Package ‘PPforest’

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Description Implements projection pursuit forest algorithm for supervised classification.
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R topics documented:

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For each bootstrap sample grow a projection pursuit tree (PPtree object).

Usage

```r
baggtree(
  data,
  class,
  m = 500,
  PPmethod = "LDA",
  lambda = 0.1,
  size.p = 1,
  parallel = FALSE,
  cores = 2
)
```

Arguments

data Data frame with the complete data set.

class A character with the name of the class variable.

m is the number of bootstrap replicates, this corresponds with the number of trees to grow. To ensure that each observation is predicted a few times we have to select this number no too small. m = 500 is by default.
crab

PPmethod is the projection pursuit index to be optimized, options LDA or PDA, by default it is LDA.

lambda a parameter for PDA index

size.p proportion of random sample variables in each split.

parallel logical condition, if it is TRUE then parallelize the function

cores number of cores used in the parallelization

Value
data frame with trees_pp output for all the bootstraps samples.

Examples

#crab data set
crab.trees <- baggtree(data = crab, class = 'Type', 
m = 200, PPmethod = 'LDA', lambda = .1, size.p = 0.5, parallel = TRUE, cores = 2)
str(crab.trees, max.level = 1)

---

Australi an crabs

Description

Measurements on rock crabs of the genus Leptograpsus. The data set contains 200 observations from two species of crab (blue and orange), there are 50 specimens of each sex of each species, collected on site at Fremantle, Western Australia.

- Type is the class variable and has 4 classes with the combinations of specie and sex (BlueMale, BlueFemale, OrangeMale and OrangeFemale).
- FLthe size of the frontal lobe length, in mm
- RWrear width, in mm
- CLlength of midline of the carapace, in mm
- CWmaximum width of carapace, in mm
- BDdepth of the body; for females, measured after displacement of the abdomen, in mm

Usage
data(crab)

Format

A data frame with 200 rows and 6 variables

Source

**fishcatch**  
*Fish catch data set*

**Description**

There are 159 fishes of 7 species are caught and measured. Altogether there are 7 variables. All the fishes are caught from the same lake (Laengelmavesi) near Tampere in Finland.

- **Type** has 7 fish classes, with 35 cases of Bream, 11 cases of Parkki, 56 cases of Perch 17 cases of Pike, 20 cases of Roach, 14 cases of Smelt and 6 cases of Whitewish.
- **weight** Weight of the fish (in grams)
- **length1** Length from the nose to the beginning of the tail (in cm)
- **length2** Length from the nose to the notch of the tail (in cm)
- **length3** Length from the nose to the end of the tail (in cm)
- **height** Maximal height as % of Length3
- **width** Maximal width as % of Length3

**Usage**

```r
data(fishcatch)
```

**Format**

A data frame with 159 rows and 7 variables

**Source**


---

**glass**  
*Glass data set*

**Description**

Contains measurements 214 observations of 6 types of glass; defined in terms of their oxide content.

- **Type** has 6 types of glasses
- **X1** refractive index
- **X2** Sodium (unit measurement: weight percent in corresponding oxide).
- **X3** Magnesium
- **X4** Aluminum
- **X5** Silicon
- **X6** Potassium
- **X7** Calcium
- **X8** Barium
- **X9** Iron
**Usage**

```
data(glass)
```

**Format**

A data frame with 214 rows and 10 variables

---

**image**

**The image data set**

**Description**

contains 2310 observations of instances from 7 outdoor images

- Type has 7 types of outdoor images, brickface, cement, foliage, grass, path, sky, and window.
- X1 the column of the center pixel of the region
- X2 the row of the center pixel of the region.
- X3 the number of pixels in a region = 9.
- X4 the results of a line extraction algorithm that counts how many lines of length 5 (any orientation) with low contrast, less than or equal to 5, go through the region.
- X5 measure the contrast of horizontally adjacent pixels in the region. There are 6, the mean and standard deviation are given. This attribute is used as a vertical edge detector.
- X6 X5 sd
- X7 measures the contrast of vertically adjacent pixels. Used for horizontal line detection.
- X8 sd X7
- X9 the average over the region of $\frac{R + G + B}{3}$
- X10 the average over the region of the R value.
- X11 the average over the region of the B value.
- X12 the average over the region of the G value.
- X13 measure the excess red: $(2R - (G + B))$
- X14 measure the excess blue: $(2B - (G + R))$
- X15 measure the excess green: $(2G - (R + B))$
- X16 3-d nonlinear transformation of RGB. (Algorithm can be found in Foley and VanDam, Fundamentals of Interactive Computer Graphics)
- X17 mean of X16
- X18 hue mean

**Usage**

```
data(image)
```

**Format**

A data frame contains 2310 observations and 19 variables
leukemia  

Description  
This dataset comes from a study of gene expression in two types of acute leukemias, acute lymphoblastic leukemia (ALL) and acute myeloid leukemia (AML). Gene expression levels were measured using Affymetrix high density oligonucleotide arrays containing 6817 human genes. A data set containing 72 observations from 3 leukemia types classes.

- Type has 3 classes with 38 cases of B-cell ALL, 25 cases of AML and 9 cases of T-cell ALL.
- Gene1 to Gen 40 gene expression levels

Usage  
data(leukemia)

Format  
A data frame with 72 rows and 41 variables

Source  

lymphoma  

Description  
Gene expression in the three most prevalent adult lymphoid malignancies: B-cell chronic lymphocytic leukemia (B-CLL), follicular lymphoma (FL), and diffuse large B-cell lymphoma (DLBCL). Gene expression levels were measured using a specialized cDNA microarray, the Lymphochip, containing genes that are preferentially expressed in lymphoid cells or that are of known immunologic or oncologic importance. This data set contain 80 observations from 3 lymphoma types.

- Type Class variable has 3 classes with 29 cases of B-cell ALL (B-CLL), 42 cases of diffuse large B-cell lymphoma (DLBCL) and 9 cases of follicular lymphoma (FL).
- Gene1 to Gen 50gene expression

Usage  
data(lymphoma)
**NCI60**

**Format**

A data frame with 80 rows and 51 variables

**Source**


---

**NCI60 data set**

**Description**

cDNA microarrays were used to examine the variation in gene expression among the 60 cell lines. The cell lines are derived from tumors with different sites of origin. This data set contain 61 observations and 30 feature variables from 8 different tissue types.

- Type has 8 different tissue types, 9 cases of breast, 5 cases of central nervous system (CNS), 7 cases of colon, 8 cases of leukemia, 8 cases of melanoma, 9 cases of non-small-cell lung carcinoma (NSCLC), 6 cases of ovarian and 9 cases of renal.
- Gene1 to Gen 30 gene expression information

**Usage**

data(NCI60)

**Format**

A data frame with 61 rows and 31 variables

**Source**

node_data  

*Data structure with the projected and boundary by node and class.*

**Description**

Data structure with the projected and boundary by node and class.

**Usage**

node_data(ppf, tr, Rule = 1)

**Arguments**

- **ppf** is a PPforest object
- **tr** numerical value to identify a tree
- **Rule** split rule 1: mean of two group means, 2: weighted mean, 3: mean of max(left group) and min(right group), 4: weighted mean of max(left group) and min(right group)

**Value**

Data frame with projected data for each class and node id and the boundaries

**Examples**

# crab data set with all the observations used as training

```r
pprf.crab <- PPforest(data = crab, std = TRUE, class = 'Type',
                      size.tr = 1, m = 200, size.p = .5, PPmethod = 'LDA')
node_data(ppf = pprf.crab, tr = 1)
```

---

olive  

*The olive data set*

**Description**

contains 572 observations and 10 variables

- Region Three super-classes of Italy: North, South and the island of Sardinia
- area Nine collection areas: three from North, four from South and 2 from Sardinia
- palmitic fatty acids percent x 100
- palmitoleic fatty acids percent x 100
- stearic fatty acids percent x 100
• oleic fatty acids percent x 100
• linoleic fatty acids percent x 100
• linolenic fatty acids percent x 100
• arachidic fatty acids percent x 100
• eicosenoic fatty acids percent x 100

Usage
data(olive)

Format
A data frame contains 573 observations and 10 variables

parkinson  Parkinson data set

Description
A data set containing 195 observations from 2 parkinson types.
• Type Class variable has 2 classes, there are 48 cases of healthy people and 147 cases with Parkinson. The feature variables are biomedical voice measures.
• X1 Average vocal fundamental frequency
• X2 Maximum vocal fundamental frequency
• X3 Minimum vocal fundamental frequency
• X4 MDVP:Jitter(%) measures of variation in fundamental frequency
• X5 MDVP:Jitter(Abs) measures of variation in fundamental frequency
• X6 MDVP:RAP measures of variation in fundamental frequency
• X7 MDVP:PPQ measures of variation in fundamental frequency
• X8 Jitter:DDP measures of variation in fundamental frequency
• X9 MDVP:Shimmer measures of variation in amplitude
• X10 MDVP:Shimmer(dB) measures of variation in amplitude
• X11 Shimmer:APQ3 measures of variation in amplitude
• X12 Shimmer:APQ5 measures of variation in amplitude
• X13 MDVP:APQ measures of variation in amplitude
• X14 Shimmer:DDA measures of variation in amplitude
• X15 NHR measures of ratio of noise to tonal components in the voice
• X16 HNR measures of ratio of noise to tonal components in the voice
• X17 RPDE nonlinear dynamical complexity measures
• X18 D2 nonlinear dynamical complexity measures
• X19 DFA - Signal fractal scaling exponent
• X20 spread1 Nonlinear measures of fundamental frequency variation
• X21 spread2 Nonlinear measures of fundamental frequency variation
• X22 PPE Nonlinear measures of fundamental frequency variation
permute_importance

Usage

data(parkinson)

Format

A data frame with 195 rows and 23 variables

Source

url https://archive.ics.uci.edu/ml/datasets/Parkinsons

permute_importance Obtain the permuted importance variable measure

Description

Obtain the permuted importance variable measure

Usage

permute_importance(ppf)

Arguments

ppf is a PPforest object

Value

A data frame with permuted importance measures, imp is the permuted importance measure defined in Brieman paper, imp2 is the permuted importance measure defined in randomForest package, the standard deviation (sd.im and sd.imp2) for each measure is computed and the also the standardized mesure.

Examples

pprf.crab <- PPforest(data = crab, class = 'Type', std = TRUE, size.tr = 1, m = 100, size.p = .4, PPmethod = 'LDA', parallel = TRUE, core = 2) permute_importance(ppf = pprf.crab)
**PPclassify2**

*Predict class for the test set and calculate prediction error after finding the PPtree structure,.*

---

**Description**

Predict class for the test set and calculate prediction error after finding the PPtree structure,.

**Usage**

```r
PPclassify2(Tree.result, test.data = NULL, Rule = 1, true.class = NULL)
```

**Arguments**

- `Tree.result`: the result of PP.Tree
- `test.data`: the test dataset
- `Rule`: split rule 1: mean of two group means, 2: weighted mean, 3: mean of max(left group) and min(right group), 4: weighted mean of max(left group) and min(right group)
- `true.class`: true class of test dataset if available

**Value**

- `predict.class`: predicted class
- `predict.error`: prediction error

**References**


**Examples**

```r
# crab data set
Tree.crab <- PPtree_split('Type~.', data = crab, PPmethod = 'LDA', size.p = 0.5)
Tree.crab

PPclassify2(Tree.crab)
```
### Description

`PPforest` implements a random forest using projection pursuit trees algorithm (based on PPtreeViz package).

### Usage

```r
PPforest(data, class, std = TRUE, size.tr, m, PPmethod, size.p,
        lambda = .1, parallel = FALSE, cores = 2, rule = 1)
```

### Arguments

- **data**: Data frame with the complete data set.
- **class**: A character with the name of the class variable.
- **std**: if TRUE standardize the data set, needed to compute global importance measure.
- **size.tr**: is the size proportion of the training if we want to split the data in training and test.
- **m**: is the number of bootstrap replicates, this corresponds with the number of trees to grow. To ensure that each observation is predicted a few times we have to select this number no too small. `m = 500` is by default.
- **PPmethod**: is the projection pursuit index to optimize in each classification tree. The options are `LDA` and `PDA`, linear discriminant and penalized linear discriminant. By default it is `LDA`.
- **size.p**: proportion of variables randomly sampled in each split.
- **lambda**: penalty parameter in PDA index and is between 0 to 1. If `lambda = 0`, no penalty parameter is added and the PDA index is the same as LDA index. If `lambda = 1` all variables are treated as uncorrelated. The default value is `lambda = 0.1`.
- **parallel**: logical condition, if it is TRUE then parallelize the function
- **cores**: number of cores used in the parallelization
- **rule**: split rule 1: mean of two group means 2: weighted mean of two group means - weight with group size 3: weighted mean of two group means - weight with group sd 4: weighted mean of two group means - weight with group se 5: mean of two group medians 6: weighted mean of two group medians - weight with group size 7: weighted mean of two group median - weight with group IQR 8: weighted mean of two group median - weight with group IQR and size

### Value

An object of class `PPforest` with components.

- **prediction.training**: predicted values for training data set.
training.error error of the training data set.

prediction.test predicted values for the test data set if testap = TRUE (default).

error.test error of the test data set if testap = TRUE (default).

oob.error.forest out of bag error in the forest.

oob.error.tree out of bag error for each tree in the forest.

boot.samp information of bootstrap samples.

output.trees output from a `trees_pp` for each bootstrap sample.

proximity Proximity matrix, if two cases are classified in the same terminal node then the proximity matrix is increased by one in PPforest there are one terminal node per class.

votes a matrix with one row for each input data point and one column for each class, giving the fraction of (OOB) votes from the PPforest.

n.tree number of trees grown in PPforest.

n.var number of predictor variables selected to use for splitting at each node.

type classification.

confusion confusion matrix of the prediction (based on OOB data).

call the original call to PPforest.

train is the training data based on `size.tr` sample proportion

test is the test data based on 1-`size.tr` sample proportion

References


Examples

# crab example with all the observations used as training

pprf.crab <- PPforest(data = crab, class = 'Type', std = FALSE, size.tr = 1, m = 200, size.p = .5, PPmethod = 'LDA', parallel = TRUE, cores = 2, rule=1)

pprf.crab
ppf_avg_imp

Global importance measure for a PPforest object as the average IMP PPtree measure over all the trees in the forest

Description

Global importance measure for a PPforest object as the average IMP PPtree measure over all the trees in the forest

Usage

ppf_avg_imp(ppf, class)

Arguments

ppf is a PPforest object
class A character with the name of the class variable.

Value

Data frame with the global importance measure

Examples

#crab data set with all the observations used as training

pprf.crab <- PPforest(data = crab, std = TRUE, class = 'Type', size.tr = 1, m = 100, size.p = .5, PPmethod = 'LDA')
ppf_avg_imp(pprf.crab, 'Type')

ppf_global_imp

Global importance measure for a PPforest object

Description

Global importance measure for a PPforest object

Usage

ppf_global_imp(data, class, ppf)

Arguments

data Data frame with the complete data set.
class A character with the name of the class variable.
ppf is a PPforest object
Value

Data frame with the global importance measure

Examples

#crab data set with all the observations used as training

pprf.crab <- PPforest(data = crab, std = TRUE, class = 'Type',
  size.tr = 1, m = 200, size.p = .5, PPmethod = 'LDA', parallel = TRUE, cores = 2)

ppf_global_imp(data = crab, class = 'Type', pprf.crab)

PPtree_split

Projection pursuit classification tree with random variable selection
in each split

Description

Find tree structure using various projection pursuit indices of classification in each split.

Usage

PPtree_split(form, data, PPmethod='LDA',
  size.p=1, lambda = 0.1,...)

Arguments

form A character with the name of the class variable.

data Data frame with the complete data set.

PPmethod index to use for projection pursuit: 'LDA', 'PDA'

size.p proportion of variables randomly sampled in each split, default is 1, returns a

PPtree.

lambda penalty parameter in PDA index and is between 0 to 1. If lambda = 0, no penalty
parameter is added and the PDA index is the same as LDA index. If lambda = 1
all variables are treated as uncorrelated. The default value is lambda = 0.1.

... arguments to be passed to methods

Value

An object of class PPtreeclass with components

Tree.Struct Tree structure of projection pursuit classification tree

projbest.node 1-dim optimal projections of each split node

splitCutoff.node cutoff values of each split node

origclass original class

origdata original data
References


Examples

# crab data set

Tree.crab <- PPtree_split('Type~.', data = crab, PPmethod = 'LDA', size.p = 0.5)
Tree.crab

---

print.PPforest

Print PPforest object

Description

Print PPforest object

Usage

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

Arguments

x is a PPforest class object
...
... additional parameter

Value

printed results for PPforest object

---

ternary_str

Data structure with the projected and boundary by node and class.

Description

Data structure with the projected and boundary by node and class.

Usage

ternary_str(ppf, id, sp, dx, dy)
trees_pred

Obtain predicted class for new data from baggtree function or PPforest.

### Description

Obtain predicted class for new data from baggtree function or PPforest.

### Usage

```r
trees_pred(object, xnew, parallel = FALSE, cores = 2, rule = 1)
```
Arguments

- **object**: Projection pursuit classification forest structure from PPforest or baggtree
- **xnew**: data frame with explicative variables used to get new predicted values.
- **parallel**: logical condition, if it is TRUE then parallelize the function
- **cores**: number of cores used in the parallelization
- **rule**: split rule 1: mean of two group means 2: weighted mean of two group means - weight with group size 3: weighted mean of two group means - weight with group sd 4: weighted mean of two group means - weight with group se 5: mean of two group medians 6: weighted mean of two group medians - weight with group size 7: weighted mean of two group median - weight with group IQR 8: weighted mean of two group median - weight with group IQR and size

Value

- Predicted values from PPforest or baggtree

Examples

```r
## Not run:
crab.trees <- baggtree(data = crab, class = 'Type', m = 200, PPmethod = 'LDA', lambda = .1, size.p = 0.4 )
pr <- trees_pred( crab.trees, xnew = crab[, -1], parallel = FALSE, cores = 2)
pprf.crab <- PPforest(data = crab, class = 'Type', std = FALSE, size.tr = 2/3, m = 100, size.p = .4, PPmethod = 'LDA', parallel = TRUE )
trees_pred(pprf.crab, xnew = pprf.crab$test, parallel = TRUE)
## End(Not run)
```

Description

A data set containing 178 observations from 3 wine grown cultivares in Italy.

Usage

data(wine)

Format

A data frame with 178 rows and 14 variables
Details

- Type Class variable has 3 classes that are 3 different wine grown cultivares in Italy.
- X1 to X13 Check vbles
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