

# 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));
+ })
> 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 4.2.0 Patched (2022-04-24 r82246 ucrt)
```

```
Platform: x86_64-w64-mingw32/x64 (64-bit)
```

```
Running under: Windows Server x64 (build 20348)
```

```
Matrix products: default
```

```
locale:
```

```
[1] LC_COLLATE=C
```

```
[2] LC_CTYPE=English_United States.utf8
```

```
[3] LC_MONETARY=English_United States.utf8
```

```
[4] LC_NUMERIC=C
```

```
[5] LC_TIME=English_United States.utf8
```

```
attached base packages:
```

```
[1] stats4      stats      graphics  grDevices  utils      datasets  methods
```

```
[8] base
```

```
other attached packages:
```

```
[1] edgeR_3.39.0      MIGSAdata_1.21.0    MIGSA_1.21.0
```

```
[4] mGSZ_1.0          ismev_1.42          mgcv_1.8-40
```

```
[7] nlme_3.1-157      MASS_7.3-57         limma_3.53.0
```

```
[10] GSA_1.03.2        BiocParallel_1.31.0 GSEABase_1.59.0
```

```
[13] graph_1.75.0      annotate_1.75.0      XML_3.99-0.9
```

```
[16] AnnotationDbi_1.59.0 IRanges_2.31.0      S4Vectors_0.35.0
```

```
[19] Biobase_2.57.0    BiocGenerics_0.43.0
```

```
loaded via a namespace (and not attached):
```

```
[1] Category_2.63.0    bitops_1.0-7        matrixStats_0.62.0
```

```
[4] bit64_4.0.5        httr_1.4.3          GenomeInfoDb_1.33.1
```

```
[7] Rgraphviz_2.41.0   tools_4.2.0         utf8_1.2.2
```

```
[10] R6_2.5.1           vegan_2.6-2         DBI_1.1.2
```

```
[13] colorspace_2.0-3   permute_0.9-7       tidyselect_1.1.2
```

```
[16] bit_4.0.4          compiler_4.2.0      cli_3.3.0
```

```
[19] formatR_1.12       gg dendro_0.1.23     labeling_0.4.2
```

```
[22] scales_1.2.0       gene filter_1.79.0   RBGL_1.73.0
```

```
[25] digest_0.6.29      stringr_1.4.0       AnnotationForge_1.39.0
```

```
[28] XVector_0.37.0     pkgconfig_2.0.3     fastmap_1.1.0
```

```
[31] rlang_1.0.2        RSQLite_2.2.13      farver_2.1.0
```

```
[34] G0stats_2.63.0     generics_0.1.2      jsonlite_1.8.0
```

```
[37] dplyr_1.0.9        RCurl_1.98-1.6      magrittr_2.0.3
```

```
[40] G0.db_3.15.0       GenomeInfoDbData_1.2.8 futile.logger_1.4.3
```

```
[43] Matrix_1.4-1       Rcpp_1.0.8.3        munsell_0.5.0
```

```
[46] fansi_1.0.3        lifecycle_1.0.1     stringi_1.7.6
```

```
[49] zlibbioc_1.43.0    org.Hs.eg.db_3.15.0 plyr_1.8.7
```

```
[52] grid_4.2.0         blob_1.2.3          parallel_4.2.0
```

[55]	crayon_1.5.1	lattice_0.20-45	Biostrings_2.65.0
[58]	splines_4.2.0	KEGGREST_1.37.0	locfit_1.5-9.5
[61]	pillar_1.7.0	codetools_0.2-18	reshape2_1.4.4
[64]	futile.options_1.0.1	glue_1.6.2	lambda.r_1.2.4
[67]	data.table_1.14.2	png_0.1-7	vctrs_0.4.1
[70]	gtable_0.3.0	purrr_0.3.4	assertthat_0.2.1
[73]	cachem_1.0.6	ggplot2_3.3.6	xtable_1.8-4
[76]	survival_3.3-1	snow_0.4-4	tibble_3.1.7
[79]	memoise_2.0.1	cluster_2.1.3	ellipsis_0.3.2

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