

Package: treefit (via r-universe)

September 27, 2024

Title The First Software for Quantitative Trajectory Inference

Version 1.0.2.9000

Description Perform two types of analysis: 1) checking the goodness-of-fit of tree models to your single-cell gene expression data; and 2) deciding which tree best fits your data.

License GPL (>= 3)

URL <https://hayamizu-lab.github.io/treefit-r/>,
<https://github.com/hayamizu-lab/treefit-r/>

BugReports <https://github.com/hayamizu-lab/treefit-r/issues>

Encoding UTF-8

LazyData true

Roxygen list(markdown=TRUE)

RoxygenNote 7.1.1

Imports ggplot2, igraph, patchwork, pracma

Suggests Seurat, gridExtra, knitr, plotly, qpdf, rmarkdown, testthat

VignetteBuilder knitr

Language en-US

Repository <https://hayamizu-lab.r-universe.dev>

RemoteUrl <https://github.com/hayamizu-lab/treefit-r>

RemoteRef HEAD

RemoteSha 1414b561a8d5e32164fa2f873c158a528972fea9