Package: BMeRL (via r-universe)

October 15, 2026

Type Package

Title Bivariate Median Residual Life Estimation

Version 1.0.0

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Description Nonparametric estimation of the bivariate median residual life function of Kayid et al. (2020) for complete and right-censored paired lifetimes. Order-restricted estimation for two groups is also provided, following Khan and Ghebremichael (2026). For censored data the bivariate survival function is estimated by the method of Lin and Ying (1993). Simultaneous confidence intervals are obtained by the percentile bootstrap approach of Mandel and Betensky (2008), and the estimated functions can be drawn as surface plots. See the accompanying vignette 'BMeRL' for a detailed introduction. Kayid, M., Shafaei Noughabi, M., and Abouammoh, A. M. (2020) <doi:10.1007/s00357-018-9300-z>; Khan, R. A., and Ghebremichael, M. (2026) <doi:10.1002/bimj.70112>; Lin, D. Y., and Ying, Z. (1993) <doi:10.1093/biomet/80.3.573>; Mandel, M., and Betensky, R. A. (2008) <doi:10.1016/j.csda.2007.07.005>.

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Encoding UTF-8

LazyData true

Depends R (>= 3.6.0)

Imports stats, utils, graphics, grDevices

Suggests knitr, rmarkdown

VignetteBuilder knitr

RoxygenNote 7.3.3

NeedsCompilation no

Repository https://cran.r-universe.dev

Date/Publication 2026-10-15 19:14:58 UTC

RemoteUrl https://github.com/cran/BMeRL

RemoteRef HEAD

RemoteSha 025e128117e4b16e8e06e6ec3177e8e4ff343304

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`BMeRL_Censored` *Bivariate Median Residual Life for Right-Censored Data*

Description

Estimates the bivariate median residual life function at one or more points from right-censored paired lifetimes and, optionally, computes bootstrap simultaneous confidence intervals (SCI).

Usage

```
BMeRL_Censored(
  x1,
  x2,
  dataset,
  time1,
  time2,
  status1,
  status2,
  SCI = FALSE,
  B = 1000,
  level = 0.95,
  seed = NULL,
  verbose = TRUE
)
```

Arguments

`x1`, `x2`	Numeric vectors of the same length specifying the points (x_1, x_2) at which the estimates are computed.
`dataset`	A data frame with one row per subject.
`time1`, `time2`	Columns of `dataset` containing the observed (possibly censored) times, specified either as unquoted column names or character strings.
`status1`, `status2`	Columns of `dataset` containing the event indicators: 1 (or `TRUE`) if the event time was observed and 0 (or `FALSE`) if it was censored.
`SCI`	Logical. If `TRUE`, simultaneous confidence intervals are computed; if `FALSE` (the default), only the point estimates are returned.
`B`	Number of bootstrap replications. Default is 1000.
`level`	Simultaneous confidence level, strictly between 0 and 1. Default is 0.95.
`seed`	Optional seed passed to `set.seed` before resampling. The default `NULL` leaves the random number generator unchanged.
`verbose`	Logical. If `TRUE` and `SCI = TRUE`, the point estimates, a progress message, and the final results are displayed, and the result is returned invisibly. If `FALSE`, nothing is displayed.

Details

Censoring model. Each subject has a common censoring time C, independent of the lifetimes (X_1, X_2). The observed data are $T_j = \min(X_j, C)$ and $\delta_j = I(X_j \le C)$, $j = 1, 2$.

Survival function. Following Lin and Ying (1993), the bivariate survival function is estimated by

$$\hat{R}(x_1, x_2) = \frac{n^{-1} \sum_i I(T_{1i} > x_1,\ T_{2i} > x_2)}{\hat{G}(\max(x_1, x_2))},$$

where $\hat{G}$ is the Kaplan-Meier estimator of $P(C > t)$, computed from $\max(T_{1i}, T_{2i})$ with censoring indicators $1 - \delta_{1i}\delta_{2i}$.

Median residual life. At a point (a, b), let $p = \hat{R}(a, b)/2$. Along the first coordinate, let $t_1^{\le}$ be the first time $t \ge a$ such that $\hat{R}(t, b) \le p$, and let $t_1^{<}$ be the first time such that $\hat{R}(t, b) < p$. The estimated median location is the midpoint of $t_1^{\le}$ and $t_1^{<}$, with $t_1^{\le}$ used alone if the strict crossing does not occur. Then $\hat{q}_1(a, b)$ is this estimated median location minus a. The estimator $\hat{q}_2(a, b)$ is defined analogously along the second coordinate. In the absence of censoring, this construction reduces to the conventional sample median and agrees with `BMeRL_Complete`.

If no paired observation lies beyond a point, both estimates are set to 0. An estimate is `NA` when $\hat{G}(\max(a, b)) = 0$ or when the estimated survival function does not reach the target level within the observed data.

SCI. The paired observations, including both observed times and their corresponding event indicators, are resampled with replacement, and $\hat{G}$ is re-estimated in every bootstrap sample. The SCI are based on the relative-rank method of Mandel and Betensky (2008), as implemented in `BMeRL_Complete`, and are simultaneous for q_1 and q_2 across all specified points. Bootstrap samples containing an undefined estimate are dropped with a warning.

Value

If SCI = FALSE, a data frame with columns x1, x2, q1, and q2, where q1 and q2 are the estimated first and second components of the bivariate median residual life at each specified point.

If SCI = TRUE, the data frame additionally contains q1_lower and q1_upper, the lower and upper simultaneous confidence limits for q1, and q2_lower and q2_upper, the corresponding simultaneous confidence limits for q2. The intervals are simultaneous across both components and all specified points. Additional bootstrap diagnostics are stored as attributes of the returned data frame.

References

Kayid, M., Shafaei Noughabi, M., and Abouammoh, A. M. (2019). A nonparametric estimator of bivariate quantile residual life model with application to tumor recurrence data set. *Journal of Classification*. doi:10.1007/s003570189300z

Lin, D. Y. and Ying, Z. (1993). A simple nonparametric estimator of the bivariate survival function under univariate censoring. *Biometrika*, 80(3), 573–581.

Mandel, M. and Betensky, R. A. (2008). Simultaneous confidence intervals based on the percentile bootstrap approach. *Computational Statistics and Data Analysis*, 52(4), 2158–2165.

See Also

BMeRL_Censored_ordered for two ordered groups, BMeRL_Complete for complete data, and BMeRL_Surface_censored for surface plots.

Examples

```
data(censored)

## Point estimates only
BMeRL_Censored(
  c(0, 5, 10), c(0, 5, 5), censored,
  time1, time2, status1, status2
)

## Point estimates with 95% simultaneous confidence intervals
out <- BMeRL_Censored(
  c(0, 5), c(0, 5), censored,
  time1, time2, status1, status2,
  SCI = TRUE, B = 200, seed = 1691, verbose = FALSE
)
out
```

BMeRL_Censored_ordered

Order-Restricted Bivariate Median Residual Life for Right-Censored Data

---

Description

Estimates the bivariate median residual life functions for two groups under an order restriction for right-censored data and, optionally, computes bootstrap simultaneous confidence intervals (SCI).

Usage

```
BMeRL_Censored_ordered(
  x1,
  x2,
  dataset,
  time1,
  time2,
  status1,
  status2,
  group,
  smaller,
  SCI = TRUE,
  B = 1000,
  level = 0.95,
  seed = NULL,
  verbose = TRUE
)
```

Arguments

`x1`, `x2`	Numeric vectors of the same length specifying the points (x_1, x_2) at which the estimates are computed.
`dataset`	A data frame with one row per subject.
`time1`, `time2`	Columns of `dataset` containing the observed (possibly censored) times, specified either as unquoted column names or character strings.
`status1`, `status2`	Columns of `dataset` containing the event indicators: 1 (or `TRUE`) if the event time was observed and 0 (or `FALSE`) if it was censored.
`group`	Column of `dataset` containing the group labels. Exactly two groups must be present. The column may be specified as an unquoted column name or a character string.
`smaller`	The group to be denoted by F and assumed to have the smaller bivariate median residual life; for example, `"Yes"`.
`SCI`	Logical. If `TRUE`, simultaneous confidence intervals are computed; if `FALSE`, only the point estimates are returned.
`B`	Number of bootstrap replications. Default is 1000.
`level`	Simultaneous confidence level, strictly between 0 and 1. Default is 0.95.
`seed`	Optional seed passed to `set.seed` before resampling. The default `NULL` leaves the random number generator unchanged.
`verbose`	Logical. If `TRUE` and `SCI = TRUE`, the point estimates, a progress message, and the final results are displayed, and the result is returned invisibly. If `FALSE`, nothing is displayed.

Details

Let $\mathbf{q}_F(x) = (q_{F1}(x), q_{F2}(x))$ denote the bivariate median residual life for the group specified by `smaller`, and let $\mathbf{q}_G(x) = (q_{G1}(x), q_{G2}(x))$ denote that for the other group, with sample sizes n_F and n_G, respectively. The componentwise order restriction $q_{Fj}(x) \leq q_{Gj}(x)$, $j = 1, 2$, is imposed at each specified point x.

Let $\hat{\mathbf{q}}_F$ and $\hat{\mathbf{q}}_G$ denote the unrestricted bivariate median residual life estimates for groups F and G, respectively, obtained as in `BMeRL_Censored`. Define the pooled estimate by

$$\hat{\mathbf{q}}_P = \frac{n_F}{n_F + n_G}\hat{\mathbf{q}}_F + \frac{n_G}{n_F + n_G}\hat{\mathbf{q}}_G.$$

The order-restricted estimates are then defined componentwise as

$$\hat{\mathbf{q}}_F^* = \min(\hat{\mathbf{q}}_F, \hat{\mathbf{q}}_P), \qquad \hat{\mathbf{q}}_G^* = \max(\hat{\mathbf{q}}_G, \hat{\mathbf{q}}_P).$$

If the unrestricted estimates already satisfy $\hat{q}_{Fj} \leq \hat{q}_{Gj}$, they remain unchanged; otherwise, the corresponding components are replaced by the pooled estimate. Thus, $\hat{q}_{Fj}^* \leq \hat{q}_{Gj}^*$, $j = 1, 2$, at every specified point.

The censoring distribution is estimated separately within each group and re-estimated in every bootstrap sample. The paired observations, including both observed times and their corresponding event indicators, are resampled with replacement separately within groups. The pooled and order-restricted estimates are then recomputed for each bootstrap sample.

The SCI are based on the relative-rank method of Mandel and Betensky (2008) and are simultaneous for both components of groups F and G across all specified points. Within each coordinate, the bootstrap estimates are ranked, and the largest absolute deviation of the coordinatewise ranks from the central rank is used to construct the simultaneous confidence limits. Near the boundary $\mathbf{q}_F = \mathbf{q}_G$, the order-restricted estimators are nonsmooth, and the percentile bootstrap may have coverage below the nominal level.

Value

A data frame with one row for each specified point and group, with columns `x1`, `x2`, `group`, `q1`, and `q2`, where `q1` and `q2` are the order-restricted estimates of the first and second components of the bivariate median residual life.

If `SCI = TRUE`, the data frame additionally contains `q1_lower` and `q1_upper`, the lower and upper simultaneous confidence limits for `q1`, and `q2_lower` and `q2_upper`, the corresponding simultaneous confidence limits for `q2`. The intervals are simultaneous across both components, both groups, and all specified points.

The unrestricted estimates are stored in the `unrestricted` attribute. Additional bootstrap diagnostics are stored as attributes of the returned data frame when `SCI = TRUE`.

References

Kayid, M., Shafaei Noughabi, M., and Abouammoh, A. M. (2019). A nonparametric estimator of bivariate quantile residual life model with application to tumor recurrence data set. *Journal of Classification*. doi:10.1007/s003570189300z

Lin, D. Y. and Ying, Z. (1993). A simple nonparametric estimator of the bivariate survival function under univariate censoring. *Biometrika*, 80(3), 573–581.

Mandel, M., and Betensky, R. A. (2008). Simultaneous confidence intervals based on the percentile bootstrap approach. *Computational Statistics and Data Analysis*, 52(4), 2158–2165.

See Also

BMeRL_Censored for unrestricted censored-data estimation, BMeRL_Complete_ordered for complete data, and BMeRL_Surface_censored_ordered for surface plots.

Examples

```
data(censored)

## Point estimates, with group "Yes" denoted by F and assumed to have
## the smaller bivariate median residual life
BMeRL_Censored_ordered(
  c(0, 5, 10), c(0, 5, 5), censored,
  time1, time2, status1, status2, disease,
  smaller = "Yes", SCI = FALSE
)

## With 95% simultaneous confidence intervals
BMeRL_Censored_ordered(
  c(0, 5), c(0, 5), censored,
  time1, time2, status1, status2, disease,
  smaller = "Yes", B = 200, seed = 1691,
  verbose = FALSE
)
```

BMeRL_Complete *Bivariate Median Residual Life for Complete Data*

Description

Estimates the bivariate median residual life function at one or more points from complete (uncensored) paired lifetimes and, optionally, computes bootstrap simultaneous confidence intervals (SCI).

Usage

```
BMeRL_Complete(
  x1,
  x2,
  dataset,
  time1,
  time2,
  SCI = TRUE,
  B = 1000,
  level = 0.95,
```

```
  seed = NULL,
  verbose = TRUE
)
```

Arguments

x1, x2	Numeric vectors of the same length specifying the points (x_1, x_2) at which the estimates are computed.
dataset	A data frame with one row per subject.
time1, time2	Columns of dataset containing the two lifetimes, specified either as unquoted column names or character strings.
SCI	Logical. If TRUE, simultaneous confidence intervals are computed; if FALSE, only the point estimates are returned.
B	Number of bootstrap replications. Default is 1000.
level	Simultaneous confidence level, strictly between 0 and 1. Default is 0.95.
seed	Optional seed passed to set.seed before resampling. The default NULL leaves the random number generator unchanged.
verbose	Logical. If TRUE and SCI = TRUE, the point estimates, a progress message, and the final results are displayed, and the result is returned invisibly. If FALSE, nothing is displayed.

Details

At a point $x = (x_1, x_2)$, the median residual lives are

$$\hat{q}_1(x_1, x_2) = \text{median}\{X_{1i} : X_{1i} > x_1,\ X_{2i} > x_2\} - x_1,$$

$$\hat{q}_2(x_1, x_2) = \text{median}\{X_{2i} : X_{1i} > x_1,\ X_{2i} > x_2\} - x_2,$$

where the conventional sample median is used, averaging the two middle values when the number of paired observations beyond the point is even. Together, $\hat{q}_1$ and $\hat{q}_2$ define the bivariate median residual life at x. If no paired observation lies beyond a point, both estimates are set to 0.

The SCI are based on the relative-rank method of Mandel and Betensky (2008) and are simultaneous for q_1 and q_2 across all specified points. The paired observations are resampled with replacement B times. Within each coordinate, the bootstrap estimates are ranked: tied values below the median receive the minimum rank of their group, tied values above the median receive the maximum rank, and values equal to the median are treated as central. For each bootstrap sample, the largest absolute deviation of the coordinatewise ranks from the central rank is computed. The central level proportion of bootstrap samples is retained, and the minimum and maximum retained bootstrap estimates in each coordinate define the simultaneous confidence limits.

Value

If SCI = FALSE, a data frame with columns x1, x2, q1, and q2, where q1 and q2 are the estimated first and second components of the bivariate median residual life at each specified point.

If SCI = TRUE, the data frame additionally contains q1_lower and q1_upper, the lower and upper simultaneous confidence limits for q1, and q2_lower and q2_upper, the corresponding simultaneous confidence limits for q2. The intervals are simultaneous across both components and all specified points. Additional bootstrap diagnostics are stored as attributes of the returned data frame.

References

Kayid, M., Shafaei Noughabi, M., and Abouammoh, A. M. (2020). A nonparametric estimator of bivariate quantile residual life model with application to tumor recurrence data set. *Journal of Classification*, 37, 237–253. doi:10.1007/s003570189300z

Mandel, M., and Betensky, R. A. (2008). Simultaneous confidence intervals based on the percentile bootstrap approach. *Computational Statistics and Data Analysis*, 52(4), 2158–2165. doi:10.1016/j.csda.2007.07.005

See Also

`BMeRL_Complete_ordered` for two ordered groups, `BMeRL_Censored` for censored data, and `BMeRL_Surface_complete` for surface plots.

Examples

```
data(complete)

## Point estimates only
BMeRL_Complete(c(0, 5, 10), c(0, 5, 5), complete, time1, time2,
               SCI = FALSE)

## Point estimates with 95% simultaneous confidence intervals
out <- BMeRL_Complete(c(0, 5), c(0, 5), complete, time1, time2,
                      B = 200, seed = 1691, verbose = FALSE)
out
```

`BMeRL_Complete_ordered`

Order-Restricted Bivariate Median Residual Life for Complete Data

---

Description

Estimates the bivariate median residual life functions for two groups under an order restriction for complete (uncensored) data and, optionally, computes bootstrap simultaneous confidence intervals (SCI).

Usage

```
BMeRL_Complete_ordered(
  x1,
  x2,
  dataset,
  time1,
  time2,
  group,
  smaller,
```

```
  SCI = TRUE,
  B = 1000,
  level = 0.95,
  seed = NULL,
  verbose = TRUE
)
```

Arguments

x1, x2	Numeric vectors of the same length specifying the points (x_1, x_2) at which the estimates are computed.
dataset	A data frame with one row per subject.
time1, time2	Columns of dataset containing the two lifetimes, specified either as unquoted column names or character strings.
group	Column of dataset containing the group labels. Exactly two groups must be present. The column may be specified as an unquoted column name or a character string.
smaller	The group to be denoted by F and assumed to have the smaller bivariate median residual life; for example, "Yes".
SCI	Logical. If TRUE, simultaneous confidence intervals are computed; if FALSE, only the point estimates are returned.
B	Number of bootstrap replications. Default is 1000.
level	Simultaneous confidence level, strictly between 0 and 1. Default is 0.95.
seed	Optional seed passed to set.seed before resampling. The default NULL leaves the random number generator unchanged.
verbose	Logical. If TRUE and SCI = TRUE, the point estimates, a progress message, and the final results are displayed, and the result is returned invisibly. If FALSE, nothing is displayed.

Details

Let $\mathbf{q}_F(x) = (q_{F1}(x), q_{F2}(x))$ denote the bivariate median residual life for the group specified by smaller, and let $\mathbf{q}_G(x) = (q_{G1}(x), q_{G2}(x))$ denote that for the other group, with sample sizes n_F and n_G, respectively. The componentwise order restriction $q_{Fj}(x) \leq q_{Gj}(x)$, $j = 1, 2$, is imposed at each specified point x.

Let $\hat{q}_F$ and $\hat{q}_G$ denote the unrestricted bivariate median residual life estimates for groups F and G, respectively, obtained as in BMeRL_Complete. Define the pooled estimate by

$$\hat{q}_P = \frac{n_F}{n_F + n_G}\hat{q}_F + \frac{n_G}{n_F + n_G}\hat{q}_G.$$

The order-restricted estimates are then defined componentwise as

$$\hat{q}_F^* = \min(\hat{q}_F, \hat{q}_P), \qquad \hat{q}_G^* = \max(\hat{q}_G, \hat{q}_P).$$

If the unrestricted estimates already satisfy $\hat{q}_F \leq \hat{q}_G$, they remain unchanged; otherwise, both are replaced by the pooled estimate. Thus, $\hat{q}_F^* \leq \hat{q}_G^*$ at every specified point.

The SCI are based on the relative-rank method of Mandel and Betensky (2008) and are simultaneous for both components of groups F and G across all specified points. The paired observations are resampled with replacement separately within each group, and the pooled and order-restricted estimates are recomputed in each bootstrap sample. Within each coordinate, the bootstrap estimates are ranked, and the largest absolute deviation of the coordinatewise ranks from the central rank is used to construct the simultaneous confidence limits.

Value

A data frame with one row for each specified point and group, with columns `x1`, `x2`, `group`, `q1`, and `q2`, where `q1` and `q2` are the order-restricted estimates of the first and second components of the bivariate median residual life.

If `SCI = TRUE`, the data frame additionally contains `q1_lower` and `q1_upper`, the lower and upper simultaneous confidence limits for `q1`, and `q2_lower` and `q2_upper`, the corresponding simultaneous confidence limits for `q2`. The intervals are simultaneous across both components, both groups, and all specified points.

The unrestricted estimates are stored in the `unrestricted` attribute. Additional bootstrap diagnostics are stored as attributes of the returned data frame when `SCI = TRUE`.

References

Kayid, M., Shafaei Noughabi, M., and Abouammoh, A. M. (2019). A nonparametric estimator of bivariate quantile residual life model with application to tumor recurrence data set. *Journal of Classification*. doi:10.1007/s003570189300z

Mandel, M., and Betensky, R. A. (2008). Simultaneous confidence intervals based on the percentile bootstrap approach. *Computational Statistics and Data Analysis*, 52(4), 2158–2165.

See Also

`BMeRL_Complete`, `BMeRL_Censored_ordered`, and `BMeRL_Surface_complete_ordered`.

Examples

```
data(complete)

## Point estimates, with group "Yes" denoted by F and assumed to have
## the smaller bivariate median residual life
est <- BMeRL_Complete_ordered(
  c(0, 5, 10), c(0, 5, 5), complete,
  time1, time2, disease, smaller = "Yes",
  SCI = FALSE
)
est

## With 95% simultaneous confidence intervals
BMeRL_Complete_ordered(
  c(0, 5), c(0, 5), complete,
  time1, time2, disease, smaller = "Yes",
  B = 200, seed = 1691, verbose = FALSE
)
```

BMeRL_Surface *Surface Plots of the Bivariate Median Residual Life*

Description

Evaluates a bivariate median residual life estimator over a grid of points and displays the two components $\hat{q}_1$ and $\hat{q}_2$ as surface plots.

Usage

```
BMeRL_Surface_complete(
  dataset,
  time1,
  time2,
  x1.grid = NULL,
  x2.grid = NULL,
  n.grid = 30,
  which = c("both", "q1", "q2"),
  plot = TRUE,
  theta = 35,
  phi = 25,
  col.palette = 50,
  main = NULL,
  ...
)

BMeRL_Surface_censored(
  dataset,
  time1,
  time2,
  status1,
  status2,
  x1.grid = NULL,
  x2.grid = NULL,
  n.grid = 30,
  which = c("both", "q1", "q2"),
  plot = TRUE,
  theta = 35,
  phi = 25,
  col.palette = 50,
  main = NULL,
  ...
)

BMeRL_Surface_complete_ordered(
```

```
  dataset,
  time1,
  time2,
  group,
  smaller,
  x1.grid = NULL,
  x2.grid = NULL,
  n.grid = 30,
  which = c("both", "q1", "q2"),
  plot = TRUE,
  theta = 35,
  phi = 25,
  col.palette = 50,
  main = NULL,
  ...
)

BMeRL_Surface_censored_ordered(
  dataset,
  time1,
  time2,
  status1,
  status2,
  group,
  smaller,
  x1.grid = NULL,
  x2.grid = NULL,
  n.grid = 30,
  which = c("both", "q1", "q2"),
  plot = TRUE,
  theta = 35,
  phi = 25,
  col.palette = 50,
  main = NULL,
  ...
)
```

Arguments

`dataset`	A data frame with one row per subject.
`time1`, `time2`	Columns of `dataset` containing the two observed times, specified either as unquoted column names or character strings.
`x1.grid`, `x2.grid`	Increasing numeric vectors specifying the grid. If `NULL`, `n.grid` equally spaced values from 0 (or the smallest observed time if negative) to the largest observed time of the corresponding component are used.
`n.grid`	Number of grid values in each direction when a grid is not supplied. Default is 30.

`which`	Component(s) to display: `"both"`, `"q1"`, or `"q2"`. The default is `"both"`.
`plot`	Logical. If `TRUE`, the surface plots are displayed. If `FALSE`, no plot is produced and only the grid of estimates is returned.
`theta, phi`	Viewing angles passed to `persp`.
`col.palette`	Number of colours, or a vector of colours, used to colour the surface facets from lower to higher values. The default is 50 colours from `hcl.colors`.
`main`	Optional plot titles, one for each component. If `NULL`, default titles are used.
`...`	Additional arguments passed to `persp`, such as `ticktype`, `expand`, or `zlim`.
`status1, status2`	Columns of `dataset` containing the event indicators: 1 (or `TRUE`) if the event time was observed and 0 (or `FALSE`) if it was censored.
`group`	Column of `dataset` containing the group labels. Exactly two groups must be present.
`smaller`	The group to be denoted by F and assumed to have the smaller bivariate median residual life.

Details

- `BMeRL_Surface_complete` uses `BMeRL_Complete`;
- `BMeRL_Surface_censored` uses `BMeRL_Censored`;
- `BMeRL_Surface_complete_ordered` uses `BMeRL_Complete_ordered`;
- `BMeRL_Surface_censored_ordered` uses `BMeRL_Censored_ordered`.

The estimator is evaluated with `SCI = FALSE` at each grid point. The surfaces of $\hat{q}_1$ and $\hat{q}_2$ are displayed side by side. For the order-restricted estimators, one row is shown for each group, with group F first and group G second. The two groups share the same vertical and colour scales for each component, allowing their surfaces to be compared directly. Surface facets are coloured according to their height. Grid points at which an estimate is `NA` are left blank. Graphical parameters modified for the layout are restored on exit.

Value

Invisibly, a list with components `x1` and `x2`, containing the grid values, and `q1` and `q2`, containing the corresponding bivariate median residual life estimates. For the unrestricted estimators, `q1` and `q2` are matrices with rows corresponding to `x1` and columns corresponding to `x2`. For the order-restricted estimators, each is a list containing one such matrix for each group.

References

Kayid, M., Shafaei Noughabi, M., and Abouammoh, A. M. (2019). A nonparametric estimator of bivariate quantile residual life model with application to tumor recurrence data set. *Journal of Classification*. doi:10.1007/s003570189300z

Examples

```
data(complete)
data(censored)

BMeRL_Surface_complete(
  complete, time1, time2,
  x1.grid = 0:30, x2.grid = 0:30
)

BMeRL_Surface_censored(
  censored, time1, time2, status1, status2,
  x1.grid = 0:30, x2.grid = 0:30
)

BMeRL_Surface_complete_ordered(
  complete, time1, time2, disease, "Yes",
  x1.grid = 0:30, x2.grid = 0:30
)

BMeRL_Surface_censored_ordered(
  censored, time1, time2, status1, status2,
  disease, "Yes",
  x1.grid = 0:30, x2.grid = 0:30,
  which = "q1"
)

## Return the grid of estimates without drawing the surfaces
s <- BMeRL_Surface_complete(
  complete, time1, time2,
  n.grid = 10, plot = FALSE
)
round(s$q1, 1)
```

`censored` *Simulated Right-Censored Bivariate Lifetimes*

Description

A simulated data set containing the subjects in `complete` observed under right censoring. The data were generated to illustrate the censored-data methods in the package and do not represent real subjects. The variables `time1`, `time2`, `status1`, and `status2` are used by `BMeRL_Censored` and `BMeRL_Surface_censored`. The order-restricted functions `BMeRL_Censored_ordered` and `BMeRL_Surface_censored_ordered` additionally use the group variable `disease`.

Usage

```
censored
```

Format

A data frame with 120 rows and 6 variables:

id Subject identifier.

time1 Observed time for the first component, in months, defined as the minimum of the lifetime and censoring time.

time2 Observed time for the second component, in months, defined as the minimum of the lifetime and censoring time.

status1 Event indicator for `time1`: 1 if the event time was observed and 0 if it was censored.

status2 Event indicator for `time2`: 1 if the event time was observed and 0 if it was censored.

disease Group indicator used by the order-restricted functions: `"Yes"` for 50 subjects and `"No"` for 70 subjects.

Details

Each subject has a single censoring time drawn from a uniform distribution on 0 to 60 months and applied to both component lifetimes in `complete`. Approximately 42% of the subjects have at least one censored component.

Source

Simulated data generated for this package.

See Also

`complete`, which contains the same subjects without censoring.

Examples

```
data(censored)
head(censored)
mean(censored$status1 == 0)
```

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complete — *Simulated Complete Bivariate Lifetimes*

Description

A simulated/artificial data set of paired lifetimes (in months) for 120 subjects, generated to illustrate the complete-data methods in the package. The data are uncensored and do not represent real subjects. The variables `time1` and `time2` are used by `BMeRL_Complete` and `BMeRL_Surface_complete`. The order-restricted functions `BMeRL_Complete_ordered` and `BMeRL_Surface_complete_ordered` additionally use the group variable `disease`.

Usage

```
complete
```

Format

A data frame with 120 rows and 4 variables:

id Subject identifier.

time1 Lifetime of the first component, in months.

time2 Lifetime of the second component, in months.

disease Group indicator used by the order-restricted functions: `"Yes"` for 50 subjects and `"No"` for 70 subjects.

Details

The paired lifetimes were simulated from Gumbel's bivariate exponential distribution with dependence parameter 0.5 and scaled to have mean lifetimes of 12 months in group `"Yes"` and 18 months in group `"No"`. Thus, group `"Yes"` has the smaller median residual life. The observed times are rounded to 0.1 month, with 0.1 as the smallest recorded value.

Source

Simulated data generated for this package.

See Also

`censored`, which contains the same subjects under right censoring.

Examples

```
data(complete)
head(complete)
table(complete$disease)
```

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