

# Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 17, 2026

## SimPhy

RRID:SCR\_024501

Type: Tool

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### Proper Citation

SimPhy (RRID:SCR\_024501)

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### 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:** 20260912T200048+0000

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### Ratings and Alerts

No rating or validation information has been found for SimPhy.

No alerts have been found for SimPhy.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

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

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).