

Package ‘lmSupport’

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Description Provides tools and a consistent interface to support analyses using General, Generalized, and Multi-level Linear Models.

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dfMerge

Merges two data frames

Description

Merges variables from two data frames (DataX, DataY) by default or merges cases (if AddVars=FALSE). When merging variables, by default matches on row names but can use other variable names in DataX (ByX) and DataY (ByY) as needed. Also by default, includes all cases in DataX and DataY but can limit to only matching (AllX=FALSE, AllY=FALSE) or left join (AllY=FALSE) or right join (AllX=FALSE).

When merging cases, will add variables to DataX or DataY as needed and set added variables to NA

Usage

```
dfMerge(DataX, DataY, ByX = 0, ByY = 0, AllX = TRUE, AllY = TRUE, AddVars=TRUE)
```

Arguments

DataX	first data frame for merge
DataY	second data frame for merge
ByX	Name of variable in DataX to match cases on. Column can be specified by name or number. Default is 0 which uses rownames
ByY	Name of variable in DataY to match cases on. Column can be specified by name or number. Default is 0 which uses rownames
AllX	logical; if TRUE, then extra rows will be added to the output, one for each row in DataX that has no matching row in DataY. These rows will have NAs in those columns that are usually filled with values from dY. The default is TRUE, so that all rows with data from both dX and dY are included in the output. In other words, it is the union of these two dataframes
AllY	analogous to AllX but for DataY
AddVars	Default is to merge variables (columns). If FALSE will merge cases (rows)

Details

see merge() or rbind() for more details on merging variables or cases, respectively.

Value

Returns merged data frame

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

See Also

merge(), rbind()

Examples

```
dX <- data.frame(v1=c(1,2,3,4,5), v2=c(1,NA,NA,2,4), data=1:5)
rownames(dX) = c(1,2,3,4,5)
dY <- data.frame(v3=c(3,2,1,4,15), v4=c(2,4,5,6,7), data=6:10)
rownames(dY) = c(1,2,3,4,6)
dNew = dfMerge(dX,dY)
```

dfReadDat	<i>Opens a tab-delimited dat file with typical Curtin lab settings</i>
-----------	--

Description

Opens a tab-delimited data file with standard Curtin lab format which include using a header and setting delimiter to tab.

If variable named SubID (default) or other text supplied by SubID variable exists in dat file, row names will be set with this variable and then variable is removed from new data frame.

Usage

```
dfReadDat(File, SubID = "SubID", SubIDDigits = NULL)
```

Arguments

File	File name for .dat file including extension
SubID	String to indicate name of SubID variable. Default is 'SubID'. If set to NULL, rownames will not be altered
SubIDDigits	Length of SubID rowname string. If NULL, will be set to max length in data

Value

returns a data frame

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

See Also

`read.table()`, `read.delim()`, `write.table()`, `dfRownames()`

Examples

```
##dfReadDat('Sample.dat) #not executable unless Sample.dat exists in path  
##dfReadDat('Sample.dat, SubID = 'subnum') #not executable unless Sample.dat exists in path
```

dfRemoveCases	<i>Removes cases from dataframe</i>
---------------	-------------------------------------

Description

Removes cases from dataframe. Cases can be numeric or character. If numeric, rownames must be able to be converted to numeric. Returns warning if cases not found in dataframe.

Usage

```
dfRemoveCases(Data, Cases)
```

Arguments

Data	a dataframe
Cases	a vector of numeric or character case IDs

Value

Returns dataframe with cases removed.

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

Examples

```
d = dfRemoveCases(Prestige, c('bookbinders')) #data from car package
d = dfRemoveCases(Davis, c(1,2,4))           #data from car package
```

dfRownames	<i>Sets rownames to SubID</i>
------------	-------------------------------

Description

Sets the row names of the data frame to the variable name listed as SubID. SubID should be text name of variable. Also keeps number of characters constant by default and removes SubID by default

Usage

```
dfRownames(Data, SubID = "SubID", FixedWidth = TRUE, Remove = TRUE, MaxNumDigits=NULL)
```

Arguments

Data	a data frame with a variable containing subject ID numbers
SubID	Text name of subject ID variable. Default is SubID
FixedWidth	logical. If TRUE (default), all rownames will be the same length by padding with leading 0's
Remove	logical. If TRUE (default), the subject ID variable will be removed from data frame after setting rownames
MaxNumDigits	Length of rowname string. If NULL, will be set to max length in data

Value

Returns data frame with rownames set (and SubID removed if requested)

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

Examples

```
d <- data.frame(SubID = c(1,2,3,10,20), v1=c(1,2,3,4,5), v2=c(1,NA,NA,2,4), data=1:5)
d=dfRownames(d)
```

dfWriteDat	<i>Saves dataframe as tab-delimited text file with typical Curtin lab parameters</i>
------------	--

Description

Saves a dataframe as a tab-delimited data file with standard Curtin lab format. Will add rownames as a first column in .dat file and label this column with SubID

Usage

```
dfWriteDat(Data, File, SubID = "SubID")
```

Arguments

Data	a dataframe
File	file name for .dat file
SubID	Name for new column with data from rownames. If NULL, rownames will not be added to .dat file) Default is 'SubID'

Details

Uses these parameters with write.table no append, no quote, separator is tab, no rownames, yes for columns.

Value

no return value but creates .dat file in current wd

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

See Also

read.table(), read.delim(), write.table()

Examples

```
dfWriteDat(Ornstein, File="Test1.dat")
dfWriteDat(Ornstein, File="Test2.dat", SubID = 'ID')
dfWriteDat(Ornstein, File="Test3.dat", SubID = NULL)
```

 figAxis

Wrapper for standardized use of axis()

Description

Wrapper function for standardized use of axis() with lab defaults for display

Usage

```
figAxis(side, lab.text, scale.at=NULL, scale.text=NULL,
        scale.lwd=NULL, scale.cex=NULL, scale.font=NULL,
        lab.line= NULL, lab.cex=NULL, lab.font=NULL)
```

Arguments

side	an integer specifying which side of the plot the axis is to be drawn on. The axis is placed as follows: 1=below, 2=left, 3=above and 4=right.
lab.text	name label for the axis
scale.at	the points at which tick-marks are to be drawn. Non-finite (infinite, NaN or NA) values are omitted. By default (when NULL) tickmark locations are computed, see 'Details' below.
scale.text	this can either be a logical value specifying whether (numerical) annotations are to be made at the tickmarks, or a character or expression vector of labels to be placed at the tickpoints.).
scale.lwd, scale.font, scale.cex	lwd, font, and cex for scale annotations. Accessed from options if NULL
lab.line, lab.cex, lab.font	line number, cex, and font for axis label. Accessed from options if NULL

Value

None

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

See Also

axis(), figLabDefaults(), figSetDefaults(), figNewDevice(), figLines(), figLines()

Examples

```

X = rep(2:9,4)+jitter(rep(0,32))
Y = X + rnorm(length(X),0,5)
m = lm(Y ~ X)
dNew = data.frame(X=seq(2,9,by=.01))
p = modelPredictions(m,dNew)
figNewDevice()
figPlotRegion(x=c(0,10),y=c(0,10))
figConfidenceBand(p$X,p$Predicted,p$CILO,p$CIHi)
figPoints(X,Y)
figLines(p$X,p$Predicted)
figAxis(side=1,lab.text='X-axis 1', scale.at=seq(from=0,to=10,by=2))
figAxis(side=2,lab.text='Startle Response', scale.at=seq(from=0,to=10,by=2))

```

figBarPlot

Wrapper for standardized use of barplot2() from gplots

Description

Wrapper function for standardized use of barplot2() with lab defaults for display

Usage

```

figBarPlot(Means, ylim, lab.text=NULL, se=NULL,
           bars.col= NULL, bars.density=NULL, bars.angle=NULL,
           scale.cex=NULL, lab.cex=NULL, lab.font=NULL,
           ci.plot=NULL, ci.col=NULL, ci.lty=NULL, ci.lwd = NULL, ci.width = NULL)

```

Arguments

Means	matrix of means to plot.
ylim	vector of min and max for y axis
lab.text	label for x-axis
se	standard error of mean for CI plotting, if needed

bars.col, bars.density, bars.angle
 color, density, and angle for bars. see barplot2 for additional detail

scale.cex cex for x axis scale

lab.font, lab.cex
 cex and font for x axis label

ci.plot boolean to indicate if CIs should be plotted

ci.col, ci.lty, ci.lwd, ci.width
 col, lty, lwd, and width of CI lines

Value

None

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

See Also

barplot2(), figLabDefaults(), figSetDefaults(), figNewDevice(), figLines(), figLines()

Examples

```
Means = matrix(c(70,65,68,91,100,90), nrow=2, ncol=3, byrow=TRUE)
colnames(Means) = c('ITI', 'CUE-', 'CUE+')
rownames(Means) = c('Non-deprived', 'Deprived')
se = matrix(c(5,10,4,5,10,4), nrow=2, ncol=3, byrow=TRUE)

bars.col = c('gray', 'white', 'black')
bars.density = c(-1,-1,10) #negative density suppresses lines
bars.angle = c(0,0,45)

figNewDevice()
figBarPlot(Means, ylim=c(0,130), lab.text='Group', ci.plot=TRUE, se=se,
           bars.col=bars.col, bars.density=bars.density,
           bars.angle = bars.angle)
figAxis(side=2, lab.text='Startle Response', scale.at=seq(0,120,by=20))
figLegend('topright', legend=colnames(Means), fill=bars.col, angle=bars.angle, density=bars.density)
```

figConfidenceBand *Creates confidence band for regression line*

Description

Adds a confidence band around a regression line in a plot

Usage

```
figConfidenceBand(X, Y, CIlo, CIhi, Color)
```

Arguments

X	Vector of data for X to plot
Y	Vector of data for Y to plot
CIlo	Vector of data for lower bound of confidence interval
CIhi	Vector of data for upper bound of confidence interval
Color	String to indicate R color. Will be .15 transparent in plot

Value

No value is returned

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

figErrBars

Wrapper for standardized use of error bars

Description

Wrapper function for standardized use of error bars with segments() with lab defaults for display

Usage

```
figErrBars(x, y, yplus, yminus, errbars.cap = NULL,
           errbars.lwd = NULL, errbars.col = NULL)
```

Arguments

x,y, yplus, yminus	coordinate vectors of x and y points for error bars
errbars.cap	Width of caps on error bars. Accessed from options if NULL
errbars.lwd	Line width. Accessed from options if NULL
errbars.col	Line color. Accessed from options if NULL

Value

None

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

See Also

lines(), figLabDefaults(), figSetDefaults(), figNewDevice(), figLines(), figPoints()

Examples

```
figNewDevice()
figPlotRegion(x=c(0,5), y=c(0,10))
figLines(c(0,10),c(0,10))
figAxis(side=1,lab.text='X-axis 1', scale.at=seq(from=0,to=10,by=2))
figAxis(side=2,lab.text='Startle Response', scale.at=seq(from=0,to=10,by=2))
```

figLabDefaults	<i>Generate list graphing parameters</i>
----------------	--

Description

Generates a list of detailed default graphing parameters that can be used by fig functions in lmSupport for standardized graphing. Need to use figSetDefaults with this list to save in options.

Usage

```
figLabDefaults()
```

Value

Returns a list that includes all graphing parameters

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

figLayout	<i>Wrapper for standardized use of layout()</i>
-----------	---

Description

Wrapper function for standardized use of layout() and layout.show()

Usage

```
figLayout(nRows, nCols, heights=rep(1,nRows), widths=rep(1,nCols),
          layout.display=NULL)
```

Arguments

nRows, nCols integers specifying number of rows and columns in matrix
 heights vector indicating relative heights of rows; Default is equal heights
 widths vector indicating relative widths of columns; Default is equal widths
 layout.display Boolean if outlines and numbers of panels should be displayed

Value

None

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

See Also

layout(), layout.show(), figLabDefaults(), figSetDefaults(), figNewDevice(), figLines(), figLines()

Examples

```
X = rep(2:9,4)+jitter(rep(0,32))
Y = X + rnorm(length(X),0,5)
m = lm(Y ~ X)
dNew = data.frame(X=seq(2,9,by=.01))
p = modelPredictions(m,dNew)

figNewDevice()
figLayout(2,1)
figPlotRegion(x=c(0,10),y=c(0,10))
figConfidenceBand(p$X,p$Predicted,p$CIlo,p$CIHi)
figLines(p$X,p$Predicted)
figAxis(side=1,lab.text='X-axis 1', scale.at=seq(from=0,to=10,by=2))
figAxis(side=2,lab.text='Startle Response', scale.at=seq(from=0,to=10,by=2))

figPlotRegion(x=c(0,10),y=c(0,10))
figPoints(X,Y)
figAxis(side=1,lab.text='X-axis 1', scale.at=seq(from=0,to=10,by=2))
figAxis(side=2,lab.text='Startle Response', scale.at=seq(from=0,to=10,by=2))
```

figLegend

Wrapper for standardized use of figLegend()

Description

Wrapper function for standardized use of Legend() with lab defaults for display

Usage

```
figLegend(x, y=NULL, legend, fill=NULL, angle=NULL, density=NULL, pch=NULL,
          leg.cex=NULL, leg.lwd=NULL, leg.font=NULL, leg.bty=NULL)
```

Arguments

`x,y` the x and y co-ordinates to be used to position the legend. They can be specified by keyword or in any way which is accepted by `xy.coords`: See 'Details' in `legend()`

`legend` a character or expression vector of length = 1 to appear in the legend. Other objects will be coerced by `as.graphicsAnnot`.

`fill` if specified, this argument will cause boxes filled with the specified colors (or shaded in the specified colors) to appear beside the legend text.

`angle` angle of shading lines.

`density` the density of shading lines, if numeric and positive. If NULL or negative or NA color filling is assumed.

`pch` the plotting symbols appearing in the legend, as numeric vector or a vector of 1-character strings (see points). Unlike points, this can all be specified as a single multi-character string. Must be specified for symbol drawing.

`leg.cex, leg.lwd, leg.font, leg.bty`
`cex, lwd, font, and bty` for legend. Defaults to values in options if NULL

Value

None

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

See Also

`legend()`, `figLabDefaults()`, `figSetDefaults()`, `figNewDevice()`, `figLines()`, `figLines()`

Examples

```
Means = matrix(c(70,65,68,91,100,90), nrow=2, ncol=3, byrow=TRUE)
colnames(Means) = c('ITI', 'CUE-', 'CUE+')
rownames(Means) = c('Non-deprived', 'Deprived')
se = matrix(c(5,10,4,5,10,4), nrow=2, ncol=3, byrow=TRUE)

bars.col = c('gray', 'white', 'black')
bars.density = c(-1,-1,10) #negative density suppresses lines
bars.angle = c(0,0,45)

figNewDevice()
figBarPlot(Means, ylim=c(0,130), lab.text='Group', ci.plot=TRUE, se=se,
           bars.col=bars.col, bars.density=bars.density, bars.angle = bars.angle)
```

```
figAxis(side=2,lab.text='Startle Response', scale.at=seq(0,120,by=20))
figLegend(x='topright', legend=colnames(Means),fill=bars.col,
          angle=bars.angle, density=bars.density)
```

 figLines

Wrapper for standardized use of lines()

Description

Wrapper function for standardized use of lines() with lab defaults for display

Usage

```
figLines(x, y, lines.lwd=NULL, lines.lty=NULL, lines.col=NULL, lines.pch=NULL)
```

Arguments

x,y	coordinate vectors of points to join
lines.lwd	Line width. Accessed from options if NULL
lines.lty	Line type. Accessed from options if NULL
lines.col	Line color. Accessed from options if NULL
lines.pch	point type. Default is no points. See points() for other types. Accessed from options if NULL

Value

None

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

See Also

lines(), figLabDefaults(), figSetDefaults(), figNewDevice(), figLines(),figPoints()

Examples

```
figNewDevice()
figPlotRegion(x=c(0,5), y=c(0,10))
figLines(c(0,10),c(0,10))
figAxis(side=1,lab.text='X-axis 1', scale.at=seq(from=0,to=10,by=2))
figAxis(side=2,lab.text='Startle Response', scale.at=seq(from=0,to=10,by=2))
```

figNewDevice	<i>Opens device for graphing</i>
--------------	----------------------------------

Description

Opens a device for graphing (window,pdf,tiff) and establishes default parameters for standardized graphs

Usage

```
figNewDevice(Width=7,Height=7, Type='window',File, Res=300)
```

Arguments

Width,Height	the (nominal) width and height of the canvas of the plotting window in inches. Default = 7.
Type	Device type: Window, pdf,tiff. Devault = 'Window'. Window will open a window using either windows(), quartz(), or X11() depending on the OS. tiff and pdf will graph to that type of file.
File	File name as string. Used by tiff and pdf
Res	The nominal resolution in ppi used by tiff. Default = 300

Value

None

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

See Also

figLabDefaults(), figSetDefaults(), windows(), tiff(), pdf()

Examples

```
figNewDevice(Type='tiff',File='Test.tiff', Res=72)
figNewDevice(Type='Windows')
```

figPlotRegion *Sets up a plot region for later plotting*

Description

Sets up a plot region for later plotting with fig functions. Typically use is to establish the x and y ranges for region and otherwise leave blank for later drawing with fig functions.

Usage

```
figPlotRegion(x, y, xlab = NA, ylab = NA, axes=FALSE, type='n')
```

Arguments

x,y	min and max for x and y plot region
xlab, ylab	Labels for x and y axes. Typically left blank (NA)
axes	a logical value indicating whether both axes should be drawn on the plot. Typically not included (FALSE)
type	1-character string giving the type of plot desired. Typically no data are plotted ('n'). see type in plot() for more info

Value

None

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

See Also

plot(), figLabDefaults(), figSetDefaults(), figNewDevice(), figLines(),figPoints()

Examples

```
figNewDevice()  
figPlotRegion(x=c(0,5), y=c(0,10))  
figLines(c(0,10),c(0,10))  
figAxis(side=1,lab.text='X-axis 1', scale.at=seq(from=0,to=10,by=2))  
figAxis(side=2,lab.text='Startle Response', scale.at=seq(from=0,to=10,by=2))
```

figPoints	<i>Wrapper for standardized use of points()</i>
-----------	---

Description

Wrapper function for standardized use of points() with lab defaults for display

Usage

```
figPoints(x, y, type='p', points.lwd=NULL, points.pch=NULL,
          points.col=NULL, points.bg=NULL, points.cex=NULL)
```

Arguments

x,y	coordinate vectors of points to join
type	character indicating the type of plotting; actually any of the types as in plot.default. Default = 'p'
points.lwd	Line width for points. Accessed from options if NULL
points.pch	plotting 'character', i.e., symbol to use. This can either be a single character or an integer code for one of a set of graphics symbols. The full set of S symbols is available with pch = 0:18, see the examples below. (NB: R uses circles instead of the octagons used in S.). Accessed from options if NULL
points.col, points.bg, points.cex	Point color, bg, and cex. Accessed from options if NULL

Value

None

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

See Also

points(), figLabDefaults(), figSetDefaults(), figNewDevice(), figLines(),figLines()

Examples

```
X = rep(2:9,4)+jitter(rep(0,32))
Y = X + rnorm(length(X),0,5)
m = lm(Y ~ X)
dNew = data.frame(X=seq(2,9,by=.01))
p = modelPredictions(m,dNew)
figNewDevice() #default is for windows(), can use quartz, tiff, or pdf as Type
figPlotRegion(x=c(0,10),y=c(0,10))
figConfidenceBand(p$X,p$Predicted,p$CIlo,p$CIHi)
```

```
figPoints(X,Y)
figLines(p$X,p$Predicted)
figAxis(side=1,lab.text='X-axis 1', scale.at=seq(from=0,to=10,by=2))
figAxis(side=2,lab.text='Startle Response', scale.at=seq(from=0,to=10,by=2))
```

figSetDefaults	<i>Saves list of graphing parameters in options</i>
----------------	---

Description

Saves a list of graphing parameters, typically created by figLabDefaults) in options for later use in graphing by fig functions.

Usage

```
figSetDefaults(FigPars)
```

Arguments

FigPars A list of graphing parameters

Value

None

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

See Also

figLabDefaults(), options()

Examples

```
FigPars = figLabDefaults()
FigPars$plot.lwd = 2
figSetDefaults(FigPars)
```

figStripChart	<i>Create strip chart on plot</i>
---------------	-----------------------------------

Description

Adds a strip chart (variant of a rug plot that includes density info) to X (or other) axis on a plot

Usage

```
figStripChart(x, side=1, sshift=0.3, adjoffset=1, strip.col='gray',  
             strip.pch=15, strip.cex= 0.2)
```

Arguments

x	vector of data to plot
side	axis for plot, 1=bottom (default), 2=left, 3= top, 4= right
sshift	scaling parameter for location of plot. Use default
adjoffset	scaling parameter for dot spacing
strip.col	color of dots. Default is gray
strip.pch	point type for dots. Default is 15 (small dot)
strip.cex	scaling parameter for size of dots

Value

No value is returned

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

figText	<i>Wrapper for standardized use of text()</i>
---------	---

Description

Wrapper function for standardized use of text() with lab defaults for display

Usage

```
figText(x, y, label, text.font = NULL, text.cex = NULL, text.adj = NULL, text.col=NULL)
```

Arguments

<code>x,y</code>	coordinates to plot text
<code>label</code>	label/text to plot
<code>text.font</code>	Text font. Accessed from options if NULL
<code>text.cex</code>	Text cex. Accessed from options if NULL
<code>text.adj</code>	Text adj. Accessed from options if NULL
<code>text.col</code>	Text color. Accessed from options if NULL

Value

None

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

See Also

`lines()`, `figLabDefaults()`, `figSetDefaults()`, `figNewDevice()`, `figLines()`, `figPoints()`

Examples

```
figNewDevice()
figPlotRegion(x=c(0,5), y=c(0,10))
figLines(c(0,10),c(0,10))
figAxis(side=1,lab.text='X-axis 1', scale.at=seq(from=0,to=10,by=2))
figAxis(side=2,lab.text='Startle Response', scale.at=seq(from=0,to=10,by=2))
figText(0,9, 'Figure label')
```

lmSupport-deprecated *Deprecated Functions in lmSupport Package*

Description

These functions are provided for compatibility with older versions of the **lmSupport** package and may be removed eventually. These functions may not necessarily work as in previous versions of the **lmSupport** package. It is strongly recommended that you update your code to use the new functions.

Usage

```
lm.boxCox(...)  
lm.codeRegressors(...)  
lm.correctSE(...)  
lm.deltaR2(...)  
lm.describeData(...)  
lm.describeGroups(...)  
lm.figSum(...)  
lm.mergeData(...)  
lm.pointEstimates(...)  
lm.readDat(...)  
lm.removeCases(...)  
lm.renameVar(...)  
lm.setContrasts(...)  
lm.setRownames(...)  
lm.stripChart(...)  
lm.sumSquares(...)  
lm.writeDat(...)
```

Arguments

... pass arguments down.

Details

`lm.boxCox` is now a synonym for the [modelBoxCox](#) function. `lm.codeRegressors` is now a synonym for the [varRegressors](#) function. `lm.correctSE` is now a synonym for the [modelCorrectSE](#) function. `lm.deltaR2` is now a synonym for the [modelCompare](#) function. `lm.describeData` is now a synonym for the [varDescribe](#) function. `lm.describeGroups` is now a synonym for the [varDescribeBy](#) function. `lm.figSum` is now a synonym for the [varPlot](#) function. `lm.mergeData` is now a synonym for the [dfMerge](#) function. `lm.pointEstimates` is now a synonym for the [modelPredictions](#) function. `lm.readDat` is now a synonym for the [dfReadDat](#) function. `lm.removeCases` is now a synonym for the [dfRemoveCases](#) function. `lm.renameVar` is now a synonym for the [varRename](#) function. `lm.setContrasts` is now a synonym for the [varContrasts](#) function. `lm.setRownames` is now a synonym for the [dfRownames](#) function. `lm.sumSquares` is now a synonym for the [modelEffectSizes](#) function. `lm.stripChart` is now a synonym for the [figStripChart](#) function. `lm.writeDat` is now a synonym for the [dfWriteDat](#) function.

modelAssumptions

Assess Linear Model Assumptions

Description

Provides diagnostic graphs and score tests to evaluate linear model assumptions of normality, constant variance and linearity. Follows best practices and uses many functions from car package.

Usage

```
modelAssumptions(Model, Type = "NORMAL", ID=row.names(Model$model), one.page = TRUE)
```

Arguments

Model	a linear model produced by <code>lm</code> .
Type	Type = c('NORMAL', 'CONSTANT', 'LINEAR') for normally distributed residuals with constant variance, and linear (e.g., mean of residuals 0 for all Y')
ID	Use to identify points. Default = row.names(model\$model). NULL = no identification
one.page	logical; display all graphs on one page if TRUE (Default).

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

References

Fox, J. (1991). Regression diagnostics. SAGE Series (79) Quantitative Applications in the Social Science.

Examples

```
m = lm(interlocks~assets+nation, data=car::Ornstein)
modelAssumptions(m, 'NORMAL')
modelAssumptions(m, 'CONSTANT')
modelAssumptions(m, 'LINEAR', ID=NULL)
```

modelBoxCox

Calculates lambda for Box-Cox power transformation

Description

Calculates and plots log-likelihoods lambda for power transformation of response variable. Reports chi-square test of lambda <> 1. All values of Y must > 0 or function will crash. Add offset to Y if necessary (see example). Default lambda range is -2 to 2. Uses `boxCox()` from car package.

Usage

```
modelBoxCox(Model, Lambdas = seq(-2, 2, by = 0.1))
```

Arguments

Model	an unweighted linear model, produced by <code>lm</code> .
Lambdas	a vector of lambda values to plot. Default is <code>seq(-2,2,by=0.1)</code>

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

References

Box, G. E. P. & Cox, D. R. (1964). An analysis of transformations (with discussion). *Journal of the Royal Statistical Society*, 26, 211-252.

See Also

boxCox(), boxcox()

Examples

```
m = lm(interlocks + 1 ~ assets+nation, data=Ornstein)
modelBoxCox(m)
```

modelCaseAnalysis *Provides graphs and/or tests for problematic cases for a linear model*

Description

Provides diagnostic graphs and visual cut points for identification of points that are univariate outliers, high leverage, regression outliers, and/or influential

Usage

```
modelCaseAnalysis(Model, Type = "RESIDUALS", Term = NULL, ID = row.names(Model$model))
```

Arguments

Model	a linear model produced by <code>lm</code> .
Type	Type = c('RESIDUALS', 'UNIVARIATE', 'HATVALUES', 'COOKSD', 'DFBETAS', 'INFLUENCEPLOT', 'COVRATIO') RESIDUALS (default) = regression outliers, UNIVARIATE = univariate outliers, HATVALUES = leverage, COOKSD = model influence, DFBETAS= individual parameter influence, INFLUENCEPLOT= leverage X influence, COVRATIO = inflation of SEs.
Term	Term from model to display. Used only by DFBETAS. DEFAULT is NULL with all terms displayed
ID	Use to identify points. Default = row.names(Model\$model). NULL = no identification

Value

Side effect of plot is main goal for function. Also returns a list with Rownames and CaseAnalysis Values for cases identified. No list returned if DFBETAS without single term identified.

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

References

Fox, J. (1991). Regression diagnostics. SAGE Series (79) Quantitative Applications in the Social Science.

Examples

```
m = lm(interlocks~assets+nation, data=Ornstein)
Cases = modelCaseAnalysis(m, 'RESIDUALS')
Ornstein[Cases$Rownames, ]

modelCaseAnalysis(m, 'DFBETAS')
modelCaseAnalysis(m, 'DFBETAS', 'assets')
```

modelCompare

F-tests for nested models

Description

Calculates F-test to compare two models to determine if ModelA significantly reduces SSE from ModelC. Also reports Partial eta² and Delta R² for this model comparison. ModelC should contain subset of ModelA regressors.

Usage

```
modelCompare(ModelC, ModelA)
```

Arguments

ModelC	a linear model, produced by lm. This compact model should include a subset of regressors from ModelA
ModelA	a linear model, produced by lm. This augmented model should include all regressors from ModelC plus additional regressors.

Details

Calculates F test for model comparison $F = ((sseC - sseA) / (pA - pC)) / (sseA / (N - pA))$ $ndf = pA - pC$ $ddf = N - P$

Value

Returns a list with results for model comparison, sses, and other relevant fields

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

Examples

```
mC = lm(interlocks~assets, data=Ornstein)
mA = lm(interlocks~assets+nation, data=Ornstein)
modelCompare(mC, mA)
```

modelCorrectSE	<i>Calculates White (1980)'s heteroscedasticity-corrected SEs and Tests for a linear model</i>
----------------	--

Description

Calculates heteroscedasticity-corrected SEs and associated tests for regression coefficients based on method described by White (1980) using `hccm()` from `car` package. Prints tables with original and corrected results and returns corrected coefficient table

Usage

```
modelCorrectSE(Model, Digits=3)
```

Arguments

Model	an unweighted linear model, produced by <code>lm</code> .
Digits	digits to print in table output. Default =3

Value

Returns the `lm` coefficients table with corrected SEs and associated tests

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

References

- Fox, J. (2008). *Applied Regression Analysis and Generalized Linear Models*, Second Edition. Sage.
- Cribari-Neto, F. (2004). Asymptotic inference under heteroskedasticity of unknown form. *Computational Statistics and Data Analysis*, 45, 215-233.
- Long, J. S. and Ervin, L. H. (2000). Using heteroscedasticity consistent standard errors in the linear regression model. *The American Statistician*, 54, 217-224.
- White, H. (1980). A heteroskedastic consistent covariance matrix estimator and a direct test of heteroskedasticity. *Econometrica*, 48, 817-838.

See Also

hccm() in car package

Examples

```
m = lm(interlocks~assets+nation, data=Ornstein)
modelCorrectSE(m)
```

modelEffectSizes *Calculates effect size indices based on Sums of Squares*

Description

Calculates unique SSRs, SSE, SST. Based on these SSS, it calculates partial eta² and delta R² for all effects in a linear model object. For categorical variables coded as factors, it calculates these for multi-df effect. Manually code regressors to get 1 df effects Uses car::Anova() with Type 3 error

Usage

```
modelEffectSizes(Model, Print = TRUE, Digits = 4)
```

Arguments

Model	a linear model, produced by lm
Print	Display results to screen. Default = TRUE
Digits	Number of digits for printing effect sizes

Value

Returns a list with fields for effect sizes, SSE, and SST.

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

See Also

Anova()

Examples

```
m = lm(interlocks~assets+nation, data=Ornstein)
modelEffectSizes(m)
```

modelErrors	Returns model errors (residuals) from lm object
-------------	---

Description

Simple wrapper to return model errors using residuals() function. Implemented simply to match terminology to 610/710 GLM course. Also prints (but does not return) model SSE

Usage

```
modelErrors(Model)
```

Arguments

Model an lm model object

Value

Returns vector of model errors (residuals) from sample

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

See Also

residuals, lm

Examples

```
m = lm(interlocks~assets+nation, data=Ornstein)
modelErrors(m)
```

modelPower	Calculate power for GLM tests
------------	-------------------------------

Description

Wrapper to calculate power for tests of parameter estimates or full model in GLM based on Cohen's tables and using pwr.f2.test in pwr package. Allows use of partial eta squared or delta R2 rather than just f2 as effect size. If you provide power, it returns v, if you provide v, it returns power. You must specify effect size as either f2, partial eta2, or delta R2 with model R2.

Usage

```
modelPower(u=NULL, v=NULL, alpha=0.05, power=NULL, f2=NULL, peta2=NULL, dR2=NULL, R2=NULL)
```

Arguments

u	numerator degrees of freedom for effect; PA-PC in model comparison terms
v	denominator degrees of freedom for effect; N-PA in model comparison terms
alpha	alpha for statistical test
power	power for statistical test
f2	f2 effect size
peta2	partial eta2 effect size
dR2	delta R2 effect size; if provided must also specify R2
R2	Model R2, only need if using Delta R2 as effect size

Value

Returns either power or v from analysis. $N^* = v + PA$

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

See Also

pwr.f2.test

Examples

```
modelPower(u=1, power=.90, peta2=.157)
modelPower(u=1, v=75, peta2=.157)
```

modelPredictions	<i>Provides predicted values for sample or new data. New predictions include SEs</i>
------------------	--

Description

If no data are provided, modelPredictions returns a numeric vector predicted values for the sample, functioning as a simple wrapper for fitted.values(). If a dataframe with new values for Xs are provided, modelPredictions adds predicted values and SEs for these new data to the dataframe using predict() from car package.

Usage

```
modelPredictions(Model, Data=NULL, Label = NULL, Type = 'response')
```

Arguments

Model	a linear model, produced by lm.
Data	a dataframe containing cases for predictions. Must include all regressors from model. Default is NULL with predictions returned for the current sample.
Label	A string label to append to variable names for predicted values, CIs and SE. Default is NULL with no append
Type	'response' or 'link'. Used only for glm objects. see predict()

Value

If Data=NULL, returns a numeric vector of predicted values for sample. If Data are provided, adds four new columns at the front of the dataframe. These variables are named Predicted (predicted value), CI_{Lo} (lower bound of - 1 SE from Predicted), CI_{Hi} (upper bound of + 1 SE), and SE (Standard error of predicted value). NOTE: For GLM, +-1 SE are calculated on the link scale and then converted to the response scale (which will be asymmetric) if Type = response. If Label is not NULL, then Label is appended to end of these four variable names.

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

See Also

predict(), fitted.values()

Examples

```
##make plot of predicted values with 1SE error bands for CAN
m = lm(interlocks~assets+nation, data=Ornstein)
dNew = data.frame(assets = seq(1000,100000, by=1000),nation='CAN')
dNew = modelPredictions(m, dNew)
plot(dNew$assets,dNew$Predicted, type = 'l', col= 'red')
lines(dNew$assets,dNew$CILo, type = 'l', col= 'gray', lwd =.5)
lines(dNew$assets,dNew$CIHi, type = 'l', col= 'gray', lwd =.5)

##Return predicted values for sample
P = modelPredictions(m)
```

modelR2

Model R2, adjusted R2 and F-test

Description

Reports model R2, adjusted R2, and F-test of model R2.

Usage

```
modelR2(Model, Print=TRUE)
```

Arguments

Model an lm model object
 Print print results to screen. Default is TRUE

Value

Returns full list object from modelSummary() with many stats

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

See Also

lm, modelSummary, summary

Examples

```
m = lm(interlocks~assets+nation, data=Ornstein)
modelR2(m)
```

modelRmd	<i>Returns a formatted string for stats reporting from a model in R Markdown</i>
----------	--

Description

Returns a formatted string to report the B, CI, partial-eta2, t, and p-value for an effect from an lm model. This formatted string is appropriate for use in an R Markdown document for a dynamic report of research results.

Usage

```
modelRmd(effect, mod, B=1, CI=B, statistic='t', pe=2)
```

Arguments

effect Text label for effect from lm
 mod object returned from lm()
 B number of decimal places for report of B; NULL if B should not be reported
 CI number of decimal places for report of Bs in 95 CI; NULL if CI should not be reported
 statistic test statistic to report: 't' or 'F'
 pe number of decimal places for report of partial eta2. Null if should not be reported

Value

Returns a formatted string that can be directly included in a R Markdown file for a dynamic report

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

modelSummary	<i>summary of results for lm model</i>
--------------	--

Description

This is a modified version of summary for use with an lm, glm, or lmer object. It provides results that align better with Brauer/Curtin perspective on these linear models from their graduate statistics series

Usage

```
modelSummary(Model, t = TRUE, Print= TRUE, Digits = 4)
```

Arguments

Model	a linear model, produced by lm.
t	Indicates if t-statistics (TRUE; Default) or F-statistics should be reported for tests of parameter estimates
Print	Print output to screen. Default is TRUE
Digits	Number of digits for values in coefficients table. Default = 4

Details

Reports model summary results from an lm object. Results include parameter estimates and their tests, SSE, model R2

Value

Returns a list with results for model.

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

See Also

summary, modelR2

Examples

```
m = lm(interlocks~assets+nation, data=Ornstein)
modelSummary(m)
```

varContrasts *Set Factor Contrasts*

Description

Calculates contrast matrix for a specified contrast type. Options include DUMMY, POC, HELMERT, EFFECTS

Usage

```
varContrasts(TheFactor, Type = "DUMMY", RefLevel = length(levels(TheFactor)),
             POCList = NULL, Labels = NULL)
```

Arguments

TheFactor	factor from dataframe
Type	type of contrast, Options include DUMMY (default), POC, HELMERT, or EFFECTS
RefLevel	Reference level for contrast. Only applies to DUMMY, HELMERT, and EFFECTS. For DUMMY: RefLevel is numeric index of control/reference category (i.e. coded 0 for all regressors). For HELMERT: RefLevel = 1 indicates reverse HELMERT (i.e., last vs. earlier, second to last vs. earlier, etc), RefLevel = 'Highest Level' indicates forward HELMERT (i.e., first vs. later, second vs. later, etc). For EFFECTS: RefLevel is numeric index of excluded level.
POCList	if Type = POC, a list of Contrasts is required in POCList; e.g., list(c(1,0,-1), c(-1,2,-1)). Best to provide as whole numbers. Function will re-scale to unit weighted contrasts.
Labels	if Type = POC, Labels can be provided. If NULL (Default), contrast labels are POC1, POC2, etc.

Details

Use the contrast matrix with contrasts() to set contrast for a specific factor in dataframe.

Value

Returns contrast matrix for indicated type of contrast.

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

See Also

[contrasts](#)

Examples

```
d = data.frame(f=factor(c('f1', 'f2', 'f3')))
contrasts(d$f)

##set as DUMMY with last category as reference
contrasts(d$f) = varContrasts(d$f, Type='DUMMY', RefLevel = 3)

##set as POC with user defined labels
contrasts(d$f) = varContrasts(d$f, Type='POC', POCList = list(c(2,-1,-1),c(0,1,-1)),
  Labels = c('f1_v_f2f3', 'f2_v_f3'))

##set as reverse HELMERT
contrasts(d$f) = varContrasts(d$f, Type='HELMERT', RefLevel = 1)

##set as EFFECTS, excluding f3 vs. grand mean contrast
contrasts(d$f) = varContrasts(d$f, Type='EFFECTS', RefLevel = 3)
```

varDescribe

Provides typical descriptive statistics for data frame

Description

Provides three levels of detail regarding descriptive statistics for a data frame. Based on describe() function from psych package

Usage

```
varDescribe(Data, Detail = 2, Digits=2)
```

Arguments

Data	a data frame
Detail	Indicates level of detail for descriptives, 1=minimal, 2=typical (default), 3= detailed
Digits	Number of decimal places to display; NULL = display all sig digits. Default =2.

Value

Returns table with descriptive statistics rounded to digits.

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

See Also

describe lm.describeGroups describe.by

Examples

```
varDescribe(Ornstein)
varDescribe(Ornstein, Detail=3)
varDescribe(Ornstein, Detail=2, Digits=1)
```

varDescribeBy	<i>Provides common descriptives for dataframe by factor(s)</i>
---------------	--

Description

Provides commons descriptive statistics for a data frame split on some factor or combination of factors. Essentially a wrapper for varDescribe() and by().

Usage

```
varDescribeBy(Data, IVList)
```

Arguments

Data	a dataframe
IVList	list of one or more factors from data frame

Value

An object of class "by", giving the results from varDescribe() applied to each subset.

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

Examples

```
varDescribeBy(Adler, list(Adler$expectation, Adler$instruction))
```

varMarkdown	<i>Returns a formatted string for stats reporting in R Markdown</i>
-------------	---

Description

Returns a formatted string to report the B, CI, partial-eta2, t, and p-value for an effect from an lm mode. This formatted string is appropriate for use in an R Markdown document for a dynamic report of research results.

Usage

```
varMarkdown(effect, mod, modsum, statistic='t', B=1, CI=B, pe=2)
```

Arguments

effect	Text label for effect from lm
mod	object returned from lm()
modsum	object returned from summary() or modelSummary()
statistic	test statistic to report: 't' or 'F'
B	number of decimal places for report of B; NULL if B should not be reported
CI	number of decimal places for report of Bs in 95 CI; NULL if CI should not be reported
pe	number of decimal places for report of partial eta2. Null if should not be reported

Value

Returns a formatted string that can be directly included in a R Markdown file for a dynamic report

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

varOdd *Tests if Number is Odd*

Description

Returns result of test if Number is Odd.

Usage

```
varOdd(Number)
```

Arguments

Number	Number to test
--------	----------------

Value

Returns boolean to indicate result of test

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

Examples

```
varOdd(3)
varOdd(4)
```

varParse	<i>Returns a subset of digits from a Number</i>
----------	---

Description

Returns a subset of digits from a Number.

Usage

```
varParse(Number, UpperDigit=1, LowerDigit=1)
```

Arguments

Number	Number to parse
UpperDigit	Location in base ten of upper end of digits to return
LowerDigit	Location in base ten of lower end of digits to return

Value

Returns a subset of the digits in Number

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

Examples

```
varParse(1234,100,10)
varParse(1234,1,1)
varParse(1234,1000,1000)
```

varPlot	<i>Creates histogram, optional rug/strip and density plots, and generates univariate descriptive statistics</i>
---------	---

Description

Represents important aspects of a variable/vector both visually (histogram, rug or strip, and density plots) and with descriptive statistics of varying detail

Usage

```
varPlot(TheVar, VarName = '', IDs = NULL, AddPoints = 'Strip',
        AddDensity = TRUE, Detail = 2)
```

Arguments

TheVar	A variable/vector to visualize
VarName	The variable name of TheVar as string. Default = ""
IDs	Rownames for interactive identification of data points, Default is NULL with no identification done
AddPoints	Strip (default), Rug, or None
AddDensity	TRUE (default) or FALSE to include density plot
Detail	1-3 of increasing detail for descriptives using varDescribe()

Value

Prints descriptive statistics table and creates graphic as side effect. Returns list with Indices, Rownames, and Values if identify is not NULL

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

See Also

hist(), rug(), varStripPlot(), density(), varDescribe(), describe(), identify()

Examples

```
varPlot(Prestige$income, 'Income') #default use strip
varPlot(Prestige$income, AddPoints='RUG')
varPlot(Prestige$income, IDs=rownames(Prestige))
```

varRecode	<i>Recode levels of variable</i>
-----------	----------------------------------

Description

Recodes levels of variable from old values to new values. Levels in Old are recoded to levels in New by matching position in these two vectors.

Usage

```
varRecode(Var, Old, New)
```

Arguments

Var	A variable to recode.
Old	Vector with original levels of Var
New	vector with new levels

Value

Returns variable with new levels

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

See Also

recode

Examples

```
##d$rIV1 = varRecode(d$IV1, c(-1,1), c(-.5, .5))
##d$rIV2 = varRecode(d$IV2, c(1,2,3), c(-.667, .333, .333))
##d$rIV3 = varRecode(d$IV3, c('A', 'B'), c('C', 'D'))
```

varRegressors	<i>Adds actual numeric regressors for factor to dataframe as new variables</i>
---------------	--

Description

Adds new variables/columns in dataframe to represent numeric regressors for a factor. Factors are coded using their currently defined contrast codes. This function is useful for control of a factor covariate when graphing and ignoring this factor and/or other lower-level control variables. For this purpose, POC coding will typically be set for factor prior to using `lm.codeRegressor`

Usage

```
varRegressors(Data, VarName, RegressorNames = NULL)
```

Arguments

Data The dataframe to add regressors
 VarName Character string name of variable to code regressor for
 RegressorNames Optional variable names for regressors.

Value

Returns original data frame (Data) with addition of new regressors.

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

Examples

```
d = Ornstein
contrasts(d$nation) = varContrasts(d$nation, Type='POC',
  POCList = list(c(3,-1,-1, -1),c(0,2,-1, -1), c(0,0,1,-1)))
d = varRegressors(d,'nation')
```

varRename

Rename Variable in Dataframe

Description

Renames a variable in specified dataframe.

Usage

```
varRename(Data, From, To)
```

Arguments

Data	a dataframe object
From	vector of original name(s) of variable(s) as strings
To	vector of new name(s) of variable(s) as strings

Value

Returns dataframe with new variable names for specified variable(s)

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

Examples

```
d = data.frame(x=1:10, y=11:20)
names(d)
d = varRename(d, c('x', 'y'), c('x1', 'y1'))
names(d)
```

varReverse	<i>Reverse score an ordinal or boolean scored item/variable</i>
------------	---

Description

Reverse scores an item that was ordinal/interval scored or boolean.

Usage

```
varReverse(Var, LowAnchor, HighAnchor)
```

Arguments

Var	A variable to reverse score.
LowAnchor	Absolute low value for variable
HighAnchor	Absolute high value for variable

Value

Returns variable new (reversed) scores

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

See Also

recode

Examples

```
##d$Item5r = varReverse(d$Item5, 1, 5)
```

varScore	<i>Creates a total score from a sum of items</i>
----------	--

Description

Creates a total score from a sum of items in a data frame. Can do range checking for items, reverse scoring of items, and prorating for missing data.

Usage

```
varScore(Data, Forward, Reverse=NULL, Range = NULL, Prorate = TRUE, MaxMiss = .20)
```


Arguments

Data	a dataframe that contains item scores among other variables
Forward	a vector of variable names to indicate the items that should be summed as is (in contrast to reverse scored). All items should be listed in EITHER Forward or Reverse argument
Reverse	a vector of variable names to indicate the items that should be summed after reverse scoring the items. Range argument (see below) must also be specified to reverse score items. Default is NULL which indicates no items are reverse scored. All items should be listed in EITHER Forward or Reverse argument
Range	A numeric vector with two values for low and high anchor values for items. Must be specified if any items will be reverse scored. Used also to do range checking for all items. Default is NULL which indicates no range checking and no reverse scored items
Prorate	A boolean to indicate if total score should be prorated for missing data. Default is TRUE.
MaxMiss	Maximum acceptable percentage of missing data before total score will be set to missing. Implemented regardless if Prorate is TRUE or FALSE. However, if Prorate is false, should probably be set to 0

Details

This is a flexible routine to score measures that consist of sums of items.

Value

Returns vector of total scores for each participant

Author(s)

John J. Curtin <jjcurtin@wisc.edu>

Examples

```
##Same code not executable with sample dataframe
##varScore(d, c('I1', 'I3', 'I4'), Reverse= c('I2', 'I5'),
##      Range = c(1,5), Prorate=TRUE, MaxMiss = .25)
```

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