Package ‘surv2sampleComp’

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Type Package

Title Inference for Model-Free Between-Group Parameters for Censored Survival Data

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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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References

Tian L, Zhao L, Wei LJ. Predicting the restricted mean event time with the subject's baseline covariates in survival analysis. Biostatistics 2014, 15, 222-233.

Zhao L, Tian L, Uno H, Solomon S, Pfeffer M, Schindler J, Wei LJ. Utilizing the integrated difference of two survival functions to quantify the treatment contrast for designing, monitoring, and analyzing a comparative clinical study. Clinical Trials 2012, 9, 570-577.

See Also

flexsurv plotrix 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

```
pbc.sample()
```

See Also

`pbc` in survival package

`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 corresponidng 0.95 confidence intervals is generatead.
`baseline`	Indicates the baseline group, 0/1. Default is 0.
`...`	For further method

See Also

`plotCI` in plotrix package

`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", conf.int=0.95)
```

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".
`conf.int`	The level for computation of the confidence intervals. The default is 0.95.

Author(s)

Lu Tian

References

Tian L, Zhao L, Wei LJ. Predicting the restricted mean event time with the subject's baseline covariates in survival analysis. Biostatistics 2014, 15, 222-233.

Examples

```
D=pbc.sample()
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", conf.int=0.95)
```

Arguments

`y`	The follow-up time.
`delta`	The censoring indicator, 1=event, and 0=censoring.
`x`	The covariate matrix. The first colomn 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".
`conf.int`	The level for computation of the confidence intervals. The default is 0.95.

Author(s)

Lu Tian

References

Tian L, Zhao L, Wei LJ. Predicting the restricted mean event time with the subject's baseline covariates in survival analysis. Biostatistics 2014, 15, 222-233.

Examples

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

`surv2sample` *Inference of model-free between-group contrasts with censored survival data*

Description

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

Usage

```
surv2sample(time, status, arm, npert=1000,
                    timepoints=c(12, 24, 36, 40), quanprobs=c(0.1, 0.15, 0.2),
                    tau_start=0, tau, SEED=NULL, procedure="KM", conf.int=0.95)
```

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_start`	The value indicates time point on the follow-up time to calculate the restricted mean survival time beyond the time point. The default is 0.
`tau`	The value indicates the restricted time point on the follow-up time to calculate the restricted mean survival time. (i.e., the minimum of the largest observed time in each of the two groups)
`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").
`conf.int`	The level for computation of the confidence intervals. The default is 0.95.

Author(s)

Hajime Uno, Miki Horiguchi

References

Tian L, Zhao L, Wei LJ. Predicting the restricted mean event time with the subject's baseline covariates in survival analysis. Biostatistics 2014, 15, 222-233.

Zhao L, Tian L, Uno H, Solomon S, Pfeffer M, Schindler J, Wei LJ. Utilizing the integrated difference of two survival functions to quantify the treatment contrast for designing, monitoring, and analyzing a comparative clinical study. Clinical Trials 2012, 9, 570-577.

Examples

```
D=pbc.sample()
surv2sample(D$time, D$status, D$group, npert=500, timepoints=c(2,4,6,8),
quanprobs =c(0.2, 0.3), tau=8, procedure="KM")
```

Index