

Package ‘lefse’

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Type Package

Title Phylogenetic and Functional Analyses for Ecology

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Description Utilizing phylogenetic and functional information for the analyses of ecological datasets. The analyses include methods for quantifying the phylogenetic and functional diversity of assemblages.

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Depends R (>= 2.10)

Imports ape, picante, geiger, fBasics, SDMTools, vegan

NeedsCompilation no

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com.trait.moments *com.trait.moments*

Description

Quantifies the moments of the community trait distribution

Usage

```
com.trait.moments(my.sample, traits)
```

Arguments

my.sample	A community data matrix.
traits	A trait file with species names as row names and trait as columns.

Details

Quantifies the moments of the community trait distribution

Value

com.mean The mean trait value of the community
com.sd The standard deviation of the trait values in the community
com.skew The skewness of the trait values in the community
com.kurt The kurtosis of the trait values in the community

Author(s)

Nathan G. Swenson

References

Swenson, N.G. 2014. Functional and Phylogenetic Ecology in R. Springer UseR! Series, Springer, New York, New York, U.S.A.

See Also

[com.trait.weighted](#)

Examples

```
data(lefse.sample)
data(lefse.traits)
com.trait.moments(lefse.sample, lefse.traits)
```

com.trait.weighted	<i>Quantifies the moments of the community trait distribution weighted by abundance</i>
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Description

Quantifies the moments of the community trait distribution weighted by abundance

Usage

```
com.trait.weighted(my.sample, traits)
```

Arguments

my.sample	A community data matrix.
traits	A trait file with species names as row names and trait as columns.

Details

Quantifies the moments of the community trait distribution weighted by abundance

Value

com.weighted.mean The abundance weighted mean trait value in the community.

com.weighted.sd The abundance weighted standard deviation of trait values in the community.

Author(s)

Nathan G. Swenson

References

Swenson, N.G. 2014. Functional and Phylogenetic Ecology in R. Springer UseR! Series, Springer, New York, New York, U.S.A.

See Also

[com.trait.moments](#)

Examples

```
data(lefse.sample)
data(lefse.traits)
com.trait.weighted(lefse.sample, lefse.traits)
```

Fmntd

Functional NND

Description

Quantifies the functional mean nearest neighbor distance with no abundance weighting

Usage

```
Fmntd(dist.mat, my.sample)
```

Arguments

<code>dist.mat</code>	A trait distance matrix.
<code>my.sample</code>	A community data matrix.

Details

Quantifies the functional mean nearest neighbor distance without abundance weighting

Value

Fntda The presence-absence weighted mean nearest functional neighbor distance for each community

Author(s)

Nathan G. Swenson

References

Swenson, N.G. 2014. Functional and Phylogenetic Ecology in R. Springer UseR! Series, Springer, New York, New York, U.S.A.

See Also

[Fmntd.a](#)

Examples

```
data(lefse.sample)
data(lefse.traits)

Fmntd(as.matrix(dist(lefse.traits)), lefse.sample)
```

`Fmntd.a`*Functional NND with abundance*

Description

Quantifies the functional mean nearest neighbor distance with abundance weighting

Usage

```
Fmntd.a(dist.mat, my.sample)
```

Arguments

<code>dist.mat</code>	A trait distance matrix.
<code>my.sample</code>	A community data matrix.

Details

Quantifies the functional mean nearest neighbor distance with abundance weighting

Value

Fntda.a The abundance weighted mean nearest functional neighbor distance for each community

Author(s)

Nathan G. Swenson

References

Swenson, N.G. 2014. Functional and Phylogenetic Ecology in R. Springer UseR! Series, Springer, New York, New York, U.S.A.

See Also

[Fmntd](#)

Examples

```
data(lefse.sample)
data(lefse.traits)
```

```
Fmntd.a(as.matrix(dist(lefse.traits)), lefse.sample)
```

`Fmpd`*Functional MPD no with abundance*

Description

Quantifies the functional mean pairwise distance with no abundance weighting

Usage

```
Fmpd(dist.mat, my.sample)
```

Arguments

<code>dist.mat</code>	A trait distance matrix.
<code>my.sample</code>	A community data matrix.

Details

Quantifies the functional mean pairwise distance without abundance weighting

Value

Fntda.a The presence-absence weighted mean pairwise distance for each community

Author(s)

Nathan G. Swenson

References

Swenson, N.G. 2014. Functional and Phylogenetic Ecology in R. Springer UseR! Series, Springer, New York, New York, U.S.A.

See Also

[Fmpd.a](#)

Examples

```
data(lefse.sample)
data(lefse.traits)

Fmpd(as.matrix(dist(lefse.traits)), lefse.sample)
```

`Fmpd.a`*Functional MPD with abundance*

Description

Quantifies the functional mean pairwise distance with abundance weighting

Usage

```
Fmpd.a(dist.mat, my.sample)
```

Arguments

<code>dist.mat</code>	A trait distance matrix.
<code>my.sample</code>	A community data matrix.

Details

Quantifies the functional mean pairwise distance with abundance weighting

Value

Fntda.a The abundance weighted mean pairwise distance for each community

Author(s)

Nathan G. Swenson

References

Swenson, N.G. 2014. Functional and Phylogenetic Ecology in R. Springer UseR! Series, Springer, New York, New York, U.S.A.

See Also

[Fmpd](#)

Examples

```
data(lefse.sample)
data(lefse.traits)

Fmpd.a(as.matrix(dist(lefse.traits)), lefse.sample)
```

Fsntd

Functional standard deviation of the NND

Description

Quantifies the functional standard deviation of the nearest neighbor distance with no abundance weighting

Usage

```
Fsntd(dist.mat, my.sample)
```

Arguments

<code>dist.mat</code>	A trait distance matrix.
<code>my.sample</code>	A community data matrix.

Details

Quantifies the functional standard deviation of the nearest neighbor distance without abundance weighting

Value

Fsntd The presence-absence weighted standard deviation of the nearest functional neighbor distance for each community

Author(s)

Nathan G. Swenson

References

Swenson, N.G. 2014. Functional and Phylogenetic Ecology in R. Springer UseR! Series, Springer, New York, New York, U.S.A.

See Also

[sntd.a](#)

Examples

```
data(lefse.sample)
data(lefse.traits)

Fsntd(as.matrix(dist(lefse.traits)), lefse.sample)
```

lefse.sample	<i>Community data matrix for lefse</i>
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Description

Community data matrix for lefse package. Matrix contains 10 species and 5 communities

Usage

```
data("lefse.sample")
```

Format

A data frame with 5 observations on the following 10 variables.

Source

Swenson, N.G. 2014. Functional and Phylogenetic Ecology in R. Springer UseR! Series, Springer, New York, New York, U.S.A.

Examples

```
data(lefse.sample)
lefse.sample
rowSums(lefse.sample)
```

lefse.traits	<i>Example trait dataset for lefse</i>
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Description

Example trait dataset for lefse package. The trait matrix contains 10 species and 3 traits

Usage

```
data("lefse.traits")
```

Format

A data frame with 10 observations on the following 3 variables.

Source

Swenson, N.G. 2014. Functional and Phylogenetic Ecology in R. Springer UseR! Series, Springer, New York, New York, U.S.A.

Examples

```
data(lefse.traits)
lefse.traits
hist(lefse.traits[,1])
```

`sntd.a`*Functional standard deviation of the NND with abundance weighting*

Description

Quantifies the functional standard deviation of the nearest neighbor distance with abundance weighting

Usage

```
sntd.a(dist.mat, my.sample)
```

Arguments

<code>dist.mat</code>	A trait distance matrix.
<code>my.sample</code>	A community data matrix.

Details

Quantifies the functional standard deviation of the nearest neighbor distance with abundance weighting

Value

sntd.a The abundance weighted standard deviation of the nearest functional neighbor distance for each community

Author(s)

Nathan G. Swenson

References

Swenson, N.G. 2014. Functional and Phylogenetic Ecology in R. Springer UseR! Series, Springer, New York, New York, U.S.A.

See Also

[Fsntd](#)

Examples

```
data(lefse.sample)
data(lefse.traits)

sntd.a(as.matrix(dist(lefse.traits)), lefse.sample)
```

trait.range	<i>Range of trait values in a community</i>
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Description

Quantifies the range of trait values present in a community

Usage

```
trait.range(my.sample, traits)
```

Arguments

my.sample	A community data.matrix.
traits	A trait matrix.

Details

Quantifies the the range of trait values in each community.

Value

trait.range The range of trait values for each community.

Examples

```
data(lefse.sample)
data(lefse.traits)

trait.range(lefse.sample, lefse.traits)
```

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