MIGSA: Getting pbcmc datasets

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Abstract

In this vignette we are going to show how we got the RData *pbcmcData.RData* which can be loaded via the **MIGSAdata** package using data(pbcmcData).

Keywords: singular enrichment analysis, over representation analysis, gene set enrichment analysis, functional class scoring, big omics data.

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1. Getting the data

Following we give the used code to download this data and their PAM50 subtypes.

```
> library(limma);
> library(pbcmc);
> # datasets included in BioConductor repository
> libNames <- c("mainz", "nki", "transbig", "unt", "upp", "vdx");
> # let's load them!
> pbcmcData <- lapply(libNames, function(actLibName) {
+     print(actLibName);
+
+     # the pbcmc package provides an easy way to download and classify them
+     actLib <- loadBCDataset(Class=PAM50, libname=actLibName, verbose=FALSE);
+     actLibFilt <- filtrate(actLib, verbose=FALSE);
+     actLibFilt <- classify(actLibFilt, std="none", verbose=FALSE);
+     actSubtypes <- classification(actLibFilt)$subtype;
+
+     # get the expression matrix and the annotation
+     actExprs <- exprs(actLib);
+     actAnnot <- annotation(actLib);
+
```

```
+     # we recommend working allways with Entrez IDs, let's match them with
+     # expression matrix rownames (and modify them)
+     if (all(actAnnot$probe == rownames(actExprs))) {
+         actExprs <- actExprs[!is.na(actAnnot$EntrezGene.ID),];
+         actAnnot <- actAnnot[!is.na(actAnnot$EntrezGene.ID),];
+         rownames(actExprs) <- as.character(actAnnot$EntrezGene.ID);
+     } else {
+         matchedEntrez <- match(rownames(actExprs), actAnnot$probe);
+         # all(rownames(actExprs) %in% actAnnot$probe == !is.na(matchedEntrez));
+
+         stopifnot(all(
+             actAnnot$probe[!is.na(matchedEntrez)] ==
+             rownames(actExprs)[!is.na(matchedEntrez)]));
+
+         actExprs <- actExprs[!is.na(matchedEntrez),];
+         actAnnot <- actAnnot[!is.na(matchedEntrez),];
+         stopifnot(all(actAnnot$probe == rownames(actExprs)));
+         actExprs <- actExprs[!is.na(actAnnot$EntrezGene.ID),];
+         actAnnot <- actAnnot[!is.na(actAnnot$EntrezGene.ID),];
+         rownames(actExprs) <- as.character(actAnnot$EntrezGene.ID);
+     }
+
+     # average repeated genes expression
+     actExprs <- avereps(actExprs);
+
+     stopifnot(all(colnames(actExprs) == names(actSubtypes)));
+     # filtrate only these two conditions
+     actExprs <- actExprs[, actSubtypes %in% c("Basal", "LumA")];
+     actSubtypes <- as.character(
+         actSubtypes[actSubtypes %in% c("Basal", "LumA")]);
+
+     return(list(geneExpr=actExprs, subtypes=actSubtypes));
+ })

[1] "mainz"
[1] "nki"
[1] "transbig"
[1] "unt"
[1] "upp"
[1] "vdx"

> names(pbcmcData) <- libNames;
```

And let's check it is the same data.

```
> # save the just created pbcmcData to newPbcmcData
> newPbcmcData <- pbcmcData;
```

```
> library(MIGSAdata);
> # and load the MIGSAdata one.
> data(pbcmcData);
> all.equal(newPbcmcData, pbcmcData);

[1] TRUE
```

Session Info

```
> sessionInfo()

R version 3.5.1 Patched (2018-07-24 r75008)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows Server 2012 R2 x64 (build 9600)

Matrix products: default

locale:
[1] LC_COLLATE=C
[2] LC_CTYPE=English_United States.1252
[3] LC_MONETARY=English_United States.1252
[4] LC_NUMERIC=C
[5] LC_TIME=English_United States.1252

attached base packages:
[1] stats4    parallel  stats     graphics  grDevices utils     datasets
[8] methods   base

other attached packages:
 [1] pbcmc_1.9.0            genefu_2.14.0          AIMS_1.14.0
 [4] e1071_1.7-0            iC10_1.4.2             iC10TrainingData_1.3.1
 [7] pamr_1.55              cluster_2.0.7-1        biomaRt_2.38.0
[10] mclust_5.4.1           survcomp_1.32.0        prodlim_2018.04.18
[13] survival_2.43-1        edgeR_3.24.0           MIGSAdata_1.5.0
[16] MIGSA_1.6.0            mGSZ_1.0               ismev_1.42
[19] mgcv_1.8-25            nlme_3.1-137           MASS_7.3-51
[22] limma_3.38.0           GSA_1.03               BiocParallel_1.16.0
[25] GSEABase_1.44.0        graph_1.60.0           annotate_1.60.0
[28] XML_3.98-1.16          AnnotationDbi_1.44.0   IRanges_2.16.0
[31] S4Vectors_0.20.0       Biobase_2.42.0         BiocGenerics_0.28.0

loaded via a namespace (and not attached):
 [1] amap_0.8-16                 colorspace_1.3-2
 [3] class_7.3-14                futile.logger_1.4.3
 [5] breastCancerTRANSBIG_1.19.0 ggdendro_0.1-20
```

```
 [7] bit64_0.9-7                splines_3.5.1
 [9] SuppDists_1.1-9.4          breastCancerVDX_1.19.0
[11] GO.db_3.7.0                compiler_3.5.1
[13] httr_1.3.1                 GOstats_2.48.0
[15] assertthat_0.2.0           Matrix_1.2-14
[17] lazyeval_0.2.1             formatR_1.5
[19] prettyunits_1.0.2          tools_3.5.1
[21] bindrcpp_0.2.2             gtable_0.2.0
[23] glue_1.3.0                 Category_2.48.0
[25] reshape2_1.4.3             dplyr_0.7.7
[27] Rcpp_0.12.19               RJSONIO_1.3-0
[29] breastCancerNKI_1.19.0     stringr_1.3.1
[31] org.Hs.eg.db_3.7.0         scales_1.0.0
[33] hms_0.4.2                  RBGL_1.58.0
[35] lambda.r_1.2.3             breastCancerUPP_1.19.0
[37] memoise_1.1.0              gridExtra_2.3
[39] breastCancerMAINZ_1.19.0   ggplot2_3.1.0
[41] stringi_1.2.4              RSQLite_2.1.1
[43] rmeta_3.0                  genefilter_1.64.0
[45] permute_0.9-4              lava_1.6.3
[47] rlang_0.3.0.1              pkgconfig_2.0.2
[49] matrixStats_0.54.0         bitops_1.0-6
[51] lattice_0.20-35            purrr_0.2.5
[53] bindr_0.1.1                labeling_0.3
[55] survivalROC_1.0.3          cowplot_0.9.3
[57] bit_1.1-14                 tidyselect_0.2.5
[59] AnnotationForge_1.24.0     plyr_1.8.4
[61] magrittr_1.5               R6_2.3.0
[63] snow_0.4-3                 bootstrap_2017.2
[65] DBI_1.0.0                  pillar_1.3.0
[67] RCurl_1.95-4.11            tibble_1.4.2
[69] crayon_1.3.4               futile.options_1.0.1
[71] KernSmooth_2.23-15         progress_1.2.0
[73] locfit_1.5-9.1             grid_3.5.1
[75] data.table_1.11.8          blob_1.1.1
[77] vegan_2.5-3                Rgraphviz_2.26.0
[79] digest_0.6.18              breastCancerUNT_1.19.0
[81] xtable_1.8-3               munsell_0.5.0
```

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