Label=="Cy5",]
> colnames(targetsCa.ch1) <- paste(colnames(targetsCa.ch1),"Cy5",sep=".")
> ###Cy3 channel
> targetsCa.ch2 <- targetsCa[targetsCa$Label=="Cy3",]
> colnames(targetsCa.ch2) <- paste(colnames(targetsCa.ch2),"Cy3", sep=".")
> #####Subset targets table extracting the rows for REFERENCE and the separate by channel
> refList <- targets$Sample.Name=="MRP"
> targetsRef <- targets[refList,]
> ###Cy5 channel
> targetsRef.ch1 <- targetsRef[targetsRef$Label=="Cy5",]
> colnames(targetsRef.ch1) <- paste(colnames(targetsRef.ch1),"Cy5",sep=".")
> ###Cy3 channel
> targetsRef.ch2 <- targetsRef[targetsRef$Label=="Cy3",]
> colnames(targetsRef.ch2) <- paste(colnames(targetsRef.ch2),"Cy3", sep=".")
```

Below is the R code chunk used to assemble the phenotypic information associated with the first set of hybridizations.

```
> ###Now combine channel information to create the new targets object
> ###Here is for the FIRST set of swapped hybridization (keep only useful columns)
```



```

> if ( all(targetsCa.ch1$Array.Data.File.Cy5==targetsRef.ch2$Array.Data.File.Cy3) ) {
  colsSel <- apply(targetsCa.ch1==targetsRef.ch2,2,function(x) sum(x) != length(x) )
  targetsSwap1 <- cbind(targetsCa.ch1,targetsRef.ch2[,colsSel],stringsAsFactors=FALSE)
  targetsSwap1 <- targetsSwap1[,apply(targetsSwap1,2,function(x) length(unique(x)) != 1 )]
  ##add Cy5 and Cy3 columns
  targetsSwap1$Cy5 <- targetsSwap1$Sample.Name
  targetsSwap1$Cy3 <- "Ref"
  targetsSwap1 <- targetsSwap1[,order(colnames(targetsSwap1))]
  ##remove dye extension to Scan name
  colnames(targetsSwap1) <- gsub("\\.Cy5$", "", colnames(targetsSwap1))
  ##reorder by sample name in Cy5
  targetsSwap1 <- targetsSwap1[order(targetsSwap1$Cy5),]
  print("Assembling the targets object for the first set of swapped hybridizations")
} else {
  stop("Check objects")
}

```

```
[1] "Assembling the targets object for the first set of swapped hybridizations"
```

Below is the R code chunk used to assemble the phenotypic information associated with the second set of hybridizations.

```

> ###create new target objects for SECOND set of swapped hybs and keep useful columns
> if ( all(targetsCa.ch2$Array.Data.File.Cy3==targetsRef.ch1$Array.Data.File.Cy5) ) {
  colsSel <- apply(targetsCa.ch2==targetsRef.ch1,2,function(x) sum(x) != length(x) )
  targetsSwap2 <- cbind(targetsCa.ch2,targetsRef.ch1[,colsSel],stringsAsFactors=FALSE)
  targetsSwap2 <- targetsSwap2[,apply(targetsSwap2,2,function(x) length(unique(x)) != 1 )]
  ##add Cy5 and Cy3 columns
  targetsSwap2$Cy5 <- "Ref"
  targetsSwap2$Cy3 <- targetsSwap2$Sample.Name
  targetsSwap2 <- targetsSwap2[,order(colnames(targetsSwap2))]
  ##remove dye extension to Scan name
  colnames(targetsSwap2) <- gsub("\\.Cy3$", "", colnames(targetsSwap2))
  ##reorder by sample name in Cy3
  targetsSwap2 <- targetsSwap2[order(targetsSwap2$Cy3),]
  print("Assembling the targets object for the second set of swapped hybridizations")
} else {
  stop("Check objects")
}

```

```
[1] "Assembling the targets object for the second set of swapped hybridizations"
```

Below is the R code chunk used to assemble the RGList object for the first set of hybridizations of the ETABM-77 series.

```

> ##Define the columns which will be read from the raw files selection
> colsList <- list(Rf="Feature Extraction Software:rMedianSignal",
  Rb="Feature Extraction Software:rBGMedianSignal",
  Gf="Feature Extraction Software:gMedianSignal",
  Gb="Feature Extraction Software:gBGMedianSignal",
  logRatio="Feature Extraction Software:LogRatio",

```

```

                logRatioError="Feature Extraction Software:LogRatioError")
> ###Swap set 1 has Reference RNA in Cy3 channel
> table(targetsSwap1$Cy3)

Ref
307

> ###This creates an instance of class "RGList", selecting specific columns from the raw data:
> RGcy3 <- read.maimages(paste(targetsSwap1$Array.Data.File, ".gz", sep=""),
                        source="generic",
                        columns=colsList, annotation="Reporter identifier",
                        path=etabm77filesLoc, verbose=FALSE)
> ###Add targets information
> RGcy3$targets <- targetsSwap1
> ###Add sample names as column names with prefix
> colnames(RGcy3) <- paste("BC",targetsSwap1$Sample.Name,sep=".")
> ###Format Reporter identifiers
> RGcy3$genes$ID <- gsub(".+A-MEXP-318\\.\\.", "", RGcy3$genes[, "Reporter identifier"])
> ###Check dimensions
> dim(RGcy3)

[1] 1900 307

```

Below is the R code chunk used to assemble the RGList object for the second set of hybridizations of the ETABM-77 series.

```

> ###This creates an instance of class "RGList", selecting specific columns from the raw data:
> RGcy5 <- read.maimages(paste(targetsSwap1$Array.Data.File, ".gz", sep=""),
                        source="generic",
                        columns=colsList, annotation="Reporter identifier",
                        path=etabm77filesLoc, verbose=FALSE)
> ###Swap set 2 has Reference RNA in Cy5 channel
> table(targetsSwap2$Cy5)

Ref
307

> ###Add targets information
> RGcy5$targets <- targetsSwap2
> ###Format Reporter identifiers
> RGcy5$genes$ID <- gsub(".+A-MEXP-318\\.\\.", "", RGcy5$genes[, "Reporter identifier"])
> ###Add sample names as column names with prefix
> colnames(RGcy5) <- paste("BC",targetsSwap2$Sample.Name,sep=".")
> ###Check dimensions
> dim(RGcy5)

[1] 1900 307

```

Below is the R code to check whether all data read is of the correct mode (i.e. numeric values are of mode “numeric”, and so on)

```

> ###Check mode of read data for first set of hybridizations
> sapply(RGcy3, mode)

```

```

          R           Rb           G           Gb           logRatio
"numeric" "numeric" "numeric" "numeric" "numeric"
logRatioError targets genes source
"numeric" "list" "list" "character"

```

```

> ###Since RGc3$logRatio is character convert to numeric
> RGc3$logRatio <- apply(RGc3$logRatio, 2, as.numeric)
> ###Check mode of read data for second set of hybridizations
> sapply(RGc5, mode)

```

```

          R           Rb           G           Gb           logRatio
"numeric" "numeric" "numeric" "numeric" "numeric"
logRatioError targets genes source
"numeric" "list" "list" "character"

```

```

> ###Since RGc3$logRatio is character convert to numeric
> RGc5$logRatio <- apply(RGc5$logRatio, 2, as.numeric)

```

Below is the R code chunk to process the microarray feature annotation for the 1.9k MammaPrint array, as it is provided in the ArrayExpress database (file A-MEXP-318.adf.txt). We will then map the microarray features from this new array to the 231-gene and the 70-gene prognostic signatures. We will finally add annotation information to the RGList objects created above.

```

> ###Read genes information for MammaPrint array from the A-MEXP-318.adf.txt
> genes <- read.table(dir(etabm77filesLoc, full.names=TRUE, pattern="A-MEXP-318.adf.txt"),
                     comment.char="", skip=21, sep="\t", header=TRUE, stringsAsFactors=FALSE)
> ###Remove special characters like points in the columns header
> colnames(genes) <- gsub("\\.$", "", gsub("\\.\\.\\.\\.\"", ".", colnames(genes)))
> ###Use the annotation information previously processed
> str(progSig)

```

List of 7

```

$ gns231acc : chr [1:231] "AL080059" "Contig63649_RC" "Contig46218_RC" "NM_016359" ...
$ gns231name: chr [1:161] "LOC51203" "ALDH4" "FGF18" "BBC3" ...
$ gns231any : chr [1:392] "AL080059" "Contig63649_RC" "Contig46218_RC" "NM_016359" ...
$ gns70acc : chr [1:70] "AL080059" "Contig63649_RC" "Contig46218_RC" "NM_016359" ...
$ gns70name : chr [1:50] "LOC51203" "ALDH4" "FGF18" "BBC3" ...
$ gns70any : chr [1:120] "AL080059" "Contig63649_RC" "Contig46218_RC" "NM_016359" ...
$ gns231Cors:'data.frame': 394 obs. of 2 variables:
..$ ID : chr [1:394] "LOC51203" "ALDH4" "FGF18" "BBC3" ...
..$ gns231Cors: num [1:394] -0.425 0.421 0.411 0.407 0.402 ...

```

```

> ###Count the features mapped to the 231-gene prognostic signature by accession number
> apply(genes, 2, function(x, y) { sum(unique(x) %in% y) }, y = progSig$gns231acc)

```

```

      Block.Column      Block.Row
      0              0
      Column          Row
      0              0
      Reporter.Name    Comment.AEReporterName
      0                68

```

Reporter.Database.Entry.embl Reporter.Database.Entry.unigene

```

              7              0
Reporter.Group.role      Control.Type
              0              0

```

```

> ###Count the features mapped to the 231-gene prognostic signature by gene symbol
> apply(genes, 2, function(x, y) { sum(unique(x) %in% y) }, y = progSig$gns231name)

```

```

      Block.Column      Block.Row
      0                0
      Column           Row
      0                0
Reporter.Name      Comment.AEReporterName
      0                161
Reporter.Database.Entry.embl Reporter.Database.Entry.unigene
      0                0
Reporter.Group.role      Control.Type
      0                0

```

```

> ###Count the features mapped to the 231-gene prognostic signature by gene symbol or accession
> apply(genes, 2, function(x, y) { sum(unique(x) %in% y) }, y = progSig$gns231any)

```

```

      Block.Column      Block.Row
      0                0
      Column           Row
      0                0
Reporter.Name      Comment.AEReporterName
      0                229
Reporter.Database.Entry.embl Reporter.Database.Entry.unigene
      7                0
Reporter.Group.role      Control.Type
      0                0

```

```

> ###Add mapping information for 229 features using both gene symbols and accession numbers
> genes$genes231 <- genes$Comment.AEReporterName %in% progSig$gns231any
> ###Count the features mapped to the 70-gene prognostic signature by accession number
> apply(genes, 2, function(x, y) { sum(unique(x) %in% y) }, y = progSig$gns70acc)

```

```

      Block.Column      Block.Row
      0                0
      Column           Row
      0                0
Reporter.Name      Comment.AEReporterName
      0                19
Reporter.Database.Entry.embl Reporter.Database.Entry.unigene
      1                0
Reporter.Group.role      Control.Type
      0                0
genes231
      0

```

```

> ###Count the features mapped to the 70-gene prognostic signature by gene symbol

```

```
> apply(genes, 2, function(x, y) { sum(unique(x) %in% y) }, y = progSig$gns70name)
```

```

      Block.Column      Block.Row
      0                0
      Column          Row
      0                0
      Reporter.Name    Comment.AEReporterName
      0                50
      Reporter.Database.Entry.embl Reporter.Database.Entry.unigene
      0                0
      Reporter.Group.role Control.Type
      0                0
      genes231
      0

```

```
> ###Count the features mapped to the 70-gene prognostic signature by gene symbol or accession number
> apply(genes, 2, function(x, y) { sum(unique(x) %in% y) }, y = progSig$gns70any)
```

```

      Block.Column      Block.Row
      0                0
      Column          Row
      0                0
      Reporter.Name    Comment.AEReporterName
      0                69
      Reporter.Database.Entry.embl Reporter.Database.Entry.unigene
      1                0
      Reporter.Group.role Control.Type
      0                0
      genes231
      0

```

```
> ###Add mapping information for 229 features using both gene symbols and accession numbers
> genes$genes70 <- genes$Comment.AEReporterName %in% progSig$gns70any
> ###The resulting gene annotation file
> str(genes)
```

```

'data.frame':      1900 obs. of  12 variables:
 $ Block.Column      : int  1 1 1 1 1 1 1 1 1 1 1 ...
 $ Block.Row        : int  1 1 1 1 1 1 1 1 1 1 1 ...
 $ Column           : int  1 2 13 20 40 42 48 49 50 1 ...
 $ Row              : int  1 1 1 1 1 1 1 1 1 2 ...
 $ Reporter.Name    : chr   "AGEN000001" "AGEN000002" "AGEN000013" "AGEN000020" ...
 $ Comment.AEReporterName : chr   "Pro25G" "3xSLv1" "eQC" "eQC" ...
 $ Reporter.Database.Entry.embl : chr   "" "" "" "" ...
 $ Reporter.Database.Entry.unigene: chr   "" "" "" "" ...
 $ Reporter.Group.role : chr   "Control" "Control" "Control" "Control" ...
 $ Control.Type     : chr   "control_biosequence" "control_biosequence" "control_bi...
 $ genes231         : logi  FALSE FALSE FALSE FALSE FALSE FALSE ...
 $ genes70          : logi  FALSE FALSE FALSE FALSE FALSE FALSE ...

```

```
> ###Add original correlation from the van't Veer study
```

```

> gns231Cors <- progSig$gns231Cors
> gns231Cors <- gns231Cors[gns231Cors$ID %in% genes$Comment.AEReporterName,]
> ###Merge and remove duplicates
> genes <- merge(genes, gns231Cors, all.x=TRUE, all.y=FALSE,
                 by.x="Comment.AEReporterName", by.y="ID")
> genes <- genes[!duplicated(genes$Reporter.Name),]
> ###Check genes
> str(genes)

'data.frame':      1900 obs. of  13 variables:
 $ Comment.AEReporterName      : chr  "3xSLv1" "3xSLv1" "3xSLv1" "3xSLv1" ...
 $ Block.Column                : int  1 1 1 1 1 1 1 1 1 1 ...
 $ Block.Row                   : int  1 1 1 1 1 1 1 1 1 1 ...
 $ Column                      : int  2 48 1 2 48 49 50 1 4 7 ...
 $ Row                         : int  1 1 2 2 2 2 2 9 9 9 ...
 $ Reporter.Name               : chr  "AGENO00002" "AGENO000048" "AGENO000051" "AGENO000052" ...
 $ Reporter.Database.Entry.embl : chr  "" "" "" "" ...
 $ Reporter.Database.Entry.unigene: chr  "" "" "" "" ...
 $ Reporter.Group.role         : chr  "Control" "Control" "Control" "Control" ...
 $ Control.Type                : chr  "control_biosequence" "control_biosequence" "control_bi
 $ genes231                    : logi  FALSE FALSE FALSE FALSE FALSE FALSE ...
 $ genes70                     : logi  FALSE FALSE FALSE FALSE FALSE FALSE ...
 $ gns231Cors                  : num  NA NA NA NA NA NA NA NA NA NA ...

```

Below is the R code chunk used to add the feature annotation the RGList objects containing the expression data (first set of hybridizations).

```

> ###Compare genes between paltform and RGList instances: first set of hybridizations
> if (nrow(genes)==nrow(RGcy3)) {
  ##Compare the identifiers' order
  if ( !all(genes$Reporter.Name == RGcy3$genes$ID) ) {
    ##Reorder if needed
    RGcy3 <- RGcy3[order(RGcy3$genes$ID),]
    genes <- genes[order(genes$Reporter.Name),]
    ##check for order AGAIN
    if ( all(genes$Reporter.Name == RGcy3$genes$ID) ) {
      ##Substitute genes or stop
      RGcy3$genes <- genes
    } else {
      stop("Wrong gene order, check objects")
    }
  } else {
    print("Updating gene annotation")
    RGcy3$genes <- genes
  }
} else {
  stop("Wrong number of features, check objects")
}
> ###Rename

```

```
> buyseRGcy3 <- RGcy3
```

Below is the R code chunk used to add the feature annotation the RGList objects containing the expression data (second set of hybridizations).

```
> ###Compare genes between paltform and RGList instances: second set of hybridizations
> if (nrow(genes)==nrow(RGcy5)) {
  ##Compare the identifiers' order
  if ( !all(genes$Reporter.Name == RGcy5$genes$ID) ) {
    ##Reorder if needed
    RGcy5 <- RGcy5[order(RGcy5$genes$ID),]
    genes <- genes[order(genes$Reporter.Name),]
    ##check for order AGAIN
    if ( all(genes$Reporter.Name == RGcy5$genes$ID) ) {
      ##Substitute genes or stop
      RGcy5$genes <- genes
    } else {
      stop("Wrong gene order, check objects")
    }
  } else {
    print("Updating gene annotation")
    RGcy5$genes <- genes
  }
} else {
  stop("Wrong number of features, check objects")
}
> ###Rename
> buyseRGcy5 <- RGcy5
```

4 Phenotypic information processing

4.1 Glas cohort: patients' phenotype curation

The chunk of R code below was used to process the clinical information associated with the 162 patients of the ArrayExpress “E-TABM-115” series, and define the final “good” and “bad” prognosis patients groups, as well as other end-points that were investigated in the our study. To this end we first identified the putative 78 patients from the van't Veer cohort [7], and the 84 cases from the Van de Vijver cohort [6] that were combined to assemble the final Glas data set. Since this information was not provided with the ArrayExpress “E-TABM-115” series, we analyzed the raw data hybridization file names, and used the 3-digits suffix code present in exactly 84 files, as follows:

```
> ###Retrieve the phenotypic information from one of the RGList intances
> phenoGlasCy3 <- glasRGcy3$targets
> phenoGlasCy5 <- glasRGcy5$targets
> ###Identification of the 78 samples from van't Veer and the 84 from VanDeVijver
> table(gsub(".+_", "", phenoGlasCy3$Scan.Name) == gsub(".+_", "", phenoGlasCy5$Scan.Name))

FALSE TRUE
   78   84
```

```

> #####
> ###There are 78 hybridizations with 1-digit suffixes, and 84 of them with 3-digit suffixes
> table(nchar(gsub(".+_", "", phenoGlasCy5$Scan.Name)))

 1  3
78 84

> table(nchar(gsub(".+_", "", phenoGlasCy3$Scan.Name)))

 1  3
78 84

> ###Use the hybridization file names suffixes to define the putative cohort of origin: FIRST SET
> phenoGlasCy5$putativeCohort <- factor(nchar(gsub(".+_", "", phenoGlasCy5$Scan.Name)))
> levels(phenoGlasCy5$putativeCohort) <- c("putativeVantVeer", "putativeVanDeVijver")
> ###Use the hybridization file names suffixes to define the putative cohort of origin: SECOND SET
> phenoGlasCy3$putativeCohort <- factor(nchar(gsub(".+_", "", phenoGlasCy3$Scan.Name)))
> levels(phenoGlasCy3$putativeCohort) <- c("putativeVantVeer", "putativeVanDeVijver")
> ###Show counts FIRST SET
> table(phenoGlasCy5$putativeCohort)

      putativeVantVeer putativeVanDeVijver
                78                84

> #####
> ###Show counts SECOND SET
> table(phenoGlasCy3$putativeCohort)

      putativeVantVeer putativeVanDeVijver
                78                84

```

We subsequently processed the “Factor.Value.overall_survival” character strings contained in the “E-TABM-115” SDRF table to define the actual overall survival (OS) time, the OS event status, and the 10-year survival status for each patient, as shown below. This was possible only for the set of hybridization for which the clinical information was provided in ArrayExpress (see `glasRGcy5$targets` below).

```

> ###Process the overall survival (OS) character strings and make numeric
> OS <- gsub("\\s+", "", phenoGlasCy5$Factor.Value.overall_survival)
> phenoGlasCy5$OS <- as.numeric(OS)
> ####Process OS event and make numeric: missing data, labeled with "n/a" strings are turned into NA
> phenoGlasCy5$OSevent <- as.numeric(phenoGlasCy5$Factor.Value.Event_Death)
> ###Count missing information by counting the number of NA
> sum(is.na(phenoGlasCy5$OSevent))

[1] 17

> ####Create binary OS at 10 years groups
> phenoGlasCy5$TenYearSurv <- phenoGlasCy5$OS < 10 & phenoGlasCy5$OSevent == 1
> phenoGlasCy5$TenYearSurv[is.na(phenoGlasCy5$OSevent)] <- NA

```

The overall survival information summary for the Glas cohort is shown below:

```

> ###Count OS events
> table(phenoGlasCy5$OSevent)

```



```

  0  1
104 41

> ###Count survival at 10 years status
> table(phenoGlasCy5$TenYearSurv)

FALSE TRUE
  106   39

```

We subsequently processed the “Factor.Value.Time_to_development_of_distant_metastases” character strings contained in the “E-TABM-115” SDRF table to define the actual time to metastasis (TTM) time, the TTM event status, and the 5-year distant recurrence status for each patient, as shown below. This was possible only for the set of hybridization for which the clinical information was provided in ArrayExpress (see `glasRGcy5$targets` below).

```

> ###Process time metastases (TTM) character strings and make numeric
> ###Note that missing data, labeled with "n/a" strings are turned into NA
> TTM <- phenoGlasCy5$Factor.Value.Time_to_development_of_distant_metastases
> phenoGlasCy5$TTM <- as.numeric(gsub("\\s+", "", TTM))
> ####Process TTM event and make numeric
> phenoGlasCy5$TTMevent <- as.numeric(phenoGlasCy5$Factor.Value.Event_distant_metastases)
> ###Use follow-up time from OS as TTM for patients without metastasis event
> phenoGlasCy5$TTM[is.na(phenoGlasCy5$TTM)] <- phenoGlasCy5$OS[is.na(phenoGlasCy5$TTM)]
> ###Create binary TTM at 5 years groups
> phenoGlasCy5$FiveYearMetastasis <- phenoGlasCy5$TTM < 5 & phenoGlasCy5$TTMevent == 1

```

The time to metastasis information summary, and the five year distant recurrence status, which corresponds to the “good” and “bad” prognosis groups used in the Glas study, are shown below.

```

> ###Count TTM events
> table(phenoGlasCy5$TTMevent)

  0  1
106 56

> ###Count metastasis events by putative cohort of origin
> table(phenoGlasCy5$FiveYearMetastasis, phenoGlasCy5$putativeCohort)

      putativeVantVeer putativeVanDeVijver
FALSE          44          72
TRUE           34          12

```

We finally replaced the processed phenotypic information in the corresponding `RGList`-class instances:

```

> ###Substitute in the RGLists
> glasRGcy3$targets <- phenoGlasCy3
> glasRGcy5$targets <- phenoGlasCy5

```

Below is the R code chunk used to save the final `RGList` objects.

```

> ###Save the final ExpressionSet object: not run
> dataDirLoc <- system.file("data", package = "mammaPrintData")
> save(glasRGcy5, glasRGcy3, file=paste(dataDirLoc, "/glasRG.rda", sep=""))

```

4.2 Buyse cohort: patients' phenotype curation

The chunk of R code below was used to process the clinical information associated with the 307 analyzed patients that were retrieved from the ArrayExpress “E-TABM-77” series, to define the final “good” and “bad” prognosis patients groups, as well as other end-points that were investigated in the present study. We hence processed the “Factor.Value.SurvivalTime” character strings contained in the “E-TABM-77” SDRF table to define the actual overall survival (OS) time, the OS event status, and the 10-year survival group for each patient, as shown below

```
> ###Retrieve the phenotypic information from one of the RGList instances
> phenoBuyseCy3 <- buyseRGcy3$targets
> phenoBuyseCy5 <- buyseRGcy5$targets
> ###Process overall survival (OS) character strings and make numeric: BOTH SETS
> OScy5 <- phenoBuyseCy5$Factor.Value.SurvivalTime
> phenoBuyseCy5$OS <- as.numeric(gsub("\\s+", "", OScy5))
> OScy3 <- phenoBuyseCy3$Factor.Value.SurvivalTime
> phenoBuyseCy3$OS <- as.numeric(gsub("\\s+", "", OScy3))
> ###Create the OS event by processing the OS character string with grep
> ###and the "plus" pattern making it a numeric vector: BOTH SETS
> phenoBuyseCy5$OSevent <- 1*( ! 1:nrow(phenoBuyseCy5) %in% grep("plus", OScy5))
> phenoBuyseCy3$OSevent <- 1*( ! 1:nrow(phenoBuyseCy3) %in% grep("plus", OScy3))
> ###Create binary OS at 10 years groups: BOTH SETS
> phenoBuyseCy5$TenYearSurv <- phenoBuyseCy5$OS < 10 & phenoBuyseCy5$OSevent == 1
> phenoBuyseCy3$TenYearSurv <- phenoBuyseCy3$OS < 10 & phenoBuyseCy3$OSevent == 1
```

The overall survival information summary for the Buyse cohort is shown below:

```
> ###Count OS survival events: BOTH SETS
> table(phenoBuyseCy5$OSevent)

 0  1
225 82

> table(phenoBuyseCy3$OSevent)

 0  1
225 82

> ###Count survival at 10 years status: BOTH SETS
> table(phenoBuyseCy5$TenYearSurv)

FALSE  TRUE
 242    65

> table(phenoBuyseCy3$TenYearSurv)

FALSE  TRUE
 242    65
```

We subsequently processed the “Factor.Value.Disease.Free.Survival” character strings contained in the “E-TABM-77” SDRF table to define the actual disease free survival (DFS) time, and the DFS event status for each patient, as shown below.

```

> ###Process disease free survival (DFS) character strings and make numeric: BOTH SETS
> DFScy5 <- phenoBuyseCy5$Factor.Value.Disease.Free.Survival
> phenoBuyseCy5$DFS <- as.numeric(gsub("\\s+", "", DFScy5))
> DFScy3 <- phenoBuyseCy3$Factor.Value.Disease.Free.Survival
> phenoBuyseCy3$DFS <- as.numeric(gsub("\\s+", "", DFScy3))
> ###Create the DFS event by processing the DFS character string with grep
> ###and the "plus" pattern making it a numeric vector: BOTH SETS
> phenoBuyseCy5$DFSevent <- 1*( ! 1:nrow(phenoBuyseCy5) %in% grep("plus", DFScy5))
> phenoBuyseCy3$DFSevent <- 1*( ! 1:nrow(phenoBuyseCy3) %in% grep("plus", DFScy3))
> ###Create binary DFS at 5 years groups:BOTH SETS
> phenoBuyseCy5$FiveYearDiseaseFree <- (phenoBuyseCy5$DFS < 5
                                         & phenoBuyseCy5$DFSevent == 1)
> phenoBuyseCy3$FiveYearDiseaseFree <- (phenoBuyseCy3$DFS < 5
                                         & phenoBuyseCy3$DFSevent == 1)

```

The disease free survival information summary for the Buyse cohort is shown below:

```

> ###Count DFS survival events: BOTH SETS
> table(phenoBuyseCy5$DFSevent)

  0   1
168 139

> table(phenoBuyseCy3$DFSevent)

  0   1
168 139

> ###Count recurrence at 5 years status: BOTH SETS
> table(phenoBuyseCy5$FiveYearDiseaseFree)

FALSE  TRUE
  226   81

> table(phenoBuyseCy3$FiveYearDiseaseFree)

FALSE  TRUE
  226   81

```

We subsequently processed the “Factor.Value.DistantMetastasis.Free.Survival” character strings contained in the “E-TABM-77” SDRF table to define the actual time to metastasis (TTM) time, the TTM event status, and the 5-year recurrence status for each patient, as shown below.

```

> ###Process time metastases (TTM) character strings and make numeric: BOTH SETS
> TTMcy5 <- phenoBuyseCy5$Factor.Value.DistantMetastasis.Free.Survival
> phenoBuyseCy5$TTM <- as.numeric(gsub("\\s+", "", TTMcy5))
> TTMcy3 <- phenoBuyseCy3$Factor.Value.DistantMetastasis.Free.Survival
> phenoBuyseCy3$TTM <- as.numeric(gsub("\\s+", "", TTMcy3))
> ###Create the TTM event by processing the TTM character string with grep
> ###and the "plus" pattern making it a numeric vector: BOTH SETS
> phenoBuyseCy5$TTMevent <- 1*( ! 1:nrow(phenoBuyseCy5) %in% grep("plus", TTMcy5))
> phenoBuyseCy3$TTMevent <- 1*( ! 1:nrow(phenoBuyseCy3) %in% grep("plus", TTMcy3))
> ###Create binary TTM at 5 years groups: BOTH SETS

```

```

> phenoBuyseCy5$FiveYearRecurrence <- (phenoBuyseCy5$TTM < 5
    & phenoBuyseCy5$TTMevent == 1)
> phenoBuyseCy3$FiveYearRecurrence <- (phenoBuyseCy3$TTM < 5
    & phenoBuyseCy3$TTMevent == 1)

```

The time to metastasis information summary, and the five year distant recurrence status, which corresponds to the “good” and “bad” prognosis groups used in the Buyse study, are shown below.

```

> ###Count TTM survival events: BOTH SETS
> table(phenoBuyseCy5$TTMevent)

  0  1
230 77

> table(phenoBuyseCy3$TTMevent)

  0  1
230 77

> ###Count recurrence at 5 years status: BOTH SETS
> table(phenoBuyseCy5$FiveYearRecurrence)

FALSE  TRUE
  260   47

> table(phenoBuyseCy3$FiveYearRecurrence)

FALSE  TRUE
  260   47

> ###Count metastasis events by European center: BOTH SETS
> table(phenoBuyseCy5$FiveYearRecurrence, phenoBuyseCy5$Characteristics.BioSourceProvider)

      CRH GUY IGR JRH KAR
FALSE  54  37  84  32  53
TRUE   5  16  12   7   7

> table(phenoBuyseCy3$FiveYearRecurrence, phenoBuyseCy3$Characteristics.BioSourceProvider)

      CRH GUY IGR JRH KAR
FALSE  54  37  84  32  53
TRUE   5  16  12   7   7

```

We finally identified the patients that were excluded from the analysis in the original study by Buyse and colleagues [2] because of missing clinical information.

```

> ###Exclude patients with missing ER status: BOTH SETSXS
> phenoBuyseCy5$toExclude <- phenoBuyseCy5$Factor.Value.ER.status=="unknown"
> phenoBuyseCy3$toExclude <- phenoBuyseCy3$Factor.Value.ER.status=="unknown"

```

We finally replaced the processed phenotypic information in the corresponding RGList-class instances:

```

> ###Substitute in the RGLists
> buyseRGcy3$targets <- phenoBuyseCy3
> buyseRGcy5$targets <- phenoBuyseCy5

```

Below is the R code chunk used to save the final RGList objects.

```
> ###Save RGList instances for later use: not run
> dataDirLoc <- system.file("data", package = "mammaPrintData")
> save(buyseRGcy5, buyseRGcy3, file=paste(dataDirLoc, "/buyseRG.rda", sep=""))
```

5 System Information

Session information:

```
> toLatex(sessionInfo())
```

- R version 3.4.4 (2018-03-15), x86_64-pc-linux-gnu
- Locale: LC_CTYPE=en_US.UTF-8, LC_NUMERIC=C, LC_TIME=en_US.UTF-8, LC_COLLATE=C, LC_MONETARY=en_US.UTF-8, LC_MESSAGES=en_US.UTF-8, LC_PAPER=en_US.UTF-8, LC_NAME=C, LC_ADDRESS=C, LC_TELEPHONE=C, LC_MEASUREMENT=en_US.UTF-8, LC_IDENTIFICATION=C
- Running under: Ubuntu 16.04.4 LTS
- Matrix products: default
- BLAS: /home/biocbuild/bbs-3.6-bioc/R/lib/libRblas.so
- LAPACK: /home/biocbuild/bbs-3.6-bioc/R/lib/libRlapack.so
- Base packages: base, datasets, grDevices, graphics, methods, parallel, stats, utils
- Other packages: Biobase 2.38.0, BiocGenerics 0.24.0, BiocInstaller 1.28.0, gdata 2.18.0, limma 3.34.9
- Loaded via a namespace (and not attached): compiler 3.4.4, gtools 3.5.0, tools 3.4.4

6 References

References

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