Package ‘Tmisc’

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Title Turner Miscellaneous
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Maintainer Stephen Turner <vustephen@gmail.com>
Description Miscellaneous utility functions for data manipulation, data tidying, and working with gene expression data.
http://stephenturner.github.io/Tmisc
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Imports dplyr, tibble, utils, rstudioapi, methods
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## addins

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
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Call these function as an addin to insert desired text at the cursor position. After installing Tmisc, hit the Addins menu, and optionally add a keyboard shortcut, e.g., Command+Shift+I, Alt+-, etc.
## Description

Aliases more pleasing to use in a dplyr pipeline:
are_all_equal

Are all equal?

Description

Are all the elements of a numeric vector (approximately) equal?

Usage

are_all_equal(x, na.rm = FALSE)

Arguments

x A numeric vector.

na.rm Remove missing values (FALSE by default; NAs in x will return NA).

Value

Logical, whether all elements of a numeric vector are equal.

Author(s)

Stephen Turner
Examples

are_all_equal(c(5, 5, 5))
are_all_equal(c(5, 5, 6))
are_all_equal(c(5, 5, NA, 6))
are_all_equal(c(5, 5, NA, 6), na.rm=TRUE)
5==5.000000001
identical(5, 5.000000001)
are_all_equal(c(5L, 5, 5.000000001))

Description

Prints the first \( n \) rows and columns of a data frame or matrix.

Usage

\( \text{corner}(x, n = 5) \)

Arguments

\( x \)  
A data.frame.

\( n \)  
The number of rows/columns to print.

Value

The corner of the data frame

Author(s)

Stephen Turner

Examples

\( \text{corner(mtcars)} \)
\( \text{corner(iris, n=4)} \)
counts2fpkm

Fragments per kilobase per million

**Description**

Takes a count matrix and a vector of gene lengths and returns an optionally log2-transformed FPKM matrix. Modified from edgeR.

**Usage**

```r
counts2fpkm(x, length, log = FALSE, prior.count = 0.25)
```

**Arguments**

- `x`: a matrix of counts
- `length`: a vector of length `nrow(x)` giving length in bases
- `log`: logical, if TRUE, then log2 values are returned.
- `prior.count`: average count to be added to each observation to avoid taking log of zero. Used only if `log`=TRUE.

**Value**

A matrix of FPKM values.

**Author(s)**

Davis McCarthy
Gordon Smyth

**Examples**

```r
## Not run:
library(readr)
library(dplyr)
countdata <- read_csv("http://files.figshare.com/2439061/GSE37704_featurecounts.csv")
counts <- countdata %>% select(countdata, starts_with("SRR")) %>% as.matrix
counts2fpkm(counts, countdata$length)

## End(Not run)
```
Description

Makes a vector of character strings from a list of valid names. Taken from Hmisc.

Usage

Cs(...)

Arguments

... any number of names separated by commas

Value

character string vector

Author(s)

Frank Harrell

Examples

Cs(a, cat, dog)
Cs(age, sex, race, bloodpressure, height)
Cs(you, must, quote, "things with spaces", 'or invalid !@#$ characters')

Description

The Datasaurus Dozen dataset

Usage

datasaurus

Format

Data frame with columns.
Source


Examples

```r
## Not run:
library(dplyr)
datasaurus %>%
group_by(set) %>%
  summarize(mean(x), mean(y), sd(x), sd(y), cor(x, y))
library(ggplot2)
ggplot(datasaurus, aes(x,y)) +
  geom_point() +
  geom_smooth(method="lm") +
  facet_wrap(~set)

## End(Not run)
```

deseqresult2tbl  Tidy DESeq2 result

Description

Returns a tidy version of a DESeq2 results table.

Usage

deseqresult2tbl(deseqresult, colname = "ensgene")

Arguments

deseqresult   Results from running results(dds) on a DESeqDataSet object.
colname       The name of the column you want to use for what DESeq puts in the row name.

Value

a tidy version of the DESeq2 results.

Author(s)

Stephen Turner
Examples

```r
## Not run:
res <- results(dds)
res <- deseqresult2tbl

## End(Not run)
```

---

**dfsigfig**  
*Round numeric columns of a data frame*

**Description**

Round the numeric columns of a data frame to a specified number of significant digits.

**Usage**

```r
dfsigfig(df, n = 3)
```

**Arguments**

- `df` A data.frame.
- `n` The number of significant digits to round off to.

**Value**

A data.frame rounded to `n` significant digits.

**Author(s)**

Stephen Turner

**Examples**

```r
## Not run:
dfsigfig(mtcars,1)

## End(Not run)
```
dokuwiki

Create tables in dokuwiki format

Description

Prints the supplied data frame or matrix using Dokuwiki's table syntax, optionally copying the data to the clipboard (Mac OS X only).

Usage

dokuwiki(x, headersep = "\^", sep = "|", clip = TRUE, ...)

Arguments

x
A data.frame.

headersep
The separator used between entries in the header row.

sep
The separator used between entries in all other rows.

clip
Whether or not to write the returned table to the clipboard (currently only supported on Mac OS X).

...
Further arguments passed to write.table.

Author(s)

Stephen Turner

Examples

dokuwiki(head(iris), clip=FALSE)
dokuwiki(head(mtcars), clip=FALSE, row.names=TRUE)

ellipses

Truncate a data frame with ellipses.

Description

Prints the specified number of rows of a data frame, followed by a row of ellipses. Useful for piping to knitr::kable() for printing a truncated table in a markdown document.

Usage

ellipses(df, n = 5L)
**fisherp**

**Arguments**
- **df** A data frame.
- **n** The number of rows to show before an ellipses row.

**Value**
A data frame truncated by a row of ellipses.

**Author(s)**
Stephen Turner

**Examples**
```r
effles(mtcars, 5)
```

---

**fisherp**  
*Fisher’s method to combine p-values.*

**Description**
Uses Fisher’s method to combine p-values from different tests.

**Usage**
```r
fisherp(x)
```

**Arguments**
- **x** A vector of p-values between 0 and 1.

**Value**
A combined p-value.

**Author(s)**
Stephen Turner

**Examples**
```r
fisherp(c(.042, .02, .001, 0.01, .89))
```
gghues

**Emulate ggplot2 default hues**

**Description**
This will emulate ggplot2’s hues, which are equally spaced hues around the color wheel, starting from 15.

**Usage**
gghues(n, start = 15)

**Arguments**
- **n** The Numeric; number of hues to generate.
- **start** Numeric; the place on the color wheel to start. ggplot2 default is 15.

**Value**
A vector of hues

**Author(s)**
Stephen Turner

**Examples**
n <- 10
gghues(3)
barplot(rep(1,n), col=gghues(n), names=gghues(n))
barplot(rep(1,n), col=gghues(n, start=15+180), names=gghues(n, start=15+180))

---

gg_na

**Plot missing data**

**Description**
Plots missing data as holes on a black canvas.

**Usage**
gg_na(df)

**Arguments**
- **df** A data.frame.
**gt2refalt**

---

**Author(s)**

Stephen Turner

**Examples**

```
# What a mess.
# Feature 10 is missing a lot. Observations 25 and 35 are completely missing.
# Most of features 40-45 are missing, except for the first few observations.
set.seed(2016-07-12)
x <- matrix(1, nrow=50, ncol=50)
x[sample(prod(dim(x)), 100)] <- NA
x <- data.frame(x)
x$X10[sample(length(x$X10), 25)] <- NA
x[c(25, 35), ] <- NA
x[1:40, 40:45] <- NA
gg_na(x)
```

---

**gt2refalt**

*Two-letter genotype from VCF GT*

---

**Description**

Get a two-letter genotype from a VCF GT field. Current implementation is quick and dirty, and only accepts 0/0, 0/1, or 1/1. Any other input to gt will return a missing value.

**Usage**

```
gt2refalt(gt, ref, alt)
```

**Arguments**

- `gt` The genotype field (must be 0/0, 0/1, or 1/1).
- `ref` The reference allele.
- `alt` The alternate allele.

**Value**

Return value

**Examples**

```
gt2refalt(gt="0/0", ref="R", alt="A")
gt2refalt(gt="0/1", ref="R", alt="A")
gt2refalt(gt="1/1", ref="R", alt="A")
gt2refalt(gt="0/2", ref="R", alt="A")
gt2refalt(gt="./.", ref="R", alt="A")
```
**Jensen-Shannon divergence**

**Description**

Calculates a distance matrix from a matrix of probability distributions using Jensen-Shannon divergence. Adapted from [http://enterotype.embl.de/enterotypes.html#dm](http://enterotype.embl.de/enterotypes.html#dm).

**Usage**

\[
\text{jsd}(M, \text{pseudocount} = 1e-06, \text{normalizeCounts} = \text{FALSE})
\]

**Arguments**

- **M**: a probability distribution matrix, e.g., normalized transcript compatibility counts.
- **pseudocount**: a small number to avoid division by zero errors.
- **normalizeCounts**: logical, whether to attempt to normalize by dividing by the column sums. Set to TRUE if this is, e.g., a count matrix.

**Value**

A Jensen-Shannon divergence-based distance matrix.

**Author(s)**

Stephen Turner

**Examples**

```r
set.seed(42)
M <- matrix(rpois(100, lambda=100), ncol=5)
colnames(M) <- paste0("sample", 1:5)
rownames(M) <- paste0("gene", 1:20)
Mnorm <- apply(M, 2, function(x) x/sum(x))
Mjsd <- jsd(Mnorm)
# equivalently
Mjsd <- jsd(M, normalizeCounts=TRUE)
Mjsd
plot(hclust(Mjsd))
```
**keep_top_n**  

*Keep rows from top groups of a column*

**Description**

Extract rows belonging to top \( n \) groups of a certain column.

**Usage**

```r
keep_top_n(.data, col, n = 10)
```

**Arguments**

- `.data` The data frame to operate on
- `col` A formula indicating the column to group over
- `n` The number of top groups to extract

**Value**

A data frame containing only rows belonging to the top \( n \) groups of the column.

**Author(s)**

Jeroen Janssens

**Examples**

```r
## Not run:
# All the cars
(nrow(mtcars))
# Only those in the top 2 groups based on the # carbs
nrow(keep_top_n(mtcars, ~carb, n=2))
## End(Not run)
```

---

**lmp**  

*Linear model p-value*

**Description**


**Usage**

```r
lmp(modelobject)
```
Arguments

modelobject  A model object of class lm.

Value

The p-value on the f-test of a linear model object testing the null hypothesis that $R^2 == 0$.

Examples

# simulate some (e.g. SNP genotype) data
set.seed(42)
n=20
d=data.frame(x1=rbinom(n,2,.5), x2=rbinom(n,2,.5))
d=transform(d, y=x1+x2+rnorm(n))
#fit the linear model
fit=lm(y ~ x1 + x2, data=d)
#shows that the F-test is 0.006641
summary(fit)
#can't access that p-value using this
names(summary(fit))
# this doesn't work either
names(fit)
coef(fit)

---

lowestnonzero  Lowest nonzero values

Description

Sometimes want to plot p-values (e.g., volcano plot or MA-plot), but if a statistical test returns a zero p-value, this causes problems with visualization on the log scale. This function returns a vector where the zero values are equal to the smallest nonzero value in the vector.

Usage

lowestnonzero(x)

Arguments

x  A vector of p-values between 0 and 1.

Value

A vector of p-values where zero values are exchanged for the lowest non-zero p-value in the original vector.
lsa

**Author(s)**
Stephen Turner

**Examples**

```r
c(.042, .02, 0, .001, 0, .89)
```

**Description**

Improved list of objects. Sorts by size by default. This was shamelessly stolen from [http://stackoverflow.com/q/1358003/654296](http://stackoverflow.com/q/1358003/654296).

**Usage**

```r
lsa(
pos = 1,
  pattern,
  order.by = "Size",
  decreasing = TRUE,
  head = TRUE,
  n = 10
)
```

**Arguments**

- `pos` numeric. Position in the stack.
- `pattern` Regex to filter the objects by.
- `order.by` character. Either 'Type', 'Size', 'PrettySize', 'Rows', or 'Columns'. This will dictate how the output is ordered.
- `decreasing` logical. Should the output be displayed in decreasing order?
- `head` logical. Use head on the output?
- `n` numeric. Number of objects to display is head is TRUE.

**Value**

A data.frame with type, size in bytes, human-readable size, rows, and columns of every object in the environment.

**Author(s)**

Dirk Eddelbuettel, Tony Breyal
## Examples

```r
## Not run:
a <- rnorm(100000)
b <- matrix(1, 1000, 100)
lsa()

## End(Not run)
```

### lsp

**List objects in package**

#### Description

Lists functions and how to call them for any package.

#### Usage

```r
lsp(package, ...)
```

#### Arguments

- `package`: The name of the package you’re examining.
- `...`: further arguments to be passed to `lsf.str`.

#### Value

A list of functions and how to call them for any package.

#### Author(s)

Stephen Turner

#### Examples

```r
## Not run:
lsp(Tmisc, pattern="un")

## End(Not run)
```
### mat2df

**Matrix to pairwise data frame**

**Description**

Turns a distance matrix into a data frame of pairwise distances.

**Usage**

mat2df(M)

**Arguments**

- **M**
  
a square pairwise matrix (e.g., of distances).

**Value**

Data frame with pairwise distances.

**Author(s)**

Stephen Turner

**Examples**

```r
set.seed(42)
M <- matrix(rnorm(25), nrow=5)
M
mat2df(M)
M <- matrix(rnorm(25), nrow=5, dimnames=list(letters[1:5], letters[1:5]))
M
mat2df(M)
```

---

### Mode

**Mode.**

**Description**

Returns the mode of a vector. First in a tie wins (see examples).

**Usage**

Mode(x, na.rm = FALSE)
Arguments

x  A vector.
na.rm  Remove missing values before calculating the mode (FALSE by default). NAs are counted just like any other element. That is, an NA in the vector won’t necessarily result in a return NA. See the first example.

Value

A combined p-value.

Author(s)

Stephen Turner

Examples

Mode(c(1,2,2,3,3, NA))
Mode(c(1,2,2,3,3, NA), na.rm=TRUE)
Mode(c(1,2,2,3,3, NA, NA, NA, NA))
Mode(c(1,2,2,3,3, NA, NA, NA, NA), na.rm=TRUE)
Mode(c("A", "Z", "Z", "B", "B"))

nn

Get names and class of all columns in a data frame

Description

Get names and class of all columns in a data frame in a friendly format.

Usage

nn(df)

Arguments

df  A data.frame.

Value

A data.frame with index and class.

Author(s)

Stephen Turner

Examples

nn(iris)
**Open the current working directory on mac**

**Description**

Opens the current working directory on mac.

**Usage**

`o()`

**Author(s)**

Stephen Turner

**Examples**

```r
## Not run:
o()
## End(Not run)
```

---

**peek**

*Peek at the top of a text file*

**Description**

This returns a character vector which shows the top n lines of a file. "Borrowed" from the rafalib package.

**Usage**

`peek(x, n = 5)`

**Arguments**

- `x`: a filename
- `n`: the number of lines to return

**Author(s)**

Michael I. Love
Examples

```r
## Not run:
filename <- tempfile()
x<-matrix(round(rnorm(10^4),2),1000,10)
colnames(x)=letters[1:10]
write.csv(x,file=filename,row.names=FALSE)
peek(filename)

## End(Not run)
```

<table>
<thead>
<tr>
<th>propmiss</th>
<th>Missing stats</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Description

Returns the number of missing values, total length, and proportion missing values for each variable in a data.frame

Usage

```r
propmiss(df)
```

Arguments

| df       | A data.frame. |

Value

A data.frame with missingness stats.

Author(s)

Stephen Turner

Examples

```r
propmiss(data.frame(a=1:5, b=c(6,NA,NA,9,10)))
```
quartet

Description
Tidy version of built-in Anscombe’s Quartet data. Four datasets that have nearly identical linear regression properties, yet appear very different when graphed.

Usage
quartet

Format
Data frame with columns.

Source
Anscombe’s Quartet, http://en.wikipedia.org/wiki/Anscombe%27s_quartet

---

read.cb

Description
Read tabular data from the clipboard.

Usage
read.cb(header = TRUE, ...)

Arguments
header
A logical value indicating whether the file contains the names of the variables as its first line. Overrides the default header=FALSE option in read.table()

... Further arguments to be passed to read.table

Value
A data.frame

Author(s)
Stephen Turner
rownames_to_symprobe  

Description

This function takes an `exprs(eset)` matrix where the rownames are probeset IDs and takes an annotated topTable output where you have an ID and Symbol column and outputs a character vector with symbol_probeid for each probeid in rownames(exprs(eset)). You can use this such that the output on a heatmap contains the gene names concatenated to the probe ID in case you have multiple symbols with the same probeID.

Usage

`rownames_to_symprobe(exprset, tt)`

Arguments

- `exprset` The output of `exprs(eset)`.  
- `tt` A topTable object.

Value

Character vector of the gene symbol with the probe ID.

Author(s)

Stephen Turner

Examples

```r
## Not run:
rownames_to_symprobe(esprs(eset), topTable(fit, number=nrow(fit)))
## End(Not run)
```
saveit

Rename objects while saving.

Description

Allows you to rename objects as you save them. See http://stackoverflow.com/a/21248218/654296.

Usage

saveit(..., file = stop("'file' must be specified"))

Arguments

... Objects to save.
file Filename/path where data will be saved.

Author(s)

Stephen Turner

Examples

## Not run:
foo <- 1
saveit(bar=foo, file="foobar.Rdata")

## End(Not run)

sicb

Write sessionInfo to the clipboard

Description

Writes output of sessionInfo() to the clipboard. Only works on Mac.

Usage

sicb()

Author(s)

Stephen Turner
Examples

## Not run:
# Write sessionInfo() to the clipboard on mac.
sicb()

## End(Not run)

---

**strSort**

*Sort characters in a string*

### Description

Alphabetically sorts characters in a string. Vectorized over x.

### Usage

`strSort(x)`

### Arguments

- `x` A string to sort.

### Value

A sorted string.

### Author(s)

Stephen Turner

### Examples

```r
strSort("cba")
strSort("zyxcBb105.a")
strSort(c("cba", "zyx"))
strSort(c("cba", NA))
```
### Tcols

**A palette of 17 diverging colors**

**Description**

17 diverging colors created by combining the Set1 and Dark2 palettes from RColorBrewer.

**Usage**

```r
Tcols
```

**Format**

Vector of 17 diverging colors.

**Source**

R Color brewer: `c(brewer.pal(9,"Set1"),brewer.pal(8,"Dark2"))`.

**Examples**

```r
## Not run:
barplot(rep(1, 17), col=Tcols, axes=F, names=c(rep("Set1", 9), rep("Dark2", 8)), horiz=TRUE, las=2)
## End(Not run)
```

### Thist

**Histograms with overlays**

**Description**

Plot a histogram with either a normal distribution or density curve overlay.

**Usage**

```r
Thist(x, overlay = "normal", col = "gray80", ...)
```

**Arguments**

- `x`: A numeric vector.
- `overlay`: Either "normal" (default) or "density" indicating whether a normal distribution or density curve should be plotted on top of the histogram.
- `col`: Color of the histogram bars.
- `...`: Other arguments to be passed to `hist()`.
Author(s)
Stephen Turner

Examples
set.seed(42)
x <- rnorm(1000, mean=5, sd=2)
Thist(x)
Thist(x, overlay="density")
Thist(x^2)
Thist(x^2, overlay="density", breaks=50, col="lightblue2")

Description
Stephen Turner's miscellaneous functions

Author(s)
Stephen Turner

Tmisc

Better scatterplot matrices.

Description
A matrix of scatter plots with rugged histograms, correlations, and significance stars. Much of the functionality borrowed from PerformanceAnalytics::chart.Correlation().

Usage
Tpairs(x, histogram = TRUE, gap = 0, ...)

Arguments
x A numeric matrix or data.frame.
histogram Overlay a histogram on the diagonals?
gap distance between subplots, in margin lines.
... arguments to be passed to or from other methods.

Author(s)
Stephen Turner
Examples

```r
Tpairs(iris[-5])
Tpairs(iris[-5], pch=21, bg=Tcols[factor(iris$Species)])
Tpairs(iris[-5], pch=21, bg=gghues(3)[factor(iris$Species)], gap=1)
```

---

**unfactor**  
Unfactor a data.frame

### Description

Did you forget to pass `stringsAsFactors=FALSE`? This converts factor variables to characters in a dataframe.

### Usage

```r
unfactor(df)
```

### Arguments

- **df**  
The dataframe you wish to change the factors into characters.

### Value

A data.frame with factors converted to characters.

### Author(s)

- [https://github.com/Dasonk](https://github.com/Dasonk)

### Examples

```r
## Not run:
df <- data.frame(a = letters[1:5], x = 1:5, y = LETTERS[1:5], stringsAsFactors = TRUE)
str(df)
df <- unfactor(df)
str(df)
## End(Not run)
```
%like%  x like y

Description

Returns a logical vector of elements of x matching the regex y.

Usage

x %like% pattern

Arguments

x  a vector (numeric, character, factor)

pattern  a vector (numeric, character, factor), matching the mode of x

Value

A logical vector with length equal to x of things in x that are like y.

See Also

%like%, %nlike%, %nin%,

Examples

(Name <- c("Mary","George","Martha"))
Name %in% c("Mary")
Name %like% "Mar"
Name %nin% c("George")
Name %nlike% "Mar"

%nin%  x not in y

Description

Returns a logical vector of elements of x that are not in y.

Usage

x %nin% table

Arguments

x  a vector (numeric, character, factor)

table  a vector (numeric, character, factor), matching the mode of x
%nlike%

Value
A logical vector with length equal to x of things in x that aren’t in y.

See Also
%like%, %nlike%, %nin%,

Examples

1:10 %nin% seq(from=2, to=10, by=2)
c("a", "b", "c") %nin% c("a", "b")
letters[letters %nin% unlist(strsplit("pack my box with five dozen liquor jugs", ""))]

%nlike%  x not like y

Description
Returns a logical vector of elements of x not matching the regex y.

Usage
x %nlike% pattern

Arguments
x          a vector (numeric, character, factor)
pattern    a vector (numeric, character, factor), matching the mode of x

Value
A logical vector with length equal to x of things in x that aren’t like y.

See Also
%like%, %nlike%, %nin%,

Examples

(Name <- c("Mary","George","Martha"))
Name %in% c("Mary")
Name %like% "^Mar"
Name %nin% c("George")
Name %nlike% "^Mar"
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