Package 'DirichletMultinomial'

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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 This package is an interface to code originally made available by Holmes, Harris, and Quince, 2012, PLoS ONE 7(2): 1-15, as discussed further in the man page for this package, ?DirichletMultinomial.

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`DirichletMultinomial-package`
Dirichlet-Multinomial Mixture Model Machine Learning for Microbiome Data

---

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 This package is an interface to code originally made available by Holmes, Harris, and Qunice, 2012, PLoS ONE 7(2): 1-15.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 Feburary 2012.

The algorithm is described in Holmes I, Harris K, Quince C, 2012 Dirichlet Multinomial Mixtures: Generative Models for Microbial Metagenomics. PLoS ONE 7(2): e30126. doi:10.1371/journal.pone.0030126.

Author(s)

Maintainer: Martin Morgan `mailto:mtmorgan.xyz@gmail.com`

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-vaildation 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 indivdual was used for testing.
additional columns	Named after classification groups, giving the posterior probability of assignment.

Author(s)

Martin Morgan mailto:mtmorgan.xyz@gmail.com

See Also

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

Examples

```
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)
```

`data` *Data objects used for examples and the vignette*

Description

These data objects correspond to steps in a typical work flow, as described in the vignette to this package. `fit` corresponds to `dmn` fits to different values of `k`. `bestgroup` is the result of the two-group generative classifier. `xval` summarizes leave-one-out cross validation of the classifier.

Usage

```
data(fit)
data(bestgrp)
data(xval)
```

Format

`fit` is a list of seven `DMN` objects.

`bestgrp` is a `DMNGroup` object.

`xval` is a `data.frame` with columns corresponding to the cross-validation group membership and the Lean and Obese posterior probabilities.

Examples

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

---

dmn *Fit Dirichlet-Multinomial models to count data.*

Description

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

Usage

```
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.xyz@gmail.com

References

Holmes I, Harris K, Quince C, 2012 Dirichlet Multinomial Mixtures: Generative Models for Microbial Metagenomics. PLoS ONE 7(2): e30126. doi:10.1371/journal.pone.0030126.

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)]]
```

DMN-class *Class* "DMN"

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.xyz@gmail.com`

See Also

dmn, mixture.

Examples

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

---

dmngroup *Dirichlet-Multinomial generative classifiers.*

Description

Fit Dirichlet-Multinomial generative classifiers to groups (rows) within a sample x taxon count matrix.

Usage

```
dmngroup(count, 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.xyz@gmail.com

References

Holmes I, Harris K, Quince C, 2012 Dirichlet Multinomial Mixtures: Generative Models for Microbial Metagenomics. PLoS ONE 7(2): e30126. doi:10.1371/journal.pone.0030126.

See Also

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

Examples

```
## 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 inheritted from SimpleList; see 'Methods', below, for information on how to manipulate this object.

Extends

Class "SimpleList", directly. Class "List", by class "SimpleList", distance 2. Class "Vector", by class "SimpleList", distance 3. Class "Annotated", by class "SimpleList", distance 4.

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 Morgan mailto:mtmorgan.xyz@gmail.com

See Also

mixture, DMN, SimpleList.

Examples

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

---

heatmapdmn *Heatmap representation of samples assigned to Dirichlet components.*

Description

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

Usage

```
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 taxanomic 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.xyz@gmail.com

Examples

```
## 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)
```

`model components` *Access model components.*

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

```
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`.

...	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))
```

---

roc *Summarize receiver-operator characteristics*

Description

Returns a data.frame summarizing the cummulative 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)

Martin Morgan mailto:mtmorgan.xyz@gmail.com

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")
```

Utilities *Helpful utility functions*

Description

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

```
## 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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