

Package: GDCRNATools (via r-universe)

June 21, 2024

Title GDCRNATools: an R/Bioconductor package for integrative analysis of lncRNA, mRNA, and miRNA data in GDC

Version 1.25.0

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Description This is an easy-to-use package for downloading, organizing, and integrative analyzing RNA expression data in GDC with an emphasis on deciphering the lncRNA-mRNA related ceRNA regulatory network in cancer. Three databases of lncRNA-miRNA interactions including spongeScan, starBase, and miRcode, as well as three databases of mRNA-miRNA interactions including miRTarBase, starBase, and miRcode are incorporated into the package for ceRNAs network construction. limma, edgeR, and DESeq2 can be used to identify differentially expressed genes/miRNAs. Functional enrichment analyses including GO, KEGG, and DO can be performed based on the clusterProfiler and DO packages. Both univariate CoxPH and KM survival analyses of multiple genes can be implemented in the package. Besides some routine visualization functions such as volcano plot, bar plot, and KM plot, a few simply shiny apps are developed to facilitate visualization of results on a local webpage.

Depends R (>= 3.5.0)

License Artistic-2.0

Encoding UTF-8

LazyData false

Imports shiny, jsonlite, rjson, XML, limma, edgeR, DESeq2, clusterProfiler, DOSE, org.Hs.eg.db, biomaRt, survival, survminer, pathview, ggplot2, gplots, DT, GenomicDataCommons, BiocParallel

Suggests knitr, testthat, prettydoc, rmarkdown

VignetteBuilder knitr

biocViews ImmunoOncology, GeneExpression, DifferentialExpression, GeneRegulation, GeneTarget, NetworkInference, Survival, Visualization, GeneSetEnrichment, NetworkEnrichment, Network, RNASeq, GO, KEGG

RoxygenNote 6.1.0

Repository <https://bioc.r-universe.dev>

RemoteUrl <https://github.com/bioc/GDCRNATools>

RemoteRef HEAD

RemoteSha fd0461c12eeff1bbc45b0abaaed36b42211ec1

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| GDCRNATools-package | <i>This is an easy-to-use package for downloading, organizing, and integrative analyzing RNA expression data in GDC with an emphasis on deciphering the lncRNA-mRNA related ceRNA regulatory network in cancer.</i> |
|---------------------|---|

Description

This is an easy-to-use package for downloading, organizing, and integrative analyzing RNA expression data in GDC with an emphasis on deciphering the lncRNA-mRNA related ceRNA regulatory network in cancer.

| | |
|--------|--|
| DEGAll | <i>Output of gdcDEAnalysis for downstream analysis</i> |
|--------|--|

Description

Output of [gdcDEAnalysis](#) for downstream analysis

| | |
|--------------|--|
| enrichOutput | <i>Output of gdcEnrichAnalysis for visualization</i> |
|--------------|--|

Description

Output of [gdcEnrichAnalysis](#) for visualization

| | |
|------------|--|
| gdcBarPlot | <i>Bar plot of differentially expressed genes/miRNAs</i> |
|------------|--|

Description

A bar plot showing the number of down-regulated and up-regulated DE genes/miRNAs of different biotypes

Usage

```
gdcBarPlot(deg, angle = 0, data.type)
```

Arguments

| | |
|-----------|--|
| deg | a dataframe generated from gdcDEReport containing DE genes/miRNAs ids, logFC, etc. |
| angle | a numeric value specifying the angle of text on x-axis. Default is 0 |
| data.type | one of 'RNAseq' and 'miRNAs' |

Value

A bar plot

Author(s)

Ruidong Li and Han Qu

Examples

```
genes <- c('ENSG00000231806', 'ENSG00000261211', 'ENSG00000260920',
           'ENSG00000228594', 'ENSG00000125170', 'ENSG00000179909',
           'ENSG00000280012', 'ENSG00000134612', 'ENSG00000213071')
symbol <- c('PCAT7', 'AL031123.2', 'AL031985.3',
            'FNDC10', 'DOK4', 'ZNF154',
            'RPL23AP61', 'FOLH1B', 'LPAL2')
group <- rep(c('long_non_coding', 'protein_coding', 'pseudogene'), each=3)
logFC <- c(2.8, 2.3, -1.1, 1.9, -1.2, -1.6, 1.5, 2.1, -1.1)
FDR <- rep(c(0.1, 0.00001, 0.0002), each=3)
deg <- data.frame(symbol, group, logFC, FDR)
rownames(deg) <- genes
gdcBarPlot(deg, angle=45, data.type='RNAseq')
```

gdcCEAnalysis

Competing endogenous RNAs (ceRNAs) analysis

Description

Identify ceRNAs by (1) number of shared miRNAs between lncRNA and mRNA; (2) expression correlation of lncRNA and mRNA; (3) regulation similarity of shared miRNAs on lncRNA and mRNA; (4) sensitivity correlation

Usage

```
gdcCEAnalysis(lnc, pc, deMIR = NULL, lnc.targets = "starBase",
              pc.targets = "starBase", rna.expr, mir.expr)
```

Arguments

| | |
|-------------|--|
| lnc | a vector of Ensembl long non-coding gene ids |
| pc | a vector of Ensembl protein coding gene ids |
| deMIR | a vector of differentially expressed miRNAs. Default is NULL |
| lnc.targets | a character string specifying the database of miRNA-lncRNA interactions. Should be one of 'spongeScan', 'starBase', and 'miRcode'. Default is 'starBase'. Or a list of miRNA-lncRNA interactions generated by users |
| pc.targets | a character string specifying the database of miRNA-lncRNA interactions. Should be one of 'spongeScan', 'starBase', and 'miRcode'. Default is 'starBase'. Or a list of miRNA-lncRNA interactions generated by users |
| rna.expr | voom transformed gene expression data |
| mir.expr | voom transformed mature miRNA expression data |

Value

A dataframe containing ceRNA pairs, expression correlation between lncRNA and mRNA, the number and hypergeometric significance of shared miRNAs, regulation similarity score, and the mean sensitivity correlation (the difference between Pearson correlation and partial correlation) of multiple lncRNA-miRNA-mRNA triplets, etc.

Author(s)

Ruidong Li and Han Qu

References

Paci P, Colombo T, Farina L. Computational analysis identifies a sponge interaction network between long non-coding RNAs and messenger RNAs in human breast cancer. *BMC systems biology*. 2014 Jul 17;8(1):83.

Examples

```
##### ceRNA network analysis #####
deLNC <- c('ENSG00000260920', 'ENSG00000242125', 'ENSG00000261211')
dePC <- c('ENSG0000043355', 'ENSG00000109586', 'ENSG00000144355')
genes <- c(deLNC, dePC)
samples <- c('TCGA-2F-A9K0-01', 'TCGA-2F-A9KP-01',
            'TCGA-2F-A9KQ-01', 'TCGA-2F-A9KR-01',
            'TCGA-2F-A9KT-01', 'TCGA-2F-A9KW-01')
rnaExpr <- data.frame(matrix(c(2.7, 7.0, 4.9, 6.9, 4.6, 2.5,
                              0.5, 2.5, 5.7, 6.5, 4.9, 3.8,
                              2.1, 2.9, 5.9, 5.7, 4.5, 3.5,
                              2.7, 5.9, 4.5, 5.8, 5.2, 3.0,
                              2.5, 2.2, 5.3, 4.4, 4.4, 2.9,
                              2.4, 3.8, 6.2, 3.8, 3.8, 4.2), 6, 6),
                      stringsAsFactors=FALSE)
```

```

rownames(rnaExpr) <- genes
colnames(rnaExpr) <- samples

mirExpr <- data.frame(matrix(c(7.7,7.4,7.9,8.9,8.6,9.5,
                             5.1,4.4,5.5,8.5,4.4,3.5,
                             4.9,5.5,6.9,6.1,5.5,4.1,
                             12.4,13.5,15.1,15.4,13.0,12.8,
                             2.5,2.2,5.3,4.4,4.4,2.9,
                             2.4,2.7,6.2,1.5,4.4,4.2),6,6),
                      stringsAsFactors=FALSE)

colnames(mirExpr) <- samples
rownames(mirExpr) <- c('hsa-miR-340-5p', 'hsa-miR-181b-5p',
                      'hsa-miR-181a-5p', 'hsa-miR-181c-5p',
                      'hsa-miR-199b-5p', 'hsa-miR-182-5p')

ceOutput <- gdcCEAnalysis(lnc      = deLNC,
                          pc       = dePC,
                          lnc.targets = 'starBase',
                          pc.targets  = 'starBase',
                          rna.expr   = rnaExpr,
                          mir.expr   = mirExpr)

```

gdcClinicalDownload *Download clinical data in GDC*

Description

Download clinical data in GDC either by providing the manifest file or specifying the project id and data type

Usage

```

gdcClinicalDownload(manifest = NULL, project.id,
                   directory = "Clinical", write.manifest = FALSE,
                   method = "gdc-client")

```

Arguments

| | |
|----------------|--|
| manifest | manifest file that is downloaded from the GDC cart. If provided, files whose UUIDs are in the manifest file will be downloaded via gdc-client, otherwise, project id argument should be provided to download data automatically. Default is NULL |
| project.id | project id in GDC |
| directory | the folder to save downloaded files. Default is 'Clinical' |
| write.manifest | logical, whether to write out the manifest file |
| method | method that is used to download data. Either 'GenomicDataCommons' which is a well established method developed in the GenomicDataCommons package, or alternatively 'gdc-client' which uses the gdc-client tool developed by GDC. Default is 'gdc-client'. |

Value

downloaded files in the specified directory

Author(s)

Ruidong Li and Han Qu

Examples

```
##### Download Clinical data by manifest file #####
manifest <- 'Clinical.manifest.txt'
## Not run: gdcClinicalDownload(manifest = manifest,
                               directory = 'Clinical')
## End(Not run)

##### Download Clinical data by project id #####
project <- 'TCGA-PRAD'
## Not run: gdcClinicalDownload(project.id = project,
                               write.manifest = TRUE,
                               directory = 'Clinical')
## End(Not run)
```

gdcClinicalMerge *Merge clinical data*

Description

Merge clinical data in .xml files that are downloaded from GDC to a dataframe

Usage

```
gdcClinicalMerge(path, key.info = TRUE, organized = FALSE)
```

Arguments

| | |
|-----------|--|
| path | path to downloaded files for merging |
| key.info | logical, whether to return the key clinical information only. If TRUE, only clinical information such as age, stage, grade, overall survival, etc. will be returned |
| organized | logical, whether the clinical data have already been organized into a single folder (eg., data downloaded by the 'GenomicDataCommons' method are already organized). Default is FALSE. |

Value

A dataframe of clinical data with rows are patients and columns are clinical traits

Author(s)

Ruidong Li and Han Qu

Examples

```
##### Merge clinical data #####
path <- 'Clinical/'
## Not run: clinicalDa <- gdcClinicalMerge(path=path, key.info=TRUE)
```

gdcCorPlot

*Correlation plot of two genes/miRNAs***Description**

Scatter plot showing the expression correlation between two genes/miRNAs

Usage

```
gdcCorPlot(gene1, gene2, rna.expr, metadata)
```

Arguments

| | |
|----------|---|
| gene1 | an Ensembl gene id or miRBase v21 mature miRNA id |
| gene2 | an Ensembl gene id or miRBase v21 mature miRNA id |
| rna.expr | voom transformed expression data |
| metadata | metadata parsed from gdcParseMetadata |

Value

A scatter plot with line of best fit

Author(s)

Ruidong Li and Han Qu

Examples

```
genes <- c('ENSG00000000938', 'ENSG00000000971', 'ENSG00000001036',
           'ENSG00000001084', 'ENSG00000001167', 'ENSG00000001460')

samples <- c('TCGA-2F-A9K0-01', 'TCGA-2F-A9KP-01',
            'TCGA-2F-A9KQ-01', 'TCGA-2F-A9KR-11',
            'TCGA-2F-A9KT-11', 'TCGA-2F-A9KW-11')

metaMatrix <- data.frame(sample_type=rep(c('PrimaryTumor',
                                           'SolidTissueNormal'), each=3),
                        sample=samples,
                        days_to_death=seq(100, 600, 100),
                        days_to_last_follow_up=rep(NA, 6))

rnaExpr <- matrix(c(2.7, 7.0, 4.9, 6.9, 4.6, 2.5,
                   0.5, 2.5, 5.7, 6.5, 4.9, 3.8,
```



```

                2.1,2.9,5.9,5.7,4.5,3.5,
                2.7,5.9,4.5,5.8,5.2,3.0,
                2.5,2.2,5.3,4.4,4.4,2.9,
                2.4,3.8,6.2,3.8,3.8,4.2),6,6)
rownames(rnaExpr) <- genes
colnames(rnaExpr) <- samples
gdcCorPlot(gene1 = 'ENSG00000000938',
           gene2  = 'ENSG0000001084',
           rna.expr = rnaExpr,
           metadata = metaMatrix)

```

gdcDEAnalysis

*Differential gene expression analysis***Description**

Performs differential gene expression analysis by **limma**, **edgeR**, and **DESeq2**

Usage

```
gdcDEAnalysis(counts, group, comparison, method = "limma",
              n.cores = NULL, filter = TRUE)
```

Arguments

| | |
|------------|--|
| counts | a dataframe or numeric matrix of raw counts data generated from gdcRNAMerge |
| group | a vector giving the group that each sample belongs to |
| comparison | a character string specifying the two groups being compared. Example: comparison='PrimaryTumor-SolidTissueNormal' |
| method | one of 'limma', 'edgeR', and 'DESeq2'. Default is 'limma' Note: It may takes long time for method='DESeq2' with a single core |
| n.cores | a numeric value of cores to be used for method='DESeq2' to accelate the analysis process. Default is NULL |
| filter | logical, whether to filter out low expression genes. If TRUE, only genes with cpm > 1 in more than half of the samples will be kept. Default is TRUE |

Value

A dataframe containing Ensembl gene ids/miRBase v21 mature miRNA ids, gene symbols, biotypes, fold change on the log2 scale, p value, and FDR etc. of all genes/miRNAs of analysis.

Note

It may takes long time for method='DESeq2' with a single core. Please use multiple cores if possible

Author(s)

Ruidong Li and Han Qu

References

Robinson MD, McCarthy DJ, Smyth GK. edgeR: a Bioconductor package for differential expression analysis of digital gene expression data. *Bioinformatics*. 2010 Jan 1;26(1):139-40.

Ritchie ME, Phipson B, Wu D, Hu Y, Law CW, Shi W, Smyth GK. limma powers differential expression analyses for RNA-sequencing and microarray studies. *Nucleic acids research*. 2015 Jan 20; 43(7):e47-e47.

Love MI, Huber W, Anders S. Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome biology*. 2014 Dec 5; 15(12):550.

Examples

```
genes <- c('ENSG00000000938', 'ENSG00000000971', 'ENSG00000001036',
          'ENSG00000001084', 'ENSG00000001167', 'ENSG00000001460')

samples <- c('TCGA-2F-A9K0-01', 'TCGA-2F-A9KP-01',
            'TCGA-2F-A9KQ-01', 'TCGA-2F-A9KR-11',
            'TCGA-2F-A9KT-11', 'TCGA-2F-A9KW-11')

metaMatrix <- data.frame(sample_type=rep(c('PrimaryTumor',
                                          'SolidTissueNormal'), each=3),
                        sample=samples,
                        days_to_death=seq(100, 600, 100),
                        days_to_last_follow_up=rep(NA, 6))

rnaMatrix <- matrix(c(6092, 11652, 5426, 4383, 3334, 2656,
                    8436, 2547, 7943, 3741, 6302, 13976,
                    1506, 6467, 5324, 3651, 1566, 2780,
                    834, 4623, 10275, 5639, 6183, 4548,
                    24702, 43, 1987, 269, 3322, 2410,
                    2815, 2089, 3804, 230, 883, 5415), 6, 6)

rownames(rnaMatrix) <- genes
colnames(rnaMatrix) <- samples
DEGall <- gdcDEAnalysis(counts = rnaMatrix,
                       group = metaMatrix$sample_type,
                       comparison = 'PrimaryTumor-SolidTissueNormal',
                       method = 'limma')
```

gdcDEReport

*Report differentially expressed genes/miRNAs***Description**

Report genes/miRNAs that are differentially expressed satisfying a given threshold

Usage

```
gdcDEReport(deg, gene.type = "all", fc = 2, pval = 0.01)
```

Arguments

| | |
|-----------|---|
| deg | A dataframe of DE analysis result from gdcDEAnalysis |
| gene.type | one of 'all', 'long_non_coding', 'protein_coding', and 'miRNAs'. Default is 'all' |
| fc | a numeric value specifying the threshold of fold change |
| pval | a numeric value specifying the threshold of p value |

Value

A dataframe or numeric matrix of differentially expressed genes/miRNAs

Author(s)

Ruidong Li and Han Qu

Examples

```
genes <- c('ENSG00000000938', 'ENSG00000000971', 'ENSG00000001036',
           'ENSG00000001084', 'ENSG00000001167', 'ENSG00000001460')

samples <- c('TCGA-2F-A9K0-01', 'TCGA-2F-A9KP-01',
            'TCGA-2F-A9KQ-01', 'TCGA-2F-A9KR-11',
            'TCGA-2F-A9KT-11', 'TCGA-2F-A9KW-11')

metaMatrix <- data.frame(sample_type=rep(c('PrimaryTumor',
                                           'SolidTissueNormal'), each=3),
                        sample=samples,
                        days_to_death=seq(100, 600, 100),
                        days_to_last_follow_up=rep(NA, 6))

rnaMatrix <- matrix(c(6092, 11652, 5426, 4383, 3334, 2656,
                    8436, 2547, 7943, 3741, 6302, 13976,
                    1506, 6467, 5324, 3651, 1566, 2780,
                    834, 4623, 10275, 5639, 6183, 4548,
                    24702, 43, 1987, 269, 3322, 2410,
                    2815, 2089, 3804, 230, 883, 5415), 6, 6)

rownames(rnaMatrix) <- genes
colnames(rnaMatrix) <- samples
DEGAll <- gdcDEAnalysis(counts = rnaMatrix,
                       group   = metaMatrix$sample_type,
                       comparison = 'PrimaryTumor-SolidTissueNormal',
                       method   = 'limma')

dePC <- gdcDEReport(deg=DEGAll)
```

gdcEnrichAnalysis *Functional enrichment analysis*

Description

Performs Gene Ontology (GO), Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway and Disease Ontology (DO) enrichment analyses by **clusterProfiler** and **DOSE** packages

Usage

```
gdcEnrichAnalysis(gene, simplify = TRUE, level = 0)
```

Arguments

| | |
|----------|---|
| gene | a vector of Ensembl gene id |
| simplify | logical, specifying whether to remove redundant GO terms. Default simplify=TRUE |
| level | a numeric value, restrict the GO enrichment result at a specific GO level. Default is 0, which means all terms should be returned |

Value

A dataframe of enrichment analysis result containing enriched terms, number of overlapped genes, p value of hypergeometric test, fdr, fold of enrichment, Ensembl gene ids, gene symbols, and functional categories, etc.

Author(s)

Ruidong Li and Han Qu

References

Yu G, Wang LG, Han Y, He QY. clusterProfiler: an R package for comparing biological themes among gene clusters. *Omics: a journal of integrative biology*. 2012 May 1;16(5):284-7.
 Yu G, Wang LG, Yan GR, He QY. DOSE: an R/Bioconductor package for disease ontology semantic and enrichment analysis. *Bioinformatics*. 2014 Oct 17;31(4):608-9.

Examples

```
##### GO, KEGG, DO enrichment analysis #####
deg <- c('ENSG00000000938', 'ENSG00000000971', 'ENSG00000001036',
        'ENSG00000001084', 'ENSG00000001167', 'ENSG00000001460')
## Not run: enrichOutput <- gdcEnrichAnalysis(gene=deg, simplify=TRUE)
```

gdcEnrichPlot *Plots for enrichment analysis*

Description

Bar plot and bubble plot for GO, KEGG, and DO functional enrichment analysis

Usage

```
gdcEnrichPlot(enrichment, type = "bar", category = "KEGG",
              num.terms = 10, bar.color = "black")
```

Arguments

| | |
|------------|--|
| enrichment | a dataframe generated from gdcEnrichAnalysis |
| type | type of the plot, should be one of 'bar' and 'bubble' |
| category | which category should be plotted. Possible values are 'KEGG', 'GO', 'GO_BP', 'GO_CC', 'GO_MF', and 'DO'. Default is 'KEGG' |
| num.terms | number of terms to be plotted. Default is 10 |
| bar.color | color of the bar plot. Default is 'black' |

Value

A bar plot or bubble plot of functional enrichment analysis

Author(s)

Ruidong Li and Han Qu

Examples

```
##### Enrichment plots #####
enrichOutput<-data.frame(Terms=c('hsa05414~Dilated cardiomyopathy (DCM)',
                                'hsa04510~Focal adhesion',
                                'hsa05205~Proteoglycans in cancer'),
                        Category=rep('KEGG',3),
                        FDR=c(0.001,0.002,0.003))
gdcEnrichPlot(enrichment=enrichOutput, type='bar', category='KEGG')
```

| | |
|------------------|-------------------------------------|
| gdcExportNetwork | <i>Export network for Cytoscape</i> |
|------------------|-------------------------------------|

Description

Export nodes and edges of ce network for **Cytoscape** visualization

Usage

```
gdcExportNetwork(ceNetwork, net)
```

Arguments

| | |
|-----------|--|
| ceNetwork | a dataframe generated from gdcCEAnalysis |
| net | one of 'nodes' and 'edges' |

Value

A dataframe of nodes or edges

Author(s)

Ruidong Li and Han Qu

Examples

```
##### ceRNA network analysis #####
ceOutput <- data.frame(lncRNAs=c('ENSG00000242125', 'ENSG00000242125',
                                'ENSG00000245532'),
                      Genes=c('ENSG0000043355', 'ENSG00000109586',
                              'ENSG00000144355'),
                      miRNAs=c('hsa-miR-340-5p', 'hsa-miR-340-5p',
                                'hsa-miR-320b, hsa-miR-320d,
                                hsa-miR-320c, hsa-miR-320a'),
                      Counts=c(1,1,4), stringsAsFactors=FALSE)
##### Export edges #####
edges <- gdcExportNetwork(ceNetwork=ceOutput, net='edges')

##### Export nodes #####
## Not run: nodes <- gdcExportNetwork(ceNetwork=ceOutput, net='nodes')
```

`gdcFilterDuplicate` *Filter out duplicated samples*

Description

Filter out samples that are sequenced for two or more times

Usage

```
gdcFilterDuplicate(metadata)
```

Arguments

`metadata` metadata parsed from [gdcParseMetadata](#)

Value

A filtered dataframe of metadata without duplicated samples

Author(s)

Ruidong Li and Han Qu

Examples

```
##### Parse metadata by project id and data type #####  
metaMatrix <- gdcParseMetadata(project.id='TARGET-RT', data.type='RNAseq')  
metaMatrix <- gdcFilterDuplicate(metadata=metaMatrix)
```

`gdcFilterSampleType` *Filter out other type of samples*

Description

Filter out samples that are neither *Solid Tissue Normal* nor *Primary Tumor*

Usage

```
gdcFilterSampleType(metadata)
```

Arguments

`metadata` metadata parsed from [gdcParseMetadata](#)

Value

A filtered dataframe of metadata with *Solid Tissue Normal* and *Primary Tumor* samples only


```

                                days_to_last_follow_up=rep(NA,6))
rnaExpr <- matrix(c(2.7,7.0,4.9,6.9,4.6,2.5,
                   0.5,2.5,5.7,6.5,4.9,3.8,
                   2.1,2.9,5.9,5.7,4.5,3.5,
                   2.7,5.9,4.5,5.8,5.2,3.0,
                   2.5,2.2,5.3,4.4,4.4,2.9,
                   2.4,3.8,6.2,3.8,3.8,4.2),6,6)
rownames(rnaExpr) <- genes
colnames(rnaExpr) <- samples
gdcHeatmap(deg.id=genes, metadata=metaMatrix, rna.expr=rnaExpr)

```

gdcKMPlot

*Kaplan Meier plot***Description**

Plot Kaplan Meier survival curve

Usage

```
gdcKMPlot(gene, rna.expr, metadata, sep = "median")
```

Arguments

| | |
|----------|---|
| gene | an Ensembl gene id |
| rna.expr | voom transformed expression data |
| metadata | metadata parsed from gdcParseMetadata |
| sep | a character string specifying which point should be used to separate low-expression and high-expression groups. Possible values are '1stQu', 'mean', 'median', and '3rdQu'. Default is 'median' |

Value

A plot of Kaplan Meier survival curve

Author(s)

Ruidong Li and Han Qu

Examples

```

##### KM plots #####
genes <- c('ENSG00000000938', 'ENSG00000000971', 'ENSG0000001036',
          'ENSG0000001084', 'ENSG0000001167', 'ENSG0000001460')

samples <- c('TCGA-2F-A9K0-01', 'TCGA-2F-A9KP-01',
            'TCGA-2F-A9KQ-01', 'TCGA-2F-A9KR-01',
            'TCGA-2F-A9KT-01', 'TCGA-2F-A9KW-01')

```

```

metaMatrix <- data.frame(sample_type=rep('PrimaryTumor',6),
                          sample=samples,
                          days_to_death=seq(100,600,100),
                          days_to_last_follow_up=rep(NA,6))
rnaExpr <- matrix(c(2.7,7.0,4.9,6.9,4.6,2.5,
                   0.5,2.5,5.7,6.5,4.9,3.8,
                   2.1,2.9,5.9,5.7,4.5,3.5,
                   2.7,5.9,4.5,5.8,5.2,3.0,
                   2.5,2.2,5.3,4.4,4.4,2.9,
                   2.4,3.8,6.2,3.8,3.8,4.2),6,6)
rownames(rnaExpr) <- genes
colnames(rnaExpr) <- samples
gdcKMPLOT(gene='ENSG00000000938', rna.expr=rnaExpr,
          metadata=metaMatrix, sep='median')

```

`gdcMatchSamples` *Match samples in metadata and expression matrix*

Description

Check if samples in the metadata and expression data match

Usage

```
gdcMatchSamples(metadata, rna.expr)
```

Arguments

`metadata` metadata parsed from [gdcParseMetadata](#)
`rna.expr` [voom](#) transformed expression data

Value

A logical value. If TRUE, all the samples matched

Author(s)

Ruidong Li and Han Qu

Examples

```

genes <- c('ENSG00000000938', 'ENSG00000000971', 'ENSG0000001036',
           'ENSG0000001084', 'ENSG0000001167', 'ENSG0000001460')

samples <- c('TCGA-2F-A9KO-01', 'TCGA-2F-A9KP-01',
            'TCGA-2F-A9KQ-01', 'TCGA-2F-A9KR-01',
            'TCGA-2F-A9KT-01', 'TCGA-2F-A9KW-01')

```

```

metaMatrix <- data.frame(sample_type=rep('PrimaryTumor',6),
                        sample=samples,
                        days_to_death=seq(100,600,100),
                        days_to_last_follow_up=rep(NA,6))
rnaExpr <- matrix(c(2.7,7.0,4.9,6.9,4.6,2.5,
                  0.5,2.5,5.7,6.5,4.9,3.8,
                  2.1,2.9,5.9,5.7,4.5,3.5,
                  2.7,5.9,4.5,5.8,5.2,3.0,
                  2.5,2.2,5.3,4.4,4.4,2.9,
                  2.4,3.8,6.2,3.8,3.8,4.2),6,6)
rownames(rnaExpr) <- genes
colnames(rnaExpr) <- samples
gdcMatchSamples(metadata=metaMatrix, rna.expr=rnaExpr)

```

| | |
|------------------|-----------------------|
| gdcParseMetadata | <i>Parse metadata</i> |
|------------------|-----------------------|

Description

Parse metadata either by providing the *.json* file that is downloaded from GDC cart or by parse metadata automatically by providing the project id and data type

Usage

```

gdcParseMetadata(metafile = NULL, project.id, data.type,
                write.meta = FALSE)

```

Arguments

| | |
|------------|---|
| metafile | metadata file in <i>.json</i> format download from GDC cart. If provided, the metadata will be parsed from this file, otherwise, project and data.type arguments should be provided to retrieve metadata automatically. Default is NULL |
| project.id | project id in GDC |
| data.type | one of 'RNAseq' and 'miRNAs' |
| write.meta | logical, whether to write the metadata to a <i>.json</i> file |

Value

A dataframe of metadata containing file_name, sample_id, etc. as well as some basic clinical data

Author(s)

Ruidong Li and Han Qu

Examples

```

##### Merge RNA expression data #####
metaMatrix <- gdcParseMetadata(project.id='TARGET-RT', data.type='RNAseq')

```

gdcRNADownload *Download RNA data in GDC*

Description

Download gene expression quantification and isoform expression quantification data from GDC either by providing the manifest file or by specifying the project id and data type

Usage

```
gdcRNADownload(manifest = NULL, project.id, data.type,
               directory = "Data", write.manifest = FALSE, method = "gdc-client")
```

Arguments

| | |
|----------------|--|
| manifest | manifest file that is downloaded from the GDC cart. If provided, files whose UUIDs are in the manifest file will be downloaded via gdc-client, otherwise, project and data.type arguments should be provided to download data automatically. Default is NULL |
| project.id | project id in GDC |
| data.type | one of 'RNAseq' and 'miRNAs' |
| directory | the folder to save downloaded files. Default is 'Data' |
| write.manifest | logical, whether to write out the manifest file |
| method | method that is used to download data. Either 'GenomicDataCommons' which is a well established method developed in the GenomicDataCommons package, or alternatively 'gdc-client' which uses the gdc-client tool developed by GDC. Default is 'gdc-client'. |

Value

Downloaded files in the specified directory

Author(s)

Ruidong Li and Han Qu

Examples

```
##### Download RNA data by manifest file #####
manifest <- 'RNAseq.manifest.txt'
## Not run: gdcRNADownload(manifest=manifest)

##### Download RNA data by project id and data type #####
project <- 'TCGA-PRAD'
## Not run: gdcRNADownload(project.id=project, data.type='RNAseq')
```

| | |
|-------------|---|
| gdcRNAMerge | <i>Merge RNA/miRNAs raw counts data</i> |
|-------------|---|

Description

Merge raw counts data that is downloaded from GDC to a single expression matrix

Usage

```
gdcRNAMerge(metadata, path, data.type, organized = FALSE)
```

Arguments

| | |
|-----------|--|
| metadata | metadata parsed from gdcParseMetadata |
| path | path to downloaded files for merging |
| data.type | one of 'RNAseq' and 'miRNAs' |
| organized | logical, whether the raw counts data have already been organized into a single folder (eg., data downloaded by the 'GenomicDataCommons' method are already organized). Default is FALSE. |

Value

A dataframe or numeric matrix of raw counts data with rows are genes or miRNAs and columns are samples

Author(s)

Ruidong Li and Han Qu

Examples

```
##### Merge RNA expression data #####
metaMatrix <- gdcParseMetadata(project.id='TARGET-RT',
  data.type='RNAseq')
## Not run: rnaExpr <- gdcRNAMerge(metadata=metaMatrix, path='RNAseq/',
  data.type='RNAseq')
## End(Not run)
```

gdcSurvivalAnalysis *Univariate survival analysis of multiple genes*

Description

Univariate Cox Proportional-Hazards and Kaplan Meier survival analysis of a vector of genes

Usage

```
gdcSurvivalAnalysis(gene, rna.expr, metadata, method = "coxph",  
  sep = "median")
```

Arguments

| | |
|----------|---|
| gene | a vector of Ensembl gene ids |
| rna.expr | voom transformed expression data |
| metadata | metadata parsed from gdcParseMetadata |
| method | method for survival analysis. Possible values are 'coxph' and 'KM'. Default is 'coxph' |
| sep | which point should be used to separate low-expression and high-expression groups for method='KM'. Possible values are '1stQu', 'mean', 'median', and '3rdQu'. Default is 'median' |

Value

A dataframe or numeric matrix of hazard ratio, 95% confidence interval, p value, and FDR

Author(s)

Ruidong Li and Han Qu

References

Therneau TM, Lumley T. Package 'survival'.
Andersen PK, Gill RD. Cox's regression model for counting processes: a large sample study. The annals of statistics. 1982 Dec 1:1100-20.
Therneau TM, Grambsch PM. Extending the Cox model. Edited by P. Bickel, P. Diggle, S. Fienberg, K. Krickeberg. 2000:51.
Harrington DP, Fleming TR. A class of rank test procedures for censored survival data. Biometrika. 1982 Dec 1;69(3):553-66.

Examples

```

genes <- c('ENSG00000000938', 'ENSG00000000971', 'ENSG00000001036',
           'ENSG00000001084', 'ENSG00000001167', 'ENSG00000001460')

samples <- c('TCGA-2F-A9K0-01', 'TCGA-2F-A9KP-01',
            'TCGA-2F-A9KQ-01', 'TCGA-2F-A9KR-01',
            'TCGA-2F-A9KT-01', 'TCGA-2F-A9KW-01')

metaMatrix <- data.frame(sample_type=rep('PrimaryTumor',6),
                        sample=samples,
                        days_to_death=seq(100,600,100),
                        days_to_last_follow_up=rep(NA,6))

rnaExpr <- matrix(c(2.7,7.0,4.9,6.9,4.6,2.5,
                  0.5,2.5,5.7,6.5,4.9,3.8,
                  2.1,2.9,5.9,5.7,4.5,3.5,
                  2.7,5.9,4.5,5.8,5.2,3.0,
                  2.5,2.2,5.3,4.4,4.4,2.9,
                  2.4,3.8,6.2,3.8,3.8,4.2),6,6)

rownames(rnaExpr) <- genes
colnames(rnaExpr) <- samples
survOutput <- gdcSurvivalAnalysis(gene=genes,
                                rna.expr=rnaExpr, metadata=metaMatrix)

```

gdcVolcanoPlot

*Volcano plot of differentially expressed genes/miRNAs***Description**

A volcano plot showing differentially expressed genes/miRNAs

Usage

```
gdcVolcanoPlot(deg.all, fc = 2, pval = 0.01)
```

Arguments

| | |
|---------|--|
| deg.all | a dataframe generated from gdcDEAnalysis containing all genes of analysis no matter they are differentially expressed or not |
| fc | a numeric value specifying the threshold of fold change |
| pval | a numeric value specifying the threshold of p value |

Value

A volcano plot

Author(s)

Ruidong Li and Han Qu

Examples

```

genes <- c('ENSG00000231806', 'ENSG00000261211', 'ENSG00000260920',
           'ENSG00000228594', 'ENSG00000125170', 'ENSG00000179909',
           'ENSG00000280012', 'ENSG00000134612', 'ENSG00000213071')
symbol <- c('PCAT7', 'AL031123.2', 'AL031985.3',
            'FNDC10', 'DOK4', 'ZNF154',
            'RPL23AP61', 'FOLH1B', 'LPAL2')
group <- rep(c('long_non_coding', 'protein_coding', 'pseudogene'), each=3)
logFC <- c(2.8, 2.3, -1.1, 1.9, -1.2, -1.6, 1.5, 2.1, -1.1)
FDR <- rep(c(0.1, 0.00001, 0.0002), each=3)
deg <- data.frame(symbol, group, logFC, FDR)
rownames(deg) <- genes
gdcVolcanoPlot(deg.all=deg)

```

gdcVoomNormalization *TMM normalization and voom transformation*

Description

Normalize raw counts data by TMM implemented in **edgeR** and then transform it by **voom** in **limma**

Usage

```
gdcVoomNormalization(counts, filter = TRUE)
```

Arguments

| | |
|--------|--|
| counts | raw counts of RNA/miRNA expression data |
| filter | logical, whether to filter out low-expression genes. If TRUE, only genes with cpm > 1 in more than half of the samples will be kept. Default is TRUE |

Value

A dataframe or numeric matrix of TMM normalized and **voom** transformed expression values on the log₂ scale

Author(s)

Ruidong Li and Han Qu

References

Robinson MD, McCarthy DJ, Smyth GK. edgeR: a Bioconductor package for differential expression analysis of digital gene expression data. *Bioinformatics*. 2010 Jan 1;26(1):139-40.

Law CW, Chen Y, Shi W, Smyth GK. Voom: precision weights unlock linear model analysis tools for RNA-seq read counts. *Genome biology*. 2014 Feb 3;15(2):R29.

Examples

```
##### Normalization #####  
rnaMatrix <- matrix(sample(1:100,100), 4, 25)  
rnaExpr <- gdcVoomNormalization(counts=rnaMatrix, filter=FALSE)
```

| | |
|-----------|----------------------------------|
| IncTarget | <i>miRNA-lncRNA interactions</i> |
|-----------|----------------------------------|

Description

miRNA-lncRNA interactions

| | |
|-----------|---------------------------------------|
| mirCounts | <i>miRNA counts data of TCGA-CHOL</i> |
|-----------|---------------------------------------|

Description

miRNA counts data of TCGA-CHOL

| | |
|----------|--------------------------------|
| pcTarget | <i>miRNA-mRNA interactions</i> |
|----------|--------------------------------|

Description

miRNA-mRNA interactions

| | |
|-----------|--|
| rnaCounts | <i>RNAseq counts data of TCGA-CHOL</i> |
|-----------|--|

Description

RNAseq counts data of TCGA-CHOL

shinyCorPlot

*Shiny correlation plot***Description**

A simple **shiny** app to show scatter plot of correlations between two genes/miRNAs on local web browser

Usage

```
shinyCorPlot(gene1, gene2, rna.expr, metadata)
```

Arguments

| | |
|----------|--|
| gene1 | a vector of Ensembl gene ids or miRBase v21 mature miRNA ids |
| gene2 | a vector of Ensembl gene ids or miRBase v21 mature miRNA ids |
| rna.expr | voom transformed expression data |
| metadata | metadata parsed from gdcParseMetadata |

Value

a local webpage for visualization of correlation plots

Author(s)

Ruidong Li and Han Qu

Examples

```
genes <- c('ENSG00000000938', 'ENSG00000000971', 'ENSG0000001036',
           'ENSG0000001084', 'ENSG0000001167', 'ENSG0000001460')

samples <- c('TCGA-2F-A9K0-01', 'TCGA-2F-A9KP-01',
            'TCGA-2F-A9KQ-01', 'TCGA-2F-A9KR-01',
            'TCGA-2F-A9KT-01', 'TCGA-2F-A9KW-01')

metaMatrix <- data.frame(sample_type=rep('PrimaryTumor',6),
                          sample=samples,
                          days_to_death=seq(100,600,100),
                          days_to_last_follow_up=rep(NA,6))

rnaExpr <- matrix(c(2.7,7.0,4.9,6.9,4.6,2.5,
                   0.5,2.5,5.7,6.5,4.9,3.8,
                   2.1,2.9,5.9,5.7,4.5,3.5,
                   2.7,5.9,4.5,5.8,5.2,3.0,
                   2.5,2.2,5.3,4.4,4.4,2.9,
                   2.4,3.8,6.2,3.8,3.8,4.2),6,6)

rownames(rnaExpr) <- genes
colnames(rnaExpr) <- samples
```

```
## Not run: shinyCorPlot(gene1=genes[1:3], gene2=genes[4:5], rna.expr=rnaExpr,
  metadata=metaMatrix)
## End(Not run)
```

shinyKMPlot

*Shiny Kaplan Meier (KM) plot***Description**

A simple **shiny** app to show KM survival curves on local web browser

Usage

```
shinyKMPlot(gene, rna.expr, metadata)
```

Arguments

| | |
|----------|---|
| gene | a vector of Ensembl gene ids |
| rna.expr | voom transformed expression data |
| metadata | metadata parsed from gdcParseMetadata |

Value

a local webpage for visualization of KM plots

Author(s)

Ruidong Li and Han Qu

Examples

```
genes <- c('ENSG00000000938', 'ENSG00000000971', 'ENSG0000001036',
  'ENSG0000001084', 'ENSG0000001167', 'ENSG0000001460')

samples <- c('TCGA-2F-A9K0-01', 'TCGA-2F-A9KP-01',
  'TCGA-2F-A9KQ-01', 'TCGA-2F-A9KR-01',
  'TCGA-2F-A9KT-01', 'TCGA-2F-A9KW-01')

metaMatrix <- data.frame(sample_type=rep('PrimaryTumor',6),
  sample=samples,
  days_to_death=seq(100,600,100),
  days_to_last_follow_up=rep(NA,6))

rnaExpr <- matrix(c(2.7,7.0,4.9,6.9,4.6,2.5,
  0.5,2.5,5.7,6.5,4.9,3.8,
  2.1,2.9,5.9,5.7,4.5,3.5,
  2.7,5.9,4.5,5.8,5.2,3.0,
  2.5,2.2,5.3,4.4,4.4,2.9,
  2.4,3.8,6.2,3.8,3.8,4.2),6,6)

rownames(rnaExpr) <- genes
```

```
colnames(rnaExpr) <- samples
## Not run: shinyKMPlot(gene=genes, rna.expr=rnaExpr,
  metadata=metaMatrix)
## End(Not run)
```

shinyPathview

Shiny pathview

Description

A simple **shiny** app to show pathways generated by **pathview** package on local web browser

Usage

```
shinyPathview(gene, pathways, directory = ".")
```

Arguments

| | |
|-----------|--|
| gene | a vector of numeric values (eg. fold change on log2 scale) with names are Ensembl gene ids |
| pathways | a vector of KEGG pathway ids |
| directory | the folder to save pathway figures. Default is the working directory |

Value

a local webpage for visualization of KEGG maps

Author(s)

Ruidong Li and Han Qu

Examples

```
genes <- c('ENSG00000000938', 'ENSG00000000971', 'ENSG0000001036',
  'ENSG00000001084', 'ENSG00000001167', 'ENSG0000001460')
pathways <- c("hsa05414~Dilated cardiomyopathy (DCM)",
  "hsa05410~Hypertrophic cardiomyopathy (HCM)",
  "hsa05412~Arrhythmogenic right ventricular cardiomyopathy",
  "hsa04512~ECM-receptor interaction",
  "hsa04510~Focal adhesion",
  "hsa04360~Axon guidance",
  "hsa04270~Vascular smooth muscle contraction",
  "hsa05205~Proteoglycans in cancer",
  "hsa04022~cGMP-PKG signaling pathway",
  "hsa00480~Glutathione metabolism")
## Not run: shinyPathview(gene=genes, pathways=pathways)
```

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