

# Package ‘Epi’

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**Depends** R (>= 2.10), utils

**Suggests** splines, nlme, survival, mstate, MASS

**Description** Functions for demographic and epidemiological analysis in the Lexis diagram, i.e. register and cohort follow-up data, including interval censored data and representation of multistate data. Also some useful functions for tabulation and plotting. Contains some epidemiological datasets.

**License** GPL-2

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apc.fit

*Fit an Age-Period-Cohort model to tabular data.***Description**

Fits the classical five models to tabulated rate data (cases, person-years) classified by two of age, period, cohort: Age, Age-drift, Age-Period, Age-Cohort and Age-period. There are no assumptions about the age, period or cohort classes being of the same length, or that tabulation should be only by two of the variables. Only requires that mean age and period for each tabulation unit is given.

**Usage**

```
apc.fit( data,
        A,
        P,
        D,
        Y,
        ref.c,
        ref.p,
        dist = c("poisson", "binomial"),
        model = c("ns", "bs", "ls", "factor"),
        dr.extr = c("weighted", "Holford"),
```

```

parm = c("ACP", "APC", "AdCP", "AdPC", "Ad-P-C", "Ad-C-P", "AC-P", "AP-C"),
npar = c( A=5, P=5, C=5 ),
scale = 1,
alpha = 0.05,
print.AOV = TRUE )

```

## Arguments

data	Data frame with (at least) variables, A (age), P (period), D (cases, deaths) and Y (person-years). Cohort (date of birth) is computed as P-A. If this argument is given the arguments A, P, D and Y are ignored.
A	Age; numerical vector with mean age at diagnosis for each unit.
P	Period; numerical vector with mean date of diagnosis for each unit.
D	Cases, deaths; numerical vector.
Y	Person-years; numerical vector. Also used as denominator for binomial data, see the <code>dist</code> argument.
ref.c	Reference cohort, numerical. Defaults to median date of birth among cases. If used with <code>parm="AdCP"</code> or <code>parm="AdPC"</code> , the residual cohort effects will be 1 at <code>ref.c</code> .
ref.p	Reference period, numerical. Defaults to median date of diagnosis among cases.
dist	Distribution (or more precisely: Likelihood) used for modelling. If a binomial model is used, Y is assumed to be the denominator; "binomial" gives a binomial model with logit link.
model	Type of model fitted: <ul style="list-style-type: none"> <li>• <code>ns</code> fits a model with natural splines for each of the terms, with <code>npar</code> parameters for the terms.</li> <li>• <code>bs</code> fits a model with B-splines for each of the terms, with <code>npar</code> parameters for the terms.</li> <li>• <code>ls</code> fits a model with linear splines.</li> <li>• <code>factor</code> fits a factor model with one parameter per value of A, P and C. <code>npar</code> is ignored in this case.</li> </ul>
dr.extr	Character. How the drift parameter should be extracted from the age-period-cohort model. "weighted" (default) lets the weighted average (by marginal no. cases, D) of the estimated period and cohort effects have 0 slope. "Holford" uses the naive average over all values for the estimated effects, disregarding the no. cases.
parm	Character. Indicates the parametrization of the effects. The first four refer to the ML-fit of the Age-Period-Cohort model, the last four give Age-effects from a smaller model and residuals relative to this. If one of the latter is chosen, the argument <code>dr.extr</code> is ignored. Possible values for <code>parm</code> are: <ul style="list-style-type: none"> <li>• "ACP": ML-estimates. Age-effects as rates for the reference cohort. Cohort effects as RR relative to the reference cohort. Period effects constrained to be 0 on average with 0 slope.</li> </ul>

- "APC": ML-estimates. Age-effects as rates for the reference period. Period effects as RR relative to the reference period. Cohort effects constrained to be 0 on average with 0 slope.
- "AdCP": ML-estimates. Age-effects as rates for the reference cohort. Cohort and period effects constrained to be 0 on average with 0 slope. These effects do not multiply to the fitted rates, the drift is missing and needs to be included to produce the fitted values.
- "AdPC": ML-estimates. Age-effects as rates for the reference period. Cohort and period effects constrained to be 0 on average with 0 slope. These effects do not multiply to the fitted rates, the drift is missing and needs to be included to produce the fitted values.
- "Ad-C-P": Age effects are rates for the reference cohort in the Age-drift model (cohort drift). Cohort effects are from the model with cohort alone, using  $\log(\text{fitted values})$  from the Age-drift model as offset. Period effects are from the model with period alone using  $\log(\text{fitted values})$  from the cohort model as offset.
- "Ad-P-C": Age effects are rates for the reference period in the Age-drift model (period drift). Period effects are from the model with period alone, using  $\log(\text{fitted values})$  from the Age-drift model as offset. Cohort effects are from the model with cohort alone using  $\log(\text{fitted values})$  from the period model as offset.
- "AC-P": Age effects are rates for the reference cohort in the Age-Cohort model, cohort effects are RR relative to the reference cohort. Period effects are from the model with period alone, using  $\log(\text{fitted values})$  from the Age-Cohort model as offset.
- "AP-C": Age effects are rates for the reference period in the Age-Period model, period effects are RR relative to the reference period. Cohort effects are from the model with cohort alone, using  $\log(\text{fitted values})$  from the Age-Period model as offset.

npar	The number of parameters to use for each of the terms in the model. It can be a list of three numerical vectors, in which case these taken as the knots for the age, period and cohort effect, the first and last element in each vector are used as the boundary knots.
alpha	The significance level. Estimates are given with $(1-\alpha)$ confidence limits.
scale	numeric(1), factor multiplied to the rate estimates before output.
print.AOV	Should the analysis of deviance table for the models be printed?

### Value

An object of class "apc" (recognized by [apc.lines](#) and [apc.plot](#)) — a list with components:

Age	Matrix with 4 colums: A.pt with the ages (equals $\text{unique}(A)$ ) and three columns giving the estimated rates with c.i.s.
Per	Matrix with 4 colums: P.pt with the dates of diagnosis (equals $\text{unique}(P)$ ) and three columns giving the estimated RRs with c.i.s.
Coh	Matrix with 4 colums: C.pt with the dates of birth (equals $\text{unique}(P-A)$ ) and three columns giving the estimated RRs with c.i.s.

Drift	A 3 column matrix with drift-estimates and c.i.s: The first row is the ML-estimate of the drift (as defined by <code>drift</code> ), the second row is the estimate from the Age-drift model. For the sequential parametrizations, only the latter is given.
Ref	Numerical vector of length 2 with reference period and cohort. If <code>ref.p</code> or <code>ref.c</code> was not supplied the corresponding element is NA.
AOV	Analysis of deviance table comparing the five classical models.
Type	Character string explaining the model and the parametrization.
Knots	If <code>model</code> is one of "ns" or "bs", a list with three components: Age, Per, Coh, each one a vector of knots. The max and the min are the boundary knots.

### Author(s)

Bendix Carstensen, <http://www.biostat.ku.dk/~bxc>

### References

The considerations behind the parametrizations used in this function are given in details in a preprint from Department of Biostatistics in Copenhagen: <http://www.pubhealth.ku.dk/bs/publikationer/rr-06-1.pdf>, later published as: B. Carstensen: Age-period-cohort models for the Lexis diagram. *Statistics in Medicine*, 10; 26(15):3018-45, 2007.

### See Also

[apc.frame](#), [apc.lines](#), [apc.plot](#).

### Examples

```
library( Epi )
data(lungDK)

# Taylor a dataframe that meets the requirements
exd <- lungDK[,c("Ax", "Px", "D", "Y")]
names(exd)[1:2] <- c("A", "P")

# Two different ways of parametrizing the APC-model, ML
ex.H <- apc.fit( exd, npar=7, model="ns", dr.extr="Holford", parm="ACP", scale=10^5 )
ex.W <- apc.fit( exd, npar=7, model="ns", dr.extr="weighted", parm="ACP", scale=10^5 )

# Sequential fit, first AC, then P given AC.
ex.S <- apc.fit( exd, npar=7, model="ns", parm="AC-P", scale=10^5 )

# Show the estimated drifts
ex.H[["Drift"]]
ex.W[["Drift"]]
ex.S[["Drift"]]

# Plot the effects
fp <- apc.plot( ex.H )
apc.lines( ex.W, frame.par=fp, col="red" )
apc.lines( ex.S, frame.par=fp, col="blue" )
```

---

apc.frame	<i>Produce an empty frame for display of parameter-estimates from Age-Period-Cohort-models.</i>
-----------	-------------------------------------------------------------------------------------------------

---

## Description

A plot is generated where both the age-scale and the cohort/period scale is on the x-axis. The left vertical axis will be a logarithmic rate scale referring to age-effects and the right a logarithmic rate-ratio scale of the same relative extent as the left referring to the cohort and period effects (rate ratios).

Only an empty plot frame is generated. Curves or points must be added with points, lines or the special utility function [apc.lines](#).

## Usage

```
apc.frame( a.lab,
           cp.lab,
           r.lab,
           rr.lab = r.lab / rr.ref,
           rr.ref = r.lab[length(r.lab)/2],
           a.tic = a.lab,
           cp.tic = cp.lab,
           r.tic = r.lab,
           rr.tic = r.tic / rr.ref,
           tic.fac = 1.3,
           a.txt = "Age",
           cp.txt = "Calendar time",
           r.txt = "Rate per 100,000 person-years",
           rr.txt = "Rate ratio",
           ref.line = TRUE,
           gap = diff(range(c(a.lab, a.tic)))/3,
           col.grid = gray(0.85),
           sides = c(1,2,4) )
```

## Arguments

a.lab	Numerical vector of labels for the age-axis.
cp.lab	Numerical vector of labels for the cohort-period axis.
r.lab	Numerical vector of labels for the rate-axis (left vertical)
rr.lab	Numerical vector of labels for the RR-axis (right vertical)
rr.ref	At what level of the rate scale is the RR=1 to be.
a.tic	Location of additional tick marks on the age-scale
cp.tic	Location of additional tick marks on the cohort-period-scale
r.tic	Location of additional tick marks on the rate-scale

<code>rr.tic</code>	Location of additional tick marks on the RR-axis.
<code>tic.fac</code>	Factor with which to diminish intermediate tick marks
<code>a.txt</code>	Text for the age-axis (left part of horizontal axis).
<code>cp.txt</code>	Text for the cohort/period axis (right part of horizontal axis).
<code>r.txt</code>	Text for the rate axis (left vertical axis).
<code>rr.txt</code>	Text for the rate-ratio axis (right vertical axis)
<code>ref.line</code>	Logical. Should a reference line at RR=1 be drawn at the calendar time part of the plot?
<code>gap</code>	Gap between the age-scale and the cohort-period scale
<code>col.grid</code>	Colour of the grid put in the plot.
<code>sides</code>	Numerical vector indicating on which sides axes should be drawn and annotated. This option is aimed for multi-panel displays where axes only are put on the outer plots.

### Details

The function produces an empty plot frame for display of results from an age-period-cohort model, with age-specific rates in the left side of the frame and cohort and period rate-ratio parameters in the right side of the frame. There is a gap of `gap` between the age-axis and the calendar time axis, vertical grid lines at `c(a.lab, a.tic, cp.lab, cp.tic)`, and horizontal grid lines at `c(r.lab, r.tic)`.

The function returns a numerical vector of length 2, with names `c("cp.offset", "RR.fac")`. The y-axis for the plot will be a rate scale for the age-effects, and the x-axis will be the age-scale. The cohort and period effects are plotted by subtracting the first element (named `"cp.offset"`) of the returned result from the cohort/period, and multiplying the rate-ratios by the second element of the returned result (named `"RR.fac"`).

### Value

A numerical vector of length two, with names `c("cp.offset", "RR.fac")`. The first is the offset for the cohort period-axis, the second the multiplication factor for the rate-ratio scale.

Side-effect: A plot with axes and grid lines but no points or curves. Moreover, the option `apc.frame.par` is given the value `c("cp.offset", "RR.fac")`, which is recognized by [apc.plot](#) and [apc.lines](#).

### Author(s)

Bendix Carstensen, Steno Diabetes Center, <http://www.pubhealth.ku.dk/~bxc/>

### References

<http://www.pubhealth.ku.dk/~bxc/APC/notes.pdf>

### See Also

[apc.lines](#), [apc.fit](#)

**Examples**

```

par( mar=c(4,4,1,4) )
res <-
apc.frame( a.lab=seq(30,90,20), cp.lab=seq(1880,2000,30), r.lab=c(1,2,5,10,20,50),
           a.tic=seq(30,90,10), cp.tic=seq(1880,2000,10), r.tic=c(1:10,1:5*10),
           gap=27 )

res
# What are the axes actually?
par(c("usr","xlog","ylog"))
# How to plot in the age-part: a point at (50,10)
points( 50, 10, pch=16, cex=2, col="blue" )
# How to plot in the cohort-period-part: a point at (1960,0.3)
points( 1960-res[1], 0.3*res[2], pch=16, cex=2, col="red" )

```

---

apc.lines

*Plot APC-estimates (and other things) in an APC-frame.*


---

**Description**

When an APC-frame has been produced by [apc.frame](#), this function draws a set of estimates from an APC-fit in the frame. An optional drift parameter can be added to the period parameters and subtracted from the cohort and age parameters.

**Usage**

```

apc.lines( A, P, C,
           scale = c("log","ln","rates","inc","RR"),
           frame.par = options()[["apc.frame.par"]],
           drift = 0,
           c0 = median( C[,1] ),
           a0 = median( A[,1] ),
           p0 = c0 + a0,
           ci = rep( FALSE, 3 ),
           lwd = c(3,1,1),
           lty = 1,
           col = "black",
           type = "l",
           knots = FALSE,
           ... )
pc.points( x, y, ... )
pc.lines( x, y, ... )
pc.matpoints( x, y, ... )
pc.matlines( x, y, ... )
cp.points( x, y, ... )
cp.lines( x, y, ... )
cp.matpoints( x, y, ... )
cp.matlines( x, y, ... )

```

**Arguments**

A	Age effects. A 4-column matrix with columns age, age-specific rates, lower and upper c.i. If A is of class <code>apc</code> (see <code>apc.fit</code> , P, C, <code>c0</code> , <code>a0</code> and <code>p0</code> are ignored, and the estimates from there plotted.
P	Period effects. Rate-ratios. Same form as for the age-effects.
C	Cohort effects. Rate-ratios. Same form as for the age-effects.
scale	Are effects given on a log-scale? Character variable, one of "log", "ln", "rates", "inc", "RR". If "log" or "ln" it is assumed that effects are $\log(\text{rates})$ and $\log(\text{RRs})$ otherwise the actual effects are assumed given in A, P and C. If A is of class <code>apc</code> , it is assumed to be "rates".
frame.par	2-element vector with the cohort-period offset and RR multiplier. This will typically be the result from the call of <code>apc.frame</code> . See this for details.
drift	The drift parameter to be added to the period effect. If <code>scale="log"</code> this is assumed to be on the log-scale, otherwise it is assumed to be a multiplicative factor per unit of the first columns of A, P and C
c0	The cohort where the drift is assumed to be 0; the subtracted drift effect is $\text{drift} * (\text{C}[, 1] - \text{c0})$ .
a0	The age where the drift is assumed to be 0.
p0	The period where the drift is assumed to be 0.
ci	Should confidence interval be drawn. Logical or character. If character, any occurrence of "a" or "A" produces confidence intervals for the age-effect. Similarly for period and cohort.
lwd	Line widths for estimates, lower and upper confidence limits.
lty	Linetypes for the three effects.
col	Colours for the three effects.
type	What type of lines / points should be used.
knots	Should knots from the model be shown?
...	Further parameters to be transmitted to <code>points</code> , <code>lines</code> , <code>matpoints</code> or <code>matlines</code> used for plotting the three sets of curves.
x	vector of x-coordinates.
y	vector of y-coordinates.

**Details**

The drawing of three effects in an APC-frame is a rather trivial task, and the main purpose of the utility is to provide a function that easily adds the functionality of adding a drift so that several sets of lines can be easily produced in the same frame.

Since the Age-part of the frame is referred to by its real coordinates plotting in the calendar time part requires translation and scaling to put things correctly there, that is done by the functions `pc.points` etc. The functions `cp.points` etc. are just synonyms for these, in recognition of the fact that you can never remember whether it is "pc" or "cp".

**Value**

APC.lines returns (invisibly) a list of three matrices with the effects plotted. The functions cp.points etc. return nothing.

**Author(s)**

Bendix Carstensen, Steno Diabetes Center, <http://www.pubhealth.ku.dk/~bxc>

**See Also**

[apc.frame](#), [apc.fit](#), [apc.plot](#)

---

apc.plot

*Plot the estimates from a fitted Age-Period-Cohort model*

---

**Description**

This function plots the estimates created by [apc.fit](#) in a single graph. It just calls [apc.frame](#) after computing some sensible values of the parameters, and subsequently plots the estimates using [apc.lines](#).

**Usage**

```
apc.plot(obj, r.txt = "Rate", ...)
```

**Arguments**

obj	An object of class apc.
r.txt	The text to put on the vertical rate axis.
...	Additional arguments passed on to <a href="#">apc.lines</a> .

**Value**

A numerical vector of length two, with names c("cp.offset", "RR.fac"). The first is the offset for the cohort period-axis, the second the multiplication factor for the rate-ratio scale. Therefore, if you want to plot at (x,y) in the right panel, use (x-res["cp.offset"], y/res["RR.fac"])=(x-res[1], y/res[2]). This vector should be supplied for the parameter frame.par to [apc.lines](#) if more sets of estimates is plotted in the same graph.

**Author(s)**

Bendix Carstensen, Steno Diabetes Center, <http://www.pubhealth.ku.dk/~bxc>

**See Also**

[apc.lines](#), [apc.frame](#), [apc.fit](#)

### Examples

```
data( lungDK )
attach( lungDK )
apc1 <- apc.fit( A=Ax, P=Px, D=D, Y=Y/10^5 )
fp <- apc.plot( apc1 )
apc.lines( apc1, frame.par=fp, drift=1.01, col="red" )
for( i in 1:11 )
  apc.lines( apc1, frame.par=fp, drift=1+(i-6)/100, col=rainbow(12)[i] )
```

---

B.dk

*Births in Denmark by year and month of birth and sex*

---

### Description

The number of live births as entered from printed publications from Statistics Denmark.

### Usage

```
data(B.dk)
```

### Format

A data frame with 1248 observations on the following 4 variables.

year Year of birth  
month Month of birth  
m Number of male births  
f Number of female births

### Details

Division of births by month and sex is only available for the years 1957–69 and 2002ff. For the remaining period, the total no. births in each month is divided between the sexes so that the fraction of boys is equal to the overall fraction for the years where the sex information is available.

There is a break in the series at 1920, when Sonderjylland was joined to Denmark.

### Source

Statistiske Undersogelser nr. 19: Befolkningsudvikling og sundhedsforhold 1901-60, Copenhagen 1966. Befolkningens bevaegelser 1957. Befolkningens bevaegelser 1958. ... Befolkningens bevaegelser 2003. Befolkningens bevaegelser 2004. Vital Statistics 2005. Vital Statistics 2006.

**Examples**

```

data( B.dk )
str( B.dk )
attach( B.dk )
# Plot the no of births and the M/F-ratio
par( las=1, mar=c(4,4,2,4) )
matplot( year+(month-0.5)/12,
         cbind( m, f ),
         bty="n", col=c("blue","red"), lty=1, lwd=1, type="l",
         ylim=c(0,5000),
         xlab="Date of birth", ylab="" )
usr <- par()$usr
mtext( "Monthly no. births in Denmark", side=3, adj=0, at=usr[1], line=1/1.6 )
text( usr[1:2] %% cbind(c(19,1),c(19,1))/20,
      usr[3:4] %% cbind(c(1,19),c(2,18))/20, c("Boys","Girls"), col=c("blue","red"), adj=0 )
lines( year+(month-0.5)/12, (m/(m+f)-0.5)*30000, lwd=1 )
axis( side=4, at=(seq(0.505,0.525,0.005)-0.5)*30000, labels=c("", "", "", "", ""), tcl=-0.3 )
axis( side=4, at=(50:53/100-0.5)*30000, labels=50:53, tcl=-0.5 )
axis( side=4, at=(0.54-0.5)*30000, labels="% boys", tick=FALSE, mgp=c(3,0.1,0) )
abline( v=1920, col=gray(0.8) )

```

bdendo

*A case-control study of endometrial cancer***Description**

The bdendo data frame has 315 rows and 13 columns. These data concern a study in which each case of endometrial cancer was matched with 4 controls. Matching was by date of birth (within one year), marital status, and residence.

**Format**

This data frame contains the following columns:

- set: Case-control set: a numeric vector
- d: Case or control: a numeric vector (1=case, 0=control)
- gall: Gall bladder disease: a factor with levels No Yes.
- hyp: Hypertension: a factor with levels No Yes.
- ob: Obesity: a factor with levels No Yes.
- est: A factor with levels No Yes.
- dur: Duration of conjugated oestrogen therapy: an ordered factor with levels 0 < 1 < 2 < 3 < 4.
- non: Use of non oestrogen drugs: a factor with levels No Yes.
- duration: Months of oestrogen therapy: a numeric vector.
- age: A numeric vector.
- cest: Conjugated oestrogen dose: an ordered factor with levels 0 < 1 < 2 < 3.
- agegrp: A factor with levels 55-59 60-64 65-69 70-74 75-79 80-84
- age3: a factor with levels <64 65-74 75+

**Source**

Breslow NE, and Day N, Statistical Methods in Cancer Research. Volume I: The Analysis of Case-Control Studies. IARC Scientific Publications, IARC:Lyon, 1980.

**Examples**

```
data(bdendo)
```

---

```
bdendo11
```

*A 1:1 subset of the endometrial cancer case-control study*

---

**Description**

The `bdendo11` data frame has 126 rows and 13 columns. This is a subset of the dataset `bdendo` in which each case was matched with a single control.

**Source**

Breslow NE, and Day N, Statistical Methods in Cancer Research. Volume I: The Analysis of Case-Control Studies. IARC Scientific Publications, IARC:Lyon, 1980.

**Examples**

```
data(bdendo11)
```

---

```
births
```

*Births in a London Hospital*

---

**Description**

Data from 500 singleton births in a London Hospital

**Usage**

```
data(births)
```

**Format**

A data frame with 500 observations on the following 8 variables.

**id:** Identity number for mother and baby.  
**bweight:** Birth weight of baby.  
**lowbw:** Indicator for birth weight less than 2500 g.  
**gestwks:** Gestation period.  
**preterm:** Indicator for gestation period less than 37 weeks.  
**matage:** Maternal age.  
**hyp:** Indicator for maternal hypertension.  
**sex:** Sex of baby: 1:Male, 2:Female.

**Source**

Anonymous

**References**

Michael Hills and Bianca De Stavola (2002). A Short Introduction to Stata 8 for Biostatistics, Timberlake Consultants Ltd <http://www.timberlake.co.uk>

**Examples**

```
data(births)
```

---

blcaIT	<i>Bladder cancer mortality in Italian males</i>
--------	--------------------------------------------------

---

**Description**

Number of deaths from bladder cancer and person-years in the Italian male population 1955–1979, in ages 25–79.

**Format**

A data frame with 55 observations on the following 4 variables:

age: Age at death. Left endpoint of age class  
 period: Period of death. Left endpoint of period  
 D: Number of deaths  
 Y: Number of person-years.

**Examples**

```
data(blcaIT)
```

---

brv	<i>Bereavement in an elderly cohort</i>
-----	-----------------------------------------

---

**Description**

The brv data frame has 399 rows and 11 columns. The data concern the possible effect of marital bereavement on subsequent mortality. They arose from a survey of the physical and mental health of a cohort of 75-year-olds in one large general practice. These data concern mortality up to 1 January, 1990 (although further follow-up has now taken place).

Subjects included all lived with a living spouse when they entered the study. There are three distinct groups of such subjects: (1) those in which both members of the couple were over 75 and therefore included in the cohort, (2) those whose spouse was below 75 (and was not, therefore, part of the main cohort study), and (3) those living in larger households (that is, not just with their spouse).

**Format**

This data frame contains the following columns:

id: subject identifier, a numeric vector  
 couple: couple identifier, a numeric vector  
 dob: date of birth, a date  
 doe: date of entry into follow-up study, a date  
 dox: date of exit from follow-up study, a date  
 dosp: date of death of spouse, a date (if the spouse was still alive at the end of follow-up, this was coded to January 1, 2000)  
 fail: status at end of follow-up, a numeric vector (0=alive, 1=dead)  
 group: see Description, a numeric vector  
 disab: disability score, a numeric vector  
 health: perceived health status score, a numeric vector  
 sex: a factor with levels Male Female

**Source**

Jagger C, and Sutton CJ, Death after Marital Bereavement. *Statistics in Medicine*, 10:395-404, 1991. (Data supplied by Carol Jagger).

**Examples**

```
data(brv)
```

---

cal.yr

*Functions to convert character, factor and various date objects into a number, and vice versa.*

---

**Description**

Dates are converted to a numerical value, giving the calendar year as a fractional number. 1 January 1970 is converted to 1970.0, and other dates are converted by assuming that years are all 365.25 days long, so inaccuracies may arise, for example, 1 Jan 2000 is converted to 1999.999. Differences between converted values will be 1/365.25 of the difference between corresponding [Date](#) objects.

**Usage**

```
cal.yr( x, format="%Y-%m-%d", wh=NULL )
## S3 method for class 'cal.yr'
as.Date( x, ... )
```

**Arguments**

x A factor or character vector, representing a date in format format, or an object of class [Date](#), [POSIXlt](#), [POSIXct](#), [date](#), [dates](#) or [chron](#) (the latter two requires the [chron](#) package). If x is a data frame, all variables in the data-frame which are of one the classes mentioned are converted to class `cal.yr`. See argument wh, though.

format	Format of the date values if x is factor or character. If this argument is supplied and x is a dataframe, all character variables are converted to class <code>cal.yr</code> . Factors in the dataframe will be ignored.
wh	Indices of the variables to convert if x is a data frame. Can be either a numerical or character vector.
...	Arguments passed on from other methods.

### Value

`cal.yr` returns a numerical vector of the same length as x, of class `c("cal.yr", "numeric")`. If x is a data frame a dataframe with some of the columns converted to class `"cal.yr"` is returned.

`as.Date.cal.yr` returns a [Date](#) object.

### Author(s)

Bendix Carstensen, Steno Diabetes Center \& Dept. of Biostatistics, University of Copenhagen, <bxc@steno.dk>, <http://www.pubhealth.ku.dk/~bxc>

### See Also

[DateTimeClasses](#), [Date](#)

### Examples

```
# Character vector of dates:
birth <- c("14/07/1852", "01/04/1954", "10/06/1987", "16/05/1990",
          "01/01/1996", "01/01/1997", "01/01/1998", "01/01/1999")
# Proper conversion to class "Date":
birth.dat <- as.Date( birth, format="%d/%m/%Y" )
# Conversion of character to class "cal.yr"
bt.yr <- cal.yr( birth, format="%d/%m/%Y" )
# Back to class "Date":
bt.dat <- as.Date( bt.yr )
# Numerical calculation of days since 1.1.1970:
days <- Days <- (bt.yr-1970)*365.25
# Blunt assignment of class:
class( Days ) <- "Date"
# Then data.frame() to get readable output of results:
data.frame( birth, birth.dat, bt.yr, bt.dat, days, Days, round(Days) )
```

### Description

Given the basic outcome variables for a cohort study: the time of entry to the cohort, the time of exit and the reason for exit ("failure" or "censoring"), this function computes risk sets and generates a matched case-control study in which each case is compared with a set of controls randomly sampled from the appropriate risk set. Other variables may be matched when selecting controls.

**Usage**

```
ccwc(entry=0, exit, fail, origin=0, controls=1, match=list(), include=list(), data=NULL, silent=F)
```

**Arguments**

entry	Time of entry to follow-up
exit	Time of exit from follow-up
fail	Status on exit (1=Fail, 0=Censored)
origin	Origin of analysis time scale
controls	The number of controls to be selected for each case
match	List of categorical variables on which to match cases and controls
include	List of other variables to be carried across into the case-control study
data	Data frame in which to look for input variables
silent	If False, echos a . to the screen for each case-control set created; otherwise produces no output.

**Value**

The case-control study, as a dataframe containing:

Set	case-control set number
Map	row number of record in input dataframe
Time	failure time of the case in this set
Fail	failure status (1=case, 0=control)

These are followed by the matching variables, and finally by the variables in the include list

**Author(s)**

David Clayton

**References**

Clayton and Hills, Statistical Models in Epidemiology, Oxford University Press, Oxford:1993.

**See Also**

[Lexis](#)

**Examples**

```
#
# For the diet and heart dataset, create a nested case-control study
# using the age scale and matching on job
#
data(diet)
dietcc <- ccwc(doe, dox, chd, origin=dob, controls=2, data=diet,
              include=energy, match=job)
```

---

<code>ci.cum</code>	<i>Compute cumulative sum of estimates.</i>
---------------------	---------------------------------------------

---

**Description**

Computes the cumulative sum of parameter functions and the standard error of it. Optionally the exponential is applied to the parameter functions before it is cumulated.

**Usage**

```
ci.cum( obj,
        ctr.mat = NULL,
        subset = NULL,
        intl = 1,
        alpha = 0.05,
        Exp = TRUE,
        sample = FALSE )
```

**Arguments**

<code>obj</code>	A model object (of class <code>lm</code> , <code>glm</code> , <code>coxph</code> , <code>survreg</code> , <code>lme</code> , <code>mer</code> , <code>nls</code> , <code>gnlm</code> , <code>MIresult</code> or <code>polr</code> ).
<code>ctr.mat</code>	Contrast matrix defining the parameter functions from the parameters of the model.
<code>subset</code>	Subset of the parameters of the model to which <code>ctr.mat</code> should be applied.
<code>intl</code>	Interval length for the cumulation. Either a constant or a numerical vector of length <code>nrow(ctr.mat)</code> .
<code>alpha</code>	Significance level used when computing confidence limits.
<code>Exp</code>	Should the parameter function be exponentiated before it is cumulated?
<code>sample</code>	Should a sample of the original parameters be used to compute a cumulative rate?

**Details**

The purpose of this function is to compute cumulative rate based on a model for the rates. If the model is a multiplicative model for the rates, the purpose of `ctr.mat` is to return a vector of rates or log-rates when applied to the coefficients of the model. If log-rates are returned from the model, they should be exponentiated before cumulated, and the variances computed accordingly. Since log-linear models are the most common the `Exp` parameter defaults to `TRUE`.

**Value**

A matrix with 4 columns: Estimate, lower and upper c.i. and standard error. If `sample` is `TRUE`, a sampled vector is returned, if `sample` is numeric a matrix with `sample` columns is returned, each column a cumulative rate based on a random sample from the distribution of the parameter estimates.

**Author(s)**

Bendix Carstensen, <http://www.pubhealth.ku.dk/~bxc>

**See Also**

See also [ci.lin](#)

**Examples**

```
# Packages required for this example
library( splines )
library( survival )
data( lung )
par( mfrow=c(1,2) )

# Plot the Kaplan-meier-estimator
plot( survfit( Surv( time, status==2 ) ~ 1, data=lung ) )

# Declare data as Lexis
lungL <- Lexis( exit=list("tfd"=time),
               exit.status=(status==2)*1, data=lung )
summary( lungL )

# Cut the follow-up every 10 days
sL <- splitLexis( lungL, "tfd", breaks=seq(0,1100,10) )
str( sL )
summary( sL )

# Fit a Poisson model with a natural spline for the effect of time.
# Extract the variables needed
D <- status(sL, "exit")
Y <- dur(sL)
tB <- timeBand( sL, "tfd", "left" )
MM <- ns( tB, knots=c(50,100,200,400,700), intercept=TRUE )
mp <- glm( D ~ MM - 1 + offset(log(Y)),
          family=poisson, eps=10^-8, maxit=25 )

# Contrast matrix to extract effects, i.e. matrix to multiply with the
# coefficients to produce the log-rates: unique rows of MM, in time order.
T.pt <- sort( unique( tB ) )
T.wh <- match( T.pt, tB )
Lambda <- ci.cum( mp, ctr.mat=MM[T.wh,], intl=diff(c(0,T.pt)) )

# Put the estimated survival function on top of the KM-estimator
matlines( c(0,T.pt[-1]), exp(-Lambda[,1:3]), lwd=c(3,1,1), lty=1, col="Red" )

# Extract and plot the fitted intensity function
lambda <- ci.lin( mp, ctr.mat=MM[T.wh,], Exp=TRUE )
matplot( T.pt, lambda[,5:7]*10^3, type="l", lwd=c(3,1,1), col="black", lty=1,
        log="y", ylim=c(0.2,20) )
```

---

ci.lin *Compute linear functions of parameters with s.e.*

---

### Description

For a given model object the function computes a linear function of the parameters and the corresponding standard errors, p-values and confidence intervals.

### Usage

```
ci.lin( obj,
        ctr.mat = NULL,
        subset = NULL,
        subint = NULL,
        diffs = FALSE,
        fnam = !diffs,
        vcov = FALSE,
        alpha = 0.05,
        df = Inf,
        Exp = FALSE,
        sample = FALSE )
Wald( obj, H0=0, ... )
ci.mat( alpha = 0.05, df=Inf )
```

### Arguments

obj	A model object (of class <code>lm</code> , <code>glm</code> , <code>coxph</code> , <code>survreg</code> , <code>lme</code> , <code>mer</code> , <code>nls</code> , <code>gnlm</code> , <code>MIresult</code> or <code>polr</code> ).
ctr.mat	Contrast matrix to be multiplied to the parameter vector, i.e. the desired linear function of the parameters.
subset	The subset of the parameters to be used. If given as a character vector, the elements are in turn matched against the parameter names (using <code>grep</code> ) to find the subset. Repeat parameters may result from using a character vector. This is considered a facility.
subint	SUBset selection like for <code>subset</code> , except that elements of a character vector given as argument will be used to select subsets of parameters and only the INTersection of these is returned.
diffs	If TRUE, all differences between parameters in the subset are computed. <code>ctr.mat</code> is ignored. If <code>obj</code> inherits from <code>lm</code> , and <code>subset</code> is given as a string <code>subset</code> is used to search among the factors in the model and differences of all factor levels for the first match are shown. If <code>subset</code> does not match any of the factors in the model, all pairwise differences between parameters matching are returned.
fnam	Should the common part of the parameter names be included with the annotation of contrasts? Ignored if <code>diffs==T</code> . If a sting is supplied this will be prefixed to the labels.

vcov	Should the covariance matrix of the set of parameters be returned? If this is set, Exp is ignored. See details.
alpha	Significance level for the confidence intervals.
df	Integer. Number of degrees of freedom in the t-distribution used to compute the quantiles used to construct the confidence intervals.
Exp	If TRUE columns 5:6 are replaced with exp( columns 1,5,6 ).
sample	Logical or numerical. If TRUE or numerical a sample of the linear parameter function as defined by subset and ctr.mat is returned.
H0	The null values for the selected/transformed parameters to be tested by a Wald test. Must have the same length as the selected parameter vector.
...	Parameters passed on to ci.lin.

### Value

ci.lin returns a matrix with number of rows and rownames as ctr.mat. The columns are Estimate, Std.Err, z, P, 2.5% and 97.5%. If vcov=TRUE a list with components est, the desired functional of the parameters and vcov, the variance covariance matrix of this, is returned but not printed. If Exp==TRUE the confidence intervals for the parameters are replaced with three columns: exp(estimate,c.i.).

Wald computes a Wald test for a subset of (possibly linearly transformed) parameters. The selection of the subset of parameters is the same as for ci.lin. Using the ctr.mat argument makes it possible to do a Wald test for equality of parameters. Wald returns a named numerical vector of length 3, with names Chisq, d.f. and P.

ci.mat returns a 2 by 3 matrix with rows c(1,0,0) and c(0,-1,1)\*1.96, devised to post-multiply to a p by 2 matrix with columns of estimates and standard errors, so as to produce a p by 3 matrix of estimates and confidence limits. Used internally in ci.lin and ci.cum. The 1.96 is replaced by the appropriate quantile from the normal or t-distribution when arguments alpha and/or df are given.

### Author(s)

Bendix Carstensen, [BendixCarstensen.com](http://www.bendixcarstensen.com) & Michael Hills <http://www.mhills.pwp.blueyonder.co.uk/>

### See Also

See also [ci.cum](#)

### Examples

```
# Bogus data:
f <- factor( sample( letters[1:5], 200, replace=TRUE ) )
g <- factor( sample( letters[1:3], 200, replace=TRUE ) )
x <- rnorm( 200 )
y <- 7 + as.integer( f ) * 3 + 2 * x + 1.7 * rnorm( 200 )

# Fit a simple model:
mm <- lm( y ~ x + f + g )
ci.lin( mm )
```

```

ci.lin( mm, subset=3:6, diff=TRUE, fnam=FALSE )
ci.lin( mm, subset=3:6, diff=TRUE, fnam=TRUE )
ci.lin( mm, subset="f", diff=TRUE, fnam="f levels:" )
print( ci.lin( mm, subset="g", diff=TRUE, fnam="gee!:", vcov=TRUE ) )

# Use character defined subset to get ALL contrasts:
ci.lin( mm, subset="f", diff=TRUE )

# A Wald test of wheter the g-parameters are 0
Wald( mm, subset="g" )
# Wald test of whether the three first f-parameters are equal:
( CM <- rbind( c(1,-1,0,0), c(1,0,-1,0)) )
Wald( mm, subset="f", ctr.mat=CM )
# or alternatively
( CM <- rbind( c(1,-1,0,0), c(0,1,-1,0)) )
Wald( mm, subset="f", ctr.mat=CM )

```

ci.pd

*Compute confidence limits for a difference of two independent proportions.*

## Description

The usual formula for the c.i. of at difference of proportions is inaccurate. Newcombe has compared 11 methods and method 10 in his paper looks like a winner. It is implemented here.

## Usage

```

ci.pd(aa, bb=NULL, cc=NULL, dd=NULL,
      method = "Nc",
      alpha = 0.05, conf.level=0.95,
      digits = 3,
      print = TRUE,
      detail.labs = FALSE )

```

## Arguments

aa	Numeric vector of successes in sample 1. Can also be a matrix or array (see details).
bb	Successes in sample 2.
cc	Failures in sample 1.
dd	Failures in sample 2.
method	Method to use for calculation of confidence interval, see "Details".
alpha	Significance level
conf.level	Confidence level
print	Should an account of the two by two table be printed.
digits	How many digits should the result be rounded to if printed.
detail.labs	Should the computing of probability differences be reported in the labels.

**Details**

Implements method 10 from Newcombe(1998) (method="Nc") or from Agresti & Caffo(2000) (method="AC").

aa, bb, cc and dd can be vectors. If aa is a matrix, the elements [1:2, 1:2] are used, with successes aa[, 1:2]. If aa is a three-way table or array, the elements aa[1:2, 1:2, ] are used.

**Value**

A matrix with three columns: probability difference, lower and upper limit. The number of rows equals the length of the vectors aa, bb, cc and dd or, if aa is a 3-way matrix, dim(aa)[3].

**Author(s)**

Bendix Carstensen, Esa Laara. <http://www.biostat.ku.dk/~bxc>

**References**

RG Newcombe: Interval estimation for the difference between independent proportions. Comparison of eleven methods. *Statistics in Medicine*, 17, pp. 873-890, 1998.

A Agresti & B Caffo: Simple and effective confidence intervals for proportions and differences of proportions result from adding two successes and two failures. *The American Statistician*, 54(4), pp. 280-288, 2000.

**See Also**

[twoby2](#), [binom.test](#)

**Examples**

```
( a <- matrix( sample( 10:40, 4 ), 2, 2 ) )
ci.pd( a )
twoby2( t(a) )
prop.test( t(a) )
( A <- array( sample( 10:40, 20 ), dim=c(2,2,5) ) )
ci.pd( A )
ci.pd( A, detail.labs=TRUE, digits=3 )
```

---

clogistic

*Conditional logistic regression*

---

**Description**

Estimates a logistic regression model by maximizing the conditional likelihood. The conditional likelihood calculations are exact, and scale efficiently to strata with large numbers of cases.

**Usage**

```
clogistic(formula, strata, data, subset, na.action, init,
model = TRUE, x = FALSE, y = TRUE, contrasts = NULL,
iter.max=20, eps=1e-6, toler.chol = sqrt(.Machine$double.eps))
```

**Arguments**

formula	Model formula
strata	Factor describing membership of strata for conditioning
data	data frame containing the variables in the formula and strata arguments
subset	subset of records to use
na.action	missing value handling
init	initial values
model	a logical value indicating whether <i>model frame</i> should be included as a component of the returned value
x,y	logical values indicating whether the response vector and model matrix used in the fitting process should be returned as components of the returned value.
contrasts	an optional list. See the <code>contrasts.arg</code> of <code>model.matrix.default</code>
iter.max	maximum number of iterations
eps	Convergence tolerance. Iteration continues until the relative change in the conditional log likelihood is less than eps. Must be positive.
toler.chol	Tolerance used for detection of a singularity during a Cholesky decomposition of the variance matrix. This is used to detect redundant predictor variables. Must be less than eps.

**Value**

An object of class "clogistic". This is a list containing the following components:

coefficients	the estimates of the log-odds ratio parameters. If the model is over-determined there will be missing values in the vector corresponding to the redundant columns in the model matrix.
var	the variance matrix of the coefficients. Rows and columns corresponding to any missing coefficients are set to zero.
loglik	a vector of length 2 containing the log-likelihood with the initial values and with the final values of the coefficients.
iter	number of iterations used.
n	number of observations used. Observations may be dropped either because they are missing, or because they belong to a homogenous stratum. For more details on which observations were used, see <code>informative</code> below.
informative	if <code>model=TRUE</code> , a logical vector of length equal to the number of rows in the model frame. This indicates whether an observation is informative, in the sense that it makes a non-zero contribution to the log-likelihood. If <code>model=FALSE</code> , this is <code>NULL</code> .

The output will also contain the following, for documentation see the `glm` object: `terms`, `formula`, `call`, `contrasts`, `xlevels`, and, optionally, `x`, `y`, and/or `frame`.

**Author(s)**

Martyn Plummer

**See Also**

[glm](#)

**Examples**

```
data(bdendo)
clogistic(d ~ cest + dur, strata=set, data=bdendo)
```

---

contr.cum

*Contrast matrices*

---

**Description**

Return a matrix of contrasts for factor coding.

**Usage**

```
contr.cum(n)
contr.diff(n)
contr.2nd(n)
contr.orth(n)
```

**Arguments**

`n` A vector of levels for a factor, or the number of levels.

**Details**

These functions are used for creating contrast matrices for use in fitting regression models. The columns of the resulting matrices contain contrasts which can be used for coding a factor with `n` levels.

`contr.cum` gives a coding corresponding to successive differences between factor levels.

`contr.diff` gives a coding that correspond to the cumulative sum of the value for each level. This is not meaningful in a model where the intercept is included, therefore `n` columns is always returned.

`contr.2nd` gives contrasts corresponding to 2nd order differences between factor levels. Returns a matrix with `n-2` columns.

`contr.orth` gives a matrix with `n-2` columns, which are mutually orthogonal and orthogonal to the matrix `cbind(1,1:n)`

**Value**

A matrix with  $n$  rows and  $k$  columns, with  $k=n$  for `contr.diff`  $k=n-1$  for `contr.cum`  $k=n-2$  for `contr.2nd` and `contr.orth`.

**Author(s)**

Bendix Carstensen

**See Also**

[contr.treatment](#)

**Examples**

```
contr.cum(6)
contr.2nd(6)
contr.diff(6)
contr.orth(6)
```

---

cutLexis

*Cut follow-up at a specified date for each person.*

---

**Description**

Follow-up intervals in a Lexis object are divided into two sub-intervals: one before and one after an intermediate event. The intermediate event may denote a change of state, in which case the entry and exit status variables in the split Lexis object are modified.

**Usage**

```
cutLexis( data, cut, timescale = 1,
          new.state = nlevels(data$lex.Cst)+1,
          new.scale = FALSE,
          split.states = FALSE,
          progressive = FALSE,
          precursor.states = NULL,
          count = FALSE)
countLexis( data, cut, timescale = 1 )
```

**Arguments**

data	A Lexis object.
cut	A numeric vector with the times of the intermediate event. If a time is missing (NA) then the event is assumed to occur at time Inf. cut can also be a dataframe, see details.
timescale	The timescale that cut refers to. Numeric or character.

<code>new.state</code>	The state to which a transition occur at time cut. It may be a single value, which is then applied to all rows of data, or a vector with a separate value for each row
<code>new.scale</code>	Name of the timescale defined as "time since entry to new.state". If TRUE a name for the new scale is constructed. See details.
<code>split.states</code>	Should states that are not precursor states be split according to whether the intermediate event has occurred.
<code>progressive</code>	a logical flag that determines the changes to exit status. See details.
<code>precursor.states</code>	an optional vector of states to be considered as "less severe" than new.state. See Details below
<code>count</code>	logical indicating whether the countLexis options should be used. Specifying count=TRUE amounts to calling countLexis, in which case the arguments new.state, progressive and precursor.states will be ignored.

## Details

The `cutLexis` function allows a number of different ways of specifying the cutpoints and of modifying the status variable.

If the `cut` argument is a dataframe it must have columns `lex.id`, `cut` and `new.state`. The values of `lex.id` must be unique. In this case it is assumed that each row represents a cutpoint (on the timescale indicated in the argument `timescale`). This cutpoint will be applied to all records in data with the corresponding `lex.id`. This makes it possible to apply `cutLexis` to a split Lexis object.

If a `new.state` argument is supplied, the status variable is only modified at the time of the cut point. However, it is often useful to modify the status variable after the cutpoint when an important event occurs. There are three distinct ways of doing this.

If the `progressive=TRUE` argument is given, then a "progressive" model is assumed, in which the status can either remain the same or increase during follow-up, but never decrease. This assumes that the state variables `lex.Cst` and `lex.Xst` are either numeric or ordered factors. In this case, if `new.state=X`, then any exit status with a value less than `X` is replaced with `X`. The Lexis object must already be progressive, so that there are no rows for which the exit status is less than the entry status. If `lex.Cst` and `lex.Xst` are factors they must be ordered factors if `progressive=TRUE` is given.

As an alternative to the `progressive` argument, an explicit vector of precursor states, that are considered less severe than the new state, may be given. If `new.state=X` and `precursor.states=c(Y,Z)` then any exit status of `Y` or `Z` in the second interval is replaced with `X` and all other values for the exit status are retained.

The `countLexis` function is a variant of `cutLexis` when the cutpoint marks a recurrent event, and the status variable is used to count the number of events that have occurred. Times given in `cut` represent times of new events. Splitting with `countLexis` increases the status variable by 1. If the current status is `X` and the exit status is `Y` before cutting, then after cutting the entry status is `X`, `X+1` for the first and second intervals, respectively, and the exit status is `X+1`, `Y+1` respectively. Moreover the values of the status is increased by 1 for all intervals for all intervals after the cut for the person in question. Hence, a call to `countLexis` is needed for as many times as the person with most events. But also it is immaterial in what order the cutpoints are entered.

**Value**

A Lexis object, for which each follow-up interval containing the cutpoint is split in two: one before and one after the cutpoint. An extra time-scale is added; the time since the event at cut. This is NA for any follow-up prior to the intermediate event.

**Note**

The cutLexis function superficially resembles the splitLexis function. However, the splitLexis function splits on a vector of common cut-points for all rows of the Lexis object, whereas the cutLexis function splits on a single time point, which may be distinct for each row, modifies the status variables, and adds a new timescale.

**Author(s)**

Bendix Carstensen, Steno Diabetes Center, <bxc@steno.dk>, Martyn Plummer, IARC, <plummer@iarc.fr>.

**See Also**

[splitLexis](#), [Lexis](#), [summary.Lexis](#), [boxes.Lexis](#)

**Examples**

```
# A small artificial example
xx <- Lexis( entry=list(age=c(17,24,33,29),per=c(1920,1933,1930,1929)),
            duration=c(23,57,12,15), exit.status=c(1,2,1,2) )

xx
cut <- c(33,47,29,50)
cutLexis(xx, cut, new.state=3, precursor=1)
cutLexis(xx, cut, new.state=3, precursor=2)
cutLexis(xx, cut, new.state=3, precursor=1:2)
# The same as the last example
cutLexis(xx, cut, new.state=3)

# The same example with a factor status variable
yy <- Lexis(entry = list(age=c(17,24,33,29),per=c(1920,1933,1930,1929)),
            duration = c(23,57,12,15),
            entry.status = factor(rep("alpha",4),
            levels=c("alpha","beta","gamma")),
            exit.status = factor(c("alpha","beta","alpha","beta"),
            levels=c("alpha","beta","gamma")))

cutLexis(yy,c(33,47,29,50),precursor="alpha",new.state="gamma")
cutLexis(yy,c(33,47,29,50),precursor=c("alpha","beta"),new.state="aleph")

## Using a dataframe as cut argument
r1 <- data.frame( lex.id=1:3, cut=c(19,53,26), timescale="age", new.state=3 )
r1
cutLexis( xx, r1 )
cutLexis( xx, r1, precursor=1 )
cutLexis( xx, r1, precursor=0:2 )
```

```
## It is immaterial in what order splitting and cutting is done
xs <- splitLexis( xx, breaks=seq(0,100,10), time.scale="age" )
xs
xsC <- cutLexis(xs, r1, precursor=0 )

xC <- cutLexis( xx, r1, pre=0 )
xC
xCs <- splitLexis( xC, breaks=seq(0,100,10), time.scale="age" )
xCs
```

---

detrend	<i>Projection of a model matrix on to the orthogonal complement of a trend.</i>
---------	---------------------------------------------------------------------------------

---

### Description

The columns of the model matrix  $M$  is projected on the orthogonal complement to the matrix  $(1, t)$ . Orthogonality is defined w.r.t. an inner product defined by the weights `weight`.

### Usage

```
detrend( M, t, weight = rep(1, nrow(M)) )
```

### Arguments

<code>M</code>	A model matrix.
<code>t</code>	The trend defining a subspace. A numerical vector of length <code>nrow(M)</code>
<code>weight</code>	Weights defining the inner product of vectors $x$ and $y$ as $\sum(x*w*y)$ . A numerical vector of length <code>nrow(M)</code> , defaults to a vector of 1s.

### Details

The functions is intended to be used in parametrization of age-period-cohort models.

### Value

A full-rank matrix with columns orthogonal to  $(1, t)$ .

### Author(s)

Bendix Carstensen, Steno Diabetes Center, <http://www.pubhealth.ku.dk/~bxc>, with help from Peter Dalgaard.

### See Also

[projection.ip](#)

diet

*Diet and heart data***Description**

The diet data frame has 337 rows and 14 columns. The data concern a subsample of subjects drawn from larger cohort studies of the incidence of coronary heart disease (CHD). These subjects had all completed a 7-day weighed dietary survey while taking part in validation studies of dietary questionnaire methods. Upon the closure of the MRC Social Medicine Unit, from where these studies were directed, it was found that 46 CHD events had occurred in this group, thus allowing a serendipitous study of the relationship between diet and the incidence of CHD.

**Format**

This data frame contains the following columns:

- id: subject identifier, a numeric vector.
- doe: date of entry into follow-up study, a [Date](#) variable.
- dox: date of exit from the follow-up study, a [Date](#) variable.
- dob: date of birth, a [Date](#) variable.
- y: - number of years at risk, a numeric vector.
- fail: status on exit, a numeric vector (codes 1, 3, 11, and 13 represent CHD events)
- job: occupation, a factor with levels Driver Conductor Bank worker
- month: month of dietary survey, a numeric vector
- energy: total energy intake (KCal per day/100), a numeric vector
- height: (cm), a numeric vector
- weight: (kg), a numeric vector
- fat: fat intake (g/day), a numeric vector
- fibre: dietary fibre intake (g/day), a numeric vector
- energy.grp: high daily energy intake, a factor with levels <=2750 KCal >2750 KCal
- chd: CHD event, a numeric vector (1=CHD event, 0=no event)

**Source**

The data are described and used extensively by Clayton and Hills, *Statistical Models in Epidemiology*, Oxford University Press, Oxford:1993. They were rescued from destruction by David Clayton and reentered from paper printouts.

**Examples**

```
data(diet)
# Illustrate the follow-up in a Lexis diagram
Lexis.diagram( age=c(30,75), date=c(1965,1990),
              entry.date=cal.yr(doe), exit.date=cal.yr(dox), birth.date=cal.yr(dob),
              fail=(fail>0), pch.fail=c(NA,16), col.fail=c(NA,"red"), cex.fail=1.0,
              data=diet )
```

---

DMconv	<i>Conversion to diabetes</i>
--------	-------------------------------

---

**Description**

Data from a randomized intervention study ("Addition") where persons with prediabetic conditions are followed up for conversion to diabetes (DM). Conversion dates are interval censored. Original data are not published yet, so id-numbers have been changed and all dates have been randomly perturbed.

**Usage**

```
data(DMconv)
```

**Format**

A data frame with 1519 observations on the following 6 variables.

`id` Person identifier

`doe` Date of entry, i.e. first visit.

`dlw` Date last seen well, i.e. last visit without DM.

`dfi` Date first seen ill, i.e. first visit with DM.

`gtol` Glucose tolerance. Factor with levels: 1="IFG" (impaired fasting glucose), 2="IGT" (impaired glucose tolerance).

`grp` Randomization. Factor with levels: 1="Intervention", 2="Control".

**Source**

Signe Saetre Rasmussen, Steno Diabetes Center. The Addition Study.

**Examples**

```
data(DMconv)
str(DMconv)
head(DMconv)
```

---

DMlate

*The Danish National Diabetes Register.*

---

### Description

These two datasets each contain a random sample of 10,000 persons from the Danish National Diabetes Register. DMrand is a random sample from the register, whereas DMlate is a random sample among those with date of diagnosis after 1.1.1995.

### Usage

```
data(DMrand)
data(DMlate)
```

### Format

A data frame with 10000 observations on the following 7 variables.

sex Sex, a factor with levels M F

dobth Date of birth

dodm Date of inclusion in the register

dodth Date of death

dooad Date of 2nd prescription of OAD

doins Date of 2nd insulin prescription

dox Date of exit from follow-up.

### Details

All dates are given in fractions of years, so 1997.00 corresponds to 1 January 1997 and 1997.997 to 31 December 1997.

### Source

Danish National Board of Health.

### References

B Carstensen, JK Kristensen, P Ottosen and K Borch-Johnsen: The Danish National Diabetes Register: Trends in incidence, prevalence and mortality, *Diabetologia*, 51, pp 2187–2196, 2008.

In particular see the appendix at the end of the paper.

## Examples

```

data(DMlate)
str(DMlate)
dml <- Lexis( entry=list(Per=dodm, Age=dodm-dobth, DMdur=0 ),
             exit=list(Per=dox),
             exit.status=factor(!is.na(dodth),labels=c("DM","Dead")),
             data=DMlate )
# Split follow-up at Insulin
dmi <- cutLexis( dml, cut=dml$doin, new.state="Ins", pre="DM" )
summary( dmi )
# Introduce a new timescale
dmi <- cutLexis( dml, cut=dml$doin, new.state="Ins", pre="DM", new.scale=TRUE )
head( dmi )
# Split the states following insulin and explicitly name the new timescale
dmi <- cutLexis( dml, cut=dml$doin, new.state="Ins",
                pre="DM", new.scale="Instime", split.states=TRUE )
summary( dmi )

```

---

 effx

*Function to calculate effects*


---

## Description

The function calculates the effects of an exposure on a response, possibly stratified by a stratifying variable, and/or controlled for one or more confounding variables.

## Usage

```

effx( response, type = "metric",
      fup = NULL,
      exposure,
      strata = NULL,
      control = NULL,
      weights = NULL,
      alpha = 0.05,
      base = 1,
      digits = 3,
      data = NULL )

```

## Arguments

response	The response variable - must be numeric
type	The type of responsetype - must be one of "metric", "binary", "failure", or "count"
fup	The fup variable contains the follow-up time for a failure response. This must be numeric.
exposure	The exposure variable can be numeric or a factor

strata	The strata stratifying variable - must be a factor
control	The control variable(s) - these are passed as a list if there are more than one.
weights	Frequency weights for binary response only
base	Baseline for the effects of a categorical exposure, default 1
digits	Number of significant digits for the effects, default 3
alpha	1 - confidence level
data	data refers to the data used to evaluate the function

### Details

The function is a wrapper for glm. Effects are calculated as differences in means for a metric response, odds ratios for a binary response, and rate ratios for a failure or count response.

The k-1 effects for a categorical exposure with k levels are relative to a baseline which, by default, is the first level. The effect of a metric (quantitative) exposure is calculated per unit of exposure.

The exposure variable can be numeric or a factor, but if it is an ordered factor the order will be ignored.

### Value

comp1	Effects of exposure
comp2	Tests of significance

### Author(s)

Michael Hills

### References

[www.mhills.pwp.blueyonder.co.uk](http://www.mhills.pwp.blueyonder.co.uk)

### Examples

```
library(Epi)
data(births)
births$hyp <- factor(births$hyp,labels=c("normal","hyper"))
births$sex <- factor(births$sex,labels=c("M","F"))

# bweight is the birth weight of the baby in gms, and is a metric
# response (the default)

# effect of hypertension on birth weight
effx(bweight,exposure=hyp,data=births)
# effect of hypertension on birth weight stratified by sex
effx(bweight,exposure=hyp,strata=sex,data=births)
# effect of hypertension on birth weight controlled for sex
effx(bweight,exposure=hyp,control=sex,data=births)
# effect of gestation time on birth weight
effx(bweight,exposure=gestwks,data=births)
```

```
# effect of gestation time on birth weight stratified by sex
effx(bweight,exposure=gestwks,strata=sex,data=births)
# effect of gestation time on birth weight controlled for sex
effx(bweight,exposure=gestwks,control=sex,data=births)

# lowbw is a binary response coded 1 for low birth weight and 0 otherwise
# effect of hypertension on low birth weight
effx(lowbw,type="binary",exposure=hyp,data=births)
# etc.
```

---

effx.match	<i>Function to calculate effects for individually matched case-control studies</i>
------------	------------------------------------------------------------------------------------

---

### Description

The function calculates the effects of an exposure on a response, possibly stratified by a stratifying variable, and/or controlled for one or more confounding variables.

### Usage

```
effx.match(response,
  exposure,
  match,
  strata=NULL,
  control=NULL,
  base=1,
  digits=3,
  alpha=0.05,
  data=NULL)
```

### Arguments

response	The response variable - must be numeric
exposure	The exposure variable can be numeric or a factor
match	The variable which identifies the matched sets
strata	The strata stratifying variable - must be a factor
control	The control variable(s). These are passed as a list if there are more than one of them.
base	Baseline for the effects of a categorical exposure, default 1
digits	Number of significant digits for the effects, default 3
alpha	1 - confidence level
data	data refers to the data used to evaluate the function

**Details**

Effects are calculated odds ratios. The function is a wrapper for `clogit`, from the `survival` package. The  $k-1$  effects for a categorical exposure with  $k$  levels are relative to a baseline which, by default, is the first level. The effect of a metric (quantitative) exposure is calculated per unit of exposure. The exposure variable can be numeric or a factor, but if it is an ordered factor the order will be ignored.

**Value**

<code>comp1</code>	Effects of exposure
<code>comp2</code>	Tests of significance

**Author(s)**

Michael Hills

**References**

[www.mhills.pwp.blueyonder.co.uk](http://www.mhills.pwp.blueyonder.co.uk)

**Examples**

```
library(Epi)
library(survival)
data(bdendo)

# d is the case-control variable, set is the matching variable.
# The variable est is a factor and refers to estrogen use (no,yes)
# The variable hyp is a factor with 2 levels and refers to hypertension (no, yes)
# effect of est on the odds of being a case
effx.match(d,exposure=est,match=set,data=bdendo)
# effect of est on the odds of being a case, stratified by hyp
effx.match(d,exposure=est,match=set,strata=hyp,data=bdendo)
# effect of est on the odds of being a case, controlled for hyp
effx.match(d,exposure=est,match=set,control=hyp,data=bdendo)
```

---

ewrates

*Rates of lung and nasal cancer mortality, and total mortality.*

---

**Description**

England and Wales mortality rates from lung cancer, nasal cancer, and all causes 1936 - 1980. The 1936 rates are repeated as 1931 rates in order to accomodate follow up for the [nickel](#) study.

**Usage**

```
data(ewrates)
```

**Format**

A data frame with 150 observations on the following 5 variables:

id:	Subject identifier (numeric)
year	Calendar period, 1931: 1931–35, 1936: 1936–40, ...
age	Age class: 10: 10–14, 15:15–19, ...
lung	Lung cancer mortality rate per 1,000,000 py.
nasal	Nasal cancer mortality rate per 1,000,000 py.
other	All cause mortality rate per 1,000,000 py.

**Source**

From Breslow and Day, Vol II, Appendix IX.

**Examples**

```
data(ewrates)
str(ewrates)
```

---

expand.data	<i>Function to expand data for regression analysis of interval censored data.</i>
-------------	-----------------------------------------------------------------------------------

---

**Description**

This is a utility function.

The original records with `first.well`, `last.well` and `first.ill` are expanded to multiple records; several for each interval where the person is known to be well and one where the person is known to fail. At the same time columns for the covariates needed to estimate rates and the response variable are generated.

**Usage**

```
expand.data(fu, formula, breaks, data)
```

**Arguments**

fu	A 3-column matrix with <code>first.well</code> , <code>last.well</code> and <code>first.ill</code> in each row.
formula	Model formula, used to derive the model matrix.
breaks	Defines the intervals in which the baseline rate is assumed constant. All follow-up before the first and after the last break is discarded.
data	Dataframe in which <code>fu</code> and <code>formula</code> is interpreted.

**Value**

Returns a list with three components

rates.frame	Dataframe of covariates for estimation of the baseline rates — one per interval defined by breaks.
cov.frame	Dataframe for estimation of the covariate effects. A data-framed version of the designmatrix from formula.
y	Response vector.

**Author(s)**

Martyn Plummer, <plummer@iarc.fr>

**References**

B Carstensen: Regression models for interval censored survival data: application to HIV infection in Danish homosexual men. *Statistics in Medicine*, 15(20):2177-2189, 1996.

**See Also**

[Icens](#) [fit.mult](#) [fit.add](#)

---

 fit.add

---

*Fit an additive excess risk model to interval censored data.*


---

**Description**

Utility function.

The model fitted assumes a piecewise constant intensity for the baseline, and that the covariates act additively on the rate scale.

**Usage**

```
fit.add( y, rates.frame, cov.frame, start )
```

**Arguments**

y	Binary vector of outcomes
rates.frame	Dataframe expanded from the original data by <a href="#">expand.data</a> , corresponding to covariates for the rate parameters.
cov.frame	do., but covariates corresponding to the formula argument of <a href="#">Icens</a>
start	Starting values for the rate parameters. If not supplied, then starting values are generated.

**Value**

A list with one component:

rates            A glm object from a binomial model with log-link function.

**Author(s)**

Martyn Plummer, <plummer@iarc.fr>

**References**

B Carstensen: Regression models for interval censored survival data: application to HIV infection in Danish homosexual men. *Statistics in Medicine*, 15(20):2177-2189, 1996.

CP Farrington: Interval censored survival data: a generalized linear modelling approach. *Statistics in Medicine*, 15(3):283-292, 1996.

**See Also**

[Icens fit.mult](#)

**Examples**

```
data( HIV.dk )
```

---

```
fit.baseline
```

*Fit a piecewise constant intensity model for interval censored data.*

---

**Description**

Utility function

Fits a binomial model with logarithmic link, with `y` as outcome and covariates in `rates.frame` to estimate rates in the intervals between breaks.

**Usage**

```
fit.baseline( y, rates.frame, start )
```

**Arguments**

<code>y</code>	Binary vector of outcomes
<code>rates.frame</code>	Dataframe expanded from the original data by <a href="#">expand.data</a>
<code>start</code>	Starting values for the rate parameters. If not supplied, then starting values are generated.

**Value**

A `glm` object, with binomial error and logarithmic link.

**Author(s)**

Martyn Plummer, <plummer@iarc.fr>

**See Also**

[fit.add](#) [fit.mult](#)

---

 fit.mult

*Fits a multiplicative relative risk model to interval censored data.*

---

**Description**

Utility function.

The model fitted assumes a piecewise constant baseline rate in intervals specified by the argument `breaks`, and a multiplicative relative risk function.

**Usage**

```
fit.mult( y, rates.frame, cov.frame, start )
```

**Arguments**

<code>y</code>	Binary vector of outcomes
<code>rates.frame</code>	Dataframe expanded from the original data by <a href="#">expand.data</a> , corresponding to covariates for the rate parameters.
<code>cov.frame</code>	do., but covariates corresponding to the formula argument of <a href="#">Icens</a>
<code>start</code>	Starting values for the rate parameters. If not supplied, then starting values are generated.

**Details**

The model is fitted by alternating between two generalized linear models where one estimates the underlying rates in the intervals, and the other estimates the log-relative risks.

**Value**

A list with three components:

<code>rates</code>	A <code>glm</code> object from a binomial model with log-link, estimating the baseline rates.
<code>cov</code>	A <code>glm</code> object from a binomial model with complementary log-log link, estimating the log-rate-ratios
<code>niter</code>	Number of iterations, a scalar

**Author(s)**

Martyn Plummer, <plummer@iarc.fr>, Bendix Carstensen, <bxc@steno.dk>

**References**

B Carstensen: Regression models for interval censored survival data: application to HIV infection in Danish homosexual men. *Statistics in Medicine*, 15(20):2177-2189, 1996.

CP Farrington: Interval censored survival data: a generalized linear modelling approach. *Statistics in Medicine*, 15(3):283-292, 1996.

**See Also**

[Icens fit.add](#)

**Examples**

```
data( HIV.dk )
```

---

float

*Calculate floated variances*

---

**Description**

Given a fitted model object, the `float()` function calculates floating variances (a.k.a. quasi-variances) for a given factor in the model.

**Usage**

```
float(object, factor, iter.max=50)
```

**Arguments**

<code>object</code>	a fitted model object
<code>factor</code>	character string giving the name of the factor of interest. If this is not given, the first factor in the model is used.
<code>iter.max</code>	Maximum number of iterations for EM algorithm

**Details**

The `float()` function implements the "floating absolute risk" proposal of Easton, Peto and Babiker(1992). This is an alternative way of presenting parameter estimates for factors in regression models, which avoids some of the difficulties of treatment contrasts. It was originally designed for epidemiological studies of relative risk, but the idea is widely applicable.

Treatment contrasts are not orthogonal. Consequently, the variances of treatment contrast estimates may be inflated by a poor choice of reference level, and the correlations between them may also

be high. The `float()` function associates each level of the factor with a "floating" variance (or quasi-variance), including the reference level. Floating variances are not real variances, but they can be used to calculate the variance error of contrast by treating each level as independent.

Plummer (2003) showed that floating variances can be derived from a covariance structure model applied to the variance-covariance matrix of the contrast estimates. This model can be fitted by minimizing the Kullback-Leibler information divergence between the true distribution of the parameter estimates and the simplified distribution given by the covariance structure model. Fitting is done using the EM algorithm.

In order to check the goodness-of-fit of the floating variance model, the `float()` function compares the standard errors predicted by the model with the standard errors derived from the true variance-covariance matrix of the parameter contrasts. The maximum and minimum ratios between true and model-based standard errors are calculated over all possible contrasts. These should be within 5 percent, or the use of the floating variances may lead to invalid confidence intervals.

### Value

An object of class `floated`. This is a list with the following components

<code>coef</code>	A vector of coefficients. These are the same as the treatment contrasts but the reference level is present with coefficient 0.
<code>var</code>	A vector of floating (or quasi-) variances
<code>limits</code>	The bounds on the accuracy of standard errors over all possible contrasts

### Note

Menezes(1999) and Firth and Menezes (2004) take a slightly different approach to this problem, using a pseudo-likelihood approach to fit the quasi-variance model. Their work is implemented in the package `qvcalc`.

### Author(s)

Martyn Plummer

### References

Easton DF, Peto J and Babiker GAG (1991) Floating absolute risk: An alternative to relative risk in survival and case control analysis avoiding an arbitrary reference group. *Statistics in Medicine*, **10**, 1025-1035.

Firth D and Mezezes RX (2004) Quasi-variances. *Biometrika* **91**, 65-80.

Menezes RX(1999) More useful standard errors for group and factor effects in generalized linear models. *D.Phil. Thesis*, Department of Statistics, University of Oxford.

Plummer M (2003) Improved estimates of floating absolute risk, *Statistics in Medicine*, **23**, 93-104.

### See Also

[ftrend](#), [qvcalc](#)

ftrend

*Fit a floating trend to a factor in generalized linear model***Description**

Fits a "floating trend" model to the given factor in a glm in a generalized linear model by centering covariates.

**Usage**

```
ftrend(object, ...)
```

**Arguments**

object	fitted lm or glm object. The model must not have an intercept term
...	arguments to the nlm function

**Details**

ftrend() calculates "floating trend" estimates for factors in generalized linear models. This is an alternative to treatment contrasts suggested by Greenland et al. (1999). If a regression model is fitted with no intercept term, then contrasts are not used for the first factor in the model. Instead, there is one parameter for each level of this factor. However, the interpretation of these parameters, and their variance-covariance matrix, depends on the numerical coding used for the covariates. If an arbitrary constant is added to the covariate values, then the variance matrix is changed.

The ftrend() function takes the fitted model and works out an optimal constant to add to the covariate values so that the covariance matrix is approximately diagonal. The parameter estimates can then be treated as approximately independent, thus simplifying their presentation. This is particularly useful for graphical display of dose-response relationships (hence the name).

Greenland et al. (1999) originally suggested centring the covariates so that their weighted mean, using the fitted weights from the model, is zero. This heuristic criterion is improved upon by ftrend() which uses the same minimum information divergence criterion as used by Plummer (2003) for floating variance calculations. ftrend() calls nlm() to do the minimization and will pass optional arguments to control it.

**Value**

A list with the following components

coef	coefficients for model with adjusted covariates.
vcov	Variance-covariance matrix of adjusted coefficients.

**Note**

The "floating trend" method is an alternative to the "floating absolute risk" method, which is implemented in the function float().

**Author(s)**

Martyn Plummer

**References**

Greenland S, Michels KB, Robins JM, Poole C and Willet WC (1999) Presenting statistical uncertainty in trends and dose-response relations, *American Journal of Epidemiology*, **149**, 1077-1086.

**See Also**[float](#)


---

gen.exp	<i>Generate covariates for drug-exposure follow-up from drug purchase records.</i>
---------	------------------------------------------------------------------------------------

---

**Description**

From records of drug purchase and possibly known treatment intensity, the time since first drug use and cumulative dose at prespecified times is computed. Optionally, lagged exposures are computed too, i.e. cumulative exposure a prespecified time ago.

**Usage**

```
gen.exp(purchase, id = "id", dop = "dop", amt = "amt", dpt = "dpt",
        fu, doe = "doe", dox = "dox",
        breaks,
        use.dpt = ( dpt %in% names(purchase) ),
        lags = NULL,
        push.max = Inf,
        pred.win = Inf,
        lag.dec = 1 )
```

**Arguments**

purchase	Data frame with columns id-person id, dop-date of purchase, amt-amount purchased, and optionally dpt-defined daily dose, that is how much is assumed to be ingested per unit time. The time unit used here is assumed to be the same as that used in dop, so despite the name it is not necessarily measured per day.
id	Name of the id variable in the data frame.
dop	Name of the date of purchase variable in the data frame.
amt	Name of the amount purchased variable in the data frame.
dpt	Name of the dose-per-time variable in the data frame.
fu	Data frame with follow-up period for each person, the person id variable must have the same name as in the purchase data frame.

doe	Name of the date of entry variable.
dox	Name of the date of exit variable.
use.dpt	Logical, should we use information on dose per time.
breaks	Numerical vector of time points where the time since exposure and the cumulative dose are computed.
lags	Numerical vector of lag-times used in computing lagged cumulative doses.
push.max	How much can purchases maximally be pushed forward in time. See details.
pred.win	The length of the window used for constructing the average dose per time used to compute the duration of the last purchase
lag.dec	How many decimals to use in the construction of names for the lagged exposure variables

### Details

Each purchase record is converted into a time-interval of exposure.

If `use.dpt` is TRUE then the dose per time information is used to compute the exposure interval associated with each purchase. Exposure intervals are stacked, that is each interval is put after any previous. This means that the start of exposure to a given purchase can be pushed into the future. The parameter `push.max` indicates the maximally tolerated push. If this is reached by a person, the assumption is that some of the purchased drug is not counted in the exposure calculations.

The `dpt` can either be a constant, basically translating the purchased amount into exposure time the same way for all persons, or it can be a vector with different treatment intensities for each purchase. In any case the cumulative dose is computed taking this into account.

If `use.dpt` is FALSE then the exposure from one purchase is assumed to stretch over the time to the next purchase, so we are effectively assuming different rates of dose per time between any two adjacent purchases. Moreover, with this approach, periods of non-exposure does not exist.

The intention of this function is to generate covariates for a particular drug for the entire follow-up of each person. The reason that the follow-up prior to drug purchase and post-exposure is included is that the covariates must be defined for these periods too, in order to be useful for analysis of disease outcomes.

### Value

A data frame with one record per follow-up interval between breaks, with columns:

`id` person id.

`dof` date of follow up, i.e. start of interval. Apart from possibly the first interval for each person, this will assume values in the set of the values in `breaks`.

`Y` the length of interval.

`tfi` time from first initiation of drug.

`tfc` time from latest cessation of drug.

`cdur` cumulative time on the drug.

`cdos` cumulative dose.

`ldos` suffixed with one value per element in `lags`, the latter giving the cumulative doses `lags` before `dof`.

**Author(s)**

Bendix Carstensen, <bxc@steno.dk>

**See Also**

[Lexis](#), [splitLexis](#)

**Examples**

```
# Construct a simple data frame of purchases for 3 persons
# The purchase units (in variable dose) correspond to
n <- c( 10, 17, 8 )
dop <- c( 1995.2+cumsum(sample(1:4/10,n[1],replace=TRUE)),
        1997.3+cumsum(sample(1:4/10,n[2],replace=TRUE)),
        1997.3+cumsum(sample(1:4/10,n[3],replace=TRUE)) )
amt <- sample( 1:3/15, sum(n), replace=TRUE )
dpt <- sample( 15:20/25, sum(n), replace=TRUE )
dfr <- data.frame( id = rep(1:3,n),
                  dop,
                  amt = amt,
                  dpt = dpt )

round( dfr, 3 )
# Construct a simple dataframe for follow-up periods for these 3 persons
fu <- data.frame( id = 1:3,
                 doe = c(1995,1997,1996)+1:3/4,
                 dox = c(2001,2003,2002)+1:3/5 )

round( fu, 3 )
dpos <- gen.exp( dfr,
               fu = fu,
               breaks = seq(1990,2015,0.5),
               lags = 2:3/5 )
xpos <- gen.exp( dfr,
               fu = fu,
               use.dpt = FALSE,
               breaks = seq(1990,2015,0.5),
               lags = 2:3/5 )

cbind( xpos, dpos )

# How many relevant columns
nvar <- ncol(xpos)-3
clrs <- rainbow(nvar)

# Show how the variables relate to the follow-up time
par( mfrow=c(3,1), mar=c(3,3,1,1), mgp=c(3,1,0)/1.6, bty="n" )
for( i in unique(xpos$id) )
matplot( xpos[xpos$id==i,"dof"],
        xpos[xpos$id==i,-(1:3)],
        xlim=range(xpos$dof), ylim=range(xpos[-(1:3)]),
        type="l", lwd=2, lty=1, col=clrs,
        ylab="", xlab="Date of follow-up" )
ytxt <- par("usr")[3:4]
ytxt <- ytxt[1] + (nvar:1)*diff(ytxt)/(nvar+2)
```

```
xtxt <- rep( sum(par("usr")[1:2]*c(0.98,0.02)), nvar )
text( xtxt, ytxt, colnames(xpos)[-(1:3)], font=2,
      col=c1rs, cex=1.5, adj=0 )
```

gmortDK

*Population mortality rates for Denmark in 5-years age groups.*

## Description

The gmortDK data frame has 418 rows and 21 columns.

## Format

This data frame contains the following columns:

- agr: Age group, 0:0–4, 5:5–9, ..., 90:90+.
- per: Calendar period, 38: 1938–42, 43: 1943–47, ..., 88:1988–92.
- sex: Sex, 1: male, 2: female.
- risk: Number of person-years in the Danish population.
- dt: Number of deaths.
- rt: Overall mortality rate in cases per 1000 person-years, i.e.  $rt=1000*dt/risk$   
Cause-specific mortality rates in cases per 1000 person-years:
- r1: Infections
- r2: Cancer.
- r3: Tumors, benign, unspecific nature.
- r4: Endocrine, metabolic.
- r5: Blood.
- r6: Nervous system, psychiatric.
- r7: Cerebrovascular.
- r8: Cardiac.
- r9: Respiratory diseases, excl. cancer.
- r10: Liver, excl. cancer.
- r11: Digestive, other.
- r12: Genitourinary.
- r13: Ill-defined symptoms.
- r14: All other, natural.
- r15: Violent.

## Source

Statistics Denmark, National board of health provided original data. Michael Andersson grouped the causes of death.

## See Also

[thoro](#), [mortDK](#)

**Examples**

```
data(gmortDK)
```

---

```
hivDK
```

```
hivDK: seroconversion in a cohort of Danish men
```

---

**Description**

Data from a survey of HIV-positivity of a cohort of Danish men followed by regular tests from 1983 to 1989.

**Usage**

```
data(hivDK)
```

**Format**

A data frame with 297 observations on the following 7 variables.

`id` ID of the person  
`entry` Date of entry to the study. Date variable.  
`well` Date last seen seronegative. Date variable.  
`ill` Date first seen seroconverted. Date variable.  
`bth` Year of birth minus 1950.  
`pyr` Annual number of sexual partners.  
`us` Indicator of whether the person has visited the USA.

**Source**

Mads Melbye, Statens Seruminstitut.

**References**

Becker N.G. and Melbye M.: Use of a log-linear model to compute the empirical survival curve from interval-censored data, with application to data on tests for HIV-positivity, *Australian Journal of Statistics*, 33, 125–133, 1990.

Melbye M., Biggar R.J., Ebbesen P., Sarngadharan M.G., Weiss S.H., Gallo R.C. and Blattner W.A.: Seroepidemiology of HTLV-III antibody in Danish homosexual men: prevalence, transmission and disease outcome. *British Medical Journal*, 289, 573–575, 1984.

**Examples**

```
data(hivDK)  
str(hivDK)
```

---

 Icens

*Fits a regression model to interval censored data.*


---

### Description

The models fitted assumes a piecewise constant baseline rate in intervals specified by the argument `breaks`, and for the covariates either a multiplicative relative risk function (default) or an additive excess risk function.

### Usage

```
Icens( first.well, last.well, first.ill,
       formula, model.type=c("MRR","AER"), breaks,
       boot=FALSE, alpha=0.05, keep.sample=FALSE,
       data )
```

### Arguments

<code>first.well</code>	Time of entry to the study, i.e. the time first seen without event. Numerical vector.
<code>last.well</code>	Time last seen without event. Numerical vector.
<code>first.ill</code>	Time first seen with event. Numerical vector.
<code>formula</code>	Model formula for the log relative risk.
<code>model.type</code>	Which model should be fitted.
<code>breaks</code>	Breakpoints between intervals in which the underlying timescale is assumed constant. Any observation outside the range of <code>breaks</code> is discarded.
<code>boot</code>	Should bootstrap be performed to produce confidence intervals for parameters. If a number is given this will be the number of bootstrap samples. The default is 1000.
<code>alpha</code>	1 minus the confidence level.
<code>keep.sample</code>	Should the bootstrap sample of the parameter values be returned?
<code>data</code>	Data frame in which the times and formula are interpreted.

### Details

The model is fitted by calling either `fit.mult` or `fit.add`.

### Value

An object of class "Icens": a list with three components:

<code>rates</code>	A glm object from a binomial model with log-link, estimating the baseline rates, and the excess risk if "AER" is specified.
--------------------	-----------------------------------------------------------------------------------------------------------------------------

cov	A glm object from a binomial model with complementary log-log link, estimating the log-rate-ratios. Only if "MRR" is specified.
niter	Nuber of iterations, a scalar
boot.ci	If boot=TRUE, a 3-column matrix with estimates and 1-alpha confidence intervals for the parameters in the model.
sample	A matrix of the parameterestimates from the bootstrapping. Rows refer to parameters, columns to bootstrap samples.

**Author(s)**

Martyn Plummer, <plummer@iarc.fr>, Bendix Carstensen, <bxc@steno.dk>

**References**

- B Carstensen: Regression models for interval censored survival data: application to HIV infection in Danish homosexual men. *Statistics in Medicine*, 15(20):2177-2189, 1996.
- CP Farrington: Interval censored survival data: a generalized linear modelling approach. *Statistics in Medicine*, 15(3):283-292, 1996.

**See Also**

[fit.add fit.mult](#)

**Examples**

```
data( hivDK )
# Convert the dates to fractional years so that rates are
# expressed in cases per year
for( i in 2:4 ) hivDK[,i] <- cal.yr( hivDK[,i] )

m.RR <- Icens( entry, well, ill,
              model="MRR", formula=~pyr+us, breaks=seq(1980,1990,5),
              data=hivDK)
# Currently the MRR model returns a list with 2 glm objects.
round( ci.lin( m.RR$rates ), 4 )
round( ci.lin( m.RR$cov, Exp=TRUE ), 4 )
# There is actually a print method:
print( m.RR )

m.ER <- Icens( entry, well, ill,
              model="AER", formula=~pyr+us, breaks=seq(1980,1990,5),
              data=hivDK)
# There is actually a print method:
print( m.ER )
```

---

lep	<i>An unmatched case-control study of leprosy incidence</i>
-----	-------------------------------------------------------------

---

**Description**

The lep data frame has 1370 rows and 7 columns. This was an unmatched case-control study in which incident cases of leprosy in a region of N. Malawi were compared with population controls.

**Format**

This data frame contains the following columns:

id:	subject identifier: a numeric vector
d:	case/control status: a numeric vector (1=case, 0=control)
age:	a factor with levels 5-9 10-14 15-19 20-24 25-29 30-44 45+
sex:	a factor with levels male, female
bcg:	presence of vaccine scar, a factor with levels no yes
school:	schooling, a factor with levels none 1-5yrs 6-8yrs sec/tert
house:	housing, a factor with levels brick sunbrick wattle temp

**Source**

The study is described in more detail in Clayton and Hills, *Statistical Models in Epidemiology*, Oxford University Press, Oxford:1993.

**Examples**

```
data(lep)
```

---

Lexis	<i>Create a Lexis object</i>
-------	------------------------------

---

**Description**

Create an object of class Lexis to represent follow-up in multiple states on multiple time scales.

**Usage**

```
Lexis(entry, exit, duration, entry.status = 0, exit.status = 0, id, data,
      merge=TRUE, states )
```

**Arguments**

<code>entry</code>	a named list of entry times. Each element of the list is a numeric variable representing the entry time on the named time scale. All time scales must have the same units (e.g. years). The names of the timescales must be different from any column name in data.
<code>exit</code>	a named list of exit times.
<code>duration</code>	a numeric vector giving the duration of follow-up.
<code>entry.status</code>	a vector or a factor giving the status at entry
<code>exit.status</code>	a vector or factor giving status at exit. Any change in status during follow-up is assumed to take place exactly at the exit time.
<code>id</code>	a vector giving a unique identity value for each row of the Lexis object.
<code>data</code>	an optional data frame, list, or environment containing the variables. If not found in data, the variables are taken from the environment from which Lexis was called.
<code>merge</code>	a logical flag. If TRUE then the data argument will be coerced to a data frame and then merged with the resulting Lexis object.
<code>states</code>	A vector of labels for the states. If given, the state variables <code>lex.Cst</code> and <code>lex.Xst</code> are returned as factors with identical levels attributes.

**Details**

The analysis of long-term population-based follow-up studies typically requires multiple time scales to be taken into account, such as age, calendar time, or time since an event. A Lexis object is a data frame with additional attributes that allows these multiple time dimensions of follow-up to be managed.

Separate variables for current and exit state allows representation of multistate data.

Lexis objects are named after the German demographer Wilhelm Lexis (1837-1914), who is credited with the invention of the "Lexis diagram" for representing population dynamics simultaneously by several timescales.

The Lexis function creates a minimal Lexis object with only those variables required to define the follow-up history in each row. Additional variables can be merged into the Lexis object using the merge method for Lexis objects. This is the default.

There are also merge, subset and transform methods for Lexis objects. They work as the corresponding methods for data-frames but ensures that the result is a Lexis object.

**Value**

An object of class Lexis. This is represented as a data frame with a column for each time scale, and additional columns with the following names:

<code>lex.id</code>	Identification of the individual (record in data, that is).
<code>lex.dur</code>	Duration of follow-up.
<code>lex.Cst</code>	Entry status (Current state), i.e. the state in which the follow up takes place.
<code>lex.Xst</code>	Exit status (eXit state), i.e. that state taken up after dur in lex.Cst.

If `merge=TRUE` (the default) then the Lexis object will also contain all variables from the data argument.

### Note

Only two of the three arguments `entry`, `exit` and `duration` need to be given. If the third parameter is missing, it is imputed.

`entry`, `exit` must be numeric, using [Date](#) variables will cause some of the utilities to crash. Transformation by `cal.yr` is recommended.

If only either `exit` or `duration` are supplied it is assumed that `entry` is 0. This is only meaningful (and therefore checked) if there is only one timescale.

If any of `entry.status` or `exit.status` are of mode character, they will both be converted to factors.

If `entry.status` is not given, then its class is automatically set to that of `exit.status`. If `exit.status` is factor, the value of `entry.status` is set to the first level. This may be highly undesirable, and therefore noted. For example, if `exit.status` is character the first level will be the first in the alphabetical ordering; slightly unfortunate if values are `c("Well", "Diseased")`. If `exit.status` is logical, the value of `entry.status` set to `FALSE`. If `exit.status` is numeric, the value of `entry.status` set to 0.

If `entry.status` or `exit.status` are factors or character, the corresponding state variables in the returned Lexis object, `lex.Cst` and `lex.Xst` will be (unordered) factors with identical set of levels, namely the union of the levels of `entry.status` and `exit.status`.

### Author(s)

Martyn Plummer

### See Also

[plot.Lexis](#), [splitLexis](#), [cutLexis](#), [merge.Lexis](#), [subset.Lexis](#), [transform.Lexis](#), [summary.Lexis](#), [timeScales](#), [timeBand](#), [entry](#), [exit](#), [dur](#)

### Examples

```
# A small bogus cohort
xcoh <- structure( list( id = c("A", "B", "C"),
  birth = c("14/07/1952", "01/04/1954", "10/06/1987"),
  entry = c("04/08/1965", "08/09/1972", "23/12/1991"),
  exit = c("27/06/1997", "23/05/1995", "24/07/1998"),
  fail = c(1, 0, 1) ),
  .Names = c("id", "birth", "entry", "exit", "fail"),
  row.names = c("1", "2", "3"),
  class = "data.frame" )

# Convert the character dates into numerical variables (fractional years)
xcoh <- cal.yr( xcoh, format="%d/%m/%Y", wh=2:4 )
# See how it looks
xcoh
```

```

# Define as Lexis object with timescales calendar time and age
Lcoh <- Lexis( entry = list( per=entry ),
              exit = list( per=exit, age=exit-birth ),
              exit.status = fail,
              data = xcoh )

Lcoh

# Using character states may have undesired effects:
xcoh$Fail <- c("Dead","Well","Dead")
Lexis( entry = list( per=entry ),
       exit = list( per=exit, age=exit-birth ),
       exit.status = Fail,
       data = xcoh )

# unless you order the levels correctly
( xcoh$Fail <- factor( xcoh$Fail, levels=c("Well","Dead") ) )
Lexis( entry = list( per=entry ),
       exit = list( per=exit, age=exit-birth ),
       exit.status = Fail,
       data = xcoh )

```

---

Lexis.diagram

*Plot a Lexis diagram*


---

### Description

Draws a Lexis diagram, optionally with life lines from a cohort, and with lifelines of a cohort if supplied. Intended for presentation purposes.

### Usage

```

Lexis.diagram( age = c( 0, 60),
              alab = "Age",
              date = c( 1940, 2000 ),
              dlab = "Calendar time",
              int = 5,
              lab.int = 2*int,
              col.life = "black",
              lwd.life = 2,
              age.grid = TRUE,
              date.grid = TRUE,
              coh.grid = FALSE,
              col.grid = gray(0.7),
              lwd.grid = 1,
              las = 1,
              entry.date = NA,
              entry.age = NA,
              exit.date = NA,
              exit.age = NA,

```

```

risk.time = NA,
birth.date = NA,
  fail = NA,
  cex.fail = 1.1,
  pch.fail = c(NA,16),
  col.fail = rep( col.life, 2 ),
  data = NULL, ... )

```

### Arguments

age	Numerical vector of length 2, giving the age-range for the diagram
alab	Label on the age-axis.
date	Numerical vector of length 2, giving the calendar time-range for the diagram
dlab	label on the calendar time axis.
int	The interval between grid lines in the diagram. If a vector of length two is given, the first value will be used for spacing of age-grid and the second for spacing of the date grid.
lab.int	The interval between labelling of the grids.
col.life	Colour of the life lines.
lwd.life	Width of the life lines.
age.grid	Should grid lines be drawn for age?
date.grid	Should grid lines be drawn for date?
coh.grid	Should grid lines be drawn for birth cohorts (diagonals)?
col.grid	Colour of the grid lines.
lwd.grid	Width of the grid lines.
las	How are the axis labels plotted?
entry.date, entry.age, exit.date, exit.age, risk.time, birth.date	Numerical vectors defining lifelines to be plotted in the diagram. At least three must be given to produce lines. Not all subsets of three will suffice, the given subset has to define life lines. If insufficient data is given, no life lines are produced.
fail	Logical of event status at exit for the persons whose life lines are plotted.
pch.fail	Symbols at the end of the life lines for censorings ( <code>fail==0</code> ) and failures ( <code>fail != 0</code> ).
cex.fail	Expansion of the status marks at the end of life lines.
col.fail	Character vector of length 2 giving the colour of the failure marks for censorings and failures respectively.
data	Dataframe in which to interpret the arguments.
...	Arguments to be passed on to the initial call to plot.

## Details

The default unit for supplied variables are (calendar) years. If any of the variables `entry.date`, `exit.date` or `birth.date` are of class "Date" or if any of the variables `entry.age`, `exit.age` or `risk.time` are of class "difftime", they will be converted to calendar years, and plotted correctly in the diagram. The returned dataframe will then have columns of classes "Date" and "difftime".

## Value

If sufficient information on lifelines is given, a data frame with one row per person and columns with entry ages and dates, birth date, risk time and status filled in.

Side effect: a plot of a Lexis diagram is produced with the life lines in it is produced. This will be the main reason for using the function. If the primary aim is to illustrate follow-up of a cohort, then it is better to represent the follow-up in a `Lexis` object, and use the generic `plot.Lexis` function.

## Author(s)

Bendix Carstensen, <http://www.biostat.ku.dk/~bxc>

## See Also

[Life.lines](#), [Lexis.lines](#)

## Examples

```
Lexis.diagram( entry.age = c(3,30,45),
              risk.time = c(25,5,14),
              birth.date = c(1970,1931,1925.7),
              fail = c(TRUE,TRUE,FALSE) )
LL <- Lexis.diagram( entry.age = sample( 0:50, 17, replace=TRUE ),
                  risk.time = sample( 5:40, 17, r=TRUE),
                  birth.date = sample( 1910:1980, 17, r=TRUE ),
                  fail = sample( 0:1, 17, r=TRUE ),
                  cex.fail = 1.1,
                  lwd.life = 2 )
# Identify the persons' entry and exits
text( LL$exit.date, LL$exit.age, paste(1:nrow(LL)), col="red", font=2, adj=c(0,1) )
text( LL$entry.date, LL$entry.age, paste(1:nrow(LL)), col="blue", font=2, adj=c(1,0) )
data( nickel )
attach( nickel )
LL <- Lexis.diagram( age=c(10,100), date=c(1900,1990),
                  entry.age=age1st, exit.age=ageout, birth.date=dob,
                  fail=(icd %in% c(162,163)), lwd.life=1,
                  cex.fail=0.8, col.fail=c("green","red") )
abline( v=1934, col="blue" )
nickel[1:10,]
LL[1:10,]
```

---

Lexis.lines

*Draw life lines in a Lexis diagram.*


---

### Description

Add life lines to a Lexis diagram.

### Usage

```
Lexis.lines( entry.date = NA,
             exit.date = NA,
             birth.date = NA,
             entry.age = NA,
             exit.age = NA,
             risk.time = NA,
             col.life = "black",
             lwd.life = 2,
             fail = NA,
             cex.fail = 1,
             pch.fail = c(NA, 16),
             col.fail = col.life,
             data = NULL )
```

### Arguments

entry.date, entry.age, exit.date, exit.age, risk.time, birth.date	Numerical vectors defining lifelines to be plotted in the diagram. At least three must be given to produce lines. Not all subsets of three will suffice, the given subset has to define life lines. If insufficient data is given, no life lines are produced.
col.life	Colour of the life lines.
lwd.life	Width of the life lines.
fail	Logical of event status at exit for the persons whose life lines are plotted.
cex.fail	The size of the status marks at the end of life lines.
pch.fail	The status marks at the end of the life lines.
col.fail	Colour of the marks for censorings and failures respectively.
data	Data frame in which to interpret values.

### Value

If sufficient information on lifelines is given, a data frame with one row per person and columns with entry ages and dates, birth date, risk time and status filled in.

Side effect: Life lines are added to an existing Lexis diagram. Lexis.lines adds life lines to an existing plot.

**Author(s)**

Bendix Carstensen, Steno Diabetes Center, <http://www.biostat.ku.dk/~bxc>

**See Also**

[Lexis.diagram](#), [Life.lines](#)

**Examples**

```
Lexis.diagram( entry.age = c(3,30,45),
               risk.time = c(25,5,14),
               birth.date = c(1970,1931,1925.7),
               fail = c(TRUE,TRUE,FALSE) )
Lexis.lines( entry.age = sample( 0:50, 100, replace=TRUE ),
             risk.time = sample( 5:40, 100, r=TRUE),
             birth.date = sample( 1910:1980, 100, r=TRUE ),
             fail = sample(0:1,100,r=TRUE),
             cex.fail = 0.5,
             lwd.life = 1 )
```

---

Life.lines

*Compute dates/ages for life lines in a Lexis diagram*

---

**Description**

Fills out the missing information for follow up of persons in a Lexis diagram if sufficient information is given.

**Usage**

```
Life.lines( entry.date = NA,
            exit.date = NA,
            birth.date = NA,
            entry.age = NA,
            exit.age = NA,
            risk.time = NA )
```

**Arguments**

entry.date, exit.date, birth.date, entry.age, exit.age, risk.time

Vectors defining lifelines to be plotted in the diagram. At least three must be given to produce a result. Not all subsets of three will suffice, the given subset has to define life lines. If insufficient data is given, nothing is returned and a warning is given.

**Value**

Data frame with variables `entry.date`, `entry.age`, `exit.date`, `exit.age`, `risk.time`, `birth.date`, with all entries computed for each person. If any of `entry.date`, `exit.date` or `birth.date` are of class `Date` or if any of `entry.age`, `exit.age` or `risk.time` are of class `difftime` the date variables will be of class `Date` and the other three of class `difftime`.

**See Also**

[Lexis.diagram](#), [Lexis.lines](#)

**Examples**

```
( Life.lines( entry.age = c(3,30,45),
             risk.time = c(25,5,14),
             birth.date = c(1970,1931,1925.7) ) )

# Draw a Lexis diagram
Lexis.diagram()

# Compute entry and exit age and date.
( LL <- Life.lines( entry.age = c(3,30,45),
                  risk.time = c(25,5,14),
                  birth.date = c(1970,1931,1925.7) ) )
segments( LL[,1], LL[,2], LL[,3], LL[,4] ) # Plot the life lines.

# Compute entry and exit age and date, supplying a date variable
bd <- ( c(1970,1931,1925.7) - 1970 ) * 365.25
class( bd ) <- "Date"
( Life.lines( entry.age = c(3,30,45),
             risk.time = c(25,5,14),
             birth.date = bd ) )
```

---

lls

*Functions to manage and explore the workspace*


---

**Description**

These functions help you to find out what has gone wrong and to start afresh if needed.

**Usage**

```
lls(pos = 1, pat = "", all=FALSE, print=TRUE )
clear()
```

**Arguments**

pos	Numeric. What position in the search path do you want listed.
pat	Character. List only objects that have this string in their name.
all	Logical. Should invisible objects be printed too - see <a href="#">ls</a> to which this argument is passed.
print	Logical. Should the result be printed?

**Details**

`lls` is designed to give a quick overview of the name, mode, class and dimension of the object in your workspace. They may not always be what you think they are.

`clear` clears all your objects from workspace, and all attached objects too — it only leaves the loaded packages in the search path; thus allowing a fresh start without closing and restarting R.

**Value**

`lls` returns a data frame with four character variables: `codename`, `codemode`, `codeclass` and `code-size` and one row per object in the workspace (if `pos=1`). `size` is either the length or the dimension of the object. The data frame is by default printed with left-justified columns.

**Author(s)**

`lls`: Unknown. Modified by Bendix Carstensen from a long forgotten snatch.

`clear`: Michael Hills / David Clayton.

**Examples**

```
x <- 1:10
y <- rbinom(10, 1, 0.5)
m1 <- glm( y ~ x, family=binomial )
M <- matrix( 1:20, 4, 5 )
.M <- M
lls()
clear()
lls()
```

---

lungDK

*Male lung cancer incidence in Denmark*

---

**Description**

Male lung cancer cases and population risks time in Denmark, for the period 1943–1992 in ages 40–89.

**Usage**

```
data(lungDK)
```

**Format**

A data frame with 220 observations on the following 9 variables.

- A5: Left end point of the age interval, a numeric vector.
- P5: Left endpoint of the period interval, a numeric vector.
- C5: Left endpoint of the birth cohort interval, a numeric vector.
- up: Indicator of upper triangles of each age by period rectangle in the Lexis diagram. ( $up=(P5-A5-C5)/5$ ).
- Ax: The mean age of diagnosis (at risk) in the triangle.
- Px: The mean date of diagnosis (at risk) in the triangle.
- Cx: The mean date of birth in the triangle, a numeric vector.
- D: Number of diagnosed cases of male lung cancer.
- Y: Risk time in the male population, person-years.

**Details**

Cases and person-years are tabulated by age and date of diagnosis (period) as well as date of birth (cohort) in 5-year classes. Each observation in the dataframe corresponds to a triangle in a Lexis diagram. Triangles are classified by age and date of diagnosis, period of diagnosis and date of birth, all in 5-year groupings.

**Source**

The Danish Cancer Registry and Statistics Denmark.

**References**

For a more thorough exposition of statistical inference in the Lexis diagram, see: <http://staff.pubhealth.ku.dk/~bxc/APC/notes.pdf>

**Examples**

```
data( lungDK )
# Draw a Lexis diagram and show the number of cases in it.
attach( lungDK )
Lexis.diagram( age=c(40,90), date=c(1943,1993), coh.grid=TRUE )
text( Px, Ax, paste( D ), cex=0.7 )
```

---

M.dk

*Mortality in Denmark 1974 ff.*

---

**Description**

Mortality in one-year classes of age (0-98,99+) and period (1974 ff.) in Denmark.

**Usage**

```
data(M.dk)
```

**Format**

A data frame with 6400 observations on the following 6 variables.

A Age-class, 0-98, 99:99+

sex Sex. 1:males, 2:females

P Period (year) of death

D Number of deaths

Y Number of person-years

rate Mortality rate per 1000 person-years

**Details**

Deaths in ages over 100 are in the class labelled 99. Risk time is computed by tabulation of the risk time in `Y.dk`, except for the class 99+ where the average of the population size in ages 99+ at the first and last date of the year is used.

**Source**

<http://www.statistikbanken.dk/statbank5a/SelectTable/omrade0.asp?SubjectCode=02&PLanguage=1&ShowNews=OFF>

**Examples**

```
data(M.dk)
str(M.dk)
```

---

<code>merge.data.frame</code>	<i>Merge data frame with a Lexis object</i>
-------------------------------	---------------------------------------------

---

**Description**

Merge two data frames, or a data frame with a Lexis object.

**Usage**

```
## S3 method for class 'data.frame'
merge(x, y, ...)
```

**Arguments**

<code>x, y</code>	data frames, or objects to be coerced into one
<code>...</code>	optional arguments for the merge method

**Details**

This version of `merge.default` masks the one in the base. It ensures that, if either `x` or `y` is a Lexis object, then `merge.Lexis` is called.

**Value**

A merged Lexis object or data frame.

**Author(s)**

Martyn Plummer

**See Also**

[Lexis](#)

---

merge.Lexis	<i>Merge a Lexis object with a data frame</i>
-------------	-----------------------------------------------

---

**Description**

Merge additional variables from a data frame into a Lexis object.

**Usage**

```
## S3 method for class 'Lexis'
merge(x, y, id, by, ...)
```

**Arguments**

x	an object of class Lexis
y	a data frame
id	the name of the variable in y to use for matching against the variable lex.id in x.
by	if matching is not done by id, a vector of variable names common to both x and y
...	optional arguments to be passed to merge.data.frame

**Details**

A Lexis object can be considered as an augmented data frame in which some variables are time-dependent variables representing follow-up. The Lexis function produces a minimal object containing only these time-dependent variables. Additional variables may be added to a Lexis object using the merge method.

**Value**

A Lexis object with additional columns taken from the merged data frame.

**Note**

The variable given as the by.y argument must not contain any duplicate values in the data frame y.

**Author(s)**

Martyn Plummer

**See Also**[merge.data.frame](#), [subset.Lexis](#)

mh

*Mantel-Haenszel analyses of cohort and case-control studies***Description**

This function carries out Mantel-Haenszel comparisons in tabulated data derived from both cohort and case-control studies.

**Usage**

```
mh(cases, denom, compare=1, levels=c(1, 2), by=NULL,
   cohort=!is.integer(denom), confidence=0.9)
```

**Arguments**

cases	the table of case frequencies (a multiway array).
denom	the denominator table. For cohort studies this should be a table of person-years observation, while for case-control studies it should be a table of control frequencies.
compare	the dimension of the table which defines the comparison groups (can be referred to either by number or by name). The default is the first dimension of the table.
levels	a vector identifying (either by number or by name) the two groups to be compared. The default is the first two levels of the selected dimension.
by	the dimensions not to be collapsed in the Mantel-Haenszel computations. Thus, this argument defines the structure of the resulting tables of estimates and tests.
cohort	an indicator whether the data derive from a cohort or a case-control study. If the denominator table is stored as an integer, a case-control study is assumed.
confidence	the approximate coverage probability for the confidence intervals to be computed.

**Details**

Multiway tables of data are accepted and any two levels of any dimension can be chosen as defining the comparison groups. The rate (odds) ratio estimates and the associated significance tests may be collapsed over all the remaining dimensions of the table, or over selected dimensions only, so that tables of estimates and tests are computed.

**Value**

A list giving tables of rate (odds) ratio estimates, their standard errors (on a log scale), lower and upper confidence limits, chi-squared tests (1 degree of freedom) and the corresponding p-values. The result list also includes numerator and denominator of the Mantel-Haenszel estimates (q, r), and score test statistics and score variance (u, v).

**Side Effects**

None

**References**

Clayton, D. and Hills, M. : Statistical Models in Epidemiology, Oxford University Press (1993).

**See Also**

[Lexis](#)

**Examples**

```
# If d and y are 3-way tables of cases and person-years
# observation formed by tabulation by two confounders
# (named "C1" and "C2") an exposure of interest ("E"),
# the following command will calculate an overall
# Mantel-Haenszel comparison of the first two exposure
# groups.
#
# Generate some bogus data
dnam <- list( E=c("low","medium","high"), C1=letters[1:2], C2=LETTERS[1:4] )
d <- array( sample( 2:80, 24 ),
            dimnames=dnam, dim=sapply( dnam, length ) )
y <- array( abs( rnorm( 24, 227, 50 ) ),
            dimnames=dnam, dim=sapply( dnam, length ) )
mh(d, y, compare="E")
#
# Or, if exposure levels named "low" and "high" are to be
# compared and these are not the first two levels of E :
#
mh(d, y, compare="E", levels=c("low", "high"))
#
# If we wish to carry out an analysis which controls for C1,
# but examines the results at each level of C2:
#
mh(d, y, compare="E", by="C2")
#
# It is also possible to look at rate ratios for every
# combination of C1 and C2 :
#
mh(d, y, compare="E", by=c("C1", "C2"))
#
# If dimensions and levels of the table are unnamed, they must
```

# be referred to by number.  
#

---

mortDK

*Population mortality rates for Denmark in 1-year age-classes.*

---

## Description

The mortDK data frame has 1820 rows and 21 columns.

## Format

This data frame contains the following columns:

age: Age class, 0–89, 90:90+.  
per: Calendar period, 38: 1938–42, 43: 1943–47, ..., 88:1988-92.  
sex: Sex, 1: male, 2: female.  
risk: Number of person-years in the Danish population.  
dt: Number of deaths.  
rt: Overall mortality rate in cases per 1000 person-years, i.e.  $rt=1000*dt/risk$   
Cause-specific mortality rates in cases per 1000 person-years:  
r1: Infections  
r2: Cancer.  
r3: Tumors, benign, unspecific nature.  
r4: Endocrine, metabolic.  
r5: Blood.  
r6: Nervous system, psychiatric.  
r7: Cerebrovascular.  
r8: Cardiac.  
r9: Respiratory diseases, excl. cancer.  
r10: Liver, excl. cancer.  
r11: Digestive, other.  
r12: Genitourinary.  
r13: Ill-defined symptoms.  
r14: All other, natural.  
r15: Violent.

## Source

Statistics Denmark, National board of health provided original data. Michael Andersson grouped the causes of death.

## See Also

[thoro](#), [gmortDK](#)

**Examples**

```
data(mortDK)
```

---

```
msdata.Lexis
```

*Create a dataframe suitable for use with the mstate package.*

---

**Description**

The mstate package requires input in the form of a stacked dataset with specific variable names. This is provided by this function. The resulting dataframe contains the same information as the result of a call to [stack.Lexis](#).

**Usage**

```
msdata(obj, ...)
## S3 method for class 'Lexis'
msdata(obj, time.scale = timeScales(obj)[1], ...)
```

**Arguments**

obj	A <a href="#">Lexis</a> object.
time.scale	Name or number of timescale in the Lexis object.
...	Not used.

**Value**

A dataframe with the Lexis specific variables stripped, and with the following added: id, Tstart, Tstop, from, to, trans, status, which are used in the mstate package.

**Author(s)**

Bendix Carstensen, <bxc@steno.dk>, [www.biostat.ku.dk/~bxc](http://www.biostat.ku.dk/~bxc)

**See Also**

[stack.Lexis](#)

**Examples**

```
data(DMlate)
str(DMlate)
dml <- Lexis( entry=list(Per=dodm, Age=dodm-dobth, DMdur=0),
             exit=list(Per=dox),
             exit.status=factor(!is.na(dodth), labels=c("DM", "Dead")),
             data=DMlate )
dmi <- cutLexis( dml, cut=dml$doin, new.state="Ins", pre="DM" )
summary( dmi )
ms.dmi <- msdata.Lexis( dmi )
```

```
summary( dmi )  
# Check that all the transitions and person-years got across.  
with( ms.dmi, rbind( table(status,trans),  
                      tapply(Tstop-Tstart,trans,sum) ) ) )
```

---

N.dk

*Population size in Denmark*

---

### Description

The population size at 1st January in ages 0-99.

### Usage

```
data(N.dk)
```

### Format

A data frame with 7200 observations on the following 4 variables.

sex Sex, 1:males, 2:females

A Age. 0:0, 1:1, ..., 98:98, 99:99+

P Year

N Number of persons alive at 1st January year P

### Source

<http://www.statistikbanken.dk/statbank5a/SelectTable/omrade0.asp?SubjectCode=02&PLanguage=1&ShowNews=OFF>

### Examples

```
data(N.dk)  
str(N.dk)  
with(N.dk, addmargins(tapply(N, list(P, sex), sum), 2))  
with(subset(N.dk, P==max(P)), addmargins(tapply(N, list(A, sex), sum)))
```

---

N2Y *Create risk time (Person-Years) in Lexis triangles from population data.*

---

### Description

Data on population size at equidistant dates and age-classes are used to estimate person-time at risk in Lexis-triangles, i.e. classes classified by age, period AND cohort.

### Usage

```
N2Y( A, P, N,
     data = NULL,
     return.dfr = TRUE)
```

### Arguments

A	Name of the age-variable, which should be numeric, corresponding to the left endpoints of the age intervals.
P	Name of the period-variable, which should be numeric, corresponding to the date of population count.
N	The population size at date P in age class A.
data	A data frame in which arguments are interpreted.
return.dfr	Logical. Should the results be returned as a data frame (default TRUE) or as a table.

### Details

The calculation of the risk time from the population figures is done as described in: B. Carstensen: Age-Period-Cohort models for the Lexis diagram. *Statistics in Medicine*, 26: 3018-3045, 2007.

### Value

A data frame with variables A, P and Y, representing the mean age and period in the Lexis triangles and the person-time in them.

If `res.dfr=FALSE` a three-way table classified by the left end point of the age-classes and the periods and a factor `wh` taking the values `up` and `lo` corresponding to upper (early cohort) and lower (late cohort) Lexis triangles.

### Author(s)

Bendix Carstensen, [BendixCarstensen.com](http://BendixCarstensen.com)

### References

B. Carstensen: Age-Period-Cohort models for the Lexis diagram. *Statistics in Medicine*, 26: 3018-3045, 2007.

**See Also**

[splitLexis](#), [apc.fit](#)

**Examples**

```
# Danish population at 1 Jan each year by sex and age
data( N.dk )
# An illustrative subset
( Nx <- subset( N.dk, sex==1 & A<5 & P<1975 ) )
# Show the data in tabular form
xtabs( N ~ A + P, data=Nx )
# Lexis triangles as data frame
Nt <- N2Y( data=Nx, return.dfr=TRUE )
xtabs( Y ~ round(A,2) + round(P,2), data=Nt )
# Lexis triangles as a 3-dim array
ftable( N2Y( data=Nx, return.dfr=FALSE ) )
```

---

ncut

*Function to group a variable in intervals.*


---

**Description**

Cuts a continuous variable in intervals. As opposed to cut which returns a factor, ncut returns a numeric variable.

**Usage**

```
ncut(x, breaks, type="left" )
```

**Arguments**

x	A numerical vector.
breaks	Vector of breakpoints. NA will results for values below min(x) if type="left", for values above max(x) if type="right" and for values outside range(x) if type="mid"
type	Character: one of c("left", "right", "mid"), indicating whether the left, right or midpoint of the intervals defined in breaks is returned.

**Details**

The function uses the base function findInterval.

**Value**

A numerical vector of the same length as x.

**Author(s)**

Bendix Carstensen, Steno Diabetes Center, <bxc@steno.dk>, <http://www.biostat.ku.dk/~bxc/>, with essential input from Martyn Plummer, IARC.

**See Also**

[cut](#), [findInterval](#)

**Examples**

```
br <- c(-2,0,1,2.5)
x <- c( rnorm( 10 ), br, -3, 3 )
cbind( x, l=ncut( x, breaks=br, type="l" ),
       m=ncut( x, breaks=br, type="m" ),
       r=ncut( x, breaks=br, type="r" ) )[order(x),]
x <- rnorm( 200 )
plot( x, ncut( x, breaks=br, type="l" ), pch=16, col="blue", ylim=range(x) )
abline( 0, 1 )
abline( v=br )
points( x, ncut( x, breaks=br, type="r" ), pch=16, col="red" )
points( x, ncut( x, breaks=br, type="m" ), pch=16, col="green" )
```

---

nice

*Nice breakpoints*

---

**Description**

The function calls [pretty](#) for linear scale. For a log-scale nice are computed using a set of specified number in a decade.

**Usage**

```
nice(x, log = F, lpos = c(1, 2, 5), ...)
```

**Arguments**

x	Numerical vector to
log	Logical. Is the scale logartimic?
lpos	Numeric. Numbers between 1 and 10 giving the desired breakpoints in this interval.
...	Arguments passed on to <a href="#">pretty</a> if log=FALSE

**Value**

A vector of breakpoints.

**Author(s)**

Bendix Carstensen, <bxc@steno.dk>, <http://www.biostat.ku.dk/~bxc>

**See Also**

pretty

**Examples**

```
nice( exp( rnorm( 100 ) ), log=TRUE )
```

---

nickel

*A Cohort of Nickel Smelters in South Wales*

---

**Description**

The nickel data frame has 679 rows and 7 columns. The data concern a cohort of nickel smelting workers in South Wales and are taken from Breslow and Day, Volume 2. For comparison purposes, England and Wales mortality rates (per 1,000,000 per annum) from lung cancer (ICDs 162 and 163), nasal cancer (ICD 160), and all causes, by age group and calendar period, are supplied in the dataset [ewrates](#).

**Format**

This data frame contains the following columns:

id:	Subject identifier (numeric)
icd:	ICD cause of death if dead, 0 otherwise (numeric)
exposure:	Exposure index for workplace (numeric)
dob:	Date of birth (numeric)
age1st:	Age at first exposure (numeric)
agein:	Age at start of follow-up (numeric)
ageout:	Age at end of follow-up (numeric)

**Source**

Breslow NE, and Day N, Statistical Methods in Cancer Research. Volume II: The Design and Analysis of Cohort Studies. IARC Scientific Publications, IARC:Lyon, 1987.

**Examples**

```
data(nickel)  
str(nickel)
```

---

 occup

*A small occupational cohort*


---

### Description

This is the data that is behind the illustrative Lexis diagram in Breslow & Day's book on case-control studies.

### Usage

```
data(occup)
```

### Format

A data frame with 13 observations on the following 4 variables.

AoE a numeric vector, Age at Entry

DoE a numeric vector, Date of entry

DoX a numeric vector, Date of eXit

Xst eXit status D-event, W-withdrawal, X-censoring

### References

Breslow & Day: Statistical Methods in Cancer Research, vol 1: The analysis of case-control studies, figure 2.2, p. 48.

### Examples

```
data(occup)
lx <- Lexis( entry = list( per=DoE, age=AoE ),
            exit = list( per=DoX ),
            entry.status = "W",
            exit.status = Xst,
            data = occup )

plot( lx )
# Split follow-up in 5-year classes
sx <- splitLexis( lx, seq(1940,1960,5), "per" )
sx <- splitLexis( sx, seq( 40, 60,5), "age" )
plot( sx )

# Plot with a bit more paraphernalia and a device to get
# the years on the same physical scale on both axes
ypi <- 2.5 # Years per inch
x11( height=15/ypi+1, width=20/ypi+1 ) # add an inch in each direction for
par( mai=c(3,3,1,1)/4, mgp=c(3,1,0)/1.6 ) # the margins set in inches by mai=
plot(sx, las=1, col="black", lty.grid=1, lwd=2, type="l",
     xlim=c(1940,1960), ylim=c(40,55), xaxs="i", yaxs="i", yaxt="n",
     xlab="Calendar year", ylab="Age (years)")
```

```
axis( side=2, at=seq(40,55,5), las=1 )
points(sx,pch=c(NA,16)[(sx$lex.Xst=="D")+1] )
box()
# Annotation with the person-years
PY.ann.Lexis( sx, cex=0.8 )
```

---

pctab *Create percentages in a table*

---

### Description

Computes percentages and a margin of totals along a given margin of a table.

### Usage

```
pctab(TT, margin = length(dim(TT)), dec=1)
```

### Arguments

TT	A table or array object
margin	Which margin should be the the total?
dec	How many decimals should be printed? If 0 or FALSE nothing is printed

### Value

A table, where all dimensions except the one specified margin has two extra levels named "All" (where all entries are 100) and "N". The function prints the table with dec decimals.

### Author(s)

Bendix Carstensen, Steno Diabetes Center, <http://www.biostat.ku.dk/~bxc>.

### See Also

[addmargins](#)

### Examples

```
Aye <- sample( c("Yes","Si","Oui"), 177, replace=TRUE )
Bee <- sample( c("Hum","Buzz"), 177, replace=TRUE )
Sea <- sample( c("White","Black","Red","Dead"), 177, replace=TRUE )
A <- table( Aye, Bee, Sea )
A
ftable( pctab( A ) )
ftable( pctab( addmargins( A, 1 ), 3 ) )
round( ftable( pctab( addmargins( A, 1 ), 3 ), row.vars=3 ), 1)
```

plot.Lexis

*Lexis diagrams***Description**

The follow-up histories represented by a Lexis object can be plotted using one or two dimensions. The two dimensional plot is a Lexis diagram showing follow-up time simultaneously on two time scales.

**Usage**

```
## S3 method for class 'Lexis'
plot(x=Lexis( entry=list(Date=1900,Age=0), exit=list(Age=0) ),
      time.scale = NULL, type="l", breaks="lightgray", ...)
## S3 method for class 'Lexis'
points(x, time.scale = options()[["Lexis.time.scale"]] , ...)
## S3 method for class 'Lexis'
lines(x, time.scale = options()[["Lexis.time.scale"]], ...)
## S3 method for class 'Lexis'
PY.ann(x, time.scale = options()[["Lexis.time.scale"]], digits=1, ...)
```

**Arguments**

x	An object of class Lexis. The default is a bogus Lexis object, so that plot.Lexis can be called without the first argument and still produce a(n empty) Lexis diagram. Unless arguments xlim and ylim are given in this case the diagram is looking pretty daft.
time.scale	A vector of length 1 or 2 giving the time scales to be plotted either by name or numerical order
type	Character indication what to draw: "n" nothing (just set up the diagram), "l" - lifelines, "p" - endpoints of follow-up, "b" - both lifelines and endpoints.
breaks	a string giving the colour of grid lines to be drawn when plotting a split Lexis object. Grid lines can be suppressed by supplying the value NULL to the breaks argument
digits	Numerical. How many digits after the demimal points should be when plotting the person-years.
...	Further graphical parameters to be passed to the plotting methods. Grids can be drawn (behind the life lines) using the following parameters in plot: <ul style="list-style-type: none"> <li>• grid If logical, a background grid is set up using the axis ticks. If a list, the first component is used as positions for the vertical lines and the last as positions for the horizontal. If a numerical vector, grids on both axes are set up using the distance between the numbers.</li> <li>• col.grid="lightgray" Color of the background grid.</li> <li>• lty.grid=2 Line type for the grid.</li> <li>• coh.grid=FALSE Should a 45 degree grid be plotted?</li> </ul>

## Details

The plot method for Lexis objects traces “life lines” from the start to the end of follow-up. The points method plots points at the end of the life lines.

If time.scale is of length 1, the life lines are drawn horizontally, with the time scale on the X axis and the id value on the Y axis. If time.scale is of length 2, a Lexis diagram is produced, with diagonal life lines plotted against both time scales simultaneously.

If lex has been split along one of the time axes by a call to splitLexis, then vertical or horizontal grid lines are plotted (on top of the life lines) at the break points.

PY.ann writes the length of each (segment of) life line at the middle of the line. Not advisable to use with large cohorts. Another example is in the example file for [occup](#).

## Author(s)

Martyn Plummer

## See Also

[Lexis](#), [splitLexis](#)

## Examples

```
# A small bogus cohort
xcoh <- structure( list( id = c("A", "B", "C"),
                        birth = c("14/07/1952", "01/04/1957", "10/06/1987"),
                        entry = c("04/08/1965", "08/09/1972", "23/12/1991"),
                        exit = c("27/06/1997", "23/05/1995", "24/07/1998"),
                        fail = c(1, 0, 1) ),
                  .Names = c("id", "birth", "entry", "exit", "fail"),
                  row.names = c("1", "2", "3"),
                  class = "data.frame" )

# Convert the character dates into numerical variables (fractional years)
xcoh$bt <- cal.yr( xcoh$birth, format="%d/%m/%Y" )
xcoh$en <- cal.yr( xcoh$entry, format="%d/%m/%Y" )
xcoh$ex <- cal.yr( xcoh$exit , format="%d/%m/%Y" )

# See how it looks
xcoh

# Define as Lexis object with timescales calendar time and age
Lcoh <- Lexis( entry = list( per=en ),
              exit = list( per=ex, age=ex-bt ),
              exit.status = fail,
              data = xcoh )

# Default plot of follow-up
plot( Lcoh )
# Show follow-up time
PY.ann( Lcoh )
```

```

# Show exit status
plot( Lcoh, type="b" )
# Same but failures only
plot( Lcoh, type="b", pch=c(NA,16)[Lcoh$fail+1] )

# With a grid and deaths as endpoints
plot( Lcoh, grid=0:10*10, col="black" )
points( Lcoh, pch=c(NA,16)[Lcoh$lex.Xst+1] )
# With a lot of bells and whistles:
plot( Lcoh, grid=0:20*5, col="black", xaxs="i", yaxs="i",
      xlim=c(1960,2010), ylim=c(0,50), lwd=3, las=1 )
points( Lcoh, pch=c(NA,16)[Lcoh$lex.Xst+1], col="red", cex=1.5 )

```

---

plotEst

*Plot estimates with confidence limits*


---

### Description

Plots parameter estimates with confidence intervals, annotated with parameter names. A dot is plotted at the estimate and a horizontal line extending from the lower to the upper limit is superimposed.

### Usage

```

plotEst( ests,
        y = dim(ests)[1]:1,
        txt = rownames(ests),
        txtpos = y,
        ylim = range(y)-c(0.5,0),
        xlab = "",
        xtic = nice(ests[!is.na(ests)]), log = xlog),
        xlim = range( xtic ),
        xlog = FALSE,
        pch = 16,
        cex = 1,
        lwd = 2,
        col = "black",
        col.lines = col,
        col.points = col,
        vref = NULL,
        grid = FALSE,
        col.grid = gray(0.9),
        restore.par = TRUE )

linesEst( ests, y = dim(ests)[1]:1, pch = 16, cex = 1, lwd = 2,
         col="black", col.lines=col, col.points=col )

pointsEst( ests, y = dim(ests)[1]:1, pch = 16, cex = 1, lwd = 2,
         col="black", col.lines=col, col.points=col )

```

**Arguments**

ests	Matrix with three columns: Estimate, lower limit, upper limit. If a model object is supplied, <code>ci.lin</code> is invoked for this object first.
y	Vertical position of the lines.
txt	Annotation of the estimates.
txtpos	Vertical position of the text. Defaults to <code>y</code> .
ylim	Extent of the vertical axis.
xlab	Annotation of the horizontal axis.
xtic	Location of tickmarks on the x-axis.
xlim	Extent of the x-axis.
xlog	Should the x-axis be logarithmic?
pch	What symbol should be used?
cex	Expansion of the symbol.
col	Colour of the points and lines.
col.lines	Colour of the lines.
col.points	Colour of the symbol.
lwd	Thickness of the lines.
vref	Where should vertical reference line(s) be drawn?
grid	If TRUE, vertical gridlines are drawn at the tickmarks. If a numerical vector is given vertical lines are drawn at <code>grid</code> .
col.grid	Colour of the vertical gridlines
restore.par	Should the graphics parameters be restored? If set to FALSE the coordinate system will still be available for additional plotting, and <code>par("mai")</code> will still have the very large value set in order to make room for the labelling of the estimates.

**Details**

`plotEst` make a news plot, whereas `linesEst` and `pointsEst` (identical functions) adds to an existing plot.

**Value**

NULL

**Author(s)**

Bendix Carstensen, <[bx@steno.dk](mailto:bx@steno.dk)>, <http://www.pubhealth.ku.dk/~bxc>

**See Also**

`ci.lin`

**Examples**

```

# Bogus data and a linear model
f <- factor( sample( letters[1:5], 100, replace=TRUE ) )
x <- rnorm( 100 )
y <- 5 + 2 * as.integer( f ) + 0.8 * x + rnorm(100) * 2
m1 <- lm( y ~ f )

# Produce some confidence intervals for contrast to first level
( cf <- summary( m1 )$coef[2:5,1:2] %*% rbind( c(1,1,1), 1.96*(c(0,-1,1) ) ) )

# Plots with increasing amount of bells and whistles
par( mfcol=c(3,2), mar=c(3,3,2,1) )
plotEst( cf )
plotEst( cf, grid=TRUE )
plotEst( cf, grid=TRUE, cex=2, lwd=3 )
plotEst( cf, grid=TRUE, cex=2, col.points="red", col.lines="green" )
plotEst( cf, grid=TRUE, cex=2, col.points="red", col.lines="green",
         xlog=TRUE, xtic=c(1:8), xlim=c(0.8,6) )
rownames( cf )[1] <- "Contrast to fa:\n\n fb"
plotEst( cf, grid=TRUE, cex=2, col.points=rainbow(4), col.lines=rainbow(4), vref=1 )

```

---

 plotevent

*Plot Equivalence Classes*


---

**Description**

For interval censored data, segments of times between last.well and first.ill are plotted for each conversion in the data. It also plots the equivalence classes.

**Usage**

```
plotevent(last.well, first.ill, data)
```

**Arguments**

last.well	Time at which the individuals are last seen negative for the event
first.ill	Time at which the individuals are first seen positive for the event
data	Data with a transversal shape

**Details**

last.well and first.ill should be written as character in the function.

**Value**

Graph

**Author(s)**

Delphine Maucort-Boulch, Bendix Carstensen, Martyn Plummer

**References**

Carstensen B. Regression models for interval censored survival data: application to HIV infection in Danish homosexual men. *Stat Med.* 1996 Oct 30;15(20):2177-89.

Lindsey JC, Ryan LM. Tutorial in biostatistics methods for interval-censored data. *Stat Med.* 1998 Jan 30;17(2):219-38.

**See Also**

[Icens](#)

---

projection.ip

*Projection of columns of a matrix.*

---

**Description**

Projects the columns of the matrix M on the space spanned by the columns of the matrix X, with respect to the inner product defined by weight:  $\langle x|y \rangle = \sum(x*w*y)$ .

**Usage**

```
projection.ip(X, M, orth = FALSE, weight = rep(1, nrow(X)))
```

**Arguments**

X	Matrix defining the space to project onto.
M	Matrix of columns to be projected. Must have the same number of rows as X.
orth	Should the projection be on the orthogonal complement to span(X)?
weight	Weights defining the inner product. Numerical vector of length nrow(X).

**Value**

A matrix of full rank with columns in span(X).

**Author(s)**

Bendix Carstensen, Steno Diabetes Center, <http://www.pubhealth.ku.dk/~bxc>, with help from Peter Dalgaard.

**See Also**

[detrrend](#)

---

rateplot	<i>Functions to plot rates from a table classified by age and calendar time (period)</i>
----------	------------------------------------------------------------------------------------------

---

### Description

Produces plots of rates versus age, connected within period or cohort (Aplot), rates versus period connected within age-groups (Pplot) and rates and rates versus date of birth cohort (Cplot). rateplot is a wrapper for these, allowing to produce the four classical displays with a single call.

### Usage

```
rateplot( rates,
          which = c("ap", "ac", "pa", "ca"),
          age = as.numeric( dimnames( rates )[[1]] ),
          per = as.numeric( dimnames( rates )[[2]] ),
          grid = FALSE,
          a.grid = grid,
          p.grid = grid,
          c.grid = grid,
          ygrid = grid,
          col.grid = gray( 0.9 ),
          a.lim = range( age, na.rm=TRUE ) + c(0,diff( range( age ) )/30),
          p.lim = range( per, na.rm=TRUE ) + c(0,diff( range( age ) )/30),
          c.lim = NULL,
          ylim = range( rates[rates>0], na.rm=TRUE ),
          at = NULL,
          labels = paste( at ),
          a.lab = "Age at diagnosis",
          p.lab = "Date of diagnosis",
          c.lab = "Date of birth",
          ylab = "Rates",
          type = "l",
          lwd = 2,
          lty = 1,
          log.ax = "y",
          las = 1,
          ann = FALSE,
          a.ann = ann,
          p.ann = ann,
          c.ann = ann,
          xannx = 1/20,
          cex.ann = 0.8,
          a.thin = seq( 1, length( age ), 2 ),
          p.thin = seq( 1, length( per ), 2 ),
          c.thin = seq( 2, length( age ) + length( per ) - 1, 2 ),
          col = par( "fg" ),
```

```

a.col = col,
p.col = col,
c.col = col,
... )

Aplot( rates, age = as.numeric( dimnames( rates )[[1]] ),
       per = as.numeric( dimnames( rates )[[2]] ), grid = FALSE,
       a.grid = grid, ygrid = grid, col.grid = gray( 0.9 ),
       a.lim = range( age, na.rm=TRUE ), ylim = range( rates[rates>0], na.rm=TRUE ),
       at = NULL, labels = paste( at ), a.lab = names( dimnames( rates ) )[[1]],
       ylab = deparse( substitute( rates ) ), type = "l", lwd = 2, lty = 1,
       col = par( "fg" ), log.ax = "y", las = 1, c.col = col, p.col = col,
       c.ann = FALSE, p.ann = FALSE, xannx = 1/20, cex.ann = 0.8,
       c.thin = seq( 2, length( age ) + length( per ) - 1, 2 ),
       p.thin = seq( 1, length( per ), 2 ), p.lines = TRUE,
       c.lines = !p.lines, ... )

Pplot( rates, age = as.numeric( dimnames( rates )[[1]] ),
       per = as.numeric( dimnames( rates )[[2]] ), grid = FALSE,
       p.grid = grid, ygrid = grid, col.grid = gray( 0.9 ),
       p.lim = range( per, na.rm=TRUE ) + c(0,diff(range(per))/30),
       ylim = range( rates[rates>0], na.rm=TRUE ), p.lab = names( dimnames( rates ) )[[2]],
       ylab = deparse( substitute( rates ) ), at = NULL, labels = paste( at ),
       type = "l", lwd = 2, lty = 1, col = par( "fg" ), log.ax = "y",
       las = 1, ann = FALSE, cex.ann = 0.8, xannx = 1/20,
       a.thin = seq( 1, length( age ), 2 ), ... )

Cplot( rates, age = as.numeric( rownames( rates ) ),
       per = as.numeric( colnames( rates ) ), grid = FALSE,
       c.grid = grid, ygrid = grid, col.grid = gray( 0.9 ),
       c.lim = NULL, ylim = range( rates[rates>0], na.rm=TRUE ),
       at = NULL, labels = paste( at ), c.lab = names( dimnames( rates ) )[[2]],
       ylab = deparse( substitute( rates ) ), type = "l", lwd = 2, lty = 1,
       col = par( "fg" ), log.ax = "y", las = 1, xannx = 1/20, ann = FALSE,
       cex.ann = 0.8, a.thin = seq( 1, length( age ), 2 ), ... )

```

## Arguments

rates	A two-dimensional table (or array) with rates to be plotted. It is assumed that the first dimension is age and the second is period.
which	A character vector with elements from <code>c("ap", "ac", "apc", "pa", "ca")</code> , indication which plots should be produced. One plot per element is produced. The first letter indicates the x-axis of the plot, the remaining which groups should be connected, i.e. "pa" will plot rates versus period and connect age-classes, and "apc" will plot rates versus age, and connect both periods and cohorts.
age	Numerical vector giving the means of the age-classes. Defaults to the rownames of rates as numeric.

per	Numerical vector giving the means of the periods. Defaults to the columnnames of rates as numeric.
grid	Logical indicating whether a background grid should be drawn.
a.grid	Logical indicating whether a background grid on the age-axis should be drawn. If numerical it indicates the age-coordinates of the grid.
p.grid	do. for the period.
c.grid	do. for the cohort.
ygrid	do. for the rate-dimension.
col.grid	The colour of the grid.
a.lim	Range for the age-axis.
p.lim	Range for the period-axis.
c.lim	Range for the cohort-axis.
ylim	Range for the y-axis (rates).
at	Position of labels on the y-axis (rates).
labels	Labels to put on the y-axis (rates).
a.lab	Text on the age-axis. Defaults to "Age".
p.lab	Text on the period-axis. Defaults to "Date of diagnosis".
c.lab	Text on the cohort-axis. Defaults to "Date of birth".
ylab	Text on the rate-axis. Defaults to the name of the rate-table.
type	How should the curves be plotted. Defaults to "1".
lwd	Width of the lines. Defaults to 2.
lty	Which type of lines should be used. Defaults to 1, a solid line.
log.ax	Character with letters from "apcyr", indicating which axes should be logarithmic. "y" and "r" both refer to the rate scale. Defaults to "y".
las	see par.
ann	Should the curves be annotated?
a.ann	Logical indicating whether age-curves should be annotated.
p.ann	do. for period-curves.
c.ann	do. for cohort-curves.
xannx	The fraction that the x-axis is expanded when curves are annotated.
cex.ann	Expansion factor for characters annotating curves.
a.thin	Vector of integers indicating which of the age-classes should be labelled.
p.thin	do. for the periods.
c.thin	do. for the cohorts.
col	Colours for the curves.
a.col	Colours for the age-curves.
p.col	do. for the period-curves.
c.col	do. for the cohort-curves.
p.lines	Should rates from the same period be connected?
c.lines	Should rates from the same cohort be connected?
...	Additional arguments passed on to <code>matlines</code> when plotting the curves.

**Details**

Zero values of the rates are ignored. They are neither in the plot nor in the calculation of the axis ranges.

**Value**

NULL. The function is used for its side-effect, the plot.

**Author(s)**

Bendix Carstensen, Steno Diabetes Center, <http://www.pubhealth.ku.dk/~bxc/>

**See Also**

[apc.frame](#)

**Examples**

```
data( blcaIT )
attach(blcaIT)

# Table of rates:
bl.rate <- tapply( D, list(age,period), sum ) /
            tapply( Y, list(age,period), sum )
bl.rate

# The four classical plots:
par( mfrow=c(2,2) )
rateplot( bl.rate*10^6 )

# The labels on the vertical axis could be nicer:
rateplot( bl.rate*10^6, at=10^(-1:3), labels=c(0.1,1,10,100,1000) )

# More bells an whistles
par( mfrow=c(1,3), mar=c(3,3,1,1), oma=c(0,3,0,0), mgp=c(3,1,0)/1.6 )
rateplot( bl.rate*10^6, ylab="", ann=TRUE, which=c("AC", "PA", "CA"),
          at=10^(-1:3), labels=c(0.1,1,10,100,1000),
          col=topo.colors(11), cex.ann=1.2 )
```

---

Relevel

---

*Reorder and combine levels of a factor*


---

**Description**

The levels of a factor are re-ordered so that the levels specified by `ref` is first and the others are moved down. This is useful for `contr.treatment` contrasts which take the first level as the reference. Levels may also be combined.

**Usage**

```
Relevel(f, ref, first = TRUE, collapse="+" )
```

**Arguments**

f	An unordered factor
ref	The names or numbers of levels to be the first. If ref is a list, factor levels mentioned in each list element are combined. If the list is named the names are used as new factor levels.
first	Should the levels mentioned in ref come before those not?
collapse	String used when collapsing factor levels.

**Value**

An unordered factor.

**Examples**

```
ff <- factor( sample( letters[1:5], 100, replace=TRUE ) )
table( ff, Relevel( ff, list( AB=1:2, "Dee"=4, c(3,5) ) ) )
table( ff, rr=Relevel( ff, list( 5:4, Z=c("c","a") ), coll="-und-", first=FALSE ) )
```

---

 ROC

---

*Function to compute and draw ROC-curves.*


---

**Description**

Computes sensitivity, specificity and positive and negative predictive values for a test based on dichotomizing along the variable test, for prediction of stat. Alternatively a model formula may given, in which case the the linear predictor is the test variable and the response is taken as the true status variable. Plots curves of these and a ROC-curve.

**Usage**

```
ROC( test = NULL,
     stat = NULL,
     form = NULL,
     plot = c("sp", "ROC"),
     PS = is.null(test),
     PV = TRUE,
     MX = TRUE,
     MI = TRUE,
     AUC = TRUE,
     grid = seq(0,100,10),
     col.grid = gray( 0.9 ),
     cuts = NULL,
```

```

    lwd = 2,
    data = parent.frame(),
    ... )

```

### Arguments

test	Numerical variable used for prediction.
stat	Logical variable of true status.
form	Formula used in a logistic regression. If this is given, test and stat are ignored. If not given then both test and stat must be supplied.
plot	Character variable. If "sp", the a plot of sensitivity, specificity and predictive values against test is produced, if "ROC" a ROC-curve is plotted. Both may be given.
PS	logical, if TRUE the x-axis in the plot "ps"-plot is the the predicted probability for stat==TRUE, otherwise it is the scale of test if this is given otherwise the scale of the linear predictor from the logistic regression.
PV	Should sensitivity, specificity and predictive values at the optimal cutpoint be given on the ROC plot?
MX	Should the “optimal cutpoint” (i.e. where sens+spec is maximal) be indicated on the ROC curve?
MI	Should model summary from the logistic regression model be printed in the plot?
AUC	Should the area under the curve (AUC) be printed in the ROC plot?
grid	Numeric or logical. If FALSE no background grid is drawn. Otherwise a grid is drawn on both axes at grid percent.
col.grid	Colour of the grid lines drawn.
cuts	Points on the test-scale to be annotated on the ROC-curve.
lwd	Thickness of the curves
data	Data frame in which to interpret the variables.
...	Additional arguments for the plotting of the ROC-curve. Passed on to plot

### Value

A list with two components:

res	dataframe with variables sn, sp, pvp, pvn and fv. The latter is the unique values of test (for PS==FALSE ) or linear predictor from the logistic regression
lr	glm object with the logistic regression result used for construction of the ROC curve

0, 1 or 2 plots are produced according to the setting of plot.

### Author(s)

Bendix Carstensen, Steno Diabetes Center & University of Copenhagen, <http://www.biostat.ku.dk/~bxc>

**Examples**

```
x <- rnorm( 100 )
z <- rnorm( 100 )
w <- rnorm( 100 )
tigol <- function( x ) 1 - ( 1 + exp( x ) )^(-1)
y <- rbinom( 100, 1, tigol( 0.3 + 3*x + 5*z + 7*w ) )
ROC( form = y ~ x + z, plot="ROC" )
```

S.typh

*Salmonella Typhimurium outbreak 1996 in Denmark.***Description**

Matched case-control study of food poisoning.

**Format**

A data frame with 136 observations on the following 15 variables:

id: Person identification  
 set: Matched set indicator  
 case: Case-control status (1:case, 0:control)  
 age: Age of individual  
 sex: Sex of individual (1:male, 2:female)  
 abroad: Within the last two weeks visited abroad (1:yes, 0:no)  
 beef: Within the last two weeks eaten beef  
 pork: Within the last two weeks eaten pork  
 veal: Within the last two weeks eaten veal  
 poultry: Within the last two weeks eaten poultry  
 liverp: Within the last two weeks eaten liverpaste  
 veg: Within the last two weeks eaten vegetables  
 fruit: Within the last two weeks eaten fruit  
 egg: Within the last two weeks eaten eggs  
 plant7: Within the last two weeks eaten meat from plant no. 7

**Details**

In the fall of 1996 an unusually large number of Salmonella Typhimurium cases were recorded in Fyn county in Denmark. The Danish Zoonosis Centre set up a matched case-control study to find the sources. Cases and two age-, sex- and residency-matched controls were telephone interviewed about their food intake during the last two weeks.

The participants were asked at which retailer(s) they had purchased meat. Retailers were independently of this linked to meat processing plants, and thus participants were linked to meat processing plants. This way persons could be linked to (amongst other) plant no. 7.

**Source**

Tine Hald.

**References**

Molbak K and Hald T: Salmonella Typhimurium outbreak in late summer 1996. A Case-control study. (In Danish: Salmonella typhimurium udbrud paa Fyn sensommeren 1996. En case-kontrol undersogelse.) Ugeskrift for Laeger., 159(36):5372-7, 1997.

**Examples**

```
data(S.typh)
```

---

splitLexis	<i>Split follow-up time in a Lexis object</i>
------------	-----------------------------------------------

---

**Description**

The splitLexis function divides each row of a Lexis object into disjoint follow-up intervals according to the supplied break points.

**Usage**

```
splitLexis(lex, breaks, time.scale, tol=.Machine$double.eps^0.5)
```

**Arguments**

lex	an object of class Lexis
breaks	a vector of break points
time.scale	the name or number of the time scale to be split
tol	numeric value $\geq 0$ . Intervals shorter than this value are dropped

**Value**

An object of class Lexis with multiple rows for each row of the argument lex. Each row of the new Lexis object contains the part of the follow-up interval that falls inside one of the time bands defined by the break points.

The variables representing the various time scales, are appropriately updated in the new Lexis object. The entry and exit status variables are also updated according to the rule that the entry status is retained until the end of follow-up. All other variables are considered to represent variables that are constant in time, and so are replicated across all rows having the same id value.

**Note**

The splitLexis() function divides follow-up time into intervals using breakpoints that are common to all rows of the Lexis object. To split a Lexis object by break points that are unique to each row, use the cut.Lexis function.



```
tapply( dur(x2), list( timeBand(x2,"age","left"),
                      timeBand(x2,"per","left") ), sum )
```

---

stack.Lexis

*Functions to facilitate analysis of multistate models.*


---

## Description

stack.Lexis produces a stacked object suited for analysis of several transitions simultaneously.

## Usage

```
## S3 method for class 'Lexis'
stack(x, ...)
tmat( x, ... )
## S3 method for class 'Lexis'
tmat(x, Y=FALSE, ...)
```

## Arguments

x	A <a href="#">Lexis</a> object.
Y	Logical. Should the risk time be put in the diagonal? This is a facility which is used by <a href="#">boxes.Lexis</a> .
...	Not used.

## Value

tmat.Lexis returns a square transition matrix, classified by the levels of lex.Cst and lex.Xst, for every transition occurring the entry is the number of transitions occurring and NA in all other entries. If Y=TRUE, the diagonal will contain the risk time in each of the states.

stack.Lexis returns a dataframe to be used for analysis of multistate data when all transitions are modelled together, for example if some parameters are required to be the same for different transitions.

The dataframe has same variables as the original Lexis object, but with each record duplicated as many times as there are possible exits from the current state, lex.Cst. Two variables are added: lex.Fail, an indicator of whether an event for the transition names in lex.Tr has occurred or not. lex.Tr is a factor with levels made up of combinations of the levels of lex.Cst and lex.Xst that do occur together in x, joined by a "->".

## Author(s)

Bendix Carstensen, <bxc@steno.dk>, [www.biostat.ku.dk/~bxc](http://www.biostat.ku.dk/~bxc)

## See Also

[splitLexis](#) [cutLexis](#) [Lexis](#)

**Examples**

```

data(DMlate)
str(DMlate)
dml <- Lexis( entry=list(Per=dodm, Age=dodm-dobth, DMdur=0 ),
              exit=list(Per=dox),
              exit.status=factor(!is.na(dodth),labels=c("DM","Dead")),
              data=DMlate )
dmi <- cutLexis( dml, cut=dml$doins, new.state="Ins", pre="DM" )
summary( dmi )
ls.dmi <- stack( dmi )
str( ls.dmi )
# Check that all the transitions and person-years got across.
with( ls.dmi, rbind( table(lex.Fail,lex.Tr),
                    tapply(lex.dur,lex.Tr,sum) ) )

```

---

start.Lexis

*Time series methods for Lexis objects*


---

**Description**

Extract the entry time, exit time, status, or duration of follow-up from a Lexis object.

**Usage**

```

entry(x, time.scale = NULL, by.id=FALSE)
exit(x, time.scale = NULL, by.id=FALSE)
status(x, at="exit"          , by.id=FALSE)
dur(x,                        by.id=FALSE)

```

**Arguments**

x	an object of class Lexis.
time.scale	a string or integer indicating the time scale. If omitted, all times scales are used.
by.id	Logical, if TRUE, only one record per unique value of lex.id is returned; either the first, the last or for dur, the sum of lex.dur. If TRUE, the returned object have the lex.id as (row)names attribute.
at	string indicating the time point(s) at which status is to be measured.

**Value**

The entry and exit functions return a vector of entry times and exit times, respectively, on the requested time scale. If multiple time scales are requested, then a matrix is returned.

The status function returns a vector giving the status at entry or exit and dur returns a vector with the lengths of the follow-up intervals.

**Author(s)**

Martyn Plummer

**See Also**[Lexis](#)


---

stat.table	<i>Tables of summary statistics</i>
------------	-------------------------------------

---

**Description**

stat.table creates tabular summaries of the data, using a limited set of functions. A list of index variables is used to cross-classify summary statistics. It does NOT work inside with()!

**Usage**

```
stat.table(index, contents = count(), data, margins = FALSE)
## S3 method for class 'stat.table'
print(x, width=7, digits,...)
```

**Arguments**

index	A factor, or list of factors, used for cross-classification. If the list is named, then the names will be used when printing the table. This feature can be used to give informative labels to the variables.
contents	A function call, or list of function calls. Only a limited set of functions may be called (See Details below). If the list is named, then the names will be used when printing the table.
data	an optional data frame containing the variables to be tabulated. If this is omitted, the variables will be searched for in the calling environment.
margins	a logical scalar or vector indicating which marginal tables are to be calculated. If a vector, it should be the same length as the index argument: values corresponding to TRUE will be retained in marginal tables.
x	an object of class stat.table.
width	a scalar giving the minimum column width when printing.
digits	a scalar, or named vector, giving the number of digits to print after the decimal point. If a named vector is used, the names should correspond to one of the permitted functions (See Details below) and all results obtained with that function will be printed with the same precision.
...	further arguments passed to other print methods.

**Details**

This function is similar to `tapply`, with some enhancements: multiple summaries of multiple variables may be mixed in the same table; marginal tables may be calculated; columns and rows may be given informative labels; pretty printing may be controlled by the associated print method.

This function is not a replacement for `tapply` as it also has some limitations. The only functions that may be used in the `contents` argument are: `count`, `mean`, `weighted.mean`, `sum`, `quantile`, `median`, `IQR`, `max`, `min`, `ratio`, `percent`, and `sd`.

The `count()` function, which is the default, simply creates a contingency table of counts. The other functions are applied to each cell created by combinations of the `index` variables.

**Value**

An object of class `stat.table`, which is a multi-dimensional array. A print method is available to create formatted one-way and two-way tables.

**Note**

The permitted functions in the `contents` list are defined inside `stat.table`. They have the same interface as the functions callable from the command line, except for two differences. If there is an argument `na.rm` then its default value is always `TRUE`. A second difference is that the `quantile` function can only produce a single quantile in each call.

**Author(s)**

Martyn Plummer

**See Also**

`table`, `tapply`, `mean`, `weighted.mean`, `sum`, `quantile`, `median`, `IQR`, `max`, `min`, `ratio`, `percent`, `count`, `sd`.

**Examples**

```
data(warpbreaks)
# A one-way table
stat.table(tension,list(count(),mean(breaks)),data=warpbreaks)
# The same table with informative labels
stat.table(index=list("Tension level"=tension),list(N=count(),
            "mean number of breaks"=mean(breaks)),data=warpbreaks)

# A two-way table
stat.table(index=list(tension,wool),mean(breaks),data=warpbreaks)
# The same table with margins over tension, but not wool
stat.table(index=list(tension,wool),mean(breaks),data=warpbreaks,
            margins=c(TRUE, FALSE))

# A table of column percentages
stat.table(list(tension,wool), percent(tension), data=warpbreaks)
# Cell percentages, with margins
stat.table(list(tension,wool),percent(tension,wool), margin=TRUE,
```

```

        data=warpbreaks)

# A table with multiple statistics
# Note how each statistic has its own default precision
a <- stat.table(index=list(wool,tension),
               contents=list(count(),mean(breaks),percent (wool)),
               data=warpbreaks)

print(a)
# Print the percentages rounded to the nearest integer
print(a, digits=c(percent=0))

```

---

stattable.funs

*Special functions for use in stat.table*


---

## Description

These functions may be used as contents arguments to the function `stat.table`. They are defined internally in `stat.table` and have no independent existence.

## Usage

```

count(id)
ratio(d,y,scale=1, na.rm=TRUE)
percent(...)

```

## Arguments

<code>id</code>	numeric vector in which identical values identify the same individual.
<code>d, y</code>	numeric vectors of equal length ( <code>d</code> for Deaths, <code>y</code> for person-Years)
<code>scale</code>	a scalar giving a value by which the ratio should be multiplied
<code>na.rm</code>	a logical value indicating whether NA values should be stripped before computation proceeds.
<code>...</code>	a list of variables taken from the <code>index</code> argument to <code>stat.table</code>

## Value

When used as a contents argument to `stat.table`, these functions create the following tables:

<code>count</code>	If given without argument ( <code>count()</code> ) it returns a contingency table of counts. If given an <code>id</code> argument it returns a table of the number of different values of <code>id</code> in each cell, i.e. how many persons contribute in each cell.
<code>ratio</code>	returns a table of values $scale * \text{sum}(d) / \text{sum}(y)$
<code>percent</code>	returns a table of percentages of the classifying variables. Variables that are in the <code>index</code> argument to <code>stat.table</code> but not in the call to <code>percent</code> are used to define strata, within which the percentages add up to 100.

**Author(s)**

Martyn Plummer

**See Also**

[stat.table](#)

---

subset.Lexis

*Subsetting Lexis objects*

---

**Description**

Return subsets of Lexis objects which meet conditions

**Usage**

```
## S3 method for class 'Lexis'  
subset(x, ...)
```

**Arguments**

x	an object of class Lexis
...	additional arguments to be passed to subset.data.frame

**Details**

The subset method for Lexis objects works exactly as the method for data frames.

**Value**

A Lexis object with selected rows and columns.

**Author(s)**

Martyn Plummer

**See Also**

[Lexis](#), [merge.Lexis](#)

---

summary.Lexis	<i>Summarize transitions and risk time from a Lexis object</i>
---------------	----------------------------------------------------------------

---

**Description**

A two-way table of records and transitions classified by states (`lex.Cst` and `lex.Xst`), as well the risk time in each state.

**Usage**

```
## S3 method for class 'Lexis'
summary( object, simplify=TRUE, scale=1, ... )
## S3 method for class 'summary.Lexis'
print( x, ..., digits=2 )
```

**Arguments**

<code>object</code>	A Lexis object.
<code>x</code>	A <code>summary.Lexis</code> object.
<code>simplify</code>	Should rows with 0 follow-up time be dropped?
<code>scale</code>	Scaling factor for the rates. The calculated rates are multiplied by this number.
<code>digits</code>	How many digits should be used for printing?
<code>...</code>	Other parameters - ignored

**Value**

An object of class `summary.Lexis`, a list with two components, `Transitions` and `Rates`, each one a matrix with rows classified by states where persons spend time, and columns classified by states to which persons transit. The `Transitions` contains number of transitions and has two extra columns of total number events and total risk time attached. The `Rates` contains the transitions rates.

**Author(s)**

Bendix Carstensen, <bx@steno.dk>

**Examples**

```
data( nickel )
# Lung cancer deaths and other deaths are coded 1 and 2
nic <- Lexis( data=nickel,
             entry=list(age=agein),
             exit=list(age=ageout, cal=ageout+dob, tfh=ageout-age1st),
             exit.status=factor( (icd > 0) + (icd %in% c(162,163)),
                               labels=c("Alive", "Other", "Lung") ) )

str( nic )
head( nic )
summary( nic )
```

---

tbox

*Draw boxes and arrows for illustration of multistate models.*


---

### Description

Boxes can be drawn with text (tbox) or a cross (dbox), and arrows pointing between the boxes (boxarr) can be drawn automatically not overlapping the boxes. The boxes method for `Lexis` objects generates displays of states with person-years and transitions with events or rates.

### Usage

```
tbox( txt, x, y, wd, ht,
      font=2, lwd=2,
      col.txt="black",
      col.border="black",
      col.bg="transparent" )
dbox( x, y, wd, ht=wd,
      font=2, lwd=2, cwd=5,
      col.cross="black",
      col.border="black",
      col.bg="transparent" )
boxarr( b1, b2, offset=FALSE, pos=0.45, ... )
## S3 method for class 'Lexis'
boxes( obj, file,
       detailed = FALSE,
       boxpos = FALSE,
       wmult = 1.5,
       hmult = 1.5*wmult,
       cex = 1.5,
       show = inherits( obj, "Lexis" ),
       show.Y = show,
       scale.Y = 1,
       digits.Y = 1,
       show.D = show,
       scale.D = FALSE,
       digits.D = as.numeric(as.logical(scale.D)),
       eq.wd = TRUE,
       eq.ht = TRUE,
       wd,
       ht,
       subset = NULL,
       exclude = NULL,
       font = 2,
       lwd = 2,
       col.txt = "black",
       col.border = col.txt,
       col.bg = "transparent",
```

```

        col.arr = "black",
        lwd.arr = 2,
        font.arr = 2,
        txt.arr = NULL,
        col.txt.arr = col.arr,
        offset.arr = 2, ... )
## S3 method for class 'matrix'
boxes( obj, ... )
      fillarr( x1, y1, x2, y2, gap=2, fr=0.8,
              angle=17, lwd=2, length=par("pin")[1]/30, ... )

```

### Arguments

txt	Text to be placed inside the box.
x	x-coordinate of center of box.
y	y-coordinate of center of box.
wd	width of boxes in percentage of the plot width.
ht	height of boxes in percentage of the plot height.
font	Font for the text. Defaults to 2 (=bold).
lwd	Line width of the boxborders.
col.txt	Color for the text in boxes.
col.border	Color of the box border.
col.bg	Background color for the interior of the box.
...	Arguments to be passed on to the call of other functions.
cwd	Width of the lines in the cross.
col.cross	Color of the cross.
b1	Coordinates of the "from" box. A vector with 4 components, x, y, w, h.
b2	Coordinates of the "to" box; like b1.
offset	Logical. Should the arrow be offset a bit to the left.
pos	Numerical between 0 and 1, determines the position of the point on the arrow which is returned.
obj	A <a href="#">Lexis</a> object or a transition matrix; that is a square matrix indexed by state in both dimensions, and the $(i, j)$ th entry different from NA if a transition $i$ to $j$ can occur. If show.D=TRUE, the arrows between states are annotated by these numbers. If show.Y=TRUE, the boxes representing states are annotated by the numbers in the diagonal of obj.
file	Name of the file with the code reproducing the plot.
detailed	Should the output of R-code be detailed, showing all parameters?
boxpos	If TRUE the boxes are positioned equidistantly on a circle, if FALSE (the default) you are queried to click on the screen for the positions. This argument can also be a named list with elements x and y, both numerical vectors, giving the centers of the boxes.

wmult	Multiplier for the width of the box relative to the width of the text in the box.
hmult	Multiplier for the height of the box relative to the height of the text in the box.
cex	Character expansion for text in the box.
show	Should person-years and transitions be put in the plot. Ignored if obj is not a Lexis object.
show.Y	If logical: Should person-years be put in the boxes. If numeric: Numbers to put in boxes.
scale.Y	What scale should be used for annotation of person-years.
digits.Y	How many digits after the decimal point should be used for the person-years.
show.D	Should transitions be put alongside the arrows. Ignored if obj is not a Lexis object.
scale.D	If this a scalar, rates instead of no. transitions are printed at the arrows, scaled by scale.D.
digits.D	How many digits after the decimal point should be used for the rates.
eq.wd	Should boxes all have the same width?
eq.ht	Should boxes all have the same height?
subset	Draw only boxes and arrows for a subset of the states. Can be given either as a numerical vector or character vector state names.
exclude	Exclude states from the plot. The complementary of subset. Ignored if subset is given.
col.arr	Color of the arrows between boxes. A vector of character strings, the arrows are referred to as the row-wise sequence of non-NA elements of the transition matrix. Thus the first ones refer to the transitions out of state 1, in order of states.
lwd.arr	Line widths of the arrows.
font.arr	Font of the text annotation the arrows.
txt.arr	Text put on the arrows.
col.txt.arr	Colors for text on the arrows.
offset.arr	The amount offset between arrows that go between the same pair of boxes (two-way transitions).
x1	x-coordinate of the starting point.
y1	y-coordinate of the starting point.
x2	x-coordinate of the end point.
y2	y-coordinate of the end point.
gap	Length of the gap between the box and the ends of the arrows.
fr	Length of the arrow as the fraction of the distance between the boxes. Ignored unless given explicitly, in which case any value given for gap is ignored.
angle	What angle should the arrow-head have?
length	Length of the arrow head in inches. Defaults to 1/30 of the physical width of the plot.

## Details

These functions are designed to facilitate the drawing of multistate models, mainly by automatic calculation of the arrows between boxes.

`tbody` draws a box with centered text, and returns a vector of location, height and width of the box. This is used when drawing arrows between boxes. `dbox` draws a box with a cross, symbolizing a death state. `boxarr` draws an arrow between two boxes, making sure it does not intersect the boxes. Only straight lines are drawn.

`boxes.Lexis` takes as input a Lexis object sets up an empty plot area (with axes 0 to 100 in both directions) and if `boxpos=FALSE` (the default) prompts you to click on the locations for the state boxes, and then draws arrows implied by the actual transitions in the Lexis object.

A transition matrix can also be supplied, in which case the row/column names are used as state names, diagonal elements taken as person-years, and off-diagonal elements as number of transitions.

Optionally returns the R-code reproducing the plot in a file, which can be useful if you want to produce exactly the same plot with differing arrow colors etc.

`boxarr` draws an arrow between two boxes, on the line connecting the two box centers. The `offset` argument is used to offset the arrow a bit to the left (as seen in the direction of the arrow) on order to accommodate arrows both ways between boxes. `boxarr` returns a named list with elements `x`, `y` and `d`, where the two former give the location of a point on the arrow used for printing (see argument `pos`) and the latter is a unit vector in the direction of the arrow, which is used by `boxes.Lexis` to position the annotation of arrows with the number of transitions. `fill.arr` is just a utility drawing nicer arrows than the default `arrows` command, basically by using filled arrow-heads; called by `boxarr`.

## Value

The functions `tbody` and `dbox` return the location and dimension of the boxes,  $c(x,y,w,h)$ , which are designed to be used as input to the `boxarr` function.

The `boxarr` function returns the coordinates (as a named list with names `x` and `y`) of a point on the arrow, designated to be used for annotation of the arrow.

## Author(s)

Bendix Carstensen

## See Also

[tmat.Lexis](#)

## Examples

```
par( mar=c(0,0,0,0), cex=1.5 )
plot( NA,
      bty="n",
      xlim=0:1*100, ylim=0:1*100, xaxt="n", yaxt="n", xlab="", ylab="" )
bw <- tbody( "Well"      , 10, 60, 22, 10, col.txt="blue" )
bo <- tbody( "other Ca" , 45, 80, 22, 10, col.txt="gray" )
```

```

bc <- tbox( "Ca"      , 45, 60, 22, 10, col.txt="red" )
bd <- tbox( "DM"      , 45, 40, 22, 10, col.txt="blue" )
bcd <- tbox( "Ca + DM" , 80, 60, 22, 10, col.txt="gray" )
bdc <- tbox( "DM + Ca" , 80, 40, 22, 10, col.txt="red" )
      boxarr( bw, bo , col=gray(0.7), lwd=3 )
# Note the argument adj= can takes values outside (0,1)
text( boxarr( bw, bc , col="blue", lwd=3 ),
      expression( lambda[Well] ), col="blue", adj=c(1,-0.2), cex=0.8 )
      boxarr( bw, bd , col=gray(0.7) , lwd=3 )
      boxarr( bc, bcd, col=gray(0.7) , lwd=3 )
text( boxarr( bd, bdc, col="blue", lwd=3 ),
      expression( lambda[DM] ), col="blue", adj=c(1.1,-0.2), cex=0.8 )

# Set up a transition matrix allowing recovery
tm <- rbind( c(NA,1,1), c(1,NA,1), c(NA,NA,NA) )
rownames(tm) <- colnames(tm) <- c("Cancer","Recurrence","Dead")
boxes.Lexis( tm, file="", boxpos=TRUE )
boxes.Lexis( tm, file="", detailed=TRUE, boxpos=TRUE )
# Illustrate textng of arrows
boxes.Lexis( tm, boxpos=TRUE, txt.arr=c("en","to","tre","fire" ) )
boxes.Lexis( tm, boxpos=TRUE, txt.arr=c(expression(lambda[C]),
                                          expression(mu[C]),
                                          "recovery",
                                          expression(mu[R]) ) )

# Set up a Lexis object
data(DMlate)
str(DMlate)
dml <- Lexis( entry=list(Per=dodm, Age=dodm-dobth, DMdur=0 ),
             exit=list(Per=dox),
             exit.status=factor(!is.na(dodth),labels=c("DM","Dead")),
             data=DMlate )
# Split follow-up at Insulin
dmi <- cutLexis( dml, cut=dml$doin, new.state="Ins", pre="DM" )
summary( dmi )
boxes( dmi, boxpos=TRUE )
# Set up a bogus recovery date
dmi$dorec <- dmi$doin + runif(nrow(dmi),0.5,10)
dmi$dorec[dmi$dorec>dmi$dox] <- NA
dmR <- cutLexis( dmi, cut=dmi$dorec, new.state="DM", pre="Ins" )
summary( dmR )
boxes( dmR, boxpos=TRUE )

```

---

thoro

*Thorotrast Study*


---

## Description

The thoro data frame has 2470 rows and 14 columns. Each row represents one patient that have had cerebral angiography (X-ray of the brain) with an injected contrast medium, either Thorotrast

or another one (the controls).

### Format

This data frame contains the following columns:

id: Identification of person.  
sex: Sex, 1: male / 2: female.  
birthdat: Date of birth, Date variable.  
contrast: Group, 1: Thorotrast / 2: Control.  
injecdat: Date of contrast injection, Date variable.  
volume: Injected volume of Thorotrast in ml. Control patients have a 0 in this variable.  
exitdat: Date of exit from the study, Date variable.  
exitstat: Status at exit, 1: dead / 2: alive, censored at closing of study, 20 February 1992 / 3: censored alive at some earlier date.  
cause: Cause of death. See causes in the helpfile for [gmortDK](#)  
liverdat: Date of liver cancer diagnosis, Date variable.  
liver: Indicator of liver cancer diagnosis. Not all livercancers are histologically verified, hence `liver >= hepcc + cholc`  
hepcc: Hepatocellular carcinoma at liverdat.  
chola: Cholangiocellular carcinoma at liverdat.  
hmang: Haemangiosarcoma carcinoma at liverdat.

### Source

M Andersson, M Vyberg, J Visfeldt, B Carstensen & HH Storm: Primary liver tumours among Danish patients exposed to Thorotrast. *Radiation Research*, 137, pp. 262–273, 1994.

M Andersson, B Carstensen HH Storm: Mortality and cancer incidence after cerebral angiography. *Radiation Research*, 142, pp. 305–320, 1995.

### See Also

[mortDK](#), [gmortDK](#)

### Examples

```
data(thoro)
str(thoro)
```

---

timeBand

*Extract time band data from a split Lexis object*

---

### Description

The break points of a Lexis object (created by a call to `splitLexis`) divide the follow-up intervals into time bands along a given time scale. The `breaks` function returns the break points, for a given time scale, and the `timeBand` classifies each row (=follow-up interval) into one of the time bands.

**Usage**

```
timeBand(lex, time.scale, type="integer")
breaks(lex, time.scale)
```

**Arguments**

lex	an object of class Lexis
time.scale	a character or integer vector of length 1 identifying the time scale of interest
type	a string that determines how the time bands are labelled. See Details below

**Details**

Time bands may be labelled in various ways according to the `type` argument. The permitted values of the `type` argument, and the corresponding return values are:

**"integer"** a numeric vector with integer codes starting from 0.

**"factor"** a factor (unordered) with labels "(left,right]"

**"left"** the left-hand limit of the time band

**"middle"** the midpoint of the time band

**"right"** the right-hand limit of the time band

**Value**

The `breaks` function returns a vector of break points for the Lexis object, or NULL if no break points have been defined by a call to `splitLexis`. The `timeBand` function returns a numeric vector or factor, depending on the value of the `type` argument.

**Note**

A newly created Lexis object has no break points defined. In this case, `breaks` will return NULL, and `timeBand` will a vector of zeros.

**Author(s)**

Martyn Plummer

**See Also**

[Lexis](#)

**Examples**

```
data(diet)
diet <- cal.yr(diet)
diet.lex <- Lexis(entry=list(period=doe),
                 exit=list(period=dox, age=dox-dob),
                 exit.status=chd,
                 data=diet)
diet.split <- splitLexis(diet.lex, breaks=seq(40,70,5), "age" )
```

```
age.left <- timeBand(diet.split, "age", "left")
table(age.left)
age.fact <- timeBand(diet.split, "age", "factor")
table(age.fact)
age.mid <- timeBand(diet.split, "age", "mid")
table(age.mid)
```

---

timeScales

*The time scales of a Lexis object*

---

### Description

Function to get the names of the time scales of a Lexis object.

### Usage

```
timeScales(x)
```

### Arguments

x                    an object of class Lexis.

### Value

A character vector containing the names of the variables in x that represent the time scales. Extracted from the `time.scales` attribute of the object.

### Author(s)

Martyn Plummer

### See Also

[Lexis](#), [splitLexis](#)

---

transform.Lexis

*Transform a Lexis objects*

---

### Description

Modify a Lexis object.

**Usage**

```
## S3 method for class 'Lexis'
transform( '_data', ... )
## S3 method for class 'Lexis'
factorize( obj, states, print = TRUE, ... )
```

**Arguments**

<code>_data</code>	an object of class <code>Lexis</code> .
<code>obj</code>	an object of class <code>Lexis</code> .
<code>states</code>	Names of the factor levels (states) for <code>lex.Cst</code> and <code>lex.Xst</code> . Can be a list, in which case some levels are collapsed, see the documentation for <a href="#">Relevel</a> . No sanity check for the latter operation is undertaken.
<code>print</code>	Should a conversion between old and new levels be printed?
<code>...</code>	Additional arguments to be passed to <a href="#">transform.data.frame</a> or <a href="#">Relevel</a> .

**Details**

The `transform` method for `Lexis` objects works exactly as the method for data frames. `factorize` transforms the variables `lex.Cst` and `lex.Xst` to factors with identical set of levels, optionally with names given in `states`, and optionally collapsing states. The default is to produce a table of old states versus new states if `states` is a list.

**Value**

A transformed `Lexis` object.

**Author(s)**

Martyn Plummer, Bendix Carstensen

**See Also**

[Lexis](#), [merge.Lexis](#), [subset.Lexis](#)

**Examples**

```
data( nickel )
nic <- Lexis( data = nickel,
             id = id,
             entry = list(age=agein),
             exit = list(age=ageout, cal=ageout+dob, tfh=ageout-age1st),
             ## Lung cancer deaths are coded 2 and other deaths are coded 1
             exit.status = ( icd > 0 ) + ( icd %in% c(162,163) ) )
str( nic )
nit <- transform( nic, cumex = exposure*(agein-age1st) )
str( nit )
## It is still a Lexis object!
```

```
summary( nic )
nix <- factorize.Lexis( nic, c("Alive","Lung","Dead"))
niw <- factorize.Lexis( nix, c("Alive","Pulm","Mort"))
niz <- factorize.Lexis( nic, states=list("Alive",c("Pulm","Mort")), coll=" \n& ")
boxes( niw, boxpos=TRUE )
par( new=TRUE )
boxes( niz, boxpos=TRUE )
```

twoby2

*Analysis of a two by two table***Description**

Computes the usual measures of association in a 2 by 2 table with confidence intervals. Also produces asymptotic and exact tests. Assumes that comparison of probability of the first column level between levels of the row variable is of interest. Output requires that the input matrix has meaningful row and column labels.

**Usage**

```
twoby2(exposure, outcome,
       alpha = 0.05, print = TRUE, dec = 4,
       conf.level = 1-alpha, F.lim = 10000)
```

**Arguments**

exposure	If a table the analysis is based on the first two rows and first two columns of this. If a variable, this variable is tabulated against
outcome	as the second variable
alpha	Significance level
print	Should the results be printed?
dec	Number of decimals in the printout.
conf.level	1-alpha
F.lim	If the table total exceeds F.lim, Fisher's exact test is not computed

**Value**

A list with elements:

table	The analysed 2 x 2 table augmented with probabilities and confidence intervals. The confidence intervals for the probabilities are computed using the normal approximation to the log-odds. Confidence intervals for the difference of proportions are computed using method 10 from Newcombe, Stat.Med. 1998, 17, pp.873 ff.
measures	A table of Odds-ratios and relative risk with confidence intervals.
p.value	Exact p-value for the null hypothesis of OR=1

**Author(s)**

Mark Myatt. Modified by Bendix Carstensen.

**Examples**

```
Treat <- sample(c("A","B"), 50, rep=TRUE )
Resp <- c("Yes","No")[1+rbinom(50,1,0.3+0.2*(Treat=="A"))]
twoby2( Treat, Resp )
twoby2( table( Treat, Resp )[ ,2:1] ) # Comparison the other way round
```

---

Y.dk

*Population risk time in Denmark*

---

**Description**

Risk time (person-years) in the Danish population, classified by sex, age, period and date of birth in 1-year classes. This corresponds to triangles in a Lexis diagram.

**Usage**

```
data(Y.dk)
```

**Format**

A data frame with 13860 observations on the following 6 variables.

sex Sex. 1:males, 2:females

A One-year age class

P Period

C Birth cohort

Y Person-years

upper Indicator of upper triangle in the Lexis diagram

**Details**

The risk time is computed from the population size figures in [N.dk](#), using the formulae devised in B. Carstensen: "Demography and epidemiology: Age-Period-Cohort models in the computer age", <http://www.pubhealth.ku.dk/bs/publikationer/rr-06-1.pdf/>

**Source**

<http://www.statistikbanken.dk/statbank5a/SelectTable/omrade0.asp?SubjectCode=02&PLanguage=1&ShowNews=OFF>

**Examples**

```
data(Y.dk)
str(Y.dk)
# Compute mean age, period for the triangles
attach( Y.dk )
age <- A + (1+upper)/3
per <- P + (2-upper)/3
# Plot a Lexis diagram
library( Epi )
Lexis.diagram( age=c(0,10), date=c(1990,2000), coh.grid=TRUE, int=1 )
box()
# Print the person-years for males there
text( per[sex==1], age[sex==1],
      formatC( Y[sex==1]/1000, format="f", digits=1 ) )
```

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