Package ‘iPath’

May 17, 2024

Type Package

Title iPath pipeline for detecting perturbed pathways at individual level

Version 1.10.0

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 predefined 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
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.
*GSDB_example*

**Value**

ggplot object containing the KM plot.

**Examples**

```r
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**

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

**Format**

A list of gene set database

**Source**

[https://www.gsea-msigdb.org/gsea/msigdb/](https://www.gsea-msigdb.org/gsea/msigdb/)

**References**

[https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3106198/](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3106198/)

**Examples**

```r
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

```r
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

```r
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


Examples

```r
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**


**References**


**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


References


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
water_fall

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

```r
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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