Package 'LCox'

July 17, 2017

Type Package

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

Version 0.1.0

Author Jiehuan Sun [aut, cre], Jose D. Herazo-Maya [aut], Jane-Ling Wang [aut], Naftali Kaminski [aut], and Hongyu Zhao [aut]

Maintainer Jiehuan Sun <jiehuan.sun@yale.edu>

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. LCox is a computationally efficient tool for selecting genes related to the survival outcome using the longitudinal genomics data. LCox 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

Repository CRAN

Date/Publication 2017-07-17 17:10:39 UTC

R topics documented:

LCox   *Hypothesis Testing for longitudinal gene profiles and the survival out-come.*

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

LCox: A tool for selecting genes related to survival outcomes using longitudinal gene expression data. Jiehuan Sun, Jose D. Herazo-Maya, Jane-Ling Wang, Naftali Kaminski, and Hongyu Zhao.

Examples

```
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)
```

---

simudata   *Function to Simulate Testing Data*

Description

simudata is a function that generates a simulated data.

Usage

```
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

LCox: A tool for selecting genes related to survival outcomes using longitudinal gene expression data. Jiehuan Sun, Jose D. Herazo-Maya, Jane-Ling Wang, Naftali Kaminski, and Hongyu Zhao.

Examples

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

Index