

# Package ‘sfsmisc’

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**Title** Utilities from 'Seminar fuer Statistik' ETH Zurich

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**Description** Useful utilities ['goodies'] from Seminar fuer Statistik ETH Zurich, some of which were ported from S-plus in the 1990s.

For graphics, have pretty (Log-scale) axes, an enhanced Tukey-Anscombe plot, combining histogram and boxplot, 2d-residual plots, a 'tachoPlot()', pretty arrows, etc.

For robustness, have a robust F test and robust range().

For system support, notably on Linux, provides 'Sys.\*()' functions with more access to system and CPU information.

Finally, miscellaneous utilities such as simple efficient prime numbers, integer codes, Duplicated(), toLatex.numeric() and is.whole().

**Depends** R (>= 3.3.0)

**Imports** grDevices, methods, utils, stats, tools

**Suggests** datasets, tcltk, cluster, lattice, MASS, Matrix, nlme, lokern

**Enhances** mgcv, rpart, nor1mix, polycor, sm, tikzDevice, e1071, Hmisc, gmp, pastecs, polynom, robustbase

**EnhancesNote** 2nd line: packages mentioned in Rd xrefs

**Encoding** latin1

**ByteCompile** yes

**License** GPL (>= 2)

**URL** <https://github.com/mmaechler/sfsmisc>

**BugReports** <https://github.com/mmaechler/sfsmisc/issues>

**NeedsCompilation** no

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AsciiToInt

*Character to and from Integer Codes Conversion***Description**

AsciiToInt returns [integer](#) codes in 0:255 for each (one byte) character in strings. `ichar` is an alias for it, for old S compatibility.

`strcodes` implements in **R** the basic engine for translating characters to corresponding integer codes.

`chars8bit()` is the *inverse* function of `AsciiToInt`, producing “one byte” characters from integer codes. Note that it (and hence `strcodes()`) depends on the locale, see [Sys.getlocale\(\)](#).

**Usage**

```

AsciiToInt(strings)
  ichar(strings)
chars8bit(i = 1:255)
strcodes(x, table = chars8bit(1:255))

```

**Arguments**

strings, x      **character** vector.

i                numeric (integer) vector of values in 1:255.

table            a vector of (unique) character strings, typically of one character each.

**Details**

Only codes in 1:127 make up the ASCII encoding which should be identical for all R versions, whereas the *'upper'* half is often determined from the ISO-8859-1 (aka "ISO-Latin 1") encoding, but may well differ, depending on the locale setting, see also [Sys.setlocale](#).

Note that  $\theta$  is no longer allowed since, R does not allow  $\backslash\theta$  aka nul characters in a string anymore.

**Value**

AsciiToInt (and hence ichar) and chars8bit return a vector of the same length as their argument.

strcodes(x, tab) returns a **list** of the same **length** and **names** as x with list components of integer vectors with codes in 1:255.

**Author(s)**

Martin Maechler, partly in 1991 for S-plus

**Examples**

```

chars8bit(65:70)#-> "A" "B" .. "F"
stopifnot(identical(LETTERS, chars8bit(65:90)),
          identical(AsciiToInt(LETTERS), 65:90))

## may only work in ISO-latin1 locale (not in UTF-8):
try( strcodes(c(a= "ABC", ch="1234", place = "Zürich")) )
## in "latin-1" gives {otherwise should give NA instead of 252}:
## Not run:
$a
[1] 65 66 67

$ch
[1] 49 50 51 52

$place
[1] 90 252 114 105 99 104

```

```
## End(Not run)

myloc <- Sys.getlocale()

if(.Platform $ OS.type == "unix") withAutoprint({ # ''should work'' here
  try( Sys.setlocale(locale = "de_CH") )# "try": just in case
  strcodes(c(a= "ABC", ch="1234", place = "Zürich")) # no NA hopefully
  AsciiToInt(chars8bit()) # -> 1:255 {if setting latin1 succeeded above}

  chars8bit(97:140)
  try( Sys.setlocale(locale = "de_CH.utf-8") )# "try": just in case
  chars8bit(97:140) ## typically looks different than above
})

## Resetting to original locale .. works "mostly":
lapply(strsplit(strsplit(myloc, ";")[[1]], "="),
       function(cc) try(Sys.setlocale(cc[1], cc[2]))) -> .scratch

Sys.getlocale() == myloc # TRUE if we have succeeded to reset it
```

---

axTexpr

*Axis Ticks Expressions in Nice 10 \*\* k Form*


---

## Description

Produce nice  $a \times 10^k$  expressions for [axis](#) labeling instead of the scientific notation "a E<k>".

## Usage

```
axTexpr(side, at = axTicks(side, axp = axp, usr = usr, log = log),
        axp = NULL, usr = NULL, log = NULL,
        drop.1 = FALSE)
```

## Arguments

side	integer in 1:4 specifying the axis side, as for <a href="#">axis</a> .
at	numeric vector; with identical default as in <a href="#">axTicks()</a> .
axp, usr, log	as for <a href="#">axTicks()</a> .
drop.1	logical indicating if $1 \times$ should be dropped from the resulting expressions.

## Details

This is just a utility with the same arguments as [axTicks](#), a wrapper [pretty10exp](#)(at, \*).

## Value

an expression of the same length as x, with elements of the form a%% 10 ^ k.

**Author(s)**

Martin Maechler

**See Also**[pretty10exp](#); [eaxis](#), [axis](#), [axTicks](#).**Examples**

```
x <- 1e7*(-10:50)
y <- dnorm(x, m=10e7, s=20e7)
plot(x,y)## not really nice, the following is better:

## For horizontal y-axis labels, need more space:
op <- par(mar= .1+ c(5,5,4,1))
plot(x,y, axes= FALSE, frame=TRUE)
aX <- axTicks(1); axis(1, at=aX, label= axExpr(1, aX))
## horizontal labels on y-axis:
aY <- axTicks(2); axis(2, at=aY, label= axExpr(2, aY), las=2)
par(op)

### -- only 'x' and using log-scale there:
plot(x,y, xaxt= "n", log = "x")
aX <- axTicks(1); axis(1, at=aX, label= axExpr(1, aX))

## Now an "engineer's version" ( more ticks; only label "10 ^ k" ) :

axp <- par("xaxp") #-> powers of 10 *inside* 'usr'
axp[3] <- 1 # such that only 10^ are labeled
aX <- axTicks(1, axp = axp)
xu <- 10 ^ par("usr")[1:2]
e10 <- c(-1,1) + round(log10(axp[1:2])) ## exponents of 10 *outside* 'usr'
v <- c(outer(1:9, e10[1]:e10[2], function(x,E) x * 10 ^ E))
v <- v[xu[1] <= v & v <= xu[2]]

plot(x,y, xaxt= "n", log = "x", main = "engineer's version of x - axis")
axis(1, at = aX, label = axExpr(1, aX, drop.1=TRUE)) # 'default'
axis(1, at = v, label = FALSE, tcl = 2/3 * par("tcl"))
```

---

 cairoSwd

*Cairo PDF Graphics Device useful for Sweave*


---

**Description**

Provides a graphics device for Sweave, based on [cairo\\_pdf](#). The advantage of `cairoSwd()` compared to `pdf()` is its support of Unicode characters.

**Usage**

```
cairoSwd(name, width, height, ...)
```

**Arguments**

name            file name prefix to which '.pdf' will be appended.  
width, height   in inches, see [cairo\\_pdf](#).  
...              further arguments, passed to [cairo\\_pdf\(\)](#)

**Note**

Sweave devices need to have an argument list as above.

Usage in a Sweave chunk:

```
<<some-plot, fig=TRUE, grdevice=cairoSwd>>=
```

**Author(s)**

Alain Hauser

**See Also**

[pdf](#), [cairo\\_pdf](#), [Sweave](#).

---

capture.and.write      *Capture output and Write / Print First and Last Parts*

---

**Description**

Capture output and print first and last parts, eliding middle parts. Particularly useful for teaching purposes, and, e.g., in Sweave ([RweaveLatex](#)).

By default, when `middle = NA`, `capture.output(EXPR, first, last)` basically does

```
co <- capture.output(EXPR)
writeLines(head(co, first))
cat( ... dotdots ...)
writeLines(tail(co, last))
```

**Usage**

```
capture.and.write(EXPR, first, last = 2, middle = NA,
                  i.middle, dotdots = " ..... ", n.dots = 2)
```



**Arguments**

EXPR	the (literal) expression the output of which is to be captured.
first	integer: how many lines should be printed at beginning.
last	integer: how many lines should be printed at the end.
middle	numeric (or NA logical):
i.middle	index start of middle part
dotdots	string to be used for elided lines
n.dots	number of dotdots lines added between parts.

**Value**

return value of `capture.output(EXPR)`.

**Author(s)**

Martin Maechler, ETH Zurich

**See Also**

[head](#), [tail](#)

**Examples**

```
x <- seq(0, 10, by = .1)

## for matrix, dataframe, .. first lines include a header line:
capture.and.write( cbind(x, log1p(exp(x))), first = 5)

## first, *middle* and last :
capture.and.write( cbind(x, x^2, x^3), first = 4, middle = 3, n.dots= 1)
```

---

col01scale

*Matrix Scaling Utilities*

---

**Description**

col01scale and colcenter (re)scale the columns of a matrix. These are simple one-line utilities, mainly with a didactical purpose.

**Usage**

```
colcenter (mat)
col01scale(mat, scale.func = function(x) diff(range(x)), location.func = mean)
```

**Arguments**

`mat` numeric matrix, to rescaled.  
`scale.func`, `location.func`  
 two functions mapping a numeric vector to a single number.

**Value**

a matrix with the same attributes as the input `mat`.

**Author(s)**

Martin Maechler

**See Also**

The standard R function [scale\(\)](#).

**Examples**

```
## See the simple function definitions:

colcenter ## simply one line

col01scale# almost as simple
```

---

compresid2way

*Plot Components + Residuals for Two Factors*

---

**Description**

For an analysis of variance or regression with (at least) two factors: Plot components + residuals for two factors according to Tukey's "forget-it plot". Try it!

**Usage**

```
compresid2way(aov, data=NULL, fac=1:2, label = TRUE, numlabel = FALSE,
              xlab=NULL, ylab=NULL, main=NULL,
              col=c(2,3,4,4), lty=c(1,1,2,4), pch=c(1,2))
```

**Arguments**

`aov` either an [aov](#) object with a formula of the form  $y \sim a + b$ , where `a` and `b` are factors, or such a formula.

`data` data frame containing `a` and `b`.

`fac` the two factors used for plotting. Either column numbers or names for argument `data`.

`label` logical indicating if levels of factors should be shown in the plot.

numlabel	logical indicating if effects of factors will be shown in the plot.
xlab,ylab,main	the usual <code>title</code> components, here with a non-trivial default constructed from <code>aov</code> and the component factors used.
col,lty,pch	colors, line types, plotting characters to be used for plotting [1] positive residuals, [2] negative residuals, [3] grid, [4] labels. If <code>pch</code> is sufficiently long, it will be used as the list of individual symbols for plotting the <code>y</code> values.

### Details

For a two-way analysis of variance, the plot shows the additive components of the fits for the two factors by the intersections of a grid, along with the residuals. The observed values of the target variable are identical to the vertical coordinate.

The application of the function has been extended to cover more complicated models. The components of the fit for two factors are shown as just described, and the residuals are added. The result is a “component plus residual” plot for two factors in one display.

### Value

Invisibly, a list with components

compy	data.frame containing the component effects of the two factors, and combined effects plus residual
coef	coefficients: Intercept and effects of the factors

### Author(s)

Werner Stahel <stahel@stat.math.ethz.ch>

### References

F. Mosteller and J. W. Tukey (1977) *Data Analysis and Regression: A Second Course in Statistics*. Addison-Wesley, Reading, Mass., p. 176.

John W. Tukey (1977) *Exploratory Data Analysis*. Addison-Wesley, Reading, Mass., p. 381.

### See Also

[interaction.plot](#)

### Examples

```
## From Venables and Ripley (2002) p.165.
N <- c(0,1,0,1,1,1,0,0,0,1,1,0,1,1,0,0,1,0,1,0,1,0,1,1,0,0)
P <- c(1,1,0,0,0,1,0,1,1,1,0,0,0,1,0,1,1,0,0,1,0,1,0,1,1,0)
K <- c(1,0,0,1,0,1,1,0,0,1,0,1,0,1,1,0,0,0,1,1,1,0,1,0)
yield <- c(49.5,62.8,46.8,57.0,59.8,58.5,55.5,56.0,62.8,55.8,69.5,55.0,
          62.0,48.8,45.5,44.2,52.0,51.5,49.8,48.8,57.2,59.0,53.2,56.0)
npk <- data.frame(block=gl(6,4), N=factor(N), P=factor(P),
                  K=factor(K), yield=yield)
npk.cr <- compresid2way(yield ~ N+P+K, data=npk, fac=c("P","K"))
```

```
## Fisher's 1926 data on potatoe yield
data(potatoes)
pot.aov <- aov(yield ~ nitrogen+potash+pos, data=potatoes)
compresid2way(pot.aov, pch=as.character(potatoes$pos))

compresid2way(yield~nitrogen+potash, data=subset(potatoes, pos == 2))

## 2 x 3 design :
data(warpbreaks)
summary(fm1 <- aov(breaks ~ wool + tension, data = warpbreaks))
compresid2way(fm1)
```

---

cum.Vert.funkt

*Kumulative Verteilung Aufzeichnen*


---

## Description

Kumulative Verteilung von x aufzeichnen, auf Wunsch auch Median und Quartile.

This is just an old German language version of `plot.ecdf()` used for teaching at ETHZ.

## Usage

```
cum.Vert.funkt(x, Quartile = TRUE, titel = TRUE, Datum = TRUE,
              rang.axis = n <= 20, xlab = "", main = "", ...)
```

## Arguments

x	numeric vector whose empirical distribution should be plotted.
Quartile	logical indicating if all 3 non-trivial quartiles should be drawn.
titel	logical indicating if a German title should be drawn.
Datum	logical indicating if <code>p.datum</code> should be added.
rang.axis	logical indicating if all the ranks should be marked at the y-axis. Defaults to true if there are not more than 20 observations.
xlab, main	x-axis label and main title; default to empty.
...	optional further arguments, passed to <code>plotStep</code> .

## Value

the return value of `plotStep()` which is called internally, *invisibly*.

## Author(s)

Martin Maechler et al.

**See Also**

[plotStep](#) on which it is based; but you should really consider using [plot.ecdf\(\)](#) from the **stats** package instead of this.

**Examples**

```
cum.Vert.funkt(runif(12))
cum.Vert.funkt(runif(20))

Z <- rnorm(50)
cum.Vert.funkt(Z)
```

D1D2

*Numerical Derivatives of (x,y) Data via Smoothing Splines***Description**

Compute numerical derivatives of  $f()$  given observations  $(x, y)$ , using cubic smoothing splines with GCV, see [smooth.spline](#). In other words, estimate  $f'()$  and/or  $f''()$  for the model

$$Y_i = f(x_i) + E_i, \quad i = 1, \dots, n,$$

**Usage**

```
D1D2(x, y, xout = x, spar.offset = 0.1384, deriv = 1:2, spl.spar = NULL)
```

**Arguments**

<code>x, y</code>	numeric vectors of same length, supposedly from a model $y \sim f(x)$ .
<code>xout</code>	abscissa values at which to evaluate the derivatives.
<code>spar.offset</code>	numeric fudge added to the smoothing parameter, see <code>spl.par</code> below.
<code>deriv</code>	integer in 1:2 indicating which derivatives are to be computed.
<code>spl.spar</code>	direct smoothing parameter for <code>smooth.spline</code> . If it is NULL (as per default), the smoothing parameter used will be <code>spar.offset + sp\$spar</code> , where <code>sp\$spar</code> is the GCV estimated smoothing parameter, see <a href="#">smooth.spline</a> .

**Details**

It is well known that for derivative estimation, the optimal smoothing parameter is larger (more smoothing) than for the function itself. `spar.offset` is really just a *fudge* offset added to the smoothing parameter. Note that in R's implementation of [smooth.spline](#), `spar` is really on the  $\log \lambda$  scale.

When `deriv = 1:2` (as per default), both derivatives are estimated with the *same* smoothing parameter which is suboptimal for the single functions individually. Another possibility is to call `D1D2(*, deriv = k)` twice with `k = 1` and `k = 2` and use a *larger* smoothing parameter for the second derivative.

**Value**

a list with several components,

x	the abscissae values at which the derivative(s) are evaluated.
D1	if deriv contains 1, estimated values of $f'(x_i)$ where $x_i$ are the values from xout.
D2	if deriv contains 2, estimated values of $f''(x_i)$ .
spar	the <b>smoothing parameter</b> used in the (final) smooth.spline call.
df	the equivalent <b>degrees of freedom</b> in that smooth.spline call.

**Author(s)**

Martin Maechler, in 1992 (for S).

**See Also**

[D2ss](#) which calls smooth.spline twice, first on y, then on the  $f'(x_i)$  values; [smooth.spline](#) on which it relies completely.

**Examples**

```
set.seed(8840)
x <- runif(100, 0, 10)
y <- sin(x) + rnorm(100)/4

op <- par(mfrow = c(2,1))
plot(x,y)
lines(ss <- smooth.spline(x,y), col = 4)
str(ss[c("df", "spar")])
if(is.R()) plot(cos, 0, 10, ylim = c(-1.5,1.5), lwd=2) else { # Splus
  xx <- seq(0,10, len=201); plot(xx, cos(xx), type = 'l', ylim = c(-1.5,1.5))
}
title(expression("Estimating f'() : " * frac(d,dx) * sin(x) == cos(x)))
offs <- c(-0.1, 0, 0.1, 0.2, 0.3)
i <- 1
for(off in offs) {
  d12 <- D1D2(x,y, spar.offset = off)
  lines(d12$x, d12$D1, col = i <- i+1)
}
legend(2,1.6, c("true cos()",paste("sp.off. = ", format(offs))), lwd=1,
      col = 1:(1+length(offs)), cex = 0.8, bg = NA)
par(op)
```

**Description**

Compute the numerical first or 2nd derivatives of  $f()$  given observations  $(x[i], y \sim f(x[i]))$ .

D1tr is the *trivial* discrete first derivative using simple difference ratios, whereas D1ss and D2ss use cubic smoothing splines (see [smooth.spline](#)) to estimate first or second derivatives, respectively.

D2ss first uses `smooth.spline` for the first derivative  $f'()$  and then applies the same to the predicted values  $\hat{f}'(t_i)$  (where  $t_i$  are the values of `xout`) to find  $\hat{f}''(t_i)$ .

**Usage**

```
D1tr(y, x = 1)
```

```
D1ss(x, y, xout = x, spar.offset = 0.1384, spl.spar=NULL)
```

```
D2ss(x, y, xout = x, spar.offset = 0.1384, spl.spar=NULL)
```

**Arguments**

<code>x,y</code>	numeric vectors of same length, supposedly from a model $y \sim f(x)$ . For <code>D1tr()</code> , <code>x</code> can have length one and then gets the meaning of $h = \Delta x$ .
<code>xout</code>	abscissa values at which to evaluate the derivatives.
<code>spar.offset</code>	numeric fudge added to the smoothing parameter(s), see <code>spl.par</code> below. Note that the current default is there for historical reasons only, and we often would recommend to use <code>spar.offset = 0</code> instead.
<code>spl.spar</code>	direct smoothing parameter(s) for <code>smooth.spline</code> . If it is <code>NULL</code> (as per default), the smoothing parameter used will be <code>spar.offset + sp\$spar</code> , where <code>sp\$spar</code> is the GCV estimated smoothing parameter for <i>both</i> smooths, see <a href="#">smooth.spline</a> .

**Details**

It is well known that for derivative estimation, the optimal smoothing parameter is larger (more smoothing needed) than for the function itself. `spar.offset` is really just a *fudge* offset added to the smoothing parameters. Note that in R's implementation of [smooth.spline](#), `spar` is really on the  $\log \lambda$  scale.

**Value**

`D1tr()` and `D1ss()` return a numeric vector of the length of `y` or `xout`, respectively.

`D2ss()` returns a list with components

<code>x</code>	the abscissae values (= <code>xout</code> ) at which the derivative(s) are evaluated.
<code>y</code>	estimated values of $f''(x_i)$ .

`spl.spar`            numeric vector of length 2, contain the `spar` arguments to the two `smooth.spline` calls.

`spar.offset`        as specified on input (maybe `rep()`eated to length 2).

### Author(s)

Martin Maechler, in 1992 (for S).

### See Also

[D1D2](#) which directly uses the 2nd derivative of the smoothing spline; [smooth.spline](#).

### Examples

```
## First Derivative --- spar.off = 0 ok "asymptotically" (?)
set.seed(330)
mult.fig(12)
for(i in 1:12) {
  x <- runif(500, 0,10); y <- sin(x) + rnorm(500)/4
  f1 <- D1ss(x=x,y=y, spar.off=0.0)
  plot(x,f1, ylim = range(c(-1,1,f1)))
  curve(cos(x), col=3, add= TRUE)
}

set.seed(8840)
x <- runif(100, 0,10)
y <- sin(x) + rnorm(100)/4

op <- par(mfrow = c(2,1))
plot(x,y)
lines(ss <- smooth.spline(x,y), col = 4)
str(ss[c("df", "spar")])
xx <- seq(0,10, len=201)
plot(xx, -sin(xx), type = 'l', ylim = c(-1.5,1.5))
title(expression("Estimating f'() : " * frac(d^2,dx^2) * sin(x) == -sin(x)))
offs <- c(0.05, 0.1, 0.1348, 0.2)
i <- 1
for(off in offs) {
  d12 <- D2ss(x,y, spar.offset = off)
  lines(d12, col = i <- i+1)
}
legend(2,1.6, c("true : -sin(x)",paste("sp.off. = ", format(offs))), lwd=1,
      col = 1:(1+length(offs)), cex = 0.8, bg = NA)
par(op)
```



---

 Deprecated

---

 Deprecated 'sfsmisc' Functions
 

---

### Description

These functions are provided for compatibility with older versions of the **sfsmisc** package only, and may be defunct as soon as of the next release.

### Usage

```
pmax.sa(scalar, arr)
pmin.sa(scalar, arr)
```

### Arguments

scalar	numeric scalar.
arr	any numeric R object, typically array.

### Details

`pmax.sa(s, a)` and `pmin.sa(s, a)` return (more-dimensional) arrays. These have been deprecated, because `pmax` and `pmin` do so too, **if** the array is used as *first* argument.

---

 diagDA

---

 Diagonal Discriminant Analysis
 

---

### Description

This function implements a simple Gaussian maximum likelihood discriminant rule, for diagonal class covariance matrices.

In machine learning lingo, this is called “Naive Bayes” (for continuous predictors). Note that naive Bayes is more general, as it models discrete predictors as multinomial, i.e., binary predictor variables as Binomial / Bernoulli.

### Usage

```
dDA(x, cll, pool = TRUE)
## S3 method for class 'dDA'
predict(object, newdata, pool = object$pool, ...)
## S3 method for class 'dDA'
print(x, ...)

diagDA(ls, cll, ts, pool = TRUE)
```

**Arguments**

<code>x, ls</code>	learning set data matrix, with rows corresponding to cases (e.g., mRNA samples) and columns to predictor variables (e.g., genes).
<code>c11</code>	class labels for learning set, must be consecutive integers.
<code>object</code>	object of class <code>dDA</code> .
<code>ts, newdata</code>	test set (prediction) data matrix, with rows corresponding to cases and columns to predictor variables.
<code>pool</code>	logical flag. If true (by default), the covariance matrices are assumed to be constant across classes and the discriminant rule is linear in the data. Otherwise ( <code>pool=FALSE</code> ), the covariance matrices may vary across classes and the discriminant rule is quadratic in the data.
<code>...</code>	further arguments passed to and from methods.

**Value**

`dDA()` returns an object of class `dDA` for which there are `print` and `predict` methods. The latter returns the same as `diagDA()`:

`diagDA()` returns an integer vector of class predictions for the test set.

**Author(s)**

Sandrine Dudoit, <sandrine@stat.berkeley.edu> and Jane Fridlyand, <janef@stat.berkeley.edu> originally wrote `stat.diag.da()` in CRAN package `sma` which was modified for speedup by Martin Maechler <maechler@R-project.org> who also introduced `dDA` etc.

**References**

S. Dudoit, J. Fridlyand, and T. P. Speed. (2000) Comparison of Discrimination Methods for the Classification of Tumors Using Gene Expression Data. (Statistics, UC Berkeley, June 2000, Tech Report #576)

**See Also**

`lda` and `qda` from the `MASS` package; `naiveBayes` from `e1071`.

**Examples**

```
## two artificial examples by Andreas Greutert:
d1 <- data.frame(x = c(1, 5, 5, 5, 10, 25, 25, 25, 25, 29),
                y = c(4, 1, 2, 4, 4, 4, 6:8, 7))
n.plot(d1)
library(cluster)
(c11P <- pam(d1,k=4)$cluster) # 4 surprising clusters
with(d1, points(x+0.5, y, col = c11P, pch =c11P))

i1 <- c(1,3,5,6)
tr1 <- d1[-i1,]
```

```

c11. <- c(1,2,1,2,1,3)
c11 <- c(2,2,1,1,1,3)
plot(tr1, cex=2, col = c11, pch = 20+c11)
(dd.<- diagDA(tr1, c11., ts = d1[ i1,]))# ok
(dd <- diagDA(tr1, c11 , ts = d1[ i1,]))# ok, too!
points(d1[ i1,], pch = 10, cex=3, col = dd)

## use new fit + predict instead :
(r1 <- dDA(tr1, c11))
(r1.<- dDA(tr1, c11.))
stopifnot(dd == predict(r1, new = d1[ i1,]),
          dd.== predict(r1., new = d1[ i1,]))

plot(tr1, cex=2, col = c11, bg = c11, pch = 20+c11,
      xlim=c(1,30), ylim= c(0,10))
xy <- cbind(x= runif(500, min=1,max=30), y = runif(500, min=0, max=10))
points(xy, cex= 0.5, col = predict(r1, new = xy))
abline(v=c( mean(c(5,25)), mean(c(25,29))))

## example where one variable xj has Var(xj) = 0:
x4 <- matrix(c(2:4,7, 6,8,5,6, 7,2,3,1, 7,7,7,7), ncol=4)
y <- c(2,2, 1,1)
m4.1 <- dDA(x4, y, pool = FALSE)
m4.2 <- dDA(x4, y, pool = TRUE)
xx <- matrix(c(3,7,5,7), ncol=4)
predict(m4.1, xx)## gave integer(0) previously
predict(m4.2, xx)

```

---

diagX

*The “Other” Diagonal Matrix*


---

## Description

Compute the *other* diagonal identity matrix. The result is basically a *fast* version of `diag(n)[, n:1]`.

## Usage

```
diagX(n)
```

## Arguments

`n` positive integer.

## Value

a numeric  $n \times n$  matrix with many zeros – apart from 1s in the *other* diagonal.

## Author(s)

Martin Maechler, 1992.

**See Also**[diag](#).**Examples**

```
diagX(4)
for(m in 1:5)
  stopifnot(identical(diagX(m), diag(m)[, m:1, drop = FALSE]))
```

---

 digitsBase

*Digit/Bit Representation of Integers in any Base*


---

**Description**

Integer number representations in other Bases.

Formally, for every element  $N = x[i]$ , compute the (vector of) “digits”  $A$  of the base  $b$  representation of the number  $N$ ,  $N = \sum_{k=0}^M A_{M-k} b^k$ .

Revert such a representation to integers.

**Usage**

```
digitsBase(x, base = 2, ndigits = 1 + floor(1e-9 + log(max(x,1), base)))
## S3 method for class 'basedInt'
as.integer(x, ...)
## S3 method for class 'basedInt'
print(x, ...)

as.intBase(x, base = 2)
bi2int(xlist, base)
```

**Arguments**

x	For <code>digitsBase()</code> : non-negative integer (vector) whose base base digits are wanted. For <code>as.intBase()</code> : a list of numeric vectors, a character vector, or an integer matrix as returned by <code>digitsBase()</code> , representing digits in base base.
base	integer, at least 2 specifying the base for representation.
ndigits	number of bits/digits to use.
...	potential further arguments passed to methods, notably <a href="#">print</a> .
xlist	a <a href="#">list</a> of integer vectors with entries typically in $0:(base-1)$ , such as resulting from <code>digitsBase()</code> .

**Value**

For `digitsBase()`, an object, say `m`, of class "basedInt" which is basically a (`ndigits` x `n`) `matrix` where `m[,i]` corresponds to `x[i]`, `n <- length(x)` and `attr(m, "base")` is the input base.

`as.integerBase()` and the `as.integer` method for `basedInt` objects return an `integer` vector. `bi2int()` is the low-level workhorse of `as.integerBase()`.

**Note**

Some of these functions existed under names `digits` and `digits.v` in previous versions of the `sfsmisc` package.

**Author(s)**

Martin Maechler, Dec 4, 1991 (for S-plus; then called `digits.v`).

**Examples**

```
digitsBase(0:12, 8) #-- octal representation
empty.dimnames(digitsBase(0:33, 2)) # binary

## This may be handy for just one number (and default decimal):
digits <- function(n, base = 10) as.vector(digitsBase(n, base = base))
digits(128982734) # 1 2 8 9 8 2 7 3 4
digits(128, base = 8) # 2 0 0

## one way of pretty printing (base <= 10!)
b2ch <- function(db)
  noquote(gsub("^0+({1,})$", " \\1",
    apply(db, 2, paste, collapse = "")))
b2ch(digitsBase(0:33, 2)) #-> 0 1 10 11 100 101 ... 100001
b2ch(digitsBase(0:33, 4)) #-> 0 1 2 3 10 11 12 13 20 ... 200 201

## Hexadecimal:
i <- c(1:20, 100:106)
M <- digitsBase(i, 16)
hexdig <- c(0:9, LETTERS[1:6])
cM <- hexdig[1 + M]; dim(cM) <- dim(M)
b2ch(cM) #-> 1 2 3 4 5 6 7 8 9 A B C D E F 10 11 ... 6A

## IP (Internet Protocol) numbers coding: <n>.<n>.<n>.<n> <--> longinteger
ip_ntoa <- function(n)
  apply(digitsBase(n, base = 256), 2, paste, collapse=".")
ip_ntoa(2130706430 + (0:9))# "126.255.255.254" ... "127.0.0.7"
## and the inverse:
ip_aton <- function(a)
  bi2int(lapply(strsplit(a, "."), fixed=TRUE), as.integer), 256)

n <- 2130706430 + (0:9)
head(ip <- ip_ntoa(n))
head(ip_aton(ip))
stopifnot( n == ip_aton(ip_ntoa(n) ),
```

```

ip == ip_ntoa(ip_aton(ip))

## Inverse of digitsBase() : as.integer method for the "basedInt" class
as.integer(M)
## or also as.intBase() working from strings:
(cb <- apply(digitsBase(0:33, 4), 2, paste, collapse = ""))
##-> "000" "001" ..... "200" "201"
all(0:33 == as.intBase(cb, base = 4))

```

---

Duplicated

*Counting-Generalization of duplicated()*


---

### Description

Duplicated() generalizes the [duplicated](#) method for vectors, by returning indices of “equivalence classes” for duplicated entries and returning nomatch (NA by default) for unique entries.

Note that duplicated() is not TRUE for the first time a duplicate appears, whereas Duplicated() only marks unique entries with nomatch (NA).

### Usage

```
Duplicated(v, incomparables = FALSE, fromLast = FALSE, nomatch = NA_integer_)
```

### Arguments

v	a vector, often character, factor, or numeric.
incomparables	a vector of values that cannot be compared, passed to both <a href="#">duplicated()</a> and <a href="#">match()</a> . FALSE is a special value, meaning that all values can be compared, and may be the only value accepted for methods other than the default. It will be coerced internally to the same type as x.
fromLast	logical indicating if duplication should be considered from the reverse side, i.e., the last (or rightmost) of identical elements would correspond to duplicated=FALSE.
nomatch	passed to <a href="#">match()</a> : the value to be returned in the case when no match is found. Note that it is coerced to integer.

### Value

an integer vector of the same length as v. Can be used as a [factor](#), e.g., in [split](#), [tapply](#), etc.

### Author(s)

Christoph Buser and Martin Maechler, Seminar fuer Statistik, ETH Zurich, Sep.2007

### See Also

[uniqueL](#) (also in this [sfsmisc](#) package); [duplicated](#), [match](#).

**Examples**

```
x <- c(9:12, 1:4, 3:6, 0:7)
data.frame(x, dup = duplicated(x),
           dupL= duplicated(x, fromLast=TRUE),
           Dup = Duplicated(x),
           DupL= Duplicated(x, fromLast=TRUE))
```

eaxis

*Extended / Engineering Axis for Graphics***Description**

An extended `axis()` function which labels more prettily, in particular for log-scale axes.

It makes use of `plotmath` or (LaTeX) *expressions* of the form  $k \times 10^k$  for labeling a log-scaled axis and when otherwise exponential formatting would be used (see `pretty10exp`).

**Usage**

```
eaxis(side, at = if(log) axTicks(side, axp=axp, log=log, nintLog=nintLog)
      else axTicks(side, axp=axp, log=log),
      labels = NULL, log = NULL,
      use.expr = log || format.info(as.numeric(at), digits=7)[3] > 0,
      f.smalltcl = 3/5, at.small = NULL, small.mult = NULL, equidist.at.tol = 0.002,
      small.args = list(),
      draw.between.ticks = TRUE, between.max = 4,
      outer.at = TRUE, drop.1 = TRUE, sub10 = FALSE, las = 1,
      nintLog = max(10, par("lab")[2 - is.x]),
      axp = NULL, n.axp = NULL, max.at = Inf,
      lab.type = "plotmath", lab.sep = "cdot",
      ...)
```

**Arguments**

<code>side</code>	integer in 1:4, specifying side of <code>axis</code> .
<code>at</code>	numeric vector of ("normalized") tick locations; by default <code>axTicks(side, ...)</code> , i.e., the same as <code>axis()</code> would use.
<code>labels</code>	NULL (default), <b>logical</b> , character or expression, as in <code>axis()</code> ; in addition, if NA, <code>labels = TRUE</code> is passed to <code>axis()</code> , i.e. <code>pretty10exp</code> is <i>not</i> used. Use FALSE to suppress any labeling.
<code>log</code>	logical or NULL specifying if log-scale should be used; the default depends on the current plot's axis.
<code>use.expr</code>	logical specifying if <code>pretty10exp(.)</code> should be used for constructing labels when they are NULL. The default is typically good enough, but you may occasionally <i>force</i> <code>use.expr = TRUE</code> .
<code>f.smalltcl</code>	factor specifying the lengths of the small ticks in proportion to the normalized, labeled ticks.

<code>at.small</code>	locations of <i>small</i> ticks; the default, <code>NULL</code> , uses <code>small.mult</code> and constructs “smart” locations.
<code>small.mult</code>	positive integer (or <code>NULL</code> ), used when <code>at.small</code> is <code>NULL</code> to indicate which multiples of <code>at</code> (typically <code>axTicks()</code> ) should be used as “small ticks”. The default <code>NULL</code> will use 9 in the log case and a number in 2:5 otherwise.
<code>equidist.at.tol</code>	a small positive number, a tolerance to be used for checking equidistant <code>at</code> values. Used to be hardwired at <code>.001</code> which was seen to be too small; increase it when necessary.
<code>small.args</code>	optional <a href="#">list</a> of further arguments to the (second) <code>axis()</code> call which draws the <i>small</i> ticks.
<code>draw.between.ticks</code>	(only if <code>log</code> is true): logical indicating that possible (non-small) ticks between the labeled (via <code>at</code> ) ones should be drawn as well (and possibly also used for <code>at.small</code> construction), see also <code>between.max</code> .
<code>between.max</code>	(only if <code>log</code> and <code>draw.between.ticks</code> are true): integer indicating ticks should be drawn (approximately) between the labeled ones.
<code>outer.at</code>	logical specifying that <code>at.small</code> should also be constructed outside the <code>at</code> range, but still inside the corresponding <code>par("usr")</code> .
<code>drop.1</code>	logical specifying if $1 \times$ should be dropped from labels, passed to <code>pretty10exp()</code> .
<code>sub10</code>	logical, integer (of length 1 or 2) or “10”, indicating if some $10^k$ should be simplified to “traditional” formats, see <code>pretty10exp</code> .
<code>nintLog</code>	only used in <code>R &gt; 2.13.x</code> , when <code>log</code> is true: approximate (lower bound on) number of intervals for log scaling.
<code>axp</code>	to be passed to <code>axTicks()</code> if <code>at</code> is not specified.
<code>n.axp</code>	to be set to <code>axp[3]</code> when <code>axp</code> and <code>at</code> are not specified, in order to tweak the <i>number</i> of (non-small) tick marks produced from <code>axTicks(. . .)</code> , notably when <code>log</code> is true, set <code>n.axp</code> to 1, 2, or 3: <b>1:</b> will produce tick marks at $10^j$ for integer $j$ , <b>2:</b> gives marks $k10^j$ with $k \in \{1, 5\}$ , <b>3:</b> gives marks $k10^j$ with $k \in \{1, 2, 5\}$ see ‘ <code>xaxp</code> ’ on the <code>par</code> help page.
<code>max.at</code>	maximal number of <code>at</code> values to be used effectively. If you don’t specify <code>at</code> yourself carefully, it is recommended to set this to something like 25, but this is not the default, for back compatibility reasons.
<code>las, . . .</code>	arguments passed to (the first) <code>axis</code> call. Note that the default <code>las = 1</code> differs from <code>axis</code> ’s default <code>las = 0</code> .
<code>lab.type</code>	string, passed to <code>pretty10exp</code> to choose between default <code>plotmath</code> or LaTeX label format.
<code>lab.sep</code>	separator between mantissa and exponent for LaTeX labels, see <code>pretty10exp</code> .

**Author(s)**

Martin Maechler



**See Also**

[axis](#), [axTicks](#), [axTexpr](#), [pretty10exp](#).

**Examples**

```
x <- lseq(1e-10, 0.1, length = 201)
plot(x, pt(x, df=3), type = "l", xaxt = "n", log = "x")
eaxis(1)
## without small ticks:
eaxis(3, at.small=FALSE, col="blue")

## If you like the ticks, but prefer traditional (non-"plotmath") labels:
plot(x, gamma(x), type = "l", log = "x")
eaxis(1, labels=NA)

x <- lseq(.001, 0.1, length = 1000)
plot(x, sin(1/x)*x, type = "l", xaxt = "n", log = "x")
eaxis(1)
eaxis(3, n.axp = 1)# -> xaxp[3] = 1: only 10^j (main) ticks

## non- log-scale : draw small ticks, but no "10^k" if not needed:
x <- seq(-100, 100, length = 1000)
plot(x, sin(x)/x, type = "l", xaxt = "n")
eaxis(1) # default -> {1, 2, 5} * 10^j ticks
eaxis(3, n.axp = 2)# -> xaxp[3] := 2 -- approximately two (main) ticks

x <- seq(-1, 1, length = 1000)
plot(x, sin(x)/x, type = "l", xaxt = "n")
eaxis(1, small.args = list(col="blue"))

x <- x/1000
plot(x, 1-sin(x)/x, type = "l", xaxt = "n", yaxt = "n")
eaxis(1)
eaxis(2)
## more labels than default:
op <- par(lab=c(10,5,7))
plot(x, sin(x)/x, type = "l", xaxt = "n")
eaxis(1) # maybe (depending on your canvas), there are too many,
## in that case, maybe use
plot(x, sin(x)/x, type = "l", xaxt = "n")
eaxis(1, axTicks(1)[c(TRUE,FALSE)]) # drop every 2nd label
eaxis(3, labels=FALSE)

## ore use 'max.at' which thins as well:
plot(x, sin(x)/x, type = "l", xaxt = "n")
eaxis(1, max.at=6)
par(op)

### Answering R-help "How do I show real values on a log10 histogram", 26 Mar 2013
## the data:
set.seed(1); summary(x <- rlnorm(100, m = 2, sdl = 3))
## the plot (w/o x-axis) :
```

```

    r <- hist(log10(x), xaxt = "n", xlab = "x [log scale]")
## the nice axis:
    axt <- axTicks(1)
    eaxis(1, at = axt, labels = pretty10exp(10^axt, drop.1=TRUE))
## Additionally demo'ing 'sub10' options:
    plot(r, xaxt="n")
    eaxis(1, at = axt, labels = pretty10exp(10^axt, drop.1=TRUE, sub10 = 2))
## or
    plot(r, xaxt="n")
    eaxis(1, at = axt, labels = pretty10exp(10^axt, drop.1=TRUE, sub10 = "10"))
## or
    plot(r, xaxt="n")
    eaxis(1, at = axt, labels = pretty10exp(10^axt, drop.1=TRUE, sub10 = c(-2, 2)))

```

---

ecdf.ksCI

---

*Plot Empirical Distribution Function With 95% Confidence Curves*


---

## Description

Plots the empirical (cumulative) distribution function (ECDF) for univariate data, together with upper and lower simultaneous 95% confidence curves, computed via Kolmogorov-Smirnov'  $D$ , see [KSd](#).

## Usage

```
ecdf.ksCI(x, main = NULL, sub = NULL, xlab = deparse(substitute(x)),
         ci.col = "red", ...)
```

## Arguments

`x`                    `x` numerical vector of observations.  
`main, sub, xlab`      arguments passed to [title](#).  
`ci.col`                color for confidence interval lines.  
`...`                   optional arguments passed to [plot.stepfun](#).

## Value

Nothing. Used for its side effect, to produce a plot.

## Note

Presently, will only work if `length(x) > 9`.

## Author(s)

Kjetil Halvorsen

**References**

Bickel and Doksum, see [KSd](#).

**See Also**

[ecdf](#) and [plot.stepfun](#) in standard R.

**Examples**

```
ecdf.ksCI( rchisq(50,3) )
```

---

ellipsePoints	<i>Compute Radially Equispaced Points on Ellipse</i>
---------------	--

---

**Description**

Compute points on (the boundary of) an ellipse which is given by elementary geometric parameters.

**Usage**

```
ellipsePoints(a, b, alpha = 0, loc = c(0, 0), n = 201, keep.ab.order=FALSE)
```

**Arguments**

a, b	length of half axes in (x,y) direction. Note that $(a, b)$ is equivalent to $(b, a)$ <i>unless</i> <code>keep.ab.order=TRUE</code> .
alpha	angle (in degrees) giving the orientation of the ellipse, i.e., the original (x,y)-axis ellipse is rotated by <code>angle</code> .
loc	center (LOCation) of the ellipse.
n	number of points to generate.
keep.ab.order	logical indicating if $(a, b)$ should be considered <i>ordered</i> . When <code>FALSE</code> , as per default, the orientation of the ellipse is solely determined by <code>alpha</code> . Note that <code>keep.ab.order = TRUE</code> seems a more natural default, but <code>FALSE</code> is there for back-compatibility.

**Value**

A numeric matrix of dimension  $n \times 2$ , each row containing the (x,y) coordinates of a point.

**Author(s)**

Martin Maechler, March 2002.

**See Also**

the 'ellipse' package and [ellipsoidhull](#) and [ellipsoidPoints](#) in the 'cluster' package.

**Examples**

```
## Simple Ellipse, centered at (0,0), x-/y- axis parallel:
ep <- ellipsePoints(5,2)
str(ep)
plot(ep, type="n",asp=1) ; polygon(ep, col = 2)
## (a,b) = (2,5) is equivalent to (5,2) :
lines(ellipsePoints(2,5), lwd=2, lty=3)
## keep.order=TRUE : Now, (2,5) are axes in x- respective y- direction:
lines(ellipsePoints(2,5, keep.ab.order=TRUE), col="blue")

## rotate by 30 degrees :
plot(ellipsePoints(5,2, alpha = 30), asp=1)
abline(h=0,v=0,col="gray")
abline(a=0,b= tan( 30 *pi/180), col=2, lty = 2)
abline(a=0,b= tan(120 *pi/180), col=3, lty = 2)

## NB: use x11(type = "Xlib") for the following if you can
if(dev.interactive(TRUE)) {
  ## Movie : rotating ellipse :
  nTurns <- 4 # #{full 360 deg turns}
  for(al in 1:(nTurns*360)) {
    ep <- ellipsePoints(3,6, alpha=al, loc = c(5,2))
    plot(ep,type="l",xlim=c(-1,11),ylim=c(-4,8),
        asp=1, axes = FALSE, xlab="", ylab="")
  }

  ## Movie : rotating _filled_ ellipse {less nice to look at}
  for(al in 1:180) {
    ep <- ellipsePoints(3,6, alpha=al, loc = c(5,2))
    plot(ep,type="n",xlim=c(-1,11),ylim=c(-4,8),
        asp=1, axes = FALSE, xlab="", ylab="")
    polygon(ep,col=2,border=3,lwd=2.5)
  }
}# only if interactive
```

---

empty.dimnames

*Empty Dimnames of an Array*


---

**Description**

Remove all dimension names from an array for compact printing.

**Usage**

```
empty.dimnames(a)
```

**Arguments**

a an [array](#), i.e., as special case a matrix.

**Value**

Returns `a` with its `dimnames` replaced by empty character strings.

**Author(s)**

Bill Venables / Martin Maechler, Sept 1993.

**See Also**

[unnname](#) removes the `dimnames`.

**Examples**

```
empty.dimnames(diag(5)) # looks much nicer

(a <- matrix(-9:10, 4,5))
empty.dimnames(a) # nicer, right?
```

---

errbar

*Scatter Plot with Error Bars*


---

**Description**

Draws a scatter plot, adding vertical “error bars” to all the points.

**Usage**

```
errbar(x, y, yplus, yminus, cap = 0.015,
       ylim = range(y,yplus,yminus),
       xlab= deparse(substitute(x)),
       ylab= deparse(substitute(y)), ...)
```

**Arguments**

<code>x</code>	vector of x values.
<code>y</code>	vector of y values.
<code>yplus</code>	vector of y values: the tops of the error bars.
<code>yminus</code>	vector of y values: the bottoms of the error bars.
<code>cap</code>	the width of the little lines at the tops and bottoms of the error bars in units of the width of the plot. Default is 0.015.
<code>ylim</code>	(numeric of length 2): the y-axis extents with a sensible default.
<code>xlab, ylab</code>	axis labels for the plot, as in <a href="#">plot.default</a> .
<code>...</code>	Graphical parameters (see <a href="#">par</a> ) may also be supplied as arguments to this function.

**Author(s)**

Originally Charles Geyer, U.Chicago, early 1991; then Martin Mächler.

**See Also**

`errbar` in package **Hmisc** is similar.

**Examples**

```
y <- rnorm(10); d <- 1 + .1*rnorm(10)
errbar(1:10, y, y + d, y - d, main="Error Bars example")
```

---

f.robftest

*Robust F-Test: Wald test for multiple coefficients of rlm() Object.*

---

**Description**

Compute a robust F-Test, i.e., a Wald test for multiple coefficients of an `rlm` object.

**Usage**

```
f.robftest(object, var = -1)
```

**Arguments**

<code>object</code>	result of <code>rlm()</code> .
<code>var</code>	variables. Either their names or their indices; the default, <code>-1</code> means all <i>but</i> the intercept.

**Details**

This builds heavily on `summary.rlm()`, the `summary` method for `rlm` results.

**Value**

An object of class `"htest"`, hence with the standard print methods for hypothesis tests. This is basically a list with components

<code>statistic</code>	the F statistic, according to ...
<code>df</code>	numerator and denominator degrees of freedom.
<code>data.name</code>	(extracted from input object.)
<code>alternative</code>	"two.sided", always.
<code>p.value</code>	the P-value, using an F-test on <code>statistic</code> and <code>df[1:2]</code> .

**Author(s)**

Werner Stahel, July 2000; updates by Martin Maechler.

## References

FIXME — Need some here !

## See Also

[rlm](#), [summary.aov](#), etc.

## Examples

```
if(require("MASS")) {  
  ## same data as example(rlm)  
  data(stackloss)  
  summary(rsl <- rlm(stack.loss ~ ., stackloss))  
  f.robftest(rsl)  
} else " forget it "
```

---

factorize

*Prime Factorization of Integers*

---

## Description

Compute the prime factorization(s) of integer(s)  $n$ .

## Usage

```
factorize(n, verbose = FALSE)
```

## Arguments

$n$  vector of integers to factorize.  
 $verbose$  logical indicating if some progress information should be printed.

## Details

works via [primes](#), currently in a cheap way, sub-optimal for large composite  $n$ .

## Value

A named [list](#) of the same length as  $n$ , each element a 2-column matrix with column "p" the prime factors and column "m" their respective exponents (or multiplities), i.e., for a prime number  $n$ , the resulting matrix is `cbind(p = n, m = 1)`.

## Author(s)

Martin Maechler, Jan. 1996.

**See Also**

[primes](#).

For factorization of moderately or really large numbers, see the [gmp](#) package, and its [factorize\(\)](#).

**Examples**

```
factorize(47)
factorize(seq(101, 120, by=2))
```

---

funEnv

*List-like Environment of Functions (and More)*


---

**Description**

Construct a “list”, really an [environment](#) typically of functions and optionally other R objects, where the [functions](#) and [formulas](#) all share the same environment. Consequently, the functions may call each other.

On technical level, this is just a simple wrapper around [list2env\(\)](#).

**Usage**

```
funEnv(..., envir = NULL, parent = parent.frame(),
       hash = (...length() > 100), size = max(29L, ...length()))
```

**Arguments**

...	an arbitrary <i>named</i> “list” of R objects, typically including several <a href="#">functions</a> .
envir	an <a href="#">environment</a> or NULL.
parent	(for the case <code>envir = NULL</code> ): a parent frame aka enclosing environment, see <a href="#">new.env</a> and <a href="#">list2env</a> .
hash, size	(for the case <code>envir = NULL</code> ): hash a logical indicating if the created environment should use hashing, and (size) the hash size, see <a href="#">list2env</a> .

**Value**

an [environment](#), say E, containing the objects from ... (plus those in `envir`), and all function objects’ [environment\(\)](#) is E.

**Author(s)**

Martin Maechler

**See Also**

[list2env](#), [environment](#)



**Examples**

```

ee <- funEnv(f = function(x) g(2*(x+1)),
            g = function(y) hh(y+1),
            hh = function(u) u^2,
            info = "Some Information (not a function)")
ls(ee) # here the same as names(ee)
## Check that it works: i.e., that "f sees g" and "g sees hh":
stopifnot(all.equal(ee$f(pi), (2*pi+3)^2))
ee$f(0:4) # [1] 9 25 49 81 121

```

hatMat

*Hat Matrix of a Smoother***Description**

Compute the hat matrix or smoother matrix, of 'any' (linear) smoother, smoothing splines, by default.

**Usage**

```

hatMat(x, trace= FALSE,
       pred.sm = function(x, y, ...)
                 predict(smooth.spline(x, y, ...), x = x)$y,
       ...)

```

**Arguments**

x	numeric vector or matrix.
trace	logical indicating if the whole hat matrix, or only its trace, i.e. the sum of the diagonal values should be computed.
pred.sm	a function of at least two arguments (x,y) which returns fitted values, i.e. $\hat{y}$ , of length compatible to x (and y).
...	optionally further arguments to the smoother function pred.sm.

**Value**

The hat matrix  $H$  (if trace = FALSE as per default) or a number,  $tr(H)$ , the *trace* of  $H$ , i.e.,  $\sum_i H_{ii}$ . Note that  $\dim(H) == c(n,n)$  where  $n <- \text{length}(x)$  also in the case where some x values are duplicated (aka *ties*).

**Author(s)**

Martin Maechler <maechler@stat.math.ethz.ch>

**References**

Hastie and Tibshirani (1990). *Generalized Additive Models*. Chapman & Hall.

**See Also**

[smooth.spline](#), etc. Note the demo, `demo("hatmat-ex")`.

**Examples**

```
require(stats) # for smooth.spline() or loess()

x1 <- c(1:4, 7:12)
H1 <- hatMat(x1, spar = 0.5) # default : smooth.spline()

matplot(x1, H1, type = "l", main = "columns of smoother hat matrix")

## Example 'pred.sm' arguments for hatMat() :
pspl <- function(x,y,...) predict(smooth.spline(x,y, ...), x = x)$y
pksm <- function(x,y,...) ksmooth(sort(x),y, "normal", x.points=x, ...)$y
## Rather than ksmooth():
if(require("lokern"))
  pksm2 <- function(x,y,...) glkerns(x,y, x.out=x, ...)$est

## Explaining 'trace = TRUE'
all.equal(sum(diag((hatMat(c(1:4, 7:12), df = 4))),
            hatMat(c(1:4, 7:12), df = 4, trace = TRUE), tol = 1e-12)

## ksmooth() :
Hk <- hatMat(x1, pr = pksm, bandwidth = 2)
cat(sprintf("df = %.2f\n", sum(diag(Hk))))
image(Hk)
Matrix::printSpMatrix(as(round(Hk, 2), "sparseMatrix"))

##---> see demo("hatmat-ex") for more (and larger) examples
```

---

histBxp

*Plot a Histogram and a Boxplot*

---

**Description**

Creates a histogram and a horizontal boxplot on the current graphics device.

**Usage**

```
histBxp(x, nclass, breaks, probability=FALSE, include.lowest=TRUE,
        xlab = deparse(substitute(x)),
        ...,
        width=0.2, boxcol=3, medcol=2, medlwd=5, whisklty=2, staplelty=1)
```

**Arguments**

<code>x</code>	numeric vector of data for histogram. Missing values (NAs) are allowed.
<code>nclass</code>	recommendation for the number of classes (i.e., bars) the histogram should have. The default is a number proportional to the logarithm of the length of <code>x</code> .
<code>breaks</code>	vector of the break points for the bars of the histogram. The count in the <i>i</i> -th bar is <code>sum(breaks[i] &lt; x &lt;= breaks[i+1])</code> except that if <code>include.lowest</code> is TRUE (the default), the first bar also includes points equal to <code>breaks[1]</code> . If omitted, evenly-spaced break points are determined from <code>nclass</code> and the extremes of the data.
<code>probability</code>	logical flag: if TRUE, the histogram will be scaled as a probability density; the sum of the bar heights times bar widths will equal 1. If FALSE, the heights of the bars will be counts.
<code>include.lowest</code>	If TRUE (the default), the lowest bar will include data points equal to the lowest break, otherwise it will act like the other bars (see the description of the <code>breaks</code> argument).
<code>xlab</code>	character or expression for x axis labeling.
<code>...</code>	additional arguments to <code>barplot</code> . The <code>hist</code> function uses the function <code>barplot</code> to do the actual plotting; consequently, arguments to the <code>barplot</code> function that control shading, etc., can also be given to <code>hist</code> . See the <code>barplot</code> documentation for arguments <code>angle</code> , <code>density</code> , <code>col</code> , and <code>inside</code> . Do not use the space or <code>histo</code> arguments.
<code>width</code>	width of the box relative to the height of the histogram. DEFAULT is <code>0.2</code> .
<code>boxcol</code>	color of filled box. The default is 3.
<code>medcol</code>	the color of the median line. The special value, NA, indicates the current plotting color ( <code>par("col")</code> ). The default is 2. If <code>boxcol=0</code> and <code>medcol</code> is not explicitly specified this is set to the current plotting color ( <code>par("col")</code> ).
<code>medlwd</code>	median line width. The special value NA, is used to indicate the current line width ( <code>par("lwd")</code> ). The default is 5.
<code>whisklty</code>	whisker line type. The special value NA indicates the current line type ( <code>par("lty")</code> ). The default is 2 (dotted line).
<code>staplelty</code>	staple (whisker end cap) line type. The special value NA indicates the current line type ( <code>par("lty")</code> ). The default is 1 (solid line). Graphical parameters (see <a href="#">par</a> ) may also be supplied as arguments to this function. In addition, the high-level graphics arguments described under <code>par</code> and the arguments to <code>title</code> may be supplied to this function.

**Details**

If `include.lowest` is FALSE the bottom breakpoint must be strictly less than the minimum of the data, otherwise (the default) it must be less than or equal to the minimum of the data. The top breakpoint must be greater than or equal to the maximum of the data.

This function has been called `hist.bxp()` for 17 years; in 2012, the increasingly strong CRAN policies required a new name (which could not be confused with an S3 method name).

**Author(s)**

S-Plus: Markus Keller, Christian Keller; port to R in 1990's: Martin Mächler.

**See Also**

[hist](#), [barplot](#), [boxplot](#), [rug](#) and [scat1d](#) in the **Hmisc** package.

**Examples**

```
lab <- "50 samples from a t distribution with 5 d.f."
mult.fig(2*3, main = "Hist() + Rug() and histBxp(*)")
for(i in 1:3) {
  my.sample <- rt(50, 5)
  hist(my.sample, main=lab); rug(my.sample)# for 50 obs., this is ok, too..
  histBxp(my.sample, main=lab)
}
```

---

integrate.xy

*Cheap Numerical Integration through Data points.*


---

**Description**

Given  $(x_i, f_i)$  where  $f_i = f(x_i)$ , compute a cheap approximation of  $\int_a^b f(x)dx$ .

**Usage**

```
integrate.xy(x, fx, a, b, use.spline=TRUE, xtol=2e-08)
```

**Arguments**

x	abscissa values.
fx	corresponding values of $f(x)$ .
a,b	the boundaries of integration; these default to min(x) and max(x) respectively.
use.spline	logical; if TRUE use an interpolating spline.
xtol	tolerance factor, typically around $\sqrt{.Machine\$double.eps}$ .....(fixme)....

**Details**

Note that this is really not good for noisy fx values; probably a smoothing spline should be used in that case.

Also, we are not yet using Romberg in order to improve the trapezoid rule. This would be quite an improvement in equidistant cases.

**Value**

the approximate integral.

**Author(s)**

Martin Maechler, May 1994 (for S).

**See Also**

[integrate](#) for numerical integration of *functions*.

**Examples**

```
x <- 1:4
integrate.xy(x, exp(x))
print(exp(4) - exp(1), digits = 10) # the true integral

for(n in c(10, 20,50,100, 200)) {
  x <- seq(1,4, len = n)
  cat(formatC(n,wid=4), formatC(integrate.xy(x, exp(x)), dig = 9),"\n")
}
```

---

inv.seq

*Inverse seq() – Short Expression for Index Vector*

---

**Description**

Compute a short expression for a given integer vector, typically an index, that can be expressed shortly, using `:` etc.

**Usage**

```
inv.seq(i)
```

**Arguments**

`i` vector of (usually increasing) integers.

**Value**

a `call` (“the inside of an [expression](#)”) to be `eval()`ed to return the original `i`.

**Author(s)**

Martin Maechler, October 1995; more elegant implementation from Tony Plate.

**See Also**

[rle](#) for another kind of integer vector coding.

### Examples

```
(rr <- inv.seq(i1 <- c(3:12, 20:24, 27, 30:33)))
eval(rr)
stopifnot(eval(rr) == i1)

e2 <- expression(c(20:13, 3:12, -1:-4, 27, 30:31))
(i2 <- eval(e2))
(r2 <- inv.seq(i2))
stopifnot(all.equal(r2, e2[[1]]))

## Had {mapply()} bug in this example:
ii <- c(1:3, 6:9, 11:16)
stopifnot(identical(ii, eval(inv.seq(ii))))
```

---

is.whole

*Test Whether a Vector or Array Consists of Whole Numbers*

---

### Description

This function tests whether a numeric or complex vector or array consists of whole numbers. The function [is.integer](#) is not appropriate for this since it tests whether the vector is of class integer (see examples).

### Usage

```
is.whole(x, tolerance = sqrt(.Machine$double.eps))
```

### Arguments

x	integer, numeric, or complex vector or array to be tested
tolerance	maximal distance to the next whole number

### Value

The return value has the same dimension as the argument x: if x is a vector, the function returns a logical vector of the same length; if x is a matrix or array, the function returns a logical matrix or array of the same dimensions. Each entry in the result indicates whether the corresponding entry in x is whole.

### Author(s)

Alain Hauser <alain@huschhus.ch>

### See Also

[is.integer](#)

**Examples**

```
## Create a random array, matrix, vector
set.seed(307)
a <- array(runif(24), dim = c(2, 3, 4))
a[4:8] <- 4:8
m <- matrix(runif(12), 3, 4)
m[2:4] <- 2:4
v <- complex(real      = seq(0.5, 1.5, by = 0.1),
             imaginary = seq(2.5, 3.5, by = 0.1))

## Find whole entries
is.whole(a)
is.whole(m)
is.whole(v)

## Numbers of class integer are always whole
is.whole(dim(a))
is.whole(length(v))
```

---

iterate.lin.recursion *Generate Sequence Iterating a Linear Recursion*

---

**Description**

Generate numeric sequences applying a linear recursion `nr.it` times.

**Usage**

```
iterate.lin.recursion(x, coeff, delta = 0, nr.it)
```

**Arguments**

<code>x</code>	numeric vector with <i>initial values</i> , i.e., specifying the beginning of the resulting sequence; must be of length (larger or) equal to <code>length(coeff)</code> .
<code>coeff</code>	coefficient vector of the linear recursion.
<code>delta</code>	numeric scalar added to each term; defaults to 0. If not zero, determines the linear drift component.
<code>nr.it</code>	integer, number of iterations.

**Value**

numeric vector, say `r`, of length `n + nr.it`, where `n = length(x)`. Initialized as `r[1:n] = x`, the recursion is `r[k+1] = sum(coeff * r[(k-m+1):k])`, where `m = length(coeff)`.

**Note**

Depending on the zeroes of the characteristic polynomial of `coeff`, there are three cases, of convergence, oscillation and divergence.

**Author(s)**

Martin Maechler

**See Also**[seq](#) can be regarded as a trivial special case.**Examples**

```
## The Fibonacci sequence:
iterate.lin.recursion(0:1, c(1,1), nr = 12)
## 0 1 1 2 3 5 8 13 21 34 55 89 144 233

## seq() as a special case:
stopifnot(iterate.lin.recursion(4,1, d=2, nr=20)
          == seq(4, by=2, length=1+20))

## 'Deterministic AR(2)' :
round(iterate.lin.recursion(1:4, c(-0.7, 0.9), d = 2, nr=15), dig=3)
## slowly decaying :
plot(ts(iterate.lin.recursion(1:4, c(-0.9, 0.95), nr=150)))
```

KSd

*Approximate Critical Values for Kolmogorov-Smirnov's D***Description**

Computes the critical value for Kolmogorov-Smirnov's  $D_n$ , for sample sizes  $n \geq 10$  and confidence level 95%.

**Usage**

KSd(n)

**Arguments**

n                    the sample size,  $n \geq 10$ .

**Details**

Based on tables values given in the reference below. For  $n \leq 80$  uses interpolations from exact values, elsewhere uses asymptotic approximation.

**Value**

The critical value for D (two-sided) for significance level 0.05 (or confidence level 95%).



**Author(s)**

Kjetil Halvorsen and Martin Maechler

**References**

Peter J. Bickel and Kjell A. Doksum (1977), *Mathematical Statistics: Basic Ideas and Selected Topics*. Holden Day. Section 9.6 and table IX.

**See Also**

Is used from [ecdf.ksCI](#).

**Examples**

```
KSd(90)
KSd(1:9)# now works

op <- par(mfrow=c(2,1))
plot(KSd, 10, 150)# nice
abline(v = c(75,85), col = "gray")
plot(KSd, 79, 81, n = 1001)# *very* tiny discontinuity at 80
par(op)
```

---

last

*Get Last Elements of a Vector*

---

**Description**

Extract the last elements of a vector.

**Usage**

```
last(x, length.out = 1, na.rm = FALSE)
```

**Arguments**

x	any vector.
length.out	integer indicating how many element are desired. If positive, return the length.out last elements of x; if negative, the last length.out elements are <i>dropped</i> .
na.rm	logical indicating if the last non-missing value (if any) shall be returned. By default (it is FALSE and) the last elements (whatever its values) are returned.

**Value**

a vector of length `abs(length.out)` of *last* values from x.

**Note**

This function may eventually be deprecated for the standard R function `tail()`.

Useful for the `turnogram()` function in package **pastecs**.

**Author(s)**

Werner Stahel (<stahel@stat.math.ethz.ch>), and independently, Philippe Grosjean (<phgrosjean@sciviews.org>),  
Frédéric Ibanez (<ibanez@obs-vlfr.fr>).

**See Also**

`first`, `turnogram`

**Examples**

```
a <- c(NA, 1, 2, NA, 3, 4, NA)
last(a)
last(a, na.rm=TRUE)

last(a, length = 2)
last(a, length = -3)
```

---

linesHyperb.lm

*Plot Confidence or Prediction Hyperbolas around a Regression Line*

---

**Description**

Add confidence/prediction hyperbolas for  $y(x_0)$  to a plot with data or regression line.

**Usage**

```
linesHyperb.lm(object, c.prob=0.95, confidence=FALSE,
               k=if (confidence) Inf else 1,
               col=2, lty=2, do.abline=TRUE)
```

**Arguments**

<code>object</code>	result of <code>lm(.)</code> .
<code>c.prob</code>	coverage probability in $(0, 1)$ .
<code>confidence</code>	logical; if true, do (small) confidence band, else, realistic prediction band for the mean of $k$ observations.
<code>k</code>	integer or <code>Inf</code> ; assume $k$ future observations; $k = \text{Inf}$ corresponds to confidence intervals (for $y$ ).
<code>col</code> , <code>lty</code>	attributes for the <code>lines</code> to be drawn.
<code>do.abline</code>	logical; if true, the regression line is drawn as well.

**Note**

With `predict.lm(*, interval=)` is available, this function `linesHyperb.lm` is only slightly more general for its `k` argument.

**Author(s)**

Martin Maechler, Oct 1995

**See Also**

`predict.lm(*, interval=)` optionally computes prediction or confidence intervals.

**Examples**

```
data(swiss)
  plot(Fertility ~ Education, data = swiss) # the data
(lmS <- lm(Fertility ~ Education, data = swiss))
linesHyperb.lm(lmS)
linesHyperb.lm(lmS, conf=TRUE, col="blue")
```

---

loessDemo

*Graphical Interactive Demo of loess()*


---

**Description**

A graphical and interactive demonstration and visualization of how `loess` works. By clicking on the graphic, the user determines the current estimation window which is visualized together with the weights.

**Usage**

```
loessDemo(x, y, span = 1/2, degree = 1, family = c("gaussian", "symmetric"),
  nearest = FALSE, nout = 501,
  xlim = numeric(0), ylim = numeric(0), strictlim = TRUE, verbose = TRUE,
  inch.sym = 0.25, pch = 4, shade = TRUE, w.symbols = TRUE,
  sym.col = "blue", w.col = "light blue", line.col = "steelblue")
```

**Arguments**

<code>x,y</code>	numeric vectors of the same length; the demo is about <code>loess(y ~ x)</code> .
<code>span</code>	the smoothing parameter $\alpha$ .
<code>degree</code>	the degree of the polynomials to be used; must be in 0, 1, 2.
<code>family</code>	if "gaussian" fitting is by least-squares, and if "symmetric" a re-descending M estimator is used with Tukey's biweight function. Can be abbreviated.
<code>nearest</code>	logical indicating how $x_0$ should be determined, the value at which $\hat{f}(x_0)$ is computed. If <code>nearest</code> is true, the closest <i>data</i> value is taken.

nout	the number of points at which to evaluate, i.e, determining $u_i, i = 1, 2, \dots, \text{nout}$ , at which $\hat{f}(u_i)$ is computed.
xlim	x-range; to extend or determine (iff <code>strictlim</code> is true) the $x$ -range for plotting.
ylim	y-range; to extend or determine (iff <code>strictlim</code> is true) the $y$ -range for plotting.
strictlim	logical determining if <code>xlim</code> and <code>ylim</code> should be strict limits (as e.g., in <code>plot.default</code> ), or just a suggestion to <i>extend</i> the data-dependent ranges.
verbose	logical .....
inch.sym	symbol size in inches of the maximal weight circle symbol.
pch	plotting character, see <code>points</code> .
shade	logical; if true, <code>polygon(..., density=..)</code> will be used to shade off the regions where the weights are zero.
w.symbols	logical indicating if the non-zero weights should be visualized by circles with radius proportional to <code>inch.sym</code> and $\sqrt{w}$ where $w$ are the weights.
sym.col, w.col, line.col	colors for the symbols, weights and lines, respectively.

### Author(s)

As function `loess.demo()`, written and posted to S-news, on 27 Sep 2001, by Greg Snow, Brigham Young University, it was modified by Henrik Aa. Nielsen, IMM, DTU, and subsequently spiffed up for R by Martin Maechler.

### See Also

[loess](#).

### Examples

```
if(dev.interactive()) {
  if(requireNamespace("lattice")) {
    data("ethanol", package = "lattice")
    attach(ethanol)
    loessDemo(E,N0x, span=.25)
    loessDemo(E,N0x, span=.25, family = "symmetric")

    loessDemo(E,N0x, degree=0)# Tricube Kernel estimate
  }

  ## Artificial Example with one outlier
  n2 <- 50; x <- 1:(1+2*n2)
  fx <- (x/10 - 5)^2
  y <- fx + 4*rnorm(x)
  y[n2+1] <- 1e4
  loessDemo(x,y, span=1/3, ylim= c(0,1000))# not robust !!
  loessDemo(x,y, span=1/3, family = "symm")
  loessDemo(x,y, span=1/3, family = "symm", w.symb = FALSE, ylim = c(0,40))
  loessDemo(x,y, span=1/3, family = "symm", ylim = c(0,40))
}
```

```
## but see warnings() --- there's a "fixup"  
}
```

---

**lseq***Generate Sequences, Equidistant on Log Scale*

---

### Description

Generate sequences which are equidistant on a log-scale.

### Usage

```
lseq(from, to, length)
```

### Arguments

from	starting value of sequence.
to	end value of the sequence.
length	desired length of the sequence.

### Value

a [numeric](#) vector of length length.

### See Also

[seq](#).

### Examples

```
(x <- lseq(1, 990, length= 21))  
plot(x, x^4, type = "b", col = 2, log = "xy")  
if(with(R.version, major >= 2 && minor >= 1))  
plot(x, exp(x), type = "b", col = 2, log = "xy")
```

---

 mat2tex

 Produce LaTeX commands to print a matrix
 

---

## Description

“Translate” an R matrix (like object) into a LaTeX table, using `\begin{tabular}` . . . .

## Usage

```
mat2tex(x, file= "mat.tex", envir = "tabular",
        nam.center = "l", col.center = "c",
        append = TRUE, digits = 3, title)
```

## Arguments

<code>x</code>	a matrix
<code>file</code>	names the file to which LaTeX commands should be written
<code>envir</code>	a string, the LaTeX environment name; default is "tabular"; useful maybe "array", or other versions of tabular environments.
<code>nam.center</code>	character specifying row names should be center; default "l".
<code>col.center</code>	character (vector) specifying how the columns should be centered; must have values from <code>c("l", "c", "r")</code> ; defaults to "c".
<code>append</code>	logical; if FALSE, will destroy the file <code>file</code> before writing commands to it; otherwise (by default), simply adds commands at the end of file <code>file</code> .
<code>digits</code>	integer; setting of <code>options(digits=..)</code> for purpose of number representation.
<code>title</code>	a string, possibly using LaTeX commands, which will span the columns of the LaTeX matrix

## Value

No value is returned. This function, when used correctly, only writes LaTeX commands to a file.

## Author(s)

For S: Vincent Carey <vjcarey@sphunix.sph.jhu.edu>, from a post on Feb.19, 1991 to S-news. Port to R (and a bit more) by Martin Maechler <maechler@stat.math.ethz.ch>.

## See Also

`latex` in package **Hmisc** is more flexible (but may surprise by its auto-printing ..).

## Examples

```
mex <- matrix(c(pi,pi/2,pi/4,exp(1),exp(2),exp(3)),nrow=2, byrow=TRUE,
             dimnames = list(c("$\\pi$","$e$"), c("a","b","c")))
mat2tex(mex, file = print(tf <- tempfile("mat", , ".tex")),
       title="$\\pi, e$, etc." )

## The last command produces the file "mat<xyz>.tex" containing

##> \begin{tabular} {| l|| c| c| c|}
##> \multicolumn{ 4 }{c}{ $\\pi, e$, etc. } \\ \hline
##> \ & a & b & c \\ \hline \hline
##> $\\pi$ & 3.14 & 1.57 & 0.785 \\ \hline
##> $e$ & 2.72 & 7.39 & 20.1 \\ \hline
##> \end{tabular}

## Now you have to properly embed the contents of this file
## in a LaTeX document -- for example, you will need a
## preamble, the \begin{document} statement, etc.

## Note that the backslash needs protection in dimnames
## or title actions.

mat2tex(mex, stdout(), col.center = c("r","r","c"))
```

---

missingCh

*Has a Formal Argument been Set or is it Missing?*

---

## Description

missingCh can be used to test whether a value was specified as an argument to a function. Very much related to the standard R function `missing`, here the argument is given by its name, a character string.

As `missingCh()` calls `missing()`, do consider the caveats about the latter, see [missing](#).

## Usage

```
missingCh(x, envir = parent.frame())
```

## Arguments

x	a <a href="#">character</a> string.
envir	a (function evaluation) <a href="#">environment</a> , in which the variable named x is to be “missing”.

## Value

a [logical](#) indicating if the argument named x is [missing](#) in the function “above”, typically the caller of `missingCh`, but see the use of `envir` in the `vapply` example.

**Author(s)**

Martin Maechler

**See Also**[missing](#)**Examples**

```

tst1 <- function(a, b, dd, ...) ## does not work an with argument named 'c' !
  c(b = missingCh("b"), dd = missingCh("dd"))
tst1(2)#-> both 'b' and 'dd' are missing
tst1(,3,,3)
##      b      dd
## FALSE TRUE  -- as 'b' is not missing but 'dd' is.

Tst <- function(a,b,cc,dd,EEE, ...)
  vapply(c("a","b","cc","dd","EEE"), missingCh, NA, envir=environment())
Tst()
## TRUE ... TRUE -- as all are missing()
Tst(1,,3)
##      a      b      cc      dd      EEE
## FALSE TRUE FALSE TRUE TRUE
## .....
## as 'a' and 'cc' where not missing()

## Formal testing:
stopifnot(tst1(), !tst1(,3,3), Tst(),
          Tst(1,,3, b=2, E="bar") == c(0,0,1,0,0))
## maybe surprising that this ^^ becomes 'dd' and only 'cc' is missing

```

mpl

*Simple Matrix Plots***Description**

Do simple matrix plots, providing an easy interface to [matplot](#) by using a default x variable.

**Usage**

```

mpl(mat, ...)
p.m(mat, ...)

```

**Arguments**

`mat` numeric matrix.  
`...` further arguments passed to [matplot](#), e.g., `type`, `xlab`, etc.



**Details**

`p.m(m)` use the first column of `m` as  $x$  variable, whereas `mpl(m)` uses the integers  $1, 2, \dots, \text{nrow}(m)$  as coordinates and `rownames(m)` as axis labels if possible.

**Note**

These were really created for playing around with curves etc, and probably should be *deprecated* since in concrete examples, using `matplot()` directly is more appropriate.

**Author(s)**

Martin Maechler

**See Also**

`matplot`, `plot.mts`(\*,`plot.type` = "single").

**Examples**

```
data(animals, package = "cluster")
mpl(animals, type = "l")
```

---

mult.fig

*Plot Setup for MULTiple FIGures, incl. Main Title*

---

**Description**

Easy Setup for plotting multiple figures (in a rectangular layout) on one page. It allows to specify a main title and uses *smart* defaults for several `par` calls.

**Usage**

```
mult.fig(nr.plots, mfrow, mfc col, marP = rep(0, 4),
         mgp = c(if(par("las") != 0) 2. else 1.5, 0.6, 0),
         mar = marP + 0.1 + c(4,4,2,1), oma = c(0,0, tit.wid, 0),
         main = NULL,
         tit.wid = if (is.null(main)) 0 else 1 + 1.5*cex.main,
         cex.main = par("cex.main"), line.main = cex.main - 1/2,
         col.main = par("col.main"), font.main = par("font.main"), ...)
```

**Arguments**

<code>nr.plots</code>	integer; the number of plot figures you'll want to draw.
<code>mfrow, mfc col</code>	<i>instead</i> of <code>nr.plots</code> : integer(2) vectors giving the rectangular figure layout for <code>par(mfrow = *)</code> , or <code>par(mfc col = *)</code> , respectively. The default is to use <code>mfrow = n2mfrow(nr.plots)</code> .
<code>marP</code>	numeric(4) vector of figure margins to <i>add</i> ("Plus") to default <code>mar</code> , see below.

mgp	argument for <code>par</code> ( <code>mgp= .</code> ) with a smaller default than usual.
mar	argument for <code>par</code> ( <code>mar= .</code> ) with a smaller default than usual, using the <code>marP</code> argument, see above.
oma	argument for <code>par</code> ( <code>oma= .</code> ), by default for adding space for the main title if necessary.
main	character. The main title to be used for the whole graphic.
tit.wid	numeric specifying the vertical width to be used for the main title; note that this is only used for the default value of <code>oma</code> (s. above).
cex.main	numeric; the character size to be used for the main title.
line.main	numeric; the margin line at which the title is written (via <code>mtext</code> ( <code>main, side=3, outer=TRUE, line = line.main, ...</code> )).
col.main, font.main	color and font for main title, passed to <code>mtext</code> (), see also <code>par</code> (*)).
...	further arguments to <code>mtext</code> for the main title.

**Value**

A `list` with two components that are lists themselves, a subset of `par`(),

<code>new.par</code>	the current <code>par</code> settings.
<code>old.par</code>	the <code>par</code> <i>before</i> the call.

**Author(s)**

Martin Maechler, UW Seattle, 1990 (for S).

**See Also**

`par`, `layout`.

**Examples**

```
opl <- mult.fig(5, main= expression("Sine Functions " * sin(n * pi * x)))
x <- seq(0, 1, len = 201)
for (n in 1:5)
  plot(x, sin(n * pi * x), ylab = "", main = paste("n = ", n))
par(opl$old.par)

rr <- mult.fig(mfrow=c(5,1), main= "Cosinus Funktionen", cex = 1.5,
  marP = - c(0, 1, 2, 0))
for (n in 1:5)
  plot(x, cos(n * pi * x), type = 'l', col="red", ylab = "")
str(rr)
par(rr$old.par)
## The *restored* par settings:
str(do.call("par", as.list(names(rr$new.par))))
```

---

`n.code`*Convert "Round" Integers to Short Strings and Back*

---

### Description

`n.code` convert “round integers” to short character strings. This is useful to build up variable names in simulations, e.g.

`code2n` is the *inverse* function of `n.code()`.

### Usage

```
n.code(n, ndig = 1, dec.codes = c("", "d", "c", "k"))
code2n(ncod, ndig = 1, dec.codes = c("", "d", "c", "k"))
```

### Arguments

<code>n</code>	integer vector.
<code>ncod</code>	character vector, typically resulting from <code>n.code</code> .
<code>ndig</code>	integer giving number of digits before the coding character.
<code>dec.codes</code>	character code for 1, 10, 100, 1000 (etc).

### Value

`n.code(n)` returns a [character](#) vector of the same length as `n`.

`code2n(ncod)` returns a [integer](#) vector of the same length as `ncod`.

Usually, `code2n(n.code(n)) == n`.

### Author(s)

Martin Maechler

### Examples

```
n10 <- c(10,20,90, 100,500, 2000,10000)
(c10 <- n.code(n10))#-> "1d" "2d" "9d" "1c" ..
stopifnot(code2n(c10) == n10)
```

---

n.plot

*Name Plot: Names or Numbers instead of Points in Plot*


---

**Description**

A utility function which basically calls `plot(*, type="n")` and `text`. To have names or numbers instead of points in a plot is useful for identification, e.g., in a residual plot, see also [TA.plot](#).

**Usage**

```
n.plot(x, y = NULL, nam = NULL, abbr = n >= 20 || max(nchar(nam))>=8,
       xlab = NULL, ylab = NULL, log = "",
       cex = par("cex"), col = par("col"), ...)
```

**Arguments**

<code>x,y</code>	coordinates at which to plot. If <code>y</code> is missing, <code>x</code> is used for both, if it's a <a href="#">data.frame</a> , <a href="#">list</a> , 2-column matrix etc – via <a href="#">xy.coords</a> ; formula do <b>not</b> work.
<code>nam</code>	the labels to plot at each (x,y). Per default, these taken from the data <code>x</code> and <code>y</code> ; case numbers <code>1:n</code> are taken if no names are available.
<code>abbr</code>	logical indicating if the <code>nam</code> labels should be abbreviated – with a sensible default.
<code>xlab,ylab</code>	labels for the x- and y- axis, the latter being empty by default.
<code>log</code>	character specifying if log scaled axes should be used, see <a href="#">plot.default</a> .
<code>cex</code>	plotting character expansion, see <a href="#">par</a> .
<code>col</code>	color to use for <code>text()</code> .
<code>...</code>	further arguments to be passed to the <a href="#">plot</a> call.

**Value**

invisibly, a character vector with the labels used.

**Author(s)**

Martin Maechler, since 1992

**See Also**

[plot.default](#), [text](#).

**Examples**

```
n.plot(1:20, cumsum(rnorm(20)))
data(cars)
with(cars, n.plot(speed, dist, cex = 0.8, col = "forest green"))
```

---

 nearcor

*Find the Nearest Proper Correlation Matrix*


---

### Description

This function “smoothes” an improper correlation matrix as it can result from `cor` with `use="pairwise.complete.obs"` or `hetcor`.

It is *deprecated* now, in favor of `nearPD()` from package **Matrix**.

### Usage

```
nearcor(R, eig.tol = 1e-06, conv.tol = 1e-07, posd.tol = 1e-08,
        maxits = 100, verbose = FALSE)
```

### Arguments

R	a square symmetric approximate correlation matrix
eig.tol	defines relative positiveness of eigenvalues compared to largest, default=1.0e-6.
conv.tol	convergence tolerance for algorithm, default=1.0e-7
posd.tol	tolerance for enforcing positive definiteness, default=1.0e-8
maxits	maximum number of iterations
verbose	logical specifying if convergence monitoring should be verbose.

### Details

This implements the algorithm of Higham (2002), then forces symmetry, then forces positive definiteness using code from `posdefify`. This implementation does not make use of direct LAPACK access for tuning purposes as in the MATLAB code of Lucas (2001). The algorithm of Knol DL and ten Berge (1989) (not implemented here) is more general in (1) that it allows constraints to fix some rows (and columns) of the matrix and (2) to force the smallest eigenvalue to have a certain value.

### Value

A `list`, with components

cor	resulting correlation matrix
fnorm	Froebenius norm of difference of input and output
iterations	number of iterations used
converged	logical

### Author(s)

Jens Oehlschlägel

## References

See those in [posdefify](#).

## See Also

the slightly more flexible [nearPD](#) which also returns a *classed* matrix (class `dpoMatrix`). For new code, `nearPD()` is really preferred to `nearcor()`, which hence is considered deprecated.

[hetcor](#), [eigen](#); [posdefify](#) for a simpler algorithm.

## Examples

```
cat("pr is the example matrix used in Knol DL, ten Berge (1989)\n")
pr <- matrix(c(1,      0.477, 0.644, 0.478, 0.651, 0.826,
0.477, 1,      0.516, 0.233, 0.682, 0.75,
0.644, 0.516, 1,      0.599, 0.581, 0.742,
0.478, 0.233, 0.599, 1,      0.741, 0.8,
0.651, 0.682, 0.581, 0.741, 1,      0.798,
0.826, 0.75, 0.742, 0.8, 0.798, 1),
  nrow = 6, ncol = 6)
```

```
ncr <- nearcor(pr)
nr <- ncr$cor
```

```
plot(pr[lower.tri(pr)],
      nr[lower.tri(nr)]); abline(0,1, lty=2)
round(cbind(eigen(pr)$values, eigen(nr)$values), 8)
```

```
cat("The following will fail:\n")
try(factanal(cov=pr, factors=2))
cat("and this should work\n")
try(factanal(cov=nr, factors=2))
```

```
if(require("polycor")) {
  n <- 400
  x <- rnorm(n)
  y <- rnorm(n)

  x1 <- (x + rnorm(n))/2
  x2 <- (x + rnorm(n))/2
  x3 <- (x + rnorm(n))/2
  x4 <- (x + rnorm(n))/2

  y1 <- (y + rnorm(n))/2
  y2 <- (y + rnorm(n))/2
  y3 <- (y + rnorm(n))/2
  y4 <- (y + rnorm(n))/2

  dat <- data.frame(x1, x2, x3, x4, y1, y2, y3, y4)

  x1 <- ordered(as.integer(x1 > 0))
```

```

x2 <- ordered(as.integer(x2 > 0))
x3 <- ordered(as.integer(x3 > 1))
x4 <- ordered(as.integer(x4 > -1))

y1 <- ordered(as.integer(y1 > 0))
y2 <- ordered(as.integer(y2 > 0))
y3 <- ordered(as.integer(y3 > 1))
y4 <- ordered(as.integer(y4 > -1))

odat <- data.frame(x1, x2, x3, x4, y1, y2, y3, y4)

xcor <- cor(dat)
pcor <- cor(data.matrix(odat)) # cor() no longer works for factors
hcor <- hetcor(odat, ML=TRUE, std.err=FALSE)$correlations
ncor <- nearcor(hcor)$cor

try(factanal(covmat=xcor, factors=2, n.obs=n))
try(factanal(covmat=pcor, factors=2, n.obs=n))
try(factanal(covmat=hcor, factors=2, n.obs=n))
try(factanal(covmat=ncor, factors=2, n.obs=n))
}

```

---

nr.sign.chg

*Number of Sign Changes in Sequence*


---

### Description

Compute the number of sign changes in the sequence  $y$ .

### Usage

```
nr.sign.chg(y)
```

### Arguments

$y$  numeric vector.

### Value

an integer giving the number of sign changes in sequence  $y$ . Note that going from positive to 0 to positive is *not* a sign change.

### Author(s)

Martin Maechler, 17 Feb 1993.

### Examples

```
(y <- c(1:2,1:-1,0:-2))
nr.sign.chg(y)## = 1
```

---

p.arrows

*Prettified Arrows Plots*


---

### Description

Draws arrows, like the [arrows](#) function, but with “nice” *filled* arrow heads.

### Usage

```
p.arrows(x1, y1, x2, y2, size = 1, width, fill = 2, ...)
```

### Arguments

x1, y1	coordinates of points <b>from</b> which to draw.
x2, y2	coordinates of points <b>to</b> which to draw.
size	symbol size as a fraction of a character height; default 1.
width	width of the arrow head; defaults to ....
fill	color for filling the arrow head.
...	further arguments passed to <a href="#">segments()</a> .

### Author(s)

Andreas Ruckstuhl, 19 May 1994; (cosmetic by MM).

### See Also

[arrows](#).

### Examples

```
example(arrows, echo = FALSE) #-> x, y, s
plot(x,y, main="p.arrows(.)")
p.arrows(x[s], y[s], x[s+1], y[s+1], col= 1:3, fill = "dark blue")
```

---

p.datum

*Plot 'Datum' (deutsch!) unten rechts*


---

### Description

Plot the date (and time, if required) in German, at the lower right hand margin of your plot.date

### Usage

```
p.datum(outer = FALSE, cex = 0.75, ...)
```



**Arguments**

outer	logical; passed to <a href="#">mtext</a> .
cex	non-negative; passed to <a href="#">mtext</a> .
...	any arguments to <a href="#">u.Datumvonheute</a> .

**See Also**

[u.date](#), [date](#).

**Examples**

```
plot(1)
p.datum()
```

---

p.dnorm

*Plot Parametric Density Functions*

---

**Description**

These are utilities for pretty plotting of often used parametric densities.

**Usage**

```
p.dnorm (mu = 0, s = 1, h0.col = "light gray",
         ms.lines = TRUE, ms.col = "gray", ...)
p.dchisq(nu, h0.col = "light gray", ...)
p.dgamma(shape, h0.col = "light gray", ...)
```

**Arguments**

mu, s	numbers, the mean and standard deviation of the normal distribution.
nu	positive number, the degrees of freedom df argument for the $\chi^2$ -density function <a href="#">dchisq</a> .
shape	number, the shape parameter for the Gamma distribution.
h0.col	color specification for the line $y = 0$ .
ms.lines	logical, used for the normal only: should lines be drawn at the mean and $\pm 1$ standard deviation.
ms.col	color for the ms lines if ms.lines is TRUE.
...	further parameter passed to <a href="#">curve()</a> , e.g., add = TRUE for adding to current plot.

**Author(s)**

Werner Stahel et al.

**See Also**

the underlying density functions, [dnorm](#), [dchisq](#), [dgamma](#).

**Examples**

```
p.dnorm()
p.dnorm(mu=1.5, add = TRUE, ms.lines = FALSE) # add to the plot above

p.dchisq(2, main= "Chi^2 Densities -- nu = 2,3,4")
p.dchisq(3, add = TRUE, col = "red")
p.dchisq(4, add = TRUE, col = "blue")

op <- par(mfrow = c(2,2), mgp = c(1.6, 0.6,0), mar = c(3,3,1,1))
for(sh in 1:4)
  p.dgamma(sh)
par(op)
```

---

p.hboxp

*Add a Horizontal Boxplot to the Current Plot*

---

**Description**

Add a horizontal boxplot to the current plot. This is mainly an auxiliary function for [histBxp](#), since [boxplot](#)(\* , horizontal = TRUE, add = TRUE) is usually much preferable to this.

**Usage**

```
p.hboxp(x, y.lo, y.hi, boxcol = 3,
        medcol = 2, medlwd = 5, whisklty = 2, staplelty = 1)
```

**Arguments**

x	univariate data set.
y.lo, y.hi	minimal and maximal <i>user</i> coordinates <b>or</b> y.lo = c(ylo,hyi).
boxcol, medcol	color of the box and the median line.
medlwd	line width of median line.
whisklty, staplelty	line types of the whisker and the staple, the latter being used for the outmost non-outliers.

**Details**

....

**Author(s)**

Martin Maechler building on code from Markus and Christian Keller.

**See Also**

`boxplot(**,horizontal = TRUE,add= TRUE)`.

**Examples**

```
## ==> See code in 'histBxp' (.) and example(histBxp) !
##
```

---

p.profileTraces      *Plot a profile.nls Object With Profile Traces*

---

**Description**

Displays a series of plots of the profile t function and the likelihood profile traces for the parameters in a nonlinear regression model that has been fitted with `nls` and profiled with `profile.nls`.

**Usage**

```
p.profileTraces(x, cex = 1,
               subtitle = paste("t-Profiles and traces of ",
                               deparse(attr(x,"summary")$formula)))
```

**Arguments**

`x`                    an object of class "profile.nls", typically resulting from `profile(nls(.))`, see `profile.nls`.

`cex`                    character expansion, see `par(cex =)`.

`subtitle`              a subtitle to set for the plot. The default now includes the `nls()` formula used.

**Note**

the `stats`-internal `stats:::plot.profile.nls` plot method just does "the diagonals".

**Author(s)**

Andreas Ruckstuhl, R port by Isabelle Flückiger and Marcel Wolbers

**See Also**

`profile`, and `nls` (which has unexported `profile` and `stats:::plot.profile.nls` methods).

**Examples**

```

require(stats)
data(Puromycin)
Treat <- Puromycin[Puromycin$state == "treated", ]
fm <- nls(rate ~ T1*conc/(T2+conc), data=Treat,
          start = list(T1=207,T2=0.06))
(pr <- profile(fm)) # quite a few things..
op <- par(mfcol=1:2)
plot(pr) # -> 2 'standard' plots
par(op)
## ours:
p.profileTraces(pr)

```

---

p.res.2fact

*Plot Numeric (e.g. Residuals) vs 2 Factors Using Boxplots*


---

**Description**

Plots a numeric “residual like” variable against two factor covariates, using boxplots.

**Usage**

```

p.res.2fact(x, y, z, restricted, notch = FALSE,
           xlab = NULL, ylab = NULL, main = NULL)

```

**Arguments**

x, y	two factors or numeric vectors giving the levels of factors.
z	numeric vector of same length as x and y, typically residuals.
restricted	positive value which truncates the size. The corresponding symbols are marked by stars.
notch	logical indicating if the boxplots should be notched, see <code>boxplot(*, notch)</code> .
xlab, ylab	axis labels, see <code>plot.default</code> , per default the actual argument expressions.
main	main title passed to plot, defaulting to the deparsed z argument.

**Details**

if values *are* restricted, this make use of the auxiliar function `u.boxplot.x`.

**Author(s)**

Lorenz Gygax <logyg@wild.unizh.ch> and Martin Maechler, Jan.95; starting from `p.res.2x()`.

**See Also**

`p.res.2x`, `boxplot`, `plot.lm`, `TA.plot`.

**Examples**

```

I <- 8; J <- 3; K <- 20
xx <- factor(rep(rep(1:I, rep(K,I)),J))
yy <- factor(rep(1:J, rep(I*K,J)))
zz <- rt(I*J*K, df=5) #-- Student t with 5 d.f.
p.res.2fact(xx,yy,zz, restr= 4, main= "i.i.d. t <- 5 random |.| <= 4")
mtext("p.res.2fact(xx,yy,zz, restr= 4, ..)",
      line=1, adj=1, outer=TRUE, cex=1)

## Real data
data(warpbreaks)
(fm1 <- lm(breaks ~ wool*tension, data = warpbreaks))
## call via formula method of p.res.2x():
p.res.2x(~ ., fm1) # is shorter than, but equivalent to
## p.res.2x(~ wool + tension, fm1) ## or the direct
## with(warpbreaks, p.res.2fact(wool, tension, residuals(fm1)))
##
## whereas this is "transposed":
p.res.2x(~ tension+wool, fm1)

```

p.res.2x

*Stahel's Residual Plot against 2 X's***Description**

Plot Residuals, e.g., of a multiple linear regression, against two (predictor) variables, using positively and negatively oriented line segments for positive and negative residuals.

This is a (S3) *generic* function with a default and a [formula](#) method.

**Usage**

```

p.res.2x(x, ...)

## Default S3 method:
p.res.2x(x, y, z, restricted, size = 1, slwd = 1, scol = 2:3,
        xlab = NULL, ylab = NULL, main = NULL,
        xlim = range(x), ylim = range(y), ...)

## S3 method for class 'formula'
p.res.2x(x = ~., data, main = deparse(substitute(data)),
        xlab = NULL, ylab = NULL, ...)

```

**Arguments**

**x, y** numeric vectors of the same length specifying 2 covariates. For the formula method, x is a [formula](#).

**z** numeric vector of same length as x and y, typically residuals.

restricted	positive value which truncates the size. The corresponding symbols are marked by stars.
size	the symbols are scaled so that size is the size of the largest symbol in cm.
slwd, scol	line width and color(s) for the residual <a href="#">segments</a> . If scol has length 2 as per default, the two colors are used for positive and negative z values, respectively.
xlab, ylab, main	axis labels, and title see <a href="#">title</a> , each with a sensible default. To suppress, use, e.g., main = "".
xlim, ylim	the basic x- and y- axis extents, see <a href="#">plot.default</a> . Note that these will be slightly extended such that segments are not cut off.
...	further arguments passed to plot, or p.res.2x.default(), respectively.
data	(for the <a href="#">formula</a> method:) a data frame or a fitted "lm" object.

### Details

Each residual  $zz[i]$  is visualized as line segment centered at  $(xx_i, yy_i)$ ,  $i = 1, \dots, n$ , where the *lengths* of the segments are proportional to the absolute values  $||zz_i||$ .

Positive residuals' line segments have slope +1, and negative ones slope -1, and scol is used to use different colors for negative and positive segments.

The formula interface calls [p.res.2fact\(\)](#) when *both* x and y are [factors](#).

### Author(s)

Andreas Ruckstuhl in June 1991 and Martin Maechler, in 1992, '94, 2003-4.

### References

Stahel, W.-A. (2008) *Statistische Datenanalyse: Eine Einföhrung fÖr Naturwissenschaftler*, 5. Auflage, Vieweg, Wiesbaden; Paragraph 13.8.r and 13.8.v.

### See Also

[p.res.2fact](#), [plot.lm](#), [TA.plot](#).

### Examples

```
xx <- rep(1:10,7)
yy <- rep(1:7, rep(10,7))
zz <- rnorm(70)
p.res.2x(xx,yy,zz, restricted = 2, main = "i.i.d. N(0,1) random residuals")

example(lm.influence, echo = FALSE)

op <- mult.fig(2, marP=c(-1,-1,-1,0), main="p.res.2x(*,*, residuals(lm.SR))")$old.par
with(LifeCycleSavings,
  { p.res.2x(pop15, ddpi, residuals(lm.SR), scol=c("red", "blue"))
    p.res.2x(pop75, dpi, residuals(lm.SR), scol=2:1)
  })
```

```
## with formula interface:
p.res.2x(~ pop15 + ddpi, lm.SR, scol=c("red", "blue"))
p.res.2x(~ pop75 + dpi, lm.SR, scol=2:1)

par(op) # revert par() settings above
```

---

p.scales

*Conversion between plotting scales: usr, cm, symbol*

---

## Description

Give scale conversion factors of three coordinate systems in use for traditional R graphics: use, cm, symbol.

## Usage

```
p.scales(unit = relsysize * 2.54 * min(pin), relsysize = 0.05)
```

## Arguments

unit	length of unit (or x and y units) of symbol coordinates in cm.
relsysize	same, as a proportion of the plotting area.

## Value

A numeric 2x2 matrix, with rows named x and y, and columns, named "sy2usr" and "usr2cm" which give the scale conversion factors from 'symbol' (as given) to 'usr' coordinates and from these to 'cm', respectively.

## Author(s)

Werner Stahel, 1990; simplification: M.Maechler, 1993, 2004

## See Also

[par\("usr"\)](#), of also ("pin") on which this is based.

## Examples

```
p.scales()
```

---

p.tachoPlot *Draw Symbol on a Plot*

---

### Description

Puts a symbol (pointer) on a plot at each of the specified locations.

### Usage

```
p.tachoPlot(x, y, z, angle=c(pi/4,3*pi/4), size,
            method = c("robust", "sensitive", "rank"),
            legend = TRUE, show.method = legend,
            xlab = deparse(substitute(x)), ylab = deparse(substitute(y)),
            xlim, ylim, ...)
```

### Arguments

x,y,z	coordinates of points. Numeric vectors of the same length. Missing values (NAs) are allowed.
angle	numeric vector whose elements give the angles between the horizontal baseline and the minimum and maximum direction of the pointer measured clockwise in radians.
size	length of the pointers in cm.
method	string specifying the method to calculate the angle of the pointer. One of "sensitive", "robust" or "rank". Only the first two characters are necessary. The minimum and maximum direction of the pointer corresponds to min(z) and max(z) if method is "sensitive" or "rank" and to the upper and lower extreme of z if method is "robust" (see boxplot or rrange for details). The angle is proportional to z or rank(z) in case of method="rank".
legend	logical flag: if TRUE (default), a legend giving the values of the minimum and maximum direction of the pointer is drawn.
show.method	logical flag, defaulting to legend; if true, the method name is printed.
xlab,ylab	labels for x and y axis; defaults to the 'expression' used in the function call.
xlim,ylim	numeric of length 2, the limits for the x and y axis, respectively; see <a href="#">plot.default</a> .
...	further arguments to <a href="#">plot</a> . Graphical parameters (see <a href="#">par</a> ) may also be supplied as arguments to this function.

### Details

A scatter plot of the variables x and y is plotted. The value of the third variable z is given by the direction of a pointer (similar to a tachometer). Observations whose z-coordinate is missing are marked by a dot.

### Side Effects

A plot is created on the current graphics device.



**Author(s)**

Christian Keller, June 1995

**See Also**

[symbols](#)

**Examples**

```
data(state)
data(USArrests)
p.tachoPlot(state.center $x, state.center $y, USArrests[, "UrbanPop"])

data(mtcars)
par(mfrow=c(2,2))
## see the difference between the three methods (not much differ. here!)

p.tachoPlot(mtcars$hp, mtcars$disp, mtcars$mpg, method="sens")
p.tachoPlot(mtcars$hp, mtcars$disp, mtcars$mpg, method="rank")
p.tachoPlot(mtcars$hp, mtcars$disp, mtcars$mpg, method="rob")
```

---

p.ts

*plot.ts with multi-plots and Auto-Title – on 1 page*

---

**Description**

For longer time-series, it is sometimes important to spread the time-series plots over several sub-plots. `p.ts(.)` does this both automatically, and under manual control.

Actually, this is a generalization of [plot.ts](#) (with different defaults).

**Usage**

```
p.ts(x, nrplots = max(1, min(8, n %/% 400)), overlap = nk %/% 16,
     date.x = NULL, do.x.axis = !is.null(date.x), do.x.rug = FALSE,
     ax.format, main.tit = NULL, ylim = NULL, ylab = "", xlab = "Time",
     quiet = FALSE, mgp = c(1.25, .5, 0), ...)
```

**Arguments**

<code>x</code>	timeseries (possibly multivariate) or numeric vector.
<code>nrplots</code>	number of sub-plots. Default: in $\{1..8\}$ , approximately $n/400$ if possible.
<code>overlap</code>	by how much should subsequent plots overlap. Defaults to about 1/16 of sub-length on each side.
<code>date.x</code>	a time “vector” of the same length as <code>x</code> and coercable to class “POSIXct” (see <a href="#">DateTimeClasses</a> ).
<code>do.x.axis</code>	logical specifying if an x axis should be drawn (i.e., tick marks and labels).

do.x.rug	logical specifying if <code>rug</code> of <code>date.x</code> values should drawn along the x axis.
ax.format	when <code>do.x.axis</code> is true, specify the format to be used in the call to <code>axis.POSIXct</code> .
main.tit	<b>Main</b> title (over all plots). Defaults to name of x.
ylim	numeric(2) or NULL; if the former, specifying the y-range for the plots. Defaults to a common pretty range.
ylab, xlab	labels for y- and x-axis respectively, see description in <code>plot.default</code> .
quiet	logical; if TRUE, there's no reporting on each subplot.
mgp	numeric(3) to be passed to <code>mult.fig()</code> , see <code>par(mgp = .)</code> .
...	further graphic parameters for each <code>plot.ts(..)</code> .

### Side Effects

A page of `nrplots` subplots is drawn on the current graphics device.

### Author(s)

Martin Maechler, <maechler@stat.math.ethz.ch>; July 1994 (for S).

### See Also

`p.ts()` calls `mult.fig()` for setup. Further, `plot.ts` and `plot`.

### Examples

```
stopifnot(require(stats))
## stopifnot(require(datasets))

data(sunspots)
p.ts(sunspots, nr=1) # == usual plot.ts(..)
p.ts(sunspots)
p.ts(sunspots, nr=3, col=2)

data(EuStockMarkets)
p.ts(EuStockMarkets[, "SMI"])
## multivariate :
p.ts(log10(EuStockMarkets), col = 2:5)

## with Date - x-axis (dense random dates):
set.seed(12)
x <- as.Date("2000-02-29") + cumsum(1+ rpois(1000, lambda= 2.5))
z <- cumsum(.1 + 2*rt(1000, df=3))
p.ts(z, 4, date.x = x)
p.ts(z, 6, date.x = x, ax.format = "%b %Y", do.x.rug = TRUE)
```

---

paste.vec	<i>Utility for 'Showing' S vectors</i>
-----------	--

---

**Description**

A simple utility for displaying simple S vectors; can be used as debugging utility.

**Usage**

```
paste.vec(name, digits = options()$digits)
```

**Arguments**

name	string with an variable name which must exist in the current environment (R session).
digits	how many decimal digits to be used; passed to <a href="#">format</a> .

**Value**

a string of the form "NAME = x1 x2 ..."

**Author(s)**

Martin Maechler, about 1992.

**Examples**

```
x <- 1:4
paste.vec(x) ##-> "x = 1 2 3 4"
```

---

pkgDesc	<i>Version of packageDescription() as Simple Vector</i>
---------	---

---

**Description**

a simple "version", or wrapper for [packageDescription\(\)](#), returning a named character vector, including "file", and still has a useful [print\(\)](#) method.

**Usage**

```
pkgDesc(pkg, lib.loc = NULL, fields = NULL, ...)
pkgBuilt(pkg, lib.loc = NULL, ...)
```

## Arguments

<code>pkg</code>	a <a href="#">character</a> string, name of an installed R package.
<code>lib.loc</code>	library location to find the package in; the default NULL uses the full <code>.libPaths()</code> .
<code>fields</code>	a character vector (or NULL) specifying fields to be returned.
<code>...</code>	further optional arguments passed to <code>packageDescription()</code> .

## Value

a named [character](#) vector, with `names`, the *fields*, identical to the names of the [list](#) returned by `packageDescription`, plus its "file" attribute. Additionally the resulting vector is of class "Dlist" which activates a useful `print()` method.

## Note

The file is always returned; not the least that the author wants to see it quite often as his `.libPaths()` is non-trivial and typically longer than 4 entries.

## Author(s)

Martin Maechler, Jan. 2021

## See Also

[packageDescription](#), [.libPaths](#).

## Examples

```
str(pd <- pkgDesc("sfsmisc"))
pd[c("Date", "Packaged", "Built", "file")]

pkgBuilt("sfsmisc")

## Show "Built" (and "file") for all packages whose namespaces are loaded:
lNs <- loadedNamespaces()
mNs <- sapply(lNs, pkgBuilt)
t(mNs) # typically prints nicely

pkgs <- c("grid", "lattice", "MASS", "Matrix", "nlme", "lme4", "sfsmisc")
pkgs <- c("foobar", "barbar", pkgs, "kitty") # + names that typically don't exist
pkgsOk <- basename(find.package(pkgs, quiet=TRUE))
mpkg <- sapply(pkgsOk, pkgBuilt)
stopifnot(is.matrix(mpkg), nrow(mpkg) == 2)
mpkg["Built",]
```

---

pkgLibs

*R Package Compiled Code Library Dependencies (on Unix-alikes)*

---

## Description

List some system level information about the compiled code library, typically its dependencies, for R packages with compiled code; for Unix-alikes or more generally when `cmd` is installed locally.

## Usage

```
pkgLibs(pkg,  
        cmd = if(Sys.info()[["sysname"]] == "Darwin") "otool -L" else "ldd")
```

## Arguments

`pkg` **character** vector of package names of *installed* R packages.

`cmd` a character string with the name of an OS / system level program (to be called via `system(cmd, . . .)`) which gives information about the shared library (of compiled code), also known as “DLL” (dynamically loadable library) or “so” ((dynamic) shared object) library. The default, “ldd” is a standard binary utility on Unix-alike platforms such as Linux. On macOS, “oTool -L” is used by default.

## Details

Note that there seems some language confusion as “DLL” on Windows is *also* used for “Dynamic-link Library” and Wikipedia warns about confusing the two concepts (“dynamically loaded ..” vs “dynamic-link ..”).

## Value

a named **list** with one entry per package in `pkg`, the **names** being the directory / folder names of the corresponding pkgs from `pkg`.

The exact structure of such entries is currently subject to change and you should not rely on its exact format for now.

## Author(s)

Martin Maechler

## References

‘Dynamic Loading’ on Wikipedia, [https://en.wikipedia.org/wiki/Dynamic\\_loading](https://en.wikipedia.org/wiki/Dynamic_loading)

On Windows, “DLL” is also used for Dynamic-link library, [https://en.wikipedia.org/wiki/Dynamic-link\\_library](https://en.wikipedia.org/wiki/Dynamic-link_library).

man ldd from a terminal on a valid OS.

**See Also**

`dyn.load()`, `library.dynam()`, and `getLoadedDLLs()`.

Also, `.C`, `.Call` which use such DLLs.

**Examples**

```
# for the example only using standard R packages :
myPkgs <- c("stats", "MASS", "rpart", "Matrix")
pl <- pkgLibs(myPkgs)
pl
stopifnot(exprs = {
  is.list(pl)
  length(pl) == length(myPkgs)
  is.character(pkgD <- names(pl))
})
## Have seen this failing when a strange development version of "Matrix" was picked up:
try( stopifnot( dir.exists(pkgD) ) )
```

---

plotDS

*Plot Data and Smoother / Fitted Values*


---

**Description**

For one-dimensional nonparametric regression, plot the data and fitted values, typically a smooth function, and optionally use segments to visualize the residuals.

**Usage**

```
plotDS(x, yd, ys, xlab = "", ylab = "", ylim = rrange(c(yd, ys)),
       xpd = TRUE, do.seg = TRUE, seg.p = 0.95,
       segP = list(lty = 2, lwd = 1, col = 2),
       linP = list(lty = 1, lwd = 2.5, col = 3),
       ...)
```

**Arguments**

<code>x</code> , <code>yd</code> , <code>ys</code>	numeric vectors all of the same length, representing $(x_i, y_i)$ and fitted (smooth) values $\hat{y}_i$ . <code>x</code> will be sorted increasingly if necessary, and <code>yd</code> and <code>ys</code> accordingly. Alternatively, <code>ys</code> can be an x-y list (as resulting from <code>xy.coords</code> ) containing fitted values on a finer grid than the observations <code>x</code> . In that case, the observational values <code>x[]</code> <b>must</b> be part of the larger set; <code>seqXtend()</code> may be applied to construct such a set of abscissa values.
<code>xlab</code> , <code>ylab</code>	x- and y- axis labels, as in <code>plot.default</code> .
<code>ylim</code>	limits of y-axis to be used; defaults to a <i>robust</i> range of the values.
<code>xpd</code>	see <code>par(xpd=.)</code> ; by default do allow to draw outside the plot region.

<code>do.seg</code>	logical indicating if residual segments should be drawn, at <code>x[i]</code> , from <code>yd[i]</code> to <code>ys[i]</code> (approximately, see <code>seg.p</code> ).
<code>seg.p</code>	segment percentage of segments to be drawn, from <code>yd</code> to <code>seg.p*ys + (1-seg.p)*yd</code> .
<code>segP</code>	list with named components <code>lty</code> , <code>lwd</code> , <code>col</code> specifying line type, width and color for the residual segments, used only when <code>do.seg</code> is true.
<code>linP</code>	list with named components <code>lty</code> , <code>lwd</code> , <code>col</code> specifying line type, width and color for “smooth curve lines”.
<code>...</code>	further arguments passed to <a href="#">plot</a> .

**Note**

Non-existing components in the lists `segP` or `linP` will result in the [par](#) defaults to be used.  
`plotDS()` used to be called `pl.ds` up to November 2007.

**Author(s)**

Martin Maechler, since 1990

**See Also**

[seqXtend\(\)](#) to construct more smooth `ys` “objects”.

**Examples**

```
data(cars)
x <- cars$speed
yd <- cars$dist
ys <- lowess(x, yd, f = .3)$y
plotDS(x, yd, ys)

## More interesting : Version of example(Theoph)
data(Theoph)
Th4 <- subset(Theoph, Subject == 4)
## just for "checking" purposes -- permute the observations:
Th4 <- Th4[sample(nrow(Th4)), ]
fm1 <- nls(conc ~ SSfol(Dose, Time, lKe, lKa, lCl), data = Th4)

## Simple
plotDS(Th4$Time, Th4$conc, fitted(fm1),
       sub = "Theophylline data - Subject 4 only",
       segP = list(lty=1,col=2), las = 1)

## Nicer: Draw the smoother not only at x = x[i] (observations):
xsm <- unique(sort(c(Th4$Time, seq(0, 25, length = 201))))
ysm <- c(predict(fm1, newdata = list(Time = xsm)))
plotDS(Th4$Time, Th4$conc, ys = list(x=xsm, y=ysm),
       sub = "Theophylline data - Subject 4 only",
       segP = list(lwd=2), las = 1)
```

plotStep

*Plot a Step Function***Description**

Plots a step function  $f(x) = \sum_i y_i 1_{[t_{i-1}, t_i]}(x)$ , i.e., a piecewise constant function of one variable. With one argument, plots **the** empirical cumulative distribution function.

**Usage**

```
plotStep(ti, y,
         cad.lag = TRUE,
         verticals = !cad.lag,
         left.points= cad.lag, right.points= FALSE, end.points= FALSE,
         add = FALSE,
         pch = par('pch'),
         xlab=deparse(substitute(ti)), ylab=deparse(substitute(y)),
         main=NULL, ...)
```

**Arguments**

ti	numeric vector = X[1:N] or t[0:n].
y	numeric vector y[1:n]; if omitted take y = k/N for empirical CDF.
cad.lag	logical: Draw 'cad.lag', i.e., " <i>continue à droite, limite à gauche</i> ". Default = TRUE.
verticals	logical: Draw vertical lines? Default= ! cad.lag
left.points	logical: Draw left points? Default= cad.lag
right.points	logical: Draw right points? Default= FALSE
end.points	logical: Draw 2 end points? Default= FALSE
add	logical: Add to existing plot? Default= FALSE
pch	plotting character for points, see <a href="#">par()</a> .
xlab,ylab	labels of x- and y-axis
main	main title; defaults to the call' if you do not want a title, use main = "".
...	Any valid argument to <a href="#">plot()</a> .

**Value**

**invisibly:** List with components t and y.

**Side Effects**

Calls [plot\(\)](#), [points\(\)](#), [segments\(\)](#) appropriately and plots on current graphics device.



**Author(s)**

Martin Maechler, Seminar for Statistics, ETH Zurich, <maechler@stat.math.ethz.ch>, 1991 ff.

**See Also**

The `plot` methods `plot.ecdf` and `plot.stepfun` in R which are conceptually nicer.  
`segments(...,method = "constant")`.

**Examples**

```
##-- Draw an Empirical CDF (and see the default title ..)
plotStep(rnorm(15))

plotStep(runif(25), cad.lag=FALSE)
plotStep(runif(25), cad.lag=FALSE, add=TRUE, lty = 2)

ui <- sort(runif(20))
plotStep(ui, ni <- cumsum(rpois(19, lambda=1.5) - 1.5), cad.lag = FALSE)
plotStep(ui, ni, verticals = TRUE, right.points = TRUE)

plotStep(rnorm(201), pch = '.') #- smaller points
```

---

 polyn.eval

*Evaluate Polynomials*


---

**Description**

Evaluate one or several univariate polynomials at several locations, i.e. compute  $\text{coef}[1] + \text{coef}[2]*x + \dots + \text{coef}[p+1]*x^p$  (in the simplest case where  $x$  is scalar and  $\text{coef}$  a vector).

**Usage**

```
polyn.eval(coef, x)
```

**Arguments**

<code>coef</code>	numeric vector or matrix. If a vector, $x$ can be an array and the result matches $x$ . If <code>coef</code> is a matrix it specifies several polynomials of the same degree as rows, $x$ must be a vector, <code>coef[,k]</code> is for $x^{k-1}$ and the result is a matrix of dimension $\text{length}(x) * \text{nrow}(\text{coef})$ .
<code>x</code>	numeric vector or array. Either $x$ or <code>coef</code> must be a vector.

**Details**

The stable ‘‘Horner rule’’ is used for evaluation in any case.

**Value**

numeric vector or array, depending on input dimensionalities, see above.

**Author(s)**

Martin Maechler, ages ago.

**See Also**

For much more sophisticated handling of polynomials, use the **polynom** package, see, e.g., [predict.polynomial](#). For multivariate polynomials (and also for nice interface to the **orthopolynom** package), consider the **mpoly** package.

**Examples**

```
polyn.eval(c(1,-2,1), x = 0:3)# (x - 1)^2
polyn.eval(c(0, 24, -50, 35, -10, 1), x = matrix(0:5, 2,3))# 5 zeros!
(cf <- rbind(diag(3), c(1,-2,1)))
polyn.eval(cf, 0:5)
```

---

 posdefify

*Find a Close Positive Definite Matrix*


---

**Description**

From a matrix *m*, construct a "close" positive definite one.

**Usage**

```
posdefify(m, method = c("someEVadd", "allEVadd"),
          symmetric = TRUE, eigen.m = eigen(m, symmetric= symmetric),
          eps.ev = 1e-07)
```

**Arguments**

<i>m</i>	a numeric (square) matrix.
<i>method</i>	a string specifying the method to apply; can be abbreviated.
<i>symmetric</i>	logical, simply passed to <a href="#">eigen</a> (unless <i>eigen.m</i> is specified); currently, we do not see any reason for <i>not</i> using TRUE.
<i>eigen.m</i>	the <a href="#">eigen</a> value decomposition of <i>m</i> , can be specified in case it is already available.
<i>eps.ev</i>	number specifying the tolerance to use, see Details below.

**Details**

We form the eigen decomposition

$$m = V\Lambda V'$$

where  $\Lambda$  is the diagonal matrix of eigenvalues,  $\Lambda_{j,j} = \lambda_j$ , with *decreasing* eigenvalues  $\lambda_1 \geq \lambda_2 \geq \dots \geq \lambda_n$ .

When the smallest eigenvalue  $\lambda_n$  are less than  $\text{Eps} < -\text{eps} \cdot \text{ev} * \text{abs}(\text{lambda}[1])$ , i.e., negative or “almost zero”, some or all eigenvalues are replaced by *positive* ( $\geq \text{Eps}$ ) values,  $\tilde{\Lambda}_{j,j} = \tilde{\lambda}_j$ . Then,  $\tilde{m} = V\tilde{\Lambda}V'$  is computed and rescaled in order to keep the original diagonal (where that is  $\geq \text{Eps}$ ).

**Value**

a matrix of the same dimensions and the “same” diagonal (i.e. [diag](#)) as `m` but with the property to be positive definite.

**Note**

As we found out, there are more sophisticated algorithms to solve this and related problems. See the references and the [nearPD\(\)](#) function in the **Matrix** package. We consider [nearPD\(\)](#) to also be the successor of this package’s [nearcor\(\)](#).

**Author(s)**

Martin Maechler, July 2004

**References**

Section 4.4.2 of Gill, P.-E., Murray, W. and Wright, M.-H. (1981) *Practical Optimization*, Academic Press.

Cheng, Sheung Hun and Higham, Nick (1998) A Modified Cholesky Algorithm Based on a Symmetric Indefinite Factorization; *SIAM J. Matrix Anal. Appl.*, **19**, 1097–1110.

Knol DL, ten Berge JMF (1989) Least-squares approximation of an improper correlation matrix by a proper one. *Psychometrika* **54**, 53–61.

Higham (2002) Computing the nearest correlation matrix - a problem from finance; *IMA Journal of Numerical Analysis* **22**, 329–343.

Lucas (2001) Computing nearest covariance and correlation matrices. A thesis submitted to the University of Manchester for the degree of Master of Science in the Faculty of Science and Engineering.

**See Also**

[eigen](#) on which the current methods rely. [nearPD\(\)](#) in the **Matrix** package. (Further, the deprecated [nearcor\(\)](#) from this package.)

**Examples**

```

set.seed(12)
m <- matrix(round(rnorm(25),2), 5, 5); m <- 1+ m + t(m); diag(m) <- diag(m) + 4
m
posdefify(m)
1000 * zapsmall(m - posdefify(m))

```

---

potatoes

*Fisher's Potato Crop Data*


---

**Description**

Fisher's potato crop data set is of historical interest as an early example of a multi-factor block design.

**Usage**

```
data(potatoes)
```

**Format**

A data frame with 64 observations on the following 5 variables.

**pos** a factor with levels 1:4.

**treat** a factor with 16 levels A to H and J to Q, i.e., LETTERS[1:17][-9].

**nitrogen** a factor specifying the amount of nitrogen sulfate ( $NH_4$ ), with the four levels 0, 1, 2, 4.

**potash** a factor specifying the amount of potassium (K, 'kalium') sulfate, with the four levels 0, 1, 2, 4.

**yield** a numeric vector giving the yield of potatoes in ...

**Source**

Bennett, J. H. (1972) *Collected Papers of R. A. Fisher* vol.~II, 1925-31; The University of Adelaide.

**References**

T.Eden and R. A. Fisher (1929) Studies in Crop Variation. VI. Experiments on the Response of the Potato to Potash and Nitrogen. *J. Agricultural Science* **19**, 201–213. Accessible from Bennett (1972), see above.

## Examples

```

data(potatoes)
## See the experimental design:
with(potatoes, {
  cat("4 blocks of experiments;",
      "each does every (nitrogen,potash) combination (aka 'treat'ment) once.",
      '\n', sep="\n")
  print(ftable(table(nitrogen, potash, treat)))
  print(ftable(tt <- table(pos,potash,nitrogen)))
  tt[cbind(pos,potash,nitrogen)] <- as.character(treat)
  cat("The 4 blocks pos = 1, 2, 3, 4:\n")
  ftable(tt)
})
## First plot:
with(potatoes, interaction.plot(potash,nitrogen, response=yield))

## ANOVAs:
summary(aov(yield ~ nitrogen * potash + Error(pos), data = potatoes))
# "==" can use simply
summary(aov(yield ~ nitrogen + potash + pos, data = potatoes))
# and
summary(aov(yield ~ nitrogen + potash, data = potatoes))

```

---

```
pretty10exp
```

```
Nice 10 ** k Label Expressions
```

---

## Description

Produce nice  $a \times 10^k$  expressions to be used instead of the scientific notation "a E<k>".

## Usage

```

pretty10exp(x, drop.1 = FALSE, sub10 = FALSE, digits = 7, digits.fuzz,
            lab.type = c("plotmath", "latex"),
            lab.sep = c("cdot", "times"))

```

## Arguments

x	numeric vector (e.g. axis tick locations)
drop.1	logical indicating if 1× should be dropped from the resulting expressions.
sub10	logical, "10", a non-negative integer number or an integer vector of length two, say $(k_1, k_2)$ , indicating if some $10^j$ expressions for $j \in J$ should be formatted traditionally, notably e.g., $10^0 \equiv 1$ . When a (non-negative) number, say $k$ , $J = \{j; j \leq k\}$ are all simplified, when a length-2 vector, $J = \{j; k_1 \leq j \leq k_2\}$ are. Special cases: sub10 = TRUE means to use 1 instead of $10^0$ and sub10 = "10" uses both 1 for $10^0$ and 10 for $10^1$ ; these are short forms of sub10 = c(0, 0) and sub10 = c(0, 1) respectively.

<code>digits</code>	number of digits for mantissa ( <i>a</i> ) construction; the number of <i>significant</i> digits, see <a href="#">signif</a> .
<code>digits.fuzz</code>	the old deprecated name for <code>digits</code> .
<code>lab.type</code>	a string indicating how the result should look like. By default, ( <a href="#">plotmath</a> -compatible) <a href="#">expressions</a> are returned. Alternatively, <code>lab.type = "plotmath"</code> returns LaTeX formatted strings for labels. (The latter is useful, e.g., when using the <a href="#">tikzDevice</a> package to generate LaTeX-processed figures.)
<code>lab.sep</code>	character separator between mantissa and exponent for LaTeX labels; it will be prepended with a backslash, i.e., " <code>\cdot</code> " will use " <code>\cdot</code> "

### Value

For the default `lab.type = "plotmath"`, an expression of the same length as `x`, typically with elements of the form `a%%10 ^ k`. Exceptions are `0` which is kept simple, if `drop.1` is true and `a = 1`, `10 ^ k` is used, and if `sub10` is not false, `a%%10 ^ 0` as `a`, and `a%%10 ^ k` as the corresponding formatted number `a * 10^k` independently of `drop.1`.

Otherwise, a [character](#) vector of the same length as `x`. For `lab.type = "latex"`, currently the only alternative to the default, these strings are LaTeX (math mode) compatible strings.

### Note

If `sub10` is set, it will typically be a small number such as 0, 1, or 2. Setting `sub10 = TRUE` will be interpreted as `sub10 = 1` where resulting exponents *k* will either be negative or  $k \geq 2$ .

### Author(s)

Martin Maechler; Ben Bolker contributed `lab.type = "latex"` and `lab.sep`.

### See Also

[axTexpr](#) and [eaxis\(\)](#) which build on `pretty10exp()`, notably the `eaxis()` example plots.

The new [toLatex.numeric](#) method which gives very similar results with option `scientific = TRUE`.

Further, [axis](#), [axTicks](#).

### Examples

```
pretty10exp(-1:3 * 1000)
pretty10exp(-1:3 * 1000, drop.1 = TRUE)
pretty10exp(c(1,2,5,10,20,50,100,200) * 1e3)
pretty10exp(c(1,2,5,10,20,50,100,200) * 1e3, drop.1 = TRUE)

set.seed(17); lx <- rlnorm(10, m=8, s=6)
pretty10exp(lx, digits = 3)
pretty10exp(lx, digits = 3, sub10 = 2)

pretty10exp(lx, digits = 3, lab.type="latex")
pretty10exp(lx, digits = 3, lab.type="latex", lab.sep="times", sub10=2)
```

```
## use regular formatted numbers from 0.03 to 300 :
pretty10exp(3*10^(-3:4), sub10 = c(-2,2))
pretty10exp(3*10^(-3:4), sub10 = c(-2,2), lab.type = "1")

ax <- 10^(-6:0) - 2e-16
pretty10exp(ax, drop.1=TRUE) # nice for plotting
pretty10exp(ax, drop.1=TRUE, sub10=TRUE)
pretty10exp(ax, drop.1=TRUE, sub10=c(-2,2))

## in sfsmisc version <= 1.0-16, no 'digits',
## i.e., implicitly had digits := #{double precision digits} ==
(dig. <- .Machine$double.digits * log10(2)) # 15.95
pretty10exp(ax, drop.1=TRUE, digits= dig.) # ''ugly''
```

primes

*Find all Primes Less Than n***Description**

Find all prime numbers aka ‘primes’ less than  $n$ .

Uses an obvious sieve method (and some care), working with [logical](#) and [integers](#) to be quite fast.

**Usage**

```
primes(n, pSeq = NULL)
```

**Arguments**

$n$	a (typically positive integer) number.
$pSeq$	optionally a vector of primes (2,3,5,...) as if from a <code>primes()</code> call; <b>must</b> be correct. The goal is a speedup, but currently we have not found one single case, where using a non-NULL $pSeq$ is faster.

**Details**

As the function only uses `max(n)`,  $n$  can also be a *vector* of numbers.

The famous prime number theorem states that  $\pi(n)$ , the *number* of primes below  $n$  is asymptotically  $n / \log(n)$  in the sense that  $\lim_{n \rightarrow \infty} \pi(n) \cdot \log(n) / n \sim 1$ .

Equivalently, the inverse of  $pi()$ , the  $n$ -th prime number  $p_n$  is around  $n \log n$ ; recent results (Pierre Dusart, 1999), prove that

$$\log n + \log \log n - 1 < \frac{p_n}{n} < \log n + \log \log n \quad \text{for } n \geq 6.$$

**Value**

numeric vector of all prime numbers  $\leq n$ .

**Author(s)**

Bill Venables (<= 2001); Martin Maechler gained another 40% speed, carefully working with logicals and integers.

**See Also**

`factorize`. For large  $n$ , use the `gmp` package and its `isprime` and `nextprime` functions.

**Examples**

```
(p1 <- primes(100))
system.time(p1k <- primes(1000)) # still lightning fast
stopifnot(length(p1k) == 168)

system.time(p.e7 <- primes(1e7)) # still only 0.3 sec (2015 (i7))
stopifnot(length(p.e7) == 664579)
## The famous pi(n) := number of primes <= n:
pi.n <- approxfun(p.e7, seq_along(p.e7), method = "constant")
pi.n(c(10, 100, 1000)) # 4 25 168
plot(pi.n, 2, 1e7, n = 1024, log="xy", axes = FALSE,
      xlab = "n", ylab = quote(pi(n)),
      main = quote("The prime number function " ~ pi(n)))
eaxis(1); eaxis(2)

## Exploring p(n) := the n-th prime number ~ n * pnn(n), where
## pnn(n) := log n + log log n
pnn <- function(n) { L <- log(n); L + log(L) }
n <- 6:(N <- length(PR <- primes(1e5)))
m.pn <- cbind(l.pn = ceiling(n*(pnn(n)-1)), pn = PR[n], u.pn = floor(n*pnn(n)))
matplot(n, m.pn, type="l", ylab = quote(p[n]), main = quote(p[n] ~
  "with lower/upper bounds" ~ n*(log(n) + log(log(n)) - (1~"or"~0))))
## (difference to the lower approximation) / n --> ~ 0.0426 (?) :
plot(n, PR[n]/n - (pnn(n)-1), type = 'l', cex = 1/8, log="x", xaxt="n")
eaxis(1); abline(h=0, col=adjustcolor(1, 0.5))
```

---

printTable2

---

*Add and Print Marginals for 2-way Contingency Tables*


---

**Description**

`printTable2()` prints a 2-way contingency table “with all bells and whistles” (currently using German labeling).

`margin2table()` computes marginals, adds them to the table and returns a `margin2table` object the print method for which adds text decorations (using “-” and “|”).



**Usage**

```
printTable2(table2, digits = 3)
margin2table(x, totName = "sum", name.if.empty=FALSE)
## S3 method for class 'margin2table'
print(x, digits = 3, quote = FALSE, right = TRUE, ...)
```

**Arguments**

table2	a matrix with non-negative integer entries, i.e. the contingency table.
x	a matrix; for print(), the result of margin2table.
digits	Anzahl Dezimalstellen, auf die die Häufigkeiten gerundet werden sollen.
quote, right	logicals passed to <code>print.default()</code> , but with different default values.
totName	string to use as row- and column- name if x has corresponding <code>dimnames</code> .
name.if.empty	logical indicating if the margin “totals” should be named in any case.
...	further potential arguments, unused currently.

**Value**

margin2table returns a matrix with *added marginals*, i.e., an extra row and column, and is of class "margin2table" (and "table" still) which has a nice print method.

printTable2 is just producing output.

**Author(s)**

Martin Maechler, Feb.1993; then Dec 2003

**See Also**

[table](#), [ftable](#).

**Examples**

```
margin2table(diag(4),,TRUE)
m <- diag(3); colnames(m) <- letters[1:3]
margin2table(m)
margin2table(m / sum(m))

data(HairEyeColor)
margin2table(HairEyeColor[, , "Male"])
printTable2(HairEyeColor[, , "Male"])
printTable2(HairEyeColor[, , "Female"])
```

---

```
prt.DEBUG
```

*Utility Printing in DEBUG mode*

---

### Description

This is **defunct** now: The global DEBUG has been a cheap precursor to R's `options(verbose=.)` (or a verbose function argument).

This function prints out its arguments as `cat()` does, additionally printing the name of function in which it's been called — only when a global variable DEBUG exists and is **TRUE**.

### Usage

```
prt.DEBUG(..., LEVEL = 1)
```

### Arguments

... arguments to be passed to `cat(...)` for printing.  
 LEVEL integer (or logical) indicating a debugging level for printing.

### Author(s)

Martin Maechler, originally for S-PLUS.

---

```
ps.end
```

*Close PostScript or Acrobat Graphics Device opened by 'ps.do' / 'pdf.do'*

---

### Description

Closes the PostScript or PDF file (`postscript, pdf`), opened by a previous `ps.do` (or `pdf.latex`, or ...) call, using `dev.off`, and additionally opens a previewer for that file, *unless* the previewer is already up. This almost provides an 'interactive' device (like `x11`) for `postscript` or `pdf`.

### Usage

```
ps.end(call.gv= NULL, command = getOption("eps_view"),
       debug = getOption("verbose"))
pdf.end(call.viewer= NULL, command = getOption("pdfviewer"),
       debug = getOption("verbose"))
```

**Arguments**

call.gv, call.viewer	logical, indicating if the postscript or acrobat reader (e.g., ghostview or acroread or the command given by command) should be called. By default, find out if the viewer is already running on this file and only call it if needed.
command	character, giving a system command for PostScript previewing. By default, getOption("eps_view") is set to gv -watch -geometry -0+0 -magstep -2 -media BBox -noantialias which assumes gv (aka <i>ghostview</i> ) to be in your OS path.
debug	logical; if TRUE print information during execution.

**Details**

Depends on Unix tools, such as ps.

**Author(s)**

Martin Maechler

**See Also**

[postscript](#), [postscript pdf.do](#), [ps.do](#), ...

**Examples**

```
if(interactive()
) {
  myPS <- tempfile("ex", fileext = ".ps")
  ps.do(myPS)
  data(sunspots)
  plot(sunspots)
  ps.end()

  tempfile("ex-sun", fileext = ".pdf") -> myPDF
  pdf.latex(myPDF)
  plot(sunspots)
  pdf.end(call. = FALSE) # basically the same as dev.off()
}
ps.latex(tempfile("ex2", fileext = ".eps"))
plot(sunspots)
ps.end(call.gv = FALSE) # basically the same as dev.off()
```

## Description

All functions start a pseudo PostScript or Acrobat preview device, using `postscript` or `pdf`, and further registering the file name for subsequent calls to `pdf.end()` or `ps.end()`.

## Usage

```
pdf.do(file, paper = "default", width = -1, height = -1, onefile = FALSE,
       title = NULL, version = "1.4", quiet = FALSE, ...)
```

```
pdf.latex(file, height = 5 + main.space * 1.25, width = 9.5,
          main.space=FALSE, lab.space = main.space,
          paper = "special", title = NULL,
          lab=c(10, 10, 7), mgp.lab=c(1.6, 0.7, 0), mar=c(4, 4, 0.9, 1.1), ...)
```

```
ps.do(file, width=-1, height=-1, onefile=FALSE, horizontal=FALSE,
      title = NULL, ...)
```

```
ps.latex(file, height = 5 + main.space * 1.25, width = 9.5,
         main.space=FALSE, lab.space = main.space,
         paper = "special", title = NULL,
         lab=c(10, 10, 7), mgp.lab=c(1.6, 0.7, 0), mar=c(4, 4, 0.9, 1.1), ...)
```

## Arguments

<code>file</code>	character giving the PostScript/PDF file name to be written.
<code>height</code>	device height in <i>inches</i> , <code>height * 2.54</code> are <i>cm</i> . The default is 5 plus 1.25 iff <code>main.space</code> .
<code>width</code>	device width in <i>inches</i> ; for this and <code>height</code> , see <code>postscript</code> .
<code>onefile</code> , <code>horizontal</code>	logicals passed to <code>postscript(..)</code> or <code>pdf(..)</code> , most probably to be left alone.
<code>title</code>	PostScript/PDF (not plot!) title passed to <code>postscript()</code> or <code>pdf()</code> ; by default use a title with <code>R</code> version and file in it.
<code>version</code>	a string describing the PDF version that will be required to view the output, see <code>pdf</code> ; our (high) default ensures alpha-transparency.
<code>quiet</code>	logical specifying that some (informative/warning) messages should not be issued.
<code>main.space</code>	logical; if true, leave space for a main title (unusual for LaTeX figures!).
<code>lab.space</code>	logical; if true, leave space for x- and y- labels (by <i>not</i> subtracting from <code>mar</code> ).

paper	character (or missing), typically "a4" or "a4r" in non-America, see <a href="#">postscript</a> . Only if this is "special" (or missing) are your choices of width and height completely honored (and this may lead to files that cannot print on A4) with resizing.
lab	integer of length 3, lab[1:2] are desired number of tick marks on x- and y-axis, see <a href="#">par</a> (lab=).
mgp.lab	three decreasing numbers determining space for axis labeling, see <a href="#">par</a> (mgp=), the default is here smaller than usual.
mar	four numbers, indicating marginal space, see <a href="#">par</a> (mar=), the default is here smaller than usual.
...	arguments passed to <a href="#">ps.do()</a> or <a href="#">pdf.do()</a> from ps.latex / pdf.latex and to <a href="#">ps.options</a> from ps.do/pdf.do.

### Details

ps.latex and pdf.latex have an additional LaTeX flavor, and just differ by some extra [par](#) settings from the \*.do siblings: E.g., after [ps.do\(\)](#) is called, the graphical parameters c("mar", "mgp", "lab") are reset (to values that typically are better than the defaults for LaTeX figures).

Whereas the defaults for paper, width, and height *differ* between [pdf](#) and [postscript](#), they are set such as to provide very similar functionality, for the functions [ps.do\(\)](#) and [pdf.do\(\)](#); e.g., by default, both use a full plot on portrait-oriented page of the default paper, as per [getOption\("papersize"\)](#). [pdf.do\(\)](#) sets the default paper to "special" when both width and height are specified.

### Value

A list with components

old.par	containing the old par values
new.par	containing the newly set par values

### Author(s)

Martin Maechler

### See Also

[ps.end](#), [pdf](#), [postscript](#), [dev.print](#).

### Examples

```
if(interactive()) {

  ps.latex("ps.latex-ex.ps", main= TRUE)
  data(sunspots)
  plot(sunspots, main=paste("Sunspots Data, n=", length(sunspots)), col="red")
  ps.end()

  pdf.latex("pdf.latex-ex.pdf", main= TRUE)
  data(sunspots)
```

```

plot(sunspots,main=paste("Sunspots Data, n=",length(sunspots)),col="red")
pdf.end()

ps.do("ps_do_ex.ps")
  example(plot.function)
ps.end()

pdf.do("pdf_do_ex.pdf", width=12, height=5)
  plot(sunspots, main="Monthly Sunspot numbers (in Zurich, then Tokyo)")
pdf.end()
}

```

---

quadrant

*Give the Quadrant Number of Planar Points*


---

### Description

Determine the quadrant of planar points, i.e. in which of the four parts cut by the  $x$ - and  $y$ - axis the points lie. Zero values (i.e. points on the axes) are treated as if *positive*.

### Usage

```
quadrant(x, y=NULL)
```

### Arguments

$x, y$  numeric vectors of the same length, or  $x$  is an  $x - y$  structure and  $y=NULL$ , see [xy.coords](#).

### Value

numeric vector of same length as  $x$  (if that's a vector) with values in 1:4 indicating the quadrant number of the corresponding point.

### Examples

```

xy <- as.matrix(expand.grid(x= -7:7, y= -7:7)); rownames(xy) <- NULL
(qu <- quadrant(xy))
plot(xy, col = qu+1, main = "quadrant() number", axes = FALSE)
abline(h=0, v=0, col="gray") # the x- and y- axis
text(xy, lab = qu, col = qu+1, adj = c(1.4,0))

```

**Description**

These functions provide quasi random numbers or *space filling* or *low discrepancy* sequences in the  $p$ -dimensional unit cube.

**Usage**

```
sHalton(n.max, n.min = 1, base = 2, leap = 1)
QUnif (n, min = 0, max = 1, n.min = 1, p, leap = 1, silent = FALSE)
```

**Arguments**

n.max	maximal (sequence) number.
n.min	minimal sequence number.
n	number of $p$ -dimensional points generated in QUnif. By default, n.min = 1, leap = 1 and the maximal sequence number is n.max = n.min + (n-1)*leap.
base	integer $\geq 2$ : The base with respect to which the Halton sequence is built.
min, max	lower and upper limits of the univariate intervals. Must be of length 1 or p.
p	dimensionality of space (the unit cube) in which points are generated.
leap	integer indicating (if $> 1$ ) if the series should be leaped, i.e., only every leapth entry should be taken.
silent	logical asking to suppress the message about enlarging the prime table for large p.

**Value**

sHalton(n,m) returns a numeric vector of length n-m+1 of values in  $[0, 1]$ .

QUnif(n,min,max,n.min,p=p) generates n-n.min+1  $p$ -dimensional points in  $[min, max]^p$  returning a numeric matrix with p columns.

**Note**

For leap Kocis and Whiten recommend values of  $L = 31, 61, 149, 409$ , and particularly the  $L = 409$  for dimensions up to 400.

**Author(s)**

Martin Maechler

## References

- James Gentle (1998) *Random Number Generation and Monte Carlo Simulation*; sec.\ 6.3. Springer.
- Kocis, L. and Whiten, W.J. (1997) Computational Investigations of Low-Discrepancy Sequences. *ACM Transactions of Mathematical Software* **23**, 2, 266–294.

## Examples

```

32*sHalton(20, base=2)

stopifnot(sHalton(20, base=3, leap=2) ==
          sHalton(20, base=3)[1+2*(0:9)])
## ----- a 2D Visualization -----

Uplot <- function(xy, axes=FALSE, xlab="", ylab="", ...) {
  plot(xy, xaxs="i", yaxs="i", xlim=0:1, ylim=0:1, xpd = FALSE,
       axes=axes, xlab=xlab, ylab=ylab, ...)
  box(lty=2, col="gray40")
}

do4 <- function(n, ...) {
  op <- mult.fig(4, main=paste("n =", n,": Quasi vs. (Pseudo) Random"),
               marP=c(-2,-2,-1,0))$old.par
  on.exit(par(op))
  for(i in 1:2) {
    Uplot(QUnif(n, p=2), main="QUnif", ...)
    Uplot(cbind(runif(n), runif(n)), main="runif", ...)
  }
}

do4(100)
do4(500)
do4(1000, cex = 0.8, col="slateblue")
do4(10000, pch= ".", col="slateblue")
do4(40000, pch= ".", col="slateblue")

```

---

read.org.table

*Read.table for an Emacs Org Table*

---

## Description

Read an emacs “Org” table (in file or text) by `read.table()`.

## Usage

```

read.org.table(file, header = TRUE, skip = 0,
              encoding = "native", fileEncoding = "", text, ...)

```



**Arguments**

file	a file name, a <a href="#">file</a> or other connection.
header	logical indicating if the org table has header line (in the usual " " -separated org table format).
skip	integer number of initial lines to skip.
encoding	to be used in the main <a href="#">readLines</a> (file, encoding=encoding) call.
fileEncoding	if file is a file name, i.e., a <a href="#">character</a> string, and fileEncoding is not the empty string, <a href="#">file</a> (file, "rt", encoding = fileEncoding) will be used.
text	instead of file, a <a href="#">character</a> or string (of a few lines, typically).
...	further arguments passed to <a href="#">read.table</a> . You should <i>not</i> use encoding (but possibly fileEncoding!) here, as we do not call <a href="#">read.table</a> on file (but on a <a href="#">textConnection</a> ).

**Value**

a [data.frame](#)

**Note**

TODO: It should be easy to extend [read.org.table\(\)](#) to also work for some of the proposed Markdown formats for tables. Please write to [maintainer](#)("sfsmisc") or open a github issue if you are interested.

**References**

Org-Mode *Manual* on tables, <https://orgmode.org/manual/Tables.html>  
 Org *tutorial* for tables, <https://orgmode.org/worg/org-tutorials/tables.html>

**See Also**

CRAN package [ascii](#) can *write* org tables. [read.table](#)

**Examples**

```
t1 <-
"
| a | var2 | C |
|---+-----+-----|
| 2 | may  | 3.4 |
| 7 | feb  | 4.7 |
"
d <- read.org.table(text = t1)
d
stopifnot(dim(d) == c(2, 3),
          identical(names(d), c("a", "var2", "C")),
          d[, "a"] == c(2,7))
```

---

relErr	<i>Relative Error When Appropriate, Absolute Otherwise</i>
--------	--

---

### Description

`relErrV()`: Compute the signed relative error componentwise (“vectorized”) between the target and current vectors, using the *absolute* error, i.e., the difference in case the relative error is not well defined, i.e., when target is zero or infinite.

`relErr()`: simply the *mean* absolute value of the relative errors between target and current vectors; typically the “same” as `all.equal.numeric(target, vector, tolerance=0, countEQ=TRUE)`. Currently useful only when both vectors are finite.

### Usage

```
relErrV(target, current, eps0 = .Machine$double.xmin)
relErr (target, current)
```

### Arguments

target	numeric, possibly scalar.
current	numeric vector of <code>length()</code> a multiple of <code>length(target)</code> .
eps0	non-negative number; values <code>abs(target) &lt; eps0</code> should be treated as zero (and hence <i>absolute</i> instead of relative error be computed). This may be crucial when target is an “mpfr”-number vector.

### Value

`relErrV()`: a numeric vector of the same length as `current`.

`relErr()`: a single number.

### Author(s)

Martin Maechler, originally as part of **Matrix** package’s ‘test-tools.R’.

### See Also

`all.equal.numeric()` is similar in spirit but returns TRUE or string containing the *mean* relative or absolute error.

### Examples

```
## relErrV() test example: showing how it works fine with {NA, Inf, 0} :
eps <- 1e-4*c(-9, -8, -6, -4, 0.5, 1, 5)
target <- c(-1:1, 0, 0, NA, NaN, Inf, -Inf, Inf, 0, Inf, 1, -3:3)
current <- c(-1:1, 1e-7, NaN, NA, 0, Inf, Inf, 0, Inf, 1, Inf, -3:3+ eps)
cbind(target, current, absE = current-target, relE = relErrV(target,current))
```

```

## relErr() is pretty simple --- (possibly too simple, currently)
relErr
relErr(target, current) # NA (of course)
all.equal.numeric(target, current) ## "'is.NA' value mismatch ..."

## comparison after dropping NA's :
hasN <- is.na(target) | is.na(current)
all.equal(target[!hasN], current[!hasN], tolerance=0) # "Mean abs. diff.: Inf"
  relErr(target[!hasN], current[!hasN]) # NaN (to improve?)

## comparison after only keeping cases where both are finite:
finN <- is.finite(target) & is.finite(current)
all.equal(target[finN], current[finN], tol=0) # "Mean abs.d.: 0.000279.."
all.equal(target[finN], current[finN], tol=0, countEQ=TRUE) # " " : 0.000239..
  relErr(target[finN], current[finN]) # 0.0002392929

```

---

repChar

*Make Simple String from Repeating a Character, e.g. Blank String*


---

## Description

Simple constructors of a constant character string from one character, notably a “blank” string of given string length.

M.M. is now *mentally deprecating* `bl.string` in favor of using `repChar()` in all cases.

With R 3.3.0 (May 2016), the *new* function `strrep()` was introduced; it is faster typically, and more flexible, e.g. accepting a *vector* for the 2nd argument.

This (for now informally) deprecates all uses of `repChar()` and `bl.string()`.

## Usage

```

repChar(char, no)
bl.string(no)

```

## Arguments

char	single character (or arbitrary string).
no	non-negative integer.

## Value

One string, i.e., `character(1)`, for `bl.string` a blank string, fulfilling `n == nchar(bl.string(n))`.

## Author(s)

Martin Maechler, early 1990’s (for `bl.string`).

## See Also

[paste](#), [character](#), [nchar](#).

**Examples**

```
r <- sapply(0:8, function(n) ccat(repChar(" ",n), n))
cbind(r)

repChar("-", 4)
repChar("_", 6)
## it may make sense to a string of more than one character:
repChar("-= ", 6)

## show the very simple function definitions:
repChar
bl.string
```

---

rot2

*Rotate Planar Points by Angle*


---

**Description**

Rotate planar (xy) points by angle phi (in radians).

**Usage**

```
rot2(xy, phi)
```

**Arguments**

xy                numeric 2-column matrix, or coercable to one.  
phi                numeric scalar, the angle in radians (i.e., phi=pi corresponds to 180 degrees)  
                  by which to rotate the points.

**Value**

A two column matrix as xy, containing the rotated points.

**Author(s)**

Martin Maechler, Oct.1994

**Examples**

```
## Rotate three points by 60 degrees :
(xy0 <- rbind(c(1,0.5), c(1,1), c(0,1)))
(Txy <- rot2(xy0, phi = 60 * pi/180))
plot(xy0, col = 2, type = "b", asp = 1,
      xlim=c(-1,1), ylim=c(0,1.5), main = "rot2(*, pi/3) : 2d rotation by 60°")
points(Txy, col = 3, type = "b")
O <- rep(0,2); P2 <- rbind(xy0[2,], Txy[2,])
arrows(0,0,P2[1],P2[2], col = "dark gray")
```

```

xy0 <- .8*rbind(c(1,0), c(.5,.6), c(.7,1), c(1,1), c(.9,.8), c(1,0)) - 0.2
plot(xy0, col= 2, type="b", main= "rot2( <polygon>, pi/4 * 1:7)", asp=1,
     xlim=c(-1,1),ylim=c(-1,1), lwd= 2, axes = FALSE, xlab="", ylab="")
abline(h=0, v=0, col="thistle"); text(1.05, -.05, "x"); text(-.05,1.05, "y")
for(phi in pi/4 * 0:7)
  do.call("arrows",c(list(0,0),rot2(xy0[2,], phi), length=0.1, col="gray40"))
for(phi in pi/4 * 1:7)
  polygon(rot2(xy0, phi = phi), col = 1+phi/(pi/4), border=2, type = "b")

```

---

rotn

*Generalized Rot13 Character Translation (Rotation)*


---

## Description

Compute generalized ‘rot13’ character translations or “rotations”

In the distant past, considered as poor man’s encryption, such rotations are way too poor nowadays and provided mainly for didactical reasons.

## Usage

```
rotn(ch, n = 13)
```

## Arguments

ch                    a [character](#) vector; often a string (of length 1).  
n                      an integer in  $\{1 \dots 26\}$ ; the default is particularly useful.

## Details

Note that the default  $n = 13$  makes `rotn` into a function that is its own inverse.

Written after having searched for it and found `seqinr::rot13()` which was generalized and rendered more transparently to my eyes.

## Value

a character as `ch`, but with each character (which belongs to [letters](#) or [LETTERS](#) “rotated” by  $n$  (positions in the alphabet).

## Author(s)

Martin Maechler

## See Also

[rot2](#), a completely different rotation (namely in the plane aka  $R^2$ ).

**Examples**

```

rotn(c("ABC", "a", "b", "c"), 1)
rotn(c("ABC", "a", "b", "c"), 2)
rotn(c("ABC", "a", "b", "c"), 26) # rotation by 26 does not change much

(ch <- paste("Hello", c("World!", "you too")))
rotn(ch)
rotn(rotn(ch) ) # rotn(*, 13) is its own inverse

```

roundfixS

*Round to Integer Keeping the Sum Fixed***Description**

Given a real numbers  $y_i$  with the particular property that  $\sum_i y_i$  is integer, find *integer* numbers  $x_i$  which are close to  $y_i$  ( $|x_i - y_i| < 1\forall i$ ), and have identical “marginal” sum,  $\text{sum}(x) == \text{sum}(y)$ .

As I found later, the problem is known as “Apportionment Problem” and it is quite an old problem with several solution methods proposed historically, but only in 1982, Balinski and Young proved that there is no method that fulfills three natural desiderata.

Note that the (first) three methods currently available here were all (re?)-invented by M.Maechler, without any knowledge of the litterature. At the time of writing, I have not even checked to which (if any) of the historical methods they match.

**Usage**

```
roundfixS(x, method = c("offset-round", "round+fix", "1greedy"))
```

**Arguments**

**x** a numeric vector which **must** sum to an integer  
**method** character string specifying the algorithm to be used.

**Details**

Without hindsight, it may be surprising that all three methods give identical results (in all situations and simulations considered), notably that the idea of ‘mass shifting’ employed in the iterative “1greedy” algorithm seems equivalent to the much simpler idea used in “offset-round”.

I am pretty sure that these algorithms solve the  $L_p$  optimization problem,  $\min_x \|y - x\|_p$ , typically for all  $p \in [1, \infty]$  *simultaneously*, but have not bothered to find a formal proof.

**Value**

a numeric vector, say  $r$ , of the same length as  $x$ , but with integer values and fulfilling  $\text{sum}(r) == \text{sum}(x)$ .



```

chk(y)

## Not run:
for(i in 1:1000)
  stopifnot(chk(makeIntSum(rpois(100, 10) +
                        c(runif(75, min= 0, max=.2),
                          runif(25, min=.5, max=.9)))))

## End(Not run)

```

---

rrange

*Robust Range using Boxplot 'Quartiles'*


---

### Description

Compute a robust range, i.e. the usual `range()` as long as there are no outliers, using the “whisker boundaries” of `boxplot`, i.e., `boxplot.stats`.

### Usage

```
rrange(x, range=1, coef = 1.5, na.rm = TRUE)
```

### Arguments

<code>x</code>	numeric vector the robust range of which shall be computed.
<code>range</code>	number for S compatibility; $1.5 * \text{range}$ is equivalent to <code>coef</code> .
<code>coef</code>	numeric multiplication factor defining the outlier boundary, see ‘Details’ below.
<code>na.rm</code>	logical indicating how NA values should be handled; they are simply dropped when <code>na.rm = TRUE</code> as by default.

### Details

The robust range is really just what `boxplot.stats(x, coef=coef)` returns as the whisker boundaries. This is the most extreme values `x[j]` still inside median plus/minus `coef * IQR`.

### Value

numeric vector `c(m, M)` with  $m \leq M$  which is (not strictly) inside `range(x) = c(min(x), max(x))`.

### Author(s)

Martin Maechler, 1990.

### See Also

`range`, `fivenum`, `boxplot` and `boxplot.stats`.

A more sophisticated robust range for (strongly) asymmetric data can be derived from the skewness adjusted boxplot statistics `adjboxStats` which is a generalization of `boxplot.stats`.



**Examples**

```
stopifnot(rrange(c(1:10,1000)) == c(1,10))
```

seqXtend

*Sequence Covering the Range of X, including X***Description**

Produce a sequence of unique values (sorted increasingly), *containing* the initial set of values  $x$ . This can be useful for setting prediction e.g. ranges in nonparametric regression.

**Usage**

```
seqXtend(x, length., method = c("simple", "aim", "interpolate"),
         from = NULL, to = NULL)
```

**Arguments**

$x$	numeric vector.
length.	integer specifying <i>approximately</i> the desired <code>length()</code> of the result.
method	string specifying the method to be used. The default, "simple" uses <code>seq(*, length.out = length.)</code> where "aim" aims a bit better towards the desired final length, and "interpolate" interpolates evenly <i>inside</i> each interval $[x_i, x_{i+1}]$ in a way to make all the new intervals of approximately the same length.
from, to	numbers to be passed to (the default method for) <code>seq()</code> , defaulting to the minimal and maximal $x$ value, respectively.

**Value**

numeric vector of increasing values, of approximate length `length.` (unless `length. < length(unique(x))` in which case, the result is simply `sort(unique(x))`), containing the original values of  $x$ .

From, `r <- seqXtend(x, *)`, the original values are at indices `ix <- match(x, r)`, i.e., `identical(x, r[ix])`.

**Note**

`method = "interpolate"` typically gives the best results. Calling `roundfixS`, it also need more computational resources than the other methods.

**Author(s)**

Martin Maechler

**See Also**

`seq`; `plotDS` can make particularly good use of `seqXtend()`

**Examples**

```

a <- c(1,2,10,12)
seqXtend(a, 12)# --> simply 1:12
seqXtend(a, 12, "interp")# ditto
seqXtend(a, 12, "aim")# really worse
stopifnot(all.equal(seqXtend(a, 12, "interp"), 1:12))

## for a "general" x, however, "aim" aims better than default
x <- c(1.2, 2.4, 4.6, 9.9)
length(print(seqXtend(x, 12)))      # 14
length(print(seqXtend(x, 12, "aim"))) # 12
length(print(seqXtend(x, 12, "int"))) # 12

## "interpolate" is really nice:
xt <- seqXtend(x, 100, "interp")
plot(xt, main="seqXtend(*, 100, \"interpol\")")
points(match(x,xt), x, col = 2, pch = 20)
# ... you don't even see that it's not equidistant
# whereas the cheap method shows ...
xt2 <- seqXtend(x, 100)
plot(xt2, col="blue")
points(match(x,xt2), x, col = 2, pch = 20)

## with "Date" objects
Drng <- as.Date(c("2007-11-10", "2012-07-12"))
(px <- pretty(Drng, n = 16)) # say, for the main labels
## say, a finer grid, for ticks -- should be almost equidistant
n3 <- 3*length(px)
summary(as.numeric(diff(seqXtend(px, n3))))      # wildly varying
summary(as.numeric(diff(seqXtend(px, n3, "aim")))) # (ditto)
summary(as.numeric(diff(seqXtend(px, n3, "int")))) # around 30

```

---

sessionInfoX

*Extended Information About the Current R Session*


---

**Description**

Collect (and print) information about the current R session and environment, using `sessionInfo()` and more mostly low-level and platform dependent information.

`isRshared()` is a utility called from `sessionInfoX()`.

**Usage**

```

sessionInfoX(pkgs = NULL, list.libP = FALSE, extraR.env = TRUE)

## S3 method for class 'sessionInfoX'
print(x, locale = TRUE, RLIBS = TRUE, Renv = TRUE, ...)

isRshared(platform = .Platform)

```

**Arguments**

pkgs	NULL (default), TRUE or a <b>character</b> vector of R package names, whose <code>packageDescription()</code> s are wanted. No packages by default, TRUE takes all currently loaded pkgs.
list.libP	a logical indicating if for all <code>.libPaths</code> entries, the files should be listed via <code>list.files</code> .
extraR.env	logical indicating if <i>all</i> environment variables should be recorded which start with "R_" or "_R_".
x	typically the result of <code>sessionInfoX()</code> .
locale	logical, passed to <code>print.sessionInfo()</code> indicating if the locale information should be printed.
RLIBS	logical indicating if the information about R_LIBS should be printed.
Renv	logical indicating if the information about R environment variables should be printed.
...	passed to <code>print</code> methods.
platform	a <b>list</b> "like" <code>.Platform</code> .

**Value**

For `isRshared()`, a **logical** indicating if R has been installed as "shared", i.e., linked to 'libR\*' shared library.

For `sessionInfoX()`, an object of S3 class "sessionInfoX", a **list** with components (there may be more, experimental and not yet listed here):

sInfo	simply the value of <code>sessionInfo()</code> .
sysInf	the value of <code>Sys.info()</code> .
capabilities	the value of <code>capabilities()</code> .
extSoft	for R 3.2.0 and newer, the value of <code>extSoftVersion()</code> .
grSoft	for R 3.2.0 and newer, the value of <code>grSoftVersion()</code> .
tclVersion	for R 3.2.0 and newer and when <code>tcltk</code> is loaded, the Tcl version ( <code>tclVersion()</code> ).
LAPACK	for R 3.0.3 and newer, the value of <code>La_version()</code> .
pcre	for R 3.1.3 and newer, the value of <code>pcre_config()</code> .
pkgDescr	If <code>pkgs</code> was non-empty, a named <b>list</b> of <code>packageDescription()</code> s for each entry in <code>pkgs</code> .
libPath	the value of <code>.libPaths()</code> .
RLIBS	a <b>character</b> vector of entries from <code>Sys.getenv("R_LIBS")</code> , typically very similar to the <code>libPaths</code> component.
n.RLIBS	simply a <code>normalizePath()</code> ed version of RLIBS.
R.env	a named character vector with the "important" R environment variables <code>R_ENVIRON</code> , <code>R_PROFILE</code> , <code>R_CHECK_ENVIRON</code> .
xR.env	if <code>extraR.env</code> was true, a named character vector of "all R related" environment variables, as specified in <code>extraR.env</code> 's description above.
shared	(not available on Windows, where it is conceptually always true:) <b>logical</b> indicating if the version of R is "shared".

**Author(s)**

Martin Maechler, December 2015 ff.

**See Also**

[sessionInfo](#), [.libPaths](#), [R.version](#), [Sys.getenv](#).

**Examples**

```
six0 <- sessionInfoX()
six0$shared # useful (for some, e.g., MM) on Unix alike

sixN <- sessionInfoX("nlme", list.libP = TRUE)
sixN # -> print() method for "sessionInfoX"
names(sixN)
str(sixN, max = 1) # outline of lower-level structure
str(sixN$pkgDescr) # list with one component "nlme"
```

---

shortRversion

*Short R Version String*

---

**Description**

From **base R**'s [R.version.string](#), produce a somewhat shorter version, with or without date, notably also for *patched* or *development* versions of R.

Main use is for plotting or construction of file of variable names.

**Usage**

```
shortRversion(Rv = R.version, Rst = Rv$status,
              Rvstring = if (!is.null(s <- Rv$version.string)) s else R.version.string,
              date = Rst != "", spaces = TRUE)
```

**Arguments**

Rv	a <a href="#">list</a> with some of the same components as <a href="#">R.version</a> .
Rst	a string specifying the <i>status</i> of R's version. For released versions of R, this is <code>""</code> ; almost always use the default <code>Rv\$status</code> .
Rvstring	a string with a default that should work even for R versions previous to 1.0.0.
date	logical specifying if the date of the R version should be included in the result; by default, this will be true only for non-released versions of R.
spaces	logical indicating if the result may contain spaces (aka 'blanks'); setting it to false, replaces the blanks by <code>"-"</code> and <code>"_"</code> .

**Value**

a [character](#) string, typically a shortened version of `Rvstring`.

**Author(s)**

Martin Maechler

**See Also**

[R.version](#), [R.version.string](#)

**Examples**

```
shortRversion() ## (including the date, typically for an R Core developer)
## but this is shorter:
(Rver <- shortRversion(date=FALSE))
shortRversion(spaces=FALSE) # e.g. for a file of even directory name
shortRversion(spaces=FALSE, date=FALSE) # even shorter, ditto

## If you want even shorter { abbreviate() will remove spaces, too }:
abbreviate(shortRversion(), 11)
abbreviate(shortRversion(date=FALSE), 13)
```

---

signi

*Rounding to Significant Digits*

---

**Description**

Rounds to significant digits similarly to [signif](#).

**Usage**

```
signi(x, digits = 6)
```

**Arguments**

x	numeric vector to be rounded.
digits	number of significant digits required.

**Value**

numeric vector “close” to x, i.e. by at least digits significant digits.

**Note**

This is really just `round(x, digits - trunc(log10(abs(x))))` and hence mainly of didactical use. Rather use `signif()` otherwise.

**Author(s)**

Martin Maechler, in prehistoric times (i.e. before 1990).

**See Also**

[signif](#), [round](#).

**Examples**

```
(x1 <- seq(-2, 4, by = 0.5))
identical(x1, signi(x1))# since 0.5 is exact in binary arithmetic
(x2 <- pi - 3 + c(-5,-1,0, .1, .2, 1, 10,100))
signi(x2, 3)
```

---

sourceAttach

*Source and Attach an R source file*

---

**Description**

Source (via [sys.source\(\)](#)) and attach ([attach](#)) an R source file.

**Usage**

```
sourceAttach(file, pos=2,
             name = paste(abbreviate(gsub(fsep,"", dirname(file))),
                          12, method="both.sides"),
             basename(file), sep=fsep),
             keep.source = getOption("keep.source.pkgs"),
             warn.conflicts = TRUE)
```

**Arguments**

file	file name
pos	passed to <a href="#">attach()</a>
name	character, with a smart default, passed to <a href="#">attach()</a> .
keep.source	logical, see <a href="#">sys.source()</a> .
warn.conflicts	logical, see <a href="#">attach</a> .

**Value**

the return value of [attach\(\)](#).

**Author(s)**

Martin Maechler, 29 Jul 2011

**See Also**

[attach](#), [sys.source](#), [source](#)

## Examples

```
sourceAttach(system.file("test-tools-1.R", package="Matrix", mustWork=TRUE))
search() # shows the new "data base" at position 2
## look what it contains:
ls.str(pos = 2)
```

---

str\_data

*Overview on All Datasets in an R Package*

---

## Description

Provide an overview over all datasets available by `data()` in a (list of) given R packages.

## Usage

```
str_data(pkgs, filterFUN, ...)
```

## Arguments

pkgs	character vector of names of R packages.
filterFUN	optionally a <a href="#">logical function</a> for filtering the R objects.
...	potential further arguments to be passed to <code>str</code> ; <code>str(utils:::str.default)</code> gives useful list.

## Value

invisibly (see [invisible](#)) a [list](#) with named components matching the `pkgs` argument. Each of these components is a named list with one entry per `data(.)` argument name. Each entry is a [character](#) vector of the names of all objects, typically only one.

The side effect is, as with `str()`, to print everything (via `cat`) to the console.

## Author(s)

Martin Maechler

## See Also

[str](#), [data](#).

## Examples

```
str_data("cluster")

str_data("datasets", max=0, give.attr = FALSE)

## Filtering (and return value)
df1 <- str_data("datasets", filterFUN=is.data.frame)
```

```
str(df.d <- dfl$datasets)
## dim() of all those data frames:
t(sapply(unlist(df.d), function(.) dim(get(.))))

### Data sets in all attached packages but "datasets" (and stubs):
s <- search()
(Apkgs <- sub("^package:", '', s[grep("^package:", s)]))
str_data(Apkgs[!Apkgs %in% c("datasets", "stats", "base")])
```

---

Sys.cpuinfo

*Provide Information about the Linux Hardware (CPU, Memory, etc)*


---

### Description

Return information about the Linux hardware, notably the CPU (the central processor unit) and memory of the computer **R** is running on. This is currently **only available for Linux**.

These functions exist on other unix-alike platforms, but produce an error when called.

### Usage

```
Sys.procinfo(procfile)
Sys.cpuinfo()
Sys.meminfo()
Sys.memGB(kind = "MemTotal")
Sys.MIPS()
```

### Arguments

procfile	name of file the lines of which give the CPU info “as on Linux”
kind	a <a href="#">character</a> string specifying which <i>kind</i> of memory is desired.

### Value

The `Sys.*info()` functions return a “simple.list”, here basically a named character vector, (where the names have been filtered through `make.names(*, unique=TRUE)` which is of importance for multi-processor or multi-core CPUs, such that vector can easily be indexed.

`Sys.memGB()` returns available memory in giga bytes [GB];

`Sys.MIPS()` returns a number giving an approximation of the **Million Instructions Per Second** that the CPU processes (using “bogomips”). This is a performance measure of the basic *non-numeric* processing capabilities. For single-core Linux systems, often about twice the basic clock rate in “MHz” (as available by `Sys.cpuinfo()[“cpu.MHz”]`); now, with multicore systems, the result is often around (but smaller than)  $2 * \#\{\text{cores}\} * \text{clock.rate}$ .



**Note**

These currently do rely on the Linux `/proc/` file system, and may not easily be portable to non-Linux environments.

On multi-processor machines, `Sys.cpuinfo()` contains each field for each processor (i.e., `names(Sys.cpuinfo())` has [duplicated](#) entries).

Conceivably, the bogomIPS source code is open and available and could be built into R.

**Author(s)**

Martin Maechler

**See Also**

[Sys.ps](#), etc.

**Examples**

```
(n.cores <- parallel::detectCores())
if(substr(R.version[["os"]], 1,5) == "linux") { ##-- only on Linux
  Sys.cpuinfo() # which is often ugly; this looks much better:
  length(Sys.cpu2 <- local({I <- Sys.cpuinfo(); I[ !grepl("^flags", names(I)) ] })))
  ## may still be too much, notably if n.cores > 2:
  (Sys3 <- Sys.cpu2[!grepl("[.][0-9]+$", names(Sys.cpu2))])

  Sys.MIPS() ## just the 'bogomips' from above:
  Sys.MIPS() / as.numeric(Sys.cpuinfo()["cpu.MHz"]) ## ~~ 2 * #{cores} ((no longer))

  ## Available Memory -- can be crucial:
  Sys.memGB() #- default "MemTotal"
  if(Sys.memGB("MemFree") > 16)
    message("Be happy! You have more than 16 Gigabytes of free memory")
}
```

---

Sys.ps

*Return Process Status (Unix 'ps') Information*

---

**Description**

These functions return process id and status information, typically about the running R process.

**Usage**

```
Sys.ps(process= Sys.getpid(),
       fields = c("pid", "pcpu", "time", "vsz", "comm"),
       usefile = length(fields) > 10,
       ps.cmd = Sys.ps.cmd(),
       verbose = getOption("verbose"),
       warn.multi = verbose || any(fields != "ALL"))
```

```
Sys.sizes(process = Sys.getpid(), ps.cmd = Sys.ps.cmd())
```

### Arguments

process	the process id, an integer.
fields	character strings of "ALL", specifying which process status fields are desired.
usefile	logical; if true, <code>system</code> writes to a temporary file and that is <code>scanned</code> subsequently.
ps.cmd	character string, giving the "ps" command name to be used.
verbose	logical ...
warn.multi	logical ...

### Details

Use `man ps` on your respective Unix system, to see what fields are supported exactly. Unix dialects *do* differ here, and, SunOS-Solaris even has more than one ps command. . .

### Value

Note, that `Sys.sizes()` currently returns two integers which are "common" to Solaris and Linux.

### Author(s)

Martin Maechler

### See Also

[Sys.info](#), [Sys.getpid](#), [proc.time](#).

### Examples

```
(.pid <- Sys.getpid()) ## process ID of current process
Sys.sizes(.pid)

## The default process statistics about the running R process
try( Sys.ps() )
```

TA.plot

*Tukey-Anscombe Plot (Residual vs. Fitted) of a Linear Model***Description**

From a linear (or glm) model fitted, produce the so-called Tukey-Anscombe plot. Useful (optional) additions include: 0-line, lowess smooth, 2sigma lines, and automatic labeling of observations.

**Usage**

```
TA.plot(lm.res,
        fit= fitted(lm.res), res= residuals(lm.res, type="pearson"),
        labels= NULL, main= mk.main(), xlab = "Fitted values",
        draw.smooth= n >= 10, show.call = TRUE, show.2sigma= TRUE,
        lo.iter = NULL, lo.cex= NULL,
        par0line = list(lty = 2, col = "gray"),
        parSmooth = list(lwd = 1.5, lty = 4, col = 2),
        parSigma = list(lwd = 1.2, lty = 3, col = 4),
        verbose = FALSE,
        ...)
```

**Arguments**

lm.res	Result of <code>lm(.)</code> , <code>aoV(.)</code> , <code>glm(.)</code> or a similar object.
fit	fitted values; you probably want the default here.
res	residuals to use. Default: <b>Weighted</b> ("Pearson") residuals if weights have been used for the model fit.
labels	strings to use as plotting symbols for each point. Default(NULL): extract observations' names or use its sequence number. Use, e.g., "*" to get simple * symbols.
main	main title to plot. Default: sophisticated, resulting in something like "Tukey-Anscombe Plot of : $y \sim x$ " constructed from <code>lm.res \$ call</code> .
xlab	x-axis label for plot.
draw.smooth	logical; if TRUE, draw a lowess smoother (with automatic smoothing fraction).
show.call	logical; if TRUE, write the "call"ing syntax with which the fit was done.
show.2sigma	logical; if TRUE, draw horizontal lines at $\pm 2\sigma$ where $\sigma$ is <code>mad(resid)</code> .
lo.iter	positive integer, giving the number of lowess robustness iterations. The default depends on the model and is 0 for non Gaussian <code>glm</code> 's.
lo.cex	character expansion ("cex") for lowess and other marginal texts.
par0line	a list of arguments (with reasonable defaults) to be passed to <code>abline(.)</code> when drawing the x-axis, i.e., the $y = 0$ line.

parSmooth, parSigma each a list of arguments (with reasonable default) for drawing the smooth curve (if `draw.smooth` is true), or the horizontal sigma boundaries (if `show.2sigma` is true) respectively.

verbose logical indicating if some construction details should be reported (`print()`ed).

... further graphical parameters are passed to `n.plot(.)`.

### Side Effects

The above mentioned plot is produced on the current graphic device.

### Author(s)

Martin Maechler, Seminar fuer Statistik, ETH Zurich, Switzerland; <maechler@stat.math.ethz.ch>

### See Also

[plot.lm](#) which also does a QQ normal plot and more.

### Examples

```
data(stackloss)
TA.plot(lm(stack.loss ~ stack.x))

example(airquality)
summary(lm0 <- lm(Ozone ~ ., data= airquality))
TA.plot(lm0)
TA.plot(lm0, label = "0") # instead of case numbers

if(FALSE) {
  TA.plot(lm(cost ~ age+type+car.age, claims, weights=number, na.action=na.omit))
}

##--- for aov(.) : -----
data(Gun, package = "nlme")
TA.plot( aov(rounds ~ Method + Physique/Team, data = Gun))

##--- Not so clear what it means for GLM, but: -----
if(require(rpart)) { # for the two datasets only
  data(solder, package = "rpart")
  TA.plot(glm(skips ~ ., data = solder, family = poisson), cex= .6)

  data(kyphosis, package = "rpart")
  TA.plot(glm(Kyphosis ~ poly(Age,2) + Start, data=kyphosis, family = binomial),
  cex=.75) # smaller title and plotting characters
}
```

---

tapplySimpl	<i>More simplification in tapply() result</i>
-------------	---

---

### Description

For the case of more than two categories or indices (in INDEX), traditional `tapply(*, simplify = TRUE)` still returns a list when an array may seem more useful and natural. This is provided by `tapplySimpl()` if the function `FUN()` is defined such as to return a vector of the same length in all cases.

### Usage

```
tapplySimpl(X, INDEX, FUN, ...)
```

### Arguments

X	an atomic object, typically a vector. All these arguments are as in <code>tapply()</code> and are passed to <code>tapply(. . .)</code> .
INDEX	list of (typically more than one) factors, each of same length as X.
FUN	the function to be applied. For the result to be simplifiable, <code>FUN()</code> must return a vector of always the same length.
...	optional arguments to FUN.

### Value

If the above conditions are satisfied, the list returned from `r <- tapply(X, INDEX, FUN, ...)` is simplified into an `array` of rank  $1 + \#\{indices\}$ , i.e.,  $1 + \text{length}(INDEX)$ ; otherwise, `tapplySimpl()` returns the list `r`, i.e., the same as `tapply()`.

### Author(s)

Martin Maechler, 14 Jun 1993 (for S-plus).

### See Also

`tapply(*, simplify=TRUE)`.

### Examples

```
## Using tapply() would give a list (with dim() of a matrix);
## here we get 3-array:

data(esoph)
with(esoph, {
  mima <- tapplySimpl(ncases/ncontrols, list(agegp, alcgp), range)
  stopifnot(dim(mima) == c(2, nlevels(agegp), nlevels(alcgp)))
})
aperm(mima)
```

tkdensity

*GUI Density Estimation using Tcl/Tk***Description**

This is graphical user interface (GUI) to [density](#), allowing for dynamic bandwidth choice and a simple kind of zooming, relying on `library(tcltk)`.

**Usage**

```
tkdensity(y, n = 1024, log.bw = TRUE, showvalue = TRUE,
          xlim = NULL, do.rug = size < 1000, kernels = NULL,
          from.f = if (log.bw) -2 else 1/1000,
          to.f   = if (log.bw) +2.2 else 2,
          col = 2)
```

**Arguments**

<code>y</code>	numeric; the data the density of which we want.
<code>n</code>	integer; the number of abscissa values for <a href="#">density</a> evaluation (and plotting).
<code>log.bw</code>	logical; if true (default), the gui scrollbar is on a <i>log</i> bandwidth scale, otherwise, simple interval.
<code>showvalue</code>	logical; if true, the value of the current (log) bandwidth is shown on top of the scrollbar.
<code>xlim</code>	initial <code>xlim</code> for plotting, see <a href="#">plot.default</a> .
<code>do.rug</code>	logical indicating if <code>rug(y)</code> should be added to each plot. This is too slow for really large sample sizes.
<code>kernels</code>	character vector of kernel names as allowable for the <code>kernels</code> argument of the standard <a href="#">density</a> function.
<code>from.f</code> , <code>to.f</code>	numeric giving the left and right limit of the bandwidth scrollbar.
<code>col</code>	color to be used for the density curve.

**Details**

`library(tcltk)` must be working, i.e., Tcl/Tk must have been installed on your platform, and must have been visible during R's configuration and/or installation.

You can not only choose the bandwidth (the most important parameter), but also the kernel, and you can zoom in and out (in x-range only).

**Value**

none.

(How could this be done? `tcltk` widgets run as separate processes!)

**Author(s)**

Martin Maechler, building on demo(tkdensity).

**Examples**

```
if (dev.interactive(TRUE)) ## does really not make sense otherwise
  if(try(require("tcltk"))) { ## sometimes (rarely) there, but broken

  data(faithful)
  tkdensity(faithful $ eruptions)

  set.seed(7)
  if(require("nor1mix"))
    tkdensity(rnormMix(1000, MW.nm9), kernels = c("gaussian", "epanechnikov"))
}
```

---

toLatex.numeric

*LaTeX or Sweave friendly Formatting of Numbers*


---

**Description**

Formats real numbers, possibly in scientific notation, with a given number of digits after the decimal point. Output can be used in LaTeX math mode, e.g., for printing numbers in a table, where each number has to be printed with the same number of digits after the decimal point, even if the last digits are zeros.

**Usage**

```
## S3 method for class 'numeric'
toLatex(object, digits = format.info(object)[2],
         scientific = format.info(object)[3] > 0, times = "\\cdot", ...)
```

**Arguments**

object	a numeric vector.
digits	number of digits <i>after the decimal point</i> (for the mantissa if scientific). The default behaves the same as R's <code>format()</code> .
scientific	logical indicating if scientific notation $a * 10^k$ should be used. The default behaves the same as R's <code>format()</code> .
times	character string indicating the LaTeX symbol to be used for the 'times' sign.
...	unused; for compatibility with <code>toLatex</code> .

**Value**

a `character` vector of the same length as `object`, containing the formatted numbers.

**Note**

We use `digits` for `round`, i.e., round after the decimal point on purpose, rather than `signif()` significant digit rounding as used by `print()` or `format()`.

**Author(s)**

Alain Hauser

**See Also**

`pretty10exp` which gives `expressions` similar to our `scientific=TRUE`. `toLatex` with other methods.

**Examples**

```
xx <- pi * 10^(-9:9)

format(xx)
formatC(xx)

toLatex(xx) #-> scientific = TRUE is chosen
toLatex(xx, scientific=FALSE)

sapply(xx, toLatex)
sapply(xx, toLatex, digits = 2)
```

---

u.assign0

*'Portable' assign / get functions (R / S-plus) for 'Frame 0'*


---

**Description**

R does not have S' concept of `frame = 0`, aka 'session frame'. These two function were an attempt to provide a portable way for working with `frame 0`, particularly when porting code *from* S.

They have been **deprecated** since August 2013.

**Usage**

```
u.assign0(x, value, immediate = FALSE)
u.get0(x)
```

**Arguments**

<code>x</code>	character string giving the <i>name</i> of the object.
<code>value</code>	any R object which is to be assigned.
<code>immediate</code>	logical, for S compatibility. No use in R.



**Note**

Really don't use these anymore...

**Author(s)**

Martin Maechler

**See Also**

[get](#), [assign](#).

---

u.boxplot.x

*Utility Returning x-Coordinates of Boxplot*

---

**Description**

Return the x-coordinates in an 'n-way' side-by-side boxplot. This is an auxiliary function and exists mainly for backcompatibility with S-plus.

**Usage**

```
u.boxplot.x(n, j = 1:n, fullrange = 100)
```

**Arguments**

n	number of boxplots.
j	indices of boxplots.
fullrange	x-coords as 'uniform' in $[0, fullrange]$ ; (f.=100, corresponds to Splus 3.x (x = 1,2)).

**Value**

a numeric vector of length n, with values inside  $(0, M)$  where  $M = fullrange$ .

**Author(s)**

Martin Maechler

**See Also**

[boxplot](#).

**Examples**

```
u.boxplot.x(7) # == 8.93 22.62 36.3 ... 91.07
```

u.date *Return Date[-Time] String in 'European' Format*

---

**Description**

Return one string of the form "day/month/year", plus "hour:minutes", optionally.

**Usage**

```
u.date(short=FALSE)
```

**Arguments**

short                    logical; if TRUE, no time is given.

**Value**

String with current date (and time).

**Author(s)**

Martin Maechler, ca. 1992

**See Also**

[u.Datumvonheute.](#)

**Examples**

```
u.date()  
u.date(short = TRUE)
```

---

u.datumdecode *Convert "Numeric" Dates*

---

**Description**

Daten der Form 8710230920 aufspalten in Jahr, Monat, Tag, Std, Min

**Usage**

```
u.datumdecode(d, YMDHMnames = c("Jahr", "Monat", "Tag", "Std", "Min"))
```

**Arguments**

d                        numeric dates in the form YYMMDDHHMM.  
YMDHMnames            (column) names to be used for the result.

**Value**

a numeric matrix (or vector) with 5 columns containing the year, month, etc.

**Note**

MM: This is a wrong concept, and also suffers from the “millenium bug” (by using only 2 digits for the year).

**Author(s)**

?? (someone at Sfs ETH)

**See Also**

R's *proper* date-time coding: [DateTimeClasses](#); [u.date](#) etc.

**Examples**

```
u.datumdecode(8710230920)
##  Jahr Monat  Tag  Std  Min
##   87   10   23   9   20

u.datumdecode(c(8710230900, 9710230920, 0210230920))
##      Jahr Monat Tag Std Min
## [1,]   87   10  23   9  00
## [2,]   97   10  23   9  20
## [3,]    2   10  23   9  20
```

---

u.Datumvonheute	<i>Datum und Uhrzeit (auf deutsch)</i>
-----------------	--

---

**Description**

Return current date and time as a string, possibly including day of the week in *German*.

**Usage**

```
u.Datumvonheute(W.tag=2, Zeit=FALSE)
```

```
C.Monatsname
C.Wochentag
C.Wochentagkurz
C.weekday
```

**Arguments**

**W.tag** logical or integer specifying you want weekday (“Wochentag”). 0 or FALSE gives no, 1 or TRUE gives a short and 2 the long version of the day of the week.

**Zeit** logical or integer specifying if time (“Zeit”) is desired. 0 or FALSE gives no, 1 or TRUE gives a hours only and 2 hours and minutes.

**Value**

A string with the current date/time, in the form specified by the arguments.

The C.\* are [character](#) vector “constants”, the German ones actually used by `u.Datumvonheute`.

**Author(s)**

Caterina Savi, Martin Maechler

**See Also**

[u.date](#) for a similar English version, and [p.datum](#) which plots. For English month names, etc [month.name](#).

**Examples**

```
u.Datumvonheute()
u.Datumvonheute(W.tag=1, Zeit=TRUE)
u.Datumvonheute(W.tag= FALSE, Zeit=2)
```

---

u.log

*(Anti)Symmetric Log High-Transform*


---

**Description**

Compute  $\log()$  only for high values and keep low ones – antisymmetrically such that `u.log(x)` is (once) continuously differentiable, it computes

$f(x) = x$  for  $|x| \leq c$  and  $\text{sign}(x)c \cdot (1 + \log(|x|/c))$  for  $|x| \geq c$ .

**Usage**

```
u.log(x, c = 1)
```

**Arguments**

x	numeric vector to be transformed.
c	scalar, > 0

**Value**

numeric vector of same length as x.

**Author(s)**

Martin Maechler, 24 Jan 1995

**Examples**

```
curve(u.log, -3, 10); abline(h=0, v=0, col = "gray20", lty = 3)
curve(1 + log(x), .01, add = TRUE, col= "brown") # simple log
curve(u.log(x, 2), add = TRUE, col=2)
curve(u.log(x, c= 0.4), add = TRUE, col=4)
```

---

u.sys

*'Portable' System function (R / S-plus)*


---

**Description**

u.sys() is a convenient wrapper (of system()) to call to the underlying operating system. The main purpose has been to provide a function with identical UI both in S-PLUS and R. MM thinks you shouldn't use this anymore, usually.

Sys.ps.cmd() returns the 'ps' ('**p**rocess **s**tatus') OS command name (as [character](#) string), and is typically usable on unix alike only.

**Usage**

```
u.sys(..., intern = TRUE)
```

```
Sys.ps.cmd()
```

**Arguments**

... any number of strings – which will be [paste\(\)](#)d together and passed to system.  
intern logical – note that the default is *reversed* from the one in [system\(\)](#).

**Author(s)**

Martin Maechler

**See Also**

[system](#), really!; on non-Windows, Sys.ps() which makes use of Sys.ps.cmd().

**Examples**

```
u.sys # shows how simply the function is defined :
## Not run:
function (... , intern = TRUE)
  system(paste(... , sep = "" ), intern = intern)

## End(Not run)

# All *running* processes of user [sometimes only R]:
try ( u.sys(Sys.ps.cmd(), "ur" ) )
```

---

`unif`*Nice Uniform Points in Interval*

---

**Description**

Give regularly spaced points on interval  $[-c, c]$  with mean 0 (exactly) and variance about 1 (very close for **even** `n` and larger `round.dig`). Note that  $c$  depends on `n`.

**Usage**

```
unif(n, round.dig = 1 + trunc(log10(n)))
```

**Arguments**

<code>n</code>	positive integer specifying the number of points desired.
<code>round.dig</code>	integer indicating to how many digits the result is rounded.

**Value**

numeric vector of length `n`, symmetric around 0, hence with exact mean 0, and variance approximately 1.

**Note**

It relies on the fact that  $Var(1, 2, \dots, n) = n(n + 1)/12$ .

**Author(s)**

Martin Maechler, ca 1990

**See Also**

[runif](#) for producing uniform *random* numbers.

**Examples**

```
(u <- unif(8))
var(u)
```

```
(u. <- unif(8, 12))# more digits in result, hence precision for Var :
var(u.)
```

---

uniqueL                      *A Reversible Version of unique()*

---

### Description

A version of [unique](#) keeping enough information to reverse (or *invert*) to the original data.

### Usage

```
uniqueL(x, isuniq = !duplicated(x), need.sort = is.unsorted(x))
```

### Arguments

`x`                      numeric vector, of length `n`, say.  
`isuniq`                logical vector of the same length as `x`. For the reversion to work this should select at least all unique values of `x`.  
`need.sort`            logical indicating if `x` is not yet sorted. Note that this argument exists only for speedup possibility when it is known, and that it *must be set correctly*.

### Value

list of two components,

`ix`                    integer vector of indices  
`xU`                    vector of values from `x`

such that both `x[isuniq] == xU` and `xU[ix] == x`.

### Author(s)

Martin Maechler

### See Also

[Duplicated](#) from the `sfsmisc` package in addition to the standard [unique](#) and [duplicated](#).

### Examples

```
x0 <- c(1:3,2:7,8:4)
str(r0 <- uniqueL(x0))
with(r0, xU[ix]) ## == x0 !
```

## Description

Concatenate vector elements or anything using `paste(*, collapse = .)`. These are simple short abbreviations I have been using in my own codes in many places.

## Usage

```
vcat(vec, sep = " ")
ccat(...)
```

## Arguments

`vec, ...` any vector and other arguments to be pasted to together.  
`sep` the separator to use, see the *Details* section.

## Details

The functions are really just defined as  
`vcat := function(vec, sep = " ") paste(vec, collapse = sep)`  
`ccat := function(...) paste(..., collapse = "", sep = "")`

## Value

a character string (of length 1) with the concatenated arguments.

## Author(s)

Martin Maechler, early 1990's.

## See Also

[paste](#), [as.character](#), [format](#). `cat()` is really for printing.

## Examples

```
ch <- "is"
ccat("This ", ch, " it: ", 100, "%")
vv <- c(1, pi, 20.4)
vcat(vv)
vcat(vv, sep = ", ")
```



---

 wrapFormula

 Enhance Formula by Wrapping each Term, e.g., by "s(.)"
 

---

### Description

The main motivation for this function has been the easy construction of a “full GAM formula” from something as simple as  $Y \sim \dots$

The potential use is slightly more general.

### Usage

```
wrapFormula(f, data, wrapString = "s(*)")
```

### Arguments

`f` the initial [formula](#); typically something like  $Y \sim \dots$

`data` [data.frame](#) to which the formula applies; see, [formula](#) or also [gam](#) or [lm](#).

`wrapString` [character](#) string, containing “\*”, specifying the wrapping expression to use.

### Value

a [formula](#) very similar to `f`; just replacing each *additive* term by its wrapped version.

### Note

There are limits for this to work correctly; notably the right hand side of the formula `f` should not be nested or otherwise complicated, rather typically just  $\dots$  as in the examples.

### Author(s)

Martin Maechler, May 2007.

### See Also

[formula](#); [gam](#) from package [mgcv](#) (or also from package [gam](#)).

### Examples

```
myF <- wrapFormula(Fertility ~ . , data = swiss)
myF # Fertility ~ s(Agriculture) + s(... ) + ...

if(require("mgcv")) {
  m1 <- gam(myF, data = swiss)
  print( summary(m1) )
  plot(m1, pages = 1) ; title(format(m1$call), line= 2.5)
}

## other wrappers:
```

```
wrapFormula(Fertility ~ . , data = swiss, wrap = "lo(*)")
wrapFormula(Fertility ~ . , data = swiss, wrap = "poly(*, 4)")
```

---

xy.grid

*Produce regular grid matrix.*

---

## Description

Produce the grid used by [persp](#), [contour](#), etc, as an N x 2 matrix. This is really outdated by [expand.grid\(\)](#) nowadays.

## Usage

```
xy.grid(x, y)
```

## Arguments

x,y                    any vectors of same mode.

## Value

a 2-column matrix of “points” for each combination of x and y, i.e. with  $\text{length}(x) * \text{length}(y)$  rows.

## Author(s)

Martin Maechler, 26 Oct 1994.

## See Also

[expand.grid](#) which didn't exist when `xy.grid` was first devised.

## Examples

```
plot(xy.grid(1:7, 10*(0:4)))

x <- 1:3 ; y <- 10*(0:4)
xyg <- xy.grid(x,y)

## Compare with expand.grid() :
m2 <- as.matrix(expand.grid(y,x)[, 2:1])
dimnames(m2) <- NULL
stopifnot(identical(xyg, m2))
```

xy.unique.x

*Uniqify (X,Y) Values using Weights***Description**

Given *smoother* data  $(x_i, y_i)$  and maybe weights  $w_i$ , with multiple  $x_i$ , use the unique x values, replacing the  $y$ 's by their (weighted) mean and updating the weights accordingly.

**Usage**

```
xy.unique.x(x, y, w, fun.mean = mean, ...)
```

**Arguments**

x,y	numeric vectors of same length. Alternatively, x can be a 'xy' like structure, see <a href="#">xy.coords</a> .
w	numeric vector of non-negative weights – or missing which corresponds to all weights equal.
fun.mean	the mean <a href="#">function</a> to use.
...	optional arguments all passed to <a href="#">unique</a> .

**Value**

Numeric matrix with three columns, named x, y and w with unique x values and corresponding y and weights w.

**Author(s)**

Martin Maechler, 8 Mar 1993.

**See Also**

e.g., [smooth.spline](#) uses something like this internally.

**Examples**

```
## simple example:
x <- c(1,1,2,4,3,1)
y <- 1:6
rbind(x, y)
xy.unique.x(x, y)
#   x y w
# 1 1 3 3
# 2 2 3 1
# 3 4 4 1
# 4 3 5 1
xy.unique.x(x, y, fromLast = TRUE)
```

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