

# Package ‘ncmR’

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**Type** Package

**Title** Fit Neutral Community Model to Microbiome or Ecological Data

**Version** 0.1.0

**Description** Provides tools for fitting the neutral community model (NCM) to assess the role of stochastic processes in community assembly. The package implements the framework of Sloan et al. (2006) <[doi:10.1111/j.1462-2920.2005.00956.x](https://doi.org/10.1111/j.1462-2920.2005.00956.x)>, enabling users to evaluate neutral dynamics in ecological and microbial communities.

**License** GPL (>= 3)

**Encoding** UTF-8

**LazyData** true

**Depends** R (>= 3.5)

**Imports** dplyr, Hmisc, minpack.lm

**RoxygenNote** 7.3.3

**URL** <https://github.com/h-xuanjiu/ncmR>

**NeedsCompilation** no

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**Repository** CRAN

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example_data	<i>Example OTU table and grouping information for NCM demonstration</i>
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**Description**

A simulated dataset containing an OTU table (ASV counts) and corresponding group labels. The data are intended to illustrate the usage of the `fit_ncm` function.

**Usage**

```
example_data
```

**Format**

A list with two components:

**otu** A data frame with 15 rows (samples) and 2000 columns (ASVs). Row names are sample identifiers, column names are ASV identifiers. Values represent counts of each ASV in each sample.

**grp** A data frame with 15 rows and 1 column named group. Row names correspond to the samples in `otu`. The group column contains character labels ("A", "A", ..., etc.) indicating group membership for each sample.

**Source**

Simulated data for package examples.

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fit_ncm	<i>Fit Neutral Community Model (NCM) with optional grouping and total pooling</i>
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**Description**

Fit Neutral Community Model (NCM) with optional grouping and total pooling

**Usage**

```
fit_ncm(  
  otu,  
  grp = NULL,  
  group_col = "group",  
  groups = NULL,  
  simplify = TRUE,  
  return_model = FALSE,  
  ...  
)
```

**Arguments**

otu	OTU table, rows = samples, columns = species (data.frame or matrix)
grp	Optional data.frame with rownames = sample IDs, and one column specifying group membership. If NULL, all samples in otu are used as one group.
group_col	Column name in grp that contains group labels (default "group").
groups	Character vector of group names to analyze. If NULL and grp is provided, the function fits models for each group AND for all samples combined (total). If non-NULL, only those groups are analyzed (no total model).
simplify	If TRUE and only one model is fitted, return the model list directly (not nested).
return_model	Whether to return the nlsLM model object (default FALSE to save space).
...	Additional arguments passed to nlsLM (e.g., lower, upper, control).

**Value**

A list containing model results. If multiple models, a named list with keys: - "all" (if total model fitted) and group names. Each value is a list with: m, N, Nm, ci, rsqr, predictions, (model optional).

**Examples**

```
# Load example data
data(example_data)
otu <- example_data$otu
grp <- example_data$grp

# 1. No grouping: fit the total model using all samples
res_total <- fit_ncm(otu)
print(paste("m =", round(res_total$m, 4)))
print(paste("R^2 =", round(res_total$rsqr, 4)))
head(res_total$predictions)

# 2. With grouping: fit models for all groups + total
res_all <- fit_ncm(otu, grp)

# 3. Only specific groups (no total model), returns a single model object
res_sub <- fit_ncm(otu, grp, groups = "A")
res_sub$status_summary
```

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print.summary\_ncm      *Print summary of NCM model*

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**Description**

Print summary of NCM model

**Usage**

```
## S3 method for class 'summary_ncm'  
print(x, ...)
```

**Arguments**

x	An object of class "summary_ncm".
...	Additional arguments (not used).

**Value**

No return value, called for side effects. Prints a formatted table of NCM results to the console.

---

```
print.summary_ncm_group  
Print summary of NCM group results
```

---

**Description**

Print summary of NCM group results

**Usage**

```
## S3 method for class 'summary_ncm_group'  
print(x, ...)
```

**Arguments**

x	An object of class "summary_ncm_group".
...	Additional arguments (not used).

**Value**

No return value, called for side effects. Prints a formatted table of NCM group results to the console.

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summary.NCM	<i>Summary method for NCM objects</i>
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**Description**

Summary method for NCM objects

**Usage**

```
## S3 method for class 'NCM'  
summary(object, ...)
```

**Arguments**

object	An object of class "NCM" (single model).
...	Additional arguments (not used).

**Value**

An object of class "summary\_ncm" containing key model statistics.

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summary.NCM_group	<i>Summary method for NCM group results</i>
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**Description**

Summary method for NCM group results

**Usage**

```
## S3 method for class 'NCM_group'  
summary(object, ...)
```

**Arguments**

object	An object of class "NCM_group" (list of NCM objects).
...	Additional arguments (not used).

**Value**

An object of class "summary\_ncm\_group" containing summary for each group.

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