

Package ‘kyotil’

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Description

Helper functions for creating formatted summary of regression models, writing publication-ready tables to latex files, and running Monte Carlo experiments.

VignetteBuilder R.rsp

License GPL (>= 2)

NeedsCompilation yes

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age_calc

*Age Calculation***Description**

Calculate age, by Jason P Becker, modified very slightly in how arguments are passed to the function.

Usage

```
age_calc(dob, enddate = Sys.Date(), units = c("days", "months", "years"), precise = TRUE)
```

Arguments

dob	POSIXlt or Date. Birthday
enddate	POSIXlt or Date. Date to compute age
units	string. Choose a unit.
precise	Boolean.

Author(s)

Jason P Becker

References

<http://blog.jsonbecker.com/2013/12/calculating-age-with-precision-in-r.html>

Examples

```
age_calc (dob=strptime("29OCT2002", format="%d%b%Y"),
          enddate=strptime("30OCT2003", format="%d%b%Y"), units='years', precise=TRUE)
age_calc (dob=strptime("29OCT2002", format="%d%b%Y"),
          enddate=strptime("30DEC2003", format="%d%b%Y"), units='years', precise=FALSE)
```

base.functions

Some Base Functions

Description

cbinduneven binds together a list of matrixes/dataframes of different lengths, rows are matched by names binary returns binary representation of an integer. binary2 returns binary representatin of an integer with leading 0, the length of string is n. msystem can call any exe file that is in the PATH f2c convert temperature from f to c/

Usage

```
cbinduneven(li)
binary(i)
```

```
multi.outer (f, ... )
```

```
myreshapelong(dat, cols.to.be.stacked, label.cols.to.be.stacked, new.col.name)
```

```
binary2(i, n)
```

```
f2c(f)
```

```
ftoi(f)
```

```
keepWarnings(expr)

meanmed(x, na.rm = FALSE)

methods4(classes, super = FALSE, ANY = FALSE)

myaggregate(x, by, FUN, new.col.name = "aggregate.value", ...)

myreshapewide(formula, dat, idvar, keep.extra.col=FALSE)

mysapply(X, FUN, ..., simplify = TRUE, USE.NAMES = TRUE, ret.mat = TRUE)

myscale(x)

mysystem(cmd, ...)

mytapply(X, INDEX, FUN = NULL, ..., simplify = TRUE)

read.csv(file, header = TRUE, ...)

read.csv(file, header = TRUE, sep = "\t", ...)

table.prop(x,y=NULL,digit=1,style=2,whole.table.add.to.1=FALSE,useNA="ifany",
  add.perc=FALSE, add.total.column = FALSE)

table.cases (case,group,include.all=TRUE,desc="cases")
table.cases.3(case,group1,group2)

unix()

mycor (x, use = "everything", method = c("pearson", "kendall", "spearman"),
  alternative = c("two.sided", "less", "greater"), exact = NULL,
  conf.level = 0.95, continuity = FALSE,
  digits.coef=2, digits.pval=3,
  ...)
```

Arguments

```
add.total.column

use
method
alternative
exact
conf.level
```

continuity
digits.coef
digits.pval
cols.to.be.stacked

label.cols.to.be.stacked

li a list
i
n
f In multi.out, f is a function.
case vector of 0/1
group vector of multi-group indicators
formula a formula object.
expr
x
na.rm
classes
super
ANY
desc
by
whole.table.add.to.1
 Boolean

new.col.name
...
dat
idvar
X
simplify
USE.NAMES
ret.mat
cmd
INDEX
file
header
sep
y

```

digit
style
FUN
keep.extra.col
useNA
add.perc
include.all
group1
group2

```

Examples

```

binary(5) ### 101
binary2(5, 4)

a=data.frame("x"=1:2)
b=data.frame("y"=3:5);#rownames(b)[3]="
cbinduneven(list(a,b))

## Not run:
# the formula in myreshapewide can only have one variable in the right hand side
myreshapewide(fi~week, dat, c("ptid","stim"))

myreshapelong(dat.201.neut, cols.to.be.stacked=c("MN.3","SF162","SVA.MLV"),
  label.cols.to.be.stacked="antigen", new.col.name="y")

myaggregate(subset(dat.poc, select=c(HIV, trt)), list(dat.poc$f), function(x)
  with(x, c(fisher.test(HIV, trt)$estimate, fisher.test(HIV, trt)$p.value)))

## End(Not run)

```

binaryloess

Using loess to Check Functional Form for Logistic Regression

Description

This function plots a smoothed line of how the average value of Y changes with X in order to check functional form for logistic regression.

Usage

```
binaryloess(x, y, scale = c("logit", "linear"), span = 0.7, weights = NULL, ...)
```

Arguments

x	
y	
scale	
span	smoothing parameter, passed to loess. If less than 1, the neighbourhood includes proportion a of the points. If greater than 1, all points are used, with the maximum distance assumed to be $a^{1/p}$ times the actual maximum distance for p explanatory variables. Missing records are removed first.
weights	sampling weights, passed to loess
...	passed to plotting function

Details

This function comes from Jonathan Bartlett (<https://thestatsgeek.com/2014/09/13/checking-functional-form-in-logistic-regression-using-loess/>).

Examples

```
set.seed(1234)
n <- 1000
x <- rnorm(n)
xb <- -2+x
pr <- exp(xb)/(1+exp(xb))
y=rbern(n, pr)

par(mfrow=c(1,2))
binaryloess(x, y, scale = "logit", span = 0.7, weights = NULL, ylab="logit(p)")
binaryloess(x, y, scale = "linear", span = 0.7, weights = NULL, ylab="prob")
```

cox.zph.2

Test the Proportional Hazards Assumption of a Cox Regression (a slightly modified version)

Description

A slightly modified test of the proportional hazards assumption for a Cox regression model fit (coxph). This version corrects some conservativeness of the test.

Usage

```
cox.zph.2(fit, transform = "km", global = TRUE, exact=TRUE)
```

Arguments

fit
transform
global
exact Boolean. If FALSE, this function is an identical copy of `cox.zph`. If TRUE, it computes the variance of the test statistic exactly, instead of approximately.

Details

When the model uses time-dependent covariates, the approximation used in Grambsch and Therneau resulted in conservativeness of the test. This is "fixed" here at a cost of up to 2.5 times longer execution time.

References

Fong, Y. and Halloran, M Elizabeth and Gilbert, P. Using Time-Dependent Age Group in Cox Regression Analysis of Vaccine Efficacy Trials, *Just Another Epi Journal*, in prep.

See Also

[cox.zph](#)

Examples

```
library(survival)
fit <- coxph(Surv(futime, fustat) ~ age + ecog.ps,
             data=ovarian)
temp <- cox.zph(fit)
print(temp)
temp.2 <- cox.zph.2(fit)
print(temp.2)
```

crossvalidation

Cross Validation Functions

Description

Cross validation utility functions.

Usage

```
sample.for.cv (dat, v, seed)
get.kfold.splits (dat, k, seed)
kfold.split (k, n1, n0)
ran.kfold.split(k, n1, n0, replicates)
```



```
lpo.split(n1, n0)
get.splits (dat, cv.scheme=c("LPO", "5fold", "50xrandom4:1"), seed)
```

Arguments

dat	a data frame. One of the columns must be named y and y should be 0/1 with 1 for case and 0 for control
v	v-fold cross validation
seed	seed for random number generators
k	
n1	
n0	
replicates	
cv.scheme	

Details

sample.for.cv: case and controls are sampled separately.

Value

sample.for.cv returns a list of two vector of integers: train and test, which refer to the rows of dat

Deming

Fit Deming regression.

Description

Deming regression fit. Assume x and y variances are the same. Slightly modified from MethComp R package.

Usage

```
Deming(x, y, vr = sdr^2, sdr = sqrt(vr), boot = TRUE, keep.boot = FALSE,
       alpha = 0.05)
```

Arguments

x	
y	
vr	
sdr	
boot	
keep.boot	
alpha	

Examples

```
## Not run:
set.seed(1)
x=rnorm(100,0,1)
y=x+rnorm(100,0,.5)
x=x+rnorm(100,0,.5)
fit=Deming(x,y, boot=TRUE)
summary(fit)
plot(x,y)
abline(fit)
# compare with lm fit
fit.1=lm(y~x, data.frame(x,y))
summary(fit.1)
abline(fit.1, col=2)

## End(Not run)
```

DMHeatMap

Better Heatmap Function

Description

Makes a heatmap representation of correlation coefficients easier.

Usage

```
DMHeatMap(x, Rowv = TRUE, Colv = if (symm) "Rowv" else TRUE,
  distfun = dist, hclustfun = hclust, dendrogram =
  c("both", "row", "column", "none"), symm = FALSE,
  scale = c("none", "row", "column"), na.rm = TRUE, revC
  = identical(Colv, "Rowv"), add.expr, breaks, symbreaks
  = min(x < 0, na.rm = TRUE) || scale != "none", col =
  "heat.colors", colsep, rowsep, sepcolor = "white",
  sepwidth = c(0.05, 0.05), cellnote, notecex = 1,
  notecol = "cyan", na.color = par("bg"), trace =
  c("column", "row", "both", "none"), tracecol = "cyan",
  hline = median(breaks), vline = median(breaks),
  linecol = tracecol, margins = c(5, 5), ColSideColors,
  RowSideColors, cexRow = 0.2 + 1/log10(nr), cexCol =
  0.2 + 1/log10(nc), labRow = NULL, labCol = NULL,
  labColor = NULL, axis = TRUE, heatmapOnly = FALSE, key
  = TRUE, keysize = 1.5, density.info = c("histogram",
  "density", "none"), denscol = tracecol, symkey = min(x
  < 0, na.rm = TRUE) || symbreaks, densadj = 0.25, main
  = NULL, xlab = NULL, ylab = NULL, lmat = NULL, lhei =
  NULL, lwid = NULL, lower.left.only = TRUE, legend =
  TRUE, legend.x = "topright", verbose = FALSE, ...)
```

Arguments

x
axis
heatmapOnly
verbose
legend.x
legend
Rowv
Colv
distfun
hclustfun
dendrogram
symm
scale
na.rm
revC
add.expr
breaks
symbreaks
col
colsep
rowsep
sepcolor
sepwidth
cellnote
notecex
notecol
na.color
trace
tracecol
hline
vline
linecol
margins
ColSideColors
RowSideColors
cexRow

```
cexCol
labRow
labCol
labColor
key
keysize
density.info
denscol
symkey
densadj
main
xlab
ylab
lmat
lhei
lwid
lower.left.only

...
```

Examples

```
cor=matrix(runif(15),5,3)
breaks=c(-1,-.7,-.5,-.3,-.1,.1,.3,.5,.7,1)
hU=DMHeatMap(cor, trace="none", symm=FALSE,dendrogram="none", col=RColorBrewer::brewer.pal(
  length(breaks)-1,"RdYlGn"), distfun = function(c) as.dist(1 - c), cexRow =1.5, cexCol =1.5,
  lmat=rbind( c(2, 1), c(4,3) ), lhei=c(4, 1 ), breaks=breaks, margins=c(2,2), key = FALSE,
  Rowv=NA, lower.left.only=FALSE)
```

get.sim.res

Read simulation results

Description

Go through a folder and read all files and combine the results into a multidimensional array.

Usage

```

get.sim.res (dir, res.name="res", verbose=TRUE)
MCsummary (dir, res.name = "res", exclude.some = TRUE,
           exclude.col = 1, verbose = TRUE)
getFormattedMCsummary (path, sim, nn, fit.method, exclude.some = TRUE,
                      exclude.col = 1, verbose = TRUE, coef.0 = NULL, digit1
                      = 2, sum.est = c("mean", "median"), sum.sd =
                      c("median", "mean"), style = 1, keep.intercept =
                      FALSE)

```

Arguments

dir	directory of MC result files
path	partial path to the directory of MC result files
res.name	name of the R object saved in the files, default is res, but may be others
verbose	Boolean
sim	a string to denote simulation setting
nn	a vector of sample sizes
fit.method	a string to denote fitting method. sim, nn and fit.method together forms the name of the directory containing MC result files
exclude.col	column number
exclude.some	whether to exclude MC results that are extreme
coef.0	simulation truth
digit1	digits
sum.est	use mean or median as location estimate summary
sum.sd	use mean or median as sd estimate summary
style	integer
keep.intercept	whether to include intercept in the table

Details

Depends on package abind to combine arrays from files.

Value

A multidimensional array.

getK

*getK***Description**

getK calculates the kernel matrix between X and itself and returns a n by n matrix. Alternatively, it calculates the kernel matrix between X and X2 and returns a n by n2 matrix.

Usage

```
getK (X, kernel, para=NULL, X2=NULL, C = NULL)
```

Arguments

X	covariate matrix with dimension n by d. Note this is not the paired difference of covariate matrix.
kernel	string specifying type of kernel: polynomial or $p(1 + \langle x, y \rangle)^{\text{para}}$, rbf or $r \exp(-\text{para} * \ x - y\ ^2)$, linear or $l \langle x, y \rangle$, ibs or $i \cdot 0.5 * \text{mean}(2.0 - x - y)$ or $\text{sum}(w * (2.0 - x - y)) / \text{sum}(w)$, with $x[i], y[i]$ in 0,1,2 and weights 'w' given in 'para'. hamming or h for $\text{sum}(x == y)$ with $x[i], y[i]$ binary, no default.
para	parameter of the kernel function. for ibs or hamming, para can be a vector of weights.
X2	optional second covariate matrix with dimension n2 by d
C	logical. If TRUE, kernels are computed by custom routines in C, which may be more memory efficient, and faster too for ibs and hamming kernels.

Details

IBS stands for 'Identical By State'. If 'x', 'y' are in 0,1,2 then

$\text{IBS}(x, y) = 0$ if $|x - y| = 2$, 1 if $|x - y| = 1$, 2 if $|x - y| = 0$, or $\text{IBS}(x, y) = 2.0 - |x - y|$.

$K(u, v) = \text{sum}(\text{IBS}(u[i], v[i])) / 2K$ where $K = \text{length}(u)$.

The 'hamming' kernel is the equivalent of the 'ibs' kernel for binary data. Note that 'hamming' kernel is based on hamming similarity(!), not on dissimilarity distance.

Within in the code, C is default to TRUE for ibs and hamming kernels and FALSE otherwise.

Value

A kernel matrix.

Author(s)

Youyi Fong <youyifong@gmail.com>

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Shuxin Yin <>

Examples

```

X = cbind(x1=rnorm(n=5), x2=rnorm(n=5))
dim(X)
X2 = cbind(x1=rnorm(n=3), x2=rnorm(n=3))
dim(X2)

K = getK(X,"linear")
dim(K)

K = getK(X,"linear",X2=X2)
dim(K)
K1 = getK(X2,"1",X2=X)
dim(K1)
all(K==t(K1))

# RBF kernel
K = getK(X,"rbf",para=1,X2=X2)
K1 = getK(X2,"r",para=1,X2=X)
all(K==t(K1))

# IBS kernel for ternary data
X <- as.matrix(expand.grid(0:2,0:2))
K = getK(X, kernel = 'ibs')

# add weight
w = runif(ncol(X))
K = getK(X, kernel = 'ibs', para = w)

# IBS kernel for binary data via option 'h' for 'hamming similarity measure'
X <- as.matrix(expand.grid(0:1,0:1))
K=getK(X, kernel = 'h')

```

```
get_count_from_xy_coor
```

Imaging analysis for spatial region

Description

Counting the number of masks in a rectangular region

Usage

```
get_count_from_xy_coor(file, topleft, bottomright, image, plot)
```

Arguments

file	_sizes_coordinates.txt
topleft	topleft (x,y) coordiate for a rectangular box
bottomright	bottomright: bottomright (x,y) coordiate for a rectangular box
image	image: an image for plotting
plot	plot: plot=TRUE shows image with rectangular box

Details

This function counts cells inside of rectangular box made by the topleft and bottomright xy-coordinates.

Value

The number of masks inside of the rectangular box

Author(s)

Sunwoo Han

Examples

```
#get_count_from_xy_coor(file='M926910_Position1_CD3-BUV395_sizes_coordinates.txt',
#topleft=c(500,0), bottomright=c(1392,500),
#image='M926910_Position1_CD3-BUV395.tiff', plot=TRUE)
```

iorw

Causal Mediation Analysis of Cowling et al.

Description

Estimate the total, direct, and indirect effects using IORW method (inverse odds ratio weighting) and compute 95

Usage

```
iorw(formula.effect, formula.mediators, data, family =
  NULL, nboot = 10000, numCores = 1, save.steps = FALSE,
  verbose = FALSE)
```

```
## S3 method for class 'iorw'
print(x, ...)
```


Arguments

<code>formula.effect</code>	a formula object for the total and direct effect regression. The first term on the right is assumed to be the binary treatment/exposure variable.
<code>formula.mediators</code>	a formula object for logistic regression. It should be of the form: <code>~ mediation marker1 + mediation marker2</code> .
<code>data</code>	a data frame.
<code>family</code>	if Cox regression, leave as <code>NULL</code> ; otherwise, it will be passed to <code>glm()</code> .
<code>nboot</code>	an integer. Number of bootstrap replicates.
<code>numCores</code>	an integer. Number of cores to use for parallel processing.
<code>save.steps</code>	boolean. Whether or not to save the fits from the three steps and the weights.
<code>x</code>	Object of type <code>iorw</code>
<code>verbose</code>	boolean.
<code>...</code>	Additional arguments passed to the print function.

Details

Code by Cowling and Lim was downloaded from <https://datadryad.org/stash/dataset/doi:10.5061/dryad.cv37539>
 If a bootstrap replicate generates warnings during regression, NA will be returned for that replicate.
 The number of such occurrences is recorded in an attribute of `boot.perc` in the return value.
 It does not handle sampling weights yet.

Value

Point estimates and percentile bootstrap confidence intervals.

Author(s)

Youyi Fong, based on code by Cowling and Lim

References

- Cowling, B. J., Lim, W. W., Perera, R. A., Fang, V. J., Leung, G. M., Peiris, J. M., & Tchetgen Tchetgen, E. J. (2019). Influenza hemagglutination-inhibition antibody titer as a mediator of vaccine-induced protection for influenza B. *Clinical Infectious Diseases*, 68(10), 1713-1717.
- Nguyen, Q. C., Osypuk, T. L., Schmidt, N. M., Glymour, M. M., & Tchetgen Tchetgen, E. J. (2015). Practical guidance for conducting mediation analysis with multiple mediators using inverse odds ratio weighting. *American journal of epidemiology*, 181(5), 349-356.
- Tchetgen Tchetgen, E. J. (2013). Inverse odds ratio-weighted estimation for causal mediation analysis. *Statistics in medicine*, 32(26), 4567-4580.
- Imai, K., Keele, L., & Tingley, D. (2010). A general approach to causal mediation analysis. *Psychological methods*, 15(4), 309.

Examples

```
#### Cox regression

# without adjusting for baseline markers
library(survival)
formula.effect=Surv(surv_time, flu)~vaccine+age
formula.mediators=~log2(postvax.B.Brisbane/5)
res.1=iorw(formula.effect, formula.mediators, kid, nboot=10, numCores=1); res.1
stopifnot(max(abs(res.1$boot[1,] - c(0.2029779,0.6070105,0.3039110,0.4283389,0.2124268)))<1e-6)

# adjust for baseline markers
formula.effect=Surv(surv_time, flu)~vaccine+log2(prevax.B.Brisbane)+age
formula.mediators=~log2(postvax.B.Brisbane/5)
res.2=iorw(formula.effect, formula.mediators, kid, nboot=10, numCores=1); res.2

#### Logistic regression

# without adjusting for baseline markers
formula.effect=flu~vaccine+age
formula.mediators=~log2(postvax.B.Brisbane/5)
res.3=iorw(formula.effect, formula.mediators, kid, family=binomial(), nboot=10, numCores=1); res.3
stopifnot(max(abs(res.3$boot[1,] - c(0.1960024,0.6154349,0.2937164,0.4145470,0.2168644)))<1e-6)

# adjust for baseline markers
formula.effect=flu~vaccine+log2(prevax.B.Brisbane)+age
formula.mediators=~log2(postvax.B.Brisbane/5)
res.4=iorw(formula.effect, formula.mediators, kid, family=binomial(), nboot=10, numCores=1); res.4
```

kid

Dataset from Cowling et al.

Description

Influenza immune response biomarkers dataset.

Usage

```
data("kid")
```

Format

A data frame with 736 observations on the following 10 variables.

hhID a numeric vector

age a numeric vector

intervention a character vector

vaccine a numeric vector

vaccine.date a Date

postvax.date a Date

prevax.B.Brisbane a numeric vector

postvax.B.Brisbane a numeric vector

surv_time a numeric vector

flu a numeric vector

References

Cowling, B. J., Lim, W. W., Perera, R. A., Fang, V. J., Leung, G. M., Peiris, J. M., & Tchetgen Tchetgen, E. J. (2019). Influenza hemagglutination-inhibition antibody titer as a mediator of vaccine-induced protection for influenza B. *Clinical Infectious Diseases*, 68(10), 1713-1717.

kyotil

kyotil

Description

Utility functions by Youyi Fong and Krisz Sebestyen, and some functions copied from other packages for convenience (acknowledged on their manual pages).

Most useful functions: mypostscript/mypdf, mytex,

See the Index link below for a list of available functions.

The package depends on Hmisc. The main reason for that, besides the usefulness of the package, is Hmisc depends on ggplot2, which also define

make.timedep.dataset *Create Dataset for Time-dependent Covariate Proportional Hazard Model Analysis*

Description

Returns a data frame that is suitable for time-dependent covariate Cox model fit.

Usage

```
make.timedep.dataset(dat, X, d, baseline.ageyrs, t.1, t.2 = NULL)
```

Arguments

dat	data frame
X	string. Name of the followup time column in dat. Unit needs to be years.
d	string. Name of the followup time column in dat.
baseline.ageyrs	string. Name of the followup time column in dat.
t.1	numerical. Cutoff for age group
t.2	numerical. Second cutoff for age group

Details

The function assumes that the followup length is such that only one change of age group is possible.

Value

Returns a data frame with the following columns added: tstart, tstop, .timedep.agegrp, .baseline.agegrp

tstart	left bound of time interval
tstop	right bound of time interval
.timedep.agegrp	time-dependent age group
.baseline.agegrp	baseline age group

Author(s)

Youyi Fong

References

Therneau, T. and Crowson, C. Using Time Dependent Covariates and Time Dependent Coefficients in the Cox Model. A vignette from the R package survival.

Examples

```
library(survival)

n=3000; followup.length=5; incidence.density=0.015; age.sim="continuous"

dat.0=sim.dat.tvarying.two(n, followup.length, incidence.density, age.sim, seed=1)
dat=subset(dat.0, for.non.tvarying.ana, select=c(ptid, X, d, baseline.age, trt))
dat.timedep = make.timedep.dataset (dat, "X", "d", "baseline.age", 6)
coxph(Surv(tstart,tstop,d) ~ trt*.timedep.agegrp, dat.timedep)
```

math.functions

Math Functions

Description

H calculates entropy.

Usage

```
as.binary(n, base = 2, r = FALSE)

binom.coef(n, m)

expit(x)

logDiffExp(logx1, logx2)

logit(x)

logMeanExp(logx, B = NULL)

logSumExp(logx)

logSumExpFor2(logx, logy)

permn(x, fun = NULL, ...)

Stirling2(n, m)

interpolate(pt1, pt2, x)
```

Arguments

n
base
r
m
pt1 a vector of length 2
pt2 a vector of length 2
x
logx1
logx2
logx
B
logy
fun
...

Examples

```
H(rep(1/5,5))  
H(rep(3,5))
```

matrix.array.functions

Matrix and Array Functions

Description

concatList returns a string that concatenates the elements of the input list or array

Usage

```
AR1(p, w)  
  
concatList(lis, sep = "")  
  
EXCH(p, rho)  
  
fill.jagged.array(a)  
  
getMidPoints(x)  
  
getUpperRight(matri, func = NULL)
```

```
last(x, n = 1, ...)  
  
mix(a, b)  
  
## S3 method for class 'data.frame'  
rep(x, times = 1, ...)  
  
## S3 method for class 'matrix'  
rep(x, times = 1, each = 1, by.row = TRUE, ...)  
  
## S3 method for class 'matrix.block'  
rep(x, times = 2, ...)  
  
shift.left(x, k = 1)  
  
shift.right(x, k = 1)  
  
thin.rows(dat, thin.factor = 10)  
  
ThinRows(dat, thin.factor = 10)  
  
tr(m)
```

Arguments

```
p  
w  
lis          list or array  
sep  
rho  
a  
x  
matri  
func  
n  
...  
b  
times  
each  
by.row  
k  
dat  
thin.factor  
m
```

Examples

```
concatList(1:3, "_")
```

 matrix2

Matrix Functions that May Be Faster than

Description

DXD computes $D \%*\% X \%*\% D$, where D is a diagonal matrix. tXDX computes $t(X) \%*\% D \%*\% X$. symprod computes $S \%*\% X$ for symmetric S . txSy computes $t(x) \%*\% S \%*\% y$ for symmetric S .

Usage

```
DXD(d1, X, d2)
tXDX(X,D)
symprod(S, X)
txSy(x, S, y)
.as.double(x, stripAttributes = FALSE)
```

Arguments

d1	a diagonal matrix or an array
d2	a diagonal matrix or an array
x	array
y	array
S	symmetric matrix
X	matix
D	matix
stripAttributes	boolean

Details

.as.double does not copying whereas as.double(x) for older versions of R when using .C(DUP = FALSE) make duplicate copy of x. In addition, even if x is a 'double', since x has attributes (dim(x)) as.double(x) duplicates

The functions do not check whether S is symmetric. If it is not symmetric, then the result will be wrong. DXD offers a big gain, while symprod and txSy gains are more incremental.

Author(s)

Krisztian Sebestyen

Examples

```
d1=1:3
d2=4:6
X=matrix(1:9,3,3)
all(DXD(d1, X, d2) == diag(d1) %** X %** diag(d2))
```

```
S=matrix(c(1,2,3,2,4,5,3,5,8),3,3)
X=matrix(1:9,3,3)
all( symprod(S, X) == S %** X )
```

```
x=1:3
y=4:6
S=matrix(c(1,2,3,2,4,5,3,5,8),3,3)
txSy(x, S, y) == drop(t(x)%**S%**y)
```

misc

Misc Functions

Description

Misc functions. summ computes iterative sum, sort of like diff.

Usage

```
pava (x, wt = rep(1, length(x)))
summ(x)
empty2na(x)
## S3 method for class 'pcc'
predict(object, newdat, ...)
rank.inv.norm(x)
INT(x)
```

Arguments

x
wt
object
newdat
...

Details

rank.inv.norm: rank-based inverse normal/gaussian transformation

Value

summ returns

p.adj.perm

Permutation-based Multitesting P Values Adjustment

Description

An implementation of Westfall and Young

Usage

```
p.adj.perm(p.unadj, p.perms, alpha = 0.05)
```

Arguments

p.unadj

p.perms

alpha

Details

This implementation is not as fast as the implementation from the package multtest. But usually the step to create p.perms is the rate-limiting step.

The smallest of the Westfall and Young FWER-controlling multitesting adjusted p values coincides with the p value for testing a global null without any assumptions. But for the multitesting adjustment to hold, it requires the subset pivotality condition.

Author(s)

Sue Li, sli@fredhutch.org

References

- Westfall, P. H., & Young, S. S. (1993). Resampling-based multiple testing: Examples and methods for p-value adjustment (Vol. 279). John Wiley & Sons.
- Westfall, P. H., & Troendle, J. F. (2008). Multiple testing with minimal assumptions. *Biometrical Journal: Journal of Mathematical Methods in Biosciences*, 50(5), 745-755.

Description

mypostscript and mypdf sets the width and height based on mfrow input.

Usage

```
myplot (object, ...)  
  
## S3 method for class 'loess'  
myplot(object, xlab="x", ylab="fitted", ...)  
  
whiskers (x, s, ...)  
  
abline.pt.slope(pt1, slope, x2=NULL, ...)  
  
abline.pts(pt1, pt2 = NULL)  
  
butterfly.plot(dat, dat2 = NULL, add = FALSE, xaxislabels = rep("", 4), x.ori = 0,  
  xlab = "", ylab = "", cex.axis = 1, ...)  
  
empty.plot()  
  
add.mtext.label (text, cex = 1.4, adj = -0.2)  
mydev.off(file = "temp", ext = c("pdf"), res = 200, mydev =  
  NULL)  
  
getMfrow(len)  
  
myhist (x, add.norm=TRUE, col.norm="blue", ...)  
  
myforestplot(dat, xlim = NULL, xlab = "", main = "", col.1 = "red",  
  col.2 = "blue", plot.labels = TRUE, order = FALSE,  
  decreasing = FALSE, vline = TRUE, cols = NULL, log =  
  "", null.val = NULL)  
  
my.interaction.plot(dat, x.ori = 0, xaxislabels = rep("", 2), cex.axis = 1, add = FALSE,  
  xlab = "", ylab = "", pcol = NULL, lcol = NULL, ...)  
  
myboxplot(object, ...)  
  
## S3 method for class 'formula'  
myboxplot(formula, data, cex = 0.5, xlab = "", ylab = "", main =  
  "", box = TRUE, at = NULL, na.action = NULL, p.val =
```

```

NULL, pch = 1, col = 1, test = "",
friedman.test.formula = NULL, reshape.formula = NULL,
reshape.id = NULL, jitter = TRUE, add.interaction =
FALSE, drop.unused.levels = TRUE, bg.pt = NULL, add =
FALSE, seed = 1, write.p.at.top = FALSE, ...)

## S3 method for class 'data.frame'
myboxplot(object, cex = 0.5, ylab = "", xlab = "", main = "",
  box = TRUE, at = NULL, pch = 1, col = 1, test = "",
  paired = FALSE, ...)

## S3 method for class 'list'
myboxplot(object, paired = FALSE, ...)

abline.shade.2(x, col=c(0,1,0))
abline.shade(pt, type = 5, col = c(0, 1, 0), alpha = 0.3)

mylegend(legend, x, y=NULL, lty = NULL, bty = "n", ...)

mymatplot(x, y, type = "b", lty = c(1, 2, 1, 2, 1, 2), pch =
  NULL, col = rep(c("darkgray", "black"), each = 3),
  xlab = NULL, ylab = "", draw.x.axis = TRUE, bg = NA,
  lwd = 1, at = NULL, make.legend = TRUE, legend = NULL,
  impute.missing.for.line = TRUE, legend.x = 9,
  legend.title = NULL, legend.cex = 1, legend.lty = lty,
  legend.inset = 0, xaxt = "s", y.intersp = 1.5,
  x.intersp = 0.3, text.width = NULL, add = FALSE, ...
)

mypairs(dat, ladder = FALSE, show.data.cloud = TRUE,
  ladder.add.line = T, ladder.add.text = T, ...)

wtd.hist (x, breaks = "Sturges", freq = NULL, probability = !freq,
  include.lowest = TRUE, right = TRUE, density = NULL, angle = 45,
  col = NULL, border = NULL, main = paste("Histogram of", xname),
  xlim = range(breaks), ylim = NULL, xlab = xname, ylab, axes = TRUE,
  plot = TRUE, labels = FALSE, nclass = NULL, weight = NULL,
  ...)

mylines(x, y, type = "l", ...)

myfigure(mfrow = c(1, 1), mfcol = NULL, width = NULL,
  height = NULL, oma = NULL, mar = NULL, main.outer = FALSE, bg=NULL)

mypdf(...)

```

```
mypng(...)
mytiff(...)

mypostscript(file = "temp", mfrow = c(1, 1), mfcol = NULL, width = NULL,
  height = NULL, ext = c("eps", "pdf", "png", "tiff"), oma = NULL,
  mar = NULL, main.outer = FALSE, save2file = TRUE, res = 200,
  ...)

panel.cor(x, y, digits = 2, prefix = "", cex.cor, cor., leading0
  = FALSE, cex.cor.dep = TRUE, ...)

panel.hist(x, ...)

panel.nothing(x, ...)

corplot(object, ...)

## Default S3 method:
corplot(object, y, ...)

## S3 method for class 'formula'
corplot(formula, data, main = "", method = c("pearson",
  "spearman"), col = 1, cex = 0.5, add.diagonal.line =
  TRUE, add.lm.fit = FALSE, add.loess.fit = FALSE,
  col.lm = 2, add.deming.fit = FALSE, col.deming = 4,
  add = FALSE, log = "", same.xyylim = FALSE, xlim =
  NULL, ylim = NULL, ...)
```

Arguments

```
legend.lty
cex.cor.dep
add.loess.fit
leading0
null.val
write.p.at.top
text.width
text
cex
adj
file
ext
```

res resolution.
add.norm Boolean, whether to add normal approximation density line
col.norm string, color of added normal density line
pt1
s
ladder
slope
friedman.test.formula

reshape.id
impute.missing.for.line

cor.
mydev
jitter Boolean
add.interaction
Boolean

...
xaxt
breaks
freq
bg.pt
probability
include.lowest
right
density
angle
border
axes
plot
labels
nclass
weight
pt2
pt
alpha
dat
lwd line width.

x.intersp controls the look of legend.
y.intersp controls the look of legend.
legend.inset legend inset
dat2
add
log
add.lm.fit
add.deming.fit
col.lm
col.deming
reshape.formula a formula object.
xaxislabels
x.ori
xlab
ylab
cex.axis
len
same.xyylim Boolean. Whether xlim and ylim should be the same
xlim
ylim
main
col.1
col.2
pcol
lcol
object
formula
data
box
at
pch
col
test string. For example, "t", "w", "f", "k", "tw"
legend
x
lty

bty
type
make.legend
legend.x
legend.title
legend.cex
draw.x.axis
bg
method
mfrow
mfcol
width
height
oma
mar
main.outer
save2file
y
digits
prefix
cex.cor
plot.labels Boolean
order Boolean
decreasing Boolean
add.diagonal.line

x2
vline
cols
na.action
drop.unused.levels

p.val
seed
paired
show.data.cloud

ladder.add.line

ladder.add.text

Details

myboxplot shows data points along with boxes. The data points are jittered and the pattern of jittering is made reproducible in repeated calls. The test can only take one type of test currently.

myforestplot is modified from code from Allan deCamp/SCHARP. dat should have three columns. first column should be point estimate, second and third lci and uci, fourth p value. col.1 is the color used for CIs that do not include null, col.2 is used for CIs that do include null. If order is TRUE, the rows are ordered by the first column of dat. descreasing can be used to change the behavior of order.

corplot.formula uses MethComp::Deming by Bendix Carstensen to fit Deming regression.

wtd.hist is copied from weights package, author: Josh Pasek.

mymatplot will use na.approx (zoo) to fill in NA before plotting in order to draw continuous lines. The filled-in values will not be shown as points.

Examples

```
set.seed(1)
x=1:50+rnorm(50,0,4)
y=1:50+rnorm(50,0,4)
dat=data.frame(x, y)
corplot(y~x,dat,add.lm.fit=TRUE,add.deming.fit=TRUE,col.lm="red",col.deming="blue")

dat=data.frame(y=c(1:10,2:11), x=rep(c("a","b"),each=10), ptid=c(1:10,1:10))
par(mfrow=c(1,2))
myboxplot(y~x, dat, test="w", jitter=FALSE)
myboxplot(y~x, dat, test="f", add.interaction=TRUE, reshape.formula=y~x, reshape.id="ptid")

myboxplot(list(jitter(1:10), jitter(3:12)), test="w")
myboxplot(list(jitter(1:10), jitter(3:12)), test="w", paired=TRUE)

## Not run:
myfigure(mfrow=c(1,2))
  plot(1:10)
  plot(1:10)
mydev.off(ext="png,pdf", file="tmp")

## End(Not run)

#myboxplot x axis may look weird if log="xy"
```

Description

Offers two approaches (Approach 2 is recommended, `pcr2` is just an alias for `predictCompetingRisk2`). Weights are allowed in the optional arguments.

Usage

```
predictCompetingRisk2(formula.list, data, t0, newdata = data, ...)
pcr2(formula.list, data, t0, newdata=data, ...)
```

```
predictCompetingRisk(formula, formula.all, data, t0, newdata=data, stype=2, ctype=2, ...)
pcr(formula, formula.all, data, t0, newdata=data, stype=2, ctype=2, ...)
```

Arguments

<code>formula.list</code>	list of formulae for cause-specific failures. Assume the first cause to be the cause of interest
<code>formula</code>	formula for the cause-specific failure
<code>formula.all</code>	formula for all-cause failure
<code>data</code>	data frame
<code>t0</code>	the time till which cumulative incidence function is computed
<code>newdata</code>	new data for making prediction, default to the data for fitting the models
<code>stype</code>	computation of the survival curve, 1=direct, 2= exponential of the cumulative hazard. Default 2, which is the default of <code>basehaz</code> and <code>predict.coxph</code>
<code>ctype</code>	whether the cumulative hazard computation should have a correction for ties, 1=no, 2=yes. Default 2, which is the default of <code>basehaz</code> and <code>predict.coxph</code>
<code>...</code>	optional arguments that are passed to <code>coxph</code> , the most import of which is <code>weights</code>

Details

Approach 2, `predictCompetingRisk2`, fits cause-specific Cox models to each cause to compute cumulative incidence function for the cause of interest under competing risk.

When there is only one cause, CIF is conceptually 1 - survival prob. (<https://www.publichealth.columbia.edu/research/population-health-methods/competing-risk-analysis>)

The function is implemented in R with matrix operation. Because looping through time points and subjects is vectorized, it is quite fast (faster than `riskRegression` in limited testing, which implements in C, but `pcr` uses more memory.)

One way to checke the implementation of this function is to compare its results with the results of `predict.coxph` when there is only one cause. The tests in the examples code below show that when the risk is small (e.g. shorter followup time), the CIF computed by this function and the 1-survival estimated via $1 - \exp(-H)$ by `predict.coxph`, where H is cumulative hazard, are close to each other. But when the risk is high, the difference between the two are more noticeable. These results make sense because, e.g.,

If t_0 = the first time failure point, $CIF = h_1 = H_1 \sim 1 - \exp(-H_1)$ If t_0 = the second time point,

$CIF = H_1 + \exp(-H_1) * h_2$ (by def)

$$\begin{aligned} &\sim H1 + \exp(-H1)(1 - \exp(-h2)) \\ &= H1 + \exp(-H1) - \exp(-H2) \\ &\sim 1 - \exp(-H2) \end{aligned}$$

Approach 1, predictCompetingRisk, fits a cause-specific Cox model and a all-cause Cox model to compute cumulative incidence function for the cause of interest under competing risk.

The difference between predictCompetingRisk and predictCompetingRisk2 is that instead of fitting a model to the overall failure, a model is fit for each cause, including the cause of interest. The overall survival is computed by adding together the cumulative hazard from individual causes.

The second approach is recommended because

Value

A vector of real numbers as the risk till t0 for each subject in newdata

References

riskRegression: Predicting the Risk of an Event using Cox Regression Models by Brice Ozenne, Anne Lyngholm Sorensen, Thomas Scheike, Christian Torp-Pedersen, Thomas Alexander Gerds <https://journal.r-project.org/archive/2017/RJ-2017-062/RJ-2017-062.pdf> Thanks to Professor Gerds for helpful discussion.

Competing Risk Analysis Columbia Public Health <https://www.publichealth.columbia.edu/research/population-health-methods/competing-risk-analysis>

Introduction to the Analysis of Survival Data in the Presence of Competing Risks Peter C Austin, Douglas S Lee, Jason P Fine <https://www.ahajournals.org/doi/full/10.1161/CIRCULATIONAHA.115.017719>

See Also

[predictCompetingRisk](#).

Examples

```
library(survival)

# prepare a dataset with competing risk
lung1=lung[order(lung$time),]
lung1$status=lung1$status-1
lung1$status[1:50]=2
with(lung1, table(status))
lung1$status.1=ifelse(lung1$status==1,1,0)
lung1$status.2=ifelse(lung1$status==2,1,0)
lung1$status.a=ifelse(lung1$status==0,0,1)
lung1$wt=rep(1, nrow(lung1))

#####
# predictCompetingRisk2
```

```

t0=1000
formula.list=list(
  Surv(time, status.1) ~ age,
  Surv(time, status.2) ~ age
)

cif.2=pcr2(formula.list, lung1, t0)

fit=coxph(formula.list[[1]], lung1)
newdata=lung1
newdata$time=t0
coxpred = 1 - exp(-predict(fit, newdata=newdata, type="expected"))

plot(cif.2, coxpred)

## results match those from riskRegression_2022.07.13 when weights are all 1
#library(riskRegression)
#fit2 <- CSC(list(Hist(time,status)~sex, Hist(time,status)~age), data=lung1, surv.type="hazard",
#cause=1)
#r2=c(predictRisk(fit2,cause=1,product.limit=F,newdata=lung1,times=t0))
#head(cbind(cif, r2))

## pcr can produce cif that is greater than 1, especially when the covariates for the overall
## failure model differs from the covariates for the cause-specific model
## because the survival prob for the overall failure for a subject can be arbitrarily high
#cif.1=pcr(Surv(time, status.1) ~ sex, Surv(time, status.a) ~ age, lung1, t0)
##
#fit3 <- CSC(list(Hist(time,status)~sex, Hist(time,status)~age), data=lung1, surv.type="surv",
# cause=1)
#r3=c(predictRisk(fit3,cause=1,product.limit=F,newdata=lung1,times=t0))

# dealing with weights
lung1$wt=c(rep(2,50), rep(1, nrow(lung1)-50))
cif=predictCompetingRisk2(formula.list, lung1, t0, weights=lung1$wt)

#####
# predictCompetingRisk

t0=1000
form =Surv(time, status.1) ~ age
form.a=Surv(time, status.a) ~ age
cif=predictCompetingRisk(form, form.a, lung1, t0, newdata=lung1, weights=lung1$wt, stype=2,ctype=2)

## results match those from riskRegression_2022.07.13 when weights are all 1
#library(riskRegression)
#fit2 <- CSC(Hist(time,status)~age, data=lung1, surv.type="survival",cause=1)
#r2=c(predictRisk(fit2,cause=1,product.limit=F,newdata=lung1,times=t0))
#head(cbind(cif, r2))

# more validation code

```

```

# when there is no covariate and one cause, CIF = 1 - KM estimate of survival prob

lung1=lung[order(lung$time),]
lung1$status=lung1$status-1
with(lung1, table(status))
lung1$status.1=ifelse(lung1$status==1,1,0)
lung1$status.a=ifelse(lung1$status==0,0,1)
lung1$wt=rep(1, nrow(lung1))

# stype=2 is surv=prod limit
fitKM <- survfit(Surv(time, status.1) ~ 1, data=lung1, stype=1, ctype=2)
cbind(summary(fitKM)$cumhaz, exp(-summary(fitKM)$cumhaz), summary(fitKM)$surv)[1:2,]
#[1,] 0.004385965 0.9956236 0.9956140
#[2,] 0.017660474 0.9824946 0.9824561
cif=predictCompetingRisk(Surv(time, status.1) ~ 1, Surv(time, status.1) ~ 1, lung1, t0=11,
  newdata=lung1[,drop=FALSE], weights=lung1$wt, stype=1, ctype=2)
cif # 0.01754386
1-cif # 0.9824561 = summary(fitKM)$surv at t=11

# when there are covariates and one cause, CIF and 1-exp(-H) are close to each other
# when H is small but not close when H is large
form =Surv(time, status.1) ~ age
form.a=Surv(time, status.a) ~ age
par(mfrow=c(1,2))
for (t0 in c(12,1000)) {
  fit=coxph(form, lung1, weights=lung1$wt)
  lung2=lung1; lung2$time=t0
  r=predict(fit, type="expected", newdata=lung2)
  print(head(basehaz(fit, centered=TRUE)))
  cif=predictCompetingRisk(form, form.a, lung1, t0, newdata=lung1, weights=lung1$wt, stype=2,
    ctype=2)
  plot(cif, 1-exp(-r), xlab="Cumulative incidence function",
    ylab="Expected number of events from predict.coxph", main="t0: a later time point")
  abline(0,1)
  print(head(cbind(cif, 1-exp(-r))))
}

```

Description

roundup prints a specified number of digits after decimal point even if 0s are needed at the end.
 formatInt prints a specified number of digits before decimal point even if 0s are needed at the beginning.

Usage

```

myprint(object, ...)

## Default S3 method:
myprint(..., newline = TRUE, digits = 3, print.name=TRUE)

## S3 method for class 'matrix'
myprint(object, ...)

formatInt(x, digits, fill = "0", ...)

make.latex.coef.table(models, model.names = NULL, row.major = FALSE, round.digits = NULL)

mysanitize.text(str)
mysanitize.numbers(x)

mytex(dat = NULL, file.name = "temp", digits = NULL, display
      = NULL, align = "r", include.rownames = TRUE,
      include.colnames = TRUE, col.headers = NULL, comment =
      FALSE, floating = FALSE, lines = TRUE, hline.after =
      NULL, add.to.row = NULL, sanitize.text.function =
      NULL, append = FALSE, preamble = "", input.foldername
      = NULL, save2input.only = NULL, caption = NULL, label
      = paste("tab", last(strsplit(file.name, "/")[1])),
      sep = " "), table.placement = "h!",
      add.clear.page.between.tables = FALSE, longtable =
      FALSE, verbose = FALSE, ...)

mytex.begin(file.name, preamble = "")

mytex.end(file.name)

mywrite(x, ...)

mywrite.csv(x, file = "tmp", row.names = FALSE, digits = NULL, ...)

roundup (value, digits, na.to.empty=TRUE, remove.leading0=TRUE)

formatDouble(value, digits, na.to.empty=TRUE, remove.leading0=TRUE)

```

Arguments

input.foldername

object

newline

print.name
save2input.only
include.colnames Boolean
col.headers string. Column headers
comment Boolean, whether to include the version and timestamp comment
hline.after vector
add.to.row a list
sanitize.text.function a function
str
remove.leading0
caption
longtable
label default to be the same as file.name stem
table.placement
na.to.empty
value
digits
fill
models
model.names
row.major
round.digits
dat
file.name
display
align
append
preamble
include.rownames
floating
lines
...
verbose
x
file
row.names
add.clear.page.between.tables

Examples

```

roundup (3.1, 2) # 3.10

formatInt(3, 2) # 03

## Not run:

# demo of dimnames
tab=diag(1:4); rownames(tab)<-colnames(tab)<-1:4; names(dimnames(tab))=c("age","height")
# for greek letter in the labels, we need sanitize.text.function=identity
rownames(tab)[1]="$\alpha$"
# note that to use caption, floating needs to be TRUE
mytex (tab, file="tmp1", sanitize.text.function=identity,
       caption="This is a caption .....", caption.placement="top",
       floating=TRUE)

# col.headers has to have the RIGHT number of columns
# but align is more flexible, may not need to include the rownames col
tab=diag(1:4); rownames(tab)<-colnames(tab)<-1:4
mytex (tab, file="tmp", include.rownames = TRUE,
       align=c("c","c","c|","c","c"), col.headers=
       "\hline\n & \multicolumn{2}{c|}{Vaccine} & \multicolumn{2}{c}{Control} \\ \n")
# not include rownames
mytex (tab, file="tmp", include.rownames = FALSE,
       align=c("c","c","c|","c","c"), col.headers=
       "\hline\n      \multicolumn{2}{c|}{Vaccine} & \multicolumn{2}{c}{Control} \\ \n")
# It should work even if some rownames are duplicated
tab=diag(1:4); rownames(tab)=rep(1,4); colnames(tab)<-1:4
mytex (tab, file="tmp", include.rownames = TRUE,
       align=c("c","c|","c","c"), col.headers=
       "\hline\n & \multicolumn{2}{c|}{Vaccine} & \multicolumn{2}{c}{Control} \\ \n")

# add.to.rows
tab=diag(1:4); rownames(tab)<-1:4; colnames(tab)<-c("a","b","c","d")
mytex (tab, file="tmp",
       add.to.row=list( list(0,2),
                        c("      \multicolumn{5}{l}{Heading 1} \\ \n",
                          "\hline\n \multicolumn{5}{l}{Heading 2}\\ \n"
                        ))
)

## End(Not run)

```

random.functions	<i>Random Functions</i>
------------------	-------------------------

Description

Generate samples from random variables.

Usage

```
dbern(x, prob, log = FALSE)
dcorbern(x, p, a, log = FALSE)
dmixnorm(x, mix.p, sd1, sd2, log = FALSE)
dnorm.norm.gamma(x, p, same.distr = FALSE, log = FALSE)
rbern(n, prob, generalized = FALSE)
rbigamma(n, shape.1, shape.2, rate.1, rate.2, rho)
rbilogistic(n, loc.1, loc.2, scale.1, scale.2, rho)
rejective.sampling(N, n, pik)
rnorm.ar(n, sd, rho)
rnorm.norm.gamma(n, mu.0, lambda, alpha, beta)
rmixnorm (n, mix.p, mu1, mu2, sd1, sd2)
rdoublexp(n, location=0, scale=1)
ddoublexp(x, location=0, scale=1)
qdoublexp(p, location=0, scale=1)
pdoublexp(q, location=0, scale=1)
rbidoublexp(n, loc.1, loc.2, scale.1, scale.2, rho)
```

Arguments

q
location
scale
x

prob
log
p
a
mix.p
sd1
sd2
same.distr
n
generalized
N
pik
mu
mu1
mu2
sd
alpha
mu.0
lambda
beta
loc.1
loc.2
scale.1
scale.2
rate.1
rate.2
shape.1
shape.2
rho

Details

rbern generates Bernoulli random variables.

rbilogistic generates a bivariate logistic distribution for correlation coefficient 0.5, or [-0.271, 0.478]. In the former case it is generated by calling `rbi-logis`, part of the VGAM package; in the latter case it is generated via the AMH copular.

rnorm.ar simulate autoregressive normal random variables, correlation is ρ^d between x_1 and $x_{(1+d)}$

Examples

```
set.seed(1)
rbern(n=10, p=1/2)
rbern(n=2, p=c(.999, .001))

## Not run:
tmp=replicate(1e4, rnorm.cor(10, 1, .81))
round(cor(t(tmp)),2)

## End(Not run)
```

```
regression.model.functions
      Regression Model Functions
```

Description

getFormattedSummary prints a table of regression coefficient estimates and standard errors.

Usage

```
getFormattedSummary(fits, type = 12, est.digits = 2, se.digits = 2,
  robust, random = FALSE, VE = FALSE, to.trim = FALSE,
  rows = NULL, coef.direct = FALSE, trunc.large.est =
  TRUE, scale.factor = 1, p.digits = 3, remove.leading0
  = FALSE, p.adj.method = "fdr", ...)

getVarComponent(object, ...)

getFixedEf(object, ...)

risk.cal(risk, binary.outcome, weights = NULL, ngroups = NULL,
  cuts = NULL, main = "", add = FALSE, show.emp.risk = TRUE,
  lcol = 2, ylim = NULL, scale = c("logit", "risk"))
interaction.table(fit, v1, v2, v1.type = "continuous", v2.type = "continuous",
  logistic.regression = TRUE)

## S3 method for class 'coxph'
getFixedEf(object, exp=FALSE,robust=FALSE, ...)

## S3 method for class 'gam'
getFixedEf(object, ...)

## S3 method for class 'gee'
```

```
getFixedEf(object, exp = FALSE, ...)  
  
## S3 method for class 'geese'  
getFixedEf(object, robust = TRUE, ...)  
## S3 method for class 'tps'  
getFixedEf(object, exp=FALSE, robust=TRUE, ...)  
  
## S3 method for class 'glm'  
getFixedEf(object, exp = FALSE, robust = TRUE, ret.robcov = FALSE,  
  ...)  
  
## S3 method for class 'svyglm'  
getFixedEf(object, exp = FALSE, robust = TRUE, ...)  
## S3 method for class 'svy_vglm'  
getFixedEf(object, exp = FALSE, robust = TRUE, ...)  
  
## S3 method for class 'svycoxph'  
getFixedEf(object, exp = FALSE, robust = TRUE, ...)  
  
## S3 method for class 'inla'  
getFixedEf(object, ...)  
  
## S3 method for class 'lm'  
getFixedEf(object, ...)  
  
## S3 method for class 'lme'  
getFixedEf(object, ...)  
  
## S3 method for class 'logistf'  
getFixedEf(object, exp = FALSE, ...)  
  
## S3 method for class 'matrix'  
getFixedEf(object, ...)  
  
## S3 method for class 'MIresult'  
getFixedEf(object, ...)  
  
## S3 method for class 'hyperpar.inla'  
getVarComponent(object, transformation = NULL, ...)  
  
## S3 method for class 'matrix'  
getVarComponent(object, ...)  
  
## S3 method for class 'geese'  
coef(object, ...)  
## S3 method for class 'tps'  
coef(object, ...)
```

```
## S3 method for class 'geese'  
predict(object, x, ...)  
## S3 method for class 'tps'  
predict(object, newdata = NULL, type = c("link", "response"), ...)  
  
## S3 method for class 'geese'  
residuals(object, y, x,...)  
  
## S3 method for class 'geese'  
vcov(object, ...)  
## S3 method for class 'tps'  
vcov(object, robust, ...)  
  
## S3 method for class 'logistf'  
vcov(object, ...)
```

Arguments

```
...  
object  
fit  
coef.direct  
robust          Boolean, whether to return robust variance estimate  
exp  
remove.leading0  
  
p.adj.method  
cuts  
ret.robcov  
fits  
type  
est.digits  
se.digits  
p.digits  
random  
VE  
transformation  
weights  
v1  
v2  
v1.type  
v2.type
```

```
logistic.regression
```

```
newdata
```

```
x
```

```
y
```

```
to.trim
```

```
rows
```

```
risk
```

```
binary.outcome
```

```
ngroups
```

```
main
```

```
add
```

```
show.emp.risk
```

```
lcol
```

```
ylim
```

```
scale
```

```
trunc.large.est
```

```
scale.factor
```

Details

getFormattedSummary: from a list of fits, say lmer, inla fits, return formatted summary controlled by "type". For a matrix, return Monte Carlo variance random=TRUE returns variance components type=1: est type=2: est (se) type=3: est (2.5 percent, 97.5 percent) type=4: est se

getFixedEf returns a matrix, first column coef, second column se,

getFixedEf.matrix used to get mean and sd from a jags or winbugs sample, getVarComponent.matrix and getFixedEf.matrix do the same thing. Each column of samples is a variable

interaction.table expects coef and vcov to work with fit.

Examples

```
## Annette Dobson (1990) "An Introduction to Generalized Linear Models".
## Page 9: Plant Weight Data.
ctl <- c(4.17,5.58,5.18,6.11,4.50,4.61,5.17,4.53,5.33,5.14)
trt <- c(4.81,4.17,4.41,3.59,5.87,3.83,6.03,4.89,4.32,4.69)
group <- gl(2, 10, 20, labels = c("Ctl","Trt"))
weight <- c(ctl, trt)
lm.D9 <- lm(weight ~ group)
glm.D9 <- glm(weight ~ group)
getFormattedSummary (list(lm.D9, glm.D9), robust=FALSE)
```

sim.dat.tvarying.two *Simulation Functions for Time-dependent Proportional Hazard Model*

Description

sim.dat.tvarying.three simulates from a model with time varying age group variable of three levels, sim.dat.tvarying.two two.

Usage

```
sim.dat.tvarying.three(n, followup.length, incidence.density,  
  age.sim = c("tvaryinggroup", "baselinegroup", "continuous", "bt"),  
  random.censoring.rate = 0.05, seed)
```

```
sim.dat.tvarying.two(n, followup.length, incidence.density,  
  age.sim = c("tvaryinggroup", "baselinegroup", "continuous", "bt"),  
  random.censoring.rate = 0.05, seed)
```

Arguments

n	integer. Sample size.
followup.length	numeric. Length of followup, in years.
incidence.density	numeric. Incidence rate per year.
age.sim	string. Choose between one of three possibilities. tvaryinggroup: age group is time-varying covariate; baselinegroup: age group is a baseline covariate; continuous: age is a continuous covariate; bt: age group by treatment interaction uses baseline age group, while age group main effect uses time-dependent age group
random.censoring.rate	numeric. Amount of random censoring.
seed	integer. Random number generator seed.

Details

In sim.dat.tvarying.three, baseline age is uniformly distributed between 2.0 and 16.0, and divided into three groups at 6 and 12. In sim.dat.tvarying.two, baseline age is uniformly distributed between 2.0 and 12.0, and divided into two groups at 6.

Value

Return a data frame with the following columns:

ptid	subject identifier
trt	treatment indicator 0/1

for.non.tvarying.ana	Boolean, used to subset dataset for non-time dependent analysis
C	censoring time
baseline.age	age years at baseline
agegrp	a factor with levels [0,6) [6,12) [12,100)
baseline.agegrp	a factor with levels [0,6) [6,12) [12,100)
tstart	left bound of time interval
tstop	right bound of time interval
d	event indicator
X	followup time, in years

Author(s)

Youyi Fong

See Also

[make.timedep.dataset](#)

Examples

```
library(survival)

dat=sim.dat.tvarying.three(n=6000, followup.length=3, incidence.density=0.05,
  age.sim="tvaryinggroup", seed=1)
f.tvarying = Surv(tstart,tstop,d) ~ trt*agegrp
f =          Surv(X,d)           ~ trt*baseline.agegrp
fits=list()
fits[["tvarying"]]=coxph(f.tvarying, dat)
fits[["baseline"]]=coxph(f, subset(dat, for.non.tvarying.ana))
fits
```

stat.functions	<i>Stat Functions</i>
----------------	-----------------------

Description

H calculates entropy.

Usage

```
H(p, logbase = c("e", "2"))  
  
mutual.info(two.way.table, logbase = c("e", "2"))  
  
cor.mixed(x, ...)  
  
## Default S3 method:  
cor.mixed(x, na.fun, method=c("pearson", "spearman"), ...)  
## S3 method for class 'vector'  
cor.mixed(x, y, na.fun, method=c("pearson", "spearman"), ...)  
## S3 method for class 'formula'  
cor.mixed(formula, data, na.fun, method=c("pearson", "spearman"), ...)  
  
skew(x, na.rm = FALSE)  
  
info.cor(two.way.table)  
  
yule.y(two.by.two.matrix)  
  
kappa.cor(two.by.two.matrix, weight = c(1, 1), maximum = FALSE)  
  
l.measure(two.by.two.matrix)
```

Arguments

p	either a count vector or a probability vector, but can not be a vector of membership indicator
logbase	
na.rm	
two.way.table	
x	
...	
na.fun	
method	
y	

formula
data
two.by.two.matrix

weight
maximum

Examples

```
H(rep(1/5,5))  
H(rep(3,5))
```

string.functions *String Functions*

Description

`%+%` concatenates its arguments and returns a string.

Usage

```
a %.% b  
  
contain(s1, s2)  
trim(x, trim.trailing=TRUE, trim.leading=TRUE)  
  
escapeUnderline(name)  
  
fileStem(file.name)  
  
firstIndex(s1, s2)  
  
getExt(file.name)  
  
getFileStem(file.name)  
  
getStem(file.name)  
  
lastIndex(s1, s2)  
  
remove.prefix(s, sep = "_")
```

Arguments

a
b
s1
s2
name
file.name
s
sep
x
trim.leading
trim.trailing

Examples

```
x=1  
x %.% "b" %.% "c"
```

testing.functions *Testing Functions*

Description

Testing functions.

Usage

```
hosmerlem(y, yhat, g = 10)  
quick.t.test(x, y, var.equal = FALSE)  
signtest(x)  
tukey.mtest(mu, ms, n)  
vector.t.test(mean.x, mean.y, var.x, var.y, n)  
myfisher.test(x,y,...)  
mycor.test(x, method = c("pearson", "kendall", "spearman"), idx =  
  NULL)
```

Arguments

```

...
y
yhat
g
x
var.equal
method
mu
ms
n
mean.x
mean.y
var.x
var.y
idx

```

Examples

```

signtest(runif(10))

```

VEplot

Vaccine Efficacy Plots

Description

Vaccine efficacy plots.

Usage

```

VEplot (object, ...)

## S3 method for class 'cox.zph'
VEplot(object, resid = TRUE, se = TRUE, df = 4, nsmo = 40,
       var, ylab="VE", xlab="Time", xaxt="s", cex.axis=1, ...)

## S3 method for class 'glm'
VEplot(object, X1, X2, x, ...)

## S3 method for class 'cox.zph'

```

```
myplot(object, resid = TRUE, se = TRUE, df = 4, nsmo = 40, var,
       coef.transform=NULL,
       ylab=NULL,
       xlab="Time", xaxt="s", cex.axis=1,
       ...)
```

Arguments

object	An object
resid	Boolean, whether to plot residuals
se	Boolean, whether to plot confidence band
df	degrees of freedom
nsmo	number of points used to plot the fitted spline
var	estimated variance matrix from the Cox model fit
xlab	x label
xaxt	x axis
cex.axis	cex for axis
ylab	y label
coef.transform	a function to transform Cox hazard ratio estimate
X1	a matrix of dimension k by p, where k is the length of x (see below) and p is the length of coef(object)
X2	a matrix of dimension k by p, where k is the length of x (see below) and p is the length of coef(object)
x	a vector of length k that represents the x coordinate of the VE plot
...	additional parameters

Details

VEplot and myplot.cox.zph are extensions of survival::plot.cox.zph to plot VE curve and other transformations.

myplot.cox.zph adds the following parameters to the original list of parameters in plot.cox.zph: coef.transform: a function to transform the coefficients ylab: y axis label xlab: x axis label

VEplot.glm computes a series of k VEs: for i in $1..k$, $VE[i] = P(Y=1|X1[i,])/P(Y=1|X2[i,])$. It returns a 3 by k matrix, whose first row contains VE estimates and the second and third rows contain lower and upper bounds, respectively.

Author(s)

Youyi Fong, Dennis Chao

References

Durham, Longini, Halloran, Clemens, Azhar and Rao (1998) "Estimation of vaccine efficacy in the presence of waning: application to cholera vaccines." American Journal of Epidemiology 147(10): 948-959.

Examples

```
library(survival)
vfit <- coxph(Surv(time,status) ~ trt + factor(celltype) +
             karno + age, data=veteran, x=TRUE)
temp <- cox.zph(vfit)

par(mfrow=c(2,2))
for (v in c("trt","age")) {
  VEplot(temp, var=v, resid=FALSE, main=v, ylab="VE", cex.axis=1.5)
  plot(temp, var=v, resid=FALSE, main=v)
}

library(survival)
fit <- glm(status ~ trt + trt*age, data=veteran)
summary(fit)
age=seq(min(veteran$age),max(veteran$age),length=10)
out = VEplot(fit, X1=cbind(1,1,age,1*age), X2=cbind(1,0,age,0*age), x=age)
out
```

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