Package ‘DirichletMultinomial’

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DirichletMultinomial-package

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 This package is an interface to code originally made available by Holmes, Harris, and Qunice, 2012, PLoS ONE 7(2): 1-15.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

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@fhcrc.org

References


See Also

DirichletMultinomial-package, vignette("DirichletMultinomial")

Examples

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

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`

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**

```r
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@fhcrc.org](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)
```

```r
## 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)

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See Also

`mixture`, `DMN`, `SimpleList`.

Examples

```r
data(bestgrp)
bestgrp
bestgrp[[1]]
```
Heatmap representation of samples assigned to Dirichlet components.

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)
```
model components

Access model components.

Description

The accessors `mixture` and `mixturewt` return information about the estimated Dirichlet components of the fitted model. `mixture` returns a sample x component matrix of estimated values, `mixturewt` returns a matrix of

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 'DMNGroup'
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.
mixtrewt 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))
Author(s)

Martin Morgan mailto:mtmorgan@fhcrc.org

Examples

```r
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")
lvls <- c("Lean", "Obese", "Overwt")
pheno <- factor(lvls[pheno0 + 1], levels=lvls)
names(pheno) <- rownames(count)

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)

Martin Morgan mailto:mtmorgan@fhcrc.org

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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