Package 'ExploreModelMatrix'

October 17, 2020

Type Package

Title Graphical Exploration of Design Matrices

Version 1.0.2

Description Given a sample data table and a design formula, generate an interactive application to explore the resulting design matrix.

License MIT + file LICENSE

Encoding UTF-8

Imports shiny, shinydashboard, DT, cowplot, utils, dplyr, magrittr, tidyr, ggplot2, stats, methods, rintrojs, scales, tibble, MASS, limma, S4Vectors

RoxygenNote 7.1.1

Suggests testthat (>= 2.1.0), knitr, rmarkdown, htmltools, BiocStyle

VignetteBuilder knitr

URL https://github.com/csoneson/ExploreModelMatrix

BugReports https://github.com/csoneson/ExploreModelMatrix/issues

biocViews ExperimentalDesign, Regression, DifferentialExpression

git_url https://git.bioconductor.org/packages/ExploreModelMatrix

git_branch RELEASE_3_11

git_last_commit 5707f6a

git_last_commit_date 2020-08-03

Date/Publication 2020-10-16

Author Charlotte Soneson [aut, cre] (<https://orcid.org/0000-0003-3833-2169>),
Federico Marini [aut] (<https://orcid.org/0000-0003-3252-7758>),
Michael Love [aut] (<https://orcid.org/0000-0001-8401-0545>),
Florian Geier [aut] (<https://orcid.org/0000-0002-9076-9264>),
Michael Stadler [aut] (<https://orcid.org/0000-0002-2269-4934>)

Maintainer Charlotte Soneson <charlottesoneson@gmail.com>

R topics documented:

1

ExploreModelMatrix   *Explore model matrix*

Description

Given a sample table and a design formula, explore the resulting design matrix graphically in an interactive application.

Usage

```
ExploreModelMatrix(sampleData = NULL, designFormula = NULL)
```

Arguments

sampleData   (optional) A `data.frame` or `DataFrame` with sample information. If set to `NULL`, the user can upload the sample information from a tab-separated text file inside the app, or choose among a collection of example designs provided in the app.

designFormula   (optional) A `formula`. All components of the terms must be present as columns in `sampleData`. If set to `NULL`, the design formula can be specified after launching the app.

Value

A Shiny app object

Author(s)

Charlotte Soneson, Federico Marini, Michael I Love, Florian Geier, Michael B Stadler

Examples

```
app <- ExploreModelMatrix(
  sampleData = data.frame(genotype = rep(c("A", "B"), each = 4),
                          treatment = rep(c("treated", "untreated"), 4)),
  designFormula = ~genotype + treatment
)
if (interactive()) shiny::runApp(app)
```

ExploreModelMatrix-pkg
                         ExploreModelMatrix

Description

ExploreModelMatrix is an R package for visualizing design matrices generated by the `model.matrix()` R function. Provided with a sample information table and a design formula, the `ExploreModelMatrix()` function launches a shiny app where the user can explore the fitted values (in terms of the model coefficients) for each combination of predictor values.

```
VisualizeDesign          Visualize design matrix
```

Description

Given a sample table and a design formula, generate a collection of static plots for exploring the resulting design matrix graphically. This function is called internally by ExploreModelMatrix(), but can also be used directly if interactivity is not required.

Usage

```
VisualizeDesign(
  sampleData,
  designFormula,
  flipCoordFitted = FALSE,
  flipCoordCoocc = FALSE,
  textSizeFitted = 5,
  textSizeCoocc = 5,
  textSizeLabsFitted = 12,
  textSizeLabsCoocc = 12,
  lineWidthFitted = 25,
  addColorFitted = TRUE,
  colorPaletteFitted = scales::hue_pal(),
  dropCols = NULL
)
```

Arguments

sampleData	A data.frame of DataFrame with sample information.
designFormula	A formula. All components of the terms must be present as columns in sampleData.
flipCoordFitted, flipCoordCoocc	
	A logical, whether to flip the coordinate axes in the fitted values/co-occurrence plot, respectively.
textSizeFitted, textSizeCoocc	
	A numeric scalar giving the text size in the fitted values/co-occurrence plot, respectively.
textSizeLabsFitted, textSizeLabsCoocc	
	A numeric scalar giving the text size for the axis labels in the fitted values/co-occurrence plot, respectively.
lineWidthFitted	
	A numeric scalar giving the maximal length of a row in the fitted values plot, before it is split and printed on multiple lines
addColorFitted	A logical scalar indicating whether the terms in the fitted values plot should be shown in different colors.
colorPaletteFitted	
	A function returning a color palette to use for coloring the model coefficients in the fitted values plot.
dropCols	A character vector with columns to drop from the design matrix, or NULL if no columns should be dropped.

Value

A list with the following elements:

- `sampledata`: A `data.frame`, expanded from the input `sampleData`
- `plotlist`: A list of plots, displaying the fitted values for each combination of predictor values, in terms of the model coefficients.
- `designmatrix`: The design matrix, after removing any columns in `dropCols`
- `pseudoinverse`: The pseudoinverse of the design matrix
- `vifs`: A `data.frame` with calculated variance inflation factors
- `colors`: A vector with colors to use for different model coefficients
- `cooccurrenceplots`: A list of plots, displaying the co-occurrence pattern for the predictors (i.e., the number of observations for each combination of predictor values)

Author(s)

Charlotte Soneson

Examples

```
VisualizeDesign(
  sampleData = data.frame(genotype = rep(c("A", "B"), each = 4),
                          treatment = rep(c("treated", "untreated"), 4)),
  designFormula = ~genotype + treatment
)
```

Index