Package 'iPath'

November 12, 2026

Type Package

Title iPath pipeline for detecting perturbed pathways at individual level

Version 1.18.0

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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Contents

density_fall . . . 2
GSDB_example . . . 3
GSEA . . . 4
iES_cal2 . . . 4
iES_surv . . . 5
iES_survPlot . . . 5
prad_cli . . . 6
prad_exprs . . . 7
prad_inds . . . 7
rem_data . . . 8
setUp_BPPARAM . . . 8
water_fall . . . 9

Index **10**

`density_fall` *density fall plot*

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 *example gene set database (GSDB)*

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 *GSEA calculation*

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 orignial GSEA score.

iES_cal2 *iES calculation Function*

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 *iES calculation Function*

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 *iES survival for a certain pathway*

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)
```

---

prad_cli *simulated clinical data for PRAD cancer patients*

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 *expression matrix for PRAD cancer patients in TCGA*

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

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` *remove genes with 0 sd*

Description

This function helps remove non-informative genes.

Usage

```
rem_data(Y)
```

Arguments

`Y`	is the expression matrix.

Value

a processed matrix

`setUp_BPPARAM` *set up for the parallel computing for biocParallel.*

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` *water fall plot*

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)
```

Index

∗ **analysis**
iES_surv, 5
∗ **and**
density_fall, 2
iES_surv, 5
iES_survPlot, 5
water_fall, 9
∗ **calculatioin.**
iES_cal2, 4
∗ **datasets**
GSDB_example, 3
prad_cli, 6
prad_exprs, 7
prad_inds, 7
∗ **densityfall**
density_fall, 2
iES_survPlot, 5
∗ **for**
density_fall, 2
iES_surv, 5
iES_survPlot, 5
water_fall, 9
∗ **groups**
iES_surv, 5
∗ **iES**
iES_cal2, 4
∗ **iPath**
iES_surv, 5
∗ **normal-like.**
iES_surv, 5
∗ **normal**
density_fall, 2
iES_survPlot, 5
water_fall, 9
∗ **of**
iES_surv, 5
∗ **patients:**
iES_surv, 5
∗ **perturbed**
iES_surv, 5
∗ **plot**
density_fall, 2
iES_survPlot, 5
water_fall, 9
∗ **sample.**
density_fall, 2
∗ **sample**
iES_survPlot, 5
water_fall, 9
∗ **statistics**
iES_cal2, 4
∗ **survival**
iES_surv, 5
∗ **tumor**
density_fall, 2
iES_survPlot, 5
water_fall, 9
∗ **two**
iES_surv, 5
∗ **waterfall**
water_fall, 9

density_fall, 2

GSDB_example, 3
GSEA, 4

iES_cal2, 4
iES_surv, 5
iES_survPlot, 5

prad_cli, 6
prad_exprs, 7
prad_inds, 7

rem_data, 8

setUp_BPPARAM, 8

water_fall, 9