

Package ‘nima’

September 5, 2017

Title Nima Hejazi's R Toolbox

Version 0.4.5

Description Miscellaneous R functions developed over the course of statistical research and scientific computing. These include, for example, utilities that supplement the existing idiosyncrasies of the R language, extend existing plotting functionality and aesthetics, provide alternative presentations of matrix decompositions, and extend access to command line tools and systems-level information.

Depends R (>= 3.2.3)

Imports utils, stats, gtools, survival, gridExtra, assertthat, ProjectTemplate, devtools, ggthemes, ggplot2, scales, plyr, grid

Suggests roxygen2, testthat

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URL <https://github.com/nhejazi/nima>

BugReports <https://github.com/nhejazi/nima/issues>

LazyData true

RoxygenNote 6.0.1

NeedsCompilation no

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Repository CRAN

Date/Publication 2017-09-05 08:30:37 UTC

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|--------|---|
| absmax | <i>Maximum of Absolute Values of Vector</i> |
|--------|---|

Description

Take the maximum of the absolute values of an input vector.

Usage

```
absmax(x, na.rm = FALSE)
```

Arguments

| | |
|-------|--|
| x | A numeric vector or array. |
| na.rm | A logical indicating whether missing values should be removed. |

Value

The maximum of the absolute values of elements of the input vector.

Examples

```
x <- c(5, 3, -9, -100, 3.14159, 7.5)
absmax(x)
```

| | |
|-----------|--------------------------------|
| attrnames | <i>Get Names of Attributes</i> |
|-----------|--------------------------------|

Description

Get the names of the attributes of an input object.

Usage

```
attrnames(obj)
```

Arguments

obj Any object.

Value

Vector of character strings with the names of the attributes.

Examples

```
x <- matrix(1:100, ncol=5)
colnames(x) <- LETTERS[1:5]
attrnames(x)
```

| | |
|------|---------------------------------------|
| bioc | <i>Conveniently Load Bioconductor</i> |
|------|---------------------------------------|

Description

Load Bioconductor's "biocLite" function by wrapping "source".

Usage

```
bioc()
```

Details

Wrapper to `source("https://bioconductor.org/biocLite.R")`

| | |
|-------|--|
| clear | <i>Clear the Current Screen/Buffer</i> |
|-------|--|

Description

Clear the screen with a call to `system` and `clear`.

Usage

```
clear()
```

Details

This function is merely a call to `system("clear")`

Examples

```
## Not run: system("clear")
```

| | |
|--------|-------------------------------------|
| commas | <i>Add Commas to a Large Number</i> |
|--------|-------------------------------------|

Description

Convert a number to a string, with commas inserted at every 3rd digit.

Usage

```
commas(numbers)
```

Arguments

`numbers` Vector of non-negative numbers (will be rounded to integers)

Value

Character string with numbers written like "5,771,009".

Examples

```
commas(c(2300, 9000, 21456, 987654890, 1256787, 345765, 1432))
```

| | |
|---------|---|
| compFun | <i>Compare Two Similar Objects including Missing Data Patterns.</i> |
|---------|---|

Description

Check whether two objects are the same, including patterns of NAs.

Usage

```
compFun(a, b)
```

Arguments

| | |
|---|--|
| a | An object of a given type. |
| b | An object similar in type to that given above. |

Value

Boolean object with TRUE indicating an element is the same.

Examples

```
x <- c(5, 8, 9, NA, 3, NA)
y <- c(5, 2, 9, 4, NA, NA)
compFun(x,y)

x <- matrix(rnorm(1000), ncol = 20)
x[sample(seq(along = x), 100)] <- NA
all(compFun(x,x))
dim(compFun(x,x))

x <- as.list(c(5, 8, 9, NA, 3, NA))
y <- as.list(y)
sapply(compFun(x,y), function(a) sum(!a))

x <- as.data.frame(x)
y <- as.data.frame(y)
sum(!compFun(x,y))
```

discrete_by_quantile *Discretize a vector*

Description

Discretizes a non-factor input vector and returns the result as numeric.

Usage

```
discrete_by_quantile(x)
```

Arguments

x A vector containing arbitrary data.

Value

A numeric vector with the data re-coded to based on the quantiles.

Examples

```
x <- rnorm(1000)
discrete_by_quantile(x)
```

exit *Exit R Without Saving*

Description

Exit R without saving workspace, using the ubiquitous UNIX syntax.

Usage

```
exit()
```

Details

This function is merely a call to `q("no")`.

| | |
|-----------|------------------------------------|
| factornum | <i>Convert a Factor to Numeric</i> |
|-----------|------------------------------------|

Description

Convert a factor with numeric levels to a non-factor (numeric).

Usage

```
factornum(x)
```

Arguments

x A vector containing a factor with numeric levels.

Value

The input factor made into a numeric vector.

Examples

```
x <- factor(c(3, 4, 9, 4, 9), levels = c(3,4,9))
factornum(x)
```

| | |
|------|--|
| hweb | <i>View HTML Version of Help Files</i> |
|------|--|

Description

View the HTML version of a help file while running R from the terminal.

Usage

```
hweb(...)
```

Arguments

... Help topics.

Details

Calls function [help](#) using argument `htmlhelp=TRUE`.

See Also

[help](#), [help.start](#)

Examples

```
## Not run: hweb(read.table)
```

`lmPlots_gg`*Linear Model Diagnostic Plots with ggplot2*

Description

Produce standard diagnostic plots for linear models using ggplot2.

Usage

```
lmPlots_gg(model)
```

Arguments

`model` A linear model object produced by `lm()`.

Examples

```
n <- 100; x1 <- rnorm(n); y1 <- rnorm(n);  
linmod <- lm(y1 ~ x1)  
lmPlots_gg(linmod)
```

`miss_ind`*Add missingness indicators to existing data.frame*

Description

Add indicator columns to a data.frame showing the pattern of missingness.

Usage

```
miss_ind(data, prefix = "miss_")
```

Arguments

`data` A numeric vector or array.
`prefix` A string used to name the indicator variables..

Value

An augmented data.frame with indicators for missingness patterns.

Examples

```
data <- data.frame(cbind(rnorm(10), runif(10)))
data[sample(nrow(data), 3), 1] <- NA
data[sample(nrow(data), 4), 2] <- NA
data <- miss_ind(data)
```

mse

Mean Squared Error (MSE)

Description

Easily compute the mean squared error for continuous predictions

Usage

```
mse(prediction, outcome)
```

Arguments

| | |
|------------|---|
| prediction | A numeric vector of predictions. |
| outcome | A numeric vector of outcomes actually observed. |

Examples

```
x <- rnorm(100)
y <- x^2
test_x <- rnorm(100)
test_y <- test_x^2
mod <- glm(y ~ x)
pred <- predict(mod, newx = as.data.frame(test_x))
error <- mse(prediction = pred, outcome = test_y)
```

newpkg

New Package Skeleton

Description

Generate a skeleton for new R packages by invoking a series of utilities from the Devtools package. This is merely a convenience utility for creating a new directory with minimal package contents.

Usage

```
newpkg(name = "new_pkg")
```

Arguments

| | |
|------|---|
| name | - Character for the name of the new package, to be passed directly to <code>devtools::create()</code> . |
|------|---|

| | |
|---------|-----------------------------|
| newproj | <i>New Project Skeleton</i> |
|---------|-----------------------------|

Description

Generate a skeleton for a data analysis project by calling `ProjectTemplate`

Usage

```
newproj(name = "ProjectTemplate", minimal = TRUE, ...)
```

Arguments

| | |
|---------|---|
| name | (character) - the name to be given to the new project directory |
| minimal | (character) - option to set up only a minimal project directory, passed to <code>ProjectTemplate::create.project</code> |
| ... | - options to be passed to <code>ProjectTemplate::create.project()</code> |

| | |
|----------|--|
| objsizes | <i>Calculate Sizes of Objects in Workspace</i> |
|----------|--|

Description

Calculate the sizes of all of the objects in the workspace.

Usage

```
objsizes(obj, bysize = TRUE)
```

Arguments

| | |
|--------|--|
| obj | Vector of object names. If missing, pull out all object names. |
| bysize | If TRUE, sort the objects from smallest to largest. |

Details

Calls `object.size` to get the sizes of a list of objects.

Value

A data frame with the only column being the size of each object in megabytes (Mb). The row names are the names of the objects.

Examples

```
print(output <- objsizes())
## Not run: sum(output)
```

| | |
|----------|--------------------|
| openfile | <i>Open a File</i> |
|----------|--------------------|

Description

Open a file using `system` and `open`.

Usage

```
openfile(file)
```

Arguments

| | |
|------|----------------------------------|
| file | File name (as character string). |
|------|----------------------------------|

Details

Open files from R by using the default operating system program.

Examples

```
## Not run: openfile("myplot.pdf")
```

| | |
|-----------|---|
| qqPlot_gg | <i>Quantile-Quantile Plots with ggplot2</i> |
|-----------|---|

Description

Produce standard quantile-quantile plots for modeling using `ggplot2`.

Usage

```
qqPlot_gg(x, distribution = "norm", ..., line.estimate = NULL,
          conf = 0.95, labels = names(x))
```

Arguments

| | |
|---------------|---|
| x | A numeric vector of residuals from a generalized linear model. |
| distribution | The reference probability distribution for residuals. |
| ... | Any additional parameters to be passed to distribution functions. |
| line.estimate | Should quantiles be estimated, if so which quantiles? |
| conf | The confidence level to be used with confidence intervals. |
| labels | The names to be used when identifying points on the Q-Q plot. |

Examples

```
n <- 100; x1 <- rnorm(n); y1 <- rnorm(n);  
linmod <- lm(y1 ~ x1)  
x <- linmod$residuals  
qqPlot_gg(x)
```

qrD

The QR decomposition of a matrix

Description

Computes the QR decomposition of a matrix.

Usage

```
qrD(x, tol = 1e-07)
```

Arguments

| | |
|-----|--|
| x | A matrix whose QR decomposition is to be computed. |
| tol | The tolerance for finding linear dependence in columns of x. |

Details

Calls function [qr](#) and returns more understandable output.

Value

A list of two matrices: Q and R.

See Also

[qr](#)

Examples

```
hilbert <- function(n) { i <- 1:n; 1/outer(i-1,i,"+") }  
h5 <- hilbert(5);  
qrD(h5)
```

| | |
|------------------|---|
| scale_color_nima | <i>Nima's ggplot2 theme - supplement: scale_color</i> |
|------------------|---|

Description

Nima's ggplot2 theme scale_color supplement: colors optimized via ColorBrewer

Usage

```
scale_color_nima(...)
```

Arguments

... Passed to [ggplot](#)

| | |
|-----------------|--|
| scale_fill_nima | <i>Nima's ggplot2 theme - supplement: scale_fill</i> |
|-----------------|--|

Description

Nima's ggplot2 theme scale_fill supplement: colors optimized via ColorBrewer

Usage

```
scale_fill_nima(...)
```

Arguments

... Passed to [ggplot](#)

| | |
|------------|-----------------------------|
| theme_nima | <i>Nima's ggplot2 theme</i> |
|------------|-----------------------------|

Description

Nima's ggplot2 theme: white background, colors optimized

Usage

```
theme_nima(base_size = 14, base_family = "Helvetica")
```

```
nima_theme(base_size = 14, base_family = "Helvetica")
```

Arguments

| | |
|-------------|---------------------------------|
| base_size | Base font size |
| base_family | Base font family |
| ... | Passed to theme |

Value

An object as returned by [theme](#)

See Also

[theme](#)

Examples

```
library(ggplot2)
p <- ggplot(mtcars, aes(y = mpg, x = disp, color = factor(cyl)))
p <- p + geom_point() + scale_fill_nima() + scale_color_nima() + theme_nima()
p
```

uniqlen

Find Number of Unique Values

Description

Get the number of unique values in an input vector.

Usage

```
uniqlen(vec, na.rm = TRUE)
```

Arguments

| | |
|-------|---------------------------------|
| vec | A vector of any type. |
| na.rm | If TRUE, remove missing values. |

Value

Number of unique values.

Examples

```
x <- c(1, 3, 1, 1, NA, 2, 2, 3, NA, NA, 1, 3, 1)
uniqlen(x)
uniqlen(x, na.rm=FALSE)
```

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