Package: FinfoMDS (via r-universe)

May 24, 2026

Type Package

Title Multidimensional Scaling with F-ratio for microbiome visualization

Version 1.2.0

Description F-informed MDS is a new multidimensional scaling-based ordination method that configures data distribution based on the F-statistic (i.e., the ratio of dispersion between groups with shared or differing labels).

License GPL-3

Encoding UTF-8

Suggests testthat (>= 3.0.0), knitr, rmarkdown, BiocStyle

VignetteBuilder knitr

biocViews DimensionReduction, MultidimensionalScaling, Visualization, Microbiome

URL https://github.com/soob-kim/FinfoMDS

BugReports https://github.com/soob-kim/FinfoMDS/issues

RoxygenNote 7.3.2

Imports phyloseq

Depends R (>= 4.4.0)

Config/testthat/edition 3

Config/pak/sysreqs libglpk-dev libicu-dev libxml2-dev zlib1g-dev

Repository https://bioc-release.r-universe.dev

Date/Publication 2026-04-28 13:05:27 UTC

RemoteUrl https://github.com/bioc/FinfoMDS

RemoteRef RELEASE_3_23

RemoteSha 01f9363f6ce7128f134d360cb946d9827cbea593

Contents

`fmds` *FMDS calculation using MM algorithm*

Description

FMDS calculation using MM algorithm

Usage

```
fmds(D = NULL, y, X, nit = 100, lambda = 0.5, threshold_p = 0.05, z0 = NULL)
```

Arguments

`D`	Square matrix of pairwise distance, size of N by N
`y`	Vector of label or group set, size of N
`X`	Object matrix; used to build distance matrix D; D is prioritized
`nit`	Number of iterations; 100 by default
`lambda`	Hyperparameter; 0.5 by default
`threshold_p`	Lower limit of p-value difference that allows iteration
`z0`	Initialization of configuration; NULL by default

Value

2D representation vector, size of N by 2

Examples

```
set.seed(100)
require(phyloseq)
data(microbiome)
D <- distance(microbiome, method = 'wunifrac') # requires phyloseq package
y <- sample_data(microbiome)$Treatment
z0 <- cmdscale(d = D)
fmds(z0 = z0, D = D, y = y)
```

`getDistMat` *Distance between vectors*

Description

Distance between vectors

Usage

```
getDistMat(z)
```

Arguments

`z`	Matrix or vector of observations

Value

Distance matrix

Examples

```
set.seed(100)
z <- rbind(matrix(rnorm(100), ncol=4),
matrix(rnorm(100, 2), ncol=4))
getDistMat(z)
```

`getIndMat` *Get index matrix*

Description

Get index matrix

Usage

```
getIndMat(y)
```

Arguments

`y`	a vector of treatments of length N

Value

A N by N matrix of indicators of equal treatment

Examples

```
require(phyloseq)
data(microbiome)
y <- sample_data(microbiome)$Treatment
getIndMat(y)
```

`getP` *Compute p-value from PERMANOVA test*

Description

Compute p-value from PERMANOVA test

Usage

```
getP(z = NULL, D = NULL, y, n_iter = 999)
```

Arguments

`z`	Object matrix; used to build distance matrix d; d is prioritized
`D`	Distance matrix; if NULL, obtain from mat using Euclidean distance
`y`	Vector of treatments
`n_iter`	Number of iterations; defaults to 999

Value

list of ratio_all: vector of obtained pseudo-F values from permutations, ratio: pseudo-F value, p: p-value from PERMANOVA

Examples

```
require(phyloseq)
data(microbiome)
D <- distance(microbiome, method = 'wunifrac') # requires phyloseq package
y <- sample_data(microbiome)$Treatment
getP(D = D, y = y)
```

`mdsObj` *Objective term of MDS*

Description

Objective term of MDS

Usage

```
mdsObj(D, z, N)
```

Arguments

`D`	Original distance matrix
`z`	Lower dimension representation
`N`	Number of observations–scaling factors

Value

Scalar of objective function value of MDS

Examples

```
require(phyloseq)
data(microbiome)
D <- distance(microbiome, method = 'wunifrac') # requires phyloseq package
z0 <- cmdscale(d = D)
N <- dim(z0)[1]
mdsObj(D = D, z = z0, N = N)
```

`microbiome` *Microbiome dataset*

Description

A phyloseq-class object representing an example microbial community dataset. The dataset consists of 36 microbiome samples, half of which were co-cultured with their diatom host (Phaeodactylum tricornutum). Each microbiome comprises 72 bacterial taxa identified by amplicon sequence variants (ASVs) of the 16S rRNA gene. ASV counts represent relative abundances after applying the cumulative sum scaling (CSS) method.

Usage

```
data(microbiome)
```

Format

A phyloseq-class object.

Value

A phyloseq-class object consisting of relative abundance table, taxonomy table, sample dataframe, and phylogenetic tree

Source

Data derived from an experimental study on host-microbe interactions.

References

Kim H., Kimbrel J.A., Vaiana C.A., Wollard J.R., Mayali X., Buie C.R. (2022). Bacterial response to spatial gradients of algal-derived nutrients in a porous microplate. *The ISME Journal*, 16(4), 1036–1045. doi:10.1038/s41396021011634

`pairByRank` *Get p-value matrix*

Description

Get p-value matrix

Usage

```
pairByRank(z, D, y)
```

Arguments

`z`	Lower dimension representation
`D`	Original distance matrix
`y`	Treatment vector

Value

pseudo-F values matrix 1st col of original data, 2nd col of reduced dim

Examples

```
require(phyloseq)
data(microbiome)
D <- distance(microbiome, method = 'wunifrac') # requires phyloseq package
y <- sample_data(microbiome)$Treatment
z0 <- cmdscale(d = D)
pairByRank(z = z0, D = D, y = y)
```

`pseudoF` *Compute pseudo-F statistic for PERMANOVA*

Description

Compute pseudo-F statistic for PERMANOVA

Usage

```
pseudoF(z = NULL, D = NULL, y)
```

Arguments

`z`	Object matrix; used to build distance matrix d; d is prioritized
`D`	Distance matrix; if NULL, obtain from mat using Euclidean distance
`y`	Vector of treatments

Value

pseudo-F value

Examples

```
require(phyloseq)
data(microbiome)
D <- distance(microbiome, method = 'wunifrac') # requires phyloseq package
y <- sample_data(microbiome)$Treatment
pseudoF(D = D, y = y)
```

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