# Package 'ivygapSE'

November 12, 2026

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

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

**Version** 1.34.0

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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

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`designOverview` *render design overview*

---

## Description

render design overview

render anatomic nomenclature

## Usage

```
designOverview()

nomenclat()
```

## Value

a rastergrob grob

## Examples

```
designOverview()
```

---

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

---

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

---

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

## 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` *ivySE: SummarizedExperiment for IvyGAP expression data and metadata*

## 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 *helper functions for data access*

---

### 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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