Package 'bqte'

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Type Package

Title Quantile treatment effects (QTE) and back-transformed QTE (BQTE)

Version 0.9.0

Description Computes QTEs and BQTEs and lower and upper tail BQTEs.

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Contents

`bqte` *Estimate backtransformed quantile treatment effects*

Description

We have observed survival/recovery times, or other numerical outcome values, in the treatment group and in the control group. Quantile treatment effect (QTE) is the difference between the two groups as a function of quantile level in (0,1). We want to transform QTE to the original scale of the outcome value, at a given grid of values ('at') in the control group. These transformed values are called backtransformed quantile treatment effects' (BQTE).

Usage

```
bqte(
  Treatment,
  Control,
  at = NULL,
  bqte.conf = 0.95,
  B = 2000,
  K = length(Control),
  bagging = TRUE,
  tails = FALSE,
  discrete.range = FALSE,
  exact.sample.quantiles = TRUE,
  interpolation.method = "linear",
  spline.df = 5,
  verbose = TRUE
)
```

Arguments

`Treatment`	vector of outcome values in Treatment group.
`Control`	vector of outcome values in Control group.
`at`	vector of outcome values in controls at which BQTE is estimated. By default, between 10 and 20 points between the empirical quantile levels of 10/N and 1 - (10/N) in controls where N = min(|Treatment|, |Control|).
`bqte.conf`	(default 0.95), confidence level for BQTE.
`B`	(default 2000), number of bootstrap samples.
`K`	(default 'length(Control)), number of quantiles where BQTE function is estimated.
`bagging`	(default TRUE), if TRUE, reports bagging estimate (mean over bootstrap samples) otherwise reports the direct estimate from the data.
`tails`	(default FALSE), if TRUE, returns also estimates and confidence intervals for UTBQTE and LTBQTE.
`discrete.range`	(default FALSE), if TRUE, returns, for every Control group value, the range of Treatment group values that correspond through the shared quantile levels.
`exact.sample.quantiles`	(default TRUE), if TRUE, uses empirical sample quantiles, that are called type = 1 in R's quantile function, if FALSE, uses R's default quantiles (type = 7).
`interpolation.method`	either "linear" for piecewise-linear model or "spline" for natural splines of df 'spline.df'.
`spline.df`	(default 5) degrees of freedom of natural spline. Relevant only if interpolation.method = "spline".
`verbose`	(default TRUE) if TRUE, prints parameters and range recommendations on console.

Details

Approach: Fix a grid of outcome values in the control group at which BQTEs are computed (parameter 'at'). Recommendation: Do not try to estimate BQTEs at values that are outside empirical

quantile levels (10/N, 1 - (10/N)), where N is the minimum sample size of the treatment and control groups because accuracy of quantile estimates is low at the tails.

Estimate the quantile treatment effects as difference between the quantiles of Treatment group and Control group at 'K' quantile levels 1/(K+1),...,K/(K+1). Make a piece-wise linear approximation of BQTE as a function of outcome value in controls, based on the observed K quantiles. If several quantiles are equal, then use average of the corresponding Treatment group values as the value of BQTE at that point. (See parameter 'discrete.range' to get more details of range of tied values.) Use that approximation to estimate the BQTE at the chosen grid of outcome values in controls. NOTE: values are returned to the user on the grid defined by 'at', with a sensible default range, and not all K values included in the computation are meant to be returned to the user.

Uses bootstrapping to estimate the uncertainty of BQTE at each grid point, by resampling with replacement a set of Treatment and Control group values that have the same sample size as the original Treatment and Control groups, respectively, and applying the procedure explained above to each bootstrap sample. Note that bootstrapping accounts for uncertainty of quantiles of both groups.

The final estimate of BQTE at a grid point is the mean over bootstrap samples ("bagging estimate") and the confidence interval for BQTE is estimated from the quantiles of the bootstrap sample. NOTE: In empirical evaluation it was observed that bagging estimate tend to have smaller mean square error in discrete distributions than the direct estimate from the data and therefore the bagging estimate is used by default. This can be switched by argument "bagging".

For discrete data, one can also compute the range of Treatment values that correspond to a single Control group value and return that range (See argument 'discrete.range'.) This range is typically wider than the confidence interval of the BQTE estimate as BQTE is defined as the expected value over those Treatment group values that correspond to the quantile levels of a particular Control roup value.

Can also compute upper tail BQTE (UTBQTE) and lower tail BQTE (LTBQTE) at each point in 'at'. UTBQTE, at outcome value 'x' is the difference in the mean outcome values of the highest 1-F(x) of the two populations, where F is the CDF of the Control population. LTBQTE, at outcome value 'x' is the difference in the mean outcome values of the lowest F(x) of the two populations, where F is the CDF of Control population. UTBQTE(x) is an upper bound for the average treatment effect of that part of the Control population who have outcome value >= x. LTBQTE(x) is a lower bound for the average treatment effect of that part of the Control population who have outcome value <= x. These bounds are general in the sense that they do not require an assumption about how the treatment operates, for example, they do not assume anything about whether the treatment preserves order. Note that the outcome value 'x' is included in the definition of both UTBQTE(x) and in LTBQTE(x). The confidence intervals of UTBQTE and LTBQTE are estimated using bootstrap and the point estimates are computed either using bagging (if bagging = TRUE) or without bagging (if bagging = FALSE).

Value

list with 1,2, or 3 data frames

$res

'at', outcome value in control group;

'bqte', backtransformed quantile treatment effect (averaged in case of ties);

'bqte.low', lower CI end point for 'bqte';

'bqte.up', upper CI end point for 'bqte';

'rbqte', relative backtransformed quantile treatment effect with respect to control outcome value;

'rbqte.low', lower CI end point for 'rbqte';

'rbqte.up', upper CI end point for 'rbqte';

$discrete.range, returned only if argument discrete.range = TRUE;

'at', outcome value in control group;

'range.low', lower CI end point of raw, non-averaged BQTE values corresponding to this Control group value;

'range.up' upper CI end point;

'rrange.low' lower CI end point of relative BQTE;

'rrange.up' upper CI end point of relative BQTE;

$tails, returned only if parameter 'tails = TRUE'

'utbqte, upper tail average treatment effect estimate;

'utbqte.low, lower CI end point for 'utbqte';

'utbqte.up, upper CI end point for 'utbqte';

'ltbqte, lower tail average treatment effect estimate;

'ltbqte.low, lower CI end point for 'ltbqte';

'ltbqte.up, upper CI end point for 'ltbqte';

'rutbqte, relative upper tail average treatment effect estimate with respect to control value;

'rutbqte.low, lower CI end point for 'rutbqte';

'rutbqte.up, upper CI end point for 'rutbqte';

'rltbqte, relative lower tail average treatment effect estimate with respect to control value;

'rltbqte.low, lower CI end point for 'rltbqte';

'rltbqte.up, upper CI end point for 'rltbqte'

Examples

```
set.seed(12); Tr = rweibull(100,1.2,1); Co = rnorm(100,3,5)
bqte(Tr, Co)
```

`bqte_doksum` *Doksum estimator*

Description

Estimator of BQTE published by Doksum (1974), Annals of Statistics Vol.2 No.2 267-277.

Usage

```
bqte_doksum(at, Treatment, Control)
```

Arguments

`at`	Control values where estimation is done.
`Treatment`	Observed values of the treatment group
`Control`	Observed values of the control group

Value

vector of estimates at the values given in 'at'.

Examples

```
set.seed(12); Tr = rweibull(30,1.2,1); Co = rnorm(30,3,5)
bqte_doksum(at = c(3,5), Tr, Co)
```

`exact_bqte_discrete` *BQTE for discrete distribution*

Description

BQTE for discrete distribution

Usage

```
exact_bqte_discrete(at, x, pr.con, pr.trt, verbose = TRUE)
```

Arguments

`at`	value at which bqte is computed.
`x`	outcome values corresponding to probabilities in pr.con and pr.trt. Value 'at' must be found among 'x'.
`pr.con`	(unnormalized) probability mass function of the control group.
`pr.trt`	(unnormalized) probability mass function of the treatment group.
`verbose`	(default TRUE), if TRUE, prints info on the console.

Value

BQTE at value 'at'

Examples

```
exact_bqte_discrete(3, x = 1:4, pr.con = c(0.1,0.2,0.3,0.4), pr.trt = c(0.3,0.5,0.15,0.05))
```

plot_bqte *Plots BQTE*

Description

Plots backtransformed quantile treatment effect (BQTE) on direct or relative scale.

Usage

```
plot_bqte(
  x,
  plot.ci = TRUE,
  plot.rbqte = FALSE,
  plot.range = FALSE,
  pch = 19,
  col = "black",
  col.ci = "red",
  col.range = "gray",
  xlim = NULL,
  ylim = NULL,
  xlab = NULL,
  ylab = NULL,
  xaxs = "r",
  yaxs = "r",
  xaxp = NULL,
  yaxp = NULL,
  cex = 1,
  cex.axis = 1,
  cex.lab = 1,
  main = "",
  lwd = 1
)
```

Arguments

x	data.frame returned by function bqte( )
plot.ci	if TRUE, plots confidence intervals around estimates using color col.ci
plot.rbqte	if TRUE, plots relative BQTEs, otherwise plots actual BQTEs
plot.range	if TRUE, plots bqte$range results (requires discrete data)
pch	pointstyle, if NULL, then lines are drawn instead of separate points
col	color
col.ci	color of confidence interval
col.range	color of range
xlim	range of x-coordinates
ylim	range of y-coordinates
xlab	label of x-axis
ylab	label of y-axis

xaxs	as R's standard plotting parameter
yaxs	as R's standard plotting parameter
xaxp	as R's standard plotting parameter
yaxp	as R's standard plotting parameter
cex	as R's standard plotting parameter
cex.axis	as R's standard plotting parameter
cex.lab	as R's standard plotting parameter
main	as R's standard plotting parameter
lwd	as R's standard plotting parameter

Value

none

Examples

```
set.seed(12); Tr = rweibull(30,1.2,1); Co = rnorm(30,3,5)
plot_bqte(bqte(Tr, Co))
```

---

plot_qte *Plot quantile treatment effect*

Description

Plot quantile treatment effect (QTE) on direct or relative scale

Usage

```
plot_qte(
  x,
  plot.ci = TRUE,
  plot.rqte = FALSE,
  pch = 19,
  col = "black",
  col.ci = "gray",
  xlim = NULL,
  ylim = NULL,
  xlab = NULL,
  ylab = NULL,
  xaxs = "r",
  yaxs = "r",
  xaxp = NULL,
  yaxp = NULL,
  lwd = 1
)
```

Arguments

x	data.frame returned by the qte () function.
plot.ci	if TRUE, plots confidence intervals around estimates.
plot.rqte	if TRUE, plots relative QTEs, otherwise plots actual QTEs.
pch	pointstyle, if NULL, then lines are drawn instead of separate points
col	color
col.ci	color of confidence interval
xlim	range of x-coordinates
ylim	range of y-coordinates
xlab	label of x-axis
ylab	label of y-axis
xaxs	as R's standard plotting parameter
yaxs	as R's standard plotting parameter
xaxp	as R's standard plotting parameter
yaxp	as R's standard plotting parameter
lwd	as R's standard plotting parameter

Value

none

Examples

```
set.seed(12); Tr = rweibull(30,1.2,1); Co = rnorm(30,3,5)
plot_qte(qte(Tr, Co))
```

---

plot_tbqte *Plot tail BQTE*

Description

Plot either lower (LTBQTE) or upper (UTBQTE) tail BQTE on direct or relative scale. For definitions of these measures, see help of bqte().

Usage

```
plot_tbqte(
  x,
  utbqte = TRUE,
  plot.ci = TRUE,
  plot.relative = FALSE,
  pch = NULL,
  col = "black",
  col.ci = "gray",
  xlim = NULL,
  ylim = NULL,
  xlab = NULL,
```

```
  ylab = NULL,
  xaxs = "r",
  yaxs = "r",
  xaxp = NULL,
  yaxp = NULL,
  cex = 1,
  cex.axis = 1,
  cex.lab = 1,
  main = "",
  lwd = 1
)
```

Arguments

x	data.frame returned by function bqte(,tails = TRUE).
utbqte	if TRUE, prints UTBQTE else prints LTBQTE.
plot.ci	if TRUE, plots confidence intervals around estimates using color col.ci.
plot.relative	if TRUE, plots relative TBQTEs, otherwise plots direct TBQTEs.
pch	pointstyle if NULL, then lines are drawn instead of separate points.
col	color.
col.ci	color of confidence interval.
xlim	range of x-coordinates.
ylim	range of y-coordinates.
xlab	label of x-axis.
ylab	label of y-axis.
xaxs	as R's standard plotting parameter.
yaxs	as R's standard plotting parameter.
xaxp	as R's standard plotting parameter.
yaxp	as R's standard plotting parameter.
cex	as R's standard plotting parameter.
cex.axis	as R's standard plotting parameter.
cex.lab	as R's standard plotting parameter.
main	as R's standard plotting parameter.
lwd	as R's standard plotting parameter.

Value

none

Examples

```
set.seed(12); Tr = rweibull(30,1.2,1); Co = rnorm(30,3,5)
plot_tbqte(bqte(Tr, Co, tails = TRUE), utbqte = FALSE, pch = 19)
```

`plot_tbqte_both` *Plot simultaneously both tail BQTEs*

Description

Plot in the same figure both UTBQTE and LTBQTE on direct or relative scale. For definitions of these measures, see help of bqte()

Usage

```
plot_tbqte_both(
  x,
  x.utbqte = NULL,
  x.ltbqte = NULL,
  plot.ci = TRUE,
  plot.relative = FALSE,
  pch.utbqte = 25,
  pch.ltbqte = 24,
  col.utbqte = "blue",
  col.ltbqte = "purple",
  col.utbqte.ci = "blue",
  col.ltbqte.ci = "purple",
  jitter = c(0, 0),
  xlim = NULL,
  ylim = NULL,
  xlab = NULL,
  ylab = NULL,
  xaxs = "r",
  yaxs = "r",
  xaxp = NULL,
  yaxp = NULL,
  cex = 1,
  cex.axis = 1,
  cex.lab = 1,
  main = "",
  lwd = 1
)
```

Arguments

`x`	data.frame returned by function bqte(,tails = TRUE).
`x.utbqte`	control group's outcome value from which utbqte is plotted towards the upper tail. If NULL, then the lowest point of data in 'x' is used.
`x.ltbqte`	control group's outcome value from which ltbqte is plotted towards the lower tail. If NULL, then highest point of data in 'x' is used.
`plot.ci`	If TRUE, plots confidence intervals around estimates using colors. col.utbqte.ci and col.ltbqte.ci
`plot.relative`	If TRUE, plots relative TBQTEs, otherwise plots direct TBQTEs.
`pch.utbqte`	pointstyle for utbqte. If NULL then the corresponding estimates are shown by a line

pch.ltbqte	pointstyle for utbqte. If NULL then the corresponding estimates are shown by a line
col.utbqte	color of utbqte.
col.ltbqte	color of ltbqte.
col.utbqte.ci	color of confidence interval for utbqte.
col.ltbqte.ci	color of confidence interval for ltbqte.
jitter	vector of length 2, gives the horizontal offsets for points to avoid overlaps. between plotted LTBQTE and UTBQTE estimates and intervals. 1st value is offset for UTBQTE, 2nd value is offset for LTBQTE default is (0,0), i.e., no offset.
xlim	range of x-coordinates.
ylim	range of y-coordinates.
xlab	label of x-axis.
ylab	label of y-axis.
xaxs	as R's standard plotting parameter.
yaxs	as R's standard plotting parameter.
xaxp	as R's standard plotting parameter.
yaxp	as R's standard plotting parameter.
cex	as R's standard plotting parameter.
cex.axis	as R's standard plotting parameter.
cex.lab	as R's standard plotting parameter.
main	as R's standard plotting parameter.
lwd	as R's standard plotting parameter.

Value

none

Examples

```
set.seed(12); Tr = rweibull(30,1.2,1); Co = rnorm(30,3,5)
plot_tbqte_both(bqte(Tr, Co, tails = TRUE))
```

---

qte *Estimate quantile treatment effects.*

Description

We have observed outcome values, such as survival or recovery times, in the treatment group and in the control group. Quantile treatment effect (QTE) is the difference between the two groups as a function of the quantile levels.

Usage

```
qte(
  Treatment,
  Control,
  at = NULL,
  qte.conf = 0.95,
  B = 2000,
  bagging = TRUE,
  exact.sample.quantiles = TRUE,
  verbose = TRUE
)
```

Arguments

Treatment	vector of outcome values (e.g. survival times) in Treatment group.
Control	vector of outcome values in Control group.
at	vector of quantiles at which QTE is estimated. By default, between 10 and 20 points between the quantile levels of 10/N and 1 - (10/N) where N = min(c(length(Control),length(Trea
qte.conf	(default 0.95), confidence level for QTE estimate.
B	(default 2000), number of bootstrap samples.
bagging	(default TRUE), if TRUE, reports bagging estimate (mean over bootstrap samples) otherwise reports the direct estimate from the data.
exact.sample.quantiles	(default TRUE), if TRUE, uses empirical sample quantiles (type = 1) if FALSE, uses R's default quantiles (type = 7), where 'type' is argument of R's quantile() function.
verbose	(default TRUE) if TRUE, prints parameters and recommendations on console.

Details

Fix a grid of quantile levels where QTEs are computed (parameter 'at'). Recommendation: Do not try to estimate QTEs at values that are outside quantile levels (10/N, 1 - (10/N)), where N is the minimum of sample sizes of treated and controls because of low accuracy at the tails.

Estimate the quantile treatment effects as difference between the quantiles of Treatment group and Control group

Use bootstrapping to estimate the uncertainty of QTE, by resampling with replacement a set of Treatment and Control group values that have the same sample size as the original Treatment and Control groups, respectively, and by applying the procedure explained above to each bootstrap sample. Note that bootstrapping accounts for uncertainty of quantiles of both groups.

The final estimate of QTE is the mean over bootstrap samples ("bagging estimate") and the confidence interval for QTE is estimated from the quantiles of the bootstrap sample. NOTE: In empirical evaluation it was observed that bagging estimate tend to have smaller mean square error in discrete distributions than the direct estimate from the data and therefore the bagging estimate is used by default. This can be switched by parameter "bagging".

Value

data frame with 7 columns

at, quantile level;

qte, quantile treatment effect;

qte.low, lower CI end point for 'qte';

qte.up, upper CI end point for 'qte';

rqte, relative quantile treatment effect with respect to control outcome value;

rqte.low, lower CI end point for 'rqte';

rqte.up, upper CI end point for 'rqte';

Examples

```
set.seed(12); Tr = rweibull(100,1.2,1); Co = rnorm(100,3,5)
qte(Tr, Co)
```

`quantiles_from_discrete`

Quantile from a discrete distribution

Description

Quantile from a discrete distribution

Usage

```
quantiles_from_discrete(p, pr)
```

Arguments

p	quantile levels.
pr	probability mass vector of non-negative values.

Value

list with two vectors: (1) quantile.level and (2) indexes. 'quantile level' equals input vector 'p' and indexes contain the indexes of 'pr' corresponding to the quantile levels in 'p'.

Examples

```
quantiles_from_discrete(p = c(0.3,0.5), pr = c(0.2,0.2,0.3,0.3))
```

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