Package ‘L Cox’

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Type Package

Title A Tool for Selecting Genes Related to Survival Outcomes using Longitudinal Gene Expression Data

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Description Longitudinal genomics data and survival outcome are common in biomedical studies. It is of great interest to select genes related to the survival outcome. L Cox is a computationally efficient tool for selecting genes related to the survival outcome using the longitudinal genomics data. L Cox is powerful to detect different forms of dependence between the longitudinal biomarkers and the survival outcome.

License GPL-2

LazyData TRUE

Depends R (>= 3.4.0), fdapace (>= 0.3.0), survival (>= 2.41-3)

RoxygenNote 6.0.1

NeedsCompilation no

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Hypothesis Testing for longitudinal gene profiles and the survival outcome.

Description

LCox is a function that performs hypothesis tests of the associations between longitudinal gene profiles and the survival outcome.

Usage

```
LCox(data = NULL, data.id = NULL, geneID = 3:4, varID = NULL, 
     PLOT = FALSE, optns = list(dataType = "Sparse", FVEthreshold = 0.95, 
                              methodBwMu = "CV"))
```

Arguments

- **data**: A data frame contains longitudinal gene expression data. This data frame must contain a column of ID to identify each patient and a column of years to indicate the follow-up time for each data point.
- **data.id**: A data frame contains the survival outcome and important covariates. This data frame must contain a column of ID to identify each patient, a column of fstat to indicate the censoring time, and a column of ftime to indicate the survival time.
- **geneID**: A vector of integers indicates the column numbers in data for the genes of interest.
- **varID**: A vector of integers indicates the column numbers in data.id for the important confounding covariates that need to be included.
- **PLOT**: A logical value indicates whether a graph showing the fitted lines is desired. If TRUE, a figure "fitted.pdf" will be saved to the current working directory.
- **optns**: A list of options control parameters for the FPCA model.

Value

returns a matrix with one column being the p values and the other column being the number of eigenfunctions (K).

References

**Examples**

```r
data.list = simudata()
data = data.list$data
data.id = data.list$data.id
res = LCox(data = data, data.id = data.id, geneID = 3:4)
res = LCox(data = data, data.id = data.id, geneID = 3:4, varID = 4)
res = LCox(data = data, data.id = data.id, geneID = 3:4, plot=TRUE)
```

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**simudata**  
*Function to Simulate Testing Data*

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**Description**

`simudata` is a function that generates a simulated data.

**Usage**

```r
simudata(n = 50, nf = 5)
```

**Arguments**

- **n**  
  Total number of patients.

- **nf**  
  The average number of follow-up visits per patient.

**Value**

returns a list with following objects.

- **data**  
  Longitudinal gene expression data.

- **data.id**  
  Survival data with important covariates.

**References**


**Examples**

```r
data.list = simudata()
```
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