

Package ‘ivygapSE’

August 17, 2025

Title A SummarizedExperiment for Ivy-GAP data

Description Define a SummarizedExperiment and exploratory app for Ivy-GAP glioblastoma image, expression, and clinical data.

Version 1.31.0

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Suggests knitr, png, limma, grid, DT, randomForest, digest, testthat, rmarkdown, BiocStyle, magick, statmod, codetools

Depends R (>= 3.5.0), SummarizedExperiment

Imports shiny, survival, survminer, hwriter, plotly, ggplot2, S4Vectors, graphics, stats, utils, UpSetR

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LazyLoad yes

biocViews Transcription, Software, Visualization, Survival, GeneExpression, Sequencing

RoxygenNote 7.2.3

VignetteBuilder knitr

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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>
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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>
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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))
```

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