

Package ‘excros’

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Title It was designed to analyze the cross-sectional data from
exposome-wide association study (EWAS)

Version 1.0.0

Description It was designed to analyze the cross-sectional data from exposome-
wide association study (EWAS).

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CrosAsso

*Association analysis***Description**

Association analysis for cross-sectional data.

Usage

```
CrosAsso(PID, OutPath = "default", EpiDesign = "cross.sectional",
  VarsY, VarsX = "all.cx", VarsN = "single.factor", VarsSel = FALSE, VarsSelThr = 0.1,
  IncCova = TRUE, Family, RepMsr = FALSE, Corstr = "ar1")
```

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. |
| EpiDesign | chr. Epidemiological design of the study, including "cohort" "case.control" and "cross.sectional". It doesn't affect the modeling, but the format of the output file. For the three designs, the effect values are usually indicated by RR (relative risk) of cohort, OR (odds ratio) of case-control, and beta value of cross-sectional. |
| VarsY | chr. Outcome variable used for modeling. 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" |
| 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. |
| VarsSelThr | num. If "VarsSel" = TRUE, provide the selection threshold of the P-value. Three value can be chosen, i.e. 0.05, 0.1, and 0.2. |
| IncCova | lgl. T (or TRUE) and F (or FALSE). Whether to include the covariate selected in the function "FindCovaCros" |
| Family | chr. The link function for the regression model according the data type of outcomes, including "gaussian" for continuous variable, "binomial" for binary variable, and "poisson" for counting variable |
| RepMsr | lgl. T (or TRUE) and F (or FALSE). Whether existing repeated measurement of the subjects. Available options. |
| Corstr | chr. If "RepMsr" = TRUE, the generalized estimating equations (GEE) will be used. For GEE, three correlation structure options are "exchangeable" "ar1" "unstructured". |

Value

A list containing the association analysis results.

Author(s)

Bin Wang

Examples

```
res <- InitCros()
  res1 = LoadCros(PID = res$PID, UseExample = "example#1")
  res2 = CrosAsso(PID=res$PID, EpiDesign = "cohort",
    VarsY = "Y1", VarsX = "X5,X6,X7,X8,X9,X10,X11", VarsN = "single.factor",
    VarsSel = FALSE, VarsSelThr = 0.1, IncCova = TRUE, Family = "gaussian",
    RepMsr = FALSE, Corstr = "ar1")
  FuncExit(PID = res$PID)
```

CrosPred

Build prediction models

Description

Build prediction models

Usage

```
CrosPred(PID, OutPath = "default", VarsY, VarsX = "all.x",
  PredType = "response", VarsSel = FALSE, VarsSelThr = 0.1, IncCova = TRUE,
  RsmplMethod = "cv", Folds = 5, Ratio = 0.667, Repeats = 5)
```

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. |
| VarsY | chr. Outcome variable used for modeling. 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" |
| PredType | chr. Prediction type of the outcome variable, including "response" for the actual values and "prob" for outcome with binary variable. |
| VarsSel | lgl. Whether to select the significant variable for the final model. Available options include T (or TRUE) and F (or FALSE). |
| VarsSelThr | num. If "VarsSel" = TRUE, provide the selection threshold of the P-value. Three value can be chosen, i.e. 0.05, 0.1, and 0.2. |

| | |
|-------------|---|
| IncCova | lgl. Whether to include the covariate selected in the function of "FindCovaCros". Available options include T (or TRUE) and F (or FALSE). |
| RsmplMethod | chr. Four resampling methods options for internal validation, including "cv" (i.e., Cross validation), "loo" (i.e., leave-one-out), "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)

Bin Wang

Examples

```
res <- InitCros()
res1 = LoadCros(PID = res$PID, UseExample = "example#1")
#res2 = TransScale(PID=res$PID, Group=TRUE, Vars="all.x", Method="normal")
#res3 = CrosPred(PID=res$PID, VarsY = "Y1", VarsX = "X5,X6,X7,X8,X9,X10,X11",
#PredType = "response", VarsSel = FALSE, VarsSelThr = 0.1, IncCova = FALSE,
#RsmplMethod = "cv", Folds = 5, Ratio = 0.667, Repeats = 5)
FuncExit(PID = res$PID)
```

FindCovaCros

Find covariates

Description

Find covariates

Usage

```
FindCovaCros(PID, OutPath = "default", VarsY, 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. |
| VarsY | chr. Outcome variable used for modeling. 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)

Bin Wang

Examples

```
res <- InitCros()
res1 = LoadCros(PID = res$PID, UseExample = "example#1")
res2 = FindCovaCros(PID=res$PID, VarsY = "Y1",
  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 must be the same with the PID generated by any initial functions. |
|-----|---|

Value

Exit status

Author(s)

Bin Wang (corresponding author)

Examples

```
res = InitCros()
res1 = LoadCros(PID = res$PID, UseExample = "example#1")
FuncExit(PID = res$PID)
```

InitCros*Initialize ExpoCros module*

Description

Initialize ExpoCros module analysis. It can generate an R6 class object.

Usage

```
InitCros()
```

Details

ExpoCros module was designed to analyze the cross-sectional data from exposome-wide association study (EWAS). This data structure can be obtained from the epidemiological designs of cross-section, case-control, and cohort.

Value

An R6 class object.

Author(s)

Bin Wang

Examples

```
res <- InitCros()
FuncExit(PID = res$PID)
```

| | |
|----------|---|
| LoadCros | <i>Load data file for ExpoCros module</i> |
|----------|---|

Description

Load data file for ExpoCros module.

Usage

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

Arguments

| | |
|------------|--|
| PID | chr. Program ID. It must be the same with the PID generated by ExpoCros |
| 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 directory of data file, e.g. "D:/test/eg_data_expocros.xlsx". It should be noted that the slash symbol is "/", not "\". |
| VocaPath | chr. Input directory of vocabulary file, e.g. "D:/test/eg_voca_expocros.xlsx". It should be noted that the slash symbol is "/", not "\". |

Value

An R6 class object containing the input data.

Author(s)

Bin Wang

Examples

```
res <- InitCros()
res1 = LoadCros(PID = res$PID, UseExample = "example#1")
FuncExit(PID = res$PID)
```

| | |
|-------------|---------------------------------------|
| VizCrosAsso | <i>Visualize association analysis</i> |
|-------------|---------------------------------------|

Description

Visualize association analysis

Usage

```
VizCrosAsso(PID, OutPath = "default", VarsN = "single.factor",
  Layout = "volcano", Brightness = "light", Palette = "default1")
```

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. |
| 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). |

Value

An R6 class object containing the results' plot.

Author(s)

Bin Wang

Examples

```
res <- InitCros()
res1 = LoadCros(PID = res$PID, UseExample = "example#1")
res2 = CrosAsso(PID=res$PID, EpiDesign = "cohort", VarsY = "Y1",
VarsX = "X5,X6,X7,X8,X9,X10,X11", VarsN = "single.factor",
VarsSel = FALSE, VarsSelThr = 0.1, IncCova = TRUE, Family = "gaussian",
RepMsr = FALSE,Corstr = "ar1")
res3 = VizCrosAsso(PID=res$PID,VarsN="single.factor", Layout = "forest",
Brightness = "dark",Palette = "default1")
FuncExit(PID = res$PID)
```

| | |
|-------------|---|
| VizCrosPred | <i>Visualize the prediction performance</i> |
|-------------|---|

Description

Visualize the prediction performance

Usage

```
VizCrosPred(PID,OutPath = "default",Layout = "bar",
Brightness = "light",Palette = "default1")
```


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. |
| Layout | chr. Visualization layout. Available options include "bar" and "roc" |
| 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)

Bin Wang

Examples

```
res <- InitCros()
  res1 = LoadCros(PID = res$PID, UseExample = "example#1")
  #res2 = TransScale(PID=res$PID, Group=TRUE, Vars="all.x", Method="normal")
  #res3 = CrosPred(PID=res$PID, VarsY = "Y1", VarsX = "X5,X6,X7,X8,X9,X10,X11",
  #PredType = "response", VarsSel = FALSE, VarsSelThr = 0.1, IncCova = FALSE,
  #RsmplMethod = "cv", Folds = 5, Ratio = 0.667, Repeats = 5)
  #res4 = VizCrosPred(PID=res$PID, Layout = "bar",
  #Brightness = "light", Palette = "science")
  #FuncExit(PID = res$PID)
```

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