

Package ‘metacart’

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Type Package

Title Meta-CART: A Flexible Approach to Identify Moderators in
Meta-Analysis

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Description Meta-CART integrates classification and regression trees (CART) into meta-
analysis. Meta-CART is a flexible approach to identify interaction effects between modera-
tors in meta-analysis. The method is described in Dussel-
dorp et al. (2014) <doi:10.1037/hea0000018> and Li et al. (2017) <doi:10.1111/bmsp.12088>.

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License GPL (>= 2)

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metacart-package	<i>R package for meta-CART</i>
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Description

In meta-analysis, heterogeneity often exists between studies. To understand this heterogeneity, researchers search for study characteristics (i.e., potential moderators) that may account for the variance in study effect sizes. When multiple potential moderators are available (e.g., intervention characteristics), traditional meta-analysis methods often lack sufficient power to investigate interaction effects between moderators, especially high-order interactions. To solve this problem, meta-CART was proposed by integrating Classification and Regression Trees (CART) into meta-analysis. The method identifies the interaction effects between influential moderators, partitions the studies into more homogeneous subgroups, and estimates summary effect size in each subgroup. The fixed effect or random effects assumption can be consistently taken into account in both tree-growing process and subgroup analysis.

Details

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 License: GPL

This method is suitable for identifying interaction effects between dichotomous, ordinal, continuous, and nominal moderators. The output of a REmrt object shows meta-CART analysis results based on the random effects model. And the output of a FEmrt object shows meta-CART analysis results based on the fixed effect model. The two objects display results for subgroup analysis including the Q-statistic and estimates for the subgroup effect sizes. Furthermore, the predict functions predict.REmrt and predict.FEmrt can be used to predict the effect size given the moderators. The plot functions plot.REmrt and plot.FEmrt show the interaction effects between identified moderators.

The core functions of the package are [FEmrt](#) and [REmrt](#).

Author(s)

Maintainer: Xinru Li <x.li@math.leidenuniv.nl>; Contributors: Elise Dusseldorp, Kaihua Liu (supported with the plot function), Jacqueline Meulman.

References

Dusseldorp, E., van Genugten, L., van Buuren, S., Verheijden, M. W., & van Empelen, P. (2014). Combinations of techniques that effectively change health behavior: Evidence from meta-cart analysis. *Health Psychology, 33*(12), 1530-1540. doi: 10.1037/hea0000018.

Li, X., Dusseldorp, E., & Meulman, J. J. (2017). Meta-CART: A tool to identify interactions between moderators in meta-analysis. *British Journal of Mathematical and Statistical Psychology, 70*(1), 118-136. doi: 10.1111/bmsp.12088.

Therneau, T., Atkinson, B., & Ripley, B. (2014) rpart: Recursive partitioning and regression trees. R package version, 4-1.

The articles of our own work can be found at <http://www.elisedusseldorp.nl/>

See Also

[FEmrt](#), [REmrt](#), [summary.FEmrt](#), [summary.REmrt](#), [plot.FEmrt](#), [plot.REmrt](#), [predict.FEmrt](#), [predict.REmrt](#)

dat.balanced	<i>A simulated meta-analytic data set with balanced pure interaction effects</i>
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Description

Data simulated from a true model with pure interactions between two moderators: x_1 , x_2 . If $x_1 = 0$ and $x_2 = 1$ or $x_1 = 1$ and $x_2 = 0$, the true effect size is 0.50. Otherwise, the true effect size is 0.

Usage

```
data(dat.balanced)
```

Format

A data frame of 60 studies with 4 moderators

- `efk`: The effect size of each study expressed as Hedges' g
- `vark`: The sampling variance of the effect size
- `x1` to `x4`: Four randomly generated moderators. x_1 , x_2 , and x_4 are dichotomous variables, x_3 is a continuous variable generated from uniform distribution.

dat.BCT2009

A subset of data from Michie et al. (2009)

Description

The complete data consist of 101 studies reporting 122 interventions targeted at physical activity and healthy eating. In this subset of the data, the interventions that include at least one of the motivation-enhancing behaviour change techniques (BCTs) were selected (N = 106).

Usage

`data(dat.BCT2009)`

Format

A data frame of 106 interventions with five motivation-enhancing behavior change techniques (BCTs).

- study: The name of the intervention.
- g: The effect size of each intervention.
- vi: The sampling variance of the effect size.
- T1: Indicating whether the BCT1 "Provide information about behavior-health link" was used by the intervention. "1" for used and "0" for not used.
- T2: Indicating whether the BCT2 "Provide information on consequences" was used by the intervention. "1" for used and "0" for not used.
- T3: Indicating whether the BCT3 "Provide information about other's approval" was used by the intervention. "1" for used and "0" for not used.
- T4: Indicating whether the BCT4 "Prompt intention formation" was used by the intervention. "1" for used and "0" for not used.
- T25: Indicating whether the BCT25 "Motivational interviewing" was used by the intervention. "1" for used and "0" for not used.

Details

IMPORTANT: for questions about these data contact Xinru Li: x.li@math.leidenuniv.nl.

References

If you use these data, please refer to: Michie, S., Abraham, C., Whittington, C., McAteer, J., & Gupta, S. (2009). Effective techniques in healthy eating and physical activity interventions: a meta-regression. *Health Psychology, 28*(6), 690.

An application of (a preliminary version of) meta-CART to this data set is given in: Dusseldorp, E., Van Genugten, L., van Buuren, S., Verheijden, M. W., & van Empelen, P. (2014). Combinations of techniques that effectively change health behavior: Evidence from Meta-CART analysis. *Health Psychology, 33*(12), 1530.

FEmrt

*Fixed effect meta-tree***Description**

A function to fit fixed effect meta-trees to meta-analytic data. The model is assuming a fixed effect within subgroups and between subgroups. The tree growing process is equivalent to the approach described in Li et al. (2017) using fixed effect weights in the function **rpart()** developed by Therneau, Atkinson & Ripley (2014).

Usage

```
FEmrt(formula, data, vi, subset, c = 1, control = rpart.control(xval =
  10, minbucket = 3, minsplit = 6, cp = 1e-04), ...)
```

Arguments

formula	A formula, with an outcome variable (usually the effect size) and the potential moderator variables but no interaction terms.
data	A data frame of a meta-analytic data set, including the study effect sizes, sampling variance, and the potential moderators.
vi	sampling variance of the effect size.
subset	optional expression that selects only a subset of the rows of the data.
c	A non-negative scalar. The pruning parameter to prune the initial tree by the "c*standard-error" rule.
control	the control object (similar to rpart.control from the rpart package) that is used in the tree algorithm
...	Additional arguments passed to the tree growing algorithm based on rpart .

Value

If (a) moderator effect(s) is(are) detected, the function will return a FEmrt object including the following components:

tree: The pruned tree that represents the moderator effect(s) and interaction effect(s) between them.

n: The number of the studies in each subgroup

Qb: The between-subgroups Q-statistic

df: The degree of freedoms of the between-subgroups Q test

pval.Qb: The p-value of the between-subgroups Q test

Qw: The within-subgroup Q-statistic in each subgroup

g: The subgroup summary effect size, based on Hedges' g

se: The standard error of the subgroup summary effect size

zval: The test statistic of the subgroup summary effect size

pval: The p-value for the test statistics of the subgroup summary effect size

ci.lb: The lower bound of the confidence interval

ci.ub: The upper bound of the confidence interval

call: The matched call

If no moderator effect is detected, the function will return a FEmrt object including the following components:

n: The total number of the studies

Q: The Q-statistic of the heterogeneity test

df: The degrees of freedom of the heterogeneity test

pval.Q: The p-value of the heterogeneity test

g: The summary effect size for all studies

se: The standard error of the summary effect size

zval: The test statistic of the summary effect size

pval: The p-value of the test statistic of the summary effect size

ci.lb: The lower bound of the confidence interval for the summary effect size

ci.ub: The upper bound of the confidence interval for the summary effect size

call: The matched call

References

Dusseldorp, E., van Genugten, L., van Buuren, S., Verheijden, M. W., & van Empelen, P. (2014). Combinations of techniques that effectively change health behavior: Evidence from meta-cart analysis. *Health Psychology, 33*(12), 1530-1540. doi: 10.1037/hea0000018.

Li, X., Dusseldorp, E., & Meulman, J. J. (2017). Meta-CART: A tool to identify interactions between moderators in meta-analysis. *British Journal of Mathematical and Statistical Psychology, 70*(1), 118-136. doi: 10.1111/bmsp.12088.

Therneau, T., Atkinson, B., & Ripley, B. (2014) rpart: Recursive partitioning and regression trees. R package version, 4-1.

See Also

[summary.FEmrt](#), [plot.FEmrt](#), [rpart](#), [rpart.control](#)

Examples

```
data(dat.BCT2009)
FEtree <- FEmrt(g ~ T1 + T2+ T4 + T25, vi = vi, data = dat.BCT2009, c = 0.5)
print(FEtree)
summary(FEtree)
plot(FEtree)
```

plot.FEmrt	<i>Visualisation of a FE meta-tree</i>
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Description

Plot function for a FEmrt object. The plot shows the result of FEmrt. The plot function uses the plot method from the package **ggplot2**

Usage

```
## S3 method for class 'FEmrt'  
plot(x, ...)
```

Arguments

x	A FEmrt object.
...	additional arguments to pass

Details

For categorical variables we recommend to use short names for levels to avoid overlapping labels at split points.

plot.REmrt	<i>Visualisation of a RE meta-tree</i>
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Description

Plot function for a REmrt object. The plot shows the result of REmrt. The plot function uses the plot method from the package **ggplot2**

Usage

```
## S3 method for class 'REmrt'  
plot(x, ...)
```

Arguments

x	A REmrt object.
...	Additional arguments to pass.

Details

For categorical variables we recommend to use short names for levels to avoid overlapping labels at split points.

predict.FEmrt	<i>Predictions from a fitted metacart object</i>
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Description

Returns a data frame of predicted effect sizes and moderators from a fitted metacart object

Usage

```
## S3 method for class 'FEmrt'
predict(object, newdata, ...)
```

Arguments

object	fitted model object of class "FEmrt".
newdata	data frame containing the values at which predictions are required.
...	Arguments that pass to other methods.

Value

A data frame containing the predicted effect size, the moderators, and the corresponding node labels in the fitted tree.

predict.REmrt	<i>Predictions from a fitted metacart object</i>
---------------	--

Description

Returns a data frame of predicted effect sizes and moderators from a fitted metacart object

Usage

```
## S3 method for class 'REmrt'
predict(object, newdata, ...)
```

Arguments

object	fitted model object of class "REmrt".
newdata	data frame containing the values at which predictions are required.
...	Arguments that pass to other methods.

Value

A data frame containing the predicted effect size, the moderators, and the corresponding node labels in the fitted tree.

print.FEmrt	<i>Print function for FEmrt</i>
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Description

Print the results of a FEmrt object

Usage

```
## S3 method for class 'FEmrt'  
print(x, ...)
```

Arguments

x	fitted tree of class FEmrt.
...	additional arguments to be passed.

Details

The function returns the objects concerning the analysis results.

print.REmrt	<i>Print function for REmrt</i>
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Description

Print the results of a REmrt object

Usage

```
## S3 method for class 'REmrt'  
print(x, ...)
```

Arguments

x	fitted tree of class FEmrt.
...	additional arguments to be passed.

Details

The function returns the results (e.g., the value of the Q-between) after each split of the tree.

REmrt

*Random effects meta-tree***Description**

A function to fit a random effects meta-tree

Usage

```
REmrt(formula, data, vi, c = 1, maxL = 5, minsplit = 6, cp = 1e-05,
      minbucket = 3, xval = 10, lookahead = FALSE, ...)
```

Arguments

formula	A formula, with a response variable (usually the effect size) and the potential moderator variables but no interaction terms.
data	A data frame of a meta-analytic data set, including the study effect sizes, sampling variance, and the potential moderators.
vi	sampling variance of the effect size.
c	A non-negative scalar. The pruning parameter to prune the initial tree by the "c*standard-error" rule.
maxL	the maximum number of splits
minsplit	the minimum number of studies in a parent node before splitting
cp	the stopping rule for the decrease of between-subgroups Q. Any split that does not decrease the between-subgroups Q is not attempted.
minbucket	the minimum number of the studies in a terminal node
xval	the number of folds to perform the cross-validation
lookahead	an argument indicating whether to apply the "look-ahead" strategy when fitting the tree
...	Additional arguments to be passed.

Value

If (a) moderator effect(s) is(are) detected, the function will return a list including the following objects:

tree: A data frame that represents the tree, with the Q-between and the residual heterogeneity (τ^2) after each split.

n: The number of the studies in each subgroup

moderators: the names of identified moderators

Qb: The between-subgroups Q-statistic

tau2: The estimate of the residual heterogeneity

df: The degrees of freedom of the between-subgroups Q test

pval.Qb: The p-value of the between-subgroups Q test
g: The subgroup summary effect size, based on Hedges' g
se: The standard error of subgroup summary effect size
zval: The test statistic of the subgroup summary effect size
pval: The p-value of the test statistic of the subgroup summary effect size
ci.lb: The lower bound of the confidence interval
ci.ub: The upper bound of the confidence interval
call: The matched call
cv.res: The cross-validation table
data: the data set subgrouped by the fitted tree

If no moderator effect is detected, the function will return a list including the following objects:

n: The total number of the studies
Q: The Q-statistics for the heterogeneity test
df: The degree of freedoms of the heterogeneity test
pval.Q: The p-value for the heterogeneity test
g: The summary effect size for all studies (i.e., the overall effect size)
se: The standard error of the summary effect size
zval: The test statistic of the summary effect size
pval: The p-value for the test statistic of the summary effect size
ci.lb: The lower bound of the confidence interval for the summary effect size
ci.ub: The upper bound of the confidence interval for the summary effect size
call: The matched call

See Also

[summary.REmrt](#), [plot.REmrt](#)

Examples

```
data(dat.BCT2009)
REtree <- REmrt(g ~ T1 + T2+ T4 +T25, vi = vi, data = dat.BCT2009, c = 0)
summary(REtree)
plot(REtree)
```

SimData	<i>A simulated meta-analytic data set</i>
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Description

Data simulated from a true model with a three-way interaction between three moderators: m1, m2 and m3. If the values of the three moderators are all "B"s the true effect size will be 0.80. Otherwise, the true effect size is 0.

Usage

```
data(SimData)
```

Format

A data frame of 120 studies with 5 moderators

- `efk`: The effect size of each study expressed as Hedges' g
- `vark`: The sampling variance of the effect size
- `m1` to `m5`: Five randomly generated moderators. `m1` and `m2` have two levels (A and B), whereas `m3`, `m4` and `m5` have three levels (A, B and C)

summary.FEmrt	<i>Summary of the results of a FE meta-tree object</i>
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Description

Summary of the results of a FE meta-tree object

Usage

```
## S3 method for class 'FEmrt'
summary(object, digits = 3, ...)
```

Arguments

<code>object</code>	fitted tree of class FEmrt.
<code>digits</code>	specified number of decimals in the printed results.
<code>...</code>	additional arguments to be passed.

Details

If no moderator effect is detected, the summary function will show the standard meta-analysis results. Otherwise, the summary function will show the subgroup meta-analysis results, with the significance test results for moderator effects, the split points of the moderators, and the estimated subgroup summary effect sizes.

summary.REmrt	<i>Summary of the results of a RE meta-tree object</i>
---------------	--

Description

Summary of the results of a RE meta-tree object

Usage

```
## S3 method for class 'REmrt'  
summary(object, digits = 3, ...)
```

Arguments

object	fitted tree of class REmrt.
digits	specified number of decimals in the printed results.
...	additional arguments to be passed.

Details

If no moderator effect is detected, the summary function will show the standard meta-analysis results. Otherwise, the summary function will show the subgroup meta-analysis results, with the significance test results for moderator effects, the split points of the moderators, and the estimated subgroup summary effect sizes.

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