

# Package: SEEPS (via r-universe)

October 25, 2024

**Title** An Agent-Based Simulator for Infectious Disease Phylodynamics

**Version** 0.0.2

**Description** A modular, modern simulation suite and toolkit for simulating transmission networks, phylogenies, and evolutionary pairwise distance matrices under different models and assumptions for viral/sequence evolution. While initially developed for HIV, SEEPS offers modular utilities for custom workflows for extension beyond HIV.

**License** BSD\_3\_clause + file LICENSE

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**Encoding** UTF-8

**LazyData** true

**Suggests** testthat (>= 2.1.0), rlang (>= 1.0.0), knitr, rmarkdown

**Imports** ape (>= 5.0.0), phyclust (>= 0.1), rngtools (>= 1.0.0), stringr (>= 1.3.1), stats

**RoxygenNote** 7.2.3

**Depends** R (>= 3.5.0)

**VignetteBuilder** knitr

**Repository** <https://molevolepid.r-universe.dev>

**RemoteUrl** <https://github.com/MolEvolEpid/SEEPS>

**RemoteRef** HEAD

**RemoteSha** 6473bd5f012c41693b7ad2a0fa1e05554757b7de