MetaGxOvarian: a package for ovarian cancer gene expression analysis

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1 Installing the Package

The MetaGxOvarian package is a compendium of Ovarian Cancer datasets. The package is publicly available and can be installed from Bioconductor into R version 3.4.1 or higher.

To install the MetaGxOvarian package from Bioconductor:

```
> if (!requireNamespace("BiocManager", quietly=TRUE))
+     install.packages("BiocManager")
> BiocManager::install("MetaGxOvarian")
```

2 Loading Datasets

First we load the MetaGxOvarian package into the workspace.

To load the packages into R, please use the following commands:

```
> library(MetaGxOvarian)
> esets = MetaGxOvarian::loadOvarianEsets()[[1]]
```

This will load 26 expression datasets, with patients selected according to the default settings in the patientselection.config file. Users can modify the file to filter and annotate gene expression datasets and individual samples within them based on the following criteria:

Datasets: Conduct probe-gene mapping to select for the 'best' probe (default = TRUE)

Datasets: Retain only genes that are common across all platforms loaded (default = FALSE)

Datasets: Retain studies with a minimum sample size (default = 40)

Datasets: Retain studies with a minimum umber of genes (default = 1000)

Datasets: Retain studies with a minimum number of survival events

Datasets: Remove duplicate samples (default = TRUE)

Datasets: Rescale genes to Z-scores (default = FALSE)

Samples: Ensure specific patient metadata is not missing

Samples: Filter samples by sample type (tumour, healthy, etc)

3 Obtaining Sample Counts in Datasets

To obtain the number of samples per dataset, run the following:

```
> numSamples <- vapply(seq_along(esets), FUN=function(i, esets){
+   length(sampleNames(esets[[i]]))
+   }, numeric(1), esets=esets)
> SampleNumberSummaryAll <- data.frame(NumberOfSamples = numSamples,
+                                      row.names = names(esets))
> total <- sum(SampleNumberSummaryAll[,"NumberOfSamples"])
> SampleNumberSummaryAll <- rbind(SampleNumberSummaryAll, total)
> rownames(SampleNumberSummaryAll)[nrow(SampleNumberSummaryAll)] <- "Total"
> require(xtable)
> print(xtable(SampleNumberSummaryAll,digits = 2), floating = FALSE)
```

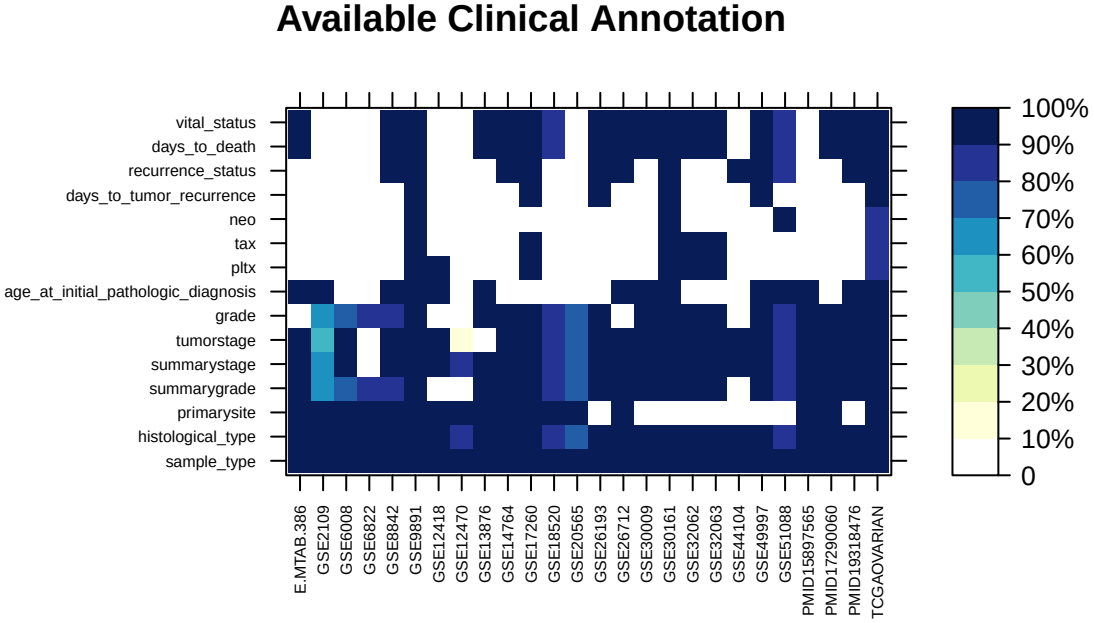
	NumberOfSamples
E.MTAB.386	129.00
GSE2109	204.00
GSE6008	103.00
GSE6822	66.00
GSE8842	83.00
GSE9891	285.00
GSE12418	54.00
GSE12470	53.00
GSE13876	157.00
GSE14764	80.00
GSE17260	110.00
GSE18520	63.00
GSE20565	140.00
GSE26193	107.00
GSE26712	195.00
GSE30009	103.00
GSE30161	58.00
GSE32062	260.00
GSE32063	40.00
GSE44104	60.00
GSE49997	204.00
GSE51088	172.00
PMID15897565	63.00
PMID17290060	117.00
PMID19318476	42.00
TCGAOVARIAN	578.00
Total	3526.00

4 Assess Phenotype Data

We can also obtain a summary of the phenotype data (pData) for each expression dataset. Here, we assess the proportion of samples in every datasets that contain a specific pData variable.

```
> #pData Variables
> pDataID <- c("sample_type", "histological_type", "primarysite", "summarygrade",
+              "summarystage", "tumorstage", "grade",
+              "age_at_initial_pathologic_diagnosis", "pltx", "tax",
+              "neo", "days_to_tumor_recurrence", "recurrence_status",
```

```
+              "days_to_death", "vital_status")
> pDataPercentSummaryTable <- NULL
> pDataSummaryNumbersTable <- NULL
> pDataSummaryNumbersList = lapply(esets, function(x)
+   vapply(pDataID, function(y) sum(!is.na(pData(x)[,y])), numeric(1)))
> pDataPercentSummaryList = lapply(esets, function(x)
+   vapply(pDataID, function(y)
+     sum(!is.na(pData(x)[,y]))/nrow(pData(x)), numeric(1))*100)
> pDataSummaryNumbersTable = sapply(pDataSummaryNumbersList, function(x) x)
> pDataPercentSummaryTable = sapply(pDataPercentSummaryList, function(x) x)
> rownames(pDataSummaryNumbersTable) <- pDataID
> rownames(pDataPercentSummaryTable) <- pDataID
> colnames(pDataSummaryNumbersTable) <- names(esets)
> colnames(pDataPercentSummaryTable) <- names(esets)
> pDataSummaryNumbersTable <- rbind(pDataSummaryNumbersTable, total)
> rownames(pDataSummaryNumbersTable)[nrow(pDataSummaryNumbersTable)] <- "Total"
> # Generate a heatmap representation of the pData
> pDataPercentSummaryTable<-t(pDataPercentSummaryTable)
> pDataPercentSummaryTable<-cbind(Name=(rownames(pDataPercentSummaryTable))
+                                 ,pDataPercentSummaryTable)
> nba<-pDataPercentSummaryTable
> gradient_colors = c("#ffffff","#ffffd9","#edf8b1","#c7e9b4","#7fcdbb",
+                     "#41b6c4","#1d91c0","#225ea8","#253494","#081d58")
> library(lattice)
> nbamat<-as.matrix(nba)
> rownames(nbamat)<-nbamat[,1]
> nbamat<-nbamat[,-1]
> Interval<-as.numeric(c(10,20,30,40,50,60,70,80,90,100))
> levelplot(nbamat,col.regions=gradient_colors,
+           main="Available Clinical Annotation",
+           scales=list(x=list(rot=90, cex=0.5),
+                       y= list(cex=0.5),key=list(cex=0.2)),
+           at=seq(from=0,to=100,length=10),
+           cex=0.2, ylab="", xlab="", lattice.options=list(),
+           colorkey=list(at=as.numeric(factor(c(seq(from=0, to=100, by=10)))),
+                  labels=as.character(c( "0","10%","20%","30%", "40%","50%",
+                                         "60%", "70%", "80%","90%", "100%"),
+                                      cex=0.2,font=1,col="brown",height=1,
+                                      width=1.4), col=(gradient_colors)))
>
```



5 Session Info

- R version 3.5.1 Patched (2018-07-12 r74967), `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 16.04.5 LTS
- Matrix products: default
- BLAS: /home/biocbuild/bbs-3.8-bioc/R/lib/libRblas.so
- LAPACK: /home/biocbuild/bbs-3.8-bioc/R/lib/libRlapack.so
- Base packages: base, datasets, grDevices, graphics, methods, parallel, stats, utils
- Other packages: AnnotationHub 2.14.0, Biobase 2.42.0, BiocGenerics 0.28.0, ExperimentHub 1.8.0, MetaGxOvarian 1.2.0, impute 1.56.0, lattice 0.20-35, xtable 1.8-3
- Loaded via a namespace (and not attached): AnnotationDbi 1.44.0, BiocManager 1.30.3, DBI 1.0.0, IRanges 2.16.0, R6 2.3.0, RSQLite 2.1.1, Rcpp 0.12.19, S4Vectors 0.20.0, bit 1.1-14, bit64 0.9-7, blob 1.1.1, compiler 3.5.1, curl 3.2, digest 0.6.18, grid 3.5.1, htmltools 0.3.6, httpuv 1.4.5, httr 1.3.1, interactiveDisplayBase 1.20.0, later 0.7.5, magrittr 1.5, memoise 1.1.0, mime 0.6, pkgconfig 2.0.2, promises 1.0.1, shiny 1.1.0, stats4 3.5.1, tools 3.5.1, yaml 2.2.0