Package: scistreer (via r-universe)

October 12, 2024

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)

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

Repository https://kharchenkolab.r-universe.dev

RemoteUrl https://github.com/kharchenkolab/scistreer

RemoteRef HEAD

RemoteSha 42b4ac56491395a04163b4e101d8430fd1382225

Contents

`annotate_tree` *Find maximum lilkelihood assignment of mutations on a tree*

Description

Find maximum lilkelihood assignment of mutations on a tree

Usage

```
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

```
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

```
get_mut_graph(gtree)
```

Arguments

`gtree`	tbl_graph The single-cell phylogeny

Value

igraph Mutation graph

Examples

```
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

```
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 Intial 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

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

`plot_phylo_heatmap` *Plot phylogeny and mutation heatmap*

Description

Plot phylogeny and mutation heatmap

Usage

```
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

```
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

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

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` *Score a tree based on maximum likelihood*

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.

`tree_upgma` *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.

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