Package ‘ERSA’

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**createERServer**

A function which returns a shiny server for Exploratory Regression

**Description**

A function which returns a shiny server for Exploratory Regression

**Usage**

```r
createERServer(  
    ERfit,  
    ERdata = NULL,  
    ERbarcols = RColorBrewer::brewer.pal(4, "Set2"),  
    ERnscpCols = 4,  
    pvalOrder = F  
)
```

**add1_models**

Constructs a list of fits by adding predictors sequentially

**Description**

Constructs a list of fits by adding predictors sequentially

**Usage**

```r
add1_models(model, preds, data = NULL)
```

**Arguments**

- `model`: A linear model
- `preds`: Predictors to be added sequentially
- `data`: The dataset (optional)

**Value**

A list of linear fits
createERUI

Arguments

- `ERfit`: the `lm` fit to be explored
- `ERdata`: the data used to fit the model. If NULL, attempts to extract from `ERfit`.
- `ERbarcols`: a vector of colours, one per term in `lm`. Will be expanded via `colorRampPalette` if not the correct length.
- `ERnpcpCols`: number of colours for the PCP
- `pvalOrder`: if TRUE, re-arranges predictors in order of p-value

Value

- a function

---

**createERUI** Constructs UI for Exploratory Regression app

---

Description

Constructs UI for Exploratory Regression app

Usage

createERUI(tablesOnly = F, gadget = TRUE)

Arguments

- `tablesOnly`: if TRUE, shows Plots 1-3 only.
- `gadget`: If TRUE, constructs a gadget, otherwise a shinyApp

Value

- the UI

---

**drop1_models** Constructs a list of fits by dropping predictors from the supplied model

---

Description

Constructs a list of fits by dropping predictors from the supplied model

Usage

drop1_models(model, preds, data = NULL)
Arguments

- **model**: A linear model
- **preds**: Predictors to be dropped
- **data**: The dataset (optional)

Value

A list of linear fits

---

**ERSA**

**ERSA: A package exploring regressions with a Shiny app**

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**exploreReg**

**A function to launch the Exploratory Regression Shiny App**

---

Description

The Exploratory Regression Shiny App (ERSA) package consists of a collection of functions for displaying the results of a regression calculation, which are then packaged together as a shiny app function.

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Usage

```r
explorereg(
  ERmfull,
  ERdata = NULL,
  ERbarcols = RColorBrewer::brewer.pal(4, "Set2"),
  npcpCols = 4,
  pvalOrder = F,
  tablesOnly = F,
  displayHeight = NULL,
  gadget = TRUE,
  viewer = "dialogViewer"
)
```
**pcpPlot**

**Arguments**

- `ERmfull`: the lm fit to be explored
- `ERdata`: the data used to fit the model. If NULL, attempts to extract from `ERmfull`.
- `ERbarcols`: a vector of colours, one per term in lm. Will be expanded via `colorRampPalette` if not the correct length.
- `npcpCols`: number of colours for the PCP
- `pvalOrder`: if TRUE, re-arranges predictors in order of p-value
- `tablesOnly`: if TRUE, shows Plots 1-3 only.
- `displayHeight`: supply a value for the display height
- `gadget`: If TRUE, constructs a gadget, otherwise a `shinyApp`.
- `viewer`: For gadget, defaults to "dialogViewer". May be "paneViewer" or "browserViewer"

**Value**

the result

**Examples**

```r
f <- lm(mpg ~ hp+wt+disp, data=mtcars)
## Not run: exploreReg(f)
```

---

**Description**

A PCP plot of the data, residuals or hat values from regression fits

**Usage**

```r
pcpPlot(
  data,
  fit,
  type = "Variables",
  npcpCols = 4,
  resDiff = F,
  absResid = F,
  sequential = F,
  selnum = NULL
)
```
plotSeqSS

Arguments

- **data**: a data frame
- **fit**: a lm for the data frame
- **type**: one of "Variables", "Residuals", "Hatvalues"
- **npcpCols**: number of colours
- **resDiff**: difference residuals, TRUE or FALSE
- **absResid**: absolute residuals, TRUE or FALSE
- **sequential**: use sequential fits (TRUE) or drop1 fits (FALSE)
- **selnum**: row numbers of cases to be highlighted

Value

ggplot

Examples

```r
f <- lm(mpg ~ wt+hp+disp, data=mtcars)
pcpPlot(mtcars, f, type="Residuals")
```

plotSeqSS  
**Plots barcharts of sequential sums of squares of lm**

Description

Plots barcharts of sequential sums of squares of lm

Usage

```r
plotSeqSS(fits, barcols = NULL, legend = F)
```

Arguments

- **fits**: list of lm objects
- **barcols**: a vector of colours, one per term in lms
- **legend**: TRUE or FALSE

Value

- a ggplot

Examples

```r
plotSeqSS(list(fit1= lm(mpg ~ wt+hp+disp, data=mtcars),
              fit2=lm(mpg ~ wt+hp+disp, data=mtcars)))
```
Description

Plots of model summaries

Usage

plotAnovaStats(
  fit0,
  barcols = NULL,
  preds = NULL,
  alpha = 0.05,
  type = "SS",
  width = 0.3
)

plottStats(fit0, barcols = NULL, preds = NULL, alpha = 0.05, width = 0.3)

plotCIStats(
  fit0,
  barcols = NULL,
  preds = NULL,
  alpha = 0.05,
  stdunits = FALSE,
  width = 0.3
)

Arguments

fit0 is an lm object
barcols a vector of colours, one per term in lm
preds terms to include in plot
alpha significance level
type "SS" or "F", from type 3 Anova
width bar width
stdunits TRUE or FALSE. If TRUE, coefficients refer to standardised predictor units.

Value

a ggplot
Functions

- plotAnovaStats: Plots bar chart of F or SS from lm
- plottStats: Plots bar chart of t stats from lm
- plotCIStats: Plots confidence intervals from lm

Examples

plotAnovaStats(lm(mpg ~ wt+hp+disp, data=mtcars))
plottStats(lm(mpg ~ wt+hp+disp, data=mtcars))
plotCIStats(lm(mpg ~ wt+hp+disp, data=mtcars))

reorderTerms Re-order model terms

Description

Re-order model terms

Usage

pvalOrder(m, d = NULL, refit = TRUE)
bselOrder(m, d = NULL, refit = TRUE, maxNPred = NULL)
fselOrder(m, d = NULL, refit = TRUE, maxNPred = NULL)
revPredOrder(m, d = NULL, refit = TRUE)
randomPredOrder(m, d = NULL, refit = TRUE)
regsubsetsOrder(m, d = NULL, refit = TRUE, collapse = TRUE)

Arguments

- m: an lm object
- d: the data frame. If NULL, attempts to extract from m.
- refit: TRUE or FALSE
- maxNPred: maximum number of predictors to use, defaults to all.
- collapse: TRUE or FALSE

Value

a vector of terms in order last to first, or an lm if refit=TRUE. regsubsetsOrder returns a list of predictor vectors, or a list of fits
Functions

- pvalOrder: Arranges model terms in order of increasing p-value
- bselOrder: Arranges model terms using backwards selection
- fse1Order: Forwards selection
- revPredOrder: Reverses order of terms in a fit
- randomPredOrder: Reorders terms in a fit randomly
- regsubsetsOrder: Best subsets regression.

Examples

bselOrder(lm(mpg~wt+hp+disp, data=mtcars))
fselOrder(lm(mpg~wt+hp+disp, data=mtcars))
revPredOrder(lm(mpg~wt+hp+disp, data=mtcars))
randomPredOrder(lm(mpg~wt+hp+disp, data=mtcars))
regsubsetsOrder(lm(mpg~wt+hp+disp, data=mtcars))

termColours

Description

Constructs colour vector for model terms

Usage

termColours(f, pal = RColorBrewer::brewer.pal(4, "Set2"))

Arguments

f a model fit with term labels
pal use this palette

Value

a vector of colours. Residuals are given a grey color

Examples

termColours(lm(mpg ~ wt+hp, data=mtcars))
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