Package ‘bossR’

January 15, 2024

Title Biomarker Optimal Segmentation System

Version 1.0.4

Description The Biomarker Optimal Segmentation System R package, 'bossR', is designed for precision medicine, helping to identify individual traits using biomarkers. It focuses on determining the most effective cutoff value for a continuous biomarker, which is crucial for categorizing patients into two groups with distinctly different clinical outcomes. The package simultaneously finds the optimal cutoff from given candidate values and tests its significance. Simulation studies demonstrate that 'bossR' offers statistical power and false positive control non-inferior to the permutation approach (considered the gold standard in this field), while being hundreds of times faster.

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Encoding UTF-8

RoxygenNote 7.2.3

Imports mvtnorm,survival,stats

Depends R (>= 2.10),

LazyData true

NeedsCompilation no

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R topics documented:

`getbeta` *Get regression coefficient*

Description

Computes the regression coefficient of certain regression based on certain cutoff.

Usage

```
getbeta(data, point, type = 2)
```

Arguments

`data`	A data frame which contains 3 columns for cox regression : survival time, censor status, Biomarker values. 2 columns for linear regression : Y, X.
`point`	A number to cut biomarker or X.
`type`	A number; if =1, will perform linear regression; if =2(default) will perform cox regression.

Value

An object with 3 class: Coefficient beta, number of samples of which the biomarker is greater than the point, standard error of coefficient estimation.

`getOC` *Select Optimal cutoff for a biomarker*

Description

Given a set of data including survival time ,censor status and Biomarker values, return the Optimal cutoff for the biomarker.

Usage

```
getOC(data, cutoff, type = 2)
```

Arguments

`data`	A data frame which contains 3 columns for cox regression : survival time, censor status, Biomarker values. 2 columns for linear regression : Y, X.
`cutoff`	Numeric vector of candidate cutoffs.
`type`	A number; if =1, will perform linear regression;if =2(default) will perform cox regerssion.

Value

Optimal cutoff for the biomarker, the FWER of the model

References

BOSS - Biomarker Optimal Segmentation System

Examples

```
cutoff=c(56,112,167,223,278,334,389,445)
    data(myGene)
    getOC(data=myGene,cutoff)
```

`getpvalue` *Computes the distribution function of the multivariate normal distribution*

Description

Computes the distribution function of the multivariate normal distribution.

Usage

```
getpvalue(threshold, mu, n, Sigma)
```

Arguments

`threshold`	A number.
`mu`	The mean vector of length n.
`n`	A number indicates dimension.
`Sigma`	The correlation matrix of dimension n.

Value

The evaluated distribution function

`myGene` *clinical dataset*

Description

This data set gives the expression levels of gene data, overall survival time, and censoring status from 500 lung adenocarcinoma cases.

Usage

```
myGene
```

Format

A dataframe containing 500 observations of 3 variables.

Source

raw survival data come from https://tau.cmmt.ubc.ca/cSurvival/project_data/TCGA-LUAD/df_survival_o.csv and raw gene expression data come from https://tau.cmmt.ubc.ca/cSurvival/project_data/TCGA-LUAD/df_gene.csv

References

Xuanjin Cheng, Yongxing Liu, Jiahe Wang, Yujie Chen, Andrew Gordon Robertson, Xuekui Zhang, Steven J M Jones, and Stefan Taubert. (2022) *cSurvival: a web resource for biomarker interactions in cancer outcomes and in cell lines*. Briefings in Bioinformatics.

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