Package: phymapnet (via r-universe)

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Type Package

Title Phylogeny-Guided Bayesian Microbial Network Inference

Version 0.1.3

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, compositions

Suggests testthat (>= 3.0.0), knitr, rmarkdown

Config/testthat/edition 3

NeedsCompilation no

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Contents

`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", "clr", "tss"),
  prune_tree = TRUE
)
```

Arguments

`otu`	samples x taxa matrix.
`tree`	`phylo` tree with tips matching taxa, or a named symmetric phylogenetic distance matrix.
`alpha`	kernel bandwidth (>0).
`k`	neighborhood scaling (integer >= 1). Uses K_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"`, `"clr"`, or `"tss"`.
`prune_tree`	prune tree tips not in OTU when `tree` is a phylogenetic tree; distance matrices are aligned directly.

Value

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

`phymapnet_prepare_inputs` *Prepare inputs for PhyMapNet*

Description

Computes a patristic distance matrix from a phylogenetic tree, or validates a supplied phylogenetic distance matrix, then aligns taxa to the OTU table.

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, or a named, symmetric taxa x taxa phylogenetic distance matrix.
`prune`	Logical; if TRUE and `tree` is a `phylo` object, prunes tree tips not found in OTU before distances are computed. Input taxa are always aligned to their shared set.

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", "clr", "tss"),
```

```
  consensus_cut = 0.5,
  prune_tree = TRUE,
  progress = TRUE,
  progress_every = 500
)
```

Arguments

`otu`	samples x taxa matrix.
`tree`	`phylo` tree, or a named symmetric phylogenetic distance matrix.
`th_fixed`	fixed quantile threshold for sparsification across all models (e.g., 0.95).
`alpha_range`	numeric vector.
`k_range`	integer vector.
`epsilon1_range`	numeric vector.
`epsilon2_range`	numeric vector.
`kernels`	character vector: "gaussian" and/or "laplacian".
`normalizations`	character vector: subset of `c("log","clr","tss")`.
`consensus_cut`	reliability cutoff for binary consensus (default 0.5).
`prune_tree`	prune tree tips not in OTU when `tree` is a phylogenetic tree; distance matrices are aligned directly.
`progress`	print progress every `progress_every` models.
`progress_every`	integer.

Value

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

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