

# Package ‘SurfR’

November 7, 2025

**Type** Package

**Title** Surface Protein Prediction and Identification

**Version** 1.7.0

**Description** Identify Surface Protein coding genes from a list of candidates.  
Systematically download data from GEO and TCGA or use your own data.  
Perform DGE on bulk RNAseq data.  
Perform Meta-analysis. Descriptive enrichment analysis and plots.

**License** GPL-3 + file LICENSE

**Encoding** UTF-8

**LazyData** false

**BugReports** <https://github.com/auroraurizio/SurfR/issues>

**URL** <https://github.com/auroraurizio/SurfR>

**biocViews** Software, Sequencing, RNASeq, GeneExpression, Transcription,  
DifferentialExpression, PrincipalComponent, GeneSetEnrichment,  
Pathways, BatchEffect, FunctionalGenomics, Visualization,  
DataImport, FunctionalPrediction, GenePrediction, GO

**VignetteBuilder** knitr

**RoxygenNote** 7.2.3

**Imports** httr, BiocFileCache, SPsimSeq, DESeq2, edgeR, openxlsx,  
stringr, rhdf5, ggplot2, ggrepel, stats, magrittr, assertr,  
tidyr, dplyr, TCGAbiolinks, biomaRt, metaRNASeq, scales, venn,  
gridExtra, SummarizedExperiment, knitr, rjson, grDevices,  
graphics, curl, utils

**Depends** R (>= 4.4.0)

**Suggests** BiocStyle, testthat (>= 3.0.0)

**Config/testthat/edition** 3

**git\_url** <https://git.bioconductor.org/packages/SurfR>

**git\_branch** devel

**git\_last\_commit** 90bbf06

**git\_last\_commit\_date** 2025-10-29

**Repository** Bioconductor 3.23  
**Date/Publication** 2025-11-06  
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|             |                                                                 |
|-------------|-----------------------------------------------------------------|
| .format_str | <i>Format a string using placeholders - function from hypeR</i> |
|-------------|-----------------------------------------------------------------|

---

Description

Format a string using placeholders - function from hypeR

**Usage**

```
.format_str(string, ...)
```

**Arguments**

|        |                                           |
|--------|-------------------------------------------|
| string | A an unformatted string with placeholders |
| ...    | Variables to format placeholders with     |

**Value**

A formatted string

**Examples**

```
## Not run:
format_str("Format with {1} and {2}", "x", "y")

## End(Not run)
```

---

Annotate\_SPID

*Annotate\_SPID*


---

**Description**

Annotate Surface Protein Coding genes according to EnrichR libraries

**Usage**

```
Annotate_SPID(
  DGE,
  enrich.database = "WikiPathway_2021_Human",
  output_tsv = FALSE
)
```

**Arguments**

|                 |                                                                                                     |
|-----------------|-----------------------------------------------------------------------------------------------------|
| DGE             | Data.frame containing annotated DEG list, as the output of DGE or Gene2SProtein functions.          |
| enrich.database | String containing the EnrichR databases you would like to consult. Default: WikiPathway_2021_Human. |
| output_tsv      | Logical. If TRUE, outputs a tsv file with the results. By default, FALSE.                           |

**Value**

A dataframe with surface protein coding DEGs annotation.

**Warning**

Be sure that `enrich.database` exists.

**See Also**

[DGE](#) function for DGE, and [Gene2SProtein](#) function for Gene2SProtein analysis

Other functional-annotation functions: [Enrichment\\_barplot\(\)](#), [Enrichment\(\)](#)

**Examples**

```
## Not run:
# Deseq2 output sample
DGE = data.frame(GeneID = c("DLK1", "TOP2A"),
                  Mean_CPM_T = c(5.92, 9.91),
                  Mean_CPM_C = c(0.04, 0.03),
                  log2FoldChange = c(10.22, 8.42),
                  lfcSE = c(0.80, 0.48),
                  stat = c(12.68, 17.69),
                  pvalue = c(7.30135e-37, 4.37011e-70),
                  padj = c(1.49936e-35, 1.12976e-67))
annotated_DGE = Annotate_SPID(DGE, "WikiPathway_2021_Human")

# Output of Gene2SProtein function
GeneNames = c("CIITA", "EPCAM", "DLK1", "CD24")
SurfaceProteins_df = Gene2SProtein(GeneNames, input_type = "gene_name")
annotated_SP = Annotate_SPID(SurfaceProteins_df, "GO_Biological_Process_2021")
## End(Not run)
```

---

```
combine_fisher_invnorm
```

```
combine_fisher_invnorm
```

---

**Description**

Combine Meta-Analysis results with individual DE tables

**Usage**

```
combine_fisher_invnorm(
  ind_deg,
  invnorm,
  fishercomb,
  adjpval = 0.05,
  output_tsv = TRUE,
  output_filename = "combine_fisher_invnorm.tsv"
)
```

**Arguments**

|                 |                                                                               |
|-----------------|-------------------------------------------------------------------------------|
| ind_deg         | List of independent DEG dataframes with p-values to be combined.              |
| invnorm         | inverse normal p-value combination technique dataframe (output of metaRNAseq) |
| fishercomb      | Fisher p-value combination technique dataframe (output of metaRNAseq)         |
| adjpval         | threshold to represent as binary the Meta-Analysis output adjpval.            |
| output_tsv      | logical. If TRUE, it outputs table with results. Default: TRUE                |
| output_filename | File name for the results file.                                               |

**Value**

A dataframe with DEindices and DName of DEG at the chosen Benjamini Hochberg threshold, and TestStatistic, rawpval, adjpval, binaryadjpval vectors for differential expression in the meta-analysis.

**See Also**

DGE function for DGE analysis, and <https://cran.r-project.org/web/packages/metaRNASeq/vignettes/metaRNASeq.pdf> for metaRNASeq package info

Other meta-analysis functions: [metaRNAseq\(\)](#)

**Examples**

```
## Not run:
# Deseq2 output samples
DGE1 <- data.frame(GeneID = c("DLK1", "EPCAM"),
  Mean_CPM_T = c(5.92, 9.91),
  Mean_CPM_C = c(0.04, 0.03),
  log2FoldChange = c(10.22, 8.42),
  lfcSE = c(0.80, 0.48),
  stat = c(12.68, 17.69),
  pvalue = c(7.30135e-37, 4.37011e-70),
  padj = c(1.49936e-35, 1.12976e-67),
  row.names = c("DLK1", "EPCAM"))
DGE2 <- data.frame(GeneID = c("DLK1", "EPCAM"),
  Mean_CPM_T = c(3.92, 8.91),
  Mean_CPM_C = c(0.04, 0.03),
  log2FoldChange = c(7.22, 5.81),
  lfcSE = c(0.80, 0.48),
  stat = c(12.68, 17.69),
  pvalue = c(7.30135e-37, 4.37011e-70),
  padj = c(1.49936e-35, 1.12976e-67),
  row.names = c("DLK1", "EPCAM"))

# input list
ind_deg <- list(DEG1_df = DGE1, DEG2_df = DGE2)
# perform invnorm meta-analysis
invnorm <- metaRNAseq(ind_deg, test_statistic = "invnorm", BHth = 0.05, nrep = c(2,2))
# perform fishercomb meta-analysis
fishercomb <- metaRNAseq(ind_deg, test_statistic = "fishercomb", BHth = 0.05)
```

```
# combine results
comb_pval_df <- combine_fisher_invnorm(ind_deg,
                                      invnorm, fishercomb,
                                      adjpval = 0.05,
                                      output_tsv = FALSE)

## End(Not run)
```

---

|           |                  |
|-----------|------------------|
| countData | <i>countData</i> |
|-----------|------------------|

---

**Description**

Simulated raw counts to use as input for DGE and plotPCA functions. metadata is available.

**Usage**

```
data(countData)
```

**Format**

dataframe

**Details**

A dataframe with 2500 rows and 4 columns (sample names).

**Value**

A dataframe.

---

|     |                     |
|-----|---------------------|
| DGE | <i>DGE function</i> |
|-----|---------------------|

---

**Description**

Perform Differential Gene Expression Analysis of RNA-Seq Data

**Usage**

```
DGE(
  expression,
  metadata,
  Nreplica,
  design = "~condition",
  condition = "condition",
  TEST,
  CTRL,
```

```

    alpha = 0.05,
    FC_filt = 0,
    output_tsv = FALSE,
    output_filename = "DEGs.tsv"
  )

```

## Arguments

|                 |                                                                                                                                                                                                         |
|-----------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| expression      | Dataframe with counts                                                                                                                                                                                   |
| metadata        | Dataframe with sample metadata                                                                                                                                                                          |
| Nreplica        | Double. Minimum number of replicates in each group                                                                                                                                                      |
| design          | Design formula for DGE                                                                                                                                                                                  |
| condition       | Column of the metadata to use for DGE results                                                                                                                                                           |
| TEST            | Character. sample name in metadata                                                                                                                                                                      |
| CTRL            | Character. sample name in metadata                                                                                                                                                                      |
| alpha           | Double. the significance cutoff used for optimizing the independent filtering (by default 0.1). If the adjusted p-value cutoff (FDR) will be a value other than 0.1, alpha should be set to that value. |
| FC_filt         | Dataframe with counts                                                                                                                                                                                   |
| output_tsv      | Logical. If TRUE, outputs a tsv file with the results. By default, FALSE.                                                                                                                               |
| output_filename | Name of the tsv output file. Default is DEGs.tsv.                                                                                                                                                       |

## Value

A dataframe with DEGs

## Examples

```

## Not run:
# Simulation of bulk RNA data
countData <- matrix(floor(runif(10000, min=0, max=101)), ncol=4)
colnames(countData) <- paste("sample", seq_len(ncol(countData)), sep = "")
rownames(countData) <- paste("gene", seq_along(seq_len(10000/4)), sep = "")
metadata <- data.frame(samplesID = paste("sample", seq_len(ncol(countData)), sep = ""),
                      condition = factor(c("A", "A", "B", "B")))
row.names(metadata) <- metadata$samplesID
# Perform DGE
DGEresults <- DGE(expression = countData, metadata = metadata,
                  Nreplica = 2,
                  design = "~condition", condition = "condition",
                  TEST = "A", CTRL = "B")
## End(Not run)

```

DownloadArchS4

*DownloadArchS4 function***Description**

Download count matrix from <https://maayanlab.cloud/archs4/>, given a vector of input GEO Sample accessions numbers (GSM).

**Usage**

```
DownloadArchS4(GSM, species, print_tsv = FALSE, filename = NULL)
```

**Arguments**

|           |                                                                                |
|-----------|--------------------------------------------------------------------------------|
| GSM       | Vector with the GSM ids of the samples to consider.                            |
| species   | Specify the specie of yuor GSM samples. Either human or mouse.                 |
| print_tsv | Logical. If TRUE, outputs a tsv file with the count matrix. By default, FALSE. |
| filename  | Name of the tsv output file. Default is matrix.tsv.                            |

**Value**

A count matrix with gene on the row and GSM ID on the column.

**Warning**

If the defined GSM ids do not have any match in ArchS4 database, we suggest to contact ArchS4 curator to add them.

**See Also**

[GEOmetadata](#) function for downloading GEO metadata. <https://www.ncbi.nlm.nih.gov/geo> for info on GSM. <https://maayanlab.cloud/archs4/> for info on ArchS4.

Other public-data functions: [GEOmetadata\(\)](#), [TCGA\\_download\(\)](#)

**Examples**

```
## Not run:
GSM <- c("GSM3447008", "GSM3447009")
GEO_count_matrix <- DownloadArchS4(GSM, species = "human",
                                   print_tsv = FALSE, filename = NULL)
## End(Not run)
```



---

|              |                     |
|--------------|---------------------|
| enrichedList | <i>enrichedList</i> |
|--------------|---------------------|

---

**Description**

Input list for Enrichment\_barplot function. enrichedList is the output of Enrichment function applied to ind\_deg object when enrich.databases is equal to GO\_Cellular\_Component\_2021, default parameters.

**Usage**

```
data(enrichedList)
```

**Format**

list

**Details**

enrichedList\$fdr\_up\$GO\_Cellular\_Component\_2021 contains upregulated gene enrichments, enrichedList\$fdr\_down\$GO\_Cellular\_Component\_2021 contains downregulated gene enrichments.

**Value**

A list of lists.

---

|            |                            |
|------------|----------------------------|
| Enrichment | <i>Enrichment function</i> |
|------------|----------------------------|

---

**Description**

Perform enrichment Analysis of RNA-Seq Data

**Usage**

```
Enrichment(  
  dfList,  
  enrich.databases = c("GO_Biological_Process_2021", "GO_Cellular_Component_2021",  
    "GO_Molecular_Function_2021", "KEGG_2021_Human", "MSigDB_Hallmark_2020",  
    "WikiPathways_2016", "BioCarta_2016", "Jensen_TISSUES", "Jensen_COMPARTMENTS",  
    "Jensen_DISEASES"),  
  p_adj = 0.05,  
  logFC = 1,  
  save.results = FALSE  
)
```

**Arguments**

|                               |                                                                 |
|-------------------------------|-----------------------------------------------------------------|
| <code>dfList</code>           | Dataframes list                                                 |
| <code>enrich.databases</code> | Vector of EnrichR databases to consult                          |
| <code>p_adj</code>            | Double. Adjusted pvalue threshold for the enrichment            |
| <code>logFC</code>            | Double. Fold change threshold for the enrichment                |
| <code>save.results</code>     | Logical. If TRUE saves input gene lists and enrichment results. |

**Value**

A list of enrichment tables for upregulated and downregulated genes in the different enrichr databases

**See Also**

<https://maayanlab.cloud/Enrichr/> for additional information about enrichR.

Other functional-annotation functions: [Annotate\\_SPID\(\)](#), [Enrichment\\_barplot\(\)](#)

**Examples**

```
## Not run:
df1 <- data.frame(GeneID = c("MEST", "CDK1", "PCLAF", "BIRC5"),
  baseMean = c(13490.22, 10490.23, 8888.33, 750.33),
  log2FoldChange = c(5.78, 6.76, -7.78, -8.78),
  padj = c(2.28e-143, 2.18e-115, 2.18e-45, 0.006),
  row.names = c("MEST", "CDK1", "PCLAF", "BIRC5"))
df2 <- data.frame(GeneID = c("MEST", "CDK1", "PCLAF", "BIRC5"),
  baseMean = c(13490.22, 10490.23, 8888.33, 750.33),
  log2FoldChange = c(5.78, 6.76, -7.78, -8.78),
  padj = c(2.28e-143, 2.18e-115, 2.18e-45, 0.006),
  row.names = c("MEST", "CDK1", "PCLAF", "BIRC5"))
dfList <- list(df1 = df1, df2 = df2)
test <- Enrichment(dfList, enrich.databases = c("GO_Cellular_Component_2021"),
  save.results = FALSE)
## End(Not run)
```

---

Enrichment\_barplot

*Enrichment\_barplot*

---

**Description**

Barplot representing the top up-regulated or down-regulated significant pathways

**Usage**

```
Enrichment_barplot(
  Enrich,
  enrich.databases = c("GO_Biological_Process_2021", "GO_Cellular_Component_2021",
    "GO_Molecular_Function_2021"),
  p_adj = 0.05,
  num_term = 10,
  cond = "UP",
  plot = FALSE
)
```

**Arguments**

|                  |                                                                                                                                                         |
|------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------|
| Enrich           | A list of enrichment tables for up and down-regulated genes in the different enrichR databases. Output of Enrichment.R function for one DGE experiment. |
| enrich.databases | Vector of EnrichR databases to consider. These databases must be present in the Enrich list.                                                            |
| p_adj            | Double. Minimum Adjusted pvalue threshold for the enrichment                                                                                            |
| num_term         | Double. Number of up-regulated and dw-regulated terms to represent                                                                                      |
| cond             | String. Title of the plot.                                                                                                                              |
| plot             | Logical. If TRUE save plot as pdf.                                                                                                                      |

**Value**

bar plot of significant pathways.

**See Also**

Other functional-annotation functions: [Annotate\\_SPID\(\)](#), [Enrichment\(\)](#)

Other plot functions: [SVenn\(\)](#), [Splot\(\)](#), [plotPCA\(\)](#)

**Examples**

```
## Not run:
dbs <- c("GO_Biological_Process_2021")
dfList <- list()
dfList[["fdr_up"]]$GO_Biological_Process_2021 <- data.frame(
  Term = c("peripheral nervous system neuron differentiation (GO:0048934)",
    "apoptotic chromosome condensation (GO:0030263)",
    "negative regulation of CD4-positive, alpha-beta T cell differentiation (GO:0043371)"),
  Overlap = c("1/5", "1/5", "1/5"),
  P.value = c(0.0007498315, 0.0007498315, 0.0007498315),
  Adjusted.P.value = c(0.00893491, 0.00893491, 0.00893491),
  Old.P.value = c(0, 0, 0),
  Old.Adjusted.P.value = c(0, 0, 0),
  Odds.Ratio = c(2499.125, 2499.125, 2499.125),
  Combined.Score = c(17982.86, 17982.86, 17982.86),
```

```

Genes = c("RUNX1", "TOP2A", "RUNX1")
dfList[["fdr_down"]] $GO_Biological_Process_2021 <- data.frame(
  Term = c("skin morphogenesis (GO:0043589)",
            "skin development (GO:0043588)",
            "collagen fibril organization (GO:0030199)"),
  Overlap = c("2/7", "2/80", "2/89"),
  P.value = c(3.149296e-07, 4.727687e-05, 5.856991e-05),
  Adjusted.P.value = c(1.291211e-05, 8.004554e-04, 8.004554e-04),
  Old.P.value = c(0, 0, 0),
  Old.Adjusted.P.value = c(0, 0, 0),
  Odds.Ratio = c(7996.8000, 510.7436, 457.7011),
  Combined.Score = c(119719.427, 5086.745, 4460.430),
  Genes = c("COL1A1;COL1A2", "COL1A1;COL1A2", "COL1A1;COL1A2"))
Enrichment_barplot(dfList,
  enrich.databases = dbs,
  p_adj = 0.01, num_term = 3, cond = "UP")

## End(Not run)

```

---

enrichr

*Gene enrichment using Enrichr*


---

## Description

Gene enrichment using Enrichr

## Usage

```
enrichr(genes, databases)
```

## Arguments

|           |                                                                                                                                                                                                                           |
|-----------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| genes     | (Required). Character vector of Entrez gene symbols as input. A data.frame of gene symbols in first column is also acceptable, optionally a score denoting the degree of membership between 0 and 1 in the second column. |
| databases | (Required). Character vector of databases to search. See <a href="https://maayanlab.cloud/Enrichr/">https://maayanlab.cloud/Enrichr/</a> for available databases.                                                         |

## Details

Gene enrichment using Enrichr, slightly modified by Aurora Maurizio.

## Value

Returns a list of data.frame of enrichment terms, p-values, ...

## Author(s)

Wajid Jawaaid <wj241@alumni.cam.ac.uk>

**Examples**

```
## Not run:
GeneID = c("MEST", "CDK1", "PCLAF", "BIRC5")
dbs <- c("GO_Molecular_Function_2023", "GO_Cellular_Component_2023",
        "GO_Biological_Process_2023")
enriched1 <- enrichr(GeneID, dbs)
print(head(enriched1[[1]]))
## End(Not run)
```

---

|                 |                                                                     |
|-----------------|---------------------------------------------------------------------|
| enrichr_connect | <i>Connect to the enrichr web application - function from hypeR</i> |
|-----------------|---------------------------------------------------------------------|

---

**Description**

Connect to the enrichr web application - function from hypeR

**Usage**

```
enrichr_connect(endpoint, db = c("Enrichr"))
```

**Arguments**

|          |                                |
|----------|--------------------------------|
| endpoint | The url endpoint to connect to |
| db       | A species                      |

**Value**

A web response

---

|                  |                                                                                     |
|------------------|-------------------------------------------------------------------------------------|
| enrichr_download | <i>Download data from enrichr in the form of a named list - function from hypeR</i> |
|------------------|-------------------------------------------------------------------------------------|

---

**Description**

Download data from enrichr in the form of a named list - function from hypeR

**Usage**

```
enrichr_download(genesets, db = c("Enrichr"))
```

**Arguments**

|          |                                            |
|----------|--------------------------------------------|
| genesets | A name corresponding to available genesets |
| db       | A species                                  |

**Value**

A list of genesets

**Examples**

```
ATLAS <- enrichr_download("Human_Gene_Atlas")
```

---

|              |                                                                                  |
|--------------|----------------------------------------------------------------------------------|
| enrichr_urls | <i>Get url base for species-specific enrichr libraries - function from hypeR</i> |
|--------------|----------------------------------------------------------------------------------|

---

**Description**

Get url base for species-specific enrichr libraries - function from hypeR

**Usage**

```
enrichr_urls(db = c("Enrichr"))
```

**Arguments**

|    |           |
|----|-----------|
| db | A species |
|----|-----------|

**Value**

A url

---

|               |                               |
|---------------|-------------------------------|
| Gene2SProtein | <i>Gene2SProtein function</i> |
|---------------|-------------------------------|

---

**Description**

Detect Surface Proteins from a vector of genes. The surface proteins are identified according to the in silico human surfaceome database, available at <https://wlab.ethz.ch/surfaceome>.

**Usage**

```
Gene2SProtein(
  genes,
  input_type = "gene_name",
  output_tsv = FALSE,
  output_filename = "surfaceProteins.tsv",
  Surfy_version = "log"
)
```

**Arguments**

|                 |                                                                                                                                                                                                                                                                              |
|-----------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| genes           | A vector of genes.                                                                                                                                                                                                                                                           |
| input_type      | The gene identification type: gene_name, ensembl, entrez or uniProt_name.<br>By default: gene_name.                                                                                                                                                                          |
| output_tsv      | Logical. If TRUE, outputs a tsv file with the results. By default, FALSE.                                                                                                                                                                                                    |
| output_filename | Name of the tsv output file. Default is surfaceProteins.tsv.                                                                                                                                                                                                                 |
| Surfy_version   | The version of surfy dataframe you wish to use. Choose between log or newest.<br>By default use the most recent log version. If a log dataframe does not exist the newest is downloaded from <a href="https://wlab.ethz.ch/surfaceome">https://wlab.ethz.ch/surfaceome</a> . |

**Value**

A data frame with filtered surface proteins from the genes array. The dataframe contains also addition information obtained from surfy.

**Warning**

The surfy database is interrogated using the gene identification type of your preference between gene\_name, ensembl, entrez or uniProt\_name. Note that you might loose some matches due to different gene version IDs.

**See Also**

[DGE](#) for DGE analysis, <https://wlab.ethz.ch/surfaceome> for info on Surfy

**Examples**

```
## Not run:
# from gene name IDs to Surface proteins
GeneNames <- c("CIITA", "EPCAM", "DLK1", "CD24", "CDCP1", "LYVE1", "ABCD1", "VAMP1")
SurfaceProteins_df <- Gene2SProtein(GeneNames, input_type = "gene_name")

# from ensembl IDs to Surface proteins
Ensembl <- c("ENSG00000178343", "ENSG00000176895", "ENSG00000162419", "ENSG00000170776",
             "ENSG00000092529", "ENSG00000135926", "ENSG00000152595", "ENSG00000121577",
             "ENSG00000186094", "ENSG00000126773", "ENSG00000198918", "ENSG00000167378",
             "ENSG00000095574", "ENSG00000140678", "ENSG00000262484", "ENSG00000133739",
             "ENSG00000172469", "ENSG00000112992", "ENSG00000148343", "ENSG00000138593")
SurfaceProteins_df <- Gene2SProtein(Ensembl, input_type = "ensembl",
                                   output_tsv = FALSE, Surfy_version = "new")
## End(Not run)
```

---

GEOmetadata*GEOmetadata function*

---

**Description**

Download metadata from <https://www.ncbi.nlm.nih.gov/geo>, given an input GEO accession series.

**Usage**

```
GEOmetadata(GSE, GPL = "")
```

**Arguments**

|     |                                                                                                                    |
|-----|--------------------------------------------------------------------------------------------------------------------|
| GSE | The GSE series ID.                                                                                                 |
| GPL | The GPL series numbers. Required only if the chosen GSE series ID include data from multiple sequencing platforms. |

**Value**

A dataframe with all the available characteristics in GEO metadata genes array.

**Warning**

If the GEO accession series has more than 1 sequencing platforms you need to specify the GPL series numbers.

**See Also**

<https://www.ncbi.nlm.nih.gov/geo> for info on GEO repository

Other public-data functions: [DownloadArchS4\(\)](#), [TCGA\\_download\(\)](#)

**Examples**

```
# only one sequencing platform
## Not run:
mGSE133671 <- GEOmetadata(GSE = "GSE133671")
# multiple sequencing platforms
mGSE59483 <- GEOmetadata("GSE59483", GPL = c("GPL11154", "GPL15520"))
## End(Not run)
```



---

|            |                                   |
|------------|-----------------------------------|
| getEnrichr | <i>Check if EnrichR is online</i> |
|------------|-----------------------------------|

---

**Description**

Helper function

**Usage**

```
getEnrichr(url, ...)
```

**Arguments**

|     |                                                  |
|-----|--------------------------------------------------|
| url | (Required). URL address to check                 |
| ... | (Optional). Additional parameters to pass to GET |

**Details**

Helper function for HTTP methods GET

**Value**

Invisible response object from GET request if successful, or NULL on failure

---

|         |                |
|---------|----------------|
| ind_deg | <i>ind_deg</i> |
|---------|----------------|

---

**Description**

Input list for metaRNAseq function made of 2 different small Deseq2 output samples dataframes for testing purposes: DEG1\_df and DEG2\_df.

**Usage**

```
data(ind_deg)
```

**Format**

dataframe list

**Details**

Each dataframe has 2 rows and 9 columns.

**Value**

A list of dataframes.

---

|                             |                                               |
|-----------------------------|-----------------------------------------------|
| <code>listEnrichrDbs</code> | <i>Look up available databases on Enrichr</i> |
|-----------------------------|-----------------------------------------------|

---

**Description**

Look up available databases on Enrichr

**Usage**

```
listEnrichrDbs()
```

**Details**

Look up available databases on Enrichr

**Value**

A data.frame of available Enrichr databases

**Author(s)**

Wajid Jawaidd <wj241@alumni.cam.ac.uk>

**Examples**

```
dbs <- listEnrichrDbs()
```

---

|                       |                 |
|-----------------------|-----------------|
| <code>metadata</code> | <i>metadata</i> |
|-----------------------|-----------------|

---

**Description**

Metadata associated with countData for testing purposes (functions DGE, plotPCA).

**Usage**

```
data(metadata)
```

**Format**

dataframe.

**Details**

A dataframe with 4 rows (sample names) and 3 columns (samplesID, condition A and B, therapy T1 and T2).

**Value**

A dataframe.

---

metaRNAseq

*metaRNAseq function*

---

**Description**

Perform Meta-Analysis of RNA-Seq Data

**Usage**

```
metaRNAseq(  
  ind_deg,  
  test_statistic = "fishercomb",  
  BHth = 0.05,  
  adjpval.t = 0.05,  
  nrep = NULL,  
  plot = FALSE  
)
```

**Arguments**

|                             |                                                                                                                                                     |
|-----------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>ind_deg</code>        | List of independent named DEG dataframes with p-values to be combined.                                                                              |
| <code>test_statistic</code> | p-value combination technique (inverse normal or Fisher): <code>fishercomb</code> , <code>invnorm</code> .<br>By default: <code>fishercomb</code> . |
| <code>BHth</code>           | Benjamini Hochberg threshold.                                                                                                                       |
| <code>adjpval.t</code>      | threshold to represent as binary the Meta-Analysis output <code>adjpval</code> .                                                                    |
| <code>nrep</code>           | Vector of numbers of replicates used in each study to calculate the previous one-sided p-values.                                                    |
| <code>plot</code>           | Logical. If TRUE plot histogram of pvalues. By default, the False Discovery Rate is controlled at 0.05.                                             |

**Value**

A list with `DEindices` of DEG at the chosen Benjamini Hochberg threshold, and `TestStatistic`, `rawpval`, `adjpval`, `binaryadjpval` vectors for differential expression in the meta-analysis.

**See Also**

[DGE](#) for DGE analysis, and <https://cran.r-project.org/web/packages/metaRNASeq/vignettes/metaRNASeq.pdf> for metaRNASeq package info.

Other meta-analysis functions: [combine\\_fisher\\_invnorm\(\)](#)

## Examples

```
## Not run:
# Deseq2 output samples
DGE1 <- data.frame(GeneID = c("DLK1", "EPCAM"),
  Mean_CPM_T = c(5.92, 9.91),
  Mean_CPM_C = c(0.04, 0.03),
  log2FoldChange = c(10.22, 8.42),
  lfcSE = c(0.80, 0.48),
  stat = c(12.68, 17.69),
  pvalue = c(7.30135e-37, 4.37011e-70),
  padj = c(1.49936e-35, 1.12976e-67),
  row.names = c("DLK1", "EPCAM"))
DGE2 <- data.frame(GeneID = c("DLK1", "EPCAM"),
  Mean_CPM_T = c(3.92, 8.91),
  Mean_CPM_C = c(0.04, 0.03),
  log2FoldChange = c(7.22, 5.81),
  lfcSE = c(0.80, 0.48),
  stat = c(12.68, 17.69),
  pvalue = c(7.30135e-37, 4.37011e-70),
  padj = c(1.49936e-35, 1.12976e-67),
  row.names = c("DLK1", "EPCAM"))

# input list
ind_deg <- list(DEG1_df = DGE1, DEG2_df = DGE2)
# perform meta-analysis
comb_pval_df <- metaRNAseq(ind_deg, test_statistic = "invnorm", BHth = 0.05, nrep = c(2,2))
## End(Not run)
```

---

plotPCA

*plotPCA function*

---

## Description

Plot PCA highlighting one or two data features

## Usage

```
plotPCA(
  matrix,
  metadata,
  nTOP = 500,
  dims = c(1, 2),
  centering = TRUE,
  scaling = TRUE,
  color.by = NULL,
  shape.by = NULL,
  pt.size = 6,
  cols.use = NULL,
  shape.use = NULL,
```

```

    main = "PCA",
    label = FALSE,
    new.label = NULL
  )

```

### Arguments

|           |                                                                                                       |
|-----------|-------------------------------------------------------------------------------------------------------|
| matrix    | Filtered count matrix in CPM or RPKM with gene on the row and sample ID on the column.                |
| metadata  | Sample metadata, row.names must be samples names.                                                     |
| nTOP      | number of top genes to use for principal components, selected by highest row variance                 |
| dims      | Dimensions to plot, must be a two-length numeric vector specifying x- and y-dimensions                |
| centering | Logical. If TRUE center PCs                                                                           |
| scaling   | Logical. If TRUE scales PCs                                                                           |
| color.by  | Name of one or more metadata columns to color point by.                                               |
| shape.by  | Name of one or more metadata columns to shape point by. If NULL, all points are circles \(\default\). |
| pt.size   | Size of the points in the plot.                                                                       |
| cols.use  | Vector of colors, each color corresponds to an identity class. By default, ggplot assigns colors.     |
| shape.use | Vector of shape, each shape corresponds to an identity class.                                         |
| main      | Plot title. Default = PCA.                                                                            |
| label     | Logical. If TRUE adds samples label. Default = FALSE.                                                 |
| new.label | If NULL, use the sample names as in metadata row.names. Otherwise you can specify new labels.         |

### Value

PCA plot object created by ggplot2, which can be assigned and further customized.

### See Also

Other plot functions: [Enrichment\\_barplot\(\)](#), [SVenn\(\)](#), [Splot\(\)](#)

### Examples

```

## Not run:
# Simulation of bulk RNA data
countData <- matrix(floor(runif(10000, min=0, max=101)),ncol=4)
colnames(countData) <- paste("sample", seq_len(ncol(countData)), sep = "")
rownames(countData) <- paste("gene", seq_along(seq_len(10000/4)), sep = "")
metadata <- data.frame(samplesID = paste("sample", seq_len(ncol(countData)), sep = ""),
                      condition = factor(c("A","A","B","B")),
                      therapy = factor(c("T1","T2","T1","T2")))

```

```

row.names(metadata) <- metadata$samplesID
library(edgeR)
SurfR::plotPCA(matrix = cpm(countData),
               metadata = metadata,
               nTOP = 100,
               dims = c(1,2),
               color.by = "condition", shape.by = "therapy",
               label = FALSE, main = "PCA")
## End(Not run)

```

---

setEnrichrSite

*Set Enrichr Website*


---

## Description

Set Enrichr Website

Set Enrichr Website

## Usage

```
setEnrichrSite(site)
```

```
setEnrichrSite(site)
```

## Arguments

site                      site requested

## Details

Set Enrichr Website

Set Enrichr Website

## Value

Changes Enrichr Website connection

Changes Enrichr Website connection

## Author(s)

Alexander Blume

---

Splot*Splot function*

---

## Description

Plot a barplot with features of Surface Protein

## Usage

```
Splot(  
  SurfaceProteins_df,  
  group.by = "Membranome.Almen.main-class",  
  cols.use = NULL,  
  main = "Almen main class"  
)
```

## Arguments

|                    |                                                                                                   |
|--------------------|---------------------------------------------------------------------------------------------------|
| SurfaceProteins_df | Output dataframe of Gene2SProtein function.                                                       |
| group.by           | Name of columns to plot. Default = Membranome.Almen.main-class.                                   |
| cols.use           | Vector of colors, each color corresponds to an identity class. By default, ggplot assigns colors. |
| main               | Plot title. Default = Almen main class.                                                           |

## Value

plot objec created by ggplot2, which can be assigned and further customized.

## See Also

Other plot functions: [Enrichment\\_barplot\(\)](#), [SVenn\(\)](#), [plotPCA\(\)](#)

## Examples

```
## Not run:  
GeneNames <- c("CIITA", "EPCAM", "DLK1", "CD24", "CDCP1", "LYVE1", "ABCD1", "VAMP1")  
SurfaceProteins_df <- Gene2SProtein(GeneNames, input_type = "gene_name")  
Splot(SurfaceProteins_df)  
## End(Not run)
```

---

|       |              |
|-------|--------------|
| SVenn | <i>SVenn</i> |
|-------|--------------|

---

**Description**

Venn diagram of common surface proteins overexpressed among up to 7 different studies

**Usage**

```
SVenn(  
  S_list,  
  cols.use = NULL,  
  opacity = 0.5,  
  output_intersectionFile = TRUE,  
  filename = "intersection.xlsx"  
)
```

**Arguments**

- S\_list            A list of a maximum of 7 surface protein sets detected in different studies.
- cols.use        Vector of colors, each color corresponds to a study. By default, ggplot assigns colors.
- opacity        Degree of opacity for the colors specified with cols.use (less opacity, more transparency).
- output\_intersectionFile  
                 logical. If TRUE (default) write an xlsx output of protein in the intersections.
- filename        Name of the output file with the intersections.

**Value**

venn plot of common genes.

**See Also**

[Gene2SProtein](#) for detection of Surface proteins from a list of genes.  
Other plot functions: [Enrichment\\_barplot\(\)](#), [Splot\(\)](#), [plotPCA\(\)](#)

**Examples**

```
## Not run:  
S_list <- list(SP1 <- c("EPCAM", "CD24", "DLK1", "CDCP1", "LYVE1"),  
              SP2 <- c("DLK1", "EPCAM", "EGFR", "UPK1A", "UPK2"))  
SP <- SVenn(S_list, cols.use = c("pink", "yellow"), output_intersectionFile = FALSE)  
## End(Not run)
```



---

|               |                               |
|---------------|-------------------------------|
| TCGA_download | <i>TCGA_download function</i> |
|---------------|-------------------------------|

---

## Description

Downloads count matrix data from TCGA

## Usage

```
TCGA_download(
  project,
  whichcounts = "unstranded",
  save.matrix = FALSE,
  save.metadata = FALSE,
  barcodes = NULL
)
```

## Arguments

|               |                                                                                                                                                |
|---------------|------------------------------------------------------------------------------------------------------------------------------------------------|
| project       | Character. A valid project from <code>TCGAbiolinks::getGDCprojects()</code> \$project_id                                                       |
| whichcounts   | Character. Counts data to use. Choose from: unstranded, stranded_first, stranded_second. By default, unstranded.                               |
| save.matrix   | Logical. If TRUE, outputs a tsv file with the Matrix. By default, FALSE.                                                                       |
| save.metadata | Logical. If TRUE, outputs a tsv file with the metadata. By default, FALSE.                                                                     |
| barcodes      | Character. A vector with names of the barcodes you want to download. If NULL (default) it downloads all the available barcodes in the project. |

## Value

A list containing the Matrix and the metadata.

## See Also

Other public-data functions: [DownloadArchS4\(\)](#), [GEOmetadata\(\)](#)

## Examples

```
## Not run:
GBM_list_s1 <- TCGA_download(project="TCGA-GBM",
                             whichcounts = "unstranded",
                             save.matrix = FALSE, save.metadata = FALSE,
                             barcodes = c("TCGA-06-0878-01A-01R-1849-01"))

remove downloaded data from TCGA
unlink('GDCdata', recursive = TRUE, force = TRUE)
file.remove("MANIFEST.txt")

## End(Not run)
```

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