

Package ‘phymapnet’

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Type Package

Title Phylogeny-Guided Bayesian Microbial Network Inference

Version 0.1.2

Description Implements a phylogeny-aware Bayesian graphical modeling framework for microbial network inference using a shrinkage precision estimator guided by a phylogenetic kernel, with optional hyperparameter-ensemble edge reliability analysis.

License GPL-3

Encoding UTF-8

RoxygenNote 7.3.3

Imports stats, ape, GUniFrac, compositions

Suggests testthat (>= 3.0.0), knitr, rmarkdown

Config/testthat/edition 3

NeedsCompilation no

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 phymapnet_fit

Fit a single PhyMapNet model

Description

Fit a single PhyMapNet model

Usage

```
phymapnet_fit(
  otu,
  tree,
  alpha = 0.05,
  k = 5,
  epsilon1 = 0,
  epsilon2 = 0,
  kernel = c("gaussian", "laplacian"),
  th_sparsity = 0.95,
  normalization = c("log", "gmp", "clr", "tss"),
  prune_tree = TRUE
)
```

Arguments

otu	samples x taxa matrix.
tree	phylo tree with tips matching taxa.
alpha	kernel bandwidth (>0).
k	neighborhood scaling (integer >= 1). Uses $K_{\text{neighbors}} = k * p$ internally.
epsilon1	diagonal jitter for omega_hat.
epsilon2	jitter for IB.
kernel	"gaussian" or "laplacian".
th_sparsity	quantile level for sparsification (e.g., 0.95).
normalization	"log","gmp","clr","tss".
prune_tree	prune tree tips not in OTU.

Value

A list with precision_map, adjacency, threshold, taxa, dist, kernel_mat.

phymapnet_prepare_inputs
Prepare inputs for PhyMapNet

Description

Computes the patristic distance matrix from a phylogenetic tree and aligns taxa between the OTU table and the tree.

Usage

```
phymapnet_prepare_inputs(otu, tree, prune = TRUE)
```

Arguments

otu	A samples x taxa count/abundance matrix (rownames=samples, colnames=taxa).
tree	A phylo object with tip labels as taxa names.
prune	Logical; if TRUE, prunes tree tips not found in OTU.

Value

A list with otu (aligned), dist (aligned), taxa.

phymapnet_reliability *Edge reliability via hyperparameter ensemble*

Description

Runs an ensemble over (alpha, k, epsilon1, epsilon2, kernel, normalization) and returns edge reliability as selection frequency under fixed sparsification threshold.

Usage

```
phymapnet_reliability(
  otu,
  tree,
  th_fixed = 0.95,
  alpha_range = seq(0.01, 0.12, by = 0.01),
  k_range = 2:10,
  epsilon1_range = seq(0, 1, by = 0.1),
  epsilon2_range = seq(0, 1, by = 0.1),
  kernels = c("gaussian"),
  normalizations = c("log", "gmp", "clr", "tss"),
  consensus_cut = 0.5,
  prune_tree = TRUE,
```

```
    progress = TRUE,  
    progress_every = 500  
  )
```

Arguments

<code>otu</code>	samples x taxa matrix.
<code>tree</code>	phylo tree.
<code>th_fixed</code>	fixed quantile threshold for sparsification across all models (e.g., 0.95).
<code>alpha_range</code>	numeric vector.
<code>k_range</code>	integer vector.
<code>epsilon1_range</code>	numeric vector.
<code>epsilon2_range</code>	numeric vector.
<code>kernels</code>	character vector: "gaussian" and/or "laplacian".
<code>normalizations</code>	character vector: subset of c("log", "gmpr", "clr", "tss").
<code>consensus_cut</code>	reliability cutoff for binary consensus (default 0.5).
<code>prune_tree</code>	prune tree tips not in OTU.
<code>progress</code>	print progress every <code>progress_every</code> models.
<code>progress_every</code>	integer.

Value

A list with `rel_mat`, `consensus_mat`, `edge_list`, `N_models`, `grid`.

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