

Package ‘iPath’

December 14, 2024

Type Package

Title iPath pipeline for detecting perturbed pathways at individual level

Version 1.13.0

Description iPath is the Bioconductor package used for calculating personalized pathway score and test the association with survival outcomes. Abundant single-gene biomarkers have been identified and used in the clinics. However, hundreds of oncogenes or tumor-suppressor genes are involved during the process of tumorigenesis. We believe individual-level expression patterns of pre-defined pathways or gene sets are better biomarkers than single genes. In this study, we devised a computational method named iPath to identify prognostic biomarker pathways, one sample at a time. To test its utility, we conducted a pan-cancer analysis across 14 cancer types from The Cancer Genome Atlas and demonstrated that iPath is capable of identifying highly predictive biomarkers for clinical outcomes, including overall survival, tumor subtypes, and tumor stage classifications. We found that pathway-based biomarkers are more robust and effective than single genes.

License GPL-2

Encoding UTF-8

Suggests rmarkdown, BiocStyle, knitr

VignetteBuilder knitr

Imports Rcpp (>= 1.0.5), matrixStats, ggpubr, ggplot2, survminer, stats

biocViews Pathways, Software, GeneExpression, Survival

NeedsCompilation yes

SystemRequirements C++11

LinkingTo Rcpp, RcppArmadillo

Depends R (>= 4.1), mclust, BiocParallel, survival

RoxygenNote 7.1.1

BugReports <https://github.com/suke18/iPath/issues>

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| | |
|--------------|--------------------------|
| density_fall | <i>density fall plot</i> |
|--------------|--------------------------|

Description

This function allows you to express your love of cats.

Usage

```
density_fall(iES_mat, gs_str, indVec, title = TRUE)
```

Arguments

`iES_mat, gs_str` is the `iES_mat` with tumor and normal and `gs` name.
`indVec` the binary indicator for normal(0) and tumor (1) patients.
`title` boolean true or false for including the title in the `ggplot`.

Value

ggplot object containing the KM plot.

Examples

```
data(PRAD_data)
data(GSDB_example)
iES_mat = iES_cal2(prad_exprs, GSDB = GSDB_example)
density_fall(iES_mat, gs_str = "SimPathway1", indVec = prad_inds)
```

| | |
|--------------|-----------------------------------------|
| GSDB_example | <i>example gene set database (GSDB)</i> |
|--------------|-----------------------------------------|

Description

includes geneset.names, genesets.

Usage

```
data("GSDB_example")
```

Format

A list of gene set database

Source

<https://www.gsea-msigdb.org/gsea/msigdb/>

References

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3106198/>

Examples

```
data("GSDB_example")
GSDB_example$geneset.names
```

| | |
|------|-------------------------|
| GSEA | <i>GSEA calculation</i> |
|------|-------------------------|

Description

This function calculates the GSEA enrichment score.

Usage

```
GSEA(gene_list, gene_set, stats_vector)
```

Arguments

| | |
|--------------|--------------------------------------------------------|
| gene_list | is a list of genes. |
| gene_set | is a set of genes. |
| stats_vector | a vector quantify the level of genes in the gene list. |

Value

the original GSEA score.

| | |
|----------|---------------------------------|
| iES_cal2 | <i>iES calculation Function</i> |
|----------|---------------------------------|

Description

This function calculates the iES matrix which is the core of iPath.

Usage

```
iES_cal2(Y, GSDB, BPPARAM = NULL, nPro = 0)
```

Arguments

| | |
|---------|-------------------------------------|
| Y | is the expression matrix. |
| GSDB | is the gene set database. |
| BPPARAM | parameters from the BiocParallel. |
| nPro | number of processors (default = 0). |

Value

a matrix with rows corresponding to the pathways and columns corresponding to the patients.

Examples

```
data(PRAD_data)
data(GSDB_example)
iES_mat = iES_cal2(prad_exprs, GSDB = GSDB_example)
```

| | |
|----------|---------------------------------|
| iES_surv | <i>iES calculation Function</i> |
|----------|---------------------------------|

Description

This function allows to investigate on one specific pathway.

Usage

```
iES_surv(iES_mat, cli, indVec = NULL, npatsThre = 5)
```

Arguments

| | |
|-----------|-------------------------------------------------------------------------------------------------|
| iES_mat | is iES matrix with rows corresponding to the pathway and columns corresponding to the patients. |
| cli | clinical data associated to the gene expression data. |
| indVec | binary vector indicating normal (0) and tumor (1). |
| npatsThre | the threshold of number of patients for survival analysis. |

Value

a matrix of survival analysis from coxph.

Examples

```
data(PRAD_data)
data(GSDB_example)
iES_mat = iES_cal2(prad_exprs, GSDB = GSDB_example)
iES_surv(iES_mat, cli = prad_cli, indVec = prad_inds)
```

| | |
|--------------|-------------------------------------------|
| iES_survPlot | <i>iES survival for a certain pathway</i> |
|--------------|-------------------------------------------|

Description

This function allows you to express your love of cats.

Usage

```
iES_survPlot(iES_mat, cli, gs_str, indVec = NULL, npatsThre = 5, title = TRUE)
```

Arguments

`iES_mat, gs_str` is the GSDB `iES_mat` with tumor and normal and gs name.
`cli` clinical data corresponding to the expression data.
`indVec` the binary indicator for normal(0) and tumor (1) patients.
`npatsThre` the threshold of number of patients for survival analysis.
`title` boolean true or false for including the title (`gs_str`) in the ggplot.

Value

ggplot object containing the KM plot.

Examples

```

data(PRAD_data)
data(GSDB_example)
iES_mat = iES_cal2(prad_exprs, GSDB = GSDB_example)
iES_survPlot(iES_mat, cli = prad_cli, gs_str = "SimPathway1", indVec = prad_inds)
  
```

| | |
|-----------------------|---------------------------------------------------------|
| <code>prad_cli</code> | <i>simulated clinical data for PRAD cancer patients</i> |
|-----------------------|---------------------------------------------------------|

Description

`prad_cli` is the clinical data containing three variables `times`, `bcr_patient_barcode`, and `patient.vital_status`.

Usage

```
data("PRAD_data")
```

Format

An object of "matrix" class contains the clinical outcomes

Source

<https://www.cancer.gov/about-nci/organization/ccg/research/structural-genomics/tcga>

References

Kosinski M, Biecek P (2021). RTCGA: The Cancer Genome Atlas Data Integration. R package version 1.22.0, <https://rtcga.github.io/RTCGA>.

Examples

```

data("PRAD_data")
prad_cli[1:10,]
  
```

| | |
|------------|-----------------------------------------------------------|
| prad_exprs | <i>expression matrix for PRAD cancer patients in TCGA</i> |
|------------|-----------------------------------------------------------|

Description

prad_exprs is the RPKM expression matrix which belongs to "matrix" class. The data includes 102 samples about human preimplantation embryos and embryonic stem cells. It contains 19304 genes after removing genes with extreme high dropout rate.

Usage

```
data("PRAD_data")
```

Format

An object of "matrix" class contains the mRNA expressions

Source

<https://www.bioconductor.org/packages/release/bioc/html/RTCGA.html>

References

Kosinski M, Biecek P (2021). RTCGA: The Cancer Genome Atlas Data Integration. R package version 1.22.0, <https://rtcga.github.io/RTCGA>.

Examples

```
data("PRAD_data")
prad_exprs[1:10, 1:4]
```

| | |
|-----------|------------------------------------------------------------------------------|
| prad_inds | <i>normal (0) and tumor (1) classes associated with PRAD expression data</i> |
|-----------|------------------------------------------------------------------------------|

Description

normal (0) and tumor (1) classes associated with PRAD expression data.

Usage

```
data("PRAD_data")
```

Format

A character vector contains the class label

Source

<https://www.bioconductor.org/packages/release/bioc/html/RTCGA.html>

References

Kosinski M, Biecek P (2021). RTCGA: The Cancer Genome Atlas Data Integration. R package version 1.22.0, <https://rtcga.github.io/RTCGA>.

Examples

```
data("PRAD_data")
table(prad_inds)
```

| | |
|----------|-------------------------------|
| rem_data | <i>remove genes with 0 sd</i> |
|----------|-------------------------------|

Description

This function helps remove non-informative genes.

Usage

```
rem_data(Y)
```

Arguments

Y is the expression matrix.

Value

a processed matrix

| | |
|---------------|------------------------------------------------------------|
| setUp_BPPARAM | <i>set up for the parallel computing for biocParallel.</i> |
|---------------|------------------------------------------------------------|

Description

This function sets up the environment for parallel computing.

Usage

```
setUp_BPPARAM(nproc = 0, BPPARAM = NULL)
```

Arguments

| | |
|---------|--------------------------|
| nproc | number of processors |
| BPPARAM | bpparameter from bpparam |

Value

BAPPARAM settings

| | |
|------------|------------------------|
| water_fall | <i>water fall plot</i> |
|------------|------------------------|

Description

This function allows you to express your love of cats.

Usage

```
water_fall(iES_mat, gs_str, indVec, title = TRUE)
```

Arguments

`iES_mat, gs_str` is the `iES_mat` with tumor and normal and `gs` name.
`indVec` the binary indicator for normal(0) and tumor (1) patients.
`title` boolean true or false for including the title (`gs_str`) in the `ggplot`.

Value

`ggplot` object containing the KM plot.

Examples

```
data(PRAD_data)
data(GSDB_example)
iES_mat = iES_cal2(prad_exprs, GSDB = GSDB_example)
water_fall(iES_mat, gs_str = "SimPathway1", indVec = prad_inds)
```

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