Package ‘survival666’

October 14, 2022

Version 0.5

Title Eliminate the Influence of Co-Expression Genes on Target Genes

Description Functions can be used for batch survival analysis,
but not only for it. Most importantly, it can verify any
P-value calculated according to the gene expression level and
eliminate the influence of co-expression genes.

Depends R (>= 3.3)

Imports survival, survminer, utils, stats, ggplot2

Suggests tidyverse, magrittr, testthat (>= 3.0.0)

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Author Honglu Zhang [aut, cre, cph] (<https://orcid.org/0000-0002-4844-5004>),
Qi Zhang [ctb] (<https://orcid.org/0000-0012-0199-6968>),
Xiaodong Pei [ctb] (<https://orcid.org/0000-0002-7897-4505>),
Jiawen Guo [ctb] (<https://orcid.org/0000-0002-0331-5038>),
Enpeng Liu [ctb] (<https://orcid.org/0000-0002-5549-957X>)

Maintainer Honglu Zhang <15738817548@163.com>

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R topics documented:

`clinic` *Clinical records of overall survival*

Description

This is a document that records the overall survival rate.

Usage

```
clinic
```

Format

An object of class `data.frame` with 454 rows and 3 columns.

Source

https://xenabrowser.net/datapages/

`super_survival` *Batch survival analysis*

Description

The super_survival is the frist function of package survival666. You can use the function to perform batch operations on the gene expression matrix to obtain the survival analysis of the entire transcriptome

Usage

```
super_survival(exp, time, status, p = 1e-04, title = "survival_rank", path)
```

Arguments

`exp` Gene expression matrix .We need to use the count matrix here.Note that symbol is required for the column name and sample for the row name.

`time` Time data for survival analysis.You need to make sure the sample as the row name is consistent with the gene expression matrix

`status` living status of patient in survival analysis,You need to make sure the sample as the row name is consistent with the gene expression matrix too.

`p` Full in the minimum significance you can accpet here.It depend on your need, but the number should not be too big,too broad results are meaningless.

`title` Give a name to the file to be output

`path` Set a save path for the output file

Examples

```
## Not run: super_survival(exp=survivaldata,
time = clinic[,3],
status = clinic[,2],
p = 0.0001,
title = 'survival_rank',
path = '/yourdir/')
## End(Not run)
```

survivaldata *A filtered transcriptome gene expression matrix.*

Description

The expression matrix was manipulated to contain less than two thousand genes. Use the symbol as the column name and the sample number as the row name. The reason of this is that to save space.It is best to use the complete transcriptome as the expression matrix when using the fundtion super_survival.

Usage

```
survivaldata
```

Format

An object of class `data.frame` with 454 rows and 1712 columns.

Source

https://xenabrowser.net/datapages/

survivalrank *Rank the significance of survival analysis*

Description

This data file is actually the output of super_survival function. The significance P value of survival analysis for each gene in survivaldata matrix were recorded

Usage

```
survivalrank
```

Format

An object of class `data.frame` with 1712 rows and 9 columns.

`survival_pie` *Visualize the factors that influence survival analysis*

Description

The checkout_survival() is the third function of survival666. We use the function to visualize the co-expression interference of a specific gene in survival analysis.

Usage

```
survival_pie(exp, survivalrank, target, pcol = 4, symbolcol = 1, path)
```

Arguments

`exp` This is a transcriptome count matrix,Note that the matrix requires symbol as column name and sample as row name

`survivalrank` This is the result calculated by the frist function in the survival666 package. However,that does not prevent you from getting results that you could get using other methods,as long as three conditions are met. Frist,you need to calculate the p value based on the expression of a particular phenotype and the level of gene expresion Second,your results must be large enough,preferably for the entire transcriptome,otherwise filtering accuracy will be reduced Finally,you need to eliminate genes that are not significant enough,and if you are using a regular PC,it is recommended to have no more than 2000 lines

`target` target gene symbols

`pcol` Digtal vector,represents the column of P value in survivalrank

`symbolcol` Digtal vector,represents the column of symbol in survivalrank

`path` Path to output file,do not omit ’/’,example:’d:/file/’.

See Also

survival_pie `super_survival`

Examples

```
## Not run: survival_pie(exp=survivaldata,
survivalrank=survivalrank[1:300,],
target=”EAF2”,
pcol=4,
symbolcol=1,
path='/yourdir/')
## End(Not run)
```

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