Package 'exviz'

December 13, 2022

Title Visualize data of different statistical and biological analysis.

Version 1.0.0

Description To visualize data of different statistical and biological analysis in a user friendly and easy way, including four typical classes of visualization. The visualization of the high dimension data is also very useful for the users in the field. The data visualization of different statistical analysis as well as the biological interaction can save much time for the data interpretation.

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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 InitViz

Author(s)

Ning Gao, Bin Wang (corresponding author)

Examples

```
res = InitViz()
  res1 = LoadViz(PID = res$PID,UseExample = "example#1")
  res2 = VizCateDot(PID=res$PID,OutPath = "default",Group = "F",
  Vars = "X4,X5,X6,X7,X8,X9,X10",Parameter = "mean",
  Brightness = "light",Palette = "default1")
  FuncExit(PID = res$PID)
```

InitViz

Initialize ExpoViz module

Description

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

Usage

```
InitViz()
```

Details

ExpoViz module is designed for the data visualization of different statistical and biological analyses in a user friendly and easy way, including four typical classes of visualization.

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Value

An R6 class object.

Author(s)

Ning Gao, Bin Wang (corresponding author)

Examples

```
res <- InitViz()
```

LoadViz

Load data file for ExpoViz module

Description

Load data for visualization.

Usage

```
LoadViz(PID, UseExample = "example#1",DataPath=NULL,VocaPath=NULL)
```

Arguments

PID chr. Program ID. It must be the same with the PID generated by InitViz.

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_expoviz_data.xlsx". It should be

noted that the slash symbol is "/", not "\".

VocaPath chr. Input vocabulary file directory, e.g. "D:/test/eg_expoviz_voca.xlsx". It

should be noted that the slash symbol is "/", not "\".

Value

An R6 class object containing the input data.

Author(s)

Ning Gao, Bin Wang (corresponding author)

```
res = InitViz()
    res1 = LoadViz(PID = res$PID, UseExample = "example#1")
```

4 VizCateDot

VizCateDot	Plot category dot	
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Description

Visualize data via dot plot.

Usage

Arguments

PID	chr. Program ID. It must be the same with the PID generated by InitViz.
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.
Group	lgl.Whether to separate dataset into train and test datasets for data imputation,including T or F.The default option is F.
Vars	chr. Specifying the variables. Available options include: "all.x", all independent variables; "all.c", all covariate variables; "all.cx", combination of All x and All x; or input a character string specifying the variables, separated by comma "," without space(e.g."X4,X5,X6,X7,X8,X9,X10"). No more than 50 variables be entered is recommended (< 50 variables).
Parameter	chr. Specifying which parameter of the data to be the ordinate of the output plot. Available options include: "mean", "median", "min", "max", "mad" or "sd".Default is "mean".
Brightness	chr. Visualization brightness. Available options include "light" and "dark".
Palette	chr. Visualization palette. Available options include "default1", "default2" and "Journal". The "Journal" option provides several journal preference styles including cell, nature, science, lancet, nejm, and jama.

Details

The dot plot is used to display the relative position of two data points in the same time period, or compare the difference between the two categorical variables.

Value

One or three ggplot plots which can be further modified using the ggplot2 package. When Group=T, (1) "all_light_default1": the whole dataset visualization result; (2) "train_light_default1": the train dataset visualization result; (3) "test_light_default1": the test dataset visualization result. When Group=F, (1) "light_default1": the whole dataset visualization result.

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Author(s)

Ning Gao, Bin Wang (corresponding author)

Examples

```
res = InitViz()
  res1 = LoadViz(PID = res$PID, UseExample = "example#1")
  res2 = VizCateDot(PID=res$PID,OutPath="default",Group="F",Vars="X4,X5,X6,X7,X8,X9,X10",
    Parameter="mean",Brightness="light",Palette="default1")
```

Viz Compo Dendrogram

Plot component dendrogram

Description

Visualize data via dendrogram plot.

Usage

```
VizCompoDendrogram(PID,OutPath="default",Group = "T",Vars,
    Parameter = "median",DistMethod = "euclidean", ClusterMethod = "ward.D",
    ClusterNum = "4",Brightness = "light",Palette = "default1")
```

Arguments

PID	chr. Program ID. It must be the same with the PID generated by InitViz.
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.
Group	lgl.Whether to separate dataset into train and test datasets for data imputation,including T or F.The default option is T.
Vars	chr. Variables to be visualized(e.g."X4,X5,X6,X7,X8,X9,X10"). Available options include: "all.x", all independent variables; "all.c", all covariate variables; "all.cx", combination of all.x and all.c; or input a character string specifying the variables, separated by comma "," without space(e.g."X4,X5,X6,X7,X8,X9,X10").
Parameter	chr. Specifying which parameter of the data to be the ordinate of the output plot. Available options include: "mean", "median", "min", "max", "mad" or "sd".Default is "mean".
DistMethod	chr.The distance measure. This must be one of "euclidean", "maximum" or "manhattan".Default is "euclidean".
ClusterMethod	chr.The agglomeration method. This should be one of "ward.D", "ward.D2" or "single".Default is "ward.D".
ClusterNum	num. The number of groups for cutting the tree.Default is 4.
Brightness	chr. Visualization brightness. Available options include "light" and "dark".
Palette	chr. Visualization palette. Available options include "default1", "default2" and "Journal". The "Journal" option provides several journal preference styles in-

cluding cell, nature, science, lancet, nejm, and jama.

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Details

The dendrogram plot is used to plot beautiful dendrograms.

Value

One or three ggplot plots which can be further modified using the ggplot2 package. When Group=T, (1) "all_light_default1": the whole dataset visualization result; (2) "train_light_default1": the train dataset visualization result; (3) "test_light_default1": the test dataset visualization result. When Group=F, (1) "light_default1": the whole dataset visualization result.

Author(s)

Ning Gao, Bin Wang (corresponding author)

Examples

```
res = InitViz()
   res1 = LoadViz(PID = res$PID, UseExample = "example#1")
   res2= VizCompoDendrogram(PID=res$PID,OutPath="default",Group = "T",
   Vars = "X4,X5,X6,X7,X8,X61,X66,X67,X200",Parameter = "median",
   DistMethod = "euclidean",ClusterMethod = "ward.D2",ClusterNum = "4",
   Brightness = "light",Palette = "default1")
```

VizDistrSierra

Plot distribution sierra

Description

Visualize data via sierra plot.

Usage

```
VizDistrSierra(PID,OutPath="default",Group = "F",Vars,Brightness = "light",
   Palette = "default1")
```

Arguments

PID	chr. Program ID. It must be the same with the PID generated by InitViz.
OutPath	chr. Output file directory. e.g. "D:/test". It should be noted that the slash s

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.

lgl. Whether to separate dataset into train and test datasets for data imputation, including Group

T or F.The default option is F.

chr. Variables to be visualized(e.g. "X4,X5,X6,X7,X8,X9,X10"). Available op-Vars

tions include: "all.x", all independent variables; "all.c", all covariate variables; "all.cx", combination of all.x and all.c; or input a character string specifying the variables, separated by comma "," without space(e.g. "X4,X5,X6,X7,X8,X9,X10").

No more than 50 variables be entered is recommended (< 20 variables).

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Brightness chr. Visualization brightness. Available options include "light" and "dark".

Palette chr. Visualization palette. Available options include "default1", "default2" and

"Journal". The "Journal" option provides several journal preference styles in-

cluding cell, nature, science, lancet, nejm, and jama.

Details

The sierra plot is used to visualize the kernel density estimation of data.

Value

One or three ggplot plots which can be further modified using the ggplot2 package. When Group=T, (1) "all_light_default1": the whole dataset visualization result; (2) "train_light_default1": the train dataset visualization result; (3) "test_light_default1": the test dataset visualization result. When Group=F, (1) "light_default1": the whole dataset visualization result.

Author(s)

Ning Gao, Bin Wang (corresponding author)

Examples

```
res = InitViz()
  res1 = LoadViz(PID = res$PID, UseExample = "example#1")
  res2 = VizDistrSierra(PID=res$PID,OutPath="default",Group = "F",
  Vars = "X14,X15,X16,X17,X18,X19,X20",Brightness = "light",Palette = "default1")
```

VizRelatEdgeBundling Plot elationship edge bundling

Description

Visualize data via edge bundling plot.

Usage

```
VizRelatEdgeBundling(PID,OutPath="default",VarsY, VarsC="all.c", VarsX = "all.x",
    Family = "gaussian", SizeFor = "pvalue",Brightness = "light",
    Palette = "default1")
```

Arguments

PID chr. Program ID. It must be the same with the PID generated by InitViz.

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. Dependent variables for visualization(e.g. "Y2").

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VarsC	chr. Covariate variable. Available options include: "all.c", all covariate variables; or input a character string specifying the variables, separated by comma "," without space(e.g. "C1,C2").
VarsX	chr. Independent variables. Available options include: "all.x", all independent variables; or input a character string specifying the variables, separated by comma "," without space(e.g. "X4,X5,X6,X7,X8,X9,X10").
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. Notice that the family are determined by data type of an outcome, or the plot can not be visualized. The default option is "gaussian".
SizeFor	chr. Parameter to represent the size of the points in the output plot. Available options include "pvalue" and "beta". The default option is "pvalue".
Brightness	chr. Visualization brightness. Available options include "light" and "dark".
Palette	chr. Visualization palette. Available options include "default1", "default2" and "Journal". The "Journal" option provides several journal preference styles in-

Details

The edge bundling plot is used to bundle the edges closely in order to reduce complexity.

cluding cell, nature, science, lancet, nejm, and jama.

Value

A ggplot plot which can be further modified using the ggplot2 package. (1) "light_default1": the visualization result;

Author(s)

Ning Gao, Bin Wang (corresponding author)

Examples

```
res = InitViz()
  res1 = LoadViz(PID = res$PID, UseExample = "example#1")
  res2 = VizRelatEdgeBundling(PID=res$PID,OutPath="default",VarsY = "Y2",
  VarsX = "all.x",VarsC = "all.c",Family = "gaussian" ,SizeFor = "pvalue",
  Brightness = "light",Palette = "default1")
```

VizRelatHeatmap

Plot relationship heatmep

Description

Visualize data via heatmap plot.

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Usage

Arguments

PID chr. Program ID. It must be the same with the PID generated by InitViz.

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.

Group lgl. Whether to separate dataset into train and test datasets for data imputation, including

T or F.The default option is F.

VarsY chr. Dependent variables for visualization(e.g. "Y2").

VarsX chr. Independent variables. Available options include: "all.x", all independent

variables; or input a character string specifying the variables, separated by comma

"," without space(e.g."X4,X5,X6,X7,X8,X9,X10").

Method chr. Method to calculate the correlation. Default option is "spearman".

Brightness chr. Visualization brightness. Available options include "light" and "dark".

Palette chr. Visualization palette. Available options include "default1", "default2" and

"Journal". The "Journal" option provides several journal preference styles in-

cluding cell, nature, science, lancet, nejm, and jama.

Details

The heatmap plot is used to display data in color changes as a matrix.

Value

One or two ggplot plots which can be further modified using the ggplot2 package. When Group=T, (1) "train_light_default1": the train dataset visualization result; (2) "test_light_default1": the test dataset visualization result. When Group=F, (1) "light_default1": the whole dataset visualization result.

Author(s)

Ning Gao, Bin Wang (corresponding author)

```
res = InitViz()
  res1 = LoadViz(PID = res$PID, UseExample = "example#1")
  res2 = VizRelatHeatmap(PID=res$PID,OutPath="default",Group = "F",
  VarsY = "Y2",VarsX = "X1,X4,X5,X6,X7,X8,X9,X10",Method = "spearman",
  Brightness = "light",Palette = "default1")
```

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VizRelatMatrix	Plot relationship matrix	

Description

Visualize data via matrix plot.

Usage

```
VizRelatMatrix(PID,OutPath="default",Group = "F",VarsY,VarsX,Method = "spearman")
```

Arguments

PID	chr. Program ID. It must be the same with the PID generated by InitViz.
OutPath	chr. Output file directory. e.g. "D:/test". It should be noted t hat the slash symbol is "/", not "\". If "default", the current working directory will be set.
Group	lgl.Whether to separate dataset into train and test datasets for data imputation, including T or F.The default option is F.
VarsY	chr. Dependent variables for visualization(e.g."Y2").
VarsX	chr. Independent variables. Available options include: "all.x", all independent variables; or input a character string specifying the variables, separated by comma "," without space(e.g. "X4,X5,X6,X7,X8,X9,X10"). Notice that no more than 20 variables can be inputed. (< 20 variables).
Method	chr. Method to calculate the correlation. Default option is "spearman".

Details

The matrix plot is used to make a matrix of plots with a given data set.

Value

One or two ggmatrix plots which can be further modified using the ggplot2 package. When Group=T, (1) "Train": the train dataset visualization result; (2) "Test": the test dataset visualization result. When Group=F, (1) "All": the whole dataset visualization result.

Author(s)

Ning Gao, Bin Wang (corresponding author)

```
res = InitViz()
  res1 = LoadViz(PID = res$PID, UseExample = "example#1")
  res2 = VizRelatMatrix(PID=res$PID,OutPath="default",Group = "F",
  VarsY = "Y2",VarsX = "X4,X5,X6,X7,X8,X9,X10",Method = "spearman")
```

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|--|

Description

Visualize data via network plot.

Usage

```
VizRelatNetwork(PID,OutPath="default",VarsY,VarsC="all.c",VarsX="all.x",
    Family="gaussian",Layout="force-directed",CutOff=0.8,Brightness="light",
    Palette="default1")
```

Arguments

PID	chr. Program ID. It must be the same with the PID generated by InitViz.
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. Specifying the dependent variables(e.g."Y2").
VarsC	chr. Specifying the covariate variable. Available options include: "all.c", all covariate variables; or input a character string specifying the variables, separated by comma "," without space(e.g. "C1,C2").
VarsX	chr. Specifying the independent variables. Available options include: "all.x", all independent variables; or input a character string specifying the variables, separated by comma "," without space(e.g. "X4,X5,X6,X7,X8,X9,X10").
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. Notice that the family are determined by data type of an outcome, or the plot can not be visualized. The default option is "gaussian".
Layout	chr. Visualization layout. Available options include "force-directed" and "degree-circle".
CutOff	num. Partial outcomes to visualize which is determined by correlation coefficient r. The range must between 0 and 1.
Brightness	chr. Visualization brightness. Available options include "light" and "dark".
Palette	chr. Visualization palette. Available options include "default1", "default2" and "Journal". The "Journal" option provides several journal preference styles including cell, nature, science, lancet, nejm, and jama.

Details

The network plot is used to visualize the relationship between the input variables by using ggraph package.

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Value

A ggplot plot which can be further modified using the ggplot2 package. (1) "light_default1": the visualization result;

Author(s)

Ning Gao, Bin Wang (corresponding author)

```
res = InitViz()
    res1 = LoadViz(PID = res$PID, UseExample = "example#1")
    res2 = VizRelatNetwork(PID=res$PID,OutPath="default",VarsY="Y2",VarsC="all.c",
    VarsX="all.x",Family="gaussian",Layout="force-directed",CutOff=0.8,
    Brightness="light",Palette="default1")
```

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