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.

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));
+ })
> 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);
```

Session Info

```
> sessionInfo()

R version 4.1.0 (2021-05-18)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows Server x64 (build 17763)

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    stats     graphics  grDevices utils     datasets  methods
[8] base

other attached packages:
 [1] edgeR_3.35.0         MIGSAdata_1.17.0     MIGSA_1.17.0
 [4] mGSZ_1.0             ismev_1.42           mgcv_1.8-36
 [7] nlme_3.1-152         MASS_7.3-54          limma_3.49.4
[10] GSA_1.03.1           BiocParallel_1.27.3  GSEABase_1.55.1
[13] graph_1.71.2         annotate_1.71.0      XML_3.99-0.6
[16] AnnotationDbi_1.55.1 IRanges_2.27.0       S4Vectors_0.31.0
[19] Biobase_2.53.0       BiocGenerics_0.39.1

loaded via a namespace (and not attached):
 [1] Category_2.59.0        bitops_1.0-7           matrixStats_0.60.0
 [4] bit64_4.0.5            httr_1.4.2             GenomeInfoDb_1.29.3
 [7] Rgraphviz_2.37.2       tools_4.1.0            utf8_1.2.2
[10] R6_2.5.0               vegan_2.5-7            DBI_1.1.1
[13] colorspace_2.0-2       permute_0.9-5          tidyselect_1.1.1
[16] bit_4.0.4              compiler_4.1.0         formatR_1.11
[19] ggdendro_0.1.22        labeling_0.4.2         scales_1.1.1
[22] genefilter_1.75.0      RBGL_1.69.0            digest_0.6.27
[25] stringr_1.4.0          AnnotationForge_1.35.0 XVector_0.33.0
[28] pkgconfig_2.0.3        fastmap_1.1.0          rlang_0.4.11
[31] rstudioapi_0.13        RSQLite_2.2.7          farver_2.1.0
[34] GOstats_2.59.1         generics_0.1.0         jsonlite_1.7.2
[37] dplyr_1.0.7            RCurl_1.98-1.3         magrittr_2.0.1
[40] GO.db_3.13.0           GenomeInfoDbData_1.2.6 futile.logger_1.4.3
[43] Matrix_1.3-4           Rcpp_1.0.7             munsell_0.5.0
[46] fansi_0.5.0            lifecycle_1.0.0        stringi_1.7.3
[49] zlibbioc_1.39.0        org.Hs.eg.db_3.13.0    plyr_1.8.6
[52] grid_4.1.0             blob_1.2.2             parallel_4.1.0
```

```
[55] crayon_1.4.1          lattice_0.20-44       Biostrings_2.61.2
[58] splines_4.1.0         KEGGREST_1.33.0       locfit_1.5-9.4
[61] pillar_1.6.2          reshape2_1.4.4        futile.options_1.0.1
[64] glue_1.4.2            lambda.r_1.2.4        data.table_1.14.0
[67] png_0.1-7             vctrs_0.3.8           gtable_0.3.0
[70] purrr_0.3.4           assertthat_0.2.1      cachem_1.0.5
[73] ggplot2_3.3.5         xtable_1.8-4          survival_3.2-12
[76] snow_0.4-3            tibble_3.1.3          memoise_2.0.0
[79] cluster_2.1.2         ellipsis_0.3.2
```

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