

Package ‘ivygapSE’

May 9, 2023

Title A SummarizedExperiment for Ivy-GAP data
Description Define a SummarizedExperiment and exploratory app for Ivy-GAP glioblastoma image, expression, and clinical data.
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Imports shiny, survival, survminer, hwriter, plotly, ggplot2, S4Vectors, graphics, stats, utils, UpSetR
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biocViews Transcription, Software, Visualization, Survival, GeneExpression, Sequencing
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R topics documented:

designOverview	2
exprByType	2
getRefLimma	3
ivyGlimpse	3
ivySE	4
makeGeneSets	5
tumorDetails	6

Index**8**

designOverview	<i>render design overview</i>
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Description

render design overview
 render anatomic nomenclature

Usage

```
designOverview()
nomenclat()
```

Value

a rastergrob grob

Examples

```
designOverview()
```

exprByType	<i>simple plot of expression values by structure/expression-based selection in IvyGAP</i>
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Description

simple plot of expression values by structure/expression-based selection in IvyGAP

Usage

```
exprByType(sym, ...)
```

Arguments

sym	a gene symbol found among 'rownames(ivySE)'
...	passed to plot, exclusive of ylab, xlab, axes

Value

invisibly returns a list with two elements: exprs, the vector of expression values, and types, the vector of structure types

Examples

```
exprByType("MYC")
```

getRefLimma	<i>provide access to a limma analysis of RNA-seq profiles for reference histology samples</i>
-------------	---

Description

provide access to a limma analysis of RNA-seq profiles for reference histology samples

Usage

```
getRefLimma()
```

Value

an instance of `MArrayLM-class` representing regularized gene-wise ANOVAs

Note

Uses [download.file](#) to acquire RDS of the output of [eBayes](#) from a public S3 bucket. The limma model was fit using [duplicateCorrelation](#) to address multiplicity of contributions per donor. Comparisons are to samples labeled CT-reference (cellular tumor, reference contributions), with coefficients 2-5 corresponding to CT-mvp (microvascular proliferation), CT-pan (pseudopalisading cells around necrosis), IT (infiltrating tumor), and LE (leading edge), respectively.

Examples

```
requireNamespace("limma")
ebout = getRefLimma() # is result of eBayes
colnames(ebout$coef)
limma::topTable(ebout,2)
```

ivyGlimpse	<i>simple app to explore image property quantifications in relation to survival and expression</i>
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Description

simple app to explore image property quantifications in relation to survival and expression

Usage

```
ivyGlimpse()
```

Value

Side effect of starting the app only.

Examples

```
if (interactive()) print(ivyGlimpse())
```

ivySE	<i>ivySE: SummarizedExperiment for IvyGAP expression data and meta- data</i>
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Description

ivySE: SummarizedExperiment for IvyGAP expression data and metadata

Usage

```
ivySE
```

Format

SummarizedExperiment instance

Details

Archive: gene_expression_matrix_2014-11-25.zip

Length	Date	Time	Name
50585	03-31-2015	13:27	columns-samples.csv
86153820	10-31-2014	14:04	fpkm_table.csv
2015	11-24-2014	18:06	README.txt
1689619	10-31-2014	13:55	rows-genes.csv
87896039	4 files		

Note

Expression data retrieved from http://glioblastoma.alleninstitute.org/api/v2/well_known_file_download/305873915

Source

processed from glioblastoma.alleninstitute.org; see Note.

Examples

```

## Not run: # how it was made
ivyFpkm = read.csv("fpkm_table.csv", stringsAsFactors=FALSE,
  check.names=FALSE)
g = read.csv("rows-genes.csv", stringsAsFactors=FALSE)
library(SummarizedExperiment)
imat = data.matrix(ivyFpkm[,-1])
ivySE = SummarizedExperiment(SimpleList(fpkm=imat))
rowData(ivySE) = g
rownames(ivySE) = g$gene_symbol
col = read.csv("columns-samples.csv", stringsAsFactors=FALSE)
rownames(col) = col$rna_well_id
stopifnot(all.equal(as.character(col$rna_well_id),
  as.character(colnames(imat))))
colData(ivySE) = DataFrame(col)
colnames(ivySE) = colnames(imat)
metadata(ivySE) = list(README=readLines("README.txt"))
metadata(ivySE)$URL = "http://glioblastoma.alleninstitute.org/static/download.html"
# metadata(ivySE)$builder = readLines("build.R")
de = read.csv("tumor_details.csv", stringsAsFactors=FALSE)
metadata(ivySE)$tumorDetails = de
subbl = read.csv("sub_block_details.csv", stringsAsFactors=FALSE)
metadata(ivySE)$subBlockDetails = subbl
bamtab = read.csv("bam.csv", stringsAsFactors=FALSE)
rownames(bamtab) = as.character(bamtab$rna_well)
bamtab[colnames(ivySE),] -> bamtreo
all.equal(rownames(bamtreo), colnames(ivySE))
colData(ivySE) = cbind(colData(ivySE), bamtreo)

## End(Not run)
data(ivySE)
names(metadata(ivySE))

```

makeGeneSets

demonstration of gene set construction for ivyGlimpse app

Description

demonstration of gene set construction for ivyGlimpse app

Usage

```
makeGeneSets()
```

Value

list of gene sets with attributes facilitating dropdown construction – attr("fullTitle") is a list of strings associated with gene set elements (named list with vectors of gene symbols constituting sets of interest)

```

List of 4
$ General: Ras-Raf-MEK-Erk/JNK signaling (26 genes)
: chr [1:26] "KRAS" "HRAS" "BRAF" "RAF1" ...
$ Glioblastoma: RTK/Ras/PI3K/AKT Signaling (17 genes)
: chr [1:17] "EGFR" "ERBB2" "PDGFRA" "MET" ...
$ General: PI3K-AKT-mTOR signaling (17 genes)
: chr [1:17] "PIK3CA" "PIK3R1" "PIK3R2" "PTEN" ...
$ Ovarian Cancer: Putative tumor-suppressor genes in epithelial ovarian cancer (16 genes)
: chr [1:16] "DIRAS3" "RASSF1" "DLEC1" "SPARC" ...
- attr(*, "fullTitle")=List of 4
..$ glioRTK : chr "Glioblastoma: RTK/Ras/PI3K/AKT Signaling (17 genes)"
..$ pi3k : chr "General: PI3K-AKT-mTOR signaling (17 genes)"
..$ ovtumsupp: chr "Ovarian Cancer: Putative tumor-suppressor genes in epithelial ovarian cancer
(16 genes)"
..$ rasraf : chr "General: Ras-Raf-MEK-Erk/JNK signaling (26 genes)"

```

Note

Should be replaced by selections from a general catalog.

Examples

```
str(makeGeneSets())
```

tumorDetails	<i>helper functions for data access</i>
--------------	---

Description

helper functions for data access

Usage

```

tumorDetails(se)

subBlockDetails(se)

vocab()

```

Arguments

se SummarizedExperiment instance, intended to work for ivySE in this package

Value

data.frames for tumorDetails, subBlockDetails and vocab

Examples

```
data(ivySE)  
dim(tumorDetails(ivySE))
```

Index

* datasets

- ivySE, [4](#)

- designOverview, [2](#)
- download.file, [3](#)
- duplicateCorrelation, [3](#)

- eBayes, [3](#)
- exprByType, [2](#)

- getRefLimma, [3](#)

- ivyGlimpse, [3](#)
- ivySE, [4](#)

- makeGeneSets, [5](#)

- nomenclat (designOverview), [2](#)

- subBlockDetails (tumorDetails), [6](#)

- tumorDetails, [6](#)

- vocab (tumorDetails), [6](#)