

# Package ‘ivygapSE’

April 12, 2022

**Title** A SummarizedExperiment for Ivy-GAP data  
**Description** Define a SummarizedExperiment and exploratory app for Ivy-GAP glioblastoma image, expression, and clinical data.  
**Version** 1.16.0  
**Author** Vince Carey  
**Suggests** knitr, png, limma, grid, DT, randomForest, digest, testthat, rmarkdown  
**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** 6.1.1  
**VignetteBuilder** knitr  
**git\_url** <https://git.bioconductor.org/packages/ivygapSE>  
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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))
```

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