Package 'exsurv'

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Title Conduct the survival analysis of the censored data.

Version 1.0.0

Description To conduct the survival analysis of the censored data.
It mainly aims to evaluate the associations between exposure
factors and health outcome, as well as predicting the survival probability.

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R topics documented:

FindCovaSurv *Find covariates*

Description

Find covariates

Usage

```
FindCovaSurv(PID, OutPath = "default", TimeY, EventY, VarsC_Prior = "default",
    VarsC_Fixed = NULL, Method = "single.factor", Thr = 0.1)
```

Arguments

PID	chr. Program ID. It must be the same with the PID generated by ExpoCros
OutPath	chr. Output file directory, e.g. "D:/test". It should be noted that the slash symbol is "/", not "\". If "default", the current working directory will be set.
TimeY	chr. Outcome variable of survival time used for modelling. Only one variable can be entered.
EventY	chr. Outcome variable of status used for modelling. Only one variable can be entered.
VarsC_Prior	chr. Potential covariates needing further statistical test. The default value is all covariate variables listed in the data file.
VarsC_Fixed	chr. Covariate variables fixed in the model by users.
Method	chr. Methods for screening the covariates, including two options, i.e. "single.factor" and "two.stage".
Thr	num. Threshold of the P-value for screening the covariates. It is ranging 0.05-0.25. The default value is 0.1.

Value

A list containing the selected covariates.

Author(s)

Changxin Lan, Bin Wang(corresponding author)

Examples

```
res <- InitSurv()
   res1 = LoadSurv(PID = res$PID, UseExample = "example#1")
   res3 = FindCovaSurv(PID=res$PID, TimeY = "Y1", EventY= 'Y2',
   VarsC_Prior = "default", VarsC_Fixed = NULL, Method = "single.factor", Thr = 0.1)
   FuncExit(PID = res$PID)
```

FuncExit *End the module analysis*

Description

End the module analysis

Usage

```
FuncExit(PID)
```

Arguments

PID	chr. Program ID. It should be the same with the PID generated by initial functions.

Value

Exit status

Author(s)

Bin Wang (corresponding author)

Examples

```
res = InitSurv()
   FuncExit(PID = res$PID)
```

InitSurv *Initialize ExpoSurvival module*

Description

Initialize ExpoSurvival module analysis. It can generate an R6 class object integrating all the analysis information.

Usage

```
InitSurv()
```

Details

InitSurv uses R6 package to generate an R6 class object where parameters to be used for the following mediation module program are initialized and save in that object. All executed function codes in the ExpoSurvival packaged will be recorded in the form of log text in that object. Furthermore, a program ID (i.e., PID) is randomly created for the users to identify their own program.

Value

An R6 class object.

Author(s)

Changxin Lan, Bin Wang(corresponding author)

Examples

```
res <- InitSurv()
```

LoadSurv *Load data file for Survival module*

Description

Load data file for Survival module

Usage

```
LoadSurv( PID, UseExample = "default", DataPath=NULL,VocaPath=NULL)
```

Arguments

PID	chr. Program ID. It must be the same with the PID generated by InitSurv.
UseExample	chr. Method of uploading data. If "default", user should upload their own data files, or use "example#1" provided by this module.
DataPath	chr. Input data file directory, e.g. "D:/test/eg_Surv_data.xlsx". It should be noted that the slash symbol is "/", not "\".
VocaPath	chr. Input vocabulary file directory, e.g. "D:/test/eg_Surv_voca.xlsx". It should be noted that the slash symbol is "/", not "\".

Details

LoadSurv function loads the data file and the vocabulary file into the R6 object that InitSurv created. Noted that there are several data format requirments for the data and vocabulary file. For data file,the first three columns should be named as "SampleID", "SubjectID", and "Group", respectively. For the "Group" variable, only two values can be used, i.e. "train" and "test". If there is no data for test, all values should be set as "train". For outcome variables, their initials must be set as "Y" and serialized by adding Arabic numerals if needed, e.g., Y1, Y2, Y3. In this module, the survival time (Y1) and status (Y2) must be provided.For exposure variables, their initials must be set as "X" and serialized by adding Arabic numerals if needed, e.g., X1, X2, X3. For covariate variables, their initials must be set as "C" and serialized by adding Arabic numerals if needed, e.g., C1, C2, C3. It should be noted the covariates are not required if users don't have. For vocabulary file, the first two columns must be named as "SerialNo" and "FullName", respectively. The list of SerialNo of outcomes, exposure, and covariates should be the same with the column names of "Data file". The list of the FullName is prepared as users' like.

Value

An R6 class object containing the input data and vocabulary file.

Author(s)

Changxin Lan, Bin Wang(corresponding author)

Examples

```
res <- InitSurv()
   res1 <- LoadSurv(PID = res$PID, UseExample = "example#1", DataPath = NULL,
   VocaPath = NULL)
```

SurvAsso *Association analysis*

Description

Association analysis for survival data

Usage

```
SurvAsso(PID, OutPath = "default",
    TimeY, EventY,VarsX='all.x',VarsN = "single.factor",VarsSel = T,
    IncCova = T)
```

Arguments

PID	chr. Program ID. It must be the same with the PID generated by InitSurv()
OutPath	chr. Output file directory, e.g. "D:/test". It should be noted that the slash symbol is "/", not "\". If "default", the current working directory will be set.
TimeY	chr. Outcome variable of survival time used for modelling. Only one variable can be entered.
EventY	chr. Outcome variable of status used for modelling. Only one variable can be entered.
VarsX	Exposure variable used for modeling. The default option is "all.x" (All exposure variables are included). Users can also choose available variables. It should be noted that there is fixed format for the entering characters separated with comma and without space, e.g., "X1,X2,X3"
VarsN	chr. Choose the single factor or multiple factor model. Available options include "single.factor" and "multiple.factor"
VarsSel	lgl. T (or TRUE) and F (or FALSE). Whether to select the significant variable for the final model. Available options includes T and F
IncCova	lgl. T (or TRUE) and F (or FALSE). Whether to include the covariate selected in the function "FindCovaSurv"

Value

A list containing the association analysis results.

Author(s)

Changxin Lan, Bin Wang(corresponding author)

Examples

```
res <- InitSurv()
   res1 = LoadSurv(PID = res$PID, UseExample = "example#1")
   res3 = FindCovaSurv(PID=res$PID, TimeY = "Y1", EventY= 'Y2',
   VarsC_Prior = "default", VarsC_Fixed = NULL, Method = "single.factor", Thr = 0.1)
   res4 = SurvAsso(PID=res$PID, TimeY = "Y1", EventY= 'Y2',VarsX='all.x',
   VarsN="single.factor",VarsSel=T,IncCova=T)
   FuncExit(PID = res$PID)
```

SurvPred *Build prediction models*

Description

Build prediction models

Usage

```
SurvPred(PID,OutPath = "default",TimeY,EventY,VarsX = "all.x",
    IncCova = T,RsmpMethod = "cv",Folds = 3,Ratio = 0.667,Repeats = 3)
```

Arguments

PID	chr. Program ID. It must be the same with the PID generated by InitSurv()
OutPath	chr. Output file directory, e.g. "D:/test". It should be noted that the slash symbol is "/", not "\". If "default", the current working directory will be set.
TimeY	chr. Outcome variable of survival time used for modelling. Only one variable can be entered.
EventY	chr. Outcome variable of status used for modelling. Only one variable can be entered.
VarsX	chr. Exposure variable used for modeling. The default option is "all.x" (All exposure variables are included). Users can also choose available variables. It should be noted that there is fixed format for the entering characters separated with comma and without space, e.g., "X1,X2,X3"
IncCova	lgl. Whether to include the covariate selected in the function of "FindCovaSurv". Available options include T (or TRUE) and F (or FALSE).
RsmpMethod	chr. Three resampling methods options for internal validation, including "cv" (i.e.,Cross validation) , "bootstrap", and "holdout".
Folds	num. Folds of Cross-validation resampling. It is ranging 2-10.
Ratio	num. Ratio of Bootstrap resampling. It is ranging 0.4-0.9.
Repeats	num. Number of Bootstrap resampling. It is ranging 2-20.

Value

A list containing the prediction performance evaluation.

Author(s)

Changxin Lan, Bin Wang(corresponding author)

Examples

```
res <- InitSurv()
   res1 = LoadSurv(PID = res$PID, UseExample = "example#1")
   res3 = FindCovaSurv(PID=res$PID, TimeY = "Y1", EventY= 'Y2',
   VarsC_Prior = "default", VarsC_Fixed = NULL, Method = "single.factor", Thr = 0.1)
   res4 = SurvPred(PID=res$PID, TimeY = "Y1", EventY= 'Y2',VarsX='all.x',
   IncCova=T,RsmpMethod="cv",Folds=3,Ratio=0.667,Repeats=3)
   FuncExit(PID = res$PID)
```

`VizSurvAsso` *Visualize association analysis*

Description

Visualize association analysis

Usage

```
VizSurvAsso(PID, OutPath = "default",VarsN = "single.factor",
   Layout = "volcano",Brightness = "light",Palette = "default1",ColorFor= "p.value",SizeFor= "p.val
```

Arguments

`PID`	chr. Program ID. It must be the same with the PID generated by InitSurv()
`OutPath`	chr. Output file directory, e.g. "D:/test". It should be noted that the slash symbol is "/", not "\". If "default", the current working directory will be set.
`VarsN`	chr. Choose the single factor or multiple factor model. Available options include "single.factor" and "multiple.factor"
`Layout`	chr. Visualization layout. Available options include "forest" and "volcano".
`Brightness`	chr. Visualization brightness. Available options include "light" and "dark".
`Palette`	chr. Visualization palette. Available options include "default1", "default2" and several journal preference styles (i.e., "cell", "nature", "science", "lancet", "nejm", and "jama").
`ColorFor`	chr. Volcano plot dot color. Available options include "p.value" and "hr".
`SizeFor`	chr. Volcano plot dot size. Available options include "p.value" and "hr".

Value

A list containing the results' plot.

Author(s)

Changxin Lan, Ning Gao, Bin Wang(corresponding author)

Examples

```
res <- InitSurv()
   res1 = LoadSurv(PID = res$PID, UseExample = "example#1")
   res3 = FindCovaSurv(PID=res$PID, TimeY = "Y1", EventY= 'Y2',
   VarsC_Prior = "default", VarsC_Fixed = NULL, Method = "single.factor", Thr = 0.1)
   res4 = SurvAsso(PID=res$PID, TimeY = "Y1", EventY= 'Y2',VarsX='all.x',
   VarsN="single.factor",VarsSel=T,IncCova=T)
  res5 = VizSurvAsso(PID=res$PID,VarsN="single.factor",Layout="volcano",Brightness= "light",
   Palette = "default1",ColorFor= "p.value",SizeFor= "p.value")
   FuncExit(PID = res$PID)
```

`VizSurvCompGroup` *Compare the survival curves of two groups*

Description

Compare the survival curves of two groups

Usage

```
VizSurvCompGroup(PID,OutPath = "default",TimeY,EventY,
   VarsG,Model='km',VarsAdj,AdjMethod='average',Brightness = "light",Palette = "default1")
```

Arguments

`PID`	chr. Program ID. It must be the same with the PID generated by InitSurv()
`OutPath`	chr. Output file directory, e.g. "D:/test". It should be noted that the slash symbol is "/", not "\". If "default", the current working directory will be set.
`TimeY`	chr. Outcome variable of survival time used for modelling. Only one variable can be entered.
`EventY`	chr. Outcome variable of status used for modelling. Only one variable can be entered.
`VarsG`	chr. Grouping variable, must be a binary variable.
`Model`	chr. Methods to depict the survival curve. Options include 'km' (Kaplan-Meier estimate) and "coxph" (Cox proportional hazards regression mode).
`VarsAdj`	If you choose the cox model, co-variables used for modelling. It should be noted that there is fixed format for the entering characters separated with comma and without space, e.g., X1,X2,X3.
`AdjMethod`	If you choose the cox model, method for adjusting model, include: "average","single","margin" and "conditional".
`Brightness`	chr. Visualization brightness. Available options include "light" and "dark".
`Palette`	chr. Visualization palette. Available options include "default1", "default2" and several journal preference styles (i.e., "cell", "nature", "science", "lancet", "nejm", and "jama").

Value

A list containing the results' plot.

Author(s)

Changxin Lan, Ning Gao, Bin Wang(corresponding author)

Examples

```
res <- InitSurv()
   res1 = LoadSurv(PID = res$PID, UseExample = "example#1")
   res6 = VizSurvCompGroup(PID=res$PID,TimeY="Y1",EventY="Y2",VarsG="C3",
   Model="km",Brightness="light",Palette='default1')
   FuncExit(PID = res$PID)
```

VizSurvPred *Visualize the prediction performance*

Description

Visualize the prediction performance

Usage

```
VizSurvPred(PID,OutPath = "default",Layout = "curve",
    Brightness = "light",Palette = "default1")
```

Arguments

PID	chr. Program ID. It must be the same with the PID generated by InitSurv()
OutPath	chr. Output file directory, e.g. "D:/test". It should be noted that the slash symbol is "/", not "\". If "default", the current working directory will be set.
Layout	chr. Visualization layout. Available options include "curve" , "bar" and 'all'.
Brightness	chr. Visualization brightness. Available options include "light" and "dark".
Palette	chr. Visualization palette. Available options include "default1", "default2" and several journal preference styles (i.e., "cell", "nature", "science", "lancet", "nejm", and "jama").

Value

A list containing the results' plot.

Author(s)

Changxin Lan, Ning Gao, Bin Wang(corresponding author)

Examples

```
res <- InitSurv()
   res1 = LoadSurv(PID = res$PID, UseExample = "example#1")
   res3 = FindCovaSurv(PID=res$PID, TimeY = "Y1", EventY= 'Y2',
   VarsC_Prior = "default", VarsC_Fixed = NULL, Method = "single.factor", Thr = 0.1)
   res4 = SurvPred(PID=res$PID, TimeY = "Y1", EventY= 'Y2',VarsX='all.x',
   IncCova=T,RsmpMethod="cv",Folds=3,Ratio=0.667,Repeats=3)
   res5 = VizSurvPred(PID=res$PID,Layout="curve",Brightness="light",Palette='default1')
   FuncExit(PID = res$PID)
```

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