

Resource Summary Report

Generated by [kravitz2](#) on Sep 4, 2026

SimPhy

RRID:SCR_024501

Type: Tool

Proper Citation

SimPhy (RRID:SCR_024501)

Resource Information

URL: <https://github.com/adamallo/SimPhy>

Proper Citation: SimPhy (RRID:SCR_024501)

Description: Software package for simulation of multiple gene families evolving under incomplete lineage sorting, gene duplication and loss, horizontal gene transfer, all three potentially leading to species tree/gene tree discordance and gene conversion. Used for phylogenomic simulation of gene, locus, and species trees.

Resource Type: simulation software, software application, software resource

Defining Citation: [PMID:26526427](#)

Keywords: phylogenomic simulation, gene phylogenomic simulation, locus phylogenomic simulation, species trees phylogenomic simulation,

Availability: Free, Available for download, Freely available

Resource Name: SimPhy

Resource ID: SCR_024501

License: GNU GPL v2.0

Record Creation Time: 20231002T161336+0000

Record Last Update: 20260903T235959+0000

Ratings and Alerts

No rating or validation information has been found for SimPhy.

No alerts have been found for SimPhy.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Morel B, et al. (2022) SpeciesRax: A Tool for Maximum Likelihood Species Tree Inference from Gene Family Trees under Duplication, Transfer, and Loss. Molecular biology and evolution, 39(2).