Package ‘RaSEn’

October 16, 2021

Type Package

Title Random Subspace Ensemble Classification and Variable Screening

Version 3.0.0

Author Ye Tian [aut, cre] and Yang Feng [aut]

Maintainer Ye Tian <ye.t@columbia.edu>

Description We propose a general ensemble classification framework, RaSE algorithm, for the sparse classification problem. In RaSE algorithm, for each weak learner, some random subspaces are generated and the optimal one is chosen to train the model on the basis of some criterion. To be adapted to the problem, a novel criterion, ratio information criterion (RIC) is put up with based on Kullback-Leibler divergence. Besides minimizing RIC, multiple criteria can be applied, for instance, minimizing extended Bayesian information criterion (eBIC), minimizing training error, minimizing the validation error, minimizing the cross-validation error, minimizing leave-one-out error. There are various choices of base classifier, for instance, linear discriminant analysis, quadratic discriminant analysis, k-nearest neighbour, logistic regression, decision trees, random forest, support vector machines. RaSE algorithm can also be applied to do feature ranking, providing us the importance of each feature based on the selected percentage in multiple subspaces. RaSE framework can be extended to the general prediction framework, including both classification and regression. We can use the selected percentages of variables for variable screening. The latest version added the variable screening function for both regression and classification problems.

Imports MASS, caret, class, doParallel, e1071, foreach, nnet, randomForest, rpart, stats, ggplot2, gridExtra, formatR, FNN, ranger, KernelKnn, utils, ModelMetrics, glmnet

License GPL-2

Encoding UTF-8

LazyData TRUE

LazyDataCompression bzip2

RoxygenNote 7.1.2

Suggests knitr, rmarkdown

VignetteBuilder knitr

Depends R (>= 3.1.0)

NeedsCompilation no
Colon data set.

Description

Alon et al.'s Colon cancer dataset containing information on 62 samples for 2000 genes. The samples belong to tumor and normal colon tissues.

Usage

colon

Format

A list with the predictor matrix x and binary 0/1 response vector y.

Source

The link to this data set: http://genomics-pubs.princeton.edu/oncology/

References


**predict.RaSE**

Predict the outcome of new observations based on the estimated RaSE classifier (Tian, Y. and Feng, Y., 2021).

**Description**

Predict the outcome of new observations based on the estimated RaSE classifier (Tian, Y. and Feng, Y., 2021).

**Usage**

```r
## S3 method for class 'RaSE'
predict(object, newx, type = c("vote", "prob", "raw-vote", "raw-prob"), ...)
```

**Arguments**

- `object`: fitted 'RaSE' object using Rase.
- `newx`: a set of new observations. Each row of `newx` is a new observation.
- `type`: the type of prediction output. Can be 'vote', 'prob', 'raw-vote' or 'raw-prob'. Default = 'vote'.
  - vote: output the predicted class (by voting and cut-off) of new observations. Available for all base learner types.
  - prob: output the predicted probabilities (posterior probability of each observation to be class 1) of new observations. It is the average probability over all base learners. Available only when base learner is not equal to 'svm' and 'tree'.
  - raw-vote: output the predicted class of new observations for all base learners. It is an \( n \times B_1 \) matrix. \( n \) is the test sample size and \( B_1 \) is the number of base learners used in RaSE. Available for all base learner types.
  - raw-prob: output the predicted probabilities (posterior probability of each observation to be class 1) of new observations for all base learners. It is an \( n \times B_1 \) matrix. Available only when base learner is not equal to 'svm' and 'tree'.
- `...`: additional arguments.

**Value**

depends on the parameter `type`. See the list above.

**References**


**See Also**

Rase.
Examples

```r
## Not run:
set.seed(0, kind = "L\'Ecuyer-CMRG")
train.data <- RaModel("classification", 1, n = 100, p = 50)
test.data <- RaModel("classification", 1, n = 100, p = 50)
xtrain <- train.data$x
ytrain <- train.data$y
xtest <- test.data$x
ytest <- test.data$y

model.fit <- Rase(xtrain, ytrain, B1 = 100, B2 = 100, iteration = 0, base = "lda",
cores = 2, criterion = 'ric', ranking = TRUE)
ypred <- predict(model.fit, xtest)
mean(ypred != ytest)

## End(Not run)
```

predict.super_RaSE

Predict the outcome of new observations based on the estimated super RaSE classifier (Zhu, J. and Feng, Y., 2021).

Description

Predict the outcome of new observations based on the estimated super RaSE classifier (Zhu, J. and Feng, Y., 2021).

Usage

```r
## S3 method for class 'super_RaSE'
predict(object, newx, type = c("vote", "prob", "raw-vote", "raw-prob"), ...)
```

Arguments

- **object**
  - fitted 'super_RaSE' object using Rase.
- **newx**
  - a set of new observations. Each row of `newx` is a new observation.
- **type**
  - the type of prediction output. Can be 'vote', 'prob', 'raw-vote' or 'raw-prob'. Default = 'vote'.
    - vote: output the predicted class (by voting and cut-off) of new observations. Available for all base learner types.
    - prob: output the predicted probabilities (posterior probability of each observation to be class 1) of new observations. It is the average probability over all base learners.
    - raw-vote: output the predicted class of new observations for all base learners. It is a `n` by `B1` matrix. `n` is the test sample size and `B1` is the number of base learners used in RaSE. Available for all base learner types.
print.RaSE

- raw-prob: output the predicted probabilities (posterior probability of each observation to be class 1) of new observations for all base learners. It is a \( n \times B_1 \) matrix.

... additional arguments.

Value
depends on the parameter type. See the list above.

References

See Also
Rase.

Examples

## Not run:
set.seed(0, kind = "L\'Ecuyer-CMRG")
train.data <- RaModel("classification", 1, n = 100, p = 50)
test.data <- RaModel("classification", 1, n = 100, p = 50)
xtrain <- train.data$x
ytrain <- train.data$y
xtest <- test.data$x
ytest <- test.data$y

# fit a super RaSE classifier by sampling base learner from kNN, LDA and logistic regression in equal probability
fit <- Rase(xtrain = xtrain, ytrain = ytrain, B1 = 100, B2 = 100,
base = c("knn", "lda", "logistic"), super = list(type = "separate", base.update = T),
criterion = "cv", cv = 5, iteration = 1, cores = 2)
ypred <- predict(fit, xtest)
mean(ypred != ytest)
## End(Not run)

print.RaSE

Print a fitted RaSE object.

Description
Similar to the usual print methods, this function summarizes results. from a fitted 'RaSE' object.

Usage

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

x  fitted 'RaSE' model object.
... additional arguments.

Value

No value is returned.

See Also

Rase.

Examples

```r
set.seed(0, kind = "L'Ecuyer-CMRG")
train.data <- RaModel("classification", 1, n = 100, p = 50)
xtrain <- train.data$x
ytrain <- train.data$y

# test RaSE classifier with LDA base classifier
fit <- Rase(xtrain, ytrain, B1 = 50, B2 = 50, iteration = 0, cutoff = TRUE,
base = "lda", cores = 2, criterion = 'ric', ranking = TRUE)

# print the summarized results
print(fit)
```

---

**print.super_RaSE**  
*Print a fitted super_RaSE object.*

Description

Similar to the usual print methods, this function summarizes results from a fitted 'super_RaSE' object.

Usage

```r
## S3 method for class 'super_RaSE'
print(x, ...)
```

Arguments

x  fitted 'super_RaSE' model object.
... additional arguments.

Value

No value is returned.
RaModel

See Also

Rase.

Examples

```r
set.seed(0, kind = "L'Ecuyer-CMRG")
train.data <- RaModel("classification", 1, n = 100, p = 50)
xtrain <- train.data$x
ytrain <- train.data$y

# test RaSE classifier with LDA base classifier
fit <- Rase(xtrain, ytrain, B1 = 50, B2 = 50, iteration = 0, cutoff = TRUE,
            base = 'lda', cores = 2, criterion = 'ric', ranking = TRUE)

# print the summarized results
print(fit)
```

RaModel

Generate data \((x, y)\) from various models in two papers.

Description

RaModel generates data from 4 models described in Tian, Y. and Feng, Y., 2021(b) and 8 models described in Tian, Y. and Feng, Y., 2021(a).

Usage

RaModel(model.type, model.no, n, p, p0 = 1/2, sparse = TRUE)

Arguments

- **model.type**: indicator of the paper covering the model, which can be 'classification' (Tian, Y. and Feng, Y., 2021(b)) or 'screening' (Tian, Y. and Feng, Y., 2021(a)).
- **model.no**: model number. It can be 1-4 when model.type = 'classification' and 1-8 when model.type = 'screening', respectively.
- **n**: sample size
- **p**: data dimension
- **p0**: marginal probability of class 0. Default = 0.5. Only used when model.type = 'classification' and model.no = 1, 2, 3.
- **sparse**: a logistic object indicating model sparsity. Default = TRUE. Only used when model.type = 'classification' and model.no = 1, 4.

Value

- **x**: \(n \times p\) matrix. \(n\) observations and \(p\) features.
- **y**: \(n\) responses.
Note

When \texttt{model.type} = 'classification' and \texttt{sparse} = TRUE, models 1, 2, 4 require $p \geq 5$ and model 3 requires $p \geq 50$. When \texttt{model.type} = 'classification' and \texttt{sparse} = FALSE, models 1 and 4 require $p \geq 50$ and $p \geq 30$, respectively. When \texttt{model.type} = 'screening', models 1, 4, 5 and 7 require $p \geq 4$. Models 2 and 8 require $p \geq 5$. Model 3 requires $p \geq 22$. Model 5 requires $p \geq 2$.

References


See Also

\texttt{Rase, RaScreen}.

Examples

```r
train.data <- RaModel("classification", 1, n = 100, p = 50)
xtrain <- train.data$x
ytrain <- train.data$y

## Not run:
train.data <- RaModel("screening", 2, n = 100, p = 50)
xtrain <- train.data$x
ytrain <- train.data$y

## End(Not run)
```

---

**RaPlot**

Visualize the feature ranking results of a fitted RaSE object.

Description

This function plots the feature ranking results from a fitted 'RaSE' object via ggplot2. In the figure, x-axis represents the feature number and y-axis represents the selected percentage of each feature in B1 subspaces.

Usage

```r
RaPlot(
    object,
    main = NULL,
    xlab = "feature",
    ylab = "selected percentage",
    ...
)
```
RaRank

Rank the features by selected percentages provided by the output from RaScreen.

Description

Rank the features by selected percentages provided by the output from RaScreen.

Usage

RaRank(object, selected.num = "all positive", iteration = object$iteration)
Arguments

object  
output from RaScreen.

selected.num  
the number of selected variables. User can either choose from the following popular options or input an positive integer no larger than the dimension.

- 'all positive': the number of variables with positive selected percentage.
- 'D': floor(D), where D is the maximum of random subspace size.
- '1.5D': floor(1.5D).
- '2D': floor(2D).
- '3D': floor(3D).
- 'n/logn': floor(n/logn), where n is the sample size.
- '1.5n/logn': floor(1.5n/logn).
- '2n/logn': floor(2n/logn).
- '3n/logn': floor(3n/logn).
- 'n-1': the sample size n - 1.
- 'p': the dimension p.

iteration  
indicates results from which iteration to use. It should be an positive integer. Default = the maximal iteration round used by the output from RaScreen.

Value

Selected variables (indexes).

References


Examples

```r
## Not run:
set.seed(0, kind = "L\'Ecuyer-CMRG")
train.data <- RaModel("screening", 1, n = 100, p = 100)
xtrain <- train.data$x
ytrain <- train.data$y

# test RaSE screening with linear regression model and BIC
fit <- RaScreen(xtrain, ytrain, B1 = 100, B2 = 50, iteration = 0, model = 'lm', cores = 2, criterion = 'bic')

# Select floor(n/logn) variables
RaRank(fit, selected.num = "n/logn")
```

## End(Not run)
RaScreen

Variable screening via RaSE.

Description
RaSE is a general framework for variable screening. In RaSE screening, to select each of the B1 subspaces, B2 random subspaces are generated and the optimal one is chosen according to some criterion. Then the selected proportions (equivalently, percentages) of variables in the B1 subspaces are used as importance measure to rank these variables.

Usage
RaScreen(
  xtrain,
  ytrain,
  xval = NULL,
  yval = NULL,
  B1 = 200,
  B2 = NULL,
  D = NULL,
  dist = NULL,
  model = NULL,
  criterion = NULL,
  k = 5,
  cores = 1,
  seed = NULL,
  iteration = 0,
  cv = 5,
  scale = FALSE,
  C0 = 0.1,
  kl.k = NULL,
  classification = NULL,
  ...
)

Arguments
- xtrain: n * p observation matrix. n observations, p features.
- ytrain: n 0/1 observations.
- xval: observation matrix for validation. Default = NULL. Useful only when criterion = 'validation'.
- yval: 0/1 observation for validation. Default = NULL. Useful only when criterion = 'validation'.
- B1: the number of weak learners. Default = 200.
- B2: the number of subspace candidates generated for each weak learner. Default = NULL, which will set B2 = 20 * floor(p/D).
D the maximal subspace size when generating random subspaces. Default = NULL. It means that $D = \min(\sqrt{n_0}, \sqrt{n_1}, p)$ when model = 'qda', and $D = \min(\sqrt{n}, p)$ otherwise.

dist the distribution for features when generating random subspaces. Default = NULL, which represents the hierarchical uniform distribution. First generate an integer $d$ from 1, ..., $D$ uniformly, then uniformly generate a subset with cardinality $d$.

model the model to use. Default = 'lda' when classification = TRUE and 'lm' when classification = FALSE.

• lm: linear regression. Only available for regression.
• lda: linear discriminant analysis. lda in MASS package. Only available for classification.
• qda: quadratic discriminant analysis. qda in MASS package. Only available for classification.
• knn: k-nearest neighbor. knn, knn.cv in class package, knn3 in caret package and knnreg in caret package.
• logistic: logistic regression. glmnet in glmnet package. Only available for classification.
• tree: decision tree. rpart in rpart package. Only available for classification.
• svm: support vector machine. If kernel is not identified by user, it will use RBF kernel. svm in e1071 package.
• randomforest: random forest. randomForest in randomForest package and ranger in ranger package.
• kernelknn: k-nearest neighbor with different kernels. It relies on function KernelKnn in KernelKnn package. Arguments method and weights_function are required. Different choices of multiple arguments are available. See documentation of function KernelKnn for details.

criterion the criterion to choose the best subspace. Default = 'ric' when model = 'lda', 'qda'; default = 'bic' when model = 'lm' or 'logistic'; default = 'loo' when model = 'knn'; default = 'cv' and set cv = 5 when model = 'tree', 'svm', 'randomforest'.

• ric: minimizing ratio information criterion (RIC) with parametric estimation (Tian, Y. and Feng, Y., 2020). Available for binary classification and model = 'lda', 'qda', or 'logistic'.
• nric: minimizing ratio information criterion (RIC) with non-parametric estimation (Tian, Y. and Feng, Y., 2020; ). Available for binary classification and model = 'lda', 'qda', or 'logistic'.
• training: minimizing training error/MSE. Not available when model = 'knn'.
• loo: minimizing leave-one-out error/MSE. Only available when model = 'knn'.
• validation: minimizing validation error/MSE based on the validation data.
• cv: minimizing k-fold cross-validation error/MSE. k equals to the value of cv. Default = 5.
• aic: minimizing Akaike information criterion (Akaike, H., 1973). Available when base = 'lm' or 'logistic'.

$AIC = -2 \times \text{log-likelihood} + |S| \times 2.$
• bic: minimizing Bayesian information criterion (Schwarz, G., 1978). Available when `model` = 'lm' or 'logistic'.
  \[ \text{BIC} = -2 \times \text{log-likelihood} + |S| \times \log(n) \]

• ebic: minimizing extended Bayesian information criterion (Chen, J. and Chen, Z., 2008; 2012). gam value is needed. When gam = 0, it represents BIC. Available when `model` = 'lm' or 'logistic'.
  \[ \text{eBIC} = -2 \times \text{log-likelihood} + |S| \times \log(n) + 2 \times |S| \times \text{gam} \times \log(p) \]

\(k\) the number of nearest neighbors considered when `model` = 'knn' or 'kernel'. Only useful when `model` = 'knn' or 'kernel'. \(k\) is required to be a positive integer. Default = 5.

`cores` the number of cores used for parallel computing. Default = 1.

`seed` the random seed assigned at the start of the algorithm, which can be a real number or NULL. Default = NULL, in which case no random seed will be set.

`iteration` the number of iterations. Default = 0.

`cv` the number of cross-validations used. Default = 5. Only useful when `criterion` = 'cv'.

`scale` whether to normalize the data. Logistic, default = FALSE.

`C0` a positive constant used when `iteration` > 1. See Tian, Y. and Feng, Y., 2021 for details. Default = 0.1.

`kl.k` the number of nearest neighbors used to estimate RIC in a non-parametric way. Default = NULL, which means that \(k0 = \text{floor}(\sqrt{n0})\) and \(k1 = \text{floor}(\sqrt{n1})\). See Tian, Y. and Feng, Y., 2020 for details. Only available when `criterion` = 'nric'.

`classification` the indicator of the problem type, which can be TRUE, FALSE or NULL. Default = NULL, which will automatically set `classification` = TRUE if the number of unique response value \(\leq 10\). Otherwise, it will be set as FALSE.

... additional arguments.

**Value**

A list including the following items.

- `model` the model used in RaSE screening.
- `criterion` the criterion to choose the best subspace for each weak learner.
- `B1` the number of selected subspaces.
- `B2` the number of subspace candidates generated for each of B1 subspaces.
- `n` the sample size.
- `p` the dimension of data.
- `D` the maximal subspace size when generating random subspaces.
- `iteration` the number of iterations.
- `selected.perc` A list of length (iteration+1) recording the selected percentages of each feature in B1 subspaces. When it is of length 1, the result will be automatically transformed to a vector.
- `scale` a list of scaling parameters, including the scaling center and the scale parameter for each feature. Equals to NULL when the data is not scaled by RaScreen.
References


See Also

RaSE, RaRank.

Examples

```r
set.seed(0, kind = "L'Ecuyer-CMRG")
train.data <- RaModel("screening", 1, n = 100, p = 100)
xtrain <- train.data$x
ytrain <- train.data$y

# test RaSE screening with linear regression model and BIC
fit <- RaScreen(xtrain, ytrain, B1 = 100, B2 = 50, iteration = 0, model = "lm",
cores = 2, criterion = "bic")

# Select D variables
RaRank(fit, selected.num = "D")

## Not run:
# test RaSE screening with knn model and 5-fold cross-validation MSE
fit <- RaScreen(xtrain, ytrain, B1 = 100, B2 = 50, iteration = 0, model = "knn",
cores = 2, criterion = "cv", cv = 5)

# Select n/logn variables
RaRank(fit, selected.num = "n/logn")

# test RaSE screening with SVM and 5-fold cross-validation MSE
fit <- RaScreen(xtrain, ytrain, B1 = 100, B2 = 50, iteration = 0, model = "svm",
cores = 2, criterion = "cv", cv = 5)

# Select n/logn variables
RaRank(fit, selected.num = "n/logn")

# test RaSE screening with logistic regression model and eBIC (gam = 0.5). Set iteration number = 1
train.data <- RaModel("screening", 6, n = 100, p = 100)
xtrain <- train.data$x
```
Construct the random subspace ensemble classifier.

Description

RaSE is a general ensemble classification framework to solve the sparse classification problem. In RaSE algorithm, for each of the B1 weak learners, B2 random subspaces are generated and the optimal one is chosen to train the model on the basis of some criterion.

Usage

Rase(xtrain, ytrain, xval = NULL, yval = NULL, B1 = 200, B2 = 500, D = NULL, dist = NULL, base = NULL, super = list(type = c("separate"), base.update = TRUE), criterion = NULL, ranking = TRUE, k = c(3, 5, 7, 9, 11), cores = 1, seed = NULL, iteration = 0, cutoff = TRUE, cv = 5, scale = FALSE, C0 = 0.1, kl.k = NULL, lower.limits = NULL, upper.limits = NULL, weights = NULL, ... )
Arguments

xtrain  n * p observation matrix. n observations, p features.
ytrain  n 0/1 observations.
xval    observation matrix for validation. Default = NULL. Useful only when criterion = 'validation'.
yval    0/1 observation for validation. Default = NULL. Useful only when criterion = 'validation'.
B1      the number of weak learners. Default = 200.
B2      the number of subspace candidates generated for each weak learner. Default = 500.
D       the maximal subspace size when generating random subspaces. Default = NULL, which is \(\min(\sqrt{n_0}, \sqrt{n_1}, p)\) when base = 'qda' and is \(\min(\sqrt{n}, p)\) otherwise. For classical RaSE with a single classifier type, D is a positive integer. For super RaSE with multiple classifier types, D is a vector indicating different D values used for each base classifier type (the corresponding classifier types should be noted in the names of the vector).
dist    the distribution for features when generating random subspaces. Default = NULL, which represents the uniform distribution. First generate an integer \(d\) from 1, ..., \(D\) uniformly, then uniformly generate a subset with cardinality \(d\).
base    the type of base classifier. Default = 'lda'. Can be either a single string chosen from the following options or a string/probability vector. When it indicates a single type of base classifiers, the classical RaSE model (Tian, Y. and Feng, Y., 2021(b)) will be fitted. When it is a string vector which includes multiple base classifier types, a super RaSE model (Zhu, J. and Feng, Y., 2021) will be fitted, by sampling base classifiers with equal probability. It can also be a probability vector with row names corresponding to the specific classifier type, in which case a super RaSE model will be trained by sampling base classifiers in the given sampling probability.

- lda: linear discriminant analysis. \texttt{lda} in MASS package.
- qda: quadratic discriminant analysis. \texttt{qda} in MASS package.
- knn: k-nearest neighbor. \texttt{knn, knn.cv} in class package and \texttt{knn3} in caret package.
- logistic: logistic regression. \texttt{glm} in stats package and \texttt{glmnet} in glmnet package.
- tree: decision tree. \texttt{rpart} in \texttt{rpart} package.
- svm: support vector machine. \texttt{svm} in \texttt{e1071} package.
- randomforest: support vector machine. \texttt{randomForest} in \texttt{randomForest} package.
- gamma: Bayesian classifier for multivariate gamma distribution with independent marginals.

super  a list of control parameters for super RaSE (Zhu, J. and Feng, Y., 2021). Not used when base equals to a single string. Should be a list object with the following components:

- type: the type of super RaSE. Currently the only option is 'separate', meaning that subspace distributions are different for each type of base classifiers.
• base.update: indicates whether the sampling probability of base classifiers should be updated during iterations or not. Logistic, default = TRUE.

**criterion**
the criterion to choose the best subspace for each weak learner. For the classical RaSE (when base includes a single classifier type), default = 'ric' when base = 'lda', 'qda', 'gamma'; default = 'ebic' and set gam = 0 when base = 'logistic'; default = 'loo' when base = 'knn'; default = 'training' when base = 'tree', 'svm', 'randomforest'. For the super RaSE (when base indicates multiple classifiers or the sampling probability of multiple classifiers), default = 'cv' with the number of folds cv = 5, and it can only be 'cv', 'training' or 'auc'.

• ric: minimizing ratio information criterion with parametric estimation (Tian, Y. and Feng, Y., 2021(b)). Available when base = 'lda', 'qda', 'gamma' or 'logistic'.
• nric: minimizing ratio information criterion with non-parametric estimation (Tian, Y. and Feng, Y., 2021(b)). Available when base = 'lda', 'qda', 'gamma' or 'logistic'.
• training: minimizing training error. Not available when base = 'knn'.
• loo: minimizing leave-one-out error. Only available when base = 'knn'.
• validation: minimizing validation error based on the validation data. Available for all base classifiers.
• auc: minimizing negative area under the ROC curve (AUC). Currently it is estimated on training data via function auc from package ModelMetrics. It is available for all classifier choices.
• cv: minimizing k-fold cross-validation error. k equals to the value of cv. Default = 5. Not available when base = 'gamma'.
• aic: minimizing Akaike information criterion (Akaike, H., 1973). Available when base = 'lda' or 'logistic'.
  \[ AIC = -2 \times \text{log-likelihood} + |S| \times 2. \]
• bic: minimizing Bayesian information criterion (Schwarz, G., 1978). Available when base = 'lda' or 'logistic'.
  \[ BIC = -2 \times \text{log-likelihood} + |S| \times \log(n). \]
• ebic: minimizing extended Bayesian information criterion (Chen, J. and Chen, Z., 2008; 2012). Need to assign value for gam. When gam = 0, it denotes the classical BIC. Available when base = 'lda' or 'logistic'.
  \[ EBIC = -2 \times \text{log-likelihood} + |S| \times \log(n) + 2 \times |S| \times \text{gam} \times \log(p). \]

**ranking**
whether the function outputs the selected percentage of each feature in B1 subspaces. Logistic, default = TRUE.

**k**
the number of nearest neighbors considered when base = 'knn'. Only useful when base = 'knn'. Default = (3, 5, 7, 9, 11).

**cores**
the number of cores used for parallel computing. Default = 1.

**seed**
the random seed assigned at the start of the algorithm, which can be a real number or NULL. Default = NULL, in which case no random seed will be set.

**iteration**
the number of iterations. Default = 0.

**cutoff**
whether to use the empirically optimal threshold. Logistic, default = TRUE. If it is FALSE, the threshold will be set as 0.5.
cv       the number of cross-validations used. Default = 5. Only useful when criterion = 'cv'.
scale    whether to normalize the data. Logistic, default = FALSE.
C0       a positive constant used when iteration > 1. Default = 0.1. See Tian, Y. and Feng, Y., 2021(b) for details.
k1,k     the number of nearest neighbors used to estimate RIC in a non-parametric way. Default = NULL, which means that \( k0 = \lfloor \sqrt{n0} \rfloor \) and \( k1 = \lfloor \sqrt{n1} \rfloor \). See Tian, Y. and Feng, Y., 2021(b) for details. Only available when criterion = 'nric'.
lower.limits the vector of lower limits for each coefficient in logistic regression. Should be a vector of length equal to the number of variables (the column number of \( xtrain \)). Each of these must be non-positive. Default = NULL, meaning that lower limits are -Inf for all coefficients. Only available when base = 'logistic'. When it’s activated, function \( glmnet \) will be used to fit logistic regression models, in which case the minimum subspace size is required to be larger than 1. The default subspace size distribution will be changed to uniform distribution on \((2, ..., D)\).
upper.limits the vector of upper limits for each coefficient in logistic regression. Should be a vector of length equal to the number of variables (the column number of \( xtrain \)). Each of these must be non-negative. Default = NULL, meaning that upper limits are Inf for all coefficients. Only available when base = 'logistic'. When it’s activated, function \( glmnet \) will be used to fit logistic regression models, in which case the minimum subspace size is required to be larger than 1. The default subspace size distribution will be changed to uniform distribution on \((2, ..., D)\).
weights  observation weights. Should be a vector of length equal to training sample size (the length of \( ytrain \)). It will be normalized inside the algorithm. Each component of weights must be non-negative. Default is NULL, representing equal weight for each observation. Only available when base = 'logistic'. When it’s activated, function \( glmnet \) will be used to fit logistic regression models, in which case the minimum subspace size is required to be larger than 1. The default subspace size distribution will be changed to uniform distribution on \((2, ..., D)\).

Value

An object with S3 class 'RASE' if base indicates a single base classifier.

marginal the marginal probability for each class.
base    the type of base classifier.
criterion the criterion to choose the best subspace for each weak learner.
B1      the number of weak learners.
B2      the number of subspace candidates generated for each weak learner.
D       the maximal subspace size when generating random subspaces.
iteration: the number of iterations.
fit.list: sequence of B1 fitted base classifiers.
cutoff: the empirically optimal threshold.
subspace: sequence of subspaces corresponding to B1 weak learners.
ranking: the selected percentage of each feature in B1 subspaces.
scale: a list of scaling parameters, including the scaling center and the scale parameter for each feature. Equals to NULL when the data is not scaled in RaSE model fitting.

An object with S3 class `super_RaSE` if base includes multiple base classifiers or the sampling probability of multiple classifiers.

marginal: the marginal probability for each class.
base: the list of B1 base classifier types.
criterion: the criterion to choose the best subspace for each weak learner.
B1: the number of weak learners.
B2: the number of subspace candidates generated for each weak learner.
D: the maximal subspace size when generating random subspaces.
iteration: the number of iterations.
fit.list: sequence of B1 fitted base classifiers.
cutoff: the empirically optimal threshold.
subspace: sequence of subspaces corresponding to B1 weak learners.
ranking.feature: the selected percentage of each feature corresponding to each type of classifier.
ranking.base: the selected percentage of each classifier type in the selected B1 learners.
scale: a list of scaling parameters, including the scaling center and the scale parameter for each feature. Equals to NULL when the data is not scaled in RaSE model fitting.

Author(s)
Ye Tian (maintainer, <ye.t@columbia.edu>) and Yang Feng. The authors thank Yu Cao (Exeter Finance) and his team for many helpful suggestions and discussions.

References


See Also

predict.RaSE,RaModel,print.RaSE,print.super_RaSE,RaPlot,RaScreen.

Examples

set.seed(0, kind = "L'Ecuyer-CMRG")
train.data <- RaModel("classification", 1, n = 100, p = 50)
test.data <- RaModel("classification", 1, n = 100, p = 50)
xtrain <- train.data$x
ytrain <- train.data$y
xtest <- test.data$x
ytest <- test.data$y

# test RaSE classifier with LDA base classifier
fit <- Rase(xtrain, ytrain, B1 = 100, B2 = 50, iteration = 0, base = 'lda',
            cores = 2, criterion = 'ric')
mean(predict(fit, xtest) != ytest)

## Not run:
# test RaSE classifier with LDA base classifier and 1 iteration round
fit <- Rase(xtrain, ytrain, B1 = 100, B2 = 50, iteration = 1, base = 'lda',
            cores = 2, criterion = 'ric')
mean(predict(fit, xtest) != ytest)

# test RaSE classifier with QDA base classifier and 1 iteration round
fit <- Rase(xtrain, ytrain, B1 = 100, B2 = 50, iteration = 1, base = 'qda',
            cores = 2, criterion = 'ric')
mean(predict(fit, xtest) != ytest)

# test RaSE classifier with kNN base classifier
fit <- Rase(xtrain, ytrain, B1 = 100, B2 = 50, iteration = 0, base = 'knn',
            cores = 2, criterion = 'loo')
mean(predict(fit, xtest) != ytest)

# test RaSE classifier with logistic regression base classifier
fit <- Rase(xtrain, ytrain, B1 = 100, B2 = 50, iteration = 0, base = 'logistic',
            cores = 2, criterion = 'bic')
mean(predict(fit, xtest) != ytest)

# test RaSE classifier with SVM base classifier
fit <- Rase(xtrain, ytrain, B1 = 100, B2 = 50, iteration = 0, base = 'svm',
            cores = 2, criterion = 'training')
mean(predict(fit, xtest) != ytest)

# test RaSE classifier with random forest base classifier
rat <- Rase(xtrain, ytrain, B1 = 20, B2 = 10, iteration = 0, base = 'randomforest', cores = 2, criterion = 'cv', cv = 3)
mean(predict(fit, xtest) != ytest)

# fit a super RaSE classifier by sampling base learner from kNN, LDA and logistic regression in equal probability
fit <- Rase(xtrain = xtrain, ytrain = ytrain, B1 = 100, B2 = 100, base = c("knn", "lda", "logistic"), super = list(type = "separate", base.update = T), criterion = "cv", cv = 5, iteration = 1, cores = 2)
mean(predict(fit, xtest) != ytest)

# fit a super RaSE classifier by sampling base learner from random forest, LDA and SVM with probability 0.2, 0.5 and 0.3
fit <- Rase(xtrain = xtrain, ytrain = ytrain, B1 = 100, B2 = 100, base = c(randomforest = 0.2, lda = 0.5, svm = 0.3), super = list(type = "separate", base.update = F), criterion = "cv", cv = 5, iteration = 0, cores = 2)
mean(predict(fit, xtest) != ytest)

## End(Not run)

---

rat Affymetrix rat genome 230 2.0 array data set.

Description

Affymetrix rat genome 230 2.0 array annotation data (chip rat2302). For this data set, 120 twelve-week old male rats were selected for tissue harvesting from the eyes and for microarray analysis. The expression of gene TRIM32 is set as the response and the 18975 probes that are expressed in the eye tissue are considered as the predictors.

Usage

rat

Format

A list with the predictor matrix x and the response vector y.

Source

The link to this data set: https://bioconductor.org/packages/release/data/annotation/html/rat2302.db.html

References

Index

* datasets
  colon, 2
  rat, 21

auc, 17

colon, 2

glm, 16
glmnet, 12, 16, 18

KernelKnn, 12
knn, 12, 16
knn.cv, 12, 16
knn3, 12, 16
knnreg, 12

lda, 12, 16

predict.RaSE, 3, 20
predict.super_RaSE, 4
print.RaSE, 5, 20
print.super_RaSE, 6, 20

qda, 12, 16

RaModel, 7, 20
randomForest, 12, 16
ranger, 12
RaPlot, 8, 20
RaRank, 9, 14
RaScreen, 8, 11, 20
Rase, 3, 5–9, 14, 15
rat, 21
rpart, 12, 16

svm, 12, 16

23