

# Package ‘FinfoMDS’

December 10, 2025

**Type** Package

**Title** Multidimensional Scaling with F-ratio for microbiome  
visualization

**Version** 1.1.0

**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

**git\_url** <https://git.bioconductor.org/packages/FinfoMDS>

**git\_branch** devel

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**Author** Soobin Kim [aut, cre],  
Hyungseok Kim [aut]

**Maintainer** Soobin Kim <soob.kim00@gmail.com>

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|      |                                            |
|------|--------------------------------------------|
| fmds | <i>FMDS calculation using MM algorithm</i> |
|------|--------------------------------------------|

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### 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)
```

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|            |                                 |
|------------|---------------------------------|
| getDistMat | <i>Distance between vectors</i> |
|------------|---------------------------------|

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**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)
```

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|           |                         |
|-----------|-------------------------|
| getIndMat | <i>Get index matrix</i> |
|-----------|-------------------------|

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**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)
```

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|        |                              |
|--------|------------------------------|
| mdsObj | <i>Objective term of MDS</i> |
|--------|------------------------------|

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**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)
```

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|            |                           |
|------------|---------------------------|
| microbiome | <i>Microbiome dataset</i> |
|------------|---------------------------|

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**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](https://doi.org/10.1038/s41396021011634)

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|            |                           |
|------------|---------------------------|
| pairByRank | <i>Get p-value matrix</i> |
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**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)
```

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

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**Description**

Compute pseudo-F statistic for PERMANOVA

**Usage**

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

**Arguments**

|                |                                                                                               |
|----------------|-----------------------------------------------------------------------------------------------|
| <code>z</code> | Object matrix; used to build distance matrix <code>d</code> ; <code>d</code> is prioritized   |
| <code>D</code> | Distance matrix; if <code>NULL</code> , obtain from <code>mat</code> using Euclidean distance |
| <code>y</code> | 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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