Package ‘OmicsMarkeR’

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Title Classification and Feature Selection for 'Omics' Datasets

Description Tools for classification and feature selection for 'omics' level datasets. It is a tool to provide multiple multivariate classification and feature selection techniques complete with multiple stability metrics and aggregation techniques. It is primarily designed for analysis of metabolomics datasets but potentially extendable to proteomics and transcriptomics applications.

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R topics documented:

aggregation .................................................... 3
bagging.wrapper .............................................. 4
canberra ....................................................... 5
canberra_stability .......................................... 6
CLA .............................................................. 7
create.corrmatrix ........................................... 7
create.discrimatrix ......................................... 9
create.random.matrix ...................................... 10
denovo.grid .................................................. 12
EE ............................................................... 13
EM ............................................................... 13
ES ............................................................... 14
extract.args .................................................. 15
extract.features ............................................ 15
feature.table ................................................ 16
fit.only.model ............................................... 17
fs.ensemble.stability ..................................... 18
fs.stability .................................................. 20
jaccard ........................................................ 23
kuncheva ...................................................... 24
modelList ..................................................... 25
modelTuner ................................................... 26
modelTuner_loo ............................................. 27
noise.matrix ................................................ 28
ochiai .......................................................... 28
optimize.model .............................................. 29
pairwise.model.stability .................................. 30
pairwise.stability .......................................... 31
params ........................................................ 32
perf.calc ...................................................... 33
performance.metrics ...................................... 34
performance.stats ......................................... 35
perm.class ................................................... 35
perm.features ............................................... 37
pof .............................................................. 38
predicting ..................................................... 39
prediction.metrics ......................................... 40
predictNewClasses .......................................... 40
RPT ............................................................. 42
sequester ..................................................... 42
sorensen ...................................................... 43
spearman ...................................................... 44
svm.weights .................................................. 44
svmrfeFeatureRanking ..................................... 45
svmrfeFeatureRankingForMulticlass ..................... 46
training ....................................................... 47
tune.instructions .......................................... 48

Index 49
aggregation

Feature Aggregation

Description

Compiles matrix of ranked features via user defined 'metric'

Usage

aggregation(efs, metric, f = NULL)

Arguments

- **efs**: A matrix of selected features
- **metric**: string indicating the type of aggregation. Available options are "CLA" (Complete Linear), "EM" (Ensemble Mean), "ES" (Ensemble Stability), and "EE" (Ensemble Exponential)
- **f**: The number of features desired. Default f = NULL

Value

- **agg**: Aggregated list of features

Author(s)

Charles Determan Jr

References


See Also

CLA, ES, EM, EE

Examples

```r
# test data
ranks <- replicate(5, sample(seq(50), 50))
row.names(ranks) <- paste0("V", seq(50))

aggregation(ranks, "CLA")
```
**Description**

Compiles results of ensemble feature selection

**Usage**

```r
bagging.wrapper(X, Y, method, bags, f, aggregation.metric, k.folds, repeats, 
res, tuning.grid, optimize, optimize.resample, metric, model.features, 
allowParallel, verbose, theDots)
```

**Arguments**

- **X**: A matrix containing numeric values of each feature
- **Y**: A factor vector containing group membership of samples
- **method**: A vector listing models to be fit
- **bags**: Number of bags to be run
- **f**: Number of features desired
- **aggregation.metric**: String indicating the type of ensemble aggregation. Available options are “CLA” (Complete Linear), “EM” (Ensemble Mean), “ES” (Ensemble Stability), and “EE” (Ensemble Exponential)
- **k.folds**: Number of folds generated during cross-validation
- **repeats**: Number of times cross-validation repeated
- **res**: Optional - Resolution of model optimization grid
- **tuning.grid**: Optional list of grids containing parameters to optimize for each algorithm. Default “tuning.grid = NULL” lets function create grid determined by “res”
- **optimize**: Logical argument determining if each model should be optimized. Default “optimize = TRUE”
- **optimize.resample**: Logical argument determining if each resample should be re-optimized. Default “optimize.resample = FALSE”. Only one optimization run, subsequent models use initially determined parameters
- **metric**: Criteria for model optimization. Available options are “Accuracy” (Prediction Accuracy), “Kappa” (Kappa Statistic), and “AUC-ROC” (Area Under the Curve - Receiver Operator Curve)
- **model.features**: Logical argument if should have number of features selected to be determined by the individual model runs. Default ”model.features = FALSE”
- **allowParallel**: Logical argument dictating if parallel processing is allowed via foreach package. Default allowParallel = FALSE
- **verbose**: Logical argument if should output progress
- **theDots**: Optional arguments provided for specific models or user defined parameters if “optimize = FALSE”.
Value

- **results**: List with the following elements:
  - **Methods**: Vector of models fit to data
  - **ensemble.results**: List of length = length(method) containing aggregated features
  - **Number.bags**: Number of bagging iterations
  - **Agg.metric**: Aggregation method applied
  - **Number.features**: Number of user-defined features

- **bestTunes**: If "optimize.resample = TRUE" then returns list of best parameters for each iteration

Author(s)

Charles Determan Jr

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**canberra**  
*Canberra Distance*

**Description**

Calculates canberra distance between two vectors. In brief, the higher the canberra distance the greater the 'distance' between the two vectors (i.e. they are less similar).

**Usage**

```r
canberra(x, y)
```

**Arguments**

- **x**: numeric vector of ranks
- **y**: numeric vector of ranks with compatible length to x

**Value**

Returns the canberra distance for the two vectors

**Note**

The `canberra_stability` function is used internally to return the canberra metric.

**Author(s)**

Charles E. Determan Jr.

**References**


canberra_stability

Examples

# Canberra demo
v1 <- seq(10)
v2 <- sample(v1, 10)
canberra(v1, v2)

canberra_stability(v1, v2)

canberra_stability  Canberra Stability

Description

Calculates canberra stability between two ranked lists. In brief, the raw canberra distance is scaled to a [0,1] distribution by the maximum canberra metric. Lastly, this value is subtracted from 1 to provide the same interpretation as the other stability metrics whereby 1 is identical and 0 is no stability.

Usage

canberra_stability(x, y)

Arguments

x  numeric vector of ranks
y  numeric vector of ranks with compatible length to x

Value

Returns the canberra stability for the two vectors

Author(s)

Charles E. Determan Jr.

References


Examples

# Canberra demo
v1 <- seq(10)
v2 <- sample(v1, 10)
canberra(v1, v2)

canberra_stability(v1, v2)
CLA

**Complete Linear Aggregation**

**Description**

Compiles matrix of ranked features via complete linear aggregation

**Usage**

```r
CLA(efs, f)
```

**Arguments**

- `efs` A matrix of selected features
- `f` The number of features desired. If rank correlation desired, `f = NULL`

**Value**

- `agg` Aggregated list of features

**Author(s)**

Charles Determan Jr

**References**


**See Also**

ES, EM, EE

---

create.corr.matrix

**Correlated Multivariate Data Generator**

**Description**

Generates a matrix of dimensions `dim(U)` with induced correlations. Blocks of variables are randomly assigned and correlations are induced. A noise matrix is applied to the final matrix to perturb 'perfect' correlations.

**Usage**

```r
create.corr.matrix(U, k = 4, min.block.size = 2, max.block.size = 5)
```
Arguments

U  Numeric matrix

k  Correlation Perturbation - The higher k, the more the data is perturbed. Default k = 4

min.block.size  minimum number of variables to correlate Default min.block.size = 2

max.block.size  maximum number of variables to correlate Default max.block.size = 5

Value

A numeric matrix of dimension dim(U) with correlations induced between variables

Note

Output does not contain classes, may provide externally as classes are irrelevant in this function.

Author(s)

Charles E. Determan Jr.

References


See Also

create.random.matrix, create.discr.matrix

Examples

# Create Multivariate Matrices
# Random Multivariate Matrix
# 50 variables, 100 samples, 1 standard deviation, 0.2 noise factor

rand.mat <- create.random.matrix(nvar = 50,
                                 nsamp = 100,
                                 st.dev = 1,
                                 perturb = 0.2)

# Induce correlations in a numeric matrix
# Default settings
# minimum and maximum block sizes (min.block.size = 2, max.block.size = 5)
# default correlation perturbation (k=4)
# see ?create.corr.matrix for citation for methods

corr.mat <- create.corr.matrix(rand.mat)

# Induce Discriminatory Variables
# 10 discriminatory variables (D = 10)
# default discrimination level (l = 1.5)
# default number of groups (num.groups=2)
# default correlation perturbation (k = 4)

dat.discr <- create.discr.matrix(corr.mat, D=10)

---

create.discr.matrix  Discriminatory Multivariate Data Generator

**Description**

Generates a matrix of dimensions $\text{dim}(U)$ with induced correlations. D variables are randomly selected as discriminatory. If $\text{num.groups} = 2$ then discrimination is induced by adding and subtracting values derived from the level of discrimination, 1, for the classes respectively. Multi-class datasets have a few further levels of randomization. For each variable, a random number of the groups are selected as discriminating while the remaining groups are not altered. For each discriminatory group, a unique change is provided by randomly assigning addition or subtraction of the discrimination factor. For example, if 3 groups are selected and two groups are assigned as addition and the third subtraction, the second addition is multiplied by its number of replicates. E.g. (1,1,-1) -> (1,2,-1). These values are randomized and then multiplied by the respective discrimination factor. The resulting values are then added/subtracted from the respective groups. A noise matrix is applied to the final matrix to perturb ‘perfect’ discrimination.

**Usage**

```r
create.discr.matrix(V, D = 20, l = 1.5, num.groups = 2, k = 4)
```

**Arguments**

- **V**  
  Numeric matrix
- **D**  
  Number of discriminatory variables induced. Default $D = 20$
- **l**  
  Level of discrimination, higher = greater separation. Default $l = 1.5$
- **num.groups**  
  Number of groups in the dataset
- **k**  
  Correlation Perturbation - The higher $k$, the more the data is perturbed. Default $k = 4$

**Value**

- **discr.mat**  
  Matrix of dimension $\text{dim}(V)+1$ with discriminatory variables induced and the classes added to the end of the matrix.
- **features**  
  Vector of features that were induced to be discriminatory.

**Author(s)**

Charles E. Determan Jr.
create.random.matrix

**Random Multivariate Data Generator**

Generates a matrix of dimensions \( n_{\text{var}} \) by \( n_{\text{samp}} \) consisting of random numbers generated from a normal distribution. This normal distribution is then perturbed to more accurately reflect experimentally acquired multivariate data.

**Usage**

create.random.matrix(nvar, nsamp, st.dev = 1, perturb = 0.2)
create.random.matrix

Arguments

- `nvar`: Number of features (i.e. variables)
- `nsamp`: Number of samples
- `st.dev`: The variation (i.e. standard deviation) that is typical in datasets of interest to the user. Default spread = 1
- `perturb`: The amount of perturbation to the normal distribution. Default perturb = 0.2

Value

Matrix of dimension `nvar` by `nsamp`

Author(s)

Charles E. Determan Jr.

References


See Also

`create.corr.matrix`, `create.discr.matrix`

Examples

```r
# Create Multivariate Matrices
# Random Multivariate Matrix
# 50 variables, 100 samples, 1 standard deviation, 0.2 noise factor
rand.mat <- create.random.matrix(nvar = 50,
                                  nsamp = 100,
                                  st.dev = 1,
                                  perturb = 0.2)

# Induce correlations in a numeric matrix
# Default settings
# minimum and maximum block sizes (min.block.size = 2, max.block.size = 5)
# default correlation perturbation (k=4)
# see ?create.corr.matrix for citation for methods
corr.mat <- create.corr.matrix(rand.mat)

# Induce Discriminatory Variables
# 10 discriminatory variables (D = 10)
# default discrimination level (l = 1.5)
# default number of groups (num.groups=2)
```
denovo.grid

# default correlation perturbation (k = 4)
dat.discr <- create.discr.matrix(corr.mat, D=10)

---

**denovo.grid**  
*Denovo Grid Generation*

**Description**  
Greatest grid for optimizing selected models

**Usage**  
denovo.grid(data, method, res)

**Arguments**  
- **data**: data of method to be tuned  
- **method**: vector indicating the models to generate grids. Available options are "plsda" (Partial Least Squares Discriminant Analysis), "rf" (Random Forest), "gbm" (Gradient Boosting Machine), "svm" (Support Vector Machines), "glmnet" (Elastic-net Generalized Linear Model), and "pam" (Prediction Analysis of Microarrays)  
- **res**: Resolution of model optimization grid.

**Value**  
A list containing dataframes of all combinations of parameters for each model:

**Author(s)**  
Charles Determan Jr

**See Also**  
"expand.grid" for generating grids of specific parameters desired. However, NOTE that you must still convert the generated grid to a list.

**Examples**

```r
# random test data
set.seed(123)
dat.discr <- create.discr.matrix(
  create.corr.matrix(
    create.random.matrix(nvar = 50, nsamp = 100, st.dev = 1, perturb = 0.2)),
    D = 10
  )
)
df <- data.frame(dat.discr$discr, .classes = dat.discr$classes)
```
# create tuning grid
denovo.grid(df, "gbm", 3)

---

**EE**  
*Ensemble Exponential Aggregation*

**Description**

Compiles matrix of ranked features via ensemble exponential aggregation

**Usage**

EE(efs, f)

**Arguments**

- **efs**
  A matrix of selected features
- **f**
  The number of features desired. If rank correlation desired, f = NULL

**Value**

- **agg**
  Aggregated list of features

**Author(s)**

Charles Determan Jr

**References**


**See Also**

CLA, ES, EM.

---

**EM**  
*Ensemble Mean Aggregation*

**Description**

Compiles matrix of ranked features via ensemble mean aggregation

**Usage**

EM(efs, f)
Arguments

efs   A matrix of selected features
f     The number of features desired. If rank correlation desired, f = NULL

Value

agg   Aggregated list of features

Author(s)

Charles Determan Jr

References


See Also

CLA, ES, EE

Description

Ensemble Stability Aggregation

Compiles matrix of ranked features via ensemble stability aggregation

Usage

ES(efs, f)

Arguments

efs   A matrix of selected features
f     The number of features desired. If rank correlation desired, f = NULL

Value

agg   Aggregated list of features

Author(s)

Charles Determan Jr

References


See Also

CLA, EM, EE
extract.args  

**Argument extractor**

**Description**

Extract arguments from previously fs.stability models

**Usage**

```
extract.args(fs.model, method)
```

**Arguments**

- `fs.model` Previously fit fs.stability model
- `method` Which model to extract from

**Value**

- `args` List of model arguments

extract.features  

**Feature Extraction**

**Description**

Extracts features from models that have been previously fit.

**Usage**

```
extract.features(x, dat = NULL, grp = NULL, method, model.features = FALSE, bestTune = NULL, f, comp.catch = NULL)
```

**Arguments**

- `x` Previously fitted model
- `dat` Numeric variable data used for fitted models (In appropriate format)
- `grp` Vector of training classes
- `method` String indicating the INDIVIDUAL model being extracted from
- `model.features` Logical argument dictating if features selected determined by models instead of user determined number of features.
- `bestTune` If `model.features = TRUE`, must provide the parameter at which to extract features from the model.
- `f` Number of features to subset
- `comp.catch` An internal check for plsda models. If the optimal model contains only 1 component, the ncomp parameter must be set to 2 for the model. However, features are still extracted only from the first component.

**Value**

Returns list of the features selected from the fitted model.
**Feature Consistency Table**

**Description**

Extracts and sorts the features identified for a given method.

**Usage**

```
feature.table(features, method)
```

**Arguments**

- `features`: A `fs.stability` fitted object
- `method`: Algorithm of interest. Available options are "plsda" (Partial Least Squares Discriminant Analysis), "rf" (Random Forest), "gbm" (Gradient Boosting Machine), "svm" (Support Vector Machines), "glmnet" (Elastic-net Generalized Linear Model), and "pam" (Prediction Analysis of Microarrays)

**Value**

A data frame containing:

- `features`: Features identified by model
- `consistency`: Number of iterations feature was identified
- `frequency`: Frequency of iterations the feature was identified

**Author(s)**

Charles Determan Jr

**Examples**

```r
dat.discr <- create.discr.matrix(
    create.corr.matrix(
        create.random.matrix(nvar = 50,
            nsamp = 100,
            st.dev = 1,
            perturb = 0.2)),
        D = 10)
)
vars <- dat.discr$discr.mat
groups <- dat.discr$classes
fits <- fs.stability(vars,
    groups,
    method = c("plsda", "rf"),
    f = 10,
    k = 3,
    k.folds = 10,
    verbose = 'none')

feature.table(fits, "plsda")
```
fit.only.model  

Fit Models without Feature Selection

Description

Applies models to high-dimensional data for classification.

Usage

fit.only.model(X, Y, method, p = 0.9, optimize = TRUE, tuning.grid = NULL, k.folds = if (optimize) 10 else NULL, repeats = if (optimize) 3 else NULL, resolution = if (optimize) 3 else NULL, metric = "Accuracy", allowParallel = FALSE, verbose = "none", ...)

Arguments

X A scaled matrix or dataframe containing numeric values of each feature
Y A factor vector containing group membership of samples
method A vector listing models to be fit. Available options are "plsda" (Partial Least Squares Discriminant Analysis), "rf" (Random Forest), "gbm" (Gradient Boosting Machine), "svm" (Support Vector Machines), "glmnet" (Elastic-net Generalized Linear Model), and "pam" (Prediction Analysis of Microarrays)
p Percent of data to by 'trained'
optimize Logical argument determining if each model should be optimized. Default "optimize = TRUE"
tuning.grid Optional list of grids containing parameters to optimize for each algorithm. Default "tuning.grid = NULL" lets function create grid determined by "res"
k.folds Number of folds generated during cross-validation. Default "k.folds = 10"
repeats Number of times cross-validation repeated. Default "repeats = 3"
resolution Resolution of model optimization grid. Default "resolution = 3"
metric Criteria for model optimization. Available options are "Accuracy" (Prediction Accuracy), "Kappa" (Kappa Statistic), and "AUC-ROC" (Area Under the Curve - Receiver Operator Curve)
allowParallel Logical argument dictating if parallel processing is allowed via foreach package. Default allowParallel = FALSE
verbose Logical argument if should output progress
...
Extra arguments that the user would like to apply to the models

Value

Methods Vector of models fit to data
performance Performance metrics of each model and bootstrap iteration
specs List with the following elements:
  • total.samples: Number of samples in original dataset
  • number.features: Number of features in original dataset
  • number.groups: Number of groups
  • group.levels: The specific levels of the groups
  • number.observations.group: Number of observations in each group
Author(s)

Charles Determan Jr

Examples

```r
dat.discr <- create.discr.matrix(
  create.corr.matrix(
    create.random.matrix(nvar = 50,
                        nsamp = 100,
                        st.dev = 1,
                        perturb = 0.2)),
    D = 10
  )
)

vars <- dat.discr$discr.mat
groups <- dat.discr$classes

fit <- fit.only.model(X = vars,
                       Y = groups,
                       method = "plsta",
                       p = 0.9)
```

Description

Applies ensembles of models to high-dimensional data to both classify and determine important features for classification. The function bootstraps a user-specified number of times to facilitate stability metrics of features selected thereby providing an important metric for biomarker investigations, namely whether the important variables can be identified if the models are refit on 'different' data.

Usage

```r
fs.ensembl.stability(X, Y, method, k = 10, p = 0.9,
                      f = ceiling(ncol(X)/10), bags = 40,
                      aggregation.metric = "CLA",
                      stability.metric = "jaccard", optimize = TRUE,
                      optimize.resample = FALSE, tuning.grid = NULL,
                      k.folds = if (optimize) 10 else NULL,
                      repeats = if (k.folds == "LOO") NULL else if (optimize) 3 else
                      NULL, resolution = if (optimize) 3 else NULL,
                      metric = "Accuracy",
                      model.features = FALSE, allowParallel = FALSE,
                      verbose = "none", ...)
```

Arguments

- `X`: A matrix containing numeric values of each feature
- `Y`: A factor vector containing group membership of samples
- `method`: A vector listing models to be fit. Available options are "plsta" (Partial Least Squares Discriminant Analysis), "rf" (Random Forest), "gbm" (Gradient Boosting Machine), "svm" (Support Vector Machines), "glmnet" (Elastic-net Generalized Linear Model), and "pam" (Prediction Analysis of Microarrays)
k
Number of bootstrapped iterations

p
Percent of data to be 'trained'

f
Number of features desired. Default is top 10 “f = ceiling(ncol(variables)/10)”. If rank correlation is desired, set “f = NULL”

bags
Number of iterations for ensemble bagging. Default "bags = 40"

aggregation.metric
String indicating which aggregation metric for features selected during bagging. Available options are "CLA" (Complete Linear), "EM" (Ensemble Mean), "ES" (Ensemble Stability), and "EE" (Ensemble Exponential)

stability.metric
String indicating the type of stability metric. Available options are "jaccard" (Jaccard Index/Tanimoto Distance), "sorensen" (Dice-Sorensen’s Index), "ochiai" (Ochiai’s Index), "pof" (Percent of Overlapping Features), "kuncheva" (Kuncheva’s Stability Measures), "spearman" (Spearman Rank Correlation), and "canberra" (Canberra Distance)

optimize
Logical argument determining if each model should be optimized. Default “optimize = TRUE”

optimize.resample
Logical argument determining if each resample should be re-optimized. Default “optimize.resample = FALSE”. Only one optimization run, subsequent models use initially determined parameters

tuning.grid
Optional list of grids containing parameters to optimize for each algorithm. Default "tuning.grid = NULL" lets function create grid determined by "res"

k.folds
Number of folds generated during cross-validation. May optionally be set to "LOO" for leave-one-out cross-validation. Default "k.folds = 10"

repeats
Number of times cross-validation repeated. Default "repeats = 3"

resolution
Optional - Resolution of model optimization grid. Default "res = 3"

metric
Criteria for model optimization. Available options are “Accuracy” (Prediction Accuracy), "Kappa" (Kappa Statistic), and "AUC-ROC" (Area Under the Curve - Receiver Operator Curve)

model.features
Logical argument if should have number of features selected to be determined by the individual model runs. Default "model.features = FALSE"

allowParallel
Logical argument dictating if parallel processing is allowed via foreach package. Default allowParallel = FALSE

verbose
Character argument specifying how much output progress to print. Options are ‘none’, ‘minimal’ or ‘full’.

... Extra arguments that the user would like to apply to the models

Value

Methods
Vector of models fit to data

performance
Performance metrics of each model and bootstrap iteration

RPT
Robustness-Performance Trade-Off as defined in Saeys 2008

features
List concerning features determined via each algorithms feature selection criteria.

  • metric: Stability metric applied
• features: Matrix of selected features
• stability: Matrix of pairwise comparions and average stability

stability.models
Function perturbation metric - i.e. how similar are the features selected by each model.

all.tunes
If "optimize.resample = TRUE" then returns list of optimized parameters for each bagging and bootstrap iteration.

final.best.tunes
If "optimize.resample = TRUE" then returns list of optimized parameters for each bootstrap of the bagged models refit to aggregated selected features.

specs
List with the following elements:

• total.samples: Number of samples in original dataset
• number.features: Number of features in original dataset
• number.groups: Number of groups
• group.levels: The specific levels of the groups
• number.observations.group: Number of observations in each group

Author(s)
Charles Determan Jr

References

Examples
## Not run:
fits <- fs.ensembl.stability(vars, groups, method = c("plsda", "rf"), f = 10, k = 3, k.folds = 10, verbose = 'none')
## End(Not run)

fs.stability Classification & Feature Selection

Description
Applies models to high-dimensional data to both classify and determine important features for classification. The function bootstraps a user-specified number of times to facilitate stability metrics of features selected thereby providing an important metric for biomarker investigations, namely whether the important variables can be identified if the models are refit on 'different' data.
fs.stability

Usage

fs.stability(X, Y, method, k = 10, p = 0.9, f = NULL,
stability.metric = "jaccard", optimize = TRUE,
optimize.resample = FALSE, tuning.grid = NULL, k.folds = if (optimize)
10 else NULL, repeats = if (k.folds == "LOO") NULL else if (optimize) 3 else
NULL, resolution = if (is.null(tuning.grid) & & optimize) 3 else NULL,
metric = "Accuracy", model.features = FALSE, allowParallel = FALSE,
verbose = "none", ...) 

Arguments

X  A scaled matrix or dataframe containing numeric values of each feature
Y  A factor vector containing group membership of samples
method  A vector listing models to be fit. Available options are "plsda" (Partial Least
Squares Discriminant Analysis), "rf" (Random Forest), "gbm" (Gradient Boosting
Machine), "svm" (Support Vector Machines), "glmnet" (Elactic-net Generalized
Linear Model), and "pam" (Prediction Analysis of Microarrays)
k  Number of bootstrapped iterations
p  Percent of data to be 'trained'
f  Number of features desired. If rank correlation is desired, set "f = NULL"
stability.metric  string indicating the type of stability metric. Avialable options are "jaccard"
(Jaccard Index/Tanimoto Distance), "sorensen" (Dice-Sorensen's Index), "ochiai"
(Ochiai's Index), "pof" (Percent of Overlapping Features), "kuncheva" (Kuncheva's
Stability Measures), "spearman" (Spearman Rank Correlation), and "canberra"
(Canberra Distance)
optimize  Logical argument determining if each model should be optimized. Default
"optimize = TRUE"
optimize.resample  Logical argument determining if each resample should be re-optimized. Default
"optimize.resample = FALSE" - Only one optimization run, subsequent
models use initially determined parameters
tuning.grid  Optional list of grids containing parameters to optimize for each algorithm. Default
"tuning.grid = NULL" lets function create grid determined by "res"
k.folds  Number of folds generated during cross-validation. May optionally be set to
"LOO" for leave-one-out cross-validation. Default "k.folds = 10"
repeats  Number of times cross-validation repeated. Default "repeats = 3"
resolution  Resolution of model optimization grid. Default "resolution = 3"
metric  Criteria for model optimization. Available options are "Accuracy" (Predication
Accuracy), "Kappa" (Kappa Statistic), and "AUC-ROC" (Area Under the Curve -
Receiver Operator Curve)
model.features  Logical argument if should have number of features selected to be determined
by the individual model runs. Default "model.features = FALSE"
allowParallel  Logical argument dictating if parallel processing is allowed via foreach package.
Default allowParallel = FALSE
verbose  Character argument specifying how much output progress to print. Options are
'none', 'minimal' or 'full'.
...  Extra arguments that the user would like to apply to the models
Value

Methods Vector of models fit to data
performance Performance metrics of each model and bootstrap iteration
RPT Robustness-Performance Trade-Off as defined in Saeys 2008
features List concerning features determined via each algorithms feature selection criteria.
  • metric: Stability metric applied
  • features: Matrix of selected features
  • stability: Matrix of pairwise comparisons and average stability

stability.models Function perturbation metric - i.e. how similar are the features selected by each model.
original.best.tunes If "optimize.resample = TRUE" then returns list of optimized parameters for each bootstrap.
final.best.tunes If "optimize.resample = TRUE" then returns list of optimized parameters for each bootstrap of models refit to selected features.
specs List with the following elements:
  • total.samples: Number of samples in original dataset
  • number.features: Number of features in orginal dataset
  • number.groups: Number of groups
  • group.levels: The specific levels of the groups
  • number.observations.group: Number of observations in each group

Author(s)

Charles Determan Jr

References


Examples

dat.discr <- create.discr.matrix(
  create.corr.matrix(
    create.random.matrix(nvar = 50,
      nsamp = 100,
      st.dev = 1,
      perturb = 0.2)),
    D = 10
  )
)

vars <- dat.discr$discr.mat
groups <- dat.discr$classes
fits <- fs.stability(vars, 
  groups,
  method = c("plsda", "rf"),
  f = 10,
  k = 3,
  k.folds = 10,
  verbose = 'none')

---

jaccard  Jaccard Index

Description

Calculates jaccard index between two vectors of features. In brief, the closer to 1 the more similar the vectors. The two vectors may have an arbitrary cardinality (i.e. don’t need same length). Also known as the Tanimoto distance metric. Defined as the size of the vectors’ intersection divided by the size of the union of the vectors.

Usage

jaccard(x, y)

Arguments

x  vector of feature names
y  vector of feature names

Value

Returns the jaccard index for the two vectors. It takes values in [0,1], with 0 meaning no overlap between two sets and 1 meaning two sets are identical.

Author(s)

Charles E. Determan Jr.

References


See Also

kuncheva, sorensen, ochiai, pof, pairwise.stability, pairwise.model.stability
Examples

```r
# Jaccard demo
v1 <- paste("Metabolite", seq(10), sep="_")
v2 <- sample(v1, 10)
jaccard(v1, v2)
```

# Kuncheva's Index

**Description**

Calculates Kuncheva’s index between two vectors of features. In brief, the closer to 1 the more similar the vectors. The two vectors must have the same cardinality (i.e. same length).

**Usage**

```r
kuncheva(x, y, num.features)
```

**Arguments**

- `x`: Character vector of feature names
- `y`: Character vector of feature names
- `num.features`: total number of features in the original dataset

**Value**

Returns the Kuncheva Index for the two vectors. It takes values in [0,1], with 0 meaning no overlap between two sets and 1 meaning two sets are identical.

**Note**

The returned Kuncheva Index has been scaled from its original [-1,1] range to [0,1] in order to make it compatible with RPT.

**Author(s)**

Charles E. Determan Jr.

**References**


**See Also**

`kuncheva, sorensen, ochiai, pof, pairwise.stability, pairwise.model.stability`
Examples

# Kuncheva demo
# Assuming 50 metabolites were measured
# But only 10 were found significant

# For demonstration purposes only!!!
some.numbers <- seq(20)

# Metabolites identified from one run
v1 <- paste("Metabolite", sample(some.numbers, 10), sep="_")
# Metabolites identified from second run
v2 <- paste("Metabolite", sample(some.numbers, 10), sep="_")
kuncheva(v1, v2, 50)

---

modellist  Model List

Description

Provide a list of currently implemented methods for OmicsMarkeR.

Usage

modellist()

Value

A data.frame containing:

methods    The abbreviated code for the method
description Full name of the method

Author(s)

Charles Determan Jr.

Examples

modellist()
modelTuner  

Model Tuner

Description

Optimizes each model based upon the parameters provided either by the internal `denovo.grid` function or by the user.

Usage

```r
modelTuner(trainData, guide, method, inTrain, outTrain, lev, 
  savePredictions = FALSE, allowParallel = FALSE, verbose = "none", 
  theDots = NULL)
```

Arguments

- `trainData`: Data used to fit the model
- `guide`: Output from `tune.instructions`. Facilitates the optimization by avoiding redundant model fitting.
- `method`: Vector of strings listing models to be fit
- `inTrain`: Indices for cross-validated training models
- `outTrain`: Indices for cross-validated testing models
- `lev`: Group levels
- `savePredictions`: Logical argument dictating if should save the prediction data. Default `savePredictions = FALSE`
- `allowParallel`: Logical argument dictating if parallel processing is allowed via foreach package
- `verbose`: Character argument specifying how much output progress to print. Options are ‘none’, ‘minimal’ or ‘full’.
- `theDots`: List of additional arguments provided in the initial classification and features selection function

Value

Returns list of fitted models

Author(s)

Charles E. Determan Jr.
modelTuner_loo  

Model Tuner for Leave-One-Out Cross-Validation

Description

Optimizes each model via LOO CV based upon the parameters provided either by the internal `denovo.grid` function or by the user.

Usage

```r
modelTuner_loo(trainData, guide, method, inTrain, outTrain, lev,
    savePredictions = FALSE, allowParallel = FALSE, verbose = "none",
    theDots = NULL)
```

Arguments

- `trainData`: Data used to fit the model
- `guide`: Output from `tune.instructions`. Facilitates the optimization by avoiding redundant model fitting.
- `method`: Vector of strings listing models to be fit
- `inTrain`: Indices for cross-validated training models
- `outTrain`: Indices for cross-validated testing models
- `lev`: Group levels
- `savePredictions`: Logical argument dictating if should save the prediction data. Default `savePredictions = FALSE`
- `allowParallel`: Logical argument dictating if parallel processing is allowed via `foreach` package
- `verbose`: Character argument specifying how much output progress to print. Options are ‘none’, ‘minimal’ or ‘full’.
- `theDots`: List of additional arguments provided in the initial classification and features selection function

Value

Returns list of fitted models

Author(s)

Charles E. Determan Jr.
noise.matrix  
*Noise Matrix Generator*

**Description**

Provides a matrix to perturb randomly generated data to facilitate a more realistic dataset.

**Usage**

`noise.matrix(matrix, k)`

**Arguments**

- `matrix` A matrix of simulated data with dimensions comparable to ’real’ datasets
- `k` Correlation Perturbation - The higher k, the more the data is perturbed.

**Value**

Returns a matrix of the same dimensions as `matrix` that can add to perturb the original simulated data.

**Author(s)**

Charles E. Determan Jr.

---

ochiai  
*Ochiai’s Index*

**Description**

Calculates Ochiai’s index between two vectors of features. In brief, the closer to 1 the more similar the vectors. The two vectors may have an arbitrary cardinality (i.e. don’t need same length). Very similar to the Jaccard Index `jaccard` but Ochiai is a geometric means of the ratio.

**Usage**

`ochiai(x, y)`

**Arguments**

- `x` Character vector of feature names
- `y` Character vector of feature names

**Value**

Returns the Ochiai Index for the two vectors. It takes values in [0,1], with 0 meaning no overlap between two sets and 1 meaning two sets are identical.

**Author(s)**

Charles E. Determan Jr.
References


See Also

kuncheva, sorensen, ochiai, pof, pairwise.stability, pairwise.model.stability

Examples

```r
# Ochiai demo
v1 <- paste("Metabolite", seq(10), sep="_")
v2 <- sample(v1, 10)
ochiai(v1, v2)
```

---

**optimize.model**  
Model Optimization and Metrics

**Description**

Optimizes each model based upon the parameters provided either by the internal `denovo.grid` function or by the user.

**Usage**

```r
optimize.model(trainVars, trainGroup, method, k.folds = 10, repeats = 3, res = 3, grid = NULL, metric = "Accuracy", allowParallel = FALSE, verbose = "none", theDots = NULL)
```

**Arguments**

- `trainVars`: Data used to fit the model
- `trainGroup`: Group identifiers for the training data
- `method`: A vector of strings listing models to be optimized
- `k.folds`: Number of folds generated during cross-validation. Default "k.folds = 10"
- `repeats`: Number of times cross-validation repeated. Default "repeats = 3"
- `res`: Resolution of model optimization grid. Default "res = 3"
- `grid`: Optional list of grids containing parameters to optimize for each algorithm. Default "grid = NULL" lets function create grid determined by "res"
- `metric`: Criteria for model optimization. Available options are "Accuracy" (Predication Accuracy), "Kappa" (Kappa Statistic), and "AUC-ROC" (Area Under the Curve - Receiver Operator Curve)
- `allowParallel`: Logical argument dictating if parallel processing is allowed via foreach package
verbose

Character argument specifying how much output progress to print. Options are 'none', 'minimal' or 'full'.

theDots

List of additional arguments provided in the initial classification and features selection function

Value

Basically a list with the following elements:

- method: Vector of strings listing models that were optimized
- performance: Performance generated internally to optimize model
- bestTune: List of parameters chosen for each model
- dots: List of extra arguments initially provided
- metric: Criteria that was used for model optimization
- finalModels: The fitted models with the 'optimum' parameters
- performance.metrics: The performance metrics calculated internally for each resulting prediction
- tune.metrics: The results from each tune
- perfNames: The names of the performance metrics
- comp.catch: If the optimal PLSDA model contains only 1 component, the model must be refit with 2 components. This catches the 1 component parameter so feature selection and further performance analysis can be conducted on the 1 component.

Author(s)

Charles E. Determan Jr.

pairwise.model.stability

Pairwise Model Stability Metrics

Description

Conducts all pairwise comparisons of each model’s selected features selected following bootstrapping. Also known as the function perturbation ensemble approach

Usage

pairwise.model.stability(features, stability.metric, nc)

Arguments

- features: A matrix of selected features
- stability.metric: String indicating the type of stability metric. Available options are "jaccard" (Jaccard Index/Tanimoto Distance), "sorensen" (Dice-Sorensen’s Index), "ochiai" (Ochiai’s Index), "pof" (Percent of Overlapping Features), "kuncheva" (Kuncheva’s Stability Measures), "spearman" (Spearman Rank Correlation), and "canberra" (Canberra Distance)
- nc: Number of original features
Value
A list is returned containing:

- comparisons: Matrix of pairwise comparisons
- overall: The average of all pairwise comparisons

Author(s)
Charles Determan Jr

References

See Also
pairwise.stability

Examples

```r
# pairwise.model.stability demo
# For demonstration purposes only!!!
some.numbers <- seq(20)

# A list containing the metabolite matrices for each algorithm
# As an example, let's say we have the output from two different models
# such as plsda and random forest.
# matrix of Metabolites identified (e.g. 5 trials)
plsda <-
  replicate(5, paste("Metabolite", sample(some.numbers, 10), sep="_"))
rf <-
  replicate(5, paste("Metabolite", sample(some.numbers, 10), sep="_"))

features <- list(plsda=plsda, rf=rf)

# nc may be omitted unless using kuncheva
pairwise.model.stability(features, "kuncheva", nc=20)
```

---

**pairwise.stability**  
Pairwise Stability Metrics

**Description**
Conducts all pairwise comparisons of features selected following bootstrapping. Also known as the data perturbation ensemble approach.

**Usage**
```
pairwise.stability(features, stability.metric, nc)
```
Arguments

features  A matrix of selected features

stability.metric  string indicating the type of stability metric.

nc  Optional argument to be used with 'kuncheva' stability. Refers to the number of variables in original data. Available options are "jaccard" (Jaccard Index/Tanimoto Distance), "sorensen" (Dice-Sorensen's Index), "ochiai" (Ochiai's Index), "pof" (Percent of Overlapping Features), "kuncheva" (Kuncheva's Stability Measures), "spearman" (Spearman Rank Correlation), and "canberra" (Canberra Distance). @param nc Number of variables in original dataset

Value

A list is returned containing:

- comparisons  Matrix of pairwise comparisons
- overall  The average of all pairwise comparisons

Author(s)

Charles Determan Jr

References


Examples

# pairwise.stability demo
# For demonstration purposes only!!!
some.numbers <- seq(20)

# matrix of Metabolites identified (e.g. 5 trials)
features <-
    replicate(5, paste("Metabolite", sample(some.numbers, 10), sep="_"))

# nc may be omitted unless using kuncheva
pairwise.stability(features, "jaccard")

params  

Model Parameters and Properties

Description

Provides a list of the models with their respective parameters and properties.

Usage

params(method = NULL)
perf.calc

Arguments

method  A vector of strings listing the models to be returned

Value

Returns a dataframe of the following components:
method  A vector of strings listing models returned
parameter  A vector of possible parameters to be optimized
label  A vector of the names for each possible parameter
seq  A logical indicator if the parameter is sequential in the model (i.e. if model is able to fit all 'lower' parameters simultaneously)

Examples

params("plsda")

perf.calc  Performance Statistics Calculations

Description

Calculates confusion matrix and ROC statistics comparing the results of the fitted models to the observed groups.

Usage

perf.calc(data, lev = NULL, model = NULL)

Arguments

data  dataframe of predicted (pred) and observed (obs) groups
lev  Group levels
model  String indicating which model was initially run

Value

Returns confusion matrix and ROC performance statistics including Accuracy, Kappa, ROC.AUC, Sensitivity, Specificity, Positive Predictive Value, and Negative Predictive Value

See Also

caret function confusionMatrix
performance.metrics  Performance Metrics of fs.stability or fs.ensembl.stability object

Description
This will provide a concise data.frame of confusion matrix and ROC statistics from the results of fs.stability or fs.ensembl.stability.

Usage
performance.metrics(fit.model, digits = max(3, getOption("digits") - 3))

Arguments
- fit.model: An fs.stability or fs.ensembl.stability object
- digits: How many digits to round values

Value
Dataframe of performance statistics by model

Author(s)
Charles E. Determan Jr.

Examples
```r
dat.discr <- create.discr.matrix(
    create.corr.matrix(
        create.random.matrix(nvar = 50,
            nsamp = 100,
            st.dev = 1,
            perturb = 0.2)),
        D = 10
    )
)

vars <- dat.discr$discr.mat
groups <- dat.discr$classes

fits <- fs.stability(vars,
    groups,
    method = c("plsda", "rf"),
    f = 10,
    k = 3,
    k.folds = 10,
    verbose = 'none')

performance.metrics(fits)
```
### performance.stats

**Performance Statistics (Internal for perf.calc)**

**Description**
Calculates confusion matrix and ROC statistics comparing the results of the fitted models to the observed groups.

**Usage**

\[
\text{performance.stats}(\text{pred}, \text{obs})
\]

**Arguments**

- **pred**: vector of groups predicted by a fitted classification model
- **obs**: vector of groups from the original dataset

**Value**
Returns confusion matrix and ROC performance statistics including Accuracy, Kappa, ROC.AUC, Sensitivity, Specificity, Positive Predictive Value, and Negative Predictive Value

**See Also**
caret function `confusionMatrix`

---

### perm.class

**Monte Carlo Permutation of Model Performance**

**Description**
Applies Monte Carlo permutations to user specified models. The user can either use the results from `fs.stability` or provide specified model parameters.

**Usage**

\[
\text{perm.class}(\text{fs.model} = \text{NULL}, \text{X}, \text{Y}, \text{method}, k.\text{folds} = 5, \\
m\text{metric} = "Accuarcy", n\text{perm} = 10, \text{allowParallel} = \text{FALSE}, \\
\text{create.plot} = \text{FALSE}, \text{verbose} = \text{TRUE}, \ldots)
\]

**Arguments**

- **fs.model**: Object containing results from `fs.stability`
- **X**: A scaled matrix or dataframe containing numeric values of each feature
- **Y**: A factor vector containing group membership of samples
- **method**: A string of the model to be fit. Available options are "plsda" (Partial Least Squares Discriminant Analysis), "rf" (Random Forest), "gbm" (Gradient Boosting Machine), "svm" (Support Vector Machines), "glmnet" (Elastic-net Generalized Linear Model), and "pam" (Prediction Analysis of Microarrays)
perm.class

k.folds  How many and what fractions of dataset held-out for prediction (i.e. 3 = 1/3, 10 = 1/10, etc.)
metric  Performance metric to assess. Available options are "Accuracy", "Kappa", and "ROC.AUC".
nperm  Number of permutations, default nperm = 10
allowParallel  Logical argument dictating if parallel processing is allowed via foreach package. Default allowParallel = FALSE
create.plot  Logical argument whether to create a distribution plot of permutation results.
verbose  Logical argument whether output printed automatically in 'pretty' format. Default create.plot = FALSE
...

Extra arguments that the user would like to apply to the models

Value

p.value  Resulting p-value of permutation test

Author(s)

Charles Determan Jr.

References


Examples

dat.discr <- create.discr.matrix(
  create.corr.matrix(
    create.random.matrix(nvar = 50,
      nsamp = 100,
      st.dev = 1,
      perturb = 0.2)),
    D = 10
  )
)

dat <- dat.discr$discr.mat
groups <- dat.discr$classes

fits <- fs.stability(vars,
  groups,
  method = c("plsda", "rf"),
  f = 10,
  k = 3,
  k.folds = 10,
  verbose = 'none')

perm.class(fits, vars, groups, "rf", k.folds=5,
  metric="Accuracy", nperm=10)
perm.features

Feature Selection via Monte Carlo Permutation

Description

Applies Monte Carlo permutations to user specified models. The user can either use the results from fs.stability or provide specified model parameters.

Usage

perm.features(fs.model = NULL, X, Y, method, sig.level = 0.05, nperm = 10,
allowParallel = FALSE, verbose = TRUE, ...)

Arguments

fs.model Object containing results from fs.stability
X A scaled matrix or dataframe containing numeric values of each feature
Y A factor vector containing group membership of samples
method A vector listing models to be fit. Available options are "plsda" (Partial Least Squares Discriminant Analysis), "rf" (Random Forest), "gbm" (Gradient Boosting Machine), "svm" (Support Vector Machines), "glmnet" (Elastic-net Generalized Linear Model), and "pam" (Prediction Analysis of Microarrays)
sig.level Desired significance level for features, default sig.level = .05
nperm Number of permutations, default nperm = 10
allowParallel Logical argument dictating if parallel processing is allowed via foreach package. Default allowParallel = FALSE
verbose Logical argument whether output printed automatically in 'pretty' format.
... Extra arguments that the user would like to apply to the models

Value

sig.level User-specified significance level
num.sig.features Number of significant features
sig.features Dataframe of significant features

Author(s)

Charles Determan Jr.

References

Examples

dat.discr <- create.discr.matrix(
create.corr.matrix(
create.random.matrix(nvar = 50,
nsamp = 100,
st.dev = 1,
perturb = 0.2)),
D = 10
)
)

vars <- dat.discr$discr.mat
groups <- dat.discr$classes

fits <- fs.stability(vars,
groups,
method = c("plsda", "rf"),
f = 10,
k = 3,
k.folds = 10,
verbose = 'none')

# permute variables/features
perm.features(fits, vars, groups, "rf",
sig.level = .05, nperm = 10)


pof

Percentage of Overlapping Features

Description

Calculates percent of overlapping features between two vectors of features. In brief, the closer to 1 the more similar the vectors. The two vectors may have an arbitrary cardinality (i.e. don’t need same length).

Usage

pof(x, y)

Arguments

x Character vector of feature names
y Character vector of feature names

Value

Returns the percent of overlapping features for the two vectors. It takes values in [0,1], with 0 meaning no overlap between two sets and 1 meaning two sets are identical.

Author(s)

Charles E. Determan Jr.
References


See Also

kuncheva, sorensen, ochiai, pof, pairwise.stability, pairwise.model.stability

Examples

# Percent-Overlapping Features demo
v1 <- paste("Metabolite", seq(10), sep="_")
v2 <- sample(v1, 10)
pof(v1, v2)

predicting Model Group Prediction

Description

This function evaluates a single fitted model and returns the predicted group memberships.

Usage

predicting(method, modelFit, orig.data, indicies, newdata, param = NULL)

Arguments

method String of the model to be evaluated
modelFit The fitted model being evaluated
orig.data The original data before subsetting training sets. Required to have the ’observed’ group membership
indicies The indicies for the training subsets
newdata The testing data to predict group membership
param The parameters being fit to the model (Determined by model optimization).

Value

Returns a list of predicted group membership
prediction.metrics  Prediction Metric Calculations

Description

Performance evaluation of all fitted models. This function concisely provides model performance metrics, including confusion matrix and ROC.

Usage

prediction.metrics(finalModel, method, raw.data, inTrain, outTrain, features, bestTune, grp.levs, stability.metric)

Arguments

- **finalModel**: List of fitted models
- **method**: Vector of strings dictating the models that were fit
- **raw.data**: Original dataset prior to any training subset
- **inTrain**: List of training indicies for each feature selection run
- **outTrain**: List of testing data indicies for each feature selection run
- **features**: List of selected features for each model
- **bestTune**: List of parameters that have been optimized for the each respective model
- **grp.levs**: Vector of group levels
- **stability.metric**: A character object specifying the stability metric

Value

Returns a dataframe consisting of each feature selection runs evaluated Accuracy, Kappa, ROC.AUC, Sensitivity, Specificity, Positive Predictive Value, and Negative Predictive Value.

See Also

- performance.stats
- perf.calc
- caret function confusionMatrix

predictNewClasses  Class Prediction

Description

This function evaluates a single fitted model and returns the predicted group memberships of new data.

Usage

predictNewClasses(modelFit, method, orig.data, newdata, param = NULL)
predictNewClasses

Arguments

modelFit The fitted model being evaluated
method String of the model to be evaluated
orig.data The original data before subsetting training sets. Required to have the 'observed' group membership
newdata The testing data to predict group membership
param Optional alternate parameters being fit to the model

Value

Returns a list of predicted group membership

Examples

dat.discr <- create.discr.matrix(
    create.corr.matrix(
        create.random.matrix(nvar = 50,
            nsamp = 100,
            st.dev = 1,
            perturb = 0.2)),
        D = 10
    )
)

vars <- dat.discr$discr.mat
groups <- dat.discr$classes

fits <- fs.stability(vars,
    groups,
    method = c("plsda", "rf"),
    f = 10,
    k = 3,
    k.folds = 10,
    verbose = 'none')

newdata <- create.discr.matrix(
    create.corr.matrix(
        create.random.matrix(nvar = 50,
            nsamp = 100,
            st.dev = 1,
            perturb = 0.2)),
        D = 10
    )$discr.mat

orig.df <- data.frame(vars, groups)

# see what the PLSDA predicts for the new data
# NOTE, newdata does not require a .classes column
predictNewClasses(fits, "plsda", orig.df, newdata)
RPT

Robustness-Performance Trade-Off

Description

A variation on the F-measure (precision and recall) to assess robustness versus classification performance.

Usage

RPT(stability, performance, beta = 1)

Arguments

- **stability**: Stability metric i.e. result from jaccard, sorensen, etc.
- **performance**: Model performance e.g. accuracy

Value

Harmonic mean of robustness and classification performance

References


Examples

```r
# RPT demo
RPT(stability=0.85, performance=0.90, beta=1)
```

sequester

Sequester Additional Parameters

Description

When the user provides additional arguments to either fs.stability or fs.ensembl.stability this function will extract the parameters to be fit if optimization is not used i.e. optimize = FALSE.

Usage

sequester(theDots, method)

Arguments

- **theDots**: List of additional arguments
- **method**: Vector of strings listing models to be fit
sorensen

Value

Returns a list of the following elements

- parameters: The parameters that will be fit to models
- pnames: The names of the specific parameters

---

Value

Returns a list of the following elements

- parameters: The parameters that will be fit to models
- pnames: The names of the specific parameters

**sorensen**  
*Dice-Sorensen’s Index*

Description

Calculates Dice-Sorensen’s index between two vectors of features. In brief, the closer to 1 the more similar the vectors. The two vectors may have an arbitrary cardinality (i.e. don’t need same length). Very similar to the Jaccard Index `jaccard` but Dice-Sorensen is the harmonic mean of the ratio.

Usage

`sorensen(x, y)`

Arguments

- `x`: vector of feature names
- `y`: vector of feature names

Value

Returns the Dice-Sorensen’s Index for the two vectors. It takes values in [0,1], with 0 meaning no overlap between two sets and 1 meaning two sets are identical.

Author(s)

Charles E. Determan Jr.

References


See Also

- `kuncheva`, `sorensen`, `ochiai`, `pof`, `pairwise.stability`, `pairwise.model.stability`

Examples

```r
# Dice-Sorensen demo
demo <- paste("Metabolite", seq(10), sep="_")
demo2 <- sample(demo, 10)
sorensen(demo, demo2)
```
spearman  

*Spearman Rank Correlation Coefficient*

**Description**

Calculates spearman rank correlation between two vectors

**Usage**

`spearman(x, y)`

**Arguments**

- `x` numeric vector of ranks
- `y` numeric vector of ranks with compatible length to `x`

**Value**

Returns the spearman rank coefficient for the two vectors

**Examples**

```r
# Spearman demo
data(v1 <- seq(10)
data(v2 <- sample(v1, 10)
spearman(v1, v2)
```

svm.weights  

*SVM Multiclass Weights Ranking*

**Description**

This calculates feature weights for multiclass Support Vector Machine (SVM) problems

**Usage**

```r
## S3 method for class 'weights'
svm(model)
```

**Arguments**

- `model` A fitted SVM model of multiclass

**Value**

Vector of feature weights

**References**

svmrfeFeatureRanking  SVM Recursive Feature Extraction (Binary)

Description
This conducts feature selection for Support Vector Machines models via recursive feature extraction. This returns a vector of the features in x ordered by relevance. The first item of the vector has the index of the feature which is more relevant to perform the classification and the last item of the vector has the feature which is less relevant. This function is specific to Binary classification problems.

Usage
```r
svmrfeFeatureRanking(x, y, c, perc.rem = 10)
```

Arguments
- `x`: A matrix where each column represents a feature and each row represents a sample.
- `y`: A vector of labels corresponding to each sample’s group membership.
- `c`: A numeric value corresponding to the ‘cost’ applied during the svm model fitting. This can be selected by the user if using this function directly or is done internally.
- `perc.rem`: A numeric value indicating the percent of features removed during each iteration. Default `perc.rem = 10`.

Value
Vector of features ranked from most important to least important.

References

See Also
- `svmrfeFeatureRankingForMulticlass`

Examples
```r
dat.discr <- create.discr.matrix(
  create.corr.matrix(
    create.random.matrix(nvar = 50,
      nsamp = 100,
      st.dev = 1,
      perturb = 0.2)),
    D = 10)

vars <- dat.discr$discr.mat
groups <- dat.discr$classes
```
# binary class feature ranking
svmrfeFeatureRanking(x = vars,
          y = groups,
          c = 0.1,
          perc.rem = 10)

svmrfeFeatureRankingForMulticlass

SVM Recursive Feature Extraction (Multiclass)

Description
This conducts feature selection for Support Vector Machines models via recursive feature extraction. This returns a vector of the features in x ordered by relevance. The first item of the vector has the index of the feature which is more relevant to perform the classification and the last item of the vector has the feature which is less relevant. This function is specific to Binary classification problems.

Usage
svmrfeFeatureRankingForMulticlass(x, y, c, perc.rem = 10)

Arguments
- x: A matrix where each column represents a feature and each row represents a sample
- y: A vector of labels corresponding to each sample’s group membership
- c: A numeric value corresponding to the ‘cost’ applied during the svm model fitting. This can be selected by the user if using this function directly or is done internally.
- perc.rem: A numeric value indicating the percent of features removed during each iteration. Default perc.rem = 10.

Value
Vector of features ranked from most important to least important.

References

See Also
svmrfeFeatureRanking
**Examples**

```r
dat.discr <- create.discr.matrix(
  create.corr.matrix(
    create.random.matrix(nvar = 50,
      nsamp = 100,
      st.dev = 1,
      perturb = 0.2),
      D = 10,
      num.groups=4
    ),
    D = 10,
    num.groups=4
  ),
  D = 10,
  num.groups=4
)

vars <- dat.discr$discr.mat
groups <- dat.discr$classes

# multiclass
svmrfeFeatureRankingForMulticlass(x = vars,
  y = groups,
  c = 0.1,
  perc.rem = 10)
```

---

**Description**

This fits each model with the defined parameters.

**Usage**

```r
training(data, method, tuneValue, obsLevels, theDots = NULL)
```

**Arguments**

- `data`: Dataframe consisting of both numeric feature values and a single column named `.classes` to denote group membership.
- `method`: String dictating which model to fit.
- `tuneValue`: List of parameters to be applied to the specific model.
- `obsLevels`: Observed group levels.
- `theDots`: List of additional parameters to be applied to the specific model.

**Value**

- `fit`: Fitted model with list with the following elements:
  - `xNames`: Names of the features.
  - `tuneValue`: Parameters applied to the fitted model.
  - `obsLevels`: Observed levels of the groups.

**Author(s)**

Charles Determan Jr
tune.instructions  Model Optimization Instructions

Description
Provides directions for which parameters to loop over during tuning. This becomes important when certain models can access 'lower' parameters without running them independently.

Usage

tune.instructions(method, grid)

Arguments

method  Vector of strings indicating which models will be fit
grid    A list of parameters grids to be applied to the models

Value

modelInfo  List of the following components

- scheme: String dictating which looping scheme to apply
- loop: Dataframe of parameters to loop through for each model
- model: Information regarding parameters of specific model
- constant: Names of the 'loop' dataframe components
- vary: Indication of parameters that vary and can access recursively

Author(s)

Charles E. Determan Jr.
# Index

aggregation, 3

bagging.wrapper, 4

canberra, 5
canberra_stability, 5, 6
CLÁ, 3, 7, 13, 14
confusionMatrix, 33, 35, 40
create.corr.matrix, 7, 11
create.discr.matrix, 8, 9, 11
create.random.matrix, 8, 10
denovo.grid, 12, 26, 27, 29
EE, 3, 7, 13, 14
EM, 3, 7, 13, 14
ES, 3, 7, 13, 14
extract.args, 15
extract.features, 15

feature.table, 16
fit.only.model, 17
fs.enssembl.stability, 18
fs.stability, 20

jaccard, 23, 28, 43
kuncheva, 23, 24, 29, 39, 43

modelList, 25
modelTuner, 26
modelTuner_loo, 27

noise.matrix, 28

ochiai, 23, 24, 29, 39, 43
optimize.model, 29

pairwise.model.stability, 23, 24, 29, 30, 39, 43
pairwise.stability, 23, 24, 29, 31, 31, 39, 43

params, 32
perf.calc, 33, 40
performance.metrics, 34
performance.stats, 35, 40

perm.class, 35
perm.features, 37
pof, 23, 24, 29, 38, 39, 43

RPT, 42

sequester, 42
sorensen, 23, 24, 29, 39, 43, 43

spearman, 44

svm.weights, 44

svmrfeFeatureRanking, 45, 46
svmrfeFeatureRankingForMulticlass, 45, 46

training, 47
tune.instructions, 26, 27, 48