

# Package ‘ERSA’

September 23, 2020

**Type** Package

**Title** Exploratory Regression 'Shiny' App

**Version** 0.1.3

**Date** 2020-9-22

**Author** Catherine B. Hurley

**Maintainer** Catherine B. Hurley <catherine.hurley@mu.ie>

**Description** Constructs a 'shiny' app function with interactive displays for summary and analysis of variance regression tables, and parallel coordinate plots of data and residuals.

**License** GPL (>= 2.0)

**Encoding** UTF-8

**LazyData** true

**Imports** shiny, miniUI, RColorBrewer, ggplot2, car, leaps, broom, dplyr, tidyrr, purrr, combinat, stats, methods

**RoxygenNote** 7.1.1

**Suggests** knitr, rmarkdown, testthat

**VignetteBuilder** knitr

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2020-09-22 23:00:02 UTC

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add1_models	<i>Constructs a list of fits by adding predictors sequentially</i>
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### Description

Constructs a list of fits by adding predictors sequentially

### Usage

```
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

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createERServer	<i>A function which returns a shiny server for Exploratory Regression</i>
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### Description

A function which returns a shiny server for Exploratory Regression

### Usage

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

**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

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createERUI	<i>Constructs UI for Exploratory Regression app</i>
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**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

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drop1_models	<i>Constructs a list of fits by dropping predictors from the supplied model</i>
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**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

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ERSA	<i>ERSA: A package exploring regressions with a Shiny app</i>
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**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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exploreReg	<i>A function to launch the Exploratory Regression Shiny App</i>
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**Description**

A function to launch the Exploratory Regression Shiny App

**Usage**

```
exploreReg(
  ERmfull,
  ERdata = NULL,
  ERbarcols = RColorBrewer::brewer.pal(4, "Set2"),
  npcCols = 4,
  pvalOrder = F,
  tablesOnly = F,
  displayHeight = NULL,
  gadget = TRUE,
  viewer = "dialogViewer"
)
```

**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**

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

---

pcpPlot

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

---

**Description**

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

**Usage**

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

**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**

```
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**

```
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**

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

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`plotSum`*Plots of model summaries*

---

**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**

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

**Value**

a ggplot

**Functions**

- plotAnovaStats: Plots barchart of F or SS from lm
- plottStats: Plots barchart 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))
```

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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
- fselOrder: Forwards selection
- revPredOrder: Reverses order of terms in a fit
- randomPredOrder: Reorders terms in a fit randomly
- regsubsetsOrder: Best subsets regression.

**Examples**

```
bse1Order(lm(mpg~wt+hp+disp, data=mtcars))
fse1Order(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***Constructs colour vector for model terms*

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**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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