Package ‘sboost’

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Type Package

Title Machine Learning with AdaBoost on Decision Stumps

Version 0.1.1

Description Creates classifier for binary outcomes using Adaptive Boosting (AdaBoost) algorithm on decision stumps with a fast C++ implementation. For a description of AdaBoost, see Freund and Schapire (1997) <doi:10.1006/jcss.1997.1504>. This type of classifier is nonlinear, but easy to interpret and visualize. Feature vectors may be a combination of continuous (numeric) and categorical (string, factor) elements. Methods for classifier assessment, predictions, and cross-validation also included.

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URL https://github.com/jadonwagstaff/sboost

BugReports https://github.com/jadonwagstaff/sboost/issues

Encoding UTF-8

LazyData true

Depends R (>= 3.4.0)

LinkingTo Rcpp (>= 0.12.17)

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RoxygenNote 6.1.1

Suggests testthat

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assess .......................... sboost Assessment Function

Description
Assesses how well an sboost classifier classifies the data.

Usage
assess(object, features, outcomes, include_scores = FALSE)

Arguments
object sboost_classifier S3 object output from sboost.
features feature set data.frame.
outcomes outcomes corresponding to the features.
include_scores if true feature_scores are included in output.

Value
An sboost_assessment S3 object containing:

performance Last row of cumulative statistics (i.e. when all stumps are included in assessment).
cumulative_statistics stump - the index of the last decision stump added to the assessment.
true_positive - number of true positive predictions.
false_negative - number of false negative predictions.
true_negative - number of true negative predictions.
false_positive - number of false positive predictions.
prevalence - true positive / total.
accuracy - correct predictions / total.
sensitivity - correct predicted positive / true positive.
specificity - correct predicted negative / true negative.
ppv - correct predicted positive / predicted positive.
npv - correct predicted negative / predicted negative.
fl - harmonic mean of sensitivity and ppv.

feature_scores If include_scores is TRUE, for each feature in the classifier lists scores for each row in the feature set.

classifier sboost sboost_classifier object used for assessment.

outcomes Shows which outcome was considered as positive and which negative.
call Shows the parameters that were used for assessment.

See Also
sboost documentation.

Examples

# malware
malware_classifier <- sboost(malware[-1], malware[1], iterations = 5, positive = 1)
assess(malware_classifier, malware[-1], malware[1])

# mushrooms
mushroom_classifier <- sboost(mushrooms[-1], mushrooms[1], iterations = 5, positive = "p")
assess(mushroom_classifier, mushrooms[-1], mushrooms[1])

malware Malware System Calls

Description
System call data for apps identified as malware and not malware.

Usage
malware

Format
A data frame with 7597 rows and 361 variables: outcomes 1 if malware, 0 if not. X1... X360 system calls.

Details
Experimental data generated in this research paper:
Data used for kaggle competition: https://www.kaggle.com/c/ml-fall2016-android-malware

Source
https://zenodo.org/record/154737#.WtoA1IjwaUl
Mushroom Classification

Description

A classic machine learning data set describing hypothetical samples from the Agaricus and Lepiota family.

Usage

mushrooms

Format

A data frame with 7597 rows and 361 variables:

- **outcomes** p=poisonous, e=edible
- **cap_shape** bell=b, conical=c, convex=x, flat=f, knobbed=k, sunken=s
- **cap_surface** fibrous=f, grooves=g, scaly=y, smooth=s
- **cap_color** brown=n, buff=b, cinnamon=c, gray=g, green=r, pink=p, purple=u, red=e, white=w, yellow=y
- **bruises** bruises=t, no=f
- **odor** almond=a, anise=l, creosote=c, fishy=y, foul=f, musty=m, none=n, pungent=p, spicy=s
- **gill_attachment** attached=a, descending=d, free=f, notched=n
- **gill_spacing** close=c, crowded=w, distant=d
- **gill_size** broad=b, narrow=n
- **gill_color** black=k, brown=n, buff=b, chocolate=h, gray=g, green=r, orange=o, pink=p, purple=u, red=e, white=w, yellow=y
- **stalk_shape** enlarging=e, tapering=t
- **stalk_root** bulbous=b, club=c, cup=u, equal=e, rhizomorphs=z, rooted=r, missing=?
- **stalk_surface_above_ring** fibrous=f, scaly=y, silky=k, smooth=s
- **stalk_surface_below_ring** fibrous=f, scaly=y, silky=k, smooth=s
- **stalk_color_above_ring** brown=n, buff=b, cinnamon=c, gray=g, orange=o, pink=p, red=e, white=w, yellow=y
- **stalk_color_below_ring** brown=n, buff=b, cinnamon=c, gray=g, orange=o, pink=p, red=e, white=w, yellow=y
- **veil_type** partial=p, universal=u
- **veil_color** brown=n, orange=o, white=w, yellow=y
- **ring_number** none=n, one=o, two=t
- **ring_type** cobwebby=c, evanescent=e, flaring=f, large=l, none=n, pendant=p, sheathing=s, zone=z
- **spore_print_color** black=k, brown=n, buff=b, chocolate=h, green=r, orange=o, purple=u, white=w, yellow=y
- **population** abundant=a, clustered=c, numerous=n, scattered=s, several=v, solitary=y
- **habitat** grasses=g, leaves=l, meadows=m, paths=p, urban=u, waste=w, woods=d
predict.sboost_classifier

Details

Data gathered from:

Source

https://archive.ics.uci.edu/ml/datasets/mushroom

predict.sboost_classifier

Make predictions for a feature set based on an sboost classifier.

Description

Make predictions for a feature set based on an sboost classifier.

Usage

## S3 method for class 'sboost_classifier'
predict(object, features, scores = FALSE, ...)

Arguments

object      sboost_classifier S3 object output from sboost.
features    feature set data.frame.
scores      if true, raw scores generated; if false, predictions are generated.
...          further arguments passed to or from other methods.

Value

Predictions in the form of a vector, or scores in the form of a vector. The index of the vector aligns the predictions or scores with the rows of the features. Scores represent the sum of all votes for the positive outcome minus the sum of all votes for the negative outcome.

See Also

sboost documentation.
Examples

```r
# malware
malware_classifier <- sboost(malware[-1], malware[1], iterations = 5, positive = 1)
predict(malware_classifier, malware[-1], scores = TRUE)
predict(malware_classifier, malware[-1])

# mushrooms
mushroom_classifier <- sboost(mushrooms[-1], mushrooms[1], iterations = 5, positive = "p")
predict(mushroom_classifier, mushrooms[-1], scores = TRUE)
predict(mushroom_classifier, mushrooms[-1])
```

sboost  

### sboost Learning Algorithm

#### Description

A machine learning algorithm using AdaBoost on decision stumps.

#### Usage

```r
sboost(features, outcomes, iterations = 1, positive = NULL, verbose = FALSE)
```

#### Arguments

- `features`: feature set data.frame.
- `outcomes`: outcomes corresponding to the features.
- `iterations`: number of boosts.
- `positive`: the positive outcome to test for; if NULL, the first outcome in alphabetical (or numerical) order will be chosen.
- `verbose`: If true, progress bar will be displayed in console.

#### Details

Factors and characters are treated as categorical features. Missing values are supported.

See [https://jadonwagstaff.github.io/sboost.html](https://jadonwagstaff.github.io/sboost.html) for a description of the algorithm.

For original paper describing AdaBoost see:

Value

An `sboost_classifier` S3 object containing:

- **classifier**  *stump* - the index of the decision stump
- **feature** - name of the column that this stump splits on.
- **vote** - the weight that this stump has on the final classifier.
- **orientation** - shows how outcomes are split. If `feature` is numeric shows split orientation, if `feature` value is less than `split` then vote is cast in favor of left side outcome, otherwise the vote is cast for the right side outcome. If `feature` is categorical, vote is cast for the left side outcome if `feature` value is found in `left_categories`, otherwise vote is cast for right side outcome.
- **split** - if `feature` is numeric, the value where the decision stump splits the outcomes; otherwise, NA.
- **left_categories** - if `feature` is categorical, shows the `feature` values that sway the vote to the left side outcome on the `orientation` split; otherwise, NA.

- **outcomes**  Shows which outcome was considered as positive and which negative.
- **training**  *stumps* - how many decision stumps were trained.
- **features** - how many features the training set contained.
- **instances** - how many instances or rows the training set contained.
- **positive_prevalence** - what fraction of the training instances were positive.

- **call**  Shows the parameters that were used to build the classifier.

See Also

- `predict.sboost_classifier` - to get predictions from the classifier.
- `assess` - to evaluate the performance of the classifier.
- `validate` - to perform cross validation for the classifier training.

Examples

```r
# malware
malware_classifier <- sboost(malware[-1], malware[,1], iterations = 5, positive = 1)
malware_classifier
malware_classifier$classifier

# mushrooms
mushroom_classifier <- sboost(mushrooms[-1], mushrooms[,1], iterations = 5, positive = "p")
mushroom_classifier
mushroom_classifier$classifier
```
validate  

sboost Validation Function

Description

A k-fold cross validation algorithm for sboost.

Usage

validate(features, outcomes, iterations = 1, k_fold = 6, positive = NULL, verbose = FALSE)

Arguments

features  
outcomes  
iterations  
k_fold  
positive  
verbose

Arguments

features  
outcomes  
iterations  
k_fold  
positive  
verbose

Arguments

features  
outcomes  
iterations  
k_fold  
positive  
verbose

Arguments

features  
outcomes  
iterations  
k_fold  
positive  
verbose

Arguments

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Value

An sboost_validation S3 object containing:

performance  
training_summary_statistics  
testing_summary_statistics  
training_statistics  
testing_statistics  
classifier_list  
outcomes  
k_fold  
call

See Also

sboost documentation.
Examples

# malware
validate(malware[-1], malware[1], iterations = 5, k_fold = 3, positive = 1)

# mushrooms
validate(mushrooms[-1], mushrooms[1], iterations = 5, k_fold = 3, positive = "p")
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