

# Package ‘ivygapSE’

November 15, 2024

**Title** A SummarizedExperiment for Ivy-GAP data

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

**Version** 1.28.0

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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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**License** Artistic-2.0

**LazyLoad** yes

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

**RoxygenNote** 7.2.3

**VignetteBuilder** knitr

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

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## Contents

designOverview . . . . .	2
exprByType . . . . .	2
getRefLimma . . . . .	3
ivyGlimpse . . . . .	3
ivySE . . . . .	4
makeGeneSets . . . . .	5
tumorDetails . . . . .	6
<b>Index</b>	<b>7</b>

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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()
```

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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")
```

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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)
```

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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())
```

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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](http://glioblastoma.alleninstitute.org/api/v2/well_known_file_download/305873915)

## Source

processed from [glioblastoma.alleninstitute.org](http://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))

```

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makeGeneSets

*demonstration of gene set construction for ivyGlimpse app*


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## 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())
```

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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))
```

# 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](#)