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Description Utility functions, datasets and extended examples for survival analysis. This includes a range of other packages, some simple wrappers for time-to-event analyses, datasets, and extensive examples in HTML with R scripts. The package also supports the course Biostatistics III entitled “Survival analysis for epidemiologists in R”.

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biostat3-package	2
addIndicators	3
brv	3

colon	4
colon_sample	5
coxphHaz	6
diet	7
eform	8
lifetab	9
lifetab2	10
lincom	11
melanoma	12
muhaz2	13
poisson.ci	14
popmort	15
smoothHaz	15
survPHplot	16
survRate	17
utilities	18
year	19
Index	20

biostat3-package	<i>Utility Functions, Datasets and Extended Examples for Survival Analysis</i>
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Description

Utility functions, datasets and extended examples for survival analysis. This includes a range of other packages, some simple wrappers for time-to-event analyses, datasets, and extensive examples in HTML with R scripts. The package also supports the course Biostatistics III entitled "Survival analysis for epidemiologists in R".

Author(s)

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Examples

```
plot(muhaz2(Surv(surv_mm, status == "Dead: cancer")~1, melanoma))
```

addIndicators	<i>Utility to add indicators from a data-frame based on a formula.</i>
---------------	--

Description

Column-bind a model matrix to the source data-frame

Usage

```
addIndicators(data, formula, drop.intercept = TRUE)
```

Arguments

`data` source data-frame or matrix.
`formula` model formula used to add columns.
`drop.intercept` logical as to whether to drop the column named '(Intercept)'.

Details

This function calls `model.matrix`, conditionally checks for and removes '(Intercept)', and binds with the original data-frame (or matrix).

Value

data-frame or matrix.

Examples

```
addIndicators(data.frame(f = c("a", "a", "b")), ~f+0)
```

brv	<i>Bereavement dataset</i>
-----	----------------------------

Description

Bereavement dataset

Usage

```
data("brv")
```

Format

A data frame with 399 observations on the following 11 variables.

id a numeric vector
 couple a numeric vector
 dob a Date
 doe a Date
 dox a Date
 dosp a Date
 fail a numeric vector
 group a numeric vector
 disab a numeric vector
 health a numeric vector
 sex a numeric vector

colon

Colon cancer dataset

Description

Colon cancer dataset

Usage

```
data("colon")
```

Format

A data frame with 15564 observations on the following 13 variables.

sex a factor for the sex of the cancer patient with levels Male and Female
 age a numeric vector for the age at cancer diagnosis
 stage a factor for the cancer stage (or extent) as cancer diagnosis, with levels Unknown, Localised, Regional and Distant
 mmdx a numeric vector for the month of cancer diagnosis
 yydx a numeric vector for the (truncated) year of cancer diagnosis
 surv_mm a numeric vector for the number of months since cancer diagnosis
 surv_yy a numeric vector for the number of years since cancer diagnosis
 status a factor for status at end of follow-up, with levels Alive, Dead: cancer, Dead: other and Lost to follow-up
 subsite a factor for the sub-site of the cancer, with levels Coecum and ascending, Transverse, Descending and sigmoid, and Other and NOS

year8594 a factor for calendar period of cancer diagnosis with levels Diagnosed 75-84 Diagnosed 85-94
agegrp a factor for age group at cancer diagnosis with levels 0-44 45-59 60-74 75+
dx a Date for the date of cancer diagnosis
exit a Date for the date of study exit
id a numeric for a row ID
ydx a numeric for the (continuous) year of cancer diagnosis
yexit a numeric for the (continuous) year of study exit

colon_sample *Sample from the colon dataset used for teaching.*

Description

Sample from the `colon` dataset used for teaching.

Usage

```
data("colon_sample")
```

Format

A data frame with 35 observations on the following 9 variables.

sex a factor with levels Male Female

age a numeric vector

stage a factor with levels Unknown Localised Regional Distant

mmdx a numeric vector

yydx a numeric vector

surv_mm a numeric vector

surv_yy a numeric vector

status a factor with levels Alive Dead: cancer Dead: other Lost to follow-up

subsite a factor with levels Coecum and ascending Transverse Descending and sigmoid
Other and NOS

coxphHaz

*Smoothed hazard estimates for coxph***Description**

Smoothed hazard estimates for coxph

Usage

```
coxphHaz(object, newdata, n.grid = 300, kernel = "epanechnikov", from,
to, ...)
## S3 method for class 'coxphHaz'
print(x, digits=NULL, ...)
## S3 method for class 'coxphHaz'
plot(x, xlab="Time", ylab="Hazard", type="l", ...)
## S3 method for class 'coxphHazList'
plot(x, xlab="Time", ylab="Hazard", type="l",
      col=1:length(x), lty=1, legend.args=list(), ...)
## S3 method for class 'coxphHazList'
lines(x, ...)
```

Arguments

object	coxph object
newdata	data-frame with covariates for prediction
n.grid	the number of grid values for which the hazard is calculated
kernel	the kernel used for smoothing
from	argument for density. Defaults to the minimum time.
to	argument for density. Defaults to the maximum time.
x	object
digits	argument passed to print.density
col	graphics argument
lty	graphics argument
xlab	graphics argument
ylab	graphics argument
type	graphics argument
legend.args	a list of options that are passed to the legend call. Defaults are list(x="topright", legend=strata(attach=TRUE, ...))
...	other arguments. For coxphHaz, these arguments are passed to density. For the plot and lines methods, these are passed to the relevant plot, matplot and matlines functions.

Details

Smooth hazard estimates from a Cox model using kernel smoothing of the Nelson-Aalen estimator.

Value

The `coxphHaz` function returns either a class of type `c("coxphHaz", "density")` when `newdata` has one row or, for multiple rows in `newdata`, a class of type `"coxphHazList"`, which is a list of type `c("coxphHaz", "density")`.

See Also

[coxph](#), [survfit](#), [density](#)

Examples

```
fit <- coxph(Surv(surv_mm/12, status=="Dead: cancer")~agegrp, data=colon)
newdata <- data.frame(agegrp=levels(colon$agegrp))
haz <- suppressWarnings(coxphHaz(fit, newdata))
plot(haz, xlab="Time since diagnosis (years)")
legend("topright", legend=newdata$agegrp, lty=1:4, col=1:4, bty="n")
```

diet

Diet data set

Description

Diet dataset

Usage

```
data("diet")
```

Format

A data frame with 337 observations on the following 12 variables.

`id` a numeric vector for the individual id
`chd` a numeric vector indicating subsequent coronary heart disease episode (0=no event, 1=event)
`y` a numeric vector for the time at risk
`hieng` a factor with levels low for low energy and high energy diet
`energy` a numeric vector for the energy level of the diet
`job` a factor with levels driver, conductor and bank
`month` a numeric vector indicating the month of study entry
`height` a numeric vector for height in cm
`weight` a numeric vector for weight in kg
`doe` a Date for date of study entry
`dox` a Date for date of study exit
`dob` a Date for date of birth
`yoe` a numeric vector for continuous year of study entry
`yox` a numeric vector for continuous year of study exit
`yob` a numeric vector for continuous year of birth

eform	<i>Calculate the exponential form for coefficients and their confidence intervals using either profile likelihood-based or Wald-based confidence intervals.</i>
-------	---

Description

irr and or use eform with a different name for the estimator.

Usage

```
eform(object, ...)
## Default S3 method:
eform(object, parm, level = 0.95, method =
c("Delta","Profile"), name = "exp(beta)", ...)
irr(..., name = "IRR")
or(..., name = "OR")
```

Arguments

object	A fitted model object with coef and confint methods
parm	a specification of which parameters are to be given confidence intervals, either a vector of numbers or a vector of names. If missing, all parameters are considered.
level	the confidence level required
method	string to determine method to use the delta method (stats::confint.default), which assumes that the parameters are asymptotically normal, or profile likelihood-based confidence intervals (MASS::confint.glm), respectively.
name	name of the estimator.
...	arguments to pass from irr or or to eform.

Value

A matrix (or vector) with columns giving lower and upper confidence limits for each parameter. These will be labelled as (1-level)/2 and 1 - (1-level)/2 in

Examples

```
## from example(glm)
counts <- c(18,17,15,20,10,20,25,13,12)
outcome <- gl(3, 1, 9); treatment <- gl(3, 3)
glm.D93 <- glm(counts ~ outcome + treatment, family = poisson())
eform(glm.D93)
eform(glm.D93, method="Profile")
```

lifetab	<i>Create cohort life table</i>
---------	---------------------------------

Description

Create cohort life table.

Usage

```
lifetab(tis, ninit, nlost, nevent)
```

Arguments

tis	a vector of end points of time intervals, whose length is 1 greater than nlost and nevent.
ninit	the number of subjects initially entering the study.
nlost	a vector of the number of individuals lost follow or withdrawn alive for whatever reason.
nevent	a vector of the number of individuals who experienced the event

Value

A data.frame with the following columns:

nsubs	the number of subject entering the intervals who have not experienced the event.
nlost	the number of individuals lost follow or withdrawn alive for whatever reason.
nrisk	the estimated number of individuals at risk of experiencing the event.
nevent	the number of individuals who experienced the event.
surv	the estimated survival function at the start of the intervals.
pdf	the estimated probability density function at the midpoint of the intervals.
hazard	the estimated hazard rate at the midpoint of the intervals.
se.surv	the estimated standard deviation of survival at the beginning of the intervals.
se.pdf	the estimated standard deviation of the prbability density function at the midpoint of the intervals.
se.hazard	the estimated standard deviation of the hazard function at the midpoint of the intervals

The row.names are the intervals.

Author(s)

Jun Yan <jyan@stat.uconn.edu>

Examples

```
tis <- c(0, 2, 3, 5, 7, 11, 17, 25, 37, 53, NA)
nsubs <- c(927, 848, 774, 649, 565, 449, 296, 186, 112, 27)
nlost <- c(2, 3, 6, 9, 7, 5, 3, rep(0, 3))
nevent <- c(77, 71, 119, 75, 109, 148, 107, 74, 85, 27)

lifetab(tis, nsubs[1], nlost, nevent)
```

lifetab2

Formula wrapper for [lifetab](#) from the `KMsurv` package.

Description

Calculate a life table using the actuarial method using a formula and a data-frame with optional breaks.

Usage

```
lifetab2(formula, data, subset, breaks = NULL)
```

Arguments

formula	formula with the left-hand side being a <code>Surv</code> object, including a time and event indicator, and the right-hand side indicated stratification.
data	optional <code>data.frame</code> for the <code>Surv</code> object. If this is not provided, then the parent frame is used for the <code>Surv</code> object.
subset	optional subset statement
breaks	optional numeric vector of breaks. If this is not provided, then the unique time values from the <code>Surv</code> object are used together with <code>Inf</code> .

Details

See `lifetab` for details. This wrapper is meant to make life easier.

A copy of the `lifetab` function has been included in the `biostat3` package to reduce dependencies.

Value

A `data.frame` as per [lifetab](#).

Author(s)

Mark Clements for the wrapper.

Examples

```
## we can use unique transformed times (colon_sample)
lifetab2(Surv(floor(surv_yy),status=="Dead: cancer")~1, colon_sample)

## we can also use the breaks argument (colon)
lifetab2(Surv(surv_yy,status=="Dead: cancer")~1, colon, breaks=0:10)
```

lincom	<i>Linear combination of regression parameters.</i>
--------	---

Description

Using results calculated by the [linearHypothesis](#) function in the car package, calculate a linear combination of regression parameters.

Usage

```
lincom(model, specification, level = 0.95, eform = FALSE, ...)
```

Arguments

model	regression model object (as per the model argument in linearHypothesis)
specification	specification of the linear combination. This is the same as a single component of the hypothesis.matrix argument in linearHypothesis .
level	the confidence level required
eform	logical for whether to exponentiate the confidence interval (default=FALSE)
...	other arguments to the linearHypothesis function.

Details

Multiple specifications of linear combinations are called individually.

Value

A matrix with columns including the estimate, a normal-based confidence interval, test statistic and p-values.

See Also

See Also [linearHypothesis](#).

Examples

```
fit <- glm(chd ~ hieng*job + offset(log(y)), data=diet, family=poisson)
lincom(fit, c("hienghigh+hienghigh:jobconductor",
             "hienghigh+hienghigh:jobbank"),
       eform=TRUE)
```

melanoma

Melanoma cancer dataset

Description

Melanoma cancer dataset

Usage

```
data("melanoma")
```

Format

A data frame with 7775 observations on the following 15 variables.

`sex` a factor for the sex of the cancer patient with levels Male and Female

`age` a numeric vector for the age at cancer diagnosis

`stage` a factor for the cancer stage (or extent) as cancer diagnosis, with levels Unknown, Localised, Regional and Distant

`mmdx` a numeric vector for the month of cancer diagnosis

`yydx` a numeric vector for the (truncated) year of cancer diagnosis

`surv_mm` a numeric vector for the number of months since cancer diagnosis

`surv_yy` a numeric vector for the number of years since cancer diagnosis

`status` a factor for status at end of follow-up, with levels Alive, Dead: cancer, Dead: other and Lost to follow-up

`subsite` a factor with levels Head and Neck, Trunk, Limbs and Multiple and NOS

`year8594` a factor for calendar period of cancer diagnosis with levels Diagnosed 75-84 Diagnosed 85-94

`dx` a Date for the date of cancer diagnosis

`exit` a Date for the date of study exit

`agegrp` a factor for age group at cancer diagnosis with levels 0-44, 45-59, 60-74 and 75+

`id` a numeric vector for row ID

`ydx` a numeric for the (continuous) year of cancer diagnosis

`yexit` a numeric for the (continuous) year of study exit

muhaz2

*Formula wrapper for the `muhaz` function from the `muhaz` package.***Description**

Formula wrapper for the `muhaz` function from the `muhaz` package.

Usage

```

muhaz2(formula, data, subset, max.time, ...)
## S3 method for class 'muhaz2'
plot(x, haz.scale=1, ylab="Hazard", ylim=NULL, log="", ...)
## S3 method for class 'muhazList'
plot(x, lty=1:5, col=1:length(x), log="", legend.args=list(), ...)
## S3 method for class 'muhaz2'
lines(x, ..., haz.scale = 1)
## S3 method for class 'muhazList'
lines(x, lty=1, col=1:length(x), ...)
## S3 method for class 'muhazList'
summary(object, ...)
## S3 method for class 'muhazList'
as.data.frame(x, row.names, optional, ...)
## S3 method for class 'muhaz'
as.data.frame(x, row.names, optional, ...)

```

Arguments

<code>formula</code>	formula with the left-hand side being a <code>Surv</code> object, including a time and event indicator, and the right-hand side indicated stratification.
<code>data</code>	optional <code>data.frame</code> for the <code>Surv</code> object. If this is not provided, then the parent frame is used for the <code>Surv</code> object.
<code>subset</code>	subset predicate for the dataset
<code>max.time</code>	maximum follow-up time for the hazards
<code>ylab</code>	graphics argument for <code>ylab</code> (y-axis label)
<code>lty</code>	graphics argument for line type
<code>col</code>	graphics argument for line colour
<code>legend.args</code>	a list of options that are passed to the legend call. Defaults are <code>list(x="topright", legend=names(x), c</code>
<code>haz.scale</code>	scale for the hazard in the plot
<code>row.names</code>	not currently used
<code>object</code>	<code>muhazList</code> object
<code>ylim</code>	graphics argument for the limits of the y axis
<code>log</code>	graphics argument for a log transformation of the x or y axes
<code>x</code>	<code>muhazList</code> or <code>muhaz</code> object
<code>optional</code>	not currently used
<code>...</code>	other arguments

Value

For a single strata, this is a [muhaz](#) object. For multiple strata, this is a [muhazList](#) object, which includes methods for

Examples

```
plot(muhaz2(Surv(surv_mm, status == "Dead: cancer")~1, melanoma))
```

poisson.ci

Exact Poisson confidence intervals.

Description

A wrapper for the [poisson.test](#) that allows for vector values.

Usage

```
poisson.ci(x, T = 1, conf.level = 0.95)
```

Arguments

x	number of events.
T	time base for event count.
conf.level	confidence level for the returned confidence interval.

Details

This uses `stats::poisson.test` for the calculations.

Value

A matrix (or vector) with columns giving lower and upper confidence limits for each parameter. These will be labelled as $(1-\text{level})/2$ and $1 - (1-\text{level})/2$ in % (by default 2.5% and 97.5%).

See Also

[poisson.test](#)

Examples

```
### These are paraphrased from data sets in the ISwR package

## SMR, Welsh Nickel workers
poisson.ci(137, 24.19893)

## eba1977, compare Fredericia to other three cities for ages 55-59
poisson.ci(c(11, 6+8+7), c(800, 1083+1050+878))
```

popmort	<i>popmort dataset, with population-based mortality rates</i>
---------	---

Description

popmort dataset, with population-based mortality rates

Usage

```
data("popmort")
```

Format

A data frame with 10600 observations on the following 5 variables.

sex a numeric vector

'_year' a numeric vector

'_age' a numeric vector

prob a numeric vector

rate a numeric vector

smoothHaz	<i>Simple implementation for kernel density smoothing of the Nelson-Aalen estimator.</i>
-----------	--

Description

Simple implementation for kernel density smoothing of the Nelson-Aalen estimator. Prefer muhaz for right censored data and bshazard for left truncated and right censored data.

Usage

```
smoothHaz(object, n.grid = 300, kernel = "epanechnikov",  
           from = NULL, to = NULL, min.n.risk = 1, ...)  
## S3 method for class 'smoothHaz'  
plot(x, xlab = "Time", ylab = "Hazard", type = "l", ...)
```

Arguments

object	survfit object
n.grid	number of grid points; passed to density
kernel	kernel used; passed to density
from	left boundary; passed to density
to	right boundary; passed to density
min.n.risk	minimum number at risk
x	object of class smoothHaz
xlab	graphics argument
ylab	graphics argument
type	graphics argument
...	Other arguments

 survPHplot

Plot to assess non-proportionality

Description

Plot of $\log(\text{time})$ versus $-\log(-\log(\text{survival}))$ to assess non-proportionality. A constant distance between curves suggest proportionality.

Usage

```
survPHplot(formula, data, subset, contrasts, weights, col = 1:5,
            lty = 1:5, pch = 19, xlab = "Time (log scale)",
            ylab = "-log(-log(Survival))", log = "x",
            legend.args = list(), ...)
```

Arguments

formula	either (i) formula with a Surv object on the left-hand-side and stratification covariates on the right-hand-side, or (ii) a survfit object
data	data argument passed to survfit
subset	subset argument passed to survfit
contrasts	contrasts argument passed to survfit
weights	weights argument passed to survfit
col	colours of the curves passed to lines
lty	line type of the curves passed to lines
pch	pch for the curves passed to points
xlab	xlab graphics argument passed to plot.default
ylab	ylab graphics argument passed to plot.default

log	log graphics argument passed to plot.default
legend.args	list of arguments passed to legend. These arguments update the base arguments, which are list(x="topright", legend=names(survfit\$strata), col=col, lty=lty, pch=pch)
...	Other arguments passed to plot.default

Details

The default plot is to use straight lines between the transformed survival values for each strata, rather than using steps.

Value

Primary purpose is for plotting (side effect). The return value is initial plot.

Examples

```
survPHplot(Surv(surv_mm/12, status == "Dead: cancer") ~ year8594,
            data=colon, subset=(stage=="Localised"),
            legend.args=list(bty="n"))
```

survRate	<i>Describe rates</i>
----------	-----------------------

Description

Describe rates using the [Surv](#) function.

Usage

```
survRate(formula, data, subset, addvars = TRUE, ci=TRUE, ...)
```

Arguments

formula	formula with the left-hand-side being a Surv function and the right-hand-side being any stratification variables.
data	source dataset
subset	subset conditions for the source dataset
addvars	logical for whether to add the stratification variables to the output (default=TRUE). This is useful for subsequent analysis.
ci	logical for whether to calculate the confidence interval (default=TRUE).
...	other arguments to the poisson.test function for calculation of the confidence intervals.

Value

data-frame with columns `tstop`, `event`, `rate`, `lower` and `upper`. Covariates are appended if `addvar=TRUE`.

Confidence intervals use `stats::poisson.test`.

Examples

```
## incidence rates for CHD for low- or high-energy diets
survRate(Surv(y,chd) ~ hieng, data=diet)
```

utilities

Utility functions for the biostat3 package

Description

Utility functions for the biostat3 package.

Usage

```
updateList(object, ...)
format_perc(probs, digits)
```

Arguments

<code>object</code>	base object (list)
<code>...</code>	arguments to update
<code>probs</code>	probability to express as a percentage
<code>digits</code>	number of significant digits

Details

Update the names in the base object list that are specified in the arguments to update.

Value

list

Examples

```
updateList(list(a=1,b=2), a=10, c=30)
```

year *Convert a Date vector to a numeric vector*

Description

Convert a Date vector to a numeric vector (either continuous or truncated).

Usage

```
year(date, trunc = FALSE, year.length = 365.24)
```

Arguments

date	Date vector
trunc	logical for whether to truncate the date to a whole year or consider the date as a double (default).
year.length	assumed length of a year

Details

For the double calculation, we use (truncated year of Date) + (date - 1 Jan of Year)/year.length.

Value

numeric vector

Examples

```
c(year(as.Date("2001-07-01")), year(as.Date("2001-01-01"), trunc=TRUE))
```

Index

- *Topic **datasets**
 - brv, 3
 - colon, 4
 - colon_sample, 5
 - diet, 7
 - melanoma, 12
 - popmort, 15
- *Topic **manip**
 - lifetab, 9
- *Topic **package**
 - biostat3-package, 2
- *Topic **survival**
 - biostat3-package, 2
 - coxphHaz, 6
 - lifetab2, 10
 - muhaz2, 13
 - smoothHaz, 15
 - survPHplot, 16
 - survRate, 17
- addIndicators, 3
- as.data.frame.muhaz (muhaz2), 13
- as.data.frame.muhazList (muhaz2), 13

- biostat3 (biostat3-package), 2
- biostat3-package, 2
- brv, 3

- colon, 4, 5
- colon_sample, 5
- coxph, 7
- coxphHaz, 6

- density, 7
- diet, 7

- eform, 8

- format_perc (utilities), 18

- irr (eform), 8

- lifetab, 9, 10
- lifetab2, 10
- lincom, 11
- linearHypothesis, 11
- lines.coxphHazList (coxphHaz), 6
- lines.muhaz2 (muhaz2), 13
- lines.muhazList (muhaz2), 13

- melanoma, 12
- muhaz, 13, 14
- muhaz2, 13

- or (eform), 8

- plot.coxphHaz (coxphHaz), 6
- plot.coxphHazList (coxphHaz), 6
- plot.muhaz2 (muhaz2), 13
- plot.muhazList (muhaz2), 13
- plot.smoothHaz (smoothHaz), 15
- poisson.ci, 14
- poisson.test, 14, 17
- popmort, 15
- print.coxphHaz (coxphHaz), 6

- smoothHaz, 15
- summary.muhazList (muhaz2), 13
- Surv, 17
- survfit, 7
- survPHplot, 16
- survRate, 17

- updateList (utilities), 18
- utilities, 18

- year, 19