Package ‘NHEMOtree’

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Description NHEMOtree performs cost-sensitive classification by solving the two-objective optimization problem of minimizing misclassification rate and minimizing total costs for classification. The three methods comprised in NHEMOtree are based on EMOAs with either tree representation or bitstring representation with an enclosed classification tree algorithm.

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NHemo

**Non-hierarchical evolutionary multi-objective tree learner to perform cost-sensitive classification**

**Description**

NHemo performs cost-sensitive classification by solving the non-hierarchical evolutionary two-objective optimization problem of minimizing misclassification rate and minimizing total costs for classification. NHemo is based on an EMOA with tree representation and cutoff optimization conducted by the EMOA.

**Usage**

```r
NHemo(data, CostMatrix,
      gens = 50, popsize = 50, max_nodes = 10,
      ngens = 14, bound = 10^-10,
      init_prob = 0.8,
      ps = c("tournament", "roulette", "winkler"), tournament_size = 4,
      crossover = c("standard", "brood", "poli"), brood_size=4,
      crossover_prob=0.5, mutation_prob=0.5,
      CV=5, vim=0, ...)  
```

**Arguments**

- `data` A data frame containing in the first column the class for each observation and in the other columns from which variables specified in formula are preferentially to be taken.
- `CostMatrix` A data frame containing the names (first column) and the costs (second column) for each explanatory variable in formula or `x`. NHEMOtree does not work with missing data in `CostMatrix`.
- `gens` Maximal number of generations of the EMOA (default: `gens=50`).
- `popsize` Population size in each generation of the EMOA (default: `popsize=50`).
- `max_nodes` Maximal number of nodes within each tree (default: `max_nodes=10`).
- `ngens` Preceeding generations for the Online Convergence Detection (OCD, default: `ngens=14`) (see below for details).
- `bound` Variance limit for the Online convergence detection (default: `bound=10^-10`).
- `init_prob` Degree of initialization \in [0, 1], i.e. the probability of a node having a subnode.
- `ps` Type of parent selection, "tournament" for tournament selection (default), "roulette" for roulette-wheel selection, and "winkler" for random selection of the first parent and the second parent by roulette-wheel selection.
- `tournament_size` Size of tournament for `ps="tournament"` (default: `tournament_size=4`).
crossover Crossover operator, "standard" for one point crossover swapping two randomly chosen subtrees of the parents, "brood" for brood crossover (for details see Tackett (1994)), "poli" for a size-dependent crossover with the crossover point from the so called common region of both parents (for details see Poli and Langdon (1998)).

brood_size Number of offspring created by brood crossover (default: brood_size=4).

crossover_prob Probability to perform crossover $\in [0, 1]$ (default: crossover_prob=0.50).

mutation_prob Probability to perform mutation $\in [0, 1]$ (default: mutation_prob=0.50).

CV Cross validation steps as natural number bigger than 1 (default: CV=5).

vim Variable importance measure to be used to improve standard crossover. vim=0 for no variable importance measure (default), vim=1 for 'simple absolute frequency', vim=2 for 'simple relative frequency', vim=3 for 'relative frequency', vim=4 for 'linear weighted relative frequency', vim=5 for 'exponential weighted relative frequency', and vim=6 for 'permutation accuracy importance'.

Details

With NHEMO a cost-sensitive classification can be performed, i.e. building a tree learner by solving a two-objective optimization problem with regard to minimizing misclassification rate and minimizing total costs for classification (sum of costs for all used variables in the classifier). The non-hierarchical evolutionary multi-objective tree learner performs this multi-objective optimization based on an EMOA with tree representation. It optimizes both objectives simultaneously without any hierarchy and generates Pareto-optimal classifiers being trees to solve the problem. Cutoffs of the tree learners are optimized with the EMOA.

Termination criteria are the maximal amount of generations and the Online Convergence Detection (OCD) proposed by Wagner and Trautmann (2010). Here, OCD uses the dominated hypervolume as quality criterion. If its variance over the last g generations is significantly below a given threshold L according to the one-sided $\chi^2$-variance test OCD stops the run. We followed the suggestion of Wagner and Trautmann (2010) and considered their parameter settings as default values.

Missing data in the grouping variable or the explanatory variables are excluded from the analysis automatically.

NHEMO does not work with missing data in CostMatrix. Costs of all explanatory variables set to 1 results in optimizing the amount of explanatory variables in the tree learner as second objective.

Author(s)

Swaantje Casjens

References


See Also

NHEMOtree

Examples

```r
# Simulation of data and costs
d <- Sim.Data(Obs=200)
CostMatrix <- Sim.Costs()

# NHEMO calculations with function NHEMOtree and type="NHEMO"
res <- NHEMOtree(method="NHEMO", formula=y2~., data=d, CostMatrix=CostMatrix,
gens=5, popsize=10,
max_nodes=5, ngens=5, bound=10^-10, init_prob=0.8,
ps="tournament", tournament_size=4, crossover="standard",
crossover_prob=0.1, mutation_prob=0.1,
CV=5, vim=1)

res
```

### NHEMOtree

**Non-hierarchical evolutionary multi-objective tree learner to perform cost-sensitive classification**

#### Description

NHEMOtree performs cost-sensitive classification by solving the two-objective optimization problem of minimizing misclassification rate and minimizing total costs for classification. The three methods comprised in NHEMOtree ("NHEMO", "NHEMO_Cutoff", "Wrapper") are based on EMOAs with either tree representation or bitstring representation with a classification tree as enclosed classifier.

#### Usage

```r
NHEMOtree(method = c("NHEMO", "NHEMO_Cutoff", "Wrapper"),
formula, data, x, grouping,
CostMatrix, ...)
```

#### Arguments

- **method**: Optimization method, "NHEMO" for standard non-hierarchical evolutionary multi-objective optimization with cutoff optimization by the EMOA, "NHEMO_Cutoff" for NHEMO with local cutoff optimization, "Wrapper" for the wrapper approach (see below for details).
- **formula**: A formula of the form groups ~ x1 + x2 + ... The response is the grouping factor and the right hand side specifies the explanatory variables.
- **data**: Data frame from which variables specified in formula are preferentially to be taken.
NHEMOtree

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<td>x</td>
<td>(Required if no formula is given as the principal argument.) A matrix or data frame containing the explanatory variables.</td>
</tr>
<tr>
<td>grouping</td>
<td>(Required if no formula is given as the principal argument.) A factor specifying the class for each observation.</td>
</tr>
<tr>
<td>CostMatrix</td>
<td>A data frame containing the names (first column) and the costs (second column) for each explanatory variable in formula or x. NHEMOtree does not work with missing data in CostMatrix.</td>
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<tr>
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Details
With NHEMOtree three types of cost-sensitive classification can be performed, i.e. building a tree learner by solving a two-objective optimization problem with regard to minimizing misclassification rate and minimizing total costs for classification (summarized costs for all used variables in the classifier).

First, the non-hierarchical evolutionary multi-objective tree learner (NHEMOtree) performs this multi-objective optimization based on an EMOA with tree representation (method="NHEMO"). It optimizes both objectives simultaneously without any hierarchy and generates Pareto-optimal classifiers being binary trees to solve the problem. Cutoffs of the tree learners are optimized with the EMOA.

Second, NHEMOtree with local cutoff optimization works like NHEMOtree but the cutoffs of the tree learner are optimized analogous to a classification tree with recursive partitioning either based on the Gini index or the misclassification rate (method="NHEMO_Cutoff").

Third, a wrapper approach based on NSGA-II with enclosed classification tree algorithm can be chosen to solve the multi-objective optimization problem (method="Wrapper"). The classification trees are built with rpart. However, wrapper approaches suffer from a hierarchy in the objectives at which misclassification is minimized at first followed by optimizing costs.

Termination criteria of the EMOAs are the maximal amount of generations and the Online Convergence Detection (OCD) proposed by Wagner and Trautmann (2010). Here, OCD uses the dominated hypervolume as quality criterion. If its variance over the last g generations is significantly below a given threshold L according to the one-sided $\chi^2$-variance test OCD stops the run. We followed the suggestion of Wagner and Trautmann (2010) and considered their parameter settings as default values.

Missing data in the grouping variable or the explanatory variables are excluded from the analysis automatically.

NHEMOtree does not work with missing data in "CostMatrix". Costs of all explanatory variables set to 1 results in optimizing the amount of explanatory variables in the tree learner as second objective.

Value
Values returned by NHEMOtree are

- **S_Metric**: S metric of the final population
- **Misclassification_total**: Range of the misclassification rate of the final population
Costs_total  Range of the costs of the final population
VIMS        Variable improtance measures of all explanatory variables for method=c("NHEMO", 
            "NHEMO_Cutoff")
Trees       Individuals of the final population
Best_Tree   Individual of the final population with the lowest misclassification rate, its mis-
            classification rate and costs for method=c("Wrapper")
S_Metrik_temp S metric values of each generation
method      Method run with NHEMOtree

Author(s)
Swaantje Casjens

References


K. Deb, A. Pratap, S. Agarwal and T. Meyarivan. A fast and elitist multiobjective genetic algorithm: 

R. Poli and W.B. Langdon. Schema theory for genetic programming with one-point crossover and 

W.A. Tackett. Recombination, selection und the genetic construction of computer programs. PhD 

T. Wagner and H. Trautmann. Online convergence detection for evolutionary multiobjective algo-

See Also

plot.NHEMOtree, NHEMO, NHEMO_Cutoff, Wrapper

Examples

# Simulation of data and costs
d <- Sim_Data(Obs=200)
CostMatrix<- Sim_Costs()

# NHEMOtree calculations
res<- NHEMOtree(method="NHEMO", formula=Y2-, data=d, CostMatrix=CostMatrix, 
                gens=5, popsize=5, crossover_prob=0.1, mutation_prob=0.1)
res
**Non-hierarchical evolutionary multi-objective optimization with local cutoff optimization**

**Description**

NHEMO_Cutoff performs cost-sensitive classification by solving the non-hierarchical evolutionary two-objective optimization problem of minimizing misclassification rate and minimizing total costs for classification. NHEMO_Cutoff is based on an EMOA with tree representation and local cutoff optimization. Cutoffs of the tree learner are optimized analogous to a classification tree with recursive partitioning either based on the Gini index or the misclassification rate.

**Usage**

```r
NHEMO_Cutoff(data, CostMatrix, gens = 50, popsize = 50, max_nodes = 10, ngens = 14, bound = 10^-10, init_prob = 0.8, ps = c("tournament", "roulette", "winkler"), tournament_size = 4, crossover = c("standard", "brood", "poli"), brood_size = 4, crossover_prob = 0.5, mutation_prob = 0.5, CV = 5, vim = 0, ncutoffs = 10, opt = c("gini", "mcr"))
```

**Arguments**

- **data**: A data frame containing in the first column the class for each observation and in the other columns from which variables specified in formula are preferentially to be taken.
- **CostMatrix**: A data frame containing the names (first column) and the costs (second column) for each explanatory variable in formula or x. NHEMOtree does not work with missing data in CostMatrix.
- **gens**: Maximal number of generations of the EMOA (default: gens=50).
- **popsize**: Population size in each generation of the EMOA (default: popsize=50).
- **max_nodes**: Maximal number of nodes within each tree (default: max_nodes=10).
- **ngens**: Preceeding generations for the Online Convergence Detection (OCD, default: ngens=14) (see below for details).
- **bound**: Variance limit for the Online convergence detection (default: bound=10^10).
- **init_prob**: Degree of initialization ∈ [0,1], i.e. the probability of a node having a subnode (default: init_prob=0.80).
- **ps**: Type of parent selection, "tournament" for tournament selection (default), "roulette" for roulette-wheel selection, and "winkler" for random selection of the first parent and the second parent by roulette-wheel selection.
- **tournament_size**: Size of tournament for ps="tournament" (default: tournament_size=4).
crossover Crossover operator, "standard" for one point crossover swapping two randomly chosen subtrees of the parents, "brood" for brood crossover (for details see Tackett (1994)), "poli" for a size-dependent crossover with the crossover point from the so called common region of both parents (for details see Poli and Langdon (1998)).
broid_size Number of offspring created by brood crossover (default: broid_size=4).
crossover_prob Probability to perform crossover \( \in [0, 1] \) (default: crossover_prob=0.50).
mutation_prob Probability to perform mutation \( \in [0, 1] \) (default: mutation_prob=0.50).
CV Cross validation steps as natural number bigger than 1 (default: CV=5).
vim Variable importance measure to be used to improve standard crossover. vim=0 for no variable importance measure (default), vim=1 for 'simple absolute frequency', vim=2 for 'simple relative frequency', vim=3 for 'relative frequency', vim=4 for 'linear weighted relative frequency', vim=5 for 'exponential weighted relative frequency', and vim=6 for 'permutation accuracy importance'.
ncutoffs Number of cutoffs per explanatory variable to be tested for optimality (default: ncutoffs=10).
opt Type of local cutoff optimization, "gini" for local cutoff optimization by Gini index (default), "mcr" for local cutoff optimization by misclassification rate.

Details

The non-hierarchical evolutionary multi-objective tree learner (NHEMOtree) with local cutoff optimization solves a two-objective optimization problem with regard to minimizing misclassification rate and minimizing total costs for classification (summarized costs for all used variables in the classifier). It is based on an EMOA with tree representation. It optimizes both objectives simultaneously without any hierarchy and generates Pareto-optimal classifiers being binary trees to solve the problem. Cutoffs of the tree learner are optimized analogous to a classification tree with recursive partitioning either based on the Gini index or the misclassification rate.

Termination criteria of NHEMO_Cutoff are the maximal amount of generations and the Online Convergence Detection (OCD) proposed by Wagner and Trautmann (2010). Here, OCD uses the dominated hypervolume as quality criterion. If its variance over the last g generations is significantly below a given threshold L according to the one-sided \( \chi^2 \)-variance test OCD stops the run. We followed the suggestion of Wagner and Trautmann (2010) and considered their parameter settings as default values.

Missing data in the grouping variable or the explanatory variables are excluded from the analysis automatically. NHEMO_Cutoff does not work with missing data in "CostMatrix". Costs of all explanatory variables set to 1 results in optimizing the amount of explanatory variables in the tree learner as second objective.

Author(s)

Swaantje Casjens

References


See Also

NHEMOtree

Examples

# Simulation of data and costs
d <- SimData(Obs=200)
CostMatrix<- Sim_Costs()

# NHEMO_Cutoff calculations with function NHEMOtree and type="NHEMO_Cutoff"
res<- NHEMOtree(method="NHEMO_Cutoff", formula=Y2~, data=d, CostMatrix=CostMatrix,
gen=5, popsize=5, max_nodes=5, ngens=5, bound=10^-10, init_prob=0.8, ps="tournament", tournament_size=4, crossover="standard", crossover_prob=0.1, mutation_prob=0.1, CV=5, vim=1, ncutoffs=5, opt="mcr")
res

plot.NHEMOtree

Plot Method for Class NHEMOtree

Description

Generates different plots for class NHEMOtree

Usage

## S3 method for class 'NHEMOtree'
plot(x, data, which = c("Pareto", "S_Metric", "VIMS", "Tree"), vim = 0, ...)

Arguments

x An object of class NHEMOtree.
data Data which was used in NHEMOtree.
which Type of plot, "Pareto" for the final Pareto front, "S_Metric" for increase of the dominated hypervolume by generation, "VIMS" for variable importance for each explanatory variable, "Tree" for the individual with the lowest misclassification rate.
Sim_Costs

vim  Variable improtance measure to be plottet for which="VIMS", vim=1 for 'simple absolute frequency', vim=2 for 'simple relative frequency', vim=3 for 'relative frequency', vim=4 for 'linear weighted relative frequency', vim=5 for 'exponential weighted relative frequency', vim=6 for 'permutation accuracy importance' (default: plots for all VIMs).

... Arguments passed to or from other methods.

Author(s)
Swaantje Casjens

See Also

NHEMOtree

Examples

# Simulation of data and costs
d <- Sim_Data(Obs=200)
CostMatrix<- Sim_Costs()

res<- NHEMOtree(type="NHEMO", formula=Y2-. , data=d, CostMatrix=CostMatrix, gens=5, popsize=5, crossover_prob=0.1, mutation_prob=0.1)
plot(data=d, x=res, which="P")
plot(data=d, x=res, which="S", col=3, type="l")
plot(data=d, x=res, which="V", vim=5)
plot(data=d, x=res, which="T")

Sim_Costs  Simulation of a cost matrix for use in NHEMOtree

Description

Simulation of a cost matrix for 10 variables in combination with 'Sim_Data' and to be analyszed with "NHEMOtree".

Usage

Sim_Costs()

Author(s)
Swaantje Casjens

See Also

Sim_Data, NHEMOtree
Examples

Sim_Costs()

---

**Description**

Simulation of data with one grouping variable containing four classes and 20 explanatory variables. Variables X1 to X3 are informative for separating the four classes. Variable X1 separates class 1, X2 separates class 1 and class 2, and X3 separates class 3 from class 4. Variables X4, X5, and X6 are created on basis of X3 and can also be used to separate class 3 from class 4 but with decreased prediction accuracy.

**Usage**

Sim_Data(Obs, VG=1, VP1=0.05, VP2=0.1, VP3=0.3)

**Arguments**

- **Obs**: Amount of observations.
- **VG**: Overall accuracy for data separation $\in [0, 1]$ with VG=1 (default) for perfect separation.
- **VP1**: Decrease of prediction accuracy for variable X4 in comparison with X3 to separate class 3 from class 4 (default: VP1=0.05).
- **VP2**: Decrease of prediction accuracy for variable X5 in comparison with X3 to separate class 3 from class 4 (default: VP2=0.1).
- **VP3**: Decrease of prediction accuracy for variable X6 in comparison with X3 to separate class 3 from class 4 (default: VP3=0.3).

**Details**

With this function data with one grouping variable containing four classes and 20 explanatory variables X1 to X10 is simulated.

Variable X1 separates class 1, X2 separates class 1 and class 2, and X3 separates class 3 from class 4. For all samples belonging to the according classes the explanatory variables X1 to X3 are drawn from a normal distribution with $\mu = 80$ and $\sigma^2 = 25$. Samples which are not allocated to the corresponding class are drawn from a uniform distribution with minimum 0 and an adjustable maximum value. The maximum values of the uniform distributions are the smallest drawn random values of each variable.

Variables X4, X5, and X6 are created on basis of X3 and separate class 3 from class 4, too. However, the prediction accuracy of these variables decreases gradually. The decrease is assigned by ‘VP1’, ‘VP2’, and ‘VP3’. Thus, the according amount of the discriminating samples of former class 3 are disturbed by assigning a value drawn from a uniform distribution. Accordingly, X4, X5 and X6
discriminate class 3 worse than X3. X7 to X10 are noisy variables drawn from a normal distribution that contain no information.

Noise is added to the class assignment by a binomial distribution. Each potential class is only with probability "VG" the equivalent class and with probability 1-"VG" one of the other classes.

Variable costs correlate with their prediction accuracy so that variables containing more information are more expensive than variables with less or none information. The costs of the variables are generated with function "Sim_Costs".

Author(s)

Swaantje Casjens

See Also

Sim_Costs, NHEMOtree

Examples

d <- Sim_Data(Obs=200)
head(d)

==

Description

This wrapper approach is based on the Nondominated Sorting Genetic Algorithm II (NSGA-II) with an enclosed classification tree algorithm. It performs cost-sensitive classification by solving the two-objective optimization problem of minimizing misclassification rate and minimizing total costs for classification.

Usage

Wrapper(data, CostMatrix,
gens = 50, popsize = 50,
gens = 14, bound = 10^-10,
init_prob = 0.8,
crossover_prob = 0.5, mutation_prob = 0.5,
CV = 5, ...)

Arguments

data A data frame containing in the first column the class for each observation and in the other columns from which variables specified in formula are preferentially to be taken.

CostMatrix A data frame containing the names (first column) and the costs (second column) for each explanatory variable in formula or x. NHEMOtree does not work with missing data in CostMatrix.
Wrapper

- **gens**: Maximal number of generations of the EMOA (default: gens=50).
- **popsize**: Population size in each generation of the EMOA (default: popsize=50).
- **ngens**: Preceeding generations for the Online Convergence Detection (OCD, default: ngens=14) (see below for details).
- **bound**: Variance limit for the Online convergence detection (default: bound=10^10).
- **init_prob**: Degree of initialization \( \in [0, 1] \), i.e. the amount of activated explanatory variables in the individuals of the initial population (default: init_prob=0.80).
- **crossover_prob**: Probability to perform crossover \( \in [0, 1] \) (default: crossover_prob=0.50).
- **mutation_prob**: Probability to perform mutation \( \in [0, 1] \) (default: mutation_prob=0.50).
- **CV**: Cross validation steps as natural number bigger than 1 (default: CV=5).
- **...**: Arguments passed to or from other methods.

**Details**

With Wrapper a wrapper approach based on the Nondominated Sorting Genetic Algorithm II (NSGA-II) with an enclosed classification tree algorithm is used to solve the two-objective optimization problem of minimizing misclassification rate and minimizing total costs for classification (summarized costs for all used variables in the classifier). The classification trees are constructed with rpart. However, wrapper approaches suffer from a hierarchy in the objectives at which misclassification is minimized at first followed by optimizing costs. Parent selection is always performed by a binary tournament and there is only one-point crossover.

Alternatives are the proposed non-hierarchical evolutionary multi-objective tree learners which do not suffer from a hierarchy in the objectives (see NHEMO NHEMOtree and NHEMO_Cutoff NHEMOtree).

Termination criteria of the NSGA-II are the maximal amount of generations and the Online Convergence Detection (OCD) proposed by Wagner and Trautmann (2010). Here, OCD uses the dominated hypervolume as quality criterion. If its variance over the last g generations is significantly below a given threshold L according to the one-sided \( \chi^2 \)-variance test OCD stops the run. We followed the suggestion of Wagner and Trautmann (2010) and considered their parameter settings as default values.

Missing data in the grouping variable or the explanatory variables are excluded from the analysis automatically. Wrapper does not work with missing data in "CostMatrix". Costs of all explanatory variables set to 1 results in optimizing the amount of explanatory variables in the tree learner as second objective.

**Author(s)**

Swaantje Casjens

**References**


See Also

- NHEMOtree

Examples

```r
# Simulation of data and costs
d <- Sim_Data(Obs=200)
CostMatrix <- Sim_Costs()

# Wrapper calculations with function NHEMOtree and type="Wrapper"
res <- NHEMOtree(method="Wrapper", formula=Y2 ~ ., data=d, CostMatrix=CostMatrix,
gens=5, popsize=5,
init_prob=0.8,
ngen=14, bound=10^-10,
crossover_prob=0.1, mutation_prob=0.1,
CV=5)

res
```
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