Package ‘FSinR’

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Ant Colony Optimization (Advanced Binary Ant Colony Optimization)

Description

The Ant Colony Optimization (Advanced Binary Ant Colony Optimization) (Kashef and Nezamabadi-pour 2015) algorithm consists of generating in each iteration a random population of individuals (ants) according to the values of a pheromone matrix (which is updated each iteration according to the paths most followed by the ants) and a heuristic (which determines how good is each path to follow by the ants). The evaluation measure is calculated for each individual. The algorithm ends once the established number of iterations has been reached.

Usage

aco(data, class, featureSetEval, population = 10, iter = 10, a = 1, b = 1, p = 0.2, q = 1, t0 = 0.2, tmin = 0, tmax = 1, mode = 1, verbose = FALSE)

Arguments

data • A data frame with the features and the class of the examples. All features must contain numerical values and not character, boolean, or factor type values since heuristics work only with numerical values. Otherwise the algorithm will generate error.
class • The name of the dependent variable
featureSetEval • The measure for evaluate features
population • The number of ants population
iter • The number of iterations
a • Parameter to control the influence of the pheromone (If a=0, no pheromone information is used)
b • Parameter to control the influence of the heuristic (If b=0, the attractiveness of the movements is not taken into account)
p • Rate of pheromone evaporation
q • Constant to determine the amount of pheromone deposited by the best ant. This amount is determined by the Q/F equation (for minimization) where F is the cost of the solution (F/Q for maximization)
t0 • Initial pheromone level
tmin • Minimum pheromone value	
tmax • Maximum pheromone value
mode • Heuristic information measurement. 1 -> min redundancy (by default). 2- > max-relevance and min-redundancy. 3-> feature-feature. 4-> based on F-score
verbose • Print the partial results in each iteration
**binaryConsistency**

**Value**

A list is returned containing for each repetition of the algorithm:

- **bestFeatures** A vector with all features. Selected features are marked with 1, unselected features are marked with 0
- **bestFitness** Evaluation measure obtained with the feature selection
- **antsIter** List that contains as many elements as iterations has the algorithm. Each of the elements in the list are matrices that represent the population in that iteration. In this matrix the individuals and the evaluation measure of each one are shown
- **pheromoneIter** List that contains as many elements as iterations have the algorithm. Each of the elements in the list are matrices that represent the amount of pheromone between the paths of the different features (the reading of the matrix is from the columns to the rows, i.e. from top to bottom) in each iteration

**Author(s)**

Francisco Aragón Royón

**References**


**Examples**

```r
## Ant Colony Optimization for iris dataset (filter method)
aco(iris, 'Species', roughsetConsistency, population = 10, iter = 5, verbose = TRUE)
```

**Description**

Calculates the binary consistency, also known as "Sufficiency test" from FOCUS (Almuallim and Dietterich 1991)

**Usage**

```r
binaryConsistency(data, class, features)
```
Arguments

- **data**: A data frame with the features and the class of the examples. Feature columns are expected to be factors, as all features should be discrete.
- **class**: The name of the dependent variable.
- **features**: The names of the selected features.

Value

- The consistency value for the selected features.

Author(s)

Adan M. Rodriguez

References


Examples

```r
code

binaryConsistency(iris, 'Species', c('Sepal.Width', 'Sepal.Length'))

```

Description

The method searches the whole features subset in breadth first order (Kozen 1992).

Usage

```r
code

breadthFirstSearch(data, class, featureSetEval)

```

Arguments

- **data**: A data frame with the features and the class of the examples.
- **class**: The name of the dependent variable.
- **featureSetEval**: The measure for evaluate features.

Value

A list is returned containing:

- **bestFeatures**: A vector with all features. Selected features are marked with 1, unselected features are marked with 0.
- **bestFitness**: Evaluation measure obtained with the feature selection.
Author(s)

Adan M. Rodriguez
Francisco Aragón Royón

References


Examples

```r
## Breadth First Search for iris dataset (filter method)
breadthFirstSearch(iris, 'Species', binaryConsistency)
```

### chiSquared

**Chi squared measure**

**Description**

Calculates the Chi squared value (F.R.S. 1900), evaluating the selected features individually.

**Usage**

```r
chiSquared(data, class, features)
```

**Arguments**

- `data`: A data frame with the features and the class of the examples
- `class`: The name of the dependent variable
- `features`: The feature or features to evaluate individually

**Value**

- The chi squared value for each selected feature

**References**

F.R.S. KP (1900). “X. On the criterion that a given system of deviations from the probable in the case of a correlated system of variables is such that it can be reasonably supposed to have arisen from random sampling.” *The London, Edinburgh, and Dublin Philosophical Magazine and Journal of Science, 50*(302), 157-175. doi: 10.1080/14786440009463897, https://doi.org/10.1080/14786440009463897.

**Examples**

```r
chiSquared(iris,'Species','Sepal.Length')
```
cramer

<table>
<thead>
<tr>
<th>cramer</th>
<th>Cramer V measure</th>
</tr>
</thead>
</table>

**Description**
Calculates Cramer’s V value (Cramer 1946), evaluating features individually.

**Usage**
cramer(data, class, features)

**Arguments**
- `data` • A data frame with the features and the class of the examples
- `class` • The name of the dependent variable
- `features` • The feature or features to evaluate individually

**Value**
- Cramer’s V value for each selected feature

**References**

**Examples**
cramer(iris,'Species','Sepal.Length')

depthFirstSearch

<table>
<thead>
<tr>
<th>depthFirstSearch</th>
<th>Exhaustive Search. Deep First Search</th>
</tr>
</thead>
</table>

**Description**
The method searches the whole features subset in deep first order (Kozen 1992).

**Usage**
depthFirstSearch(data, class, featureSetEval)

**Arguments**
- `data` • A data frame with the features and the class of the examples
- `class` • The name of the dependent variable
- `featureSetEval` • The measure for evaluate features
**determinationCoefficient**

**Value**

A list is returned containing:

- **bestFeatures** A vector with all features. Selected features are marked with 1, unselected features are marked with 0
- **bestFitness** Evaluation measure obtained with the feature selection

**Author(s)**

Francisco Aragón Royón

**References**


**Examples**

```r
## Deep First Search for iris dataset (filter method)
depthFirstSearch(iris, 'Species', binaryConsistency)
```

```r
determinationCoefficient
  R Squared, to continuous features
```

**Description**

This measure calculates the determinantation coefficient (Dodge 2008) of continuous features

**Usage**

determinationCoefficient(data, class, features)

**Arguments**

- **data** A data frame with the features and the class of the examples
- **class** The name of the dependent variable
- **features** The names of the selected features

**Value**

- The R squared value for the selected features

**Author(s)**

Adan M. Rodriguez
**entropy**

**References**


**Examples**

```r
determinationCoefficient(iris,'Species',c('Sepal.Width', 'Sepal.Length'))
```

<table>
<thead>
<tr>
<th>entropy</th>
<th>Entropy</th>
</tr>
</thead>
</table>

**Description**

Calculates the entropy value, using the information theory.

**Usage**

```r
entropy(x)
```

**Arguments**

- `x` • Collection of values

**Value**

- Entropy value

**Author(s)**

Adan M. Rodriguez
Alfonso Jiménez-Vílchez

**Examples**

```r
entropy(iris$Sepal.Length)
```
**entropyJ**  
*EntropyJ*

**Description**
Calculates the entropyJ value, using the information theory.

**Usage**
```
entropyJ(x)
```

**Arguments**
- **x**  
  - Collection of values

**Value**
- EntropyJ value

**Author(s)**
- Adan M. Rodriguez
- Alfonso Jiménez-Vilchez

**Examples**
```
entropyJ(iris$Sepal.Length)
```

---

**fscore**  
*F-score measure*

**Description**
Evaluates a feature using the F-score approach defined in (Wang et al. 2018).

**Usage**
```
fscore(data, class, features)
```

**Arguments**
- **data**  
  - A data frame with the features and the class of the examples
- **class**  
  - The name of the dependent variable
- **features**  
  - The name of the selected feature (only 1 feature)
**Value**
- The value of the function for the selected feature

**References**

**Examples**
```r
fscore(ToothGrowth, 'supp', c('len'))
```

---

**ga**

---

**Genetic Algorithm**

**Description**
The `ga` method (Yang and Honavar 1998) starts with an initial population of solutions and at each step applies a series of operators to the individuals in order to obtain new and better population of individuals. These operators are selection, crossing and mutation methods. This method uses the GA package implementation (Scrucca 2013) (Scrucca 2017).

**Usage**
```r
ga(data, class, featureSetEval, popSize = 20, pcrossover = 0.8, pmutation = 0.1, maxiter = 100, run = 100, verbose = FALSE)
```

**Arguments**
- `data` • A data frame with the features and the class of the examples
- `class` • The name of the dependent variable
- `featureSetEval` • The measure for evaluate features
- `popSize` • The population size
- `pcrossover` • The probability of crossover between individuals
- `pmutation` • The probability of mutation between individuals
- `maxiter` • The number of iterations
- `run` • Number of consecutive iterations without fitness improvement to stop the algorithm
- `verbose` • Print the partial results in each iteration. This functionality is not available if the objective of the evaluation method is to minimize the target value (e.g. regression methods)
Value

A list is returned containing for each repetition of the algorithm:

- **bestFeatures**: A vector with all features. Selected features are marked with 1, unselected features are marked with 0
- **bestFitness**: Evaluation measure obtained with the feature selection
- **population**: Matrix with the population of the last iteration of the algorithm along with the evaluation measure of each individual

Author(s)

Francisco Aragón Royón

References


Examples

```r
## Genetic algorithm for iris dataset (filter method)
ga(iris, 'Species', roughsetConsistency, popSize = 10, maxiter=5, verbose=TRUE)
```

<table>
<thead>
<tr>
<th>gainRatio</th>
<th><em>The gain ratio measure</em></th>
</tr>
</thead>
</table>

Description

This measure calculates the gain ratio value (Quinlan 1986), using the information theory.

Usage

```r
gainRatio(data, class, features)
```

Arguments

- **data**: A data frame with the features and the class of the examples. Feature columns are expected to be factors, as all features should be discrete.
- **class**: The name of the dependent variable
- **features**: The names of the selected features
Value

- The gain ratio value for the selected features.

Author(s)

Adan M. Rodriguez

References


Examples

gainRatio(iris, 'Species', c('Sepal.Width', 'Sepal.Length'))

Description

get.data.frame.from.formula

Usage

get.data.frame.from.formula(formula, data)

Arguments

- formula
- data

Value

- data.frame
**giniIndex**  
*Gini index measure*

**Description**
This measure calculates the gini index (Ceriani and Verme 2012) of discrete features

**Usage**
giniIndex(data, class, features)

**Arguments**
- **data**  • A data frame with the features and the class of the examples
- **class**  • The name of the dependent variable
- **features**  • The names of the selected features

**Value**
- The Gini index value for the selected features

**Author(s)**
Adan M. Rodriguez

**References**

**Examples**
giniIndex(iris,'Species',c('Sepal.Width', 'Sepal.Length'))

---

**hc**  
*Hill-Climbing*

**Description**
The hc (Russell and Norvig 2009) method starts with a certain set of features and in each iteration it searches among its neighbors to advance towards a better solution. The method ends as soon as no better solutions are found.
Usage

hc(data, class, featureSetEval, start = NULL, nneigh = length(data) - 1, repeats = 1, verbose = FALSE)

Arguments

data • A data frame with the features and the class of the examples
class • The name of the dependent variable
featureSetEval • The measure for evaluate features
start • Binary vector with the set of initial features
nneigh • Number of neighbors to evaluate in each iteration of the algorithm
repeats • Number of repetitions of the algorithm
verbose • Print the partial results in each iteration

Value

A list is returned containing for each repetition of the algorithm:

- **bestFeatures** A vector with all features. Selected features are marked with 1, unselected features are marked with 0
- **bestFitness** Evaluation measure obtained with the feature selection
- **initialVector** The vector with which the algorithm started
- **initialFitness** The evaluation measure of the initial vector
- **trace** Matrix with the results of each iteration. It contains the number of the iteration, the best set of features selected by the algorithm up to that iteration (1: selected, 0: not selected) and the value of the evaluation measure obtained from that best set of features

Author(s)

Francisco Aragón Royón

References


Examples

```r
## Hill-Climbing method for iris dataset (filter method)
hc(iris, 'Species', roughsetConsistency)
```
IEConsistency

Description
Calculates the inconsistent examples consistency value (Dash and Liu 2003), using hash tables

Usage
IEConsistency(data, class, features)

Arguments
- data: A data frame with the features and the class of the examples. Feature columns are expected to be factors, as all features should be discrete.
- class: The name of the dependent variable
- features: The names of the selected features

Value
- The consistency value for the selected features

Author(s)
Adan M. Rodriguez

References

Examples
IEConsistency(iris,'Species',c('Sepal.Width', 'Sepal.Length'))
IEPConsistency

Inconsistent Examples Pairs consistency measure

Description

Calculates the inconsistent examples pairs consistency value, using hash tables (Arauzo-Azofra et al. 2007)

Usage

IEPConsistency(data, class, features)

Arguments

data • A data frame with the features and the class of the examples. Feature columns are expected to be factors, as all features should be discrete.

class • The name of the dependent variable

features • The names of the selected features

Value

• The consistency value for the selected features

Author(s)

Adan M. Rodriguez

References


Examples

IEPConsistency(iris,'Species',c('Sepal.Width', 'Sepal.Length'))
Description
Applies the discriminant function designed by Narendra and Fukunaga (Narendra and Fukunaga 1977) to evaluate a set of features.

Usage
Jd(data, class, features)

Arguments
- data: A data frame with the features and the class of the examples
- class: The name of the dependent variable
- features: The names of the selected features

Value
- The value of the function for the selected features

Author(s)
Alfonso Jiménez-Vilchez

References

Examples
Jd(ToothGrowth, 'supp', c('len', 'dose'))

Description
Linear Consistency-Constrained algorithm described in (Shin and Xu 2009).

Usage
LCC(data, class, featureSetEval, featureEval = symmetricalUncertain, threshold = 0.9)
Arguments

data • A data frame with the features and the class of the examples
class • The name of the dependent variable
featureSetEval • The measure for evaluate feature sets
featureEval • The measure for evaluate individual features
threshold • Threshold

Value

A list is returned containing:

bestFeatures A vector with all features. Selected features are marked with 1, unselected features are marked with 0
bestFitness Evaluation measure obtained with the feature selection

Author(s)

Alfonso Jiménez-Vílchez

References


Examples

## sfbs method for iris dataset (filter method)
LCC(iris, 'Species', IEConsistency)

Description

The lvw method (Liu and Setiono 1996) starts with a certain set of features and in each step a new set is randomly generated, if the new set is better it is saved as the best solution. The algorithm ends when there are no improvements in a certain number of iterations.

Usage

lvw(data, class, featureSetEval, start = sample(0:1, ncol(data) - 1, replace = TRUE), K = 50, verbose = FALSE)
**Arguments**

- **data**
  - A data frame with the features and the class of the examples
- **class**
  - The name of the dependent variable
- **featureSetEval**
  - The measure for evaluate features
- **start**
  - Binary vector with the set of initial features (1: selected and 0: unselected) for the algorithm
- **K**
  - The maximum number of iterations without improvement to finalize the algorithm
- **verbose**
  - Print the partial results in each iteration

**Value**

A list is returned containing:

- **bestFeatures** A vector with all features. Selected features are marked with 1, unselected features are marked with 0
- **bestFitness** Evaluation measure obtained with the feature selection
- **initialVector** The vector with which the algorithm started
- **initialFitness** The evaluation measure of the initial vector
- **trace** Matrix with the results of each iteration. It contains the number of the iteration, the value of K, the best set of features selected by the algorithm up to that iteration (1: selected, 0: not selected) and the value of the evaluation measure obtained from that best set of features

**Author(s)**

Francisco Aragón Royón

**References**


**Examples**

```r
## lvw method for iris dataset (filter method)
lvw(iris, 'Species', roughsetConsistency, K=15, verbose=TRUE)
```
MDLC

**MDLC evaluation measure**

**Description**

Applies the Minimum-Description-Length-Criterion (MDLC) (Sheinvald et al. 1990) to evaluate a set of features.

**Usage**

```r
MDLC(data, class, features)
```

**Arguments**

- **data**
  - A data frame with the features and the class of the examples
- **class**
  - The name of the dependent variable
- **features**
  - The names of the selected features

**Value**

- MDLC value for the selected features

**Author(s)**

Alfonso Jiménez-Vilchez

**References**


**Examples**

```r
```
mutualInformation

The mutual information measure

Description

This measure calculates the mutual information value, using the information theory (Qian and Shu 2015).

Usage

mutualInformation(data, class, features)

Arguments

data
  • A data frame with the features and the class of the examples. Feature columns are expected to be factors, as all features should be discrete.

class
  • The name of the dependent variable

features
  • The names of the selected features

Value

• The mutual information value for the selected features

Author(s)

Adan M. Rodriguez

References


Examples

mutualInformation(iris,'Species',c('Sepal.Width', 'Sepal.Length'))
**normalization**

*Normalize a data frame*

**Description**

Takes in any data frame and normalize the data of their features.

**Usage**

```r
normalization(data, class)
```

**Arguments**

- `data` • A data frame with the features and the class of the examples
- `class` • The dependent variable

**Value**

- The dataframe with the independent variables or features normalized

**Author(s)**

Adan M. Rodriguez

**Examples**

```r
normalization(iris, 'Species')
```

---

**normalize.min.max**

**Description**

`normalize.min.max`

**Usage**

```r
normalize.min.max(data)
```

**Arguments**

- `data` • data

**Value**

- normalized data
Description

The relief algorithm (Kira and Rendell 1992) finds weights of continuous and discrete attributes basing on a distance between instances. Adapted from Piotr Romanski’s Fselector package (Romanski and Kotthoff 2018).

Usage

relief(data, class, features, neighbours.count = 5, sample.size = 10)

Arguments

data • A data frame with the features and the class of the examples
class • The name of the dependent variable
features • The feature or features to evaluate individually
neighbours.count • number of neighbours to find for every sampled instance
sample.size • number of instances to sample

Details

relief classification and regression continuous and discrete data

Value

• a data.frame containing the worth of attributes in the first column and their names as row names

Author(s)

Alfonso Jiménez-Vílchez

References


Examples

relief(iris, 'Species', c('Sepal.Width', 'Sepal.Length'))
**RFSM**

**RFSM evaluation measure**

---

**Description**

Feature set measure based on relief. Described in (Arauzo-Azofra et al. 2004)

**Usage**

```
RFSM(data, class, features, m = 5, k = 4)
```

**Arguments**

- `data`: A data frame with the features and the class of the examples
- `class`: The name of the dependent variable
- `features`: The names of the selected features
- `m`: Number of iterations
- `k`: Number of neighbours

**Value**

- The value of the function for the selected features

**Author(s)**

Alfonso Jiménez-Vilchez

**References**


**Examples**

```
RFSM(iris, 'Species', c('Sepal.Width', 'Sepal.Length'))
```
roughsetConsistency  Rough Set consistency measure

Description

Calculates the rough sets consistency value (Pawlak 1982) (Pawlak 1991), using hash tables

Usage

roughsetConsistency(data, class, features)

Arguments

data  • A data frame with the features and the class of the examples. Feature
columns are expected to be factors, as all features should be discrete.
class  • The name of the dependent variable
features  • The names of the selected features

Value

• The consistency value for the selected features

Author(s)

Adan M. Rodriguez

References

science/article/pii/S0377042717302078.


Examples

roughsetConsistency(iris,'Species',c('Sepal.Width', 'Sepal.Length'))
Simulated Annealing

Description

The sa method (Kirkpatrick et al. 1983) starts with a certain set of features and in each iteration modifies an element of the previous feature vector and decreases the temperature. If the energy of the new feature vector is better than that of the old vector, it is accepted and moved towards it, otherwise it is moved towards the new vector according to an acceptance probability. The algorithm ends when the minimum temperature has been reached. Additionally, a number of internal iterations can be performed within each iteration of the algorithm. In this case, the same temperature value of the outer iteration is used for the inner iterations.

Usage

```r
sa(data, class, featureSetEval, start = sample(0:1, ncol(data) - 1, replace = TRUE), temperature = 1, temperature_min = 0.01, reduction = 0.6, innerIter = 1, verbose = FALSE)
```

Arguments

- **data**: A data frame with the features and the class of the examples
- **class**: The name of the dependent variable
- **featureSetEval**: The measure for evaluate features
- **start**: Binary vector with the set of initial features
- **temperature**: Temperature initial
- **temperature_min**: Temperature to stops in the outer loop
- **reduction**: Temperature reduction in the outer loop
- **innerIter**: Number of iterations of inner loop. By default no inner iterations are established
- **verbose**: Print the partial results in each iteration

Value

A list is returned containing for each repetition of the algorithm:
- **bestFeatures**: A vector with all features. Selected features are marked with 1, unselected features are marked with 0
- **bestFitness**: Evaluation measure obtained with the feature selection
- **initialVector**: The vector with which the algorithm started
- **initialEnergy**: The evaluation measure of the initial vector
tracOutter Matrix with the results of each iteration. Contains the number of the iteration, the value of the temperature, the subset of features of the iteration, its evaluation measure and whether there has been a movement from the previous iteration to obtain the subset of features in the current iteration.

traceInnner List containing as many lists as outer iterations have been performed. In each iteration of these lists the same values are shown as for traceOutter but referring to each internal iteration.

Author(s)
Francisco Aragón Royón

References

Examples
## Simulated Annealing for iris dataset (filter method)
sa(iris, 'Species', roughsetConsistency, temperature = 5, temperature_min=0.01, reduction=0.6, verbose=TRUE)

---

sbs Sequential Backward Selection

Description
The SBS method (Marill and Green 1963) starts with all the features and removes a single feature at each step with a view to improving the evaluation of the set.

Usage
sbs(data, class, featureSetEval, stopCriterion = -1, stop = FALSE)

Arguments
data • A data frame with the features and the class of the examples
class • The name of the dependent variable
featureSetEval • The measure for evaluate features
stopCriterion • Define a maximum number of iterations. Disabled if the value is -1 (default: -1 )
stop • If true, the function stops if next iteration does not improve current results (default: FALSE)
selectDifference

Value

A list is returned containing:

bestFeatures A vector with all features. Selected features are marked with 1, unselected features are marked with 0

bestFitness Evaluation measure obtained with the feature selection

Author(s)

Adan M. Rodriguez
Alfonso Jiménez-Vílchez
Francisco Aragón Royón

References


Examples

```r
## sbs method for iris dataset (filter method)
sbs(iris, "Species", giniIndex)
```

selectDifference Select difference

Description

Selects features (in descending order from the best evaluation measure to the lowest) until evaluation difference is over a threshold.

Usage

```
selectDifference(data, class, featureEval, d.threshold = 0.1)
```

Arguments

data • A data frame with the features and the class of the examples
class • The name of the dependent variable
featureEval • The measure used to evaluate features
d.threshold • Number between 0 and 1, to calculate the slope
Value

A list is returned containing:

- **bestFeatures**: A vector with all features. Selected features are marked with 1, unselected features are marked with 0
- **featuresSelected**: The names of the returned features sorted according to the result of the evaluation measure
- **valuePerFeature**: The evaluation measures of the returned features

Author(s)

Adan M. Rodriguez
Francisco Aragón Royón

Examples

```r
## Select Difference for iris dataset (filter method)
# Selects features in descending order as long as the difference between them is less than 0.1
selectDifference(iris, 'Species', chiSquared, 0.1)
```

---

**selectKBest**  
*Select K best*

Description

Takes the 'k' features with the greatest evaluations

Usage

```r
selectKBest(data, class, featureEval, k = 1)
```

Arguments

- **data**: A data frame with the features and the class of the examples
- **class**: The name of the dependent variable
- **featureEval**: The measure used to evaluate features
- **k**: Number (positive integer) of returned features

Value

A list is returned containing:

- **bestFeatures**: A vector with all features. Selected features are marked with 1, unselected features are marked with 0
- **featuresSelected**: The names of the k returned features sorted according to the result of the evaluation measure
- **valuePerFeature**: The evaluation measures of the k returned features
selectPercentile

Author(s)
Adan M. Rodriguez
Francisco Aragón Royón

Examples

## Select K best for iris dataset (filter method)
selectKBSelectKBestKBest(iris, 'Species', roughsetConsistency, 2) # 2 best features

---

selectPercentile Select Percentile

Description
Selects a fraction, given as a percentage, of the total number of available features

Usage
selectPercentile(data, class, featureEval, percentile = 10)

Arguments
- **data**
  - A data frame with the features and the class of the examples
- **class**
  - The name of the dependent variable
- **featureEval**
  - The measure used to evaluate features
- **percentile**
  - Number (positive integer) between 0 and 100

  - **bestFeatures** A vector with all features. Selected features are marked with 1, unselected features are marked with 0
  - **featuresSelected** The names of the returned features sorted according to the result of the evaluation measure
  - **valuePerFeature** The evaluation measures of the returned features

Author(s)
Adan M. Rodriguez
Francisco Aragón Royón

Examples

## Select Percentile for iris dataset (filter method)
selectPercentile(iris, 'Species', giniIndex, 80) # 80% best features
Description

Selects features (in descending order from the best evaluation measure to the lowest) until the slope to the next feature is over a threshold. The slope is calculated as: (s.threshold) / (number of features)

Usage

selectSlope(data, class, featureEval, s.threshold = 0.8)

Arguments

data • A data frame with the features and the class of the examples
class • The name of the dependent variable
featureEval • The measure used to evaluate features
s.threshold • Number between 0 and 1

Value

A list is returned containing:

bestFeatures A vector with all features. Selected features are marked with 1, unselected features are marked with 0
featuresSelected The names of the returned features sorted according to the result of the evaluation measure
valuePerFeature The evaluation measures of the returned features

Author(s)

Adan M. Rodriguez

Examples

## Select Slope for iris dataset (filter method)
selectSlope(iris, 'Species', IEPConsistency, 0.8)
\textit{selectThreshold} \hspace{2cm} Select \: threshold

\textbf{Description}

Selects the features whose evaluation is over/under a user given threshold (It depends on the method that generates the evaluation measure. For example: under for regression methods, over for classification methods, etc.). Features that do not satisfy the threshold, will be removed.

\textbf{Usage}

\begin{verbatim}
selectThreshold(data, class, featureEval, threshold = 0.5)
\end{verbatim}

\textbf{Arguments}

\begin{itemize}
  \item \textbf{data} \hspace{1cm} A data frame with the features and the class of the examples
  \item \textbf{class} \hspace{1cm} The name of the dependent variable
  \item \textbf{featureEval} \hspace{1cm} The measure used to evaluate features
  \item \textbf{threshold} \hspace{1cm} Number between 0 and 1
\end{itemize}

\textbf{Value}

A list is returned containing:

\begin{itemize}
  \item \textbf{bestFeatures} \hspace{1cm} A vector with all features. Selected features are marked with 1, unselected features are marked with 0
  \item \textbf{featuresSelected} \hspace{1cm} The names of the returned features sorted according to the result of the evaluation measure
  \item \textbf{valuePerFeature} \hspace{1cm} The evaluation measures of the returned features
\end{itemize}

\textbf{Author(s)}

Adan M. Rodriguez
Francisco Aragón Royón

\textbf{Examples}

\begin{verbatim}
## Select Threshold for iris dataset (filter method)
# Features with a evaluation measure higher than 0.7
selectThreshold(iris, 'Species', mutualInformation, 0.7)
\end{verbatim}
selectThresholdRange  
*Select threshold range*

**Description**

Selects the features whose evaluation is over a threshold, where this threshold is given as: \(((\text{min} - \text{max}) \times \text{p.threshold}) + \text{max})\)

**Usage**

```
selectThresholdRange(data, class, featureEval, p.threshold = 0.3)
```

**Arguments**

- **data**: A data frame with the features and the class of the examples
- **class**: The name of the dependent variable
- **featureEval**: The measure used to evaluate features
- **p.threshold**: Number between 0 and 1

**Value**

A list is returned containing:

- **bestFeatures**: A vector with all features. Selected features are marked with 1, unselected features are marked with 0
- **featuresSelected**: The names of the returned features sorted according to the result of the evaluation measure
- **valuePerFeature**: The evaluation measures of the returned features

**Author(s)**

Adan M. Rodriguez

Francisco Aragón Royón

**Examples**

```r
## Select Threshold range for iris dataset (filter method)
selectThresholdRange(iris, 'Species', determinationCoefficient, 0.3)
```
Sequential Floating Backward Selection

Description

The sfbs method (Pudil et al. 1994) starts with all the features and removes a single feature at each step with a view to improving the evaluation of the set. In addition, it checks whether adding any of the removed features, improve the value of the set.

Usage

sfbs(data, class, featureSetEval)

Arguments

data • A data frame with the features and the class of the examples
class • The name of the dependent variable
featureSetEval • The measure for evaluate features

Value

A list is returned containing:

bestFeatures A vector with all features. Selected features are marked with 1, unselected features are marked with 0
bestFitness Evaluation measure obtained with the feature selection

Author(s)

Adan M. Rodriguez
Francisco Aragón Royón

References


Examples

```r
## sfbs method for iris dataset (filter method)
sfbs(iris, 'Species', determinationCoefficient)
```
Description

The sffs method (Pudil et al. 1994) starts with an empty set of features and add a single feature at each step with a view to improving the evaluation of the set. In addition, it checks whether removing any of the included features, improve the value of the set.

Usage

sffs(data, class, featureSetEval)

Arguments

data • A data frame with the features and the class of the examples
class • The name of the dependent variable
featureSetEval • The measure for evaluate features

Value

A list is returned containing:

bestFeatures A vector with all features. Selected features are marked with 1, unselected features are marked with 0

bestFitness Evaluation measure obtained with the feature selection

Author(s)

Adan M. Rodriguez
Francisco Aragón Royón

References


Examples

```r
## sffs method for mtcars dataset (filter method)
sffs(mtcars, 'mpg', mutualInformation)
```
Sequential Forward Selection

Description

The SFS method (Whitney 1971) starts with an empty set of features and add a single feature at each step with a view to improving the evaluation of the set.

Usage

```r
sfs(data, class, featureSetEval, stopCriterion = -1, stop = FALSE)
```

Arguments

- `data`: A data frame with the features and the class of the examples
- `class`: The name of the dependent variable
- `featureSetEval`: The measure for evaluate features
- `stopCriterion`: Define a maximum number of iterations. Disabled if the value is -1 (default: -1)
- `stop`: If true, the function stops if next iteration does not improve current results (default: FALSE)

Value

A list is returned containing:

- `bestFeatures`: A vector with all features. Selected features are marked with 1, unselected features are marked with 0
- `bestFitness`: Evaluation measure obtained with the feature selection

Author(s)

Adan M. Rodriguez
Alfonso Jiménez-Vilchez
Francisco Aragón Royón

References


Examples

```r
## sfs method for iris dataset (filter method)
sfs(iris, 'Species', roughsetConsistency)
```
symmetricalUncertain  Symmetrical uncertain measure

Description

This measure calculates the symmetrical uncertain value (Witten and Frank 2005), using the information theory.

Usage

symmetricalUncertain(data, class, features)

Arguments

data • A data frame with the features and the class of the examples. Feature columns are expected to be factors, as all features should be discrete.

class • The name of the dependent variable

features • The names of the selected features

Value

• The symmetrical uncertain value for the selected features

Author(s)

Adan M. Rodriguez

References


Examples

symmetricalUncertain(iris,'Species',c('Sepal.Width', 'Sepal.Length'))
Tabu Search

**Description**

The Tabu Search (Glover 1986) (Glover 1989) method starts with a certain set of features and in each iteration it searches among its neighbors to advance towards a better solution. The method has a memory (tabu list) that prevents returning to recently visited neighbors. The method ends when a certain number of iterations are performed, or when a certain number of iterations are performed without improvement, or when there are no possible neighbors. Once the method is finished, an intensification phase can be carried out that begins in the space of the best solutions found, or a diversification phase can be carried out in which solutions not previously visited are explored.

**Usage**

```r
ts(data, class, featureSetEval, start = NULL, numNeigh = (ncol(data) - 1), tamTabuList = 5, iter = 100, iterNoImprovement = NULL, intensification = NULL, iterIntensification = 50, interPercentaje = 75, tamIntermediateMemory = 5, diversification = NULL, iterDiversification = 50, forgetTabuList = TRUE, verbose = FALSE)
```

**Arguments**

- `data` • A data frame with the features and the class of the examples
- `class` • The name of the dependent variable
- `featureSetEval` • The measure for evaluate features
- `start` • Binary vector with the set of initial features
- `numNeigh` • The number of neighbor to consider in each iteration. By default: all possibilities. It is important to note that a high value of this parameter considerably increases the computation time.
- `tamTabuList` • The size of the tabu list. By default: 5
- `iter` • The number of iterations of the algorithm. By default: 100
- `iterNoImprovement` • Number of iterations without improvement to start/reset the intensification/diversification phase. By default, it is not taken into account (all iterations are performed)
- `intensification` • Number of times the intensification phase is applied. None by default
- `iterIntensification` • Number of iterations of the intensification phase
- `interPercentaje` • Percentage of the most significant features to be taken into account in the intensification phase
tamIntermediateMemory
• Number of best solutions saved in the intermediate memory
diversification
• Number of times the diversification phase is applied. None by default
iterDiversification
• Number of iterations of the diversification phase
forgetTabuList
• Forget tabu list for intensification/diversification phases. By default: TRUE
verbose
• Print the partial results in each iteration

Value
A list is returned containing for each repetition of the algorithm:

Author(s)
Francisco Aragón Royón

References
http://dx.doi.org/10.1016/0305-0548(86)90048-1.

ijoc.1.3.190, https://doi.org/10.1287/ijoc.1.3.190, https://doi.org/10.1287/ijoc.1.3.190.

bestFeatures A vector with all features. Selected features are marked with 1, unselected features
are marked with 0
bestFitness Evaluation measure obtained with the feature selection
basicStage List containing the best neighbour in each iteration along with its obtained evaluation
measure, and the content of the taboo list in each iteration
intensificationStage List containing for each repetition of the intensification phase the best neigh-
bour in each iteration along with its obtained evaluation measure, and the content of the taboo
list in each iteration.
diversificationStage List containing for each repetition of the diversification phase the best neigh-
bour in each iteration along with its obtained evaluation measure, and the content of the taboo
list in each iteration.

Examples
## Taboo-Search algorithm for iris dataset (filter method)
ts(iris, ’Species’, roughsetConsistency, iter = 5)
**Whale Optimization Algorithm (Binary Whale Optimization Algorithm)**

**Description**

Binary Whale Optimization Algorithm (Kumar and Kumar 2018) is an algorithm that simulates the social behavior of humpback whales. This algorithm employs a binary version of the bubble-net hunting strategy. The algorithm starts with an initial population of individuals, and in each iteration updates the individuals according to several possible actions: Encircling prey, Bubble-net attacking or Search for prey.

**Usage**

```r
woa(data, class, featureSetEval, population = 10, iter = 10,
    verbose = FALSE)
```

**Arguments**

- `data` • A data frame with the features and the class of the examples
- `class` • The name of the dependent variable
- `featureSetEval` • The measure for evaluate features
- `population` • The number of whales population
- `iter` • The number of iterations of the algorithm
- `verbose` • Print the partial results in each iteration

**Value**

A list is returned containing for each repetition of the algorithm:

- `bestFeatures` • A vector with all features. Selected features are marked with 1, unselected features are marked with 0
- `bestFitness` • Evaluation measure obtained with the feature selection
- `popIter` • List that contains as many elements as iterations has the algorithm. Each of the elements in the list are matrices that represent the population in that iteration. In this matrix the individuals and the evaluation measure of each one are shown

**Author(s)**

Francisco Aragón Royón

**References**

Examples

```r
## Whale Optimization Algorithm for iris dataset (filter method)
woa(iris, 'Species', roughsetConsistency, population = 10, iter = 5, verbose = TRUE)
```

---

**wrapperGenerator**

*Wrapper measure generator*

**Description**

Generates a wrapper function to be used as an evaluator (Kohavi and John 1997), given a learner algorithm and related customizable parameters (from Jed Wing et al. 2018). More specifically, the result of calling this function is another function that is used as an evaluator in the search methods, although you can also call it up to generate an evaluation measure individually.

**Usage**

`wrapperGenerator(learner, resamplingParams, fittingParams)`

**Arguments**

- `learner` • Learner to be used. The models available are the models available in caret: http://topepo.github.io/caret/available-models.html
- `resamplingParams` • Control parameters for evaluating the impact of model tuning parameters. The arguments are the same as those of the caret trainControl function
- `fittingParams` • Control parameters for choose the best model across the parameters. The arguments are the same as those of the caret train function (minus the parameters: x, y, form, data, method and trainControl).

**Details**

`generaWrapper`

**Value**

Returns a wrapper function that is used to generate an evaluation measure

**Author(s)**

Alfonso Jiménez-Vilchez
Francisco Aragón Royón
References


Examples

```r
# Values for the caret trainControl function
resamplingParams <- list(method = "repeatedcv", repeats = 3)
# Values for the caret train function
fittingParams <- list(preProc = c("center", "scale"), metric="Accuracy",
    tuneGrid = expand.grid(k = c(1:20)))
# Generation of the wrapper function
wrapper <- wrapperGenerator("knn", resamplingParams, fittingParams)
# The function call generates the evaluation measure
wrapper(iris, 'Species', c('Sepal.Length','Sepal.Width','Petal.Length'))
```
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