# Package ‘phymapnet’

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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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**Repository** CRAN

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## Contents

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`phymapnet_fit` *Fit a single PhyMapNet model*

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## 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.

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## `phymapnet_prepare_inputs` *Prepare inputs for PhyMapNet*

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### 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.

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## `phymapnet_reliability` *Edge reliability via hyperparameter ensemble*

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### 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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