Package ‘RcmdrPlugin.survival’

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Description This package provides an R Commander plug-in for the survival package, with dialogs for Cox models, parametric survival regression models, estimation of survival curves, and testing for differences in survival curves, along with data-management facilities and a variety of tests, diagnostics and graphs.
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RcmdrPlugin.survival-package

Rcmdr Plug-In Package for the survival Package

Description

This package provides an R Commander plug-in for the survival package, with dialogs for managing survival data (this to a limited extent), Cox models, parametric survival regression models, estimation of survival curves, testing for differences in survival curves, and a variety of diagnostics, tests, and displays.

Details

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The plug-in is tightly integrated with the R Commander interface; see the following menus: Data -> Survival data", Statistics -> Survival analysis, Statistics -> Fit Models, Models -> Hypothesis tests, Models -> Numerical diagnostics, Models -> Graphs.

Acknowledgments

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Author(s)

John Fox

Maintainer: John Fox <jfox@mcmaster.ca>

References

Hemodialysis Data from Brazil

Description

This data set is analyzed in Sa Carvalho et al. (2003), and consists of data on 6805 hemodialysis patients in all federally funded clinics in Rio de Janeiro State, Brazil.

Usage

data(Dialysis)

Format

A data frame with 6805 observations on the following 7 variables.

center  a numeric code indicating in which of 67 centers the patient was treated.
age  of the patient.
begin  The month in which treatment began, with 1 representing January 1998.
end  The month in which observation terminated, either because of death or censoring. The study ended in month 44 (August, 2000).
event  1, death, or 0, censoring.
time  the difference between end and begin.
disease  a factor with levels congen, (congenital); diabetes; hypert (hypertension); other; and renal.

Source


References


Examples

summary(Dialysis)
table(Dialysis$center)
**mfrow**  
*Function to Compute Layout for Plot Array*

**Description**  
Given a number of plots \( n \), find a arrangement for showing the plots in an array, set by \( \text{par}(\text{mfrow}=\text{mfrow}(n)) \).

**Usage**  
\[
\text{mfrow}(n, \text{max.plot} = 0)
\]

**Arguments**  
- \( n \): number of plots  
- \( \text{max.plot} \): maximum number of plots; 0, the default, means no maximum.

**Author(s)**  
John Fox <jfox@mcmaster.ca>

**See Also**  
- \( \text{par} \)

**Examples**  
\[
\text{mfrow}(4)  
\text{mfrow}(5)  
\text{mfrow}(6)
\]

---

**plot.coxph**  
*Plot Method for coxph Objects*

**Description**  
Plots the predicted survival function from a coxph object, setting covariates to particular values.

**Usage**  
\[
\#
\text{S3 method for class 'coxph'}
\text{plot}(x, \text{newdata}, \text{typical} = \text{mean}, \text{byfactors} = \text{FALSE},
\text{col} = \text{palette}(), \text{lty}, \text{conf.level} = 0.95, \ldots)
\]
Arguments

arguments

x
newdata
typical
byfactors
col
ty
conf.level
...

Details

If newdata is missing then all combinations of levels of factor-predictors (or strata), if present, are combined with "typical" values of numeric predictors.

Value

Invisibly returns the summary resulting from applying survfit.coxph to the coxph object.

Author(s)

John Fox <jfox@mcmaster.ca>.

References


See Also

coxph, survfit.coxph, plot.survfit.

Examples

require(survival)
cancer$sex <- factor(ifelse(cancer$sex == 1L, "male", "female"))

mod.1 <- coxph(Surv(time, status) ~ age + wt.loss, data=cancer)
plot(mod.1)
plot(mod.1, typical=function(x) quantile(x, c(.25, .75)))

mod.2 <- coxph(Surv(time, status) ~ age + wt.loss + sex, data=cancer)
plot(mod.2)
mod.3 <- coxph(Surv(time, status) ~ (age + wt.loss)*sex, data=cancer)
plot(mod.3)
mod.4 <- coxph(Surv(time, status) ~ age + wt.loss + strata(sex), data=cancer)
plot(mod.4)
mods.1 <- survreg(Surv(time, status) ~ age + wt.loss, data=cancer)

Rossi et al.'s Criminal Recidivism Data

Description
This data set is originally from Rossi et al. (1980), and is used as an example in Allison (1995). The data pertain to 432 convicts who were released from Maryland state prisons in the 1970s and who were followed up for one year after release. Half the released convicts were assigned at random to an experimental treatment in which they were given financial aid; half did not receive aid.

Usage
Rossi

Format
A data frame with 432 observations on the following 62 variables.

- week: week of first arrest after release or censoring; all censored observations are censored at 52 weeks.
- arrest: 1 if arrested, 0 if not arrested.
- fin: financial aid: no yes.
- age: in years at time of release.
- race: black or other.
- wexp: full-time work experience before incarceration: no or yes.
- mar: marital status at time of release: married or not married.
- paro: released on parole? no or yes.
- prio: number of convictions prior to current incarceration.
- educ: level of education: 2 = 6th grade or less; 3 = 7th to 9th grade; 4 = 10th to 11th grade; 5 = 12th grade; 6 = some college.
- emp1: employment status in the first week after release: no or yes.
- emp2: as above.
- emp3: as above.
- emp4: as above.
emp5 as above.
emp6 as above.
emp7 as above.
emp8 as above.
emp9 as above.
emp10 as above.
emp11 as above.
emp12 as above.
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emp38 as above.
emp39 as above.
emp40 as above.
emp41 as above.
SurvivalData

emp42 as above.
emp43 as above.
emp44 as above.
emp45 as above.
emp46 as above.
emp47 as above.
emp48 as above.
emp49 as above.
emp50 as above.
emp51 as above.
emp52 as above.

Source

References


Examples
summary(rossi)

---

**SurvivalData**

**Define Survival Data Dialog Box**

**Description**

This dialog box permits you to define a time variable (or start and stop variables), an event indicator, a strata variable or variables, and a cluster variable to be associated with the current data set. If these characteristics are defined, then they will become default choices where appropriate in other dialog boxes.

**Usage**

SurvivalData() # normally not called directly

**Value**

Used only for its side effect.
**unfold**

**Author(s)**

John Fox <jfox@mcmaster.ca>

**References**


---

**Convert a Survival Data Set from "Wide" to "Long" Format**

**Description**

Converts a survival-analysis data frame from "wide" format, in which time-varying covariates are separate variables, one per occasion, to "long" or counting-process format in which each occasion is a separate row in the data frame.

**Usage**

```r
unfold(dataL ...)
```

## S3 method for class 'data.frame'

```r
unfold(data, time, event, cov, 
    cov.names = paste("covariate",".", 1:ncovs, sep = ""),
    suffix = ".time", cov.times = 0:ncov, common.times = TRUE, lag = 0,
    show.progress=TRUE, ...)
```

**Arguments**

- `data`: a data frame to be "unfolded" from wide to long.
- `time`: the column number or quoted name of the event/censoring-time variable in data.
- `event`: the column number or quoted name of the event/censoring-indicator variable in data.
- `cov`: a vector giving the column numbers of the time-dependent covariate in data, or a list of vectors if there is more than one time-varying covariate.
- `cov.names`: a character string or character vector giving the name or names to be assigned to the time-dependent covariate(s) in the output data set.
- `suffix`: the suffix to be attached to the name of the time-to-event variable in the output data set; defaults to ".time".
- `cov.times`: the observation times for the covariate values, including the start time. This argument can take several forms: (1) The default is integers from 0 to the number of covariate values (i.e., one more than the length of each vector in cov). (2) An arbitrary numerical vector with one more entry than the length of each vector in cov. (3) The columns in the input data set that give the observations times for each individual. There should be one more column than the length of each vector in cov.
common.times  a logical value indicating whether the times of observation are the same for all individuals; defaults to TRUE.

lag number of observation periods to lag each value of the time-varying covariate(s); defaults to 0.

show.progress  if TRUE, the default, show a progress bar as the observations are processed.

... arguments to be passed down.

Value

A data frame containing the "long" version of the data set.

Author(s)

John Fox <jfox@mcmaster.ca>

References


Examples

if (interactive()){
  head(Rossi, 2)
  Rossi.long <- unfold(Rossi, time="week", event="arrest", cov=1:6, cov.names="emp")
  head(Rossi.long, 50)
}

Unfold-dialog  

Dialog to Convert a Survival Data Set from "Wide" to "Long" Format

Description

Converts a survival-analysis data frame from "wide" format, in which time-varying covariates are separate variables, one per occasion, to "long" or counting-process format in which each occasion is a separate row in the data frame.

Usage

Unfold() # called via the R Commander menus
Details

Most of the dialog box is self-explanatory. A time-varying covariate is identified by selecting the variables constituting the covariate in the "wide" version of the data set using the variable-list box at the lower-left; specifying a name to be used for the covariate in the "long" version of the data set; and pressing the Select button. This process is repeated for each time-varying covariate. All time-varying covariates have to be measured on the same occasions, which are assigned times 0, 1, ... in the output data set. If the covariates are to be lagged, this is indicated via the Lag covariates slider near the lower right. The default lag is 0 — i.e., no lag. The output data set will include variables named start and stop, which give the counting-process start and stop times for each row, and an event indicator composed of the name of the event indicator in the "wide" form of the data set and the suffix .time.

The Unfold dialog calls the unfold function, which is somewhat more flexible.

Author(s)

John Fox <jfox@mcmaster.ca>

References


See Also

unfold
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