

# Package ‘OmicsMarkeR’

April 15, 2017

**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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**VignetteBuilder** knitr

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**BugReports** <http://github.com/cdeterman/OmicsMarkeR/issues/new>

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**Repository** Bioconductor

**Suggests** testthat, BiocStyle, knitr

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**R topics documented:**

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aggregation	<i>Feature Aggregation</i>
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**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. Avialable 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
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**Author(s)**

Charles Determan Jr

**References**

Abeel T., Helleputte T., Van de Peer Y., Dupont P., Saeys Y. (2010) *Robust biomarker identification for cancer diagnosis with ensemble feature selection methods*. *Bioinformatics* 26(3) 392-398.

Meinshausen N., Buhlmann P. (2010) *Stability selection*. *J.R. Statist. Soc. B.* 72(4) 417-473.

Haury A., Gestraud P., Vert J. (2011) *The Influence of Features Selection Methods on Accuracy, Stability, and Interpretability of Molecular Signatures*. *PLoS ONE* 6(12) e28210. doi: 10.1371/journal.pone.0028210.

**See Also**

[CLA](#), [ES](#), [EM](#), [EE](#)

**Examples**

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

aggregation(ranks, "CLA")
```

---

 bagging.wrapper

*Bagging Wrapper for Ensemble Features Selection*


---

## Description

Compiles results of ensemble feature selection

## Usage

```
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: <ul style="list-style-type: none"> <li>• Methods: Vector of models fit to data</li> <li>• ensemble.results: List of length = length(method) containing aggregated features</li> <li>• Number.bags: Number of bagging iterations</li> <li>• Agg.metric: Aggregation method applied</li> <li>• Number.features: Number of user-defined features</li> </ul>
bestTunes	If "optimize.resample = TRUE" then returns list of best parameters for each iteration

**Author(s)**

Charles Determan Jr

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canberra	<i>Canberra Distance</i>
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**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**

```
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**

- Jurman G., Merler S., Barla A., Paoli S., Galea A., & Furlanello C. (2008) *Algebraic stability indicators for ranked lists in molecular profiling*. *Bioinformatics* 24(2): 258-264.
- He. Z. & Weichuan Y. (2010) *Stable feature selection for biomarker discovery*. *Computational Biology and Chemistry* 34 215-225.

**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**

Jurman G., Merler S., Barla A., Paoli S., Galea A., & Furlanello C. (2008) *Algebraic stability indicators for ranked lists in molecular profiling*. *Bioinformatics* 24(2): 258-264.

He. Z. & Weichuan Y. (2010) *Stable feature selection for biomarker discovery*. *Computational Biology and Chemistry* 34 215-225.

**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**

```
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**

Abeel T., Helleputte T., Van de Peer Y., Dupont P., Saeys Y. (2010) *Robust biomarker identification for cancer diagnosis with ensemble feature selection methods*. *Bioinformatics* 26:3 392-398.

**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**

```
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**

Wongravee, K., Lloyd, G R., Hall, J., Holmboe, M. E., & Schaefer, M. L. (2009). *Monte-Carlo methods for determining optimal number of significant variables. Application to mouse urinary profiles*. *Metabolomics*, 5(4), 387-406. <http://dx.doi.org/10.1007/s11306-009-0164-4>

**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  $\dim(U)$  with induced correlations.  $D$  variables are randomly selected as discriminatory. If `num.groups = 2` then discrimination is induced by adding and subtracting values derived from the level of discrimination,  $l$ , 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)  $\rightarrow$  (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

```
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

List of the following elements

discr.mat	Matrix of dimension $\dim(V)+1$ 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.

## References

Wongravee, K., Lloyd, G R., Hall, J., Holmboe, M. E., & Schaefer, M. L. (2009). *Monte-Carlo methods for determining optimal number of significant variables. Application to mouse urinary profiles*. *Metabolomics*, 5(4), 387-406. <http://dx.doi.org/10.1007/s11306-009-0164-4>

## 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.random.matrix *Random Multivariate Data Generator*

---

## Description

Generates a matrix of dimensions nvar by nsamp 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)
```

**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**

Wongravee, K., Lloyd, G R., Hall, J., Holmboe, M. E., & Schaefer, M. L. (2009). *Monte-Carlo methods for determining optimal number of significant variables. Application to mouse urinary profiles*. *Metabolomics*, 5(4), 387-406. <http://dx.doi.org/10.1007/s11306-009-0164-4>

**See Also**

[create.corr.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)
```

---

denovo.grid

*Denovo Grid Generation*


---

## Description

Creates 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

```
# 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$discr.mat, .classes = dat.discr$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
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**Author(s)**

Charles Determan Jr

**References**

Haury A., Gestraud P., Vert J. (2011) *The Influence of Features Selection Methods on Accuracy, Stability, and Interpretability of Molecular Signatures*. PLoS ONE 6(12) e28210. doi: 10.1371/journal.pone.0028210

**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**

Abeel T., Helleputte T., Van de Peer Y., Dupont P., Saeys Y. (2010) *Robust biomarker identification for cancer diagnosis with ensemble feature selection methods*. *Bioinformatics* 26:3 392-398.

**See Also**

[CLA](#), [ES](#), [EE](#)

---

ES

*Ensemble Stability Aggregation*

---

**Description**

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**

Meinshausen N., Buhlmann P. (2010) *Stability selection*. *J.R. Statist. Soc. B.* 72:4 417-473.

**See Also**

[CLA](#), [EM](#), [EE](#)

---

extract.args	<i>Argument extractor</i>
--------------	---------------------------

---

**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	<i>Feature Extraction</i>
------------------	---------------------------

---

**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 paramter 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.table                      *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**

```
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	<i>Fit Models without Feature Selection</i>
----------------	---

---

**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" (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. 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: <ul style="list-style-type: none"> <li>• total.samples: Number of samples in original dataset</li> <li>• number.features: Number of features in orginal dataset</li> <li>• number.groups: Number of groups</li> <li>• group.levels: The specific levels of the groups</li> <li>• number.observations.group: Number of observations in each group</li> </ul>

**Author(s)**

Charles Determan Jr

**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

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

```

---

 fs.ensembl.stability *Ensemble Classification & Feature Selection*


---

**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**

```

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 "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)

k	Number of bootstrapped iterations
p	Percent of data to by 'trained'
f	Number of features desired. Default is top 10 " $f = \text{ceiling}(\text{ncol}(\text{variables})/10)$ ". If rank correlation is desired, set " $f = \text{NULL}$ "
bags	Number of iterations for ensemble bagging. Default " $\text{bags} = 40$ "
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 " $\text{optimize} = \text{TRUE}$ "
optimize.resample	Logical argument determining if each resample should be re-optimized. Default " $\text{optimize.resample} = \text{FALSE}$ " - Only one optimization run, subsequent models use initially determined parameters
tuning.grid	Optional list of grids containing parameters to optimize for each algorithm. Default " $\text{tuning.grid} = \text{NULL}$ " 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 " $\text{k.folds} = 10$ "
repeats	Number of times cross-validation repeated. Default " $\text{repeats} = 3$ "
resolution	Optional - Resolution of model optimization grid. Default " $\text{res} = 3$ "
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 " $\text{model.features} = \text{FALSE}$ "
allowParallel	Logical argument dictating if parallel processing is allowed via foreach package. Default $\text{allowParallel} = \text{FALSE}$
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.

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

Saeys Y., Abeel T., et. al. (2008) *Machine Learning and Knowledge Discovery in Databases*. 313-325. [http://link.springer.com/chapter/10.1007/978-3-540-87481-2\\_21](http://link.springer.com/chapter/10.1007/978-3-540-87481-2_21)

#### 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.

**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" (Elastic-net Generalized Linear Model), and "pam" (Prediction Analysis of Microarrays)
k	Number of bootstrapped iterations
p	Percent of data to by 'trained'
f	Number of features desired. If rank correlation is desired, set "f = NULL"
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	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)
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.
	<ul style="list-style-type: none"> <li>• metric: Stability metric applied</li> <li>• features: Matrix of selected features</li> <li>• stability: Matrix of pairwise comparions and average stability</li> </ul>
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: <ul style="list-style-type: none"> <li>• total.samples: Number of samples in original dataset</li> <li>• number.features: Number of features in orginal dataset</li> <li>• number.groups: Number of groups</li> <li>• group.levels: The specific levels of the groups</li> <li>• number.observations.group: Number of observations in each group</li> </ul>

**Author(s)**

Charles Determan Jr

**References**

Saeys Y., Abeel T., et. al. (2008) *Machine Learning and Knowledge Discovery in Databases*. 313-325. [http://link.springer.com/chapter/10.1007/978-3-540-87481-2\\_21](http://link.springer.com/chapter/10.1007/978-3-540-87481-2_21)

**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

- Jaccard P. (1908) *Nouvelles recherches sur la distribution florale*. Bull. Soc. Vaudoise Sci. Nat. 44: 223-270.
- Real R. & Vargas J.M. (1996) *The Probabilistic Basis of Jaccard's Index of Similarity* Systematic Biology 45(3): 380-385.
- He. Z. & Weichuan Y. (2010) *Stable feature selection for biomarker discovery*. Computational Biology and Chemistry 34 215-225.

### See Also

[kuncheva](#), [sorensen](#), [ochiai](#), [pof](#), [pairwise.stability](#), [pairwise.model.stability](#)

## Examples

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

---

kuncheva

*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

```
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

Kuncheva L. (2007) *A stability index for feature selection*. Proceedings of the 25th IASTED International Multi-Conference: Artificial Intelligence and Applications. pp. 390-395.

He. Z. & Weichuan Y. (2010) *Stable feature selection for biomarker discovery*. Computational Biology and Chemistry 34 215-225.

## 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)
```

---

modellList

*Model List*

---

**Description**

Provide a list of currently implemented methods for OmicsMarkeR.

**Usage**

```
modellList()
```

**Value**

A data.frame containing:

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

**Author(s)**

Charles Determan Jr.

**Examples**

```
modellList()
```

---

 modelTuner

*Model Tuner*


---

### Description

Optimizes each model based upon the parameters provided either by the internal [denovo.grid](#) function or by the user.

### Usage

```
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 <a href="#">tune.instructions</a> . 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	<i>Model Tuner for Leave-One-Out Cross-Validation</i>
----------------	---

---

### Description

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

### Usage

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

### Arguments

<code>trainData</code>	Data used to fit the model
<code>guide</code>	Output from <code>tune.instructions</code> . Facilitates the optimization by avoiding redundant model fitting.
<code>method</code>	Vector of strings listing models to be fit
<code>inTrain</code>	Indices for cross-validated training models
<code>outTrain</code>	Indices for cross-validated testing models
<code>lev</code>	Group levels
<code>savePredictions</code>	Logical argument dictating if should save the prediction data. Default <code>savePredictions = FALSE</code>
<code>allowParallel</code>	Logical argument dictating if parallel processing is allowed via <code>foreach</code> package
<code>verbose</code>	Character argument specifying how much output progress to print. Options are 'none', 'minimal' or 'full'.
<code>theDots</code>	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	<i>Noise Matrix Generator</i>
--------------	-------------------------------

---

**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	<i>Ochiai's Index</i>
--------	-----------------------

---

**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

- Ochiai A. (1957) *Zoogeographical studies on the soleoid fishes found in Japan and its neighbouring regions*. Bulletin of the Japanese Society of Scientific Fisheries. 22: 526-530.
- Zucknick M., Richardson S., & Stronach E.A. (2008) *Comparing the characteristics of gene expression profiles derived by univariate and multivariate classification methods*. Statistical Applications in Genetics and Molecular Biology. 7(1): Article 7. doi:10.2202/1544-6115.1307
- He. Z. & Weichuan Y. (2010) *Stable feature selection for biomarker discovery*. Computational Biology and Chemistry 34 215-225.

## See Also

[kuncheva](#), [sorensen](#), [ochiai](#), [pof](#), [pairwise.stability](#), [pairwise.model.stability](#)

## Examples

```
# 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

```
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" (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   |

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**

He. Z. & Weichuan Y. (2010) *Stable feature selection for biomarker discovery*. Computational Biology and Chemistry 34 215-225.

**See Also**

[pairwise.stability](#)

**Examples**

```
# 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**

He. Z. & Weichuan Y. (2010) *Stable feature selection for biomarker discovery*. Computational Biology and Chemistry 34 215-225.

**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)
```



**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

```
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	<i>Performance Statistics (Internal for perf.calc)</i>
-------------------	--

---

**Description**

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

**Usage**

```
performance.stats(pred, 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	<i>Monte Carlo Permutation of Model Performance</i>
------------	---

---

**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.class(fs.model = NULL, X, Y, method, k.folds = 5,
  metric = "Accuracy", nperm = 10, allowParallel = FALSE,
  create.plot = FALSE, verbose = TRUE, ...)
```

**Arguments**

fs.model	Object containing results from <code>fs.stability</code>
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)

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**

Guo Y., et. al. (2010) *Sample size and statistical power considerations in high-dimensionality data settings: a comparative study of classification algorithms*. BMC Bioinformatics 11:447.

**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')

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**

<code>fs.model</code>	Object containing results from <code>fs.stability</code>
<code>X</code>	A scaled matrix or dataframe containing numeric values of each feature
<code>Y</code>	A factor vector containing group membership of samples
<code>method</code>	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)
<code>sig.level</code>	Desired significance level for features, default <code>sig.level = .05</code>
<code>nperm</code>	Number of permutations, default <code>nperm = 10</code>
<code>allowParallel</code>	Logical argument dictating if parallel processing is allowed via <code>foreach</code> package. Default <code>allowParallel = FALSE</code>
<code>verbose</code>	Logical argument whether output printed automatically in 'pretty' format.
<code>...</code>	Extra arguments that the user would like to apply to the models

**Value**

<code>sig.level</code>	User-specified significance level
<code>num.sig.features</code>	Number of significant features
<code>sig.features</code>	Dataframe of significant features

**Author(s)**

Charles Determan Jr.

**References**

Wongravee K., et. al. (2009) *Monte-Carlo methods for determining optimal number of significant variables. Application to mouse urinary profiles*. *Metabolomics* 5:387-406.

**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

Shi L., et al. (2005) *Cross-platform comparability of microarray technology: intra-platform consistency and appropriate data analysis procedures are essential*. BMC Bioinformatics. 6 (Suppl. 2) S12. He. Z. & Weichuan Y. (2010) *Stable feature selection for biomarker discovery*. Computational Biology and Chemistry 34 215-225.

## 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)
```



**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
beta	Relative of importance of stability versus performance. Default beta = 1 treats stability and performance equally.

**Value**

Harmonic mean of robustness and classification performance

**References**

Saeys Y., Abeel T., et. al. (2008) *Machine Learning and Knowledge Discovery in Databases*. 313-325. [http://link.springer.com/chapter/10.1007/978-3-540-87481-2\\_21](http://link.springer.com/chapter/10.1007/978-3-540-87481-2_21)

**Examples**

```
# 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

**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	<i>Dice-Sorensen's Index</i>
----------	------------------------------

---

**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**

Sorensen T. (1948) *A method of establishing groups of equal amplitude in plant sociology based on similarity of species and its application to analyses of the vegetation on Danish commons*. Kongelige Danske Videnskabernes Selskab. 5(4): 1-34.

Dice, Lee R. (1945) *Measures of the Amount of Ecologic Association Between Species*. Ecology 26 (3): 297-302. doi:10.2307/1932409

He. Z. & Weichuan Y. (2010) *Stable feature selection for biomarker discovery*. Computational Biology and Chemistry 34 215-225.

**See Also**

[kuncheva](#), [sorensen](#), [ochiai](#), [pof](#), [pairwise.stability](#), [pairwise.model.stability](#)

**Examples**

```
# Dice-Sorensen demo
v1 <- paste("Metabolite", seq(10), sep="_")
v2 <- sample(v1, 10)
sorensen(v1, v2)
```

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**

```
# Spearman demo  
v1 <- seq(10)  
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**

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

**Arguments**

model                A fitted SVM model of multiclass

**Value**

Vector of feature weights

**References**

Guyon I. et. al. (2010) *Gene Selection for Cancer Classification using Support Vector Machines*. Machine Learning 46 389-422.

---

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

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

### Arguments

<code>x</code>	A matrix where each column represents a feature and each row represents a sample
<code>y</code>	A vector of labels corresponding to each sample's group membership
<code>c</code>	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.
<code>perc.rem</code>	A numeric value indicating the percent of features removed during each iteration. Default <code>perc.rem = 10</code> .

### Value

Vector of features ranked from most important to least important.

### References

Guyon I. et. al. (2010) *Gene Selection for Cancer Classification using Support Vector Machines*. Machine Learning 46 389-422.

### See Also

[svmrfeFeatureRankingForMulticlass](#)

### 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
```

```
# 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

<code>x</code>	A matrix where each column represents a feature and each row represents a sample
<code>y</code>	A vector of labels corresponding to each sample's group membership
<code>c</code>	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.
<code>perc.rem</code>	A numeric value indicating the percent of features removed during each iteration. Default <code>perc.rem = 10</code> .

### Value

Vector of features ranked from most important to least important.

### References

Guyon I. et. al. (2010) *Gene Selection for Cancer Classification using Support Vector Machines*. Machine Learning 46 389-422.

### See Also

[svmrfeFeatureRanking](#)

**Examples**

```

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
)

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

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

```

training

*Model Training***Description**

This fits each model with the defined parameters

**Usage**

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

**Arguments**

data	Dataframe consisting of both numeric feature values and a single column named '.classes' to denoted 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.



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