Package ‘NBLDA’

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Type Package
Title Negative Binomial Linear Discriminant Analysis
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Description We proposed a package for the classification task which uses Negative Binomial distribution within Linear Discriminant Analysis (NBLDA). It is an extension of the 'PoiClaClu' package to Negative Binomial distribution. The classification algorithms are based on the papers Dong et al. (2016, ISSN: 1471-2105) and Witten, DM (2011, ISSN: 1932-6157) for NBLDA and PLDA, respectively. Although PLDA is a sparse algorithm and can be used for variable selection, the algorithm proposed by Dong et al. is not sparse. Therefore, it uses all variables in the classifier. Here, we extend Dong et al.’s algorithm to the sparse case by shrinking overdispersion towards 0 (Yu et al., 2013, ISSN: 1367-4803) and offset parameter towards 1 (as proposed by Witten DM, 2011). We support only the classification task with this version.

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'control.R' 'copiedFromOtherPackages.R' 'generateCountData.R'
'getShrinkedDispersions.R' 'helper_functions.R'
'normalize_counts.R' 'package_and_supplementary.R'
'plot.nblda.R' 'predict.nblda.R' 'trainNBLDA.R' 'zzz_methods.R'

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NBLDA-package

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NBLDA-package

Classifying count data using Poisson/Negative Binomial linear discriminant analysis

Description

This package applies linear discriminant analysis using Poisson (PLDA) and Negative Binomial (NBLDA) distributions for the classification of count data, such as gene expression data from RNA-sequencing. PLDA algorithms have been proposed by Witten (2011) through an R package PoiClaClu, which is available at CRAN. Dong et al. (2016) proposed an extension of PLDA to negative Binomial distribution. However, the algorithm is not provided through an R package. Hence, we develop an R package NBLDA to make the proposed algorithm available through CRAN. Detailed information about mathematical backgrounds is available in the references given below.
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References

See Also
https://CRAN.R-project.org/package=PoiClaClu

Package: NBLDA
Type: Package
License: GPL (>= 2)

---

cervical  
**Cervical cancer data**

description
Cervical cancer data measures the gene expression levels of 714 miRNAs of human samples. There are 29 tumor and 29 non-tumor cervical samples, and these two groups correspond to two separate classes.

format
A data frame with 58 observations and 715 variables (including the class labels).

source
https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2880020/
References


Examples

## Not run:
data(cervical)

## End(Not run)

control

Accessors for the 'control' slot.

Description

This slot stores control parameters for training NBLDA model.

Usage

## S4 method for signature 'nblda'
control(object)

## S4 method for signature 'nblda_trained'
control(object)

Arguments

object

an nblda or nblda_trained object.

See Also

trainNBLDA

Examples

set.seed(2128)
counts <- generateCountData(n = 20, p = 10, K = 2, param = 1, sdsignal = 0.5, DE = 0.8, allZero.rm = FALSE, tag.samples = TRUE)
x <- t(counts$x + 1)
y <- counts$y
xte <- t(counts$xte + 1)
ctrl <- nbldaControl(folds = 2, repeats = 2)
fit <- trainNBLDA(x = x, y = y, type = "mle", tuneLength = 10, metric = "accuracy", train.control = ctrl)
control(fit)
FindBestTransform

Find the Power Transformation Parameter.

Description

Use this function to find a constant value of alpha to be used for transforming count data. The power transformation parameter alpha, which approximately fits transformed data to the Poisson log-linear model, is selected using a grid search within the interval [0, 1].

Usage

FindBestTransform(x, grid.length = 50)

Arguments

x an n-by-p data frame or matrix of count data. Samples should be in the rows.
grid.length how many distinct points of alpha should be searched within the interval [0, 1]? Default is 50.

Value

the value of alpha to be used within the power transformation.

Note

This function is copied from PoiClaClu package and modified to control the total number of grid search.

Author(s)

Dincer Goksuluk

Examples

set.seed(2128)
counts <- generateCountData(n = 20, p = 10, K = 2, param = 1, sdsignal = 0.5, DE = 0.8, allZero.rm = FALSE, tag.samples = TRUE)

x <- counts$x
FindBestTransform(x)
generateCountData  

**Generate Count Data**

**Description**

This function can be used to generate counts, e.g., RNA-Sequencing data, for both the classification and clustering purposes.

**Usage**

```r
generateCountData(n, p, K, param, sdsignal = 1, DE = 0.3, allZero.rm = TRUE, 
tag.samples = FALSE)
```

**Arguments**

- `n` number of samples.
- `p` number of variables/features.
- `K` number of classes.
- `param` overdispersion parameter. This parameter is matched with the argument `size` in the `rnbinom` function. Hence, the Negative Binomial distribution approximates to the Poisson distribution as `param` increases.
- `sdsignal` a nonzero numeric value. As `sdsignal` increases, the observed counts greatly differs among `K` classes.
- `DE` a numeric value within the interval [0, 1]. This is the proportion of total number of variables that is significantly different among `K` classes. The remaining part is assumed to be having no contribution to the discrimination function.
- `allZero.rm` a logical. If TRUE, the columns having all zero cells are dropped.
- `tag.samples` a logical. If TRUE, the row names are automatically generated using a tag for each sample such as "S1", "S2", etc.

**Value**

- `x, xte` count data matrix for training and test set.
- `y, yte` class labels for training and test set.
- `truesf, truesfte` true size factors for training and test set. See Witten (2011) for more information on estimating size factors.

**Author(s)**

Dincer Goksuluk
getShrinkedDispersions

Examples

```r
set.seed(2128)
counts <- generateCountData(n = 20, p = 10, K = 2, param = 1, sdsignal = 0.5, DE = 0.8,
allZero.rm = FALSE, tag.samples = TRUE)
head(counts$x)
```

getShrinkedDispersions

*Estimate Shrinked Overdispersions*

Description

Use this function to shrink initial estimates of overdispersions towards a target value.

Usage

```r
getShrinkedDispersions(obs, shrinkTarget = NULL, delta = NULL)
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>obs</code></td>
<td>a numeric vector. Initial dispersion estimates for each feature.</td>
</tr>
<tr>
<td><code>shrinkTarget</code></td>
<td>a numeric value. Initial dispersion estimates are shrunk towards this value. If NULL, target value is estimated from the initial dispersion estimates. See notes.</td>
</tr>
<tr>
<td><code>delta</code></td>
<td>a numeric value. This is the weight that is used within the shrinkage algorithm. If 0, no shrinkage is performed on initial values. If equals 1, initial values are forced to be shrunk to the target value. If NULL, weights are automatically estimated from the initial dispersion estimates.</td>
</tr>
</tbody>
</table>

Value

A list with the elements of initial and adjusted (shrunken) dispersion estimates, shrinkage target, and weights that are used to shrink towards the target value. See the related paper for detailed information on shrinkage algorithm (Yu et al., 2013).

<table>
<thead>
<tr>
<th>Element</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>initial</code></td>
<td>initial dispersion estimates using the method-of-moments.</td>
</tr>
<tr>
<td><code>adj</code></td>
<td>shrunken dispersion estimates.</td>
</tr>
<tr>
<td><code>cmp</code></td>
<td>the means and variances of initial estimates.</td>
</tr>
<tr>
<td><code>delta</code></td>
<td>a weight used for shrinkage estimates. See Yu et al. (2013) for details.</td>
</tr>
<tr>
<td><code>target</code></td>
<td>shrinkage target for initial dispersion estimates.</td>
</tr>
</tbody>
</table>

Note

This function is modified from the source codes of `getAdjustDisp` function in the `sSeq` Bioconductor package.
Author(s)
Dincer Goksuluk

References

See Also
getT, getAdjustDisp

Examples
set.seed(2128)
initial <- runif(10, 0, 4)

getShrinkedDispersions(initial, 0)  # shrink towards 0.
getShrinkedDispersions(initial, 0, delta = 1)  # force to shrink 0.

inputs
Accessors for the 'input' slot.

Description
This slot stores the input data for trained model.

Usage
## S4 method for signature 'nblda'
inputs(object)

Arguments
object an nblda object.

See Also
trainNBLDA
Examples

```r
set.seed(2128)
counts <- generateCountData(n = 20, p = 10, K = 2, param = 1, sdsignal = 0.5, DE = 0.8,
allZero.rm = FALSE, tag.samples = TRUE)
x <- t(counts$x + 1)
y <- counts$y
xte <- t(counts$xte + 1)
ctrl <- nbldaControl(folds = 2, repeats = 2)

fit <- trainNBLDA(x = x, y = y, type = "mle", tuneLength = 10,
metric = "accuracy", train.control = ctrl)

inputs(fit)
```

---

nblda-class nblda object

Description

This object is the main class for the NBLDA package. It stores inputs, results, and call info for the trained model.

Details

Objects can be created by calls of the form `new("nblda",...)`. This type of object is returned from `trainNBLDA` function of the NBLDA package. It is then used in `predict` function for predicting class labels of new samples.

Slots

- **input**: an `nblda_input` object including the count matrix (or data.frame) and class labels.
- **result**: an `nblda_trained` object with elements from the cross-validated and final models.
- **call**: a call expression.

Author(s)

Dincer Goksuluk

See Also

- `nblda_trained`, `nblda_input`
nbldaControl  

*Control parameters for trained NBLDA model.*

**Description**

Define control parameters to be used within `trainNBLDA` function.

**Usage**

```r
nbldaControl(folds = 5, repeats = 2, foldIdx = NULL, rhos = NULL, 
beta = 1, prior = NULL, transform = FALSE, alpha = NULL, truephi = NULL, 
target = 0, phi.epsilon = 0.15, normalize.target = FALSE, delta = NULL, 
multicore = FALSE, ...)
```

**Arguments**

- **folds**: A positive integer. The number of folds for k-fold model validation.
- **repeats**: A positive integer. This is the number of repeats for k-fold model validation. If NULL, 0 or negative, it is set to 1.
- **foldIdx**: a list with indices of hold-out samples for each fold. It should be a list where folds are nested within repeats. If NULL, `folds` and `repeats` are used to define hold-out samples.
- **rhos**: A vector of tuning parameters that control the amount of soft thresholding performed. If NULL, it is automatically generated within `trainNBLDA` using `tuneLength`, i.e., the length of grid search. See details.
- **beta**: A smoothing term. A Gamma(beta,beta) prior is used to fit the Poisson model. Recommendation is to just leave it at 1, the default value. See Witten (2011) and Dong et al. (2016) for details.
- **prior**: A vector with a length equal to the number of classes indicates the prior class probabilities. If NULL, all classes are assumed to be equally distributed.
- **transform**: a logical. If TRUE, count data is transformed using power transformation. If alpha is not specified the power transformation parameter is automatically calculated using a goodness-of-fit test. See Witten (2011) for details.
- **alpha**: a numeric value within [0, 1] to be used for power transformation.
- **truephi**: a vector with a length equal to the number of variables. Its elements represent the true overdispersion parameters for each variable. If a single value is given, it is recycled for all variables. If a vector whose length is not equal to the number of variables given, the first element of this vector is used and recycled for all variables. If NULL, estimated overdispersions are used in the classifier. See details.
- **target**: a value for the shrinkage target of dispersion estimates. If NULL, then then a value that is small and minimizes the average squared difference is automatically used as the target value. See `getT` for details.
phi.epsilon  a positive value for controlling the number of features whose dispersions are shrinked towards 0. See details.

normalize.target  a logical. If TRUE and target is NULL, the target value is estimated using the normalized dispersion estimates. See getT for details.

delta  a weight within the interval [0, 1] that is used while shrinking dispersions towards 0. When "delta = 0", initial dispersion estimates are forced to be shrunk to 1. Similarly, if "delta = 0", no shrinkage is performed on the initial estimates.

multicore  a logical. If a parallel backend is loaded and available, the function runs in parallel setting for speeding up the computations.

...  further arguments passed to trainNBLDA.

Details

rhos is used to control the level of sparsity, i.e., the number of variables (or features) used in the classifier. If a variable has no contribution to the discrimination function, it should be removed from the model. By setting rhos within the interval [0, Inf], it is possible to control the number of variables that are removed from the model. As the upper bound of rhos decreases towards 0, fewer variables are removed. If rhos = 0, all variables are included in the classifier.

truephi controls how the Poisson model differs from the Negative Binomial model. If overdispersion is zero, the Negative Binomial model converges to the Poisson model. Hence, the results from trainNBLDA are identical to PLDA results from Classify when truephi = 0.

phi.epsilon is a value used to shrink estimated overdispersions towards 0. The Poisson model assumes that there is no overdispersion in the observed counts. However, this is not a valid assumption in highly overdispersed count data. NBLDA performs a shrinkage on estimated overdispersions. Although the amount of shrinkage is dependent on several parameters such as delta, target, and truephi, some of the shrunken overdispersions might be very close to 0. By defining a threshold value for shrunken overdispersions, it is possible to shrink very small overdispersions towards 0. If estimated overdispersion is below phi.epsilon, it is shrunk to 0. If phi.epsilon = NULL, threshold value is set to 0. Hence, all the variables with very small overdispersion are included in the NBLDA model.

Value

a list with all the control elements.

Author(s)

Dincer Goksuluk

References


See Also
getT, getAdjustDisp

Examples

nbldaControl() # return default control parameters.

---

nbldaTrained

**Accessors for the 'crossValidated' slot.**

**Description**

This slot stores the results for cross-validated model, e.g. tuning results, optimum model parameters etc.

**Usage**

```r
## S4 method for signature 'nblda'
nbldaTrained(object)

## S4 method for signature 'nblda_trained'
nbldaTrained(object)
```

**Arguments**

- `object` an nblda or nblda_trained object.

**See Also**

trainNBLDA

**Examples**

```r
set.seed(2128)
counts <- generateCountData(n = 20, p = 10, K = 2, param = 1, sdsignal = 0.5, DE = 0.8,
                           allZero.rm = FALSE, tag.samples = TRUE)
x <- t(counts$x + 1)
y <- counts$y
xte <- t(counts$xte + 1)
ctrl <- nbldaControl(folds = 2, repeats = 2)

fit <- trainNBLDA(x = x, y = y, type = "mle", tuneLength = 10,
                  metric = "accuracy", train.control = ctrl)

nbldaTrained(fit)
```
### nblda_input-class

**nblda_input object**

**Description**

This object is the subclass for the NBLDA package. It stores input objects, i.e., count data and class labels.

**Slots**

- `x`: a data.frame or matrix containing the count data input for the NBLDA classifier.
- `y`: a vector of length equal to the number of rows of `x`. This is the class label of each subject. Should be either a numeric vector or factor.

**Author(s)**

Dincer Goksuluk

---

### nblda_trained-class

**nblda_trained object**

**Description**

This object is the subclass for the NBLDA package. It stores the cross-validated results and the final model.

**Slots**

- `crossValidated`: a list. Returns the results from cross-validation.
- `finalModel`: a list with the elements from the final model that is fitted using optimum model parameters from the cross-validated model.
- `control`: a list with controlling parameters for fitting NBLDA classifier.

**Author(s)**

Dincer Goksuluk
normalization

Accessors for the 'type' slot.

Description

This slot stores the name of normalization method. Normalization is defined using type argument in trainNBLDA function.

Usage

```r
## S4 method for signature 'nblda'
normalization(object)

## S4 method for signature 'nblda_trained'
normalization(object)
```

Arguments

- `object`: an nblda or nblda_trained object.

See Also

trainNBLDA

Examples

```r
set.seed(2128)
counts <- generateCountData(n = 20, p = 10, K = 2, param = 1, sdsignal = 0.5, DE = 0.8,
allZero.rm = FALSE, tag.samples = TRUE)
x <- t(counts$x + 1)
y <- counts$y
xte <- t(counts$xte + 1)
ctrl <- nbldaControl(folds = 2, repeats = 2)

fit <- trainNBLDA(x = x, y = y, type = "mle", tuneLength = 10,
metric = "accuracy", train.control = ctrl)

normalization(fit)
```
NullModel

**Description**

Fit a training set to the NBLDA model and estimate normalized counts. The related model parameters, which are used while normalizing training sets, are also returned to normalize test sets using training set parameters.

**Usage**

```r
NullModel(x, type = c("mle", "deseq", "quantile", "none", "tmm"))

NullModelTest(null.out, xte = NULL)
```

**Arguments**

- `x`: an n-by-p data frame or matrix of count data. Samples should be in the rows.
- `type`: the normalization method. See `control` for details.
- `null.out`: an object returned from `NullModel`.
- `xte`: an n-by-p count matrix or data frame of test set. These counts are normalized using the training set parameters.

**Value**

a list with the normalized counts and the training set parameters that are used for normalizing the raw counts.

**Note**

These functions are copied from the PoiClaClu package and modified here to make "tmm" and "none" methods available.

**Author(s)**

Dincer Goksuluk

**Examples**

```r
set.seed(2128)
counts <- generateCountData(n = 20, p = 10, K = 2, param = 1, sdsignal = 0.5, DE = 0.8, allZero.rm = FALSE, tag.samples = TRUE)
x <- counts$x
oxte <- counts$xte

x.out <- NullModel(x, "mle")
x.out$n # Normalized counts using "mle" method
```
xte.out <- NullModelTest(x.out, xte)
xte.out$n  # Normalized counts for test set using train set parameters.

---

**Plot Method for the `nblda` and `nblda_trained` Classes**

**Description**

This function is used to generate model performance plots using *ggplot2* functions.

**Usage**

```r
## S3 method for class 'nblda'
plot(
  x,
  y,
  ...,
  theme = c("nblda", "default"),
  metric = c("accuracy", "error", "sparsity"),
  return = c("plot", "aes")
)
```

```r
## S3 method for class 'nblda_trained'
plot(
  x,
  y,
  ...,
  theme = c("nblda", "default"),
  metric = c("accuracy", "error", "sparsity"),
  return = c("plot", "aes")
)
```

```r
## S4 method for signature 'nblda'
plot(
  x,
  y,
  ...,
  theme = c("nblda", "default"),
  metric = c("accuracy", "error", "sparsity"),
  return = c("plot", "aes")
)
```

```r
## S4 method for signature 'nblda_trained'
plot(
  x,
  y,
  ...
)
```r
...,
  theme = c("nblda", "default"),
  metric = c("accuracy", "error", "sparsity"),
  return = c("plot", "aes")
)

Arguments

x  
a nblda object returned from the `trainNBLDA` or nblda_trained object returned from the `nbldaTrained`.
y  
same as x and not required to be defined. If x is missing or NULL, nblda or nblda_trained object is imported from y.
...  
further arguments to be passed to plotting function `ggplot`.
theme  
pre-defined plot themes. It can be defined outside plot function using the ggplot's library. See examples.
metric  
which metric should be used in the y-axis?
return  
should a complete plot or a ggplot object from ggplot be returned? One may select "aes" in order to add plot layers to a returned ggplot aesthetics. See examples.

Value

A list of class ggplot.

Author(s)

Dincer Goksuluk

See Also

ggplot

Examples

```r
set.seed(2128)
counts <- generateCountData(n = 20, p = 10, K = 2, param = 1, sdsignal = 0.5,
  DE = 0.8, allZero.rm = FALSE, tag.samples = TRUE)
x <- t(counts$x + 1)
y <- counts$y
xte <- t(counts$xte + 1)
ctrl <- nbldaControl(folds = 2, repeats = 2)

fit <- trainNBLDA(x = x, y = y, type = "mle", tuneLength = 10,
  metric = "accuracy", train.control = ctrl)

plot(fit)

# Use pre-defined theme
plot(fit, theme = "nblda")
```

# Externally defining plot theme
plot(fit, theme = "default") + theme_dark(base_size = 14)

# Return empty ggplot object and add layers.
plot(fit, theme = "nblda", return = "aes") +
    geom_point() + geom_line(linetype = 2)

## S3 method for class 'nblda'
predict(object, test.data, return = c("predictions", "everything"), ...)

## S4 method for signature 'nblda'
predict(object, test.data, return = c("predictions", "everything"), ...)

object a nblda object returned from the \texttt{trainNBLDA}.
test.data a data frame or matrix whose class labels to be predicted.
return what should be returned? Predicted class labels or everything?
... further arguments to be passed to or from methods.

It is possible to return only predicted class labels or a list with elements which are used within prediction process. These arguments are as follows:

xte count data for test set.
nste normalized count data for test set.
ns estimates of offset parameter for each variable. See notes.
discriminant discriminant scores of each subject.
prior prior probabilities for each class.
ytehat predicted class labels for test set.
alpha power transformation parameter. If no transformation is requested, it returns NULL.
type normalization method.
dispensions dispersion estimates of each variable.
Note

d_{kj} is simply used to re-parameterize the Negative Binomial mean as s_i*g_j*d_{kj} where s_i is the size factor for subject i, g_j is the total count of variable j and d_{kj} is the offset parameter for variable j at class k.

Author(s)

Dincer Goksuluk

Examples

```r
set.seed(2128)
counts <- generateCountData(n = 20, p = 10, K = 2, param = 1, sdsignal = 0.5, DE = 0.8,
   allZero.rm = FALSE, tag.samples = TRUE)
x <- t(counts$x + 1)
y <- counts$y
xte <- t(counts$xte + 1)
ctrl <- nbldaControl(folds = 2, repeats = 2)

fit <- trainNBLDA(x = x, y = y, type = "mle", tuneLength = 10,
   metric = "accuracy", train.control = ctrl)
predict(fit, xte)
```

selectedFeatures

Accessors for the 'selectedFeatures' slot.

Description

This slot, if not NULL, stores the selected features/variables for sparse model.

Usage

```r
## S4 method for signature 'nblda'
selectedFeatures(object)

## S4 method for signature 'nblda_trained'
selectedFeatures(object)
```

Arguments

- **object**: an nblda or nblda_trained object.
show

Value

a list of selected features info including the followings:

idx     column indices of selected features/variables
names   column names of selected features/variables if input data have pre-defined col-
        umn names.

Note

If return.selected.features = FALSE within nbldaControl or all features/variables are se-
lected and used in discrimination function, idx and names are returned NULL.

See Also

trainNBLDA, nblda, nblda_trained

Examples

set.seed(2128)
counts <- generateCountData(n = 20, p = 50, K = 2, param = 1, sdsignal = 0.5, DE = 0.6,
    allZero.rm = FALSE, tag.samples = TRUE)
x <- t(counts$x + 1)
y <- counts$y
xte <- t(counts$xte + 1)
ctrl <- nbldaControl(folds = 2, repeats = 2, return.selected.features = TRUE,
    transform = TRUE, phi.epsilon = 0.10)
fit <- trainNBLDA(x = x, y = y, type = "mle", tuneLength = 10,
    metric = "accuracy", train.control = ctrl)

selectedFeatures(fit)

Description

Pretty print the objects in S4 classes on R console.

Usage

## S3 method for class 'nblda'
show(object)

## S4 method for signature 'nblda'
show(object)
### S3 method for class 'nblda_trained'
show(object)

### S4 method for signature 'nblda_trained'
show(object)

### S3 method for class 'nblda_input'
show(object)

### S4 method for signature 'nblda_input'
show(object)

**Arguments**

- **object**
  - an object of class nblda, nblda_trained and nblda_input to be printed.

**Author(s)**

Dincer Goksuluk

**Examples**

```r
set.seed(2128)
counts <- generateCountData(n = 20, p = 10, K = 2, param = 1, sdsignal = 0.5, DE = 0.8,
                           allZero.rm = FALSE, tag.samples = TRUE)
x <- t(counts$x + 1)
y <- counts$y
xte <- t(counts$xte + 1)
ctrl <- nbldaControl(folds = 2, repeats = 2)

fit <- trainNBLDA(x = x, y = y, type = "mle", tuneLength = 10,
                   metric = "accuracy", train.control = ctrl)

show(fit)
show(inputs(fit))
show(nbldaTrained(fit))
```

---

**trainNBLDA**

*Train Model over Different Tuning Parameters*

**Description**

This function fits the Negative Binomial classifier using various model parameters and finds the best model parameter using the resampling based performance measures.

**Usage**

```r
trainNBLDA(x, y, type = c("mle", "deseq", "quantile", "tmm"),
tuneLength = 10, metric = c("accuracy", "error"), train.control = nbldaControl(), ...)
```
trainNBLDA

Arguments

- **x**: a n-by-p data frame or matrix. Samples should be in the rows and variables in the columns. Used to train the classifier.

- **y**: a vector of length n. Each element corresponds to a class label of a sample. Integer and/or factor types are allowed.

- **type**: a character string indicating the type of normalization method within the NBLDA model. See details.

- **tuneLength**: a positive integer. This is the total number of levels to be used while tuning the model parameter(s) in grid search.

- **metric**: which criteria should be used while determining the best model parameter? overall accuracy or average number of misclassified samples?

- **train.control**: a list with control parameters to be used in the NBLDA model. See nbldaControl for details.

- ... further arguments. Deprecated.

Details

NBLDA is proposed to classify count data from any field, e.g., economics, social sciences, genomics, etc. In RNA-Seq studies, for example, normalization is used to adjust between-sample differences for downstream analysis. type is used to define normalization method. Available options are "mle", "deseq", "quantile", and "tmm". Since "deseq", "quantile", and "tmm" methods are originally proposed as robust methods to be used in RNA-Sequencing studies, one should carefully define normalization types. In greater detail, "deseq" estimates the size factors by dividing each sample by the geometric means of the transcript counts (Anders and Huber, 2010). "tmm" trims the lower and upper side of the data by log-fold changes to minimize the log-fold changes between the samples and by absolute intensity (Robinson and Oshlack, 2010). "quantile" is quantile normalization approach of Bullard et al. (2010). "mle" (less robust) divided total counts of each sample to the total counts (Witten, 2010). See related papers for mathematical backgrounds.

Value

- an nblda object with following slots:
  - **input**: an nblda_input object including the raw count data and response variable. See nblda_input for details.
  - **result**: an nblda_trained object including the results from cross-validated and final models. See nblda_trained for details.
  - **call**: a call expression.

Author(s)

Dincer Goksuluk
References


Examples

```
set.seed(2128)
counts <- generateCountData(n = 20, p = 10, K = 2, param = 1, sdsignal = 0.5, DE = 0.8,
allZero.rm = FALSE, tag.samples = TRUE)
x <- t(counts$x + 1)
y <- counts$y
xte <- t(counts$xte + 1)
ctrl <- nbldaControl(folds = 2, repeats = 2)

fit <- trainNBLDA(x = x, y = y, type = "mle", tuneLength = 10,
metric = "accuracy", train.control = ctrl)

fit
nbldaTrained(fit)  # Cross-validated model summary.
```
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