

# Package ‘quint’

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**Type** Package

**Title** Qualitative Interaction Trees

**Version** 1.0

**Date** 2013-11-08

**Description** Grows a qualitative interaction tree. Quint is a tool for subgroup analysis, suitable for data from a two-arm randomized controlled trial.

**Depends** R (>= 3.0.2), partykit, Formula, rpart

**License** GPL-2

**Author** Elise Dusseldorp [aut, cre, cph], Lisa Doove [aut], Cor Ninaber [ctb] (supported with the plot function), Iven Van Mechelen [aut, cph]

**Maintainer** Elise Dusseldorp <elise.dusseldorp@tno.nl>

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## Description

When two treatment alternatives (say A and B) are available for some problem, one may be interested in qualitative treatment-subgroup interactions. Such interactions imply the existence of subgroups of persons (patients) which are such that in one subgroup Treatment A outperforms Treatment B, whereas the reverse holds in another subgroup. Obviously, this type of interactions is crucial for optimal treatment assignment of future patients. Given baseline characteristics and outcome data from a two-arm Randomized Controlled Trial (RCT), QQualitative INteraction Trees (QUINT) is a tool to identify subgroups that are involved in meaningful qualitative treatment-subgroup interactions. The result of QUINT is a tree that partitions the total group of participants (patients) on the basis of their baseline characteristics into three subgroups (i.e., partition classes): Subgroup 1: Those for whom Treatment A is better than Treatment B (P1), Subgroup 2: Those for whom Treatment B is better than Treatment A (P2), and Subgroup 3: Those for whom it does not make any difference (P3).

## Details

Package: quint  
Type: Package  
Version: 1.0  
Date: 2013-11-08  
License: GPL

Version 1.0 is suitable for a continuous outcome variable. The baseline characteristics (i.e., possible splitting variables) may be continuous, ordinal or dichotomous. The core function of the package is [quint](#).

## Author(s)

Maintainer: Elise Dusseldorp <elise.dusseldorp@tno.nl>

## References

Dusseldorp E. and Van Mechelen I. (2013). Qualitative interaction trees: a tool to identify qualitative treatment-subgroup interactions. *Statistics in Medicine*, first online 6 Aug 2013. DOI: 10.1002/sim.5933.

Scheier M.F., Helgeson V.S., Schulz R., et al.(2007). Moderators of interventions designed to enhance physical and psychological functioning among younger women with early-stage breast cancer. *Journal of Clinical Oncology*, 25, 5710-5714. DOI: 10.1200/JCO.2007.11.7093.

**See Also**

[quint,summary.quint,quint.control,prune.quint](#)

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bcrp

*Breast Cancer Recovery Project*

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**Description**

Data from a three-arm randomized controlled trial. Women with early-stage breast cancer were randomly assigned to a nutrition intervention ( $n = 85$ ), an education intervention ( $n = 83$ ) or standard care ( $n = 84$ ). They were measured before and after treatment. These data contain the baseline measurement and the 9-month follow-up.

**Usage**

```
data(bcrp)
```

**Format**

A data frame with 252 observations on the following 14 variables:

physt1 physical functioning (from SF-36) at baseline.

cesdt1 depression score (CESD) at baseline.

physt3 physical functioning (from SF-36) at 9 months follow-up.

cesdt3 depression score (CESD) at 9 months follow-up.

negsoct1 negative social interaction at baseline.

uncomt1 unmitigated communion at baseline.

disopt1 dispositional optimism at baseline.

comorbid number of comorbidities (e.g. diabetes, migraines, arthritis, or angina).

age age at baseline.

wcht1 weight change since diagnosis: yes [1] or no [0].

nationality Caucasian [1] or not [0].

marital married [1] or not [0].

trext treatment extensiveness index: lumpectomy without or with one form of adjuvant therapy (radiation or chemo) [-1.77], lumpectomy with radiation and chemotherapy [0.26], mastectomy without or with lumpectomy, and without or with one form of adjuvant therapy [0.56], mastectomy without or with lumpectomy, and radiation and chemotherapy [2.59].

cond experimental condition: nutrition [1], education [2] or standard care [3].

**Details**

IMPORANT: for questions about these data contact Elise Dusseldorp: [elise.dusseldorp@tno.nl](mailto:elise.dusseldorp@tno.nl).

**Source**

The authors thank M.F. Scheier for making his data available.

**References**

If you use these data, please refer to: Scheier M.F., Helgeson V.S., Schulz R., et al. (2007). Moderators of interventions designed to enhance physical and psychological functioning among younger women with early-stage breast cancer. *Journal of Clinical Oncology*, 25, 5710-5714.

An application of quint to these data is given in: Dusseldorp E. and Van Mechelen I. (2013). Qualitative interaction trees: a tool to identify qualitative treatment-subgroup interactions. *Statistics in Medicine*, first online 6 Aug 2013. DOI: 10.1002/sim.5933.

**Examples**

```
data(bcrp)
names(bcrp)
dim(bcrp)
```

---

plot.quint

*Visualisation of a Qualitative Interaction Tree*

---

**Description**

Plot function for a quint object. The plot shows the result of quint: a binary tree with (a) splitting variable(s) and split point(s). The colors of the leaves of the tree correspond to the final subgroups: Subgroup 1 (P1), those patients for whom the mean treatment outcome (Y) is higher for Treatment A than B, is GREEN; Subgroup 2 (P2), those patients for whom the mean treatment outcome (Y) is higher for Treatment B than A, is RED, and Subgroup 3 (P3), those for whom the mean treatment outcome (Y) is about the same for both treatments. Within the leaves the effect size  $d$  is displayed, with its 95 percent confidence interval. This effect size is the standardized mean difference between Treatment A and B. The plot function uses the plot method from the package **partykit** of Hothorn & Zeileis (2013).

**Usage**

```
## S3 method for class 'quint'
plot(x, digits=2,...)
```

**Arguments**

x	fitted tree of class quint.
digits	specified number of decimal places of the splitpoints in the graph (default is 2).
...	additional arguments to be passed.

**Author(s)**

Cor Ninaber and Elise Dusseldorp

## References

Torsten Hothorn and Achim Zeileis (2013). partykit: A Toolkit for Recursive Partytioning. R package version 0.1-5. <http://CRAN.R-project.org/package=partykit>.

## See Also

[quint](#), [quint.control](#), [bcrp](#)

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prune

*Pruning of a Qualitative Interaction Tree*

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## Description

Determines the optimally pruned size of the tree by applying the one standard error rule to the results from the bias-corrected bootstrap procedure.

## Usage

```
## S3 method for class 'quint'  
prune(tree, pp=1, ...)
```

## Arguments

tree	fitted tree of class <code>quint</code> .
pp	constant ( $c$ ) to be used in the $c$ *standard error rule. The default value is 1.
...	generic function.

## Details

The pruning algorithm of `quint` is explained in Dusseldorp & Van Mechelen (2013), Appendix B of the online supplementary material. It is based on the bias-corrected bootstrap pruning procedure (Le Blanc & Crowley, 1993) and the one standard error rule (Breiman, Friedman, Olshen, & Stone, 1984). The one standard error rule for `quint` uses the estimates of the bias-corrected criterion value ( $C$ ) and its standard error for each value of  $L$  (= maximum number of leaves). The optimally pruned tree corresponds to the smallest tree with a bias-corrected  $C$  higher or equal to the maximum bias-corrected  $C$  minus its standard error.

## Value

Returns an object of class `quint`. The number of leaves of this object is equal to the optimally pruned size of the tree.

## References

Breiman L., Friedman J.H., Olshen R.A. and Stone C.J. (1984). *Classification and Regression Trees*. Chapman & Hall/CRC: Boca Raton.

Dusseldorp E. and Van Mechelen I. (2013). Qualitative interaction trees: a tool to identify qualitative treatment-subgroup interactions. *Statistics in Medicine*, first online 6 Aug 2013. DOI: 10.1002/sim.5933.

LeBlanc M. and Crowley J. (1993). Survival trees by goodness of split. *Journal of the American Statistical Association*, 88, 457-467.

## See Also

[quint.control](#), [quint](#)

## Examples

```
data(bcrp)
formula2<- I(cesdt1-cesdt3)~cond |age+trestt++uncomt1+ disopt1+negsoct1
#Adjust the control parameters only to save computation time in the example;
#The default control parameters are preferred
control2<-quint.control(maxl=6,B=2)
set.seed(2) #this enables you to repeat the results of the bootstrap procedure
quint2<-quint(formula2, data= subset(bcrp,cond<3),control=control2)
quint2pr<-prune(quint2)
summary(quint2pr)
```

---

quint

*Qualitative Interaction Trees*

---

## Description

This is the core function of the package. It performs a subgroup analysis by Qualitative Interaction Trees (QUINT; Dusseldorp & Van Mechelen, 2013) and is suitable for data from a two-arm randomized controlled trial. Ingredients of the analysis are: one continuous outcome variable  $Y$  (the effect variable), one dichotomous treatment variable  $T$  (indicating two treatment conditions, A and B), and several background characteristics  $X_1, \dots, X_J$ . These background characteristics are measured at baseline and may be continuous, ordinal, or dichotomous. They are used to identify the following subgroups (i.e., partition classes): Subgroup 1: Those patients for whom Treatment A is better than Treatment B (P1); Subgroup 2: Those for whom Treatment B is better than Treatment A (P2), and Subgroup 3: Those for whom it does not make any difference (P3).

## Usage

```
quint(formula, data, control = NULL)
```

**Arguments**

formula	a description of the model to be fit. The format is $Y \sim T \mid X_1 + \dots + X_J$ , where the variable before the   represents the dichotomous treatment variable $T$ and the variables after the   are the baseline characteristics used for partitioning. If the data are in the order $Y, T, X_1, \dots, X_J$ , no formula is needed. The lay-out of this formula is based on Zeileis & Croissant (2010).
data	a dataframe containing the variables in the model.
control	a list with control parameters as returned by <code>quint.control</code> .

**Details**

The method QUINT uses a sequential partitioning algorithm. The algorithm starts with a tree consisting of a single node, that is, the root node containing all patients. Next, it follows a stepwise binary splitting procedure. This procedure implies that in each step a node, a baseline characteristic, a split of that characteristic, and an assignment of the leaves of the current tree to partition classes 1, 2, and 3 (P1 to P3) are chosen that maximize the partitioning criterion. Note that this means that after each split, all leaves of the tree are re-assigned afresh to the partition classes P1, P2, and P3.

**Value**

Returns an object of class `quint` with components:

call	the call that created the object.
crit	the partitioning criterion used to grow the tree. The default is the Effect size criterion. Use <code>crit="dm"</code> for the Difference in means criterion.
control	the control parameters used in the analysis.
fi	the fit information of the final tree.
si	the split information of the final tree.
li	the leaf information of the final tree.
data	the data used to grow the tree.
nind	an $N \times L$ matrix indicating leaf membership.
siboot	an $L \times 9 \times B$ array with split information for each bootstrap sample: <code>C_boot</code> = value of $C$ ; <code>C_compdif</code> = value of Difference in treatment outcome component; <code>checkdif</code> = indicates if pooled Difference in treatment outcome component in test set (i.e., original sample) is positive, with values: 0 = yes, 1 = negative in P1, 2 = negative in P2, 3 = negative in P1 and P2; <code>C_compcard</code> = value of Cardinality component; <code>checkcard</code> = indicates if value of pooled cardinality in test set is zero, with values: 0 = no, 1 = zero in P1, 2 = zero in P2, 3 = zero in P1 and P2; <code>opt</code> = value of optimism ( $C_{boot} - C_{orig}$ ).
indexboot	an $N \times B$ matrix indicating bootstrap sample membership.

**References**

Dusseldorp E. and Van Mechelen I. (2013). Qualitative interaction trees: a tool to identify qualitative treatment-subgroup interactions. *Statistics in Medicine*, first online 6 Aug 2013. DOI: 10.1002/sim.5933.

Zeileis A. and Croissant Y. (2010). Extended model formulas in R: Multiple parts and multiple responses. *Journal of Statistical Software*, 34(1), 1-13.

### See Also

[summary.quint](#), [quint.control](#), [prune.quint](#), [bcrp](#)

### Examples

```
#EXAMPLE with data from the Breast Cancer Recovery Project
data(bcrp)

#Start with expliciting the model for quint
#The outcome Y is a change score between timepoint 3 and timepoint 1
#A positive Y value indicates an improvement in depression (i.e., a decrease)

formula1<- I(cesdt1-cesdt3)~cond | nationality+marital+wcht1+age+
trext+comorbid+disopt1+uncomt1+negsoct1

#Perform a quint analysis
#The BCRP data contain 3 conditions. Quint only works now for 2 conditions.
#For the example, we disregard the control condition
#To save computation time, we also adjust the control parameters

set.seed(2)
control1<-quint.control(maxl=5,B=2)
quint1<-quint(formula1, data= subset(bcrp,cond<3),control=control1)

#Inspect the main results of the analysis:
summary(quint1)

#Inspect the assignments of the patients to the leaves of the tree
quint1$nind

#plot the tree
plot(quint1)
```

---

quint.control

*Control Parameters for Quint Algorithm*

---

### Description

Various parameters that control aspects of the “quint” algorithm. Appendix A of Dusseldorp & Van Mechelen (2013) gives a detailed overview of the choices that can be made.

### Usage

```
quint.control(crit = "es", maxl=10, a1 = NULL, a2 = NULL, w = NULL,
Bootstrap = TRUE, B = 25, dmin = 0.3)
```

**Arguments**

crit	the type of difference in treatment outcome used in the partitioning criterion: "es" (Treatment effect sizes) or "dm" (Difference in treatment means).
maxl	maximum number of leaves ( $L$ ) of the tree. Default value is 10.
a1	the minimal sample size of Treatment A ( $T = 1$ ) in a leaf.
a2	the minimal sample size of Treatment B ( $T = 2$ ) in a leaf.
w	a vector with $w_1$ and $w_2$ representing the weights of, respectively, the Difference in treatment outcome component and the Cardinality component of the partitioning criterion. If crit = "dm", the default value of $w_1$ is $1/\log(1 + IQR(Y))$ . If crit = "es", the default value of $w_1$ is $1/\log(1 + 3)$ . The default of $w_2$ is $1/\log(0.50N)$ .
Bootstrap	whether the bias-corrected bootstrap procedure should be performed. The default is TRUE.
B	the number of bootstrap samples to be drawn. The default is 25.
dmin	the minimum absolute standardized mean difference in treatment outcome in each of the two leaves after the first split of the tree. This value is used to check whether a qualitative interaction is present in the data (the qualitative interaction condition); dmin controls the balance between Type I error and Type II error. The default value of dmin is 0.30.

**Value**

A list containing the options.

**References**

Dusseldorp E. and Van Mechelen I. (2013). Qualitative interaction trees: a tool to identify qualitative treatment-subgroup interactions. *Statistics in Medicine*, first online 6 Aug 2013. DOI: 10.1002/sim.5933.

**See Also**

[quint](#)

**Examples**

```
data(bcrp)
formula1<- I(cesdt1-cesdt3)~cond | nationality+marital+wcht1+age+
trext+comorbid+disopt1+uncomt1+negsoct1
#Specify the Difference in treatment outcome as Difference in means
#and skip the bias-corrected bootstrap procedure
#and change the maximum number of leaves
control3<-quint.control(crit="dm",Bootstrap=FALSE,maxl=3)
quint3<-quint(formula1, data= subset(bcrp,cond<3),control=control3)
summary(quint3)

#Set number of bootstrap samples at 10
control4<-quint.control(B=10)
```

```
#Set minimal sample size in each treatment group at 5
control5<-quint.control(a1=5,a2=5)
```

---

summary.quint

*Summarizing Qualitative Interaction Tree Information*


---

### Description

Summary method for an object of class quint.

### Usage

```
## S3 method for class 'quint'
summary(object,...,digits=2)
```

### Arguments

object	a quint object. This can be the output of <a href="#">quint</a> .
...	optional additional arguments.
digits	specified number of decimal places (default is 2).

### Details

This function is a method for the generic function summary for class quint. It extracts the following essential components from a quint object: 1) Specification of the partitioning criterion; 2) Fit information; 3) Split information, and 4) Leaf information.

### Examples

```
data(bcrp)
formula1<- I(cesdt1-cesdt3)~cond | nationality+marital+wcht1+
age+trext+comorbid+disopt1+uncomt1+negsoct1
control1<-quint.control(max1=5,Bootstrap=FALSE)
quint1<-quint(formula1, data= subset(bcrp,cond<3),control=control1 )
summary(quint1)
```

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