Package ‘Sstack’

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Type Package

Title Bootstrap Stacking of Random Forest Models for Heterogeneous Data

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Description Generates and predicts a set of linearly stacked Random Forest models using bootstrap sampling. Individual datasets may be heterogeneous (not all samples have full sets of features). Contains support for parallelization but the user should register their cores before running. This is an extension of the method found in Matlock (2018) <doi:10.1186/s12859-018-2060-2>.

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LazyData true

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Depends R (>= 2.10)

Imports randomForest, foreach, dplyr, parallel, doParallel

NeedsCompilation no

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BSHorizontalStack

**Horizontal stacking Random Forest models.**

**Description**

Generate the weights for a horizontally stacked set of Random Forest (RF) models given a set of heterogeneous datasets. For horizontal stacking some subset of samples must be common among all datasets. Subfunction of BSstack but can be used stand-alone.

**Usage**

```r
BSHorizontalStack(T = 100, mtry = NA, nodesize = 5, iter = 100,
                   Xn = NULL, ECHO = TRUE, Cf = NULL, Y, X1, X2, ...)
```

**Arguments**

- `T`: Number of trees for the individual RF models. (int)
- `mtry`: Number of variables available for splitting at each tree node. If a scalar is given then all models use the given values. If a 1D array is given then each individual model uses the given value.
- `nodesize`: Minimum size of terminal nodes. If a scalar is given then all models use the given values. If a 1D array is given then each individual model uses the given value. By default all models use 5.
- `iter`: The number of time to bootstrap sample the data. (int)
- `Xn`: List containing each dataset to be stacked. If not supplied will be generated from X1, X2, ...
- `ECHO`: Bool, enable to provide output to the user in terms of overlapping samples and runtime for CV.
- `Cf`: Character vector listing set of samples common among all given datasets. If not found will generate on it’s own.
- `Y`: Nsample x 1 data table of responses for ALL samples. Must have matching rownames with each individual dataset.
- `X1`: Data table of first dataset to be stacked. Rownames should be contained within Y.
- `X2`: Data table of second dataset to be stacked. Rownames should be contained within Y.
- `...`: Further data tables, X3, X4, ..., Xl.

**Details**

Required Packages: dplyr, randomForest, foreach

**Value**

Weights and offsets for each individual RF model.
**BSstack**

*Bootstrap Stacking model builder.*

**Description**

Creates a bootstrapped linear stacked set of Random Forest (RF) models given a set of heterogeneous datasets.

**Usage**

```r
BSstack(T = 50, mtry = NULL, nodesize = 5, iter = 25, CV = NA,
Xn = NULL, ECHO = TRUE, Y, X1, X2, ...)
```

**Arguments**

- `T` Number of trees for the individual RF models. (int)
- `mtry` Number of variables available for splitting at each tree node. If a scalar is given then all models use the given values. If a 1D array is given then each individual model uses the given value. If NA then for each model it will be set to Nfeats/3
- `nodesize` Minimum size of terminal nodes. If a scalar is given then all models use the given values. If a 1D array is given then each individual model uses the given value. By default all models use 5.
- `iter` The number of time to bootstrap sample the data. (int)
- `CV` Cross validation (CV) to measure mean-absolute error and correlation coefficient, if NA (default) no CV is performed. Otherwise the value gives the number of folds for CV. If CV<2 then leave-one-out CV is performed. CV is performed utilizing the samples that have full record.
- `Xn` List containing each dataset to be stacked. If not supplied will be generated from X1, X2, ...
- `ECHO` Bool, enable to provide output to the user in terms of overlapping samples and runtime for CV.
- `Y` Nsample x 1 data table of responses for ALL samples. Must have matching rownames with each individual dataset.
- `X1` Data table of first dataset to be stacked. Rownames should be contained within Y.
- `X2` Data table of second dataset to be stacked. Rownames should be contained within Y.
- `...` Further data tables, X3, X4, ..., Xl.

**Details**

Required Packages: dplyr, randomForest, foreach
BSstack_predict

Value


Examples

library(Sstack)
library(doParallel)
data(StackData)

AUC=StackData[[1]]
GE=StackData[[2]]
RPPA=StackData[[3]]

X1 <- GE[1:400,1:75]
X2 <- GE[200:400,76:150]
Xt <- GE[401:487,]

set.seed(1)
cl <- makeCluster(2)
registerDoParallel(cl)

Hbs <- BSstack(T = 25, iter = 20, Y = AUC, X1 = X1, X2 = X2)

stopCluster(cl)

Yp <- BSstack_predict(Hbs[[1]],Xt)

maeH1 <- mean(abs(AUC[401:487,]-Yp[,1]))
maeH2 <- mean(abs(AUC[401:487,]-Yp[,2]))
maeHs <- mean(abs(AUC[401:487,]-Yp[,3]))

BSstack_predict

Predict using a set of Stacked Random Forest models.

Description

Gives predictions for a linear bootstrapped stacked Random Forest predictors. Gives the predictions of each individual model as well as the linearly combined predictions.

Usage

BSstack_predict(BSmodel, Xi)
**BSVerticalStack**

**Arguments**

- **BSmodel**: List containing the individual Random Forest models, their weights, and feature names. Generated using BSstack function.
- **Xi**: NxM datatable containing input features to be predicted. Must contain all features used in the individual RF models.

**Details**

Required Packages: randomForest

**Value**

NxL+1 matrix where L is the number of individual RF models. Predictions for the ith RF model is found in the ith column of this matrix while predictions for the stacked model is in the final column.

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**BSVerticalStack**

*Vertical stacking Random Forest models.*

**Description**

Generate the weights for a vertically stacked set of Random Forest (RF) models given a set of heterogeneous datasets. For vertical stacking at least one dataset must contain full record (all features). Subfunction of BSstack but can be used stand-alone.

**Usage**

BSVerticalStack(T = 50, mtry = NULL, nodesize = 5, iter = 25, ECHO = TRUE, Y, Xfull = NULL, Xn = NULL, X1, X2, ...)

**Arguments**

- **T**: Number of trees for the individual RF models. (int)
- **mtry**: Number of variables available for splitting at each tree node. If a scalar is given then all models use the given values. If a 1D array is given then each individual model uses the given value.
- **nodesize**: Minimum size of terminal nodes. If a scalar is given then all models use the given values. If a 1D array is given then each individual model uses the given value. By default all models use 5.
- **iter**: The number of time to bootstrap sample the data. (int)
- **ECHO**: Bool, enable to provide output to the user in terms of overlapping samples and runtime for CV.
- **Y**: Nsample x 1 data table of responses for ALL samples. Must have matching rownames with each individual dataset.
- **Xfull**: Data table containing samples with full record. Used for generating the weights. Will attempt to find if not given.
StackData

Xn List containing each dataset to be stacked. If not supplied will be generated from X1, X2, ...

X1 Data table of first dataset to be stacked. Rownames should be contained within Y.

X2 Data table of second dataset to be stacked. Rownames should be contained within Y.

... Further data tables, X3, X4, ..., Xl.

Details

Required Packages: dplyr, randomForest, foreach

Value

Weights and offsets for each individual RF model.

Sample Stack Data

StackData Description

A demo dataset containing Gene Expression (GE), Reverse Phase Protein Array (RPPA) and drug sensitivity measure (AUC) for cancer cell lines that have been tested for the drug 17-AAG. Used to demonstrate the benefits of stacking by building an integrated model that will more effectively predict the AUC values given both GE and RPPA data.

Usage

StackData

Format

A list of 3 variables containing Gene Expression (GE), Reverse Phase Protein Array (RPPA) and drug sensitivity measure (AUC):

GE Gene Expression (GE) data corresponding to cell lines tested by the drug 17-AAG taken from the Cancer Cell Line Encyclopedia. Relieff has been run to select the top 150 genes.

RPPA Reverse Phase Protein Array (RPPA) data corresponding to cell lines tested by the drug 17-AAG taken from the MD Anderson Cell Lines Project. Relieff has been run to select the top 150 proteins.

AUC Area under the Dose-Responsce Curve (AUC) corresponding to the drug 17-AAG applied to each cell line. Taken from the Cancer Cell Line Encyclopedia.

Source

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