

# Package ‘expanel’

December 13, 2022

**Title** Conduct the analysis of the panel data.

**Version** 1.0.0

**Description** To conduct the analysis of the panel data. It mainly aims to evaluate the associations between exposure factors and the health outcome.

**License** GPL (>= 3)

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.2.2

**Imports** httr,vroom,ggplot2,readxl,gridExtra

**NeedsCompilation** no

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FindCovaPanel	<i>Find covariates</i>
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## Description

Find covariates

**Usage**

```
FindCovaPanel(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 ExpoPanel
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 defaults value is 0.1.

**Value**

A list containing the selected covariates.

**Author(s)**

Bin Wang

**Examples**

```
res <- InitPanel()
res1 = LoadPanel(PID = res$PID, UseExample = "example#1")
res2 = FindCovaPanel(PID=res$PID, VarsY = "Y1",
  VarsC_Prior = "default", VarsC_Fixed ="C1", Method = "single.factor", Thr = 0.1)
```

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FuncExit

*End the module analysis*

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**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 <- InitPanel()
res1 = LoadPanel(PID = res$PID, UseExample = "example#1")
FuncExit(PID = res$PID)
```

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InitPanel

*Initialize ExpoPanel module*

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**Description**

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

**Usage**

```
InitPanel()
```

**Details**

ExpoPanel module is designed to conduct the analysis of the panel data. It mainly aims to evaluate the associations between exposure factors and the health outcome.

**Value**

An R6 class object.

**Author(s)**

Bin Wang (corresponding author)

**Examples**

```
res <- InitPanel()
```

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LoadPanel	<i>Load data file for ExpoPanel module</i>
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### Description

Load data file for ExpoPanel module

### Usage

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

### Arguments

PID	chr. Program ID. It must be the same with the PID generated by ExpoPanel
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_biolink.xlsx". It should be noted that the slash symbol is "/", not "\".
VocaPath	chr. Input directory of vocabulary file, e.g. "D:/test/eg_voca_biolink.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 <- InitPanel()
res = LoadPanel(PID = res$PID, UseExample = "example#1")
```

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PanelAsso	<i>Association analysis of panel data</i>
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### Description

Association analysis of panel data

### Usage

```
PanelAsso(PID, OutPath = "default", VarsY, VarsX, VarsN = "single.factor",
  VarsRandomIpt = "SubjectID", VarsRandomSlp = "none", IncCova = F)
```

**Arguments**

PID	chr. Program ID. It must be the same with the PID generated by ExpoPanel
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"
VarsN	chr. Choose the single factor or multiple factor model. Available options include "single.factor" and "multiple.factor"
VarsRandomIpt	chr. Random intercept variable for the linear mixed-effect model. The default is "SubjectID".
VarsRandomSlp	chr. Random slope variable for the linear mixed-effect model. The default is "none". 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. T (or TRUE) and F (or FALSE). Whether to include the covariate(s) selected in the function "FindCovaPanel"

**Value**

A list containing the association analysis results.

**Author(s)**

Bin Wang

**Examples**

```
res <- InitPanel()
res1 = LoadPanel(PID = res$PID, UseExample = "example#1")
res2 = PanelAsso(PID=res$PID, VarsY = "Y1",
  VarsX = "X1,X2,X3,X4,X5,X6,X7,X8,X9,X10,X11,X12", VarsN = "single.factor",
  VarsRandomIpt = "SubjectID", VarsRandomSlp = "none", IncCova = F)
```

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VizPanelAsso

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*Visualize the results of association analysis for panel data*


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**Description**

Visualize the results of association analysis for panel data

**Usage**

```
VizPanelAsso(PID, OutPath = "default", VarsY, VarsN, EffectThr = 0.5,
  Layout = "volcano", Brightness = "dark", Palette = "default1")
```

**Arguments**

PID	chr. Program ID. It must be the same with the PID generated by ExpoPanel
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.
VarsN	chr. Choose the single factor or multiple factor model. Available options include "single.factor" and "multiple.factor"
EffectThr	num. Insert the cutoff line for the effect values.
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**

A list containing the plots of association analysis results.

**Author(s)**

Bin Wang

**Examples**

```
res <- InitPanel()
res1 = LoadPanel(PID = res$PID, UseExample = "example#1")
res2 = PanelAsso(PID=res$PID, VarsY = "Y1",
  VarsX = "X1,X2,X3,X4,X5,X6,X7,X8,X9,X10,X11,X12", VarsN = "single.factor",
  VarsRandomIpt = "SubjectID", VarsRandomSlp = "none", IncCova = F)
res3 = VizPanelAsso(PID = res$PID, VarsY = "Y1",
  VarsN = "single.factor", Layout = "forest", Brightness = "dark", Palette = "default1")
```

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