

Package ‘ymse’

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Title Various more or less useful functions and methods

Version 0.4.1

Description What the package does (one paragraph).

Depends R (>= 3.5.0)

Imports stats, utils, graphics, grDevices, forecast

License GPL (>= 2)

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LazyData true

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addrows	<i>Add rows to a data.frame</i>
---------	---------------------------------

Description

An "rbind for data.frames", sort of.

Usage

```
addrows(dtf, nrw, top = FALSE)
```

Arguments

dtf	data.frame; original data.frame
nrw	data.frame; the new row(s) to be added
top	logical; should the new rows be added to the top or the bottom (default)?

Details

Can only bind two objects at a time, but will bind data.frames with non-matching column names and -classes. In such cases the original data.frame will serve as template.

Examples

```
dtf <- data.frame(A=letters[1:5],
                  B=1:5,
                  C=as.factor(5:1),
                  D=as.Date(0:4, origin="2000-01-01"),
                  stringsAsFactors=FALSE)

nrw <- data.frame(A=letters[1:5],
                  B=4:8,
```

```

C=5:1,
D=as.Date(5:1, origin="1990-01-01"),
stringsAsFactors=FALSE)

str(dtf)

dtf.a <- addrows(dtf, nrw, top=FALSE)
str(dtf.a)

# adding a single row with little concern for data types and column names
b <- type.convert(beaver1[80:90,])
b$activ <- as.logical(b$activ)

addrows(b, data.frame(350, 1200, 37.02, 1))

```

adjustcolorHSV

*Adjust Colors in One or More Directions Conveniently.***Description**

Adjust or modify a vector of colors by "turning knobs" on one or more coordinates in (h,s,v, α) space, typically by up or down scaling them.

Usage

```
adjustcolorHSV(col, alpha.f = 1, h.f = 1, s.f = 1, v.f = 1,
  offset = c(0, 0, 0, 0), transform = diag(c(h.f, s.f, v.f, alpha.f)))
```

Arguments

<code>col</code>	vector of colors, in any format that <code>col2rgb()</code> accepts
<code>alpha.f</code> , <code>h.f</code> , <code>s.f</code> , <code>v.f</code>	factors scaling the opacity, hue, saturation and value of <code>col</code>
<code>offset</code>	a length 4 numeric vector specifying the linear offset applied to the <i>hue</i> , <i>saturation</i> , <i>value</i> and <i>alpha</i> values
<code>transform</code>	a 4x4 diagonal matrix specifying the scaling applied to the <i>hue</i> , <i>saturation</i> , <i>value</i> and <i>alpha</i> values

Details

Essentially an HSV version of the RGB-based [adjustcolor](#). One important distinction is that the `h.f` value wraps around to fit the [0, 1] range, rather than simply "clamping" it between 0 and 1.

Value

A character vector the same length as `col` containing color data in standard hexadecimal RGBA format.

Examples

```
# Halve the saturation and value of the default palette colours
plot(2:8, cex=5, lwd=4, pch=21, bg=2:8,
     col=adjustcolorHSV(2:8, s.f=0.5, v.f=0.6))

# Offset the hue of the default palette colours by 0.5, inverting the colours
plot(2:8, cex=5, lwd=4, pch=21, bg=2:8,
     col=adjustcolorHSV(2:8, offset=c(0.5, 0, 0, 0)))
```

ahist

Average shifted histogram

Description

Create a smoothed histogram by averaging several histograms shifted by fractions of a bin-width

Usage

```
ahist(x, n.breaks = nclass.FD(x), n.shifts = 3, type = c("histogram",
  "polygon", "line", "table"), freq = FALSE, plot = TRUE, add = FALSE,
  ...)
```

Arguments

x	a vector of values for which the histogram is desired
n.breaks	an integer giving the number of bins to be used
n.shifts	an integer giving the number of shifts to be performed
type	if plot=TRUE, the type of plot to be used
freq	should frequency counts be used, or density (default)
plot	logical; if TRUE (default), a graphical output will be returned
add	logical; if TRUE the plot will be added to the current plot
...	further graphical parameters to ymse::plot.histogram, polygon, or lines

Value

an object of class "histogram"

Examples

```
set.seed(1)
n <- 6

x <- sample(sample(0:20, 8), 6*n, replace=TRUE) + rnorm(6*n, -8, 0.5)
x <- c(x, rgamma(5*n, 3, 0.5), rnorm(4*n, 15, 2))
x <- round(x*5)/5

hist(x, freq=FALSE, breaks="FD", col="lightblue")
ahist(x, type="hist", border=2, col=7, freq=FALSE, lwd=2)
ahist(x, type="poly", border=2, col=7, freq=FALSE, lwd=2)
ahist(x, type="line", col=2, freq=FALSE, lwd=2)
ahist(x, type="table", col=2, freq=FALSE, lwd=2)
ahist(x, plot=FALSE)
```

arfilter	<i>AR filter</i>
----------	------------------

Description

Filter a time series using AR coefficients

Usage

```
arfilter(x, mod, x.mean = mod$x.mean, init = "focb")
```

Arguments

x	a time series
mod	an AR model
x.mean	the mean used. By default the mean of the original model. Set to zero for no demeaning
init	how the initial values should be chosen. First observation carried backwards (default), mean of the first values, or the first values in reverse.

See Also

[armodel](#)

Examples

```
set.seed(1)
arap <- ar(AirPassengers)
spec.ar(arap)
spec.pgram(arfilter(rnorm(10000), arap), span=21, na.action=na.omit)

arm <- armodel(c(1.3, -0.4))
spec.ar(arm)
plot(x <- rnorm(200), type="l")
lines(scale(arfilter(x, arm), center=FALSE), col="red", lwd=2)
```

arfit	<i>AR model fit</i>
-------	---------------------

Description

Fit a specified AR model to a univariate time series

Usage

```
arfit(x, mod, x.mean = mod$x.mean)
```

Arguments

x	a time series
mod	an AR model
x.mean	the mean used. By default the mean of the original model. Set to zero for no demeaning

See Also

[armodel](#) for examples

Examples

```
set.seed(1)
x <- runif(50) + sin(1:50/10)
plot(x); lines(arfilter(x, armodel(c(1.5, -0.5, 0.5)), x.mean=mean(x)))
```

arimpulse

Impulse response of an AR model

Description

Get and plot the impulse response of an AR model

Usage

```
arimpulse(mod, pulse = 1, n.ahead = 20, plot = TRUE, ...)
```

Arguments

mod	an AR model
pulse	numeric vector; the initial pulse. Magnitude is added to the model mean
n.ahead	the length of the computed response
plot	logical; should the result be plotted?
...	further arguments to plot

See Also

[armodel](#) for examples

armodel	Create an AR model object
---------	---------------------------

Description

Specify the characteristics of an AR model

Usage

```
armodel(coefs, mean = 0, intercept = 0, var.pred = 1, frequency = 1,
        x.name = "Synthetic AR model")
```

Arguments

coefs	a vector of model coefficients
mean	the mean of the process
intercept	the intercept in the model
var.pred	the portion of the variance not explained by this model
frequency	the sampling frequency of the process
x.name	name of the series

See Also

[arimpulse](#)

Examples

```
# short decay
ar.mod <- armodel(c(0.5))
arimpulse(ar.mod, pulse=1)

# long decay
ar.mod <- armodel(c(0.8))
arimpulse(ar.mod, pulse=1)

# negative second coefficient reduce damping, signal returns to normal
# more quickly
ar.mod <- armodel(c(0.8, -0.1))
arimpulse(ar.mod, pulse=1)

# second coefficient reduce damping too much, overdamping, oscillations
ar.mod <- armodel(c(0.8, -0.5))
arimp <- arimpulse(ar.mod, pulse=1, n.ahead=40)$pred
polyroot(c(1, -ar.mod$ar)) # complex conjugate roots
acf(arimp) # period ~= 6?
phi1 <- ar.mod$ar[1]
phi2 <- ar.mod$ar[2]
f <- (1/(2*pi)) * acos((phi1*(phi2-1))/(4*phi2))
1/f # period = 6.78
sp <- spec.ar(ar.mod, plot=FALSE)
1/sp$freq[which.max(sp$spec)] # period = 6.79
```

```
# decaying oscillations
ar.mod1 <- armodel(c(0.8, -0.6, -0.5, 0.2, -0.2))
arimpulse(ar.mod1, n.ahead=100)
Mod(1/polyroot(c(1, -ar.mod1$ar))) # barely inside the unit circle

# growing oscillations
ar.mod2 <- armodel(c(0.8, -0.7, -0.5, 0.2, -0.2))
arimpulse(ar.mod2, n.ahead=100)
Mod(1/polyroot(c(1, -ar.mod2$ar))) # barely outside the unit circle

ar.mod3 <- armodel(c(1.8, -1.1, 0.2, -0.2, 0.2))
arimpulse(ar.mod3, n.ahead=100)
spec.ar(ar.mod3)

resid(arfit(rnorm(10), armodel(c(0.5, -0.1), frequency=2)))
```

as.array.list

Coerce a list to an array

Description

Coerce a list consisting of data.frames or matrices of equal size to a 3d array

Usage

```
## S3 method for class 'list'
as.array(x, ...)
```

Arguments

x	a list of equal sized data.frames or matrices
...	(not used)

Value

A list of length l with elements of m rows and n columns will result in an $m \times n \times l$ array.

Examples

```
df1 <- data.frame(x=c(1, 2, 3), y=c(2, 3, 4), z=c(3, 4, 5))
df2 <- data.frame(x=c(4, 2, 3), y=c(2, 5, 4), z=c(3, 4, 6))
df3 <- data.frame(x=c(1, 4, 2), y=c(3, 3, 8), z=c(4, 3, 5))

l <- list(df1, df2, df3)

as.array(l)

llm <- list(matrix(LETTERS[1:6], 2),
            matrix(LETTERS[7:12], 2))

as.array(llm)

as.array(speedskate)
```

bartlett*Maurice Stevenson Bartlett's car data*

Description

This is an example data set Bartlett used for a lecture course on stochastic processes, Statistics Department, University College, London. The data represents the times, in seconds, when cars passed an observation point by a road.

Bartlett attributes the data to a Dr A. J. Miller who supplied them as a class example. According to Adery C. A. Hope the data was recorded on a rural Swedish road.

Usage

bartlett

Format

A numeric vector representing time points in seconds

M. S. Bartlett's notes

Analyse the above data with a view to examining:

- i whether the times of passing constitute a Poisson process;
- ii if not, whether some form of "bunching" or "clustering" seems to be present.

Possible analyses include:

- a testing the homogeneity of the consecutive random time-intervals, by means of a partitioning of the degrees of freedom for the total (approximate) χ^2 ;
- b testing the homogeneity of counts in consecutive fixed time-intervals, choosing an appropriate interval, and partitioning the degrees of freedom corresponding to the total dispersion by means of an analysis of variance;
- c testing the correlation between the consecutive random time-intervals;
- d examining the overall distribution of counts in fixed time-intervals;
- e examining the overall distribution of the consecutive random time-intervals

You should undertake at least sufficient of these to answer the questions asked.

Source

The Spectral Analysis of Point Processes (p. 280), M. S. Bartlett, 1963

Also mentioned in:

Statistical Estimation of Density Functions (p. 252), M. S. Bartlett, 1963

A Simplified Monte Carlo Significance Test Procedure (p. 583), Adery C. A. Hope, 1968

Examples

```

cpgram(diff(bartlett))

bartlett2 <- bartlett - bartlett[1]

x <- rep(0, tail(bartlett2, 1)*10)
x[bartlett2*10] <- 1

par(mfrow=c(2, 1), mar=c(2, 3, 1, 1))
plot(x, type="l", ann=FALSE)
lines(cumsum(x)/sum(x), col="red", lwd=2)

sp <- spectrum(x, main="", xlim=c(0, 0.1), ylim=c(1e-3, 0.04))
spec <- predict(loess(sp$spec[1:3000] ~ sp$freq[1:3000], span=0.15), se=TRUE)
lines(sp$freq[1:3000], spec$fit, col="red", lwd=2)
lines(sp$freq[1:3000], spec$fit - qt((0.99 + 1)/2, spec$df)*spec$se,
      lty=1, col="lightblue")
lines(sp$freq[1:3000], spec$fit + qt((0.99 + 1)/2, spec$df)*spec$se,
      lty=1, col="lightblue")

```

binsearch

*Binary search***Description**

Find the position of a given value in a sorted array

Usage

```

binsearch(val, arr, L = 1L, H = length(arr))

binclosest(val, arr, L = 1L, H = length(arr))

```

Arguments

val	the value to search for
arr	a sorted array to make the search in
L	a lower bound
H	an upper bound

Details

While both `val` and `arr` can be either integer or double, the algorithm is limited by integer storage in how long the array can be. `L` and `H` can be used to limit the range of indices to be search within. `binsearch` will return either the index of the exact match, or the index just below if no exact match is found. This means that if `val` is less than the lowest value in `arr` (and `L=1`), a `0` will be returned, which can lead to issues as such an index does not exist in R. An array indexed by `0` will return a zero length object. `binclosest` will return the index of the closest match, and therefore a `1` in the situation where `binsearch` returns a `0`. If there is a tie the lower index will be returned. In either case, if there are duplicate matches, the lower index will be returned.

Value

A single integer representing an index on the input array.

Examples

```
binsearch(15, (1:9)*3.333)
binsearch(2, (1:9)*3.333)
binclosest(2, (1:9)*3.333)

binsearch(18, seq_len(2e9))
## Not run:
binsearch(18, seq_len(3e9))
## End(Not run)
binsearch(18, seq_len(3e9), H=2e9)
binsearch(2000, seq_len(3e7)*100 + 0.1)

set.seed(1)
x <- sort(sample(1:300, 30))
r <- sort(sample(1:300, 30))

plot(sapply(r, binsearch, x), type="l")
lines(sapply(r, binclosest, x), col="red")

x <- c(1, 2, 3, 5, 8, 9)
binclosest(6, x)
binclosest(7, x)
binclosest(5, x)
```

caleidoscope

Caleidoscopic effect on a matrix

Description

Flip a matrix vertically and horizontally before recombining into a new large matrix

Usage

```
caleidoscope(m, odd = TRUE)
```

Arguments

m	a matrix
odd	logical; should the resulting matrix have odd dimensions?

Details

Three copies of m will be made. One flipped horizontally, one flipped vertically, and one flipped both horizontally and vertically. Then they are recombined with the original matrix in the upper right corner, and the flipped copies in the upper left, lower right and lower left corners, respectively.

Value

A matrix of either $2 \times$ or 2×-1 the number of rows and columns of the input matrix.

Examples

```
caleidoscope(matrix(1:4, 2), odd=FALSE)

image(caleidoscope(1:9 %o% 1:9))

image(caleidoscope(matrix(runif(180*200)^2, 180)), col=rainbow(256, start=0.58))
```

central.tendency	<i>Central tendency measures</i>
------------------	----------------------------------

Description

Central tendency measures

Usage

```
pseudomedian(x, na.rm = TRUE)

cmode(x, ...)
```

Arguments

x	numeric vector
na.rm	remove NAs before starting calculations
...	send further arguments to underlying function, e.g. density for cmode

See Also

[means](#)

Examples

```
xx <- c(1, 3, 4, 5, 7, 8, 9, 9, 7, 5, 4, 5, 3, 8)
median(xx) #'
pseudomedian(xx)
```

combodice	<i>Combine dice</i>
-----------	---------------------

Description

Generate probability density functions for combinations of dice.

Usage

```
combodice(x, FUN, ..., method = c("outer", "expand.grid", "convolve"), name)
```

Arguments

x	a list of dice objects, or objects that can be interpreted as such
FUN	function passed on to outer or apply, depending on method
...	further arguments passed to FUN
method	method for computation. One of outer, expand.grid or convolve
name	name used for the resulting PDF. Will use x object if none is given

Details

Each of the methods have their advantages and disadvantages. Outer and expand.grid work with roughly the same speed and memory, and can take the same kind of input, but FUN is interpreted differently, reflecting their use of outer and apply respectively. Convolve is much quicker than the other two, but is restricted to only summing distributions. While the first two can handle non-integer values, but only integer probabilities, the third can handle non-integer probabilities, but only integer values.

Value

A table giving the relative probability of each value

See Also

[dusd](#)

Examples

```
# Fudge dice
dF.2 <- as.table(c("-1"=2, "0"=2, "1"=2))
dF.1 <- as.table(c("-1"=1, "0"=4, "1"=1))
fudgedice2221 <- list(dF.2, dF.2, dF.2, dF.1)

combodice(fudgedice2221)

# Heterogeneous-class list and non-integer values
die1 <- as.table(c("2.6"=2, "3"=1, "5"=1))
die2 <- c(0, 1.4)
die3 <- as.dice(as.table(c("1"=2, "2"=2, "3"=2)))
diel <- list(die1, die2, die3)

combodice(diel)

# Regular d6 pair
re <- combodice(list(1:6, 1:6))

# Sichermann pair
si <- combodice(list(c(1, 2, 2, 3, 3, 4), c(1, 3, 4, 5, 6, 8)))
re; si # Identical

# One regular and one "average" d6
combodice(list(1:6, c(2, 3, 3, 4, 4, 5)))

# One 1/2 coin, one D4 and one d6, multiplied together
combodice(list(1:2, 1:4, 1:6, "*"))
```

```
# 3d6, and d6+d10+d20. Discard lowest
discard_lowest <- function(x) sum(sort(x)[-1])
combodice(list(1:6, 1:6, 1:6), discard_lowest, method="ex")
combodice(list(1:6, 1:10, 1:20), discard_lowest, method="ex")

# Dice pool. 3 d10 with target value 7
f <- function(x) sum(x >= 7)
combodice(lapply(rep(1, 3), seq, 10), f, method="ex")/10

# Equivalent using binomial PDF
dbinom(0:3, 3, 0.4)*100

# I have a d20 with a slight bump at the 4 and 10 facets,
# which makes 16 and 11 less likely, but the nearby 3, 18, 19 and 20
# correspondingly more likely. How does this affect the PDF?
d20l <- dice(20)
d20l[c(16, 11)] <- 0.6
d20l[c(3, 20, 18, 19)] <- 1.2
mean(d20l)

c0 <- combodice(list(dice(6), dice(10), dice(20)), method="conv", name="fair")
c1 <- combodice(list(dice(6), dice(10), d20l), method="conv", name="uneven")

set_mar()
plot(c0, type="o", pch=16, col="grey")
points(c1, col=2, type="o", lwd=1, pch=16, cex=0.6)
legend("topright", c("fair", "bumpy"), bty="n", col=c("grey", "red"), lwd=2:1)
```

compare_forecasts	<i>Compare forecast accuracies</i>
-------------------	------------------------------------

Description

Test the efficacy of time series models by comparing forecasts with actual data

Usage

```
compare_forecasts(m, y = NULL, holdout = NULL)
```

Arguments

<code>m</code>	a list of models to compare
<code>y</code>	a monovariate time series; the data to train and test the models on
<code>holdout</code>	single integer; the last <code>n</code> points will be forecasted

Examples

```
library(forecast)
set.seed(1)
extr <- aggregate(sunspot.month, nfrequency=2, mean)[100:349]
extr <- ts(extr, f=21)

mod1 <- StructTS(extr)
```

```

mod2 <- ar(extr)
mod3 <- nnetar(extr)
mod4 <- arfima(extr)
mod5 <- Arima(extr, order=c(3, 0, 1))
mod6 <- Arima(extr, order=c(2, 0, 2), seasonal=c(2, 1, 0))

mod.l <- list(mod1, mod2, mod3, mod4, mod5, mod6)

l <- compare_forecasts(mod.l, extr, 21)

diffs <- sapply(l, function(y) y[["fcast"]] - y[["test"]])
matplot(diffs, type="l",
        col=c("red", "lightgreen", "blue", "orange", "pink", "cyan"), lty=1)

par(mfrow=c(3, 2), mar=c(3, 3, 2, 1), mgp=c(2, 0.6, 0), oma=c(0, 0, 0, 0))
invisible(lapply(l, function(x) {
  plot(x$fcast.obj, shaded=FALSE, PI=FALSE, include=66, type="l",
       cex.main=0.9, xpd=NA)
  lines(x$test, col="#00FF4488")
}))
summary(l)
head(forecasts(l))
1

```

comparison_with_ties *Comparison with ties*

Description

Compare numeric values, returning an inbetween value for ties

Usage

```
x %tgt% y
```

```
tgt(x, y, bias = 0.5)
```

```
x %tlt% y
```

```
tlt(x, y, bias = 0.5)
```

Arguments

x, y	numeric values to be compared
bias	what bias should be given to ties? 0.5, the default, is considered neutral as it's halfway between 1 and 0 (true and false).

See Also

[Comparison](#), [tied_triple_test](#)

Examples

```
1:5 %tlt% 3
1:5 %tgt% 3

c(1, 4, 3, 1) %tlt% c(1, 3, 3, 2)
c(1, 4, 3, 1) %tgt% c(1, 3, 3, 2)
```

default_par	<i>Default par</i>
-------------	--------------------

Description

Sets par settings to their default values

Usage

```
default_par()
```

Details

Default par settings can be retrieved by `data(.def.par)`. A new default can be specified by editing `def.par` or making a `def.par <- par(no.readonly=TRUE)` type call.

See Also

Other `par_and_plot_margins_functions`: [revert_par](#), [set_mar](#)

dput2	<i>Write an Object to console</i>
-------	-----------------------------------

Description

Writes an ASCII text representation of an R object to the console for easy copy/paste sharing

Usage

```
dput2(x, width = 65, assign = c("front", "end", "none"),
      breakAtParen = FALSE, compact = TRUE)
```

Arguments

<code>x</code>	an object
<code>width</code>	integer; column width
<code>assign</code>	character; should assignment be included?
<code>breakAtParen</code>	logical; should lines break at parenthesis begins (default FALSE)
<code>compact</code>	remove spaces around ' = ' assignments

Details

This is similar to the way dput is used to print ASCII representations of objects to the console. The differences are that dput2 lets you specify the width of the resulting column, and assignment of the object to the name used in the call will by default be included. Line breaks are by default only done on whitespace, but can be set to happen at parenthesis begins as well. This should not break code and can make for a more compact representation, but it can also make the code harder to read.

See Also

[dput](#), [deparse](#)

Examples

```
xmpl <- faithful[sort(sample(1:nrow(faithful), 50)), ]
dput(xmpl)
cat(deparse(xmpl, width.cutoff=65), sep='\n')
dput2(xmpl, compact=FALSE)
dput2(xmpl)
dput2(xmpl, assign="end")
dput2(xmpl, assign="none")
dput2(xmpl, 80)

# no line breaks on whitespaces or parens within character strings
xmpl <- mtcars[1:5, ]
rownames(xmpl) <- c("bbbb (hhhhhhh\u00A0hhhhhhh)",
                    " rrrrrrrr ( bbbbbb )",
                    "v v v v v v v v v v",
                    "( g-god, d-god, _-___)",
                    "100*(part)/(total)")
dput2(xmpl, 15)
dput2(xmpl, 15, breakAtParen=TRUE)
```

dtf_clean	<i>Data cleanup</i>
-----------	---------------------

Description

Create a data.frame from a messy table

Usage

```
dtf_clean(x, header = TRUE, na.strings = c("NA", "N/A"),
          stringsAsFactors = FALSE, ...)
```

Arguments

- x a messy table the form of a character string
- header does the table include headers? (default TRUE)
- na.strings a vector of character strings which will be interpreted as missing values
- stringsAsFactors should strings be read as factors? (default FALSE)
- ... further arguments passed to read.table

Examples

```
x1 <- "
```

```
+-----+-----+-----+-----+
|   Date   | Emp1 | Case | Priority | PriorityCountinLast7days |
+-----+-----+-----+-----+
| 2018-06-01 | A    | A1   | 0       | 0 |
| 2018-06-03 | A    | A2   | 0       | 1 |
| 2018-06-02 | B    | B2   | 0       | 2 |
| 2018-06-03 | B    | B3   | 0       | 3 |
+-----+-----+-----+-----+
```

```
"
```

```
x2 <- '
```

```
+-----+-----+-----+-----+
|   Date   | Emp1 | Case | Priority | PriorityCountinLast7days |
+-----+-----+-----+-----+
| 2018-06-01 | A    | "A 1" | 0       | 0 |
| 2018-06-03 | A    | "A 2" | 0       | 1 |
| 2018-06-02 | B    | "B 2" | 0       | 2 |
| 2018-06-03 | B    | "B 3" | 0       | 3 |
+-----+-----+-----+-----+
```

```
'
```

```
x3 <- "
```

```
      Date   | Emp1 | Case | Priority | PriorityCountinLast7days
2018-06-01 | A    | A|1  | 0       | 0
2018-06-03 | A    | A|2  | 0       | 1
2018-06-02 | B    | B|2  | 0       | 2
2018-06-03 | B    | B|3  | 0       | 3
```

```
"
```

```
x4 <- "
```

```
Maths | English | Science | History | Class
0.1   | 0.2     | 0.3     | 0.2     | Y2
0.9   | 0.5     | 0.7     | 0.4     | Y1
0.2   | 0.4     | 0.6     | 0.2     | Y2
0.9   | 0.5     | 0.2     | 0.7     | Y1
```

```
"
```

```
x5 <- "
```

```
      Season   | Team | W | AHWO
-----+-----+-----+-----+
1 | 2017/2018 | TeamA | 2 | 1.75
2 | 2017/2018 | TeamB | 1 | 1.85
3 | 2017/2018 | TeamC | 1 | 1.70
4 | 2017/2018 | TeamD | 0 | 3.10
5 | 2016/2017 | TeamA | 1 | 1.49
6 | 2016/2017 | TeamB | 3 | 1.51
7 | 2016/2017 | TeamC | 2 | 1.90
```

```
8 | 2016/2017 | TeamD | 0 | N/A
"
```

```
lapply(c(x1, x2, x3, x4), dtf_clean)
```

dusd

Discrete (Uniform) Sum Distributions

Description

Generate distributions of the sum of discrete (uniform) random variables. Two different approaches.

Usage

```
dusd1(xr = 1:6, n = 2, FUN = "+")
```

```
dusd2(xi = rep(1, 6), n = 2, bix = 1, round, limit = 1e-13)
```

Arguments

xr	numeric vector; a vector of equiprobable values
n	integer; the number of distributions to be summed
FUN	function passed on to outer
xi	numeric vector; a vector of probabilities, with indices representing values
bix	logical; where does the index of xi start?
round	integer; number of digits to round to after each convolution
limit	numeric; values (frequencies or counts) less than this will be omitted.

Details

dusd1 works by recursively taking the outer sum of xr, while dusd2 recursively convolves xi. Although convolution is more efficient, it can introduce small errors, and with repeated convolutions those errors can compound. By rounding to a slightly lower precision after each convolution the generation of spurious singletons and general imprecisions can be mitigated.

Value

dusd1 returns an array of size $\text{length}(\text{xr})^n$ representing every possible outcome. dusd2 returns a probability mass function in the form of a table.

See Also

[combodice](#) for a more flexible implementation of the same ideas

Examples

```
# five coin flips
plot(table(dusd1(0:1, 5)))
plot(dusd2(c(1, 1), 5, bix=0))
plot(as.table(dbinom(0:5, 5, 0.5)))

# ten flips with a loaded coin
plot(table(dusd1(c(1, 1, 2), 10)))
plot(dusd2(c(2, 1), 10))
plot(dbinom(0:10, 10, 1/3), type="h", lwd=2)

# sample from a multi-roll d4 distribution
sample(dusd1(1:4, 5), 20, replace=TRUE)
plot(ecdf(dusd1(1:4, 5)))

tt <- dusd2(xi=rep(1, 4), n=3)
plot(tt)
tt <- tt/sum(tt)
rr <- replicate(50000, sample(names(tt), prob=tt))
barplot(apply(rr, 1, table), beside=TRUE)

# distribution of the sum of three d6 rolls
plot(table(dusd1(xr=1:6, 3)))
plot(dusd2(xi=rep(1, 6), n=3))

# d6 die with faces 2, 3, 5, 7, 11, 13 (prime numbers)
plot(table(dusd1(xr=c(2, 3, 5, 7, 11, 13), 3)))

# Loaded die
p <- c(0.5, 1, 1, 1, 1, 1.5); sum(p)
plot(dusd2(xi=p, n=2))

# A loaded die with prime number faces
s <- vector(length=13)
s[c(2, 3, 5, 7, 11, 13)] <- c(0.5, 1, 1, 1, 1, 1.5)
plot(dusd2(xi=s, n=3))

# tricky to do with dusd2
plot(table(dusd1(xr=c(0.1105, 2, exp(1)), 10)))

# Demonstrating CLT
# dusd1 struggles with many iterations
# remember it returns an array of size length(xr)^n
plot(table(dusd1(xr=c(1, 2, 9), 12)))

s <- vector(length=9)
s[c(1, 2, 9)] <- 1
plot(dusd2(xi=s, 12, round=9)) # much quicker
plot(dusd2(xi=s/sum(s), 12)) # for frequencies instead of counts

# Impossible with dusd1
clt <- dusd2(xi=s, 15, round=9)
plot(clt, lwd=0.5, col="#00000088")

# small floating-point errors from convolution.
tail(dusd2(xi=s, 15))
```

```
# dusd2 isn't always quicker
plot(table(dusd1(xr=c(1, 220, 3779), 12)), lwd=1)
## Not run:
s2 <- vector(length=3779)
s2[c(1, 220, 3779)] <- 1
plot(dusd2(xi=s2, 12, round=8), lwd=1)

## End(Not run)
# making sure the length of xi is highly composite (or more precicely 'smooth')
# improves speed
# 3779 is prime, 3780 == 2*2*3*3*3*5*7
s3 <- vector(length=3780)
s3[c(1, 220, 3779)] <- 1
plot(dusd2(xi=s3, 12, round=9), lwd=1)
```

entropy	<i>Information entropy</i>
---------	----------------------------

Description

Computes the information entropy (also called Shannon entropy) of a set of discrete values, or a tabulated such set.

Usage

```
entropy(x, ...)
```

```
## S3 method for class 'table'
entropy(x, base = 2, ...)
```

```
## S3 method for class 'data.frame'
entropy(x, base = 2, ...)
```

```
## S3 method for class 'matrix'
entropy(x, base = 2, ...)
```

```
## Default S3 method:
entropy(x, base = 2, ...)
```

Arguments

x	a vector, table, data.frame or matrix. In the case of table, data.frame and matrix each row is treated as a separate set of counts or proportions, with columns representing species, types, categories etc.
...	further arguments passed to methods
base	the log base to be used.

Examples

```

entropy(c(5, 5, 4, 4, 2, 3, 5)) # default is unit bits
entropy(c(5, 5, 4, 4, 2, 3, 5), base=exp(1)) # unit nats

entropy(rep(1:4, 1:4), 4)
entropy(rep(1:4, 1), 4)

entropy(as.factor(c(1, 1, 2, 3, 4, 4)))
entropy(as.character(c(1, 1, 2, 3, 4, 4)))

mtctab <- table(mtcars$cyl, mtcars$carb)
entropy(mtctab, 6)

xx <- data.frame(bee=c(0, 0, 1, 2, 3, 2, 0, 3),
                 wasp=c(1, 3, 2, 0, 1, 1, 2, 1),
                 fly=c(1, 2, 4, 2, 1, 0, 1, 0),
                 beetle=c(1, 0, 0, 1, 2, 2, 0, 2),
                 butterfly=c(0, 0, 0, 0, 3, 1, 0, 1))

entropy(xx)

```

every_nth

*Select every n'th element***Description**

Select every second, third, fourth etc. element (or slice/hyperplane) of an object

Usage

```

every_nth(...)

## Default S3 method:
every_nth(x, n = 2, start = 1, ...)

## S3 method for class 'matrix'
every_nth(x, n = 2, start = 1, margin = 1, ...)

## S3 method for class 'array'
every_nth(x, n = 2, start = 1, margin = 1, ...)

## S3 method for class 'data.frame'
every_nth(x, n = 2, start = 1, margin = 1, ...)

## S3 method for class 'list'
every_nth(x, n = 2, start = 1, ...)

```

Arguments

...	further arguments passed to methods
x	an object to be selected from
n	selection "step size"

start	integer in [1:n] specifying the start of selection
margin	what margin to select along

Examples

```
m <- matrix(1:64, 8)
every_nth(m, n=3, start=3, margin=2)

d <- data.frame(A=1:8, B=2:9, Q=letters[rep(1:3, length.out=8)])
every_nth(d, start=2)

a <- array(1:6^4, rep(6, 4))
every_nth(a)

l <- list(a=1:3, b=2:6, c=8:5, d=9:7, e=list(ea=1:2, eb=1), f=2:6)
every_nth(l, n=2, start=2)
```

fitrange	<i>Fit to a range</i>
----------	-----------------------

Description

Linearly shift and scale a numeric vector so that it fits to a given range.

Usage

```
fitrange(x, lower = -1, upper = 1)
```

Arguments

x	a numeric vector
lower	the lower bound of the new vector
upper	the upper bound of the new vector

See Also

[norma](#)

Examples

```
range(fitrange(runif(10, -2, 1.5), 0, 1))

fitrange(c(2, 3, 5, 7, 4), 1, 0)
# same, but without warning
1 - fitrange(c(2, 3, 5, 7, 4), 0, 1)
```

 forecasts

Return forecasts

Description

Return forecasts and actual data from compare_forecasts object

Usage

```
forecasts(x)
```

Arguments

x a compare_forecasts object

Value

A multivariate time series (mts) with the actual data, the holdout, on the first column, and the forecasts on the rest.

 incdiff

Increase difference

Description

Rearrange a sorted numeric sequence so that the difference between subsequent elements is increased

Usage

```
incdiff(x, step = 2)
```

Arguments

x a numeric sequence
 step how long a step the difference is considered for.

Details

With step=2 (default) only the difference between immediate neighbours are considered; the difference between every second element will remain small, or rather reduced, compared to the original sequence. With step=3 say, differences of both lag 1 and 2 is increased, but the difference of lag 1 will be less than if a step of 2 was used.

Examples

```

x <- 1:100
diff(x)

diff(incdiff(x, 2))
diff(incdiff(x, 3))

diff(incdiff(x, 2), 2)
diff(incdiff(x, 3), 2)

# incdiff will introduce a periodicity equal to the step length
acf(incdiff(x, 10))

# useful for making a sequence of colours more distinct
y <- seq(0.4, 1, l=18)
cols1 <- hsv(y, 1, y)
cols2 <- hsv(y, 1, incdiff(y, 3))

plot(y, col=cols1, pch=16, cex=5, ylim=c(0.4, 1.5))
points(y+0.5, col=cols2, pch=16, cex=5)

```

indexvalue

*Index-value representation of arrays***Description**

Represent an array as columns of dimensional indices and value

Usage

```
indexvalue(x, reverse = FALSE)
```

Arguments

x	an array or something that can be coerced into an array
reverse	logical; convert from Index-value representation to regular array representation?

Details

An n-dimensional array will be unfolded to a n+1-column data.frame where the first n columns represent the indices of the n dimensions, and the last column gives the value found at each index tuple. The reverse process can also be performed.

See Also

[latin_sq](#)

Examples

```

arr <- array(1:(2*3*4), dim=c(2, 3, 4))
arr.is <- indexvalue(arr)

# can be used to permute an array
indexvalue(arr.is[,c(2, 1, 3, 4)], rev=TRUE)
aperm(arr, c(2, 1, 3))

# can interpret values (symbols) as dimensional indices and permute them as well
arr2 <- array(rep(1:6, 4), dim=c(2, 3, 4))
arr2.is <- indexvalue(arr2)
indexvalue(arr2.is[,c(1, 2, 4, 3)], rev=TRUE)

# a latin square will produce an "orthogonal array"
set.seed(1)
lsq <- latin_sq(5)
iv <- indexvalue(lsq)
iv

# any permutation of a latin square is also a latin square
indexvalue(iv[, c(1, 3, 2)], reverse=TRUE)

```

isPrime

*Primality check***Description**

Test an integer for whether it is prime or not

Usage

```
isPrime(x)
```

Arguments

x integer; one or more prime candidates

See Also

[primes](#)

latin_sq

*Latin square***Description**

Generate latin squares, either randomly or ordered

Usage

```
latin_sq(n, random = TRUE, reduce = TRUE)
```

Arguments

n	integer; number of unique values (aka. symbols)
random	logical; should the square be generated randomly?
reduce	logical; should the square be in reduced form?

Details

Computation time increases rapidly with n. On my computer generating a random square with n=12 takes about ten minutes, marking the upper limit of practicability, or even stretching it a little. A latin square in reduced form will have elements in the first row and the first column in a sorted order. By setting reduced=TRUE the first row and the first column will always be 1:n.

Value

A square integer matrix of size n^2

See Also

[indexvalue](#)

Examples

```
set.seed(1)
ls <- latin_sq(9, reduce=TRUE)
image(ls, col=randcolours(ncol(ls)))

# The more "classic" representation with latin capital letters
ls[] <- LETTERS[ls]
ls
```

math_constants

Mathematical constants

Description

Various mathematical constants available as global variables

Format

An object of class `numeric` of length 1.

Details

e Euler's number
pi Archimedes' number, the circle constant
phi Golden ratio
feig1 Feigenbaum's first constant, δ ; bifurcation velocity
feig2 Feigenbaum's second constant, α ; reduction parameter
eu.ma Euler–Mascheroni constant
khin Khintchine's constant
glai.kin Glaisher–Kinkelin constant

math_constants_char	<i>High precision mathematical constants</i>
---------------------	--

Description

Character strings representing various mathematical constants to ~100 decimal points

Format

An object of class character of length 1.

Details

e.char Euler's number
 pi.char Archimedes' number, the circle constant
 phi.char Golden ratio
 feig1.char Feigenbaum's first constant, δ ; bifurcation velocity
 feig2.char Feigenbaum's second constant, α ; reduction parameter
 eu.ma.char Euler–Mascheroni constant
 khin.char Khintchine's constant
 glai.kin.char Glaisher-Kinkelin constant

means	<i>Generalized means</i>
-------	--------------------------

Description

Harmonic, geometric, quadratic, cubic, power and Lehmer means.

Usage

```
harm(x, na.rm = TRUE)

geom(x, zero.rule = c("1p", "rm", "1"), na.rm = TRUE)

quad(x, na.rm = TRUE)

cubi(x, na.rm = TRUE)

powr(x, p = 1.5, na.rm = TRUE)

lehm(x, p = 2, na.rm = TRUE)
```

Arguments

<code>x</code>	numeric vector of values whose *mean is to be computed
<code>na.rm</code>	logical; should NA values be removed? (default TRUE)
<code>zero.rule</code>	for the geometric mean, how should zeros be dealt with? Add one before, and subtract one after the calculation (see <code>lop1p</code>), remove all zeros, or replace all zeros with 1.
<code>p</code>	exponential power. For the power mean $p=-1$, $p=2$ and $p=3$ gives the harmonic, quadratic and cubic means, respectively. For the Lehmer mean $p=0$, $p=1$ and $p=2$ gives the harmonic, arithmetic and contraharmonic means, respectively.

Notice

For some of these means zeros and/or negative values are undefined, or make otherwise little sense in context. Workarounds are given for the geometric mean, but if you end up using it on data ≤ 0 , the wise call would be to reconsider whether using a geometric mean really makes sense in that case.

Examples

```
fun1 <- substitute(c(harm, geom, mean, quad, cubi))

x1 <- list(c( 1, 2, 3, 5),
          c(-1, 1, 2, 3, 5),
          c( 0, 1, 2, 3, 5),
          c(-1, 0, 1, 2, 3, 5))

m <- sapply(x1, function(x) sapply(eval(fun1), function(f) f(x)))
rownames(m) <- as.character(fun1)[-1]
colnames(m) <- c("posi", "1neg", "zero", "1ngz")
round(m, 3)

harm(x1[[1]]); powr(x1[[1]], -1); lehm(x1[[1]], 0)

y <- c(0, 1, 5, 0, 6, 5, 9)

geom(y, zero.rule="1p")
geom(y, zero.rule="rm")
geom(y, zero.rule="1")
```

narm

Remove NAs

Description

Remove NAs from vector or matrix

Usage

```
narm(x, ...)
```

```
## Default S3 method:
narm(x, ...)
```

```
## S3 method for class 'matrix'
narm(x, margin = 1, keep = c("any", "complete"), ...)
```

```
## S3 method for class 'data.frame'
narm(x, margin = 1, keep = c("any", "complete"), ...)
```

Arguments

<code>x</code>	a vector or matrix
<code>...</code>	further arguments passed to methods
<code>margin</code>	if <code>x</code> is matrix, which margin to remove NAs by
<code>keep</code>	if <code>x</code> is matrix, keep rows/columns with any non-NA values, or keep only complete rows/columns.

Value

If `x` is a matrix and `margin` is 1 or 2, a matrix is returned. Else a vector.

Examples

```
m1 <- matrix(c(10, 20, 30, 43,
               10, NA, 32, 50,
               NA, NA, NA, NA,
               13, 22, 70, 81,
               NA, 29, NA, 41), 5, byrow=TRUE,
             dimnames=list(letters[1:5], LETTERS[1:4]))
```

```
narm(m1)
matplot(narm(apply(m1, 2, sort, na.last=TRUE))), type="l")
```

```
m1[complete.cases(m1),]
narm(m1, 1, "c") #same
narm(m1, 2, "complete") #no complete columns
```

```
m1.df <- as.data.frame(t(m1))
narm(m1.df, 2, "complete")
```

 norma

Normalize

Description

Linearly shift and scale a numeric vector so that it has a given range, about a given centre.

Usage

```
norma(x, c = 0, r = 2)
```

Arguments

x a numeric vector
 c the centre (as in the midrange) for the new vector
 r the range of the new vector

See Also

[fitrange](#)

Examples

```
range(norma(runif(9, -2, 0.1), 0, 2))
```

pcamean	<i>PCA mean</i>
---------	-----------------

Description

Takes the average of several PCA objects

Usage

```
pcamean(...)
```

Arguments

... prcomp, princomp or factanal objects, or a single list of such objects

Details

I don't know if this kind of calculation has any sort of merit. It was written more as an impromptu challenge than as a solution to any problem

See Also

[prcomp](#), [princomp](#), [factanal](#)

Examples

```
xx <- data.frame(bee=c(0, 0, 1, 2, 3, 2, 0, 3),
                 wasp=c(1, 3, 2, 0, 1, 1, 2, 1),
                 fly=c(1, 2, 4, 2, 1, 0, 1, 0),
                 beetle=c(1, 0, 0, 1, 2, 2, 0, 2))

set.seed(1)
r <- 1000
xxs <- replicate(r, {
  xx$random <- sample(c(0:1, 0:4), 8, r=TRUE)
```

```

      xx
    }, simplify=FALSE)

xxm <- Reduce("+", xxs) / r
xxl <- lapply(xxs, princomp)

biplot(pcamean(xxl))
biplot(princomp(xxm))

```

plot.histogram	<i>Plot histogram object</i>
----------------	------------------------------

Description

A very minor modification of `graphics::plot.histogram`.
Only difference is that `lwd` now specifies the width of the histogram bars' outline.

See Also

[plot.histogram](#), [plot.stl](#), [ahist](#)

plot.stl	<i>Plot stl object</i>
----------	------------------------

Description

A very minor modification of `stats::stl`.
Only difference is that the distance between the plotting window and the x and y labels is set by `par("mgp")[1]`, as it is for regular plots.

See Also

[plot.stl](#), [plot.histogram](#)

primes	<i>Prime number generator</i>
--------	-------------------------------

Description

Prime generator based on the sieve of Eratosthenes

Usage

```
primes(n)
```

Arguments

`n` integer; all prime numbers up to this will be returned

Details

Effective for primes up to ~100,000,000.

On my lightweight laptop: 1e7 -> 0.32s, 5e7 -> 1.7s, 1e8 -> 3.7s, 2e8 -> 7.6s, 3e8 -> 15s

Source

<https://stackoverflow.com/questions/3789968/generate-a-list-of-primes-up-to-a-certain-number/3791284#3791284>

See Also

[isPrime](#)

randcolours	<i>Random colours</i>
-------------	-----------------------

Description

Generate a randomly selected colour palette

Usage

```
randcolours(n, l = c(0.2, 0.9), c1 = c(0, 1), c2 = c(0, 1), alpha = 1,  
  space = c("Luv", "Lab"))
```

Arguments

n	number of colours
l	lightness range
c1	colour channel one range
c2	colour channel two range
alpha	alpha channel range
space	should the parameters be interpreted as Luv or Lab components?

Details

The range of l, c1, c2 and alpha, will be interpreted as the wanted range of each colour component, whether their length is 1, 2, or more. Although they all should nominally lie within [0, 1], only alpha must do so to achieve a valid output. The others can exceed this range, at an increased risk of clipping.

Examples

```
set.seed(3)  
n <- 20  
plot(1:n, col=randcolours(n), pch=16, cex=5)
```

revert_par	<i>Revert par</i>
------------	-------------------

Description

Reverts par settings back to old.par

Usage

revert_par()

See Also

Other par_and_plot_margins_functions: [default_par](#), [set_mar](#)

set_mar	<i>Set plot margins</i>
---------	-------------------------

Description

Moves axis titles and labels closer to the plotting window and shrinks the margins

Usage

set_mar(x = 1.8, y = 1.8, main = 1, right = 1)

Arguments

- | | |
|-------|--|
| x | margin width for the x axis, default 2 |
| y | margin width for the x axis, default 2 |
| main | margin width for the main title, default 1, no title |
| right | margin width for the right edge, default 1 |

Details

Old par settings are stored in .old.par before a call to par of the form par(mar=c(x, y, main, right), mgp=c(1.9, 0.5), ...), is made.

See Also

Other par_and_plot_margins_functions: [default_par](#), [revert_par](#)

Examples

```
ymse:::.old.par
get("old.par", envir=ymse::ymseEnv)
ls(envir=ymse::ymseEnv)

par(col.axis=2)
plot(1:4)

set_mar()
plot(1:4)

default_par()
plot(1:4)

revert_par()
plot(1:4)

ymse:::.old.par
head(get("old.par", envir=ymse::ymseEnv))
```

simple_loess

Simplified Local Polynomial Regression Fitting

Description

A simplified interface to the loess and predict.loess combo.

Usage

```
simple_loess(...)

## Default S3 method:
simple_loess(y, x = seq_along(y), xout = sort(x),
  span = 0.75, periodic = FALSE, ...)

## S3 method for class 'data.frame'
simple_loess(df, xout = sort(df[, 1]), ...)
```

Arguments

...	further arguments passed to loess
y	the response values to be regressed
x	the regressor, by default an integer sequence along y
xout	values used for prediction, unless it is an integer of length 1. In that case xout specifies the number of equally spaced values on the interval of x to be used. By default the same as x
span	parameter controlling the degree of smoothing
periodic	should the input be treated as periodic?
df	a data.frame with x-values in the first column and y-vlues in the second

Value

A data.frame with columns *xout* and *y.predicted*

Examples

```
# Simple equally spaced vector
h <- c(-0.63, 0.2, -0.44, 1.6, 0.33, -0.74, -0.82, 0.29, 0.74, 0.58, -0.3)

plot(h)
lines(simple_loess(h))

# More complicated unequally space x-values
x <- c(4, 3, 2, 5, 6, 7, 9, 10, 12, 13, 14, 15, 16, 17, 18, 19)
y <- c(3, 2, 4, 5, 6, 5, 5, 3, 4, 7, 10, 10, 8, 9, 7, 8)

plot(x, y)
lines(simple_loess(y, x), col="gray40")
points(simple_loess(y=y, x=x, xout=5L), col=2, cex=2)
points(simple_loess(y=y, x=x, xout=17), col=3, cex=2)
points(simple_loess(y=y, x=x, xout=seq(8, 12, 0.3)), col=3, pch=16)
lines(simple_loess(y=y, x=x, xout=50L), col=4, lty=2)

# data.frame input
dtf <- data.frame(x, y)
simple_loess(dtf)
```

speedskate

2018 MarbleLympics speed skating times

Description

Intermediate and total times for all 16 runs, arranged by lane and heat number.

Usage

```
speedskate
```

Format

A list containing two data.frames, one for each lane. Columns are heat and rows are time checks in seconds.

Source

https://www.youtube.com/watch?v=fA-O6f_jArk

Examples

```
tt <- t(do.call(cbind, speedskate))
pairs(tt)
cor(tt)
outer(
  colnames(tt),
  colnames(tt),
  Vectorize(function(i,j) cor.test(tt[,i],tt[,j])$p.value)
)
```

tied_triple_test	<i>Tied triple test</i>
------------------	-------------------------

Description

Compare numeric values, returning an inbetween value for ties

Usage

```
x %ttt% y

ttt(x, y)

is.ttt(x)

## S3 method for class 'ttt'
print(x, symbols = TRUE, ...)

## S3 method for class 'ttt'
table(...)
```

Arguments

x, y	numeric values to be compared
symbols	should symbols be used instead of numeric values?
...	further arguments passed to methods

See Also

[Comparison](#), [comparison_with_ties](#)

Examples

```
1:5 %ttt% 3

ttt(1:3, 2)
print(ttt(1:3, 2), FALSE)

c(1, 6, 3, 0) %ttt% c(1, 3, 3, 2)

# Equivalent
as.integer(c(1, 6, 3, 0) %ttt% c(1, 3, 3, 2))
```

```

sign(c(1, 6, 3, 0) - c(1, 3, 3, 2))

# Demonstrating table method
dtf <- data.frame(x=1:5, y=3)
dtf$`?` <- ttt(dtf$x, dtf$y)
dtf

x <- c(8, 4, 6, 8, 9, 6, 5, 7, 0, 3, 2, 1, 5, 6, 4, 7, 6,
      3, 1, 9, 5, 6, 7, 7, 4, 5, 8, 6, 2, 5, 9, 5, 4, 8)
y <- c(1, 3, 2, 4, 6, 0, 5, 3, 7, 5, 7, 4, 5, 6, 0, 1, 4,
      2, 4, 3, 1, 5, 3, 9, 2, 2, 4, 7, 5, 6, 8)

ou <- outer(sort(x), sort(y), "%ttt%")
ta <- table(ou)

pa <- capture.output(ta)

par(mar=c(1, 2, 3, 2))
image(ou, col=topo.colors(length(ta)), axes=FALSE)
title(pa)
box()

```

Description

There is no grand "theme" to ymse, other than that none of the functions, and in some cases function groups and classes, seemed to fit too well in any other package or merit their own package entirely.

ymse functions

[addrows](#) Add rown to a data.frame [ahist](#) Create an average shifted histogram

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