

# Package ‘Microbialdiversity’

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**Title** What the Package Does (One Line, Title Case)

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**Description** What the package does (one paragraph).

**License** MIT + file LICENSE

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`calculate_inverse_simpson`*Calculate Inverse Simpson Diversity Index*

---

**Description**

This function calculates the Inverse Simpson diversity index for a vector of species counts or proportions. The Inverse Simpson index ranges from 1 (low diversity) to the number of species (high diversity).

**Usage**

```
calculate_inverse_simpson(abundances)
```

**Arguments**

`abundances`      A numeric vector of species counts or proportions.

**Value**

The Inverse Simpson diversity index.

**Author(s)**

Akinsuyi Oluwamayowa Samuel

**Examples**

```
# Example with equal abundances
calculate_inverse_simpson(c(1, 1, 1, 1)) # Should return 4

# Example with unequal abundances
calculate_inverse_simpson(c(10, 20, 30, 40)) # Should return ~3.57
```

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`calculate_observed_otus`*Calculate Observed OTUs*

---

**Description**

This function calculates the number of observed OTUs (Operational Taxonomic Units) or ASVs (Amplicon Sequence Variants) in a sample by counting non-zero abundances.

**Usage**

```
calculate_observed_otus(abundances)
```

**Arguments**

`abundances`      A numeric vector of species counts or proportions.

**Value**

The number of observed OTUs/ASVs (species richness).

**Author(s)**

Akinsuyi Oluwamayowa Samuel

**Examples**

```
# Example with some zero abundances
calculate_observed_otus(c(1, 0, 3, 0, 5)) # Should return 3
```

---

calculate_shannon	<i>Calculate Shannon Diversity Index</i>
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**Description**

This function calculates the Shannon diversity index for a vector of species counts or proportions.

**Usage**

```
calculate_shannon(abundances)
```

**Arguments**

abundances      A numeric vector of species counts or proportions.

**Value**

The Shannon diversity index.

**Author(s)**

Akinsuyi Oluwamayowa Samuel

**Examples**

```
# Example with equal abundances
calculate_shannon(c(1, 1, 1, 1)) # Should return ~1.386

# Example with unequal abundances
calculate_shannon(c(10, 20, 30, 40)) # Should return ~1.279
```

---

calculate_simpson	<i>Calculate Simpson Diversity Index This function calculates the Simpson diversity index (1-D) for a vector of species counts or proportions. The Simpson index ranges from 0 (low diversity) to 1 (high diversity).</i>
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---

**Description**

Calculate Simpson Diversity Index This function calculates the Simpson diversity index (1-D) for a vector of species counts or proportions. The Simpson index ranges from 0 (low diversity) to 1 (high diversity).

**Usage**

```
calculate_simpson(abundances)
```

**Arguments**

abundances      A numeric vector of species counts or proportions.

**Value**

The Simpson diversity index (1-D).

**Author(s)**

Akinsuyi Oluwamayowa Samuel

**Examples**

```
# Example with equal abundances
calculate_simpson(c(1, 1, 1, 1)) # Should return 0.75

# Example with unequal abundances
calculate_simpson(c(10, 20, 30, 40)) # Should return ~0.72
```

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compare_inverse_simpson_multiple	<i>Compare Inverse Simpson Diversity Between Multiple Groups</i>
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**Description**

Compare Inverse Simpson Diversity Between Multiple Groups

**Usage**

```
compare_inverse_simpson_multiple(abundance_matrix)
```

**Arguments**

abundance\_matrix  
Matrix where rows are species and columns are samples

**Value**

Matrix of p-values for pairwise comparisons

**Author(s)**

Akinsuyi Oluwamayowa Samuel

**Examples**

```
communities <- matrix(c(10,20,30,40, 40,30,20,10, 25,25,25,25),  
                      nrow=4, ncol=3)  
compare_inverse_simpson_multiple(communities)
```

---

compare\_inverse\_simpson\_two

*Compare Inverse Simpson Diversity Between Two Groups*

---

**Description**

Compare Inverse Simpson Diversity Between Two Groups

**Usage**

```
compare_inverse_simpson_two(x, y)
```

**Arguments**

x	Numeric vector of abundances for first community
y	Numeric vector of abundances for second community

**Value**

List containing test statistics and p-value

**Author(s)**

Akinsuyi Oluwamayowa Samuel

**Examples**

```
sample1 <- c(10, 20, 30, 40)  
sample2 <- c(40, 30, 20, 10)  
compare_inverse_simpson_two(sample1, sample2)
```

---

`compare_observed_otus_multiple`*Compare Observed OTUs Between Multiple Groups*

---

**Description**

Compare Observed OTUs Between Multiple Groups

**Usage**

```
compare_observed_otus_multiple(abundance_matrix)
```

**Arguments**

`abundance_matrix`

Matrix where rows are species and columns are samples

**Value**

Matrix of p-values for pairwise comparisons

**Author(s)**

Akinsuyi Oluwamayowa Samuel

**Examples**

```
communities <- matrix(c(10,20,0,40, 40,30,20,0, 25,0,25,25),  
                      nrow=4, ncol=3)  
compare_observed_otus_multiple(communities)
```

---

`compare_observed_otus_two`*Compare Observed OTUs Between Two Groups*

---

**Description**

Compare Observed OTUs Between Two Groups

**Usage**

```
compare_observed_otus_two(x, y)
```

**Arguments**

`x` Numeric vector of abundances for first community

`y` Numeric vector of abundances for second community

**Value**

List containing test statistics and p-value

**Author(s)**

Akinsuyi Oluwamayowa Samuel

**Examples**

```
sample1 <- c(10, 20, 30, 0, 40)
sample2 <- c(40, 0, 30, 20, 10)
compare_observed_otus_two(sample1, sample2)
```

---

`compare_shannon_multiple`

*Compare Shannon Diversity Between Multiple Groups*

---

**Description**

Compare Shannon Diversity Between Multiple Groups

**Usage**

```
compare_shannon_multiple(abundance_matrix, shannon_base = exp(1))
```

**Arguments**

`abundance_matrix`      Matrix where rows are species and columns are samples

`shannon_base`      Base for logarithm calculation (default: `exp(1)`)

**Value**

Matrix of p-values for pairwise comparisons

**Author(s)**

Akinsuyi Oluwamayowa Samuel

**Examples**

```
communities <- matrix(c(10,20,30,40, 40,30,20,10, 25,25,25,25),
                      nrow=4, ncol=3)
compare_shannon_multiple(communities)
```

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compare_shannon_two	<i>Compare Shannon Diversity Between Two Groups</i>
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---

**Description**

Compare Shannon Diversity Between Two Groups

**Usage**

```
compare_shannon_two(x, y, shannon_base = exp(1))
```

**Arguments**

x	Numeric vector of abundances for first community
y	Numeric vector of abundances for second community
shannon_base	Base for logarithm calculation (default: exp(1))

**Value**

List containing test statistics and p-value

**Author(s)**

Akinsuyi Oluwamayowa Samuel

**Examples**

```
sample1 <- c(10, 20, 30, 40)
sample2 <- c(40, 30, 20, 10)
compare_shannon_two(sample1, sample2)
```

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compare_simpson_multiple	<i>Compare Simpson Diversity Between Multiple Groups</i>
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**Description**

Compare Simpson Diversity Between Multiple Groups

**Usage**

```
compare_simpson_multiple(abundance_matrix)
```

**Arguments**

abundance_matrix	Matrix where rows are species and columns are samples
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**Value**

Matrix of p-values for pairwise comparisons



**Author(s)**

Akinsuyi Oluwamayowa Samuel

**Examples**

```
communities <- matrix(c(10,20,30,40, 40,30,20,10, 25,25,25,25),
                      nrow=4, ncol=3)
compare_simpson_multiple(communities)
```

---

compare_simpson_two	<i>Compare Simpson Diversity Between Two Groups</i>
---------------------	---

---

**Description**

Compare Simpson Diversity Between Two Groups

**Usage**

```
compare_simpson_two(x, y)
```

**Arguments**

x	Numeric vector of abundances for first community
y	Numeric vector of abundances for second community

**Value**

List containing test statistics and p-value

**Author(s)**

Akinsuyi Oluwamayowa Samuel

**Examples**

```
sample1 <- c(10, 20, 30, 40)
sample2 <- c(40, 30, 20, 10)
compare_simpson_two(sample1, sample2)
```

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Microbialdiversity	<i>Microbialdiversity: A package for calculating microbial diversity indices</i>
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**Description**

Microbialdiversity: A package for calculating microbial diversity indices

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`microbiome_data`*Example Microbiome Dataset*

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## Description

A small example dataset containing microbial abundance data with associated metadata and taxonomy information. The dataset includes 5 taxa across 10 samples, with samples divided between Control and Treatment conditions.

## Usage

```
data(microbiome_data)
```

## Format

A list containing three elements:

**abundances** A matrix with 5 taxa (rows) and 10 samples (columns)

**metadata** A data frame with 10 rows and 2 columns:

- `sample_id`: Sample identifier (Sample\_1 to Sample\_10)
- `condition`: Factor with levels Control and Treatment

**taxonomy** A data frame with 5 rows and 2 columns:

- `taxa_id`: Taxa identifier (Taxa\_1 to Taxa\_5)
- `genus`: Genus classification

## Source

Generated example dataset for demonstration purposes

## Examples

```
# Load the dataset
data(microbiome_data)

# Calculate Shannon diversity for each sample
shannon_values <- apply(microbiome_data$abundances, 2, calculate_shannon)

# Compare diversity between conditions
control_samples <- microbiome_data$abundances[,
  microbiome_data$metadata$condition == "Control"]
treatment_samples <- microbiome_data$abundances[,
  microbiome_data$metadata$condition == "Treatment"]
diversity_comparison <- compare_shannon_two(control_samples, treatment_samples)

# View first few rows of abundance data
head(microbiome_data$abundances)

# View sample metadata
print(microbiome_data$metadata)
```

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shannon_diversity	<i>Shannon Diversity Functions</i>
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**Description**

Shannon Diversity Functions

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simpson_diversity	<i>Simpson Diversity Functions</i>
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**Description**

Simpson Diversity Functions