

# Package ‘scistreer’

May 9, 2026

**Title** Maximum-Likelihood Perfect Phylogeny Inference at Scale

**URL** <https://github.com/kharchenkolab/scistreer>,  
<https://kharchenkolab.github.io/scistreer/>

**Version** 1.2.1

## Description

Fast maximum-likelihood phylogeny inference from noisy single-cell data using the 'ScisTree' algorithm by Yufeng Wu (2019) <[doi:10.1093/bioinformatics/btz676](https://doi.org/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** CRAN

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annotate_tree	<i>Find maximum likelihood assignment of mutations on a tree</i>
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### Description

Find maximum likelihood 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	<i>Convert a single-cell phylogeny with mutation placements into a mutation graph</i>
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---

**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	<i>Smaller example annotated tree built from P_small</i>
-------------	--

---

**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	<i>From ape; will remove once new ape version is released <a href="https://github.com/emmanuelparadis/ape/issues/54">https://github.com/emmanuelparadis/ape/issues/54</a></i>
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**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	<i>Mutation placements calculated from tree_small and P_small</i>
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---

**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	<i>Transfer mutation assignment onto a single-cell phylogeny</i>
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---

**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	<i>Maximum likelihood tree search via NNI</i>
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**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**

```
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	<i>Example genotype probability matrix</i>
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---

**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	<i>Smaller example genotype probability matrix</i>
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---

**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	<i>Run the scistree workflow</i>
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---

**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	<i>Convert the phylogeny from tidygraph to phylo object modified from R package alakazam, converts a tbl_graph to a phylo object</i>
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---

**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	<i>Smaller example tree built from P_small</i>
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---

**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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