Package: SAFEMCN (via r-universe)

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Type Package

Title Network Topology Parameter Analysis with Rarefaction

Version 1.0.0

Description Calculate network topology parameters from Operational Taxonomic Unit (OTU) tables with customizable correlation thresholds, parallel processing options, and visualization capabilities including trend fitting, prediction of future sample sizes, and lag-1 autocorrelation (AR1) analysis. Methods are based on co-occurrence network construction via correlation thresholds and graph-theoretic metrics computed with 'igraph'.

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Encoding UTF-8

Depends R (>= 3.5.0)

Imports igraph, Hmisc, parallel, ggplot2, grDevices, graphics, rlang, stats, utils

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

RoxygenNote 7.3.3

NeedsCompilation no

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Contents

`analyze_network_topology`

Analyze Network Topology Parameters with Rarefaction

Description

Calculate network topology parameters from OTU tables with customizable correlation thresholds, parallel processing options, and visualization capabilities including topology parameter plots, exponential formula fitting, prediction of future sample sizes, and AR1 analysis.

Usage

```
analyze_network_topology(
  otu_file,
  r_threshold = 0.6,
  p_threshold = 0.05,
  cor_method = "spearman",
  start_size = 5,
  end_size = NULL,
  step_size = 1,
  replicates = 50,
  use_parallel = FALSE,
  output_prefix = "network_parameters",
  plot_topology = FALSE,
  plot_start_size = 11,
  fit_formula = FALSE,
  fit_start_size = 11,
  predict_end_size = NULL,
  run_ar1 = FALSE,
  ar1_input_file = NULL,
  ar1_windows = c(5, 10, 15)
)
```

Arguments

`otu_file`	OTU table file name (full path)
`r_threshold`	Correlation coefficient threshold (default: 0.6)
`p_threshold`	P-value threshold (default: 0.05)
`cor_method`	Correlation method: "spearman" or "pearson" (default: "spearman")
`start_size`	Starting sample size (default: 5)
`end_size`	Ending sample size (default: NULL, uses total samples)
`step_size`	Step size for sample sizes (default: 1)
`replicates`	Number of replicates (default: 50)
`use_parallel`	Use parallel processing (default: FALSE)

`output_prefix`	Output file prefix (default: "network_parameters")
`plot_topology`	Whether to plot topology parameters vs sample size (default: FALSE)
`plot_start_size`	Starting sample size for topology plots (default: 11)
`fit_formula`	Whether to perform exponential formula fitting (default: FALSE)
`fit_start_size`	Starting sample size for formula fitting (default: 11)
`predict_end_size`	End sample size for prediction (default: NULL, no prediction)
`run_ar1`	Whether to run AR1 analysis (default: FALSE)
`ar1_input_file`	Input file name for AR1 analysis (default: NULL, auto-select)
`ar1_windows`	Sliding window sizes for AR1 (default: c(5, 10, 15))

Value

A list containing raw results, summary statistics, fit parameters, and predictions

Examples

```
# Create a small toy dataset (8 OTUs x 10 samples)
set.seed(42)
otu_data <- data.frame(
  matrix(rpois(80, lambda = 10), nrow = 8, ncol = 10)
)
rownames(otu_data) <- paste0("OTU", 1:8)
colnames(otu_data) <- paste0("Sample", 1:10)
tmp_file <- tempfile(fileext = ".csv")
write.csv(otu_data, tmp_file)

results <- analyze_network_topology(
  otu_file = tmp_file,
  r_threshold = 0.4,
  p_threshold = 0.05,
  start_size = 5,
  end_size = 7,
  step_size = 1,
  replicates = 2,
  use_parallel = FALSE
)
# Check structure of returned list
names(results)
head(results$summary)


# Larger run with fitting and prediction (takes longer)
set.seed(100)
otu_big <- data.frame(
  matrix(rpois(200, lambda = 10), nrow = 10, ncol = 20)
)
rownames(otu_big) <- paste0("OTU", 1:10)
```

```
colnames(otu_big) <- paste0("Sample", 1:20)
tmp_file2 <- tempfile(fileext = ".csv")
write.csv(otu_big, tmp_file2)

results2 <- analyze_network_topology(
  otu_file = tmp_file2,
  r_threshold = 0.4,
  start_size = 5,
  end_size = 18,
  step_size = 1,
  replicates = 5,
  fit_formula = TRUE,
  fit_start_size = 5,
  predict_end_size = 25
)
str(results2$fit_parameters)
```

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