

Package ‘classifly’

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Type Package

Title Explore classification models in high dimensions

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Depends rpart, MASS, nnet, class, e1071, reshape

Suggests randomForest, rggobi

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Description Given p -dimensional training data containing d groups (the design space), a classification algorithm (classifier) predicts which group new data belongs to. Generally the input to these algorithms is high dimensional, and the boundaries between groups will be high dimensional and perhaps curvilinear or multi-faceted. This package implements methods for understanding the division of space between the groups.

URL <http://had.co.nz/classifly>

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LazyData true

Collate ‘classification.r’ ‘data.r’ ‘explore.r’ ‘knn.r’

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| | |
|-----------|--|
| advantage | <i>Calculate the advantage the most likely class has over the next most...</i> |
|-----------|--|

Description

Calculate the advantage the most likely class has over the next most likely.

Usage

```
advantage(post)
```

Arguments

| | |
|------|-----------------------------------|
| post | matrix of posterior probabilities |
|------|-----------------------------------|

Details

This is used to identify the boundaries between classification regions. Points with low (close to 0) advantage are likely to be near boundaries.

| | |
|----------|--|
| classify | <i>Classify provides a convenient method to fit a classification function...</i> |
|----------|--|

Description

Classify provides a convenient method to fit a classification function and then explore the results in the original high dimensional space.

Usage

```
classify(data, model, classifier, ..., n=10000,
         method="nonaligned", type="range")
```

Arguments

| | |
|------------|---|
| data | Data set use for classification |
| model | Classification formula, usually of the form response ~ predictors |
| classifier | Function to use for the classification, eg. lda |
| ... | Other arguments passed to classification function. For example. if you use svm you need to use <code>probability = TRUE</code> so that posterior probabilities can be retrieved. |
| n | Number of points to simulate. To maintain the illusion of a filled solid this needs to increase with dimension. 10,000 points seems adequate for up to four of five dimensions, but if you have more predictors than that, you will need to increase this number. |
| method | method to simulate points: grid, random or nonaligned (default). See simvar for more details on the methods used. |
| type | type of scaling to apply to data. Defaults to common range. See rescaler for more details. |

Details

This is a convenient function to fit a classification function and then explore the results using GGobi. You can also do this in two separate steps using the classification function and then [explore](#).

By default in GGobi, points that are not on the boundary (ie. that have an advantage greater than the 5 percentile) are hidden. To show them, switch to brush mode and choose include shadowed points from the brush menu on the plot window. You can then brush them yourself to explore how the certainty of classification varies throughout the space

Special notes:

- You should make sure the response variable is a factor
- For SVM, make sure to include `probability = TRUE` in the arguments to `classify`

See Also

[explore](#), <http://had.co.nz/classify>

Examples

```

classify(kyphosis, Kyphosis ~ . , lda)
classify(kyphosis, Kyphosis ~ poly(Age,2) + poly(Number,2) +
poly(Start,2) , lda)
classify(kyphosis, Kyphosis ~ . , qda)
classify(kyphosis, Kyphosis ~ . , rpart)
classify(kyphosis, Kyphosis ~ . , knnf, k=3)
classify(kyphosis, Kyphosis ~ . , glm, family="binomial")

classify(kyphosis, Kyphosis ~ . , svm, probability=TRUE)
classify(kyphosis, Kyphosis ~ . , svm, probability=TRUE, kernel="linear")
classify(kyphosis, Kyphosis ~ . , best.svm, probability=TRUE,
kernel="linear")

```

```
# Also can use explore directly
bsvm <- best.svm(Species~., data = iris, gamma = 2^(-1:1),
cost = 2^(2:+ 4), probability=TRUE)
explore(bsvm, iris)
```

explore

Default method for exploring objects...

Description

Default method for exploring objects

Usage

```
explore(model, data, n=10000, method="nonaligned",
  advantage=TRUE, ...)
```

Arguments

| | |
|-----------|--|
| model | classification object |
| data | data set used with classifier |
| n | number of points to generate when searching for boundaries |
| method | method to generate points, see generate_data |
| advantage | only display boundaries |
| ... | other arguments not currently used |

Details

The default method currently works for classification functions.

It generates a data set filling the design space, finds class boundaries (if desired) and then displays in a new ggobi instance.

Value

A [invisible](#) data frame of class `classify` that contains all the simulated and true data. This can be saved and then printed later to open with `rggobi`.

See Also

[generate_classification_data](#), <http://had.co.nz/classify>

Examples

```
bsvm <- best.svm(Species~., data = iris, gamma = 2^(-1:1),
cost = 2^(2:+ 4), probability=TRUE)
explore(bsvm, iris)
```

generate_classification_data
Generate classification data.

Description

Generate classification data.

Usage

```
generate_classification_data(model, data, n, method,  
                             advantage)
```

Arguments

| | |
|-----------|---|
| model | classification model |
| data | data set used in model |
| n | number of points to generate |
| method | method to use, currently either grid (an evenly spaced grid), random (uniform random distribution across cube), or nonaligned (grid + some random perturbation) |
| advantage | if TRUE, compute advantage, otherwise don't |

Details

Given a model, this function generates points within the range of the data, classifies them, and attempts to locate boundaries by looking at advantage.

If posterior probabilities of classification are available, then the `advantage` will be calculated directly. If not, `knn` is used to calculate the advantage based on the number of neighbouring points that share the same classification. Because `knn` is $O(n^2)$ this method is rather slow for large (>20,000 say) data sets.

By default, the boundary points are identified as those below the 5th-percentile for advantage.

Value

data.frame of classified data

| | |
|---------------|---|
| generate_data | <i>Generate new data from a data frame.</i> |
|---------------|---|

Description

Generate new data from a data frame.

Usage

```
generate_data(data, n=10000, method="grid")
```

Arguments

| | |
|--------|---|
| data | data frame |
| n | desired number of new observations |
| method | method to use, see simvar |

Details

This method generates new data that fills the range of the supplied datasets.

| | |
|------|---|
| knnf | <i>A wrapper function for knn to allow use...</i> |
|------|---|

Description

A wrapper function for [knn](#) to allow use with `classify`.

Usage

```
knnf(formula, data, k=2)
```

Arguments

| | |
|---------|-----------------------------|
| formula | classification formula |
| data | training data set |
| k | number of neighbours to use |

Olives

Olive oil data

Description

The olive oil data consists of the percentage composition of 8 fatty acids (palmitic, palmitoleic, stearic, oleic, linoleic, linolenic, arachidic, eicosenoic) found in the lipid fraction of 572 Italian olive oils. There are 9 collection areas, 4 from southern Italy (North and South Apulia, Calabria, Sicily), two from Sardinia (Inland and Coastal) and 3 from northern Italy (Umbria, East and West Liguria).

Usage

```
data(olives)
```

Format

A data frame with 244 rows and 7 variables

References

Forina, M. and Armanino, C. and Lanteri, S. and Tiscornia, E., Classification of olive oils from their fatty acid composition, 1983, in Food Research and Data Analysis, edited by Martens, H. and Russwurm Jr, H, pages 189-214.

posterior

Extract posterior group probabilities...

Description

Extract posterior group probabilities

Usage

```
posterior(model, data)
```

Arguments

| | |
|-------|------------------------|
| model | model object |
| data | data set used in model |

Details

Every classification method seems to provide a slightly different way of retrieving the posterior probability of group membership. This function provides a common interface to all of them

| | |
|--------|---|
| simvar | <i>Simulate observations from a vector...</i> |
|--------|---|

Description

Simulate observations from a vector

Usage

```
simvar(x, n=10, method="grid")
```

Arguments

| | |
|--------|--|
| x | data vector |
| n | desired number of points (will not always be achieved) |
| method | grid simulation method. See details. |

Details

Given a vector of data this function will simulate data that could have come from that vector.

There are three methods to choose from:

- nonaligned (default): grid + some random perturbation
- grid: grid of evenly spaced observations. If a factor, all levels in a factor will be used, regardless of n
- random: a random uniform sample from the range of the variable

| | |
|-----------|---|
| variables | <i>Extract predictor and response variables for a model object.</i> |
|-----------|---|

Description

Extract predictor and response variables for a model object.

Usage

```
variables(model)
```

Arguments

| | |
|-------|--------------|
| model | model object |
|-------|--------------|

Details

Due to the way that most model objects are stored, you also need to supply the data set you used with the original data set. It currently doesn't support models fitted without using a data argument.

Value

list containing response and predictor variables

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