

# MIGSA: Getting TCGA datasets

**Juan C Rodriguez**

CONICET

Universidad Católica de Córdoba

Universidad Nacional de Córdoba

**Cristóbal Fresno**

Instituto Nacional de Medicina Genómica

**Andrea S Llera**

CONICET

Fundación Instituto Leloir

**Elmer A Fernández**

CONICET

Universidad Católica de Córdoba

Universidad Nacional de Córdoba

---

## Abstract

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

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

---

## 1. Getting the data

From the TCGA data portal the breast invasive carcinoma (BRCA) microarray and RNAseq datasets present at the date were downloaded. PAM50 subtypes Basal vs. Luminal A were evaluated. With these subjects, *tcgaMAdata.RData* and *tcgaRNAseqData.RData* were built.

### 1.1. Basal-like subjects

Basal-like TCGA subjects identifiers used:

```
> library(MIGSAdata);
> data(tcgaMAdata);
> names(tcgaMAdata$subtypes)[ tcgaMAdata$subtypes == "Basal" ];

[1] "TCGA-BH-A0E0-01A-11R-A056-07" "TCGA-A0-A0JL-01A-11R-A056-07"
[3] "TCGA-B6-A0RE-01A-11R-A056-07" "TCGA-BH-A0B3-01A-11R-A056-07"
[5] "TCGA-AN-A0AL-01A-11R-A00Z-07" "TCGA-A2-A0YJ-01A-11R-A109-07"
[7] "TCGA-AR-A0U4-01A-11R-A109-07" "TCGA-B6-A0WX-01A-11R-A109-07"
[9] "TCGA-A2-A0YM-01A-11R-A109-07" "TCGA-A2-A0YE-01A-11R-A109-07"
[11] "TCGA-B6-A0X1-01A-11R-A109-07" "TCGA-AR-A0TU-01A-31R-A109-07"
[13] "TCGA-BH-A0WA-01A-11R-A109-07" "TCGA-AN-A0XU-01A-11R-A109-07"
```

```

[15] "TCGA-AR-AOU0-01A-11R-A109-07" "TCGA-E2-A108-01A-13R-A10J-07"
[17] "TCGA-A0-A124-01A-11R-A10J-07" "TCGA-A0-A128-01A-11R-A10J-07"
[19] "TCGA-A0-A129-01A-21R-A10J-07" "TCGA-BH-AOBG-01A-11R-A115-07"
[21] "TCGA-BH-AODL-01A-11R-A115-07" "TCGA-A0-A12F-01A-11R-A115-07"
[23] "TCGA-C8-A131-01A-11R-A115-07" "TCGA-E2-A14R-01A-11R-A115-07"
[25] "TCGA-BH-AOBL-01A-11R-A115-07" "TCGA-AR-AOU1-01A-11R-A115-07"
[27] "TCGA-A2-A04U-01A-11R-A115-07" "TCGA-C8-A12K-01A-21R-A115-07"
[29] "TCGA-C8-A134-01A-11R-A115-07" "TCGA-D8-A142-01A-11R-A115-07"
[31] "TCGA-E2-A14X-01A-11R-A115-07" "TCGA-C8-A12V-01A-11R-A115-07"
[33] "TCGA-D8-A143-01A-11R-A115-07" "TCGA-BH-AOAV-01A-31R-A115-07"
[35] "TCGA-BH-AOBW-01A-11R-A115-07" "TCGA-A7-AODA-01A-31R-A115-07"
[37] "TCGA-D8-A147-01A-11R-A115-07" "TCGA-BH-AOBW-11A-12R-A115-07"
[39] "TCGA-AR-AOTS-01A-11R-A115-07" "TCGA-D8-A13Z-01A-11R-A115-07"
[41] "TCGA-A8-A08H-01A-21R-A00Z-07" "TCGA-A2-AODO-01A-11R-A00Z-07"
[43] "TCGA-AN-AOFJ-01A-11R-A00Z-07" "TCGA-A8-A07O-01A-11R-A00Z-07"
[45] "TCGA-AN-AOAT-01A-11R-A034-07" "TCGA-A2-AOCM-01A-31R-A034-07"
[47] "TCGA-A2-A04T-01A-21R-A034-07" "TCGA-A7-AOCE-01A-11R-A00Z-07"
[49] "TCGA-A0-A03R-01A-21R-A034-07" "TCGA-AN-A04D-01A-21R-A034-07"
[51] "TCGA-AQ-A04J-01A-02R-A034-07" "TCGA-A2-A04P-01A-31R-A034-07"
[53] "TCGA-A2-A04Q-01A-21R-A034-07" "TCGA-A8-A07C-01A-11R-A034-07"
[55] "TCGA-A8-A07R-01A-21R-A034-07" "TCGA-A8-A07U-01A-11R-A034-07"
[57] "TCGA-A8-A08R-01A-11R-A034-07" "TCGA-A2-AOD2-01A-21R-A034-07"
[59] "TCGA-BH-AOE6-01A-11R-A034-07" "TCGA-AN-AOFL-01A-11R-A034-07"
[61] "TCGA-AN-AOFX-01A-11R-A034-07" "TCGA-AN-AOGO-01A-11R-A034-07"
[63] "TCGA-B6-AOI2-01A-11R-A034-07" "TCGA-B6-AOI6-01A-11R-A034-07"
[65] "TCGA-B6-AOIJ-01A-11R-A034-07" "TCGA-A0-AOJ4-01A-11R-A034-07"
[67] "TCGA-A0-AOJ6-01A-11R-A034-07" "TCGA-B6-AOIQ-01A-11R-A034-07"
[69] "TCGA-BH-AORX-01A-21R-A084-07" "TCGA-A2-AOST-01A-12R-A084-07"
[71] "TCGA-B6-AORU-01A-11R-A084-07" "TCGA-A1-AOSO-01A-22R-A084-07"
[73] "TCGA-A2-AOTO-01A-22R-A084-07" "TCGA-A1-AOSP-01A-11R-A084-07"
[75] "TCGA-A1-AOSK-01A-12R-A084-07" "TCGA-A2-AOSX-01A-12R-A084-07"
[77] "TCGA-B6-AORT-01A-21R-A084-07" "TCGA-AR-AOTP-01A-11R-A084-07"
[79] "TCGA-A7-AODB-11A-33R-A089-07" "TCGA-A2-AOT2-01A-11R-A084-07"
[81] "TCGA-AR-A1AH-01A-11R-A12D-07" "TCGA-E2-A158-01A-11R-A12D-07"
[83] "TCGA-BH-A18V-01A-11R-A12D-07" "TCGA-E2-A14Y-01A-21R-A12D-07"
[85] "TCGA-E2-A150-01A-11R-A12D-07" "TCGA-BH-A18G-01A-11R-A12D-07"
[87] "TCGA-BH-A18Q-01A-12R-A12D-07" "TCGA-A7-A13D-01A-13R-A12P-07"
[89] "TCGA-AR-A1A0-01A-11R-A12P-07" "TCGA-A7-A13E-01A-11R-A12P-07"
[91] "TCGA-AR-A1AY-01A-21R-A12P-07" "TCGA-AR-A1AQ-01A-11R-A12P-07"
[93] "TCGA-AR-A1AR-01A-31R-A137-07" "TCGA-E2-A14N-01A-31R-A137-07"
[95] "TCGA-BH-A1F0-01A-11R-A137-07"

```

## 1.2. Luminal A subjects

Luminal A TCGA subjects identifiers used:

```
> library(MIGSadata);
```

```
> data(tcgaMadata);
> names(tcgaMadata$subtypes)[ tcgaMadata$subtypes == "LumA" ];

[1] "TCGA-BH-A0BA-01A-11R-A056-07" "TCGA-BH-A0DS-01A-11R-A056-07"
[3] "TCGA-BH-A0H6-01A-21R-A056-07" "TCGA-A0-A0JJ-01A-11R-A056-07"
[5] "TCGA-A8-A0A6-01A-12R-A056-07" "TCGA-BH-A0BJ-01A-11R-A056-07"
[7] "TCGA-BH-A0DP-01A-21R-A056-07" "TCGA-A8-A080-01A-21R-A056-07"
[9] "TCGA-A8-A0AD-01A-11R-A056-07" "TCGA-BH-A0BM-01A-11R-A056-07"
[11] "TCGA-BH-A0HF-01A-11R-A056-07" "TCGA-A7-A0D9-01A-31R-A056-07"
[13] "TCGA-BH-A0HK-01A-11R-A056-07" "TCGA-BH-A0GZ-01A-11R-A056-07"
[15] "TCGA-A0-A0JF-01A-11R-A056-07" "TCGA-B6-A0WT-01A-11R-A109-07"
[17] "TCGA-AN-A0XV-01A-11R-A109-07" "TCGA-AN-A0X0-01A-11R-A109-07"
[19] "TCGA-AN-A0XP-01A-11R-A109-07" "TCGA-A2-A0YD-01A-11R-A109-07"
[21] "TCGA-BH-A0W4-01A-11R-A109-07" "TCGA-B6-A0WZ-01A-11R-A109-07"
[23] "TCGA-AN-A0XS-01A-22R-A109-07" "TCGA-BH-A0W5-01A-11R-A109-07"
[25] "TCGA-AN-A0XT-01A-11R-A109-07" "TCGA-B6-A0X4-01A-11R-A109-07"
[27] "TCGA-A0-A12G-01A-11R-A10J-07" "TCGA-A0-A125-01A-11R-A10J-07"
[29] "TCGA-A0-A126-01A-11R-A10J-07" "TCGA-BH-A0B2-01A-11R-A10J-07"
[31] "TCGA-A2-A0YI-01A-31R-A10J-07" "TCGA-E2-A10E-01A-21R-A10J-07"
[33] "TCGA-A0-A12C-01A-11R-A10J-07" "TCGA-E2-A10F-01A-11R-A10J-07"
[35] "TCGA-A0-A12E-01A-11R-A10J-07" "TCGA-E2-A106-01A-11R-A10J-07"
[37] "TCGA-B6-A0X7-01A-11R-A10J-07" "TCGA-AN-A0XL-01A-11R-A10J-07"
[39] "TCGA-A0-A03V-01A-11R-A115-07" "TCGA-BH-A0H5-01A-21R-A115-07"
[41] "TCGA-A2-A04N-01A-11R-A115-07" "TCGA-A0-A12H-01A-11R-A115-07"
[43] "TCGA-C8-A132-01A-31R-A115-07" "TCGA-D8-A141-01A-11R-A115-07"
[45] "TCGA-E2-A15P-01A-11R-A115-07" "TCGA-BH-A0BP-01A-11R-A115-07"
[47] "TCGA-A2-A0CS-01A-11R-A115-07" "TCGA-B6-A0IH-01A-11R-A115-07"
[49] "TCGA-BH-A0BQ-01A-21R-A115-07" "TCGA-A2-A0CV-01A-31R-A115-07"
[51] "TCGA-B6-A0WS-01A-11R-A115-07" "TCGA-BH-A0EA-01A-11R-A115-07"
[53] "TCGA-B6-A0X0-01A-21R-A115-07" "TCGA-D8-A145-01A-11R-A115-07"
[55] "TCGA-BH-A0B0-01A-21R-A115-07" "TCGA-A2-A0D3-01A-11R-A115-07"
[57] "TCGA-BH-A0EI-01A-11R-A115-07" "TCGA-A1-A0SD-01A-11R-A115-07"
[59] "TCGA-C8-A12N-01A-11R-A115-07" "TCGA-D8-A146-01A-31R-A115-07"
[61] "TCGA-A0-A12A-01A-21R-A115-07" "TCGA-E2-A15D-01A-11R-A115-07"
[63] "TCGA-BH-A0DE-01A-11R-A115-07" "TCGA-A2-A0EW-01A-21R-A115-07"
[65] "TCGA-A8-A08T-01A-21R-A00Z-07" "TCGA-A7-A0CH-01A-21R-A00Z-07"
[67] "TCGA-A8-A07J-01A-11R-A00Z-07" "TCGA-A8-A06Y-01A-21R-A00Z-07"
[69] "TCGA-A8-A09A-01A-11R-A00Z-07" "TCGA-A8-A091-01A-11R-A00Z-07"
[71] "TCGA-A8-A09B-01A-11R-A00Z-07" "TCGA-A7-A0CD-01A-11R-A00Z-07"
[73] "TCGA-A7-A0DB-01A-11R-A00Z-07" "TCGA-A8-A09V-01A-11R-A034-07"
[75] "TCGA-A8-A0A2-01A-11R-A034-07" "TCGA-A2-A0CP-01A-11R-A034-07"
[77] "TCGA-A2-A0CQ-01A-21R-A034-07" "TCGA-A8-A06P-01A-11R-A00Z-07"
[79] "TCGA-A8-A093-01A-11R-A00Z-07" "TCGA-A7-A0DC-01A-11R-A00Z-07"
[81] "TCGA-AN-A046-01A-21R-A034-07" "TCGA-AN-A04A-01A-21R-A034-07"
[83] "TCGA-A8-A07G-01A-11R-A034-07" "TCGA-BH-A0E7-01A-11R-A034-07"
[85] "TCGA-A2-A0EM-01A-11R-A034-07" "TCGA-A2-A0EX-01A-21R-A034-07"
[87] "TCGA-BH-A0EB-01A-11R-A034-07" "TCGA-BH-A0HO-01A-11R-A034-07"
```

```

[89] "TCGA-B6-A0I5-01A-11R-A034-07" "TCGA-B6-A0I8-01A-11R-A034-07"
[91] "TCGA-A2-A0EO-01A-11R-A034-07" "TCGA-A2-A0EV-01A-11R-A034-07"
[93] "TCGA-AN-A0FS-01A-11R-A034-07" "TCGA-BH-A0HQ-01A-11R-A034-07"
[95] "TCGA-AN-A0FN-01A-11R-A034-07" "TCGA-A7-A0CG-01A-12R-A056-07"
[97] "TCGA-A0-A0J8-01A-21R-A034-07" "TCGA-B6-A0IP-01A-11R-A034-07"
[99] "TCGA-AR-A0TR-01A-11R-A084-07" "TCGA-BH-A0DH-01A-11R-A084-07"
[101] "TCGA-A0-A0JG-01A-31R-A084-07" "TCGA-B6-A0RV-01A-11R-A084-07"
[103] "TCGA-BH-A0DQ-01A-11R-A084-07" "TCGA-B6-A0RN-01A-12R-A084-07"
[105] "TCGA-A2-A0EN-01A-13R-A084-07" "TCGA-B6-A0RO-01A-22R-A084-07"
[107] "TCGA-BH-A0HI-01A-11R-A084-07" "TCGA-A1-A0SE-01A-11R-A084-07"
[109] "TCGA-A2-A0SU-01A-11R-A084-07" "TCGA-A1-A0SH-01A-11R-A084-07"
[111] "TCGA-A2-A0T5-01A-21R-A084-07" "TCGA-B6-A0RP-01A-21R-A084-07"
[113] "TCGA-A2-A0T6-01A-11R-A084-07" "TCGA-BH-A0HP-01A-12R-A084-07"
[115] "TCGA-A2-A0SY-01A-31R-A084-07" "TCGA-BH-A18I-01A-11R-A12D-07"
[117] "TCGA-E2-A14Q-01A-11R-A12D-07" "TCGA-BH-A0BO-01A-23R-A12D-07"
[119] "TCGA-BH-A18S-01A-11R-A12D-07" "TCGA-E2-A15E-06A-11R-A12D-07"
[121] "TCGA-BH-A0DO-01B-11R-A12D-07" "TCGA-BH-A0DT-01A-21R-A12D-07"
[123] "TCGA-BH-A18M-01A-11R-A12D-07" "TCGA-E2-A15C-01A-31R-A12D-07"
[125] "TCGA-BH-A18N-01A-11R-A12D-07" "TCGA-C8-A133-01A-32R-A12D-07"
[127] "TCGA-E2-A15G-01A-11R-A12D-07" "TCGA-BH-A18H-01A-11R-A12D-07"
[129] "TCGA-E2-A153-01A-12R-A12D-07" "TCGA-E2-A15J-01A-11R-A12P-07"
[131] "TCGA-BH-A0AZ-01A-21R-A12P-07" "TCGA-E2-A1B4-01A-11R-A12P-07"
[133] "TCGA-BH-A0BS-01A-11R-A12P-07" "TCGA-BH-A0H3-01A-11R-A12P-07"
[135] "TCGA-AR-A1AN-01A-11R-A12P-07" "TCGA-BH-A0BT-01A-11R-A12P-07"
[137] "TCGA-BH-A0HA-01A-11R-A12P-07" "TCGA-BH-A1EU-01A-11R-A137-07"
[139] "TCGA-E2-A15I-01A-21R-A137-07" "TCGA-BH-A1EW-11B-33R-A137-07"
[141] "TCGA-BH-A1ET-01A-11R-A137-07" "TCGA-C8-A1HI-01A-11R-A137-07"

```

## 2. Getting the data with TCGAbiolinks R package

All the subject's data mentioned in section 1 was downloaded by means of the **TCGAbiolinks** R package, however, at the present this library had been greatly refactored, causing that this code does not work unless some files are present in your hard drive, these files are available upon request as they weigh too much. Below we show the code used to get both RDataS.

```

> ## Not run:
>
> library(TCGAbiolinks);
> R.Version()$version.string;
> # [1] "R version 3.2.3 (2015-12-10)"
> packageVersion("TCGAbiolinks");
> # [1] '1.0.10'
>
> query <- TCGAquery(tumor="BRCA");
> matSamples <- TCGAquery_integrate(query);

```

```

> # subjects in both microarray and RNAseq data
> matSamples["AgilentG4502A_07_3", "IlluminaHiSeq_RNASeq"];
> # [1] 495
>
> # we filter only microarray data
> geneExprSubjects <- TCGAquery(tumor="BRCA", platform="AgilentG4502A_07_3",
+   level=3);
> # we filter only RNAseq data
> rnaSeqSubjects <- TCGAquery(tumor="BRCA", platform="IlluminaHiSeq_RNASeq",
+   level=3);
> geneExprbarcodes <- geneExprSubjects$barcode;
> geneExprbarcodes <- strsplit(geneExprbarcodes, ",");
> geneExprbarcodes <- Reduce(union, geneExprbarcodes);
> rnaSeqbarcodes <- rnaSeqSubjects$barcode;
> rnaSeqbarcodes <- strsplit(rnaSeqbarcodes, ",");
> rnaSeqbarcodes <- Reduce(union, rnaSeqbarcodes);
> commonSubjects <- intersect(geneExprbarcodes, rnaSeqbarcodes);
> rm(geneExprbarcodes); rm(rnaSeqbarcodes);
> length(commonSubjects);
> # [1] 547
>
> # we filter microarray and RNAseq data (but just common subjects)
> geneExprSubjects <- TCGAquery(tumor="BRCA", platform="AgilentG4502A_07_3",
+   samples=commonSubjects, level=3);
> rnaSeqSubjects <- TCGAquery(tumor="BRCA", platform="IlluminaHiSeq_RNASeq",
+   samples=commonSubjects, level=3);
> ##### this lines are the ones which are not working any more (TCGAdownload)
> # TCGAdownload(geneExprSubjects, path="geneExpr/", samples=commonSubjects);
> # TCGAdownload(rnaSeqSubjects, path="rnaSeq/", samples=commonSubjects,
> #   type="gene.quantification");
>
> ## However, we can provide you necessary files to skip the TCGAdownload step.
>
> ## type is any of:
> # RNASeq:          exon.quantification
> #                  spljxn.quantification
> #                  gene.quantification
> # genome_wide_snp_6: hg18.seg
> #                  hg19.seg,nocnv_hg18.seg
> #                  nocnv_hg19.seg
>
> geneExpr <- TCGAprepare(geneExprSubjects, dir="geneExpr/");
> rnaSeq <- TCGAprepare(rnaSeqSubjects, dir="rnaSeq/",
+   type="gene.quantification");
> library(SummarizedExperiment);
> assays(geneExpr);
> # names(1): raw_counts

```

```

>
> # It would be a better way of conversion
> geneExpr <- head(assay(geneExpr, "raw_counts"), n=nrow(geneExpr));
> assays(rnaSeq);
> # names(3): raw_counts median_length_normalized RPKM
> rnaSeq_raw <- head(assay(rnaSeq, "raw_counts"), n=nrow(rnaSeq));
> rnaSeq_medianNorm <- head(assay(rnaSeq, "median_length_normalized"),
+   n=nrow(rnaSeq));
> rnaSeq_rpkM <- head(assay(rnaSeq, "RPKM"), n=nrow(rnaSeq));
> ## checking if we have the same subjects in every experiment
> stopifnot(all(colnames(geneExpr) %in% colnames(rnaSeq_raw)));
> stopifnot(all(colnames(rnaSeq_raw) %in% colnames(rnaSeq_medianNorm)));
> stopifnot(all(colnames(rnaSeq_medianNorm) %in% colnames(rnaSeq_rpkM)));
> stopifnot(all(colnames(rnaSeq_rpkM) %in% colnames(geneExpr)));
> mapping <- do.call(rbind, strsplit(rownames(rnaSeq_raw), "|", fixed=!F));
> colnames(mapping) <- c("Symbol", "Entrez");
> ##### Now let's get subjects subtypes
>
> library(genefu);
> rnaSeq <- rnaSeq_rpkM;
> rm(rnaSeq_rpkM);
> ## Also request this file!
> pam50Annot <- read.csv("pam50_annotation.txt", sep="\t");
> library(limma);
> dim(geneExpr);
> geneExpr <- avereps(geneExpr);
> dim(geneExpr);
> rownames(rnaSeq) <- mapping[, "Symbol" ];
> dim(rnaSeq);
> rnaSeq <- rnaSeq[ mapping[, "Symbol" ] != "?" , ];
> dim(rnaSeq);
> rnaSeq <- avereps(rnaSeq);
> dim(rnaSeq);
> geneExpr <- geneExpr[as.character(pam50Annot$GeneName),, drop=F];
> dim(geneExpr);
> rnaSeq <- rnaSeq[as.character(pam50Annot$GeneName),, drop=F];
> dim(rnaSeq);
> rnaSeq <- log(rnaSeq);
> pam50Annot <- pam50Annot[,c("GeneName", "EntrezGene")];
> colnames(pam50Annot) <- c("probe", "EntrezGene.ID");
> pam50Annot$probe <- as.character(pam50Annot$probe);
> ## get subtypes
> dataset <- apply(geneExpr, 1, as.numeric);
> rownames(dataset) <- colnames(geneExpr);
> subtypesGeneExpr <- intrinsic.cluster.predict(sbt.model=pam50.scale,
+   data=dataset, annot=pam50Annot, do.mapping=!F, do.prediction.strength=!F,
+   verbose=!F);

```

```

> ## get subtypes
> dataset <- apply(rnaSeq, 1, as.numeric);
> rownames(dataset) <- colnames(rnaSeq);
> subtypesRnaSeq <- intrinsic.cluster.predict(sbt.model=pam50.scale,
+     data=dataset, annot=pam50Annot, do.mapping=!F, do.prediction.strength=!F,
+     verbose=!F);
> table(subtypesGeneExpr$subtype);
> # Basal Her2 LumA LumB Normal
> # 101 77 150 157 62
>
> table(subtypesRnaSeq$subtype);
> # Basal Her2 LumA LumB Normal
> # 101 81 165 137 63
>
> subtypesGeneExpr <- subtypesGeneExpr$subtype;
> subtypesRnaSeq <- subtypesRnaSeq$subtype[names(subtypesGeneExpr)];
> ## how many subjects got the same subtype between microarray and RNAseq data
> concSubtypes <- table(subtypesGeneExpr, subtypesRnaSeq);
> concSubtypes;
> # Basal Her2 LumA LumB Normal
> # Basal 95 2 1 2 1
> # Her2 0 72 0 4 1
> # LumA 1 0 142 4 3
> # LumB 3 7 19 127 1
> # Normal 2 0 3 0 57
> sum(diag(concSubtypes)) / sum(concSubtypes);
> # [1] 0.9012797 # 90% of concordant subjects
>
> stopifnot(all(names(subtypesGeneExpr) == names(subtypesRnaSeq)));
> ## I am going to use the subjects that got the same classification in both
> subtypes <- subtypesGeneExpr[subtypesGeneExpr == subtypesRnaSeq];
> length(subtypes);
> # [1] 493
>
> ##### Now just translate GeneSymbols to EntrezGene IDs
>
> ## Also request this file!
> annotAgi <- read.csv("AgilentG4502A_07_3.csv", sep="|");
> geneExprSymbol <- rownames(geneExpr);
> # we first search into Agilent annotation file
> geneExprEntrez <- annotAgi[ match(geneExprSymbol, annotAgi[, "Symbol"]),
+     "Entrez" ];
> sum(is.na(geneExprEntrez));
> # [1] 796
> # then we look into the mapping given by RNASeq TCGA data
> geneExprEntrez[ is.na(geneExprEntrez) ] <- mapping[ match(geneExprSymbol[
+     is.na(geneExprEntrez) ], mapping[, "Symbol"]), "Entrez" ];

```

```

> sum(is.na(geneExprEntrez));
> # [1] 772
>
> geneExpr <- geneExpr[ !is.na(geneExprEntrez), ];
> rownames(geneExpr) <- geneExprEntrez[ !is.na(geneExprEntrez) ];
> dim(geneExpr);
> geneExpr <- avereps(geneExpr);
> dim(geneExpr);
> rownames(rnaSeq) <- do.call(rbind, strsplit(rownames(rnaSeq), "|",
+   fixed=!F))[,2];
> dim(rnaSeq);
> rnaSeq <- avereps(rnaSeq);
> dim(rnaSeq);
> load("rnaSeq_raw.RData");
> rownames(rnaSeq_raw) <- do.call(rbind, strsplit(rownames(rnaSeq_raw), "|",
+   fixed=!F))[,2];
> dim(rnaSeq_raw);
> rnaSeq_raw <- avereps(rnaSeq_raw);
> dim(rnaSeq_raw);
> #### And keep only Basal and Luminal A subjects
> rnaSeq_raw <- rnaSeq_raw[, names(subtypes)[subtypes %in% c("Basal", "LumA")]] ];
> geneExpr <- geneExpr[, names(subtypes)[subtypes %in% c("Basal", "LumA")]] ];
> subtypes <- subtypes[subtypes %in% c("Basal", "LumA")];
> ## And these are the two data objects used.
> tcgaRNAseqData <- list(rnaSeq=rnaSeq_raw, subtypes=subtypes);
> tcgaMAdata <- list(geneExpr=geneExpr, subtypes=subtypes);
> ## End(Not run)

```

## Session Info

```
> sessionInfo()
```

```

R version 4.1.1 (2021-08-10)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 20.04.3 LTS

```

```
Matrix products: default
```

```

BLAS: /home/biocbuild/bbs-3.14-bioc/R/lib/libRblas.so
LAPACK: /home/biocbuild/bbs-3.14-bioc/R/lib/libRlapack.so

```

```
locale:
```

```

[1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
[3] LC_TIME=en_GB             LC_COLLATE=C
[5] LC_MONETARY=en_US.UTF-8   LC_MESSAGES=en_US.UTF-8
[7] LC_PAPER=en_US.UTF-8      LC_NAME=C

```



```
[9] LC_ADDRESS=C                LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
```

attached base packages:

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

other attached packages:

```
[1] edgeR_3.36.0      MIGSadata_1.17.0    MIGSA_1.18.0
[4] mGSZ_1.0          ismev_1.42          mgcv_1.8-38
[7] nlme_3.1-153      MASS_7.3-54         limma_3.50.0
[10] GSA_1.03.1        BiocParallel_1.28.0 GSEABase_1.56.0
[13] graph_1.72.0      annotate_1.72.0      XML_3.99-0.8
[16] AnnotationDbi_1.56.0 IRanges_2.28.0      S4Vectors_0.32.0
[19] Biobase_2.54.0     BiocGenerics_0.40.0
```

loaded via a namespace (and not attached):

```
[1] Category_2.60.0      bitops_1.0-7        matrixStats_0.61.0
[4] bit64_4.0.5          httr_1.4.2          GenomeInfoDb_1.30.0
[7] Rgraphviz_2.38.0     tools_4.1.1         utf8_1.2.2
[10] R6_2.5.1             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_4.1.1      formatR_1.11
[19] gg dendro_0.1.22     labeling_0.4.2      scales_1.1.1
[22] genefilter_1.76.0    RBGL_1.70.0         digest_0.6.28
[25] stringr_1.4.0        AnnotationForge_1.36.0 XVector_0.34.0
[28] pkgconfig_2.0.3      fastmap_1.1.0       rlang_0.4.12
[31] rstudioapi_0.13      RSQLite_2.2.8       farver_2.1.0
[34] GOstats_2.60.0       generics_0.1.1      jsonlite_1.7.2
[37] dplyr_1.0.7          RCurl_1.98-1.5      magrittr_2.0.1
[40] GO.db_3.14.0         GenomeInfoDbData_1.2.7 futile.logger_1.4.3
[43] Matrix_1.3-4         Rcpp_1.0.7          munsell_0.5.0
[46] fansi_0.5.0          lifecycle_1.0.1     stringi_1.7.5
[49] zlibbioc_1.40.0      org.Hs.eg.db_3.14.0 plyr_1.8.6
[52] grid_4.1.1           blob_1.2.2          parallel_4.1.1
[55] crayon_1.4.1         lattice_0.20-45     Biostrings_2.62.0
[58] splines_4.1.1        KEGGREST_1.34.0     locfit_1.5-9.4
[61] pillar_1.6.4         reshape2_1.4.4      futile.options_1.0.1
[64] glue_1.4.2           lambda.r_1.2.4      data.table_1.14.2
[67] png_0.1-7            vctrs_0.3.8         gtable_0.3.0
[70] purrr_0.3.4          assertthat_0.2.1    cachem_1.0.6
[73] ggplot2_3.3.5        xtable_1.8-4        survival_3.2-13
[76] tibble_3.1.5         memoise_2.0.0       cluster_2.1.2
[79] ellipsis_0.3.2
```

**Affiliation:**

Juan C Rodriguez & Elmer A Fernández

Bioscience Data Mining Group

Facultad de Ingeniería

Universidad Católica de Córdoba - CONICET

X5016DHK Córdoba, Argentina

E-mail: [jcrodriguez@bdmg.com.ar](mailto:jcrodriguez@bdmg.com.ar), [efernandez@bdmg.com.ar](mailto:efernandez@bdmg.com.ar)

URL: <http://www.bdmg.com.ar/>