Package 'NMcalc'

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Title Basic Calculations for PK/PD Modeling

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Description Essentials for PK/PD (pharmacokinetics/pharmacodynamics) such as area under the curve, (geometric) coefficient of variation, and other calculations that are not part of base R. This is not a noncompartmental analysis (NCA) package.

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Imports stats, data.table

Suggests ggplot2

NeedsCompilation no

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R topics documented:

`CV` *Calculate coefficient of variation of data*

Description

Calculate coefficient of variation of data

Usage

```
CV(x, log = FALSE)
```

Arguments

`x`	The data
`log`	If TRUE, the geometric coefficient of variation is calculated. This is sqrt(exp(var(log(x))-1).

Details

This function is intended to be used on data. For a log-normal THETA1*EXP(OMEGA[1]) 'Nonmem' parameter, do CV=sqrt(exp(OMEGA[1,1])-1).

Value

A numeric

Examples

```
set.seed(139)
x1 <- rnorm(1000,mean=5)
CV(x1)
CV(x1,log=TRUE)
x2 <- exp(x1)
CV(x2)
CV(x2,log=TRUE)
```

`means` *calculate arithmetic or geometric mean and confidence intervals*

Description

calculate arithmetic or geometric mean and confidence intervals

Usage

```
means(
  x,
  type = "arithmetic",
  na.rm = FALSE,
  z.rm = FALSE,
  ci = FALSE,
  dist.ci = "t",
  p.ci = 0.95,
  colnames = c("est", "ll", "ul"),
  format = "df"
)
```

Arguments

`x`	vector to calculate the geometric mean of
`type`	type of mean or median. Default is arithmetic, geometric and median are available as well. Only first letters needed, so say "geo" or even "g" is enough.
`na.rm`	Remove NA's before doing calculations?
`z.rm`	removes zeros before calculation? Default is FALSE. Can only be TRUE if type="geometric".
`ci`	if TRUE, a data.frame including point estimate and confidence interval returned. If FALSE, a numeric representing the mean value returned.
`dist.ci`	The distribution to use for the confidence interval. Default and only supported is "t". If type=geometric, this is applied after transformation to gaussian.
`p.ci`	probability covered by confidence interval. Default is 0.95
`colnames`	If ci, this defines the column names of the resulting data frame. Default is c("est","ll","ul").
`format`	The format of the result. Possible values are df and num.

Value

If ci=FALSE, a numeric. If ci=TRUE, a data.frame.

Examples

```
x <- 1:100
means(x, type="arithmetic", ci=TRUE)
means(x, type="geometric", ci=TRUE)
means(x, type="median", ci=TRUE)
```

`quantbin` *Bin observations by quantiles. Label by bin number or by interval.*

Description

This is simple stuff, but I can never remember the exact quantile and findInterval/cut commands to use. quantbin finds quantiles using quantile and then assigns bins using either findInterval or cut.

Usage

```
quantbin(x, nbins, label = "num", ...)
```

Arguments

`x`	The observations
`nbins`	Number of bins to use
`label`	label="num" gives a numeric bin number (findInterval). label="interval" gives a character representation of the interval (cut).
`...`	additional arguments passed to quantile.

Details

quantbin uses stats::quantile for quantile estimation. Except for x and probs, all parameters can be controlled using na.rm and ... arguments. See ?stats::quantile for details.

na.rm na.rm=TRUE is needed for quantile to be able to estimate the distribution if x contains NA's. Notice, if na.rm=T, an NA element in x will still result in an NA element in return. If na.rm=F and there are NA's in x, all elements will be NA in result (quantiles cannot be determined, nor can the binning of x by those quantiles).

If data is not continuous, this method may not lead to balanced distributions.

Value

If label="num", integers. If label="interval", factors.

Examples

```
set.seed(134)
library(data.table)
dt1 <- data.table(x=rnorm(n=1000))
dt1[,bin:=quantbin(x,nbins=4,label="num")]
dt1[,int:=quantbin(x,nbins=4,label="interval")]
## perfect - flat distribution
dt1[,.N,keyby=.(bin,int)]

dt2 <- data.table(x=c(rnorm(n=100000),NA))
dt2[,bin:=quantbin(x,nbins=4,label="num",na.rm=TRUE)]
dt2[,int:=quantbin(x,nbins=4,label="interval",na.rm=TRUE)]
```

```
## perfect - flat distribution
dt2[,.N,keyby=.(bin,int)]
unique(dt2[,.(bin,int)])[order(bin)]


## we may not get a flat distribution in case of discrete observations
dt3 <- data.table(x=c(sample(1:3,100,replace=TRUE)))
dt3[,bin:=quantbin(x,nbins=2,label="num",na.rm=TRUE)]
dt3[,int:=quantbin(x,nbins=2,label="interval",na.rm=TRUE)]
## Not a flat distribution
dt3[,.N,keyby=.(x,bin,int)]
```

`seqlog` *Log-scale equidistant sequences*

Description

Useful for generating sequences to be plotted on log scale. This is really simple - seq is run on from and to after log transformation, then the exponential is reported.

Usage

```
seqlog(from, to, length.out)
```

Arguments

`from`	start of sequence
`to`	end of sequence
`length.out`	length of sequence

Value

A numeric vector.

Examples

```
library(ggplot2)
df <- data.frame(x=seqlog(1,100,100))
df <- transform(df, y=x/(10+x))
## the points are equidistant on the log x scale
ggplot(df,aes(x,y))+geom_point()+scale_x_log10()
```

`signif2` *round to fixed number of significant digits*

Description

Even if theoretically correct, the built-in ’R’ functions ’round’ and ’signif’ can be confusing (see examples). ’signif2’ is a simple solution that can be used for reporting results consistently.

Usage

```
signif2(x, digits = 1, add, ...)
```

Arguments

`x`	a numeric vector.
`digits`	number of significant digits to round to. Must be an integer larger than 0.
`add`	pad with zeros where digits>nchar(x[i]). Currently not used.
`...`	additional arguments passed to formatC.

Value

A character vector.

Examples

```
x <- c(1.24e-4,1.1334e6,1.1,22.00000,10.00,1)
data.frame(x,s.3=signif(x,3),sc.3=as.character(signif(x,3)),s2.3=signif2(x,3))
signif2(c(.2,11.84),2)
## digits has no effect when x==0
signif2(0,1)
signif2(0,3)
```

`trapez` *trapezoidal area under the curve on linear scale*

Description

This is a numerical integration of y with respect to x by the trapezoidal method on linear scale.

Usage

```
trapez(x, y, cum = FALSE, na.rm = FALSE)
```

Arguments

`x`	The vector to integrate y with respect to (typically TIME to get area under the curve).
`y`	The variable to integrate.
`cum`	Return the cumulative trapezoidal area under the curve? If false (default) a single number is returned. If true, a vector is returned. Notice, the vector is one element shorter than x and y.
`na.rm`	Remove indexes in x and y wherever x or y are NA.

Value

a numeric

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