Package ‘DirichletMultinomial’

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Type Package

Title Dirichlet-Multinomial Mixture Model Machine Learning for Microbiome Data

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Description Dirichlet-multinomial mixture models can be used to describe variability in microbial metagenomic data. This package is an interface to code originally made available by Holmes, Harris, and Quince, 2012, PLoS ONE 7(2): 1-15, as discussed further in the man page for this package, ?DirichletMultinomial.

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Depends S4Vectors, IRanges

Imports stats4, methods, BiocGenerics

Suggests lattice, parallel, MASS, RColorBrewer, xtable


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Description

Dirichlet-multinomial mixture models can be used to describe variability in microbial metagenomic data. This package is an interface to code originally made available by Holmes, Harris, and Quince, 2012, PLoS ONE 7(2): 1-15.

Details

The estimation routine is from the LGPL-licensed (as stated on the corresponding googlecode page) source http://microbedmm.googlecode.com/files/MicrobeDMMv1.0.tar.gz, retrieved 17 February 2012.


Author(s)

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cvdmngroup

Cross-validation on Dirichlet-Multinomial classifiers.

Description

Run cross-validation on Dirichlet-Multinomial generative classifiers.

Usage

cvdmngroup(ncv, count, k, z, ..., verbose = FALSE, 
  .lapply = parallel::mclapply)

Arguments

ncv     integer(1) number of cross-validation groups, between 2 and nrow(count).
count   matrix of sample x taxon counts, subsets of which are used for training and 
        cross-validation.
k       named integer() vector of groups and number of Dirichlet components; e.g., 
        c(Lean=1, Obese=3) performs cross-validation for models with k=1 Dirichlet 
        components for the ‘Lean’ group, k=3 Dirichlet components for ‘Obese’.
z       True group assignment.
...     Additional arguments, passed to dmn during each cross-validation.
verbose logical(1) indicating whether progress should be reported
.lapply A function used to perform the outer cross-validation loop, e.g., lapply for 
        calculation on a single processor, parallel::mclapply for parallel evaluation.

Value

A data.frame summarizing classifications of test samples in cross-validation groups. Columns 
are:

  group       The cross-validation group in which the individual was used for testing.

  additional columns       Named after classification groups, giving the posterior probability of assignment.

Author(s)

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See Also

dmn, DirichletMultinomial-package, vignette("DirichletMultinomial")
Examples

```r
data(xval)  ## result of following commands
head(xval)

## Not run:
## count matrix
fl <- system.file(package="DirichletMultinomial", "extdata",
                   "Twins.csv")
count <- t(as.matrix(read.csv(fl, row.names=1)))

## phenotype
fl <- system.file(package="DirichletMultinomial", "extdata",
                   "TwinStudy.t")
pheno0 <- scan(fl)
lvls <- c("Lean", "Obese", "Overwt")
pheno <- factor(lvls[pheno0 + 1], levels=lvls)
names(pheno) <- rownames(count)

## subset
keep <- c("Lean", "Obese")
count <- count[pheno]
pheno <- factor(pheno[pheno]

## cross-validation, single Dirichlet component for Lean, 3 for Obese
xval <- cvdmngroup(nrow(count), count, c(Lean=1, Obese=3), pheno,
                    verbose=TRUE, mc.preschedule=FALSE)

## End(Not run)
```
Fit Dirichlet-Multinomial models to count data.

**Examples**

```r
data(fit); fit[1:2]
plot(sapply(fit, laplace), type="b")
data(bestgrp); bestgrp
data(xval); head(xval, 3)
```

**Description**

Fit Dirichlet-Multinomial models to a sample x taxon count matrix.

**Usage**

```r
dmn(count, k, verbose = FALSE, seed = runif(1, 0, .Machine$integer.max))
```

**Arguments**

- `count` matrix() of sample x taxon counts.
- `k` integer(1), the number of Dirichlet components to fit.
- `verbose` logical(1) indicating whether progress in fit should be reported.
- `seed` numeric(1) random number seed.

**Details**

This implements Dirichlet-multinomial mixture models describe in the package help page, *DirichletMultinomial-package*.

**Value**

An object of class `dmn`, with elements (elements are usually retrieved via functions defined in the package, not directly).

- `GoodnessOfFit` NLE, LogDet, Laplace, AIC, and BIC criteria assessing goodness-of-fit.
- `Group` matrix of dimension samples x k, providing the Dirichlet parameter vectors.
- `Mixture Weight` numeric() of length k, with relative weight of each component.
- `Fit Lower` matrix() of dimension taxa x k with 95% lower bounds on Dirichlet component vector estimates.
- `Estimate` matrix() of dimension taxa x k with Dirichlet component vector estimates.
- `Upper` matrix() of dimension taxa x k with 95% upper bounds on Dirichlet component vector estimates.

**Author(s)**

Martin Morgan mailto:mtmorgan@fhcrc.org
References

See Also
DirichletMultinomial-package, vignette("DirichletMultinomial")

Examples
data(fit)
## k = 1:7; full example in vignette
lplc <- sapply(fit, laplace)
plot(lplc, type="b")
fit[[which.min(lplc)]]

<table>
<thead>
<tr>
<th>DMN-class</th>
<th>Class &quot;DMN&quot;</th>
</tr>
</thead>
</table>

Description
Result from fitting a Dirichlet-Multinomial model.

Objects from the Class
Objects can be created by calls to dmn.

Slots
The contents of a slot is usually retrieved via the methods described on the mixture help page.

goodnessOfFit NLE, LogDet, Laplace, AIC, and BIC criteria assessing goodness-of-fit.
group matrix of dimension samples x k, providing the Dirichlet parameter vectors.
mixture Weight numeric() of length k, with relative weight of each component.
fit Lower matrix() of dimension taxa x k with 95% lower bounds on Dirichlet component vector estimates.
   Estimate matrix() of dimension taxa x k with Dirichlet component vector estimates.
   Upper matrix() of dimension taxa x k with 95% upper bounds on Dirichlet component vector estimates.

Methods
See the mixture help page.

Author(s)
Martin Morgan mailto:mtmorgan@fhcrc.org
dmngroup

See Also
dmn, mixture.

Examples

```r
data(fit)
fitt[[4]]
```

dmngroup(matrix, group, k, ..., simplify = TRUE, .lapply = parallel::mclapply)

Arguments

- `count` matrix() of sample x taxon counts.
- `group` factor() or vector to be coerced to a factor, with as many elements as there are rows in count, indicating the group to which the corresponding sample belongs.
- `k` integer(), the number(s) of Dirichlet components to fit.
- `...` Additional arguments, passed to dmn.
- `simplify` Return only the best-fit model for each group?
- `.lapply` An lapply-like function for application of group x k fits.

Details

This function divided count into groups defined by group, creates all combinations of group x k, and evaluates each using dmn. When simplify=TRUE, the best (Laplace) fit is selected for each group.

Value

An object of class dmngroup, a list of fitted models of class dmn. When simplify=TRUE, elements are named by the group to which they correspond.

Author(s)

Martin Morgan mailto:mtmorgan@fhcrc.org
References


See Also
dmn, DirichletMultinomial-package, vignette("DirichletMultinomial")

Examples

```r
## best fit for groups 'Lean' and 'Obese'; full example in vignette.
## Not run: bestgrp <- dmngroup(count, pheno, k=1:5, verbose=TRUE,
## mc.preschedule=FALSE)
## End(Not run)
data(bestgrp)
bestgrp
bestgrp[["Obese"]]
```

---

DMNGroup-class

Class "DMNGroup"

Description

Result from fitting a Dirichlet-Multinomial generative classifier.

Objects from the Class

Objects can be created by calls to dmngroup.

Slots

All slots in this class are inherited from SimpleList; see 'Methods', below, for information on how to manipulate this object.

Extends


Methods

See the mixture help page for functions that operate on DMNGroup and DMN. DMNGroup can be manipulated as a list; see SimpleList for a description of typical list-like functions.

Author(s)

Martin Morganmailto:mtmorgan@fhcrc.org
**heatmapdmn**

See Also

*mixture, DMN, SimpleList.*

Examples

```r
data(bestgrp)
bestgrp
bestgrp[[1]]
```

<table>
<thead>
<tr>
<th>heatmapdmn</th>
<th>Heatmap representation of samples assigned to Dirichlet components.</th>
</tr>
</thead>
</table>

**Description**

Produce a heat map summarizing count data, grouped by Dirichlet component.

**Usage**

```r
heatmapdmn(count, fit1, fitN, ntaxa = 30, ..., 
transform = sqrt, lblwidth = 0.2 * nrow(count), col = .gradient)
```

**Arguments**

- `count`: A matrix of sample x taxon counts, as supplied to `dmn`.
- `fit1`: An instance of class `dmn`, from a model fit to a single Dirichlet component, k=1 in `dmn`.
- `fitN`: An instance of class `dmn`, from a model fit to N != 1 components, k=N in `dmn`.
- `ntaxa`: The `ntaxa` most numerous taxa to display counts for.
- `...`: Additional arguments, ignored.
- `transform`: Transformation to apply to count data prior to visualization; this does not influence mixture membership or taxonomic ordering.
- `lblwidth`: The proportion of the plot to dedicate to taxonomic labels, as a fraction of the number of samples to be plotted.
- `col`: The colors used to display (possibly transformed, by `transform`) count data, as used by `image`.

**Details**

Columns of the heat map correspond to samples. Samples are grouped by Dirichlet component, with average (Dirichlet) components summarized as a separate wide column. Rows correspond to taxonomic groups, ordered based on contribution to Dirichlet components.

**Author(s)**

Martin Morgan `mailto:mtmorgan@fhcrc.org`
Examples

```r
## counts
fl <- system.file(package="DirichletMultinomial", "extdata", "Twins.csv")
count <- t(as.matrix(read.csv(fl, row.names=1)))

## all and best-fit clustering
data(fit)
lplc <- sapply(fit, laplace)
best <- fit[[which.min(lplc)]]

heatmapdmn(count, fit[[1]], best, 30)
```

Description

The accessors mixture and mixturewt return information about the estimated Dirichlet components of the fitted model. Return values are described in the Values section, below.

Usage

```r
mixture(object, ..., assign=FALSE)
mixturewt(object, ...)
goodnessOfFit(object, ...)
laplace(object, ...)
## S4 method for signature 'DMN'
AIC(object, ..., k = 2)
## S4 method for signature 'DMN'
BIC(object, ...)

## S4 method for signature 'DMN'
fitted(object, ..., scale=FALSE)
## S4 method for signature 'DMN'
predict(object, newdata, ..., logevidence=FALSE)
## S4 method for signature 'DMNGroup'
fitted(object, ...)
## S4 method for signature 'DMNGroup'
predict(object, newdata, ..., assign=FALSE)
## S4 method for signature 'DMNGroup'
summary(object, ...)
```

Arguments

object An instance of class dmn.
newdata A matrix of new sample x taxon data to be fitted to the model of object.
roc

... Additional arguments, available to methods, when applicable.

assign logical(1) indicating whether the maximum per-sample mixture component should be returned (assign=FALSE), or the full mixture matrix (assign=TRUE).

scale logical(1) indicating whether fitted values should be returned unscaled (default, scaled=FALSE) or scaled by the variability of mixturewt parameter theta.

logevidence logical(1) indicating whether posterior probability (default, logevidence=FALSE) or log evidence logical=TRUE should be returned.

k ignored.

Value

mixture with assign=FALSE returns a matrix of sample x Dirichlet component estimates. With assign=TRUE mixture returns a named vector indexing the maximal Dirichlet component of each sample.

mixturewt returns a matrix with rows corresponding to mixture components, and columns pi (component weight) and theta (component variability). Small values of theta correspond to highly variable components.

goodnessOfFit returns a named numeric vector of measures of goodness of fit.

laplace, AIC, and BIC return the corresponding measures of goodness of fit.

Author(s)

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Examples

data(fit)
best <- fit[[4]]
mixturewt(best)
head(mixture(best), 3)
head(mixture(best, assign=TRUE), 3)
goodnessOfFit(best)

fl <- system.file(package="DirichletMultinomial", "extdata", "Twins.csv")
count <- t(as.matrix(read.csv(fl, row.names=1)))
data(bestgrp)
bestgrp
head(predict(bestgrp, count))

detectorroc

Summarize receiver-operator characteristics

Description

Returns a data.frame summarizing the cumulative true- and false-positive probabilities from expected and observed classifications.
Usage

roc(exp, obs, ...)

Arguments

exp logical() vector of expected classifications to a particular group.
obs Predicted probability of assignment to the group identified by TRUE values in exp. The length of exp and obs must be identical.
... Additional arguments, available to methods.

Value

A data.frame with columns

TruePositive Cummulative probability of correct assignment.
FalsePositive Cummulative probability of incorrect assignment.

Author(s)

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Examples

library(lattice)

## count matrix
fl <- system.file(package="DirichletMultinomial", "extdata", "Twins.csv")
count <- t(as.matrix(read.csv(fl, row.names=1)))

## phenotype
fl <- system.file(package="DirichletMultinomial", "extdata", "TwinStudy.t")
pheno0 <- scan(fl)
lvls <- c("Lean", "Obese", "Overwt")
pheno <- factor(lvls[pheno0 + 1], levels=lvls)
names(pheno) <- rownames(count)

## count data used for cross-validation, and cross-validation
count <- csubset(c("Lean", "Obese"), count, pheno)
data(bestgrp)

## true, false positives from single-group classifier
bst <- roc(pheno[rownames(count)] == "Obese",
predict(bestgrp, count)[,"Obese"])
head(bst)

## lattice plot
xyplot(TruePostive ~ FalsePositive, bst, type="l",
       xlab="False Positive", ylab="True Positive")

csubset creates a subset of a count matrix, based on identity of column phenotypes to a specified value.

Usage

csubset(val, x, pheno, cidx = TRUE)

Arguments

val character(1) specifying the subset of phenotype to select.

x A matrix of counts, with rows corresponding to samples and columns to taxonomic groups.

pheno A character() vector of length equal to the number of rows in count, indicating the phenotype of the corresponding sample.

cidx A logical(1) indicating whether columns (taxa) with zero counts in the count matrix following removal of taxa not satisfying pheno %in% val should be removed. cidx=FALSE removes the 0-count columns.

Value

A matrix of counts, with rows satisfying pheno %in% val and with columns equal either to ncol(x) (when cidx=TRUE) or the number of columns with non-zero counts after row subsetting (cidx=FALSE).

Author(s)

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Examples

```R
## count matrix
fl <- system.file(package="DirichletMultinomial", "extdata", "Twins.csv")
count <- t(as.matrix(read.csv(fl, row.names=1)))

## phenotype
fl <- system.file(package="DirichletMultinomial", "extdata", "TwinStudy.t")
pheno0 <- scan(fl)
lvls <- c("Lean", "Obese", "Overwt")
pheno <- factor(lvls[pheno0 + 1], levels=lvls)
names(pheno) <- rownames(count)

## subset
```
dim(count)
sum("Lean" == pheno)
dim(csubset("Lean", count, pheno))
dim(csubset("Lean", count, pheno, cidx=FALSE))
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