

Package ‘surv2sampleComp’

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Type Package

Title Inference for model-free between-group parameters for censored survival data.

Version 1.0-4

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Depends survival, plotrix, flexsurv, survC1

Description Performs inference of several model-free group contrast measures, which include difference/ratio of cumulative incidence rates at given time points, quantiles, and restricted mean survival times (RMST). Two kinds of covariate adjustment procedures (i.e., regression and augmentation) for inference of the metrics based on RMST are also included.

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surv2sampleComp-package

Inference for model-free between-group parameters for censored survival data.

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Details

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Author(s)

Lu Tian, Hajime Uno

Maintainer: Hajime Uno <huno@jimmy.harvard.edu>

References

Tian, Lu; Zhao, Lihui; and Wei, LJ. "On the Restricted Mean Event Time in Survival Analysis." (February 2013). Harvard University Biostatistics Working Paper Series. Working Paper 156. <http://biostats.bepress.com/harvardbiostat/paper156>

See Also

flexsurv, survival

pbc.sample

Edit pbc data to run sample code

Description

Edit pbc data in survival package and make it ready to run the sample code in this manual

Usage

```
pbcsample()
```

```
plot.surv2sample      Plot method for surv2sample objects
```

Description

Creates plots from a surv2sample object.

Usage

```
## S3 method for class 'surv2sample'
plot(x, measure=NULL, baseline=0, ...)
```

Arguments

x	surv2sample object
measure	The type of measure used for the plot. When default(=NULL), plot.survfit() is called and KM plots are given. When "relative time" is specified, a plot of relative percentiles with corresponding 0.95 confidence intervals is generated.
baseline	Indicates the baseline group, 0/1. Default is 0.
...	for future method

See Also

```
plotCI(plotrix)
```

```
rmstaug      Adjusted difference/ratio of restricted mean survival times
```

Description

Compares restricted mean survival time between two groups, adjusting for imbalance of baseline factors.

Usage

```
rmstaug(y, delta, x, arm, tau, type = "difference")
```

Arguments

y	The follow-up time.
delta	The censoring indicator, 1=event, and 0= censoring.
x	The covariate matrix. The group indicator, arm (below) should not be included in this matrix.
arm	The group indicator, 1/0.
tau	The value indicates the restricted time point on the follow-up time to calculate the restricted mean survival time.
type	The type of the between-group contrast measure: "difference"(default), "ratio" or "lossratio"

Author(s)

Lu Tian

References

Tian, Lu; Zhao, Lihui; and Wei, LJ. "On the Restricted Mean Event Time in Survival Analysis." (February 2013). Harvard University Biostatistics Working Paper Series. Working Paper 156. <http://biostats.bepress.com/harvardbiostat/paper156>

Examples

```
D=pbcsample()
rmstaug(D$time, D$status, D$covariates, D$group, tau=8, type="difference")
```

rmstreg

Adjusted difference/ratio of restricted mean survival times

Description

Compares restricted mean survival time between two groups, adjusting for imbalance of baseline factors via a regression model.

Usage

```
rmstreg(y, delta, x, arm, tau, type = "difference")
```

Arguments

y	The follow-up time.
delta	The censoring indicator, 1=event, and 0= censoring.
x	The covariate matrix. The first column of this matrix should be the group indicator, arm (below).
arm	The group indicator, 1/0.
tau	The value indicates the restricted time point on the follow-up time to calculate the restricted mean survival time.
type	The type of the between-group contrast measure: "difference"(default), "ratio" or "lossratio."

Author(s)

Lu Tian

References

Tian, Lu; Zhao, Lihui; and Wei, LJ. "On the Restricted Mean Event Time in Survival Analysis." (February 2013). Harvard University Biostatistics Working Paper Series. Working Paper 156. <http://biostats.bepress.com/harvardbiostat/paper156>

Examples

```
D=pbcsample()
x=cbind(D$group, D$covariates)
rmstreg(D$time, D$status, x, D$group, tau=8, type="difference")
```

surv2sample	<i>Inference of model-free between-group contrasts with censored survival data</i>
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Description

Performs inference of several model-free group contrast measures, which include difference/ratio of cumulative incidence rates, quantiles, and restricted mean survival times.

Usage

```
surv2sample(time, status, arm, npert = 1000, timepoints = c(12, 24, 36, 40),
  quanprobs = c(0.1, 0.15, 0.2), tau = NULL, SEED = NULL, procedure="KM")
```

Arguments

time	The follow-up time.
status	The censoring indicator, 1=event, and 0= censoring.
arm	The indicator for groups to compare 1/0.
npert	The number of resampling. The default is 1000.
timepoints	specifies the time points at which difference and ratio of the survival rates are computed.
quanprobs	specifies the probabilities at which difference and ratio of the corresponding quantiles are computed.
tau	The value indicates the restricted time point on the follow-up time to calculate the restricted mean survival time. If NULL, the function automatically calculates the largest time among non-censored observations for each group and picks the smaller one.
SEED	A random seed used for the resampling. Default is NULL.
procedure	Specifies the inference procedure. A non-parametric procedure by the method of Kaplan-Meier ("KM") is the default. Another option is a parametric inference procedure by fitting a generalized gamma distribution to each group ("GG").

Author(s)

Hajime Uno

Examples

```
D=pbcsample()
```

```
surv2sample(D$time, D$status, D$group, npert=500, timepoints=c(2,4,6,8),  
            quanprobs =c(0.25, 0.5), tau=8, procedure="KM")
```

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*Topic **ANCOVA, augmentation,
generalized gamma,
resampling, restricted mean
survival time**
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