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 Fits meta-CART by integrating classification and regression trees (CART) into meta-analysis. Meta-CART is a flexible approach to identify interaction effects between moderators in meta-analysis. The methods are described in Dusseldorp et al. (2014) <doi:10.1037/hea0000018> and Li et al. (2017) <doi:10.1111/bmsp.12088>.

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Description

In many areas, there are multiple moderators available (e.g., intervention characteristics). In such cases, 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, splits the studies into more homogeneous subgroups, and test the interaction effects by Q-statistic. The fixed effect or random effects assumption can be consistently taken into account in both detection and testing process.

Details

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This method is suitable for identifying interaction effects between dichotomous, ordinal, continuous, and nominal moderators. The output of a \texttt{REMrt} object shows meta-CART analysis results based on the random effects model. And the output of a \texttt{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 \texttt{predict.REmrt} and \texttt{predict.FEmrt} can be used to predict the effect size given the moderators. The plot functions \texttt{plot.REmrt} and \texttt{plot.FEmrt} show the interaction effects between identified moderators.

The core functions of the package are \texttt{FEmrt} and \texttt{REMrt}.
Author(s)

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References


The articles of our own work can be found at [http://www.elisedusseldorp.nl/](http://www.elisedusseldorp.nl/)

See Also

femrt, remrt, summary.femrt, summary.REmrt, plot.femrt, plot.REmrt, predict.femrt, predict.REmrt

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

References


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**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**

```r
FEmrt(formula, data, vi, subset, c = 0, control = rpart.control(xval = 10,
    minbucket = 5, msplit = 10, cp = 1e-04), ...)
```

**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.
- `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 \texttt{rpart}.

\textbf{Value}

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

- \texttt{n}: The total number of the studies
- \texttt{Q}: The \texttt{Q}-statistic of the heterogeneity test
- \texttt{df}: The degrees of freedom of the heterogeneity test
- \texttt{pval.Q}: The p-value of the heterogeneity test
- \texttt{g}: The summary effect size for all studies
- \texttt{se}: The standard error of the summary effect size
- \texttt{zval}: The test statistic of the summary effect size
- \texttt{pval}: The p-value of the test statistic of the summary effect size
- \texttt{ci.lb}: The lower bound of the confidence interval for the summary effect size
- \texttt{ci.ub}: The upper bound of the confidence interval for the summary effect size
- \texttt{call}: The matched call

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

- \texttt{tree}: The pruned tree that represents the moderator effect(s) and interaction effect(s) between them.
- \texttt{n}: The number of the studies in each subgroup
- \texttt{Qb}: The between-subgroups \texttt{Q}-statistic
- \texttt{df}: The degree of freedoms of the between-subgroups \texttt{Q} test
- \texttt{pval.Qb}: The p-value of the between-subgroups \texttt{Q} test
- \texttt{Qw}: The within-subgroup \texttt{Q}-statistic in each subgroup
- \texttt{g}: The subgroup summary effect size, based on Hedges’ $g$
- \texttt{se}: The standard error of the subgroup summary effect size
- \texttt{zval}: The test statistic of the subgroup summary effect size
- \texttt{pval}: The p-value for the test statistics of the subgroup summary effect size
- \texttt{ci.lb}: The lower bound of the confidence interval
- \texttt{ci.ub}: The upper bound of the confidence interval
- \texttt{call}: The matched call
References


See Also

`summary.FEmrt`, `plot.FEmrt`, `rpart.rpart.control`

Examples

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

plot.FEmrt

*Visualisation of a FE meta-tree*

Description

Plot function for a `FEmrt` object. The plot shows the result of `FEmrt`. The plot function uses the plot method from the package `rpart.plot` of Stephen Milborrow (2016).

Usage

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

Arguments

- `x` A `FEmrt` object.
- `...` Arguments that pass to `prp()`

Details

For categorical variables we recommend to use short names for levels to avoid overlapping labels at split points. For each split of the tree it holds that if the condition (in the parent node) is satisfied, then the study goes to the left node and if not it goes to the right node.
plot.REmrt

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
Predictions from a fitted metacart object

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**  
*Predictions from a fitted metacart object*

**Description**

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

**Usage**

```r
# 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.

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**print.REmrt**  
*Print function for REmrt*

**Description**

Print the results of a REmrt object.

**Usage**

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

**Arguments**

- `x` fitted tree of class REmrt.
- `...` additional arguments to be passed.

**Details**

The function returns the objects concerning the analysis results.
**print.REmrt**

*print.REmrt*

---

**Examples**

```r
data(SimData)
test <- FEmrt(efk~m1+m2+m3+m4+m5, vark=SimData, c=1)
print(test)
```

---

**Description**

Print function for REmrt

**Usage**

```r
## 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.

**Examples**

```r
data(SimData)
test <- REmrt(efk~m1+m2+m3+m4+m5, vark = SimData, maxL = 2, c= 0.5)
print(test)
```

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**REmrt**

Random effects meta-tree

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**Description**

A function to fit a random effects meta-tree

**Usage**

```r
REmrt(formula, data, vi, c = 1, maxL = 10L, minsplit = 2L, delQ = 0.001, n.fold = 10, ...)
```
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.
- **delQ**: The stopping rule for the decrease of between-subgroups Q. Any split that does not decrease the between-subgroups Q is not attempted.
- **n.fold**: The number of folds to perform the cross-validation.
- **...**: Additional arguments to be passed.

Value

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.

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 ($\tau^2$) 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

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)

SimData

A simulated meta-analytic data set

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**  
*Summary function for metacart*

**Description**

Summary of the results of a FE meta-tree object

**Usage**

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

**Arguments**

- `object`: fitted tree of class `FEmrt`.
- `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 splitting points of the moderators, and the estimated subgroup overall effect sizes.

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**summary.REmrt**  
*Summary of the results of a RE meta-tree object*

**Description**

Summary of the results of a RE meta-tree object

**Usage**

```r
## 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 splitting points of the moderators, and the estimated subgroup overall effect sizes.
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