Package ‘scistreer’

June 15, 2023

Title  Maximum-Likelihood Perfect Phylogeny Inference at Scale

URL  https://github.com/kharchenkolab/scistreer,  
https://kharchenkolab.github.io/scistreer/

Version  1.2.0

Description  
Fast maximum-likelihood phylogeny inference from noisy single-cell data using the 'ScisTree' algorithm by Yufeng Wu (2019) <doi:10.1093/bioinformatics/btz676>. 'scistreer' provides an 'R' interface and improves speed via 'Rcpp' and 'RcppParallel', making the method applicable to massive single-cell datasets (>10,000 cells).

License  GPL-3

Encoding  UTF-8

LazyData  true

Depends  R (>= 4.1.0)

biocViews

Imports  ape, dplyr, ggplot2, ggtree, igraph, parallelDist, patchwork, phangorn, Rcpp, reshape2, RcppParallel, RhpcBLASctl, stringr, tidygraph

Suggests  testthat (>= 3.0.0)

Config/testthat/edition  3

LinkingTo  Rcpp, RcppArmadillo, RcppParallel

NeedsCompilation  yes

SystemRequirements  GNU make

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RoxygenNote  7.2.2

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### annotate_tree

**Find maximum likelihood assignment of mutations on a tree**

#### Description

Find maximum likelihood assignment of mutations on a tree

#### Usage

```r
annotate_tree(tree, P)
```

#### Arguments

- `tree` phylo Single-cell phylogenetic tree
- `P` matrix Genotype probability matrix

#### Value

`tbl_graph` A single-cell phylogeny with mutation placements

#### Examples

```r
gtree_small = annotate_tree(tree_small, P_small)
```
**get_mut_graph**

Convert a single-cell phylogeny with mutation placements into a mutation graph

**Description**

Convert a single-cell phylogeny with mutation placements into a mutation graph

**Usage**

```r
get_mut_graph(gtree)
```

**Arguments**

- `gtree` tbl_graph The single-cell phylogeny

**Value**

igraph Mutation graph

**Examples**

```r
mut_graph = get_mut_graph(gtree_small)
```

**gtree_small**

Smaller example annotated tree built from P_small

**Description**

Smaller example annotated tree built from P_small

**Usage**

```r
gtree_small
```

**Format**

An object of class tbl_graph (inherits from igraph) of length 199.
ladderize  

From ape; will remove once new ape version is released
https://github.com/emmanuelparadis/ape/issues/54

Description

From ape; will remove once new ape version is released https://github.com/emmanuelparadis/ape/issues/54

Usage

ladderize(phy, right = TRUE)

Arguments

phy  
phylo The phylogeny
right  
logical Whether ladderize to the right

Examples

tree_small = ladderize(tree_small)

mut_nodes_small  

Mutation placements calculated from tree_small and P_small

Description

Mutation placements calculated from tree_small and P_small

Usage

mut_nodes_small

Format

An object of class data.frame with 9 rows and 2 columns.
mut_to_tree

Transfer mutation assignment onto a single-cell phylogeny

Description
Transfer mutation assignment onto a single-cell phylogeny

Usage
mut_to_tree(gtree, mut_nodes)

Arguments

  gtree tbl_graph The single-cell phylogeny
  mut_nodes dataframe Mutation placements

Value

  tbl_graph A single-cell phylogeny with mutation placements

Examples

  gtree_small = mut_to_tree(gtree_small, mut_nodes_small)

perform_nni

Maximum likelihood tree search via NNI

Description
Maximum likelihood tree search via NNI

Usage

  perform_nni(
    tree_init,
    P,
    max_iter = 100,
    eps = 0.01,
    ncores = 1,
    verbose = TRUE
  )
Arguments

- **tree_init**: phylo Initial tree
- **P**: matrix Genotype probability matrix
- **max_iter**: integer Maximum number of iterations
- **eps**: numeric Tolerance threshold in likelihood difference for stopping
- **ncores**: integer Number of cores to use
- **verbose**: logical Verbosity

Value

- multiPhylo List of trees corresponding to the rearrangement steps

Examples

```r
  tree_list = perform_nni(tree_upgma, P_small)
```

---

**plot_phylo_heatmap**  
*Plot phylogeny and mutation heatmap*

Description

Plot phylogeny and mutation heatmap

Usage

```r
  plot_phylo_heatmap(tree, P, branch_width = 0.5, root_edge = TRUE)
```

Arguments

- **tree**: phylo or tbl_graph Phylogeny
- **P**: matrix Genotype probability matrix
- **branch_width**: numeric Branch width
- **root_edge**: logical Whether to plot root edge

Value

- `ggplot` Plot visualizing the single-cell phylogeny and mutation probability heatmap

Examples

```r
  p = plot_phylo_heatmap(tree_small, P_small)
```
**P_example**

*Example genotype probability matrix*

**Description**

Example genotype probability matrix

**Usage**

`P_example`

**Format**

An object of class `matrix` (inherits from `array`) with 1000 rows and 25 columns.

---

**P_small**

*Smaller example genotype probability matrix*

**Description**

Smaller example genotype probability matrix

**Usage**

`P_small`

**Format**

An object of class `matrix` (inherits from `array`) with 100 rows and 25 columns.

---

**run_scistree**

*Run the scistree workflow*

**Description**

Run the scistree workflow

**Usage**

```r
run_scistree(
P,
init = "UPGMA",
ncores = 1,
max_iter = 100,
eps = 0.01,
verbose = TRUE
)
```
score_tree

Arguments

P matrix Genotype probability matrix (cell x mutation). Each entry is a probability (0-1) that the cell harbors the mutation
init character Initialization strategy; UPGMA or NJ
ncores integer Number of cores to use
max_iter integer Maximum number of iterations
eps numeric Tolerance threshold in likelihood difference for stopping
verbose logical Verbosity

Value

phylo A maximum-likelihood phylogeny

Examples

tree_small = run_scistree(P_small)

score_tree tree likelihood = score_tree(tree_upgma, P_small)$l_tree

Description

Score a tree based on maximum likelihood

Usage

score_tree(tree, P, get_l_matrix = FALSE)

Arguments

tree phylo object
P genotype probability matrix
get_l_matrix whether to compute the whole likelihood matrix

Value

list Likelihood scores of a tree

Examples

tree_likelihood = score_tree(tree_upgma, P_small)$l_tree
to_phylo

Convert the phylogeny from tidygraph to phylo object modified from R package alakazam, converts a tbl_graph to a phylo object

Description
Convert the phylogeny from tidygraph to phylo object modified from R package alakazam, converts a tbl_graph to a phylo object

Usage

to_phylo(graph)

Arguments

graph tbl_graph The single-cell phylogeny

Value

phylo The single-cell phylogeny

Examples

tree_small = to_phylo(annotate_tree(tree_small, P_small))


tree_small Smaller example tree built from P_small

Description
Smaller example tree built from P_small

Usage

tree_small

Format
An object of class phylo of length 5.
Example tree built using UPGMA from P_small

Description
Example tree built using UPGMA from P_small

Usage
tree_upgma

Format
An object of class phylo of length 4.
Index

* datasets
  gtree_small, 3
  mut_nodes_small, 4
  P_example, 7
  P_small, 7
  tree_small, 9
  tree_upgma, 10

annotate_tree, 2
get_mut_graph, 3
gtree_small, 3
ladderize, 4
mut_nodes_small, 4
mut_to_tree, 5
P_example, 7
P_small, 7
perform_nni, 5
plot_phylo_heatmap, 6
run_scistree, 7
score_tree, 8
to_phylo, 9
tree_small, 9
tree_upgma, 10