

Resource Summary Report

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Seq-Gen

RRID:SCR_014934

Type: Tool

Proper Citation

Seq-Gen (RRID:SCR_014934)

Resource Information

URL: <http://tree.bio.ed.ac.uk/software/seqgen/>

Proper Citation: Seq-Gen (RRID:SCR_014934)

Description: Software program that simulates the evolution of nucleotide or amino acid sequences along a phylogeny using common models of the substitution process. A range of models of molecular evolution are implemented, including the general reversible model. State frequencies and other parameters of the model may be given and site-specific rate heterogeneity may also be incorporated in a number of ways. Any number of trees may be read in and the program will produce any number of data sets for each tree.

Resource Type: software resource, software application, simulation software

Defining Citation: [DOI:10.1093/bioinformatics/13.3.235](https://doi.org/10.1093/bioinformatics/13.3.235)

Keywords: simulator, simulation software, molecular evolution, nucleotide, amino acid, sequence, phylogeny, phylogenetic tree

Funding: Wellcome Trust ;
BBSRC ;
Fogarty ;
The Royal Society

Availability: Available for download

Resource Name: Seq-Gen

Resource ID: SCR_014934

Alternate IDs: OMICS_15373

Alternate URLs: <https://sources.debian.org/src/seq-gen/>

Record Creation Time: 20220129T080323+0000

Ratings and Alerts

No rating or validation information has been found for Seq-Gen.

No alerts have been found for Seq-Gen.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 155 mentions in open access literature.

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

Thawornwattana Y, et al. (2026) On the robustness of Bayesian inference of gene flow to intragenic recombination and natural selection. *Molecular biology and evolution*, 43(1).

Featherstone LA, et al. (2025) How does date-rounding affect phylodynamic inference for public health? *PLoS computational biology*, 21(4), e1012900.

Ndovie W, et al. (2025) Exploration of the genetic landscape of bacterial dsDNA viruses reveals an ANI gap amid extensive mosaicism. *mSystems*, 10(2), e0166124.

Paredes MI, et al. (2025) Viral introductions and return to baseline sexual behaviors maintain low-level mpox incidence in Los Angeles County, USA, 2023-2024. *medRxiv* : the preprint server for health sciences.

Taylor DJ, et al. (2024) Genomic transfers help to decipher the ancient evolution of filoviruses and interactions with vertebrate hosts. *PLoS pathogens*, 20(9), e1011864.

Rees J, et al. (2024) Ancient Loss of Catalytic Selenocysteine Spurred Convergent Adaptation in a Mammalian Oxidoreductase. *Genome biology and evolution*, 16(3).

Gay SA, et al. (2024) Phylogenetic inference of inter-population transmission rates for infectious diseases. *Briefings in bioinformatics*, 25(4).

Aoki S, et al. (2024) Kernel density estimation of allele frequency including undetected alleles. *PeerJ*, 12, e17248.

Wu Z, et al. (2024) Ultrafast learning of four-node hybridization cycles in phylogenetic networks using algebraic invariants. *Bioinformatics advances*, 4(1), vbae014.

Ma B, et al. (2024) Bases-dependent Rapid Phylogenetic Clustering (Bd-RPC) enables precise and efficient phylogenetic estimation in viruses. *Virus evolution*, 10(1), veae005.

Rosser N, et al. (2024) Hybrid speciation driven by multilocus introgression of ecological traits. *Nature*, 628(8009), 811.

Fleming JF, et al. (2023) nRCFV: a new, dataset-size-independent metric to quantify compositional heterogeneity in nucleotide and amino acid datasets. *BMC bioinformatics*, 24(1), 145.

Casanellas M, et al. (2023) Designing Weights for Quartet-Based Methods When Data are Heterogeneous Across Lineages. *Bulletin of mathematical biology*, 85(7), 68.

Zhang L, et al. (2023) A fast and scalable method for inferring phylogenetic networks from trees by aligning lineage taxon strings. *Genome research*, 33(7), 1053.

Tay JH, et al. (2023) Detecting Episodic Evolution through Bayesian Inference of Molecular Clock Models. *Molecular biology and evolution*, 40(10).

Barido-Sottani J, et al. (2023) Estimating the Age of Poorly Dated Fossil Specimens and Deposits Using a Total-Evidence Approach and the Fossilized Birth-Death Process. *Systematic biology*, 72(2), 466.

Liu L, et al. (2023) Short branch attraction in phylogenomic inference under the multispecies coalescent. *Frontiers in ecology and evolution*, 11.

Fiedler L, et al. (2023) Detecting gene breakpoints in noisy genome sequences using position-annotated colored de-Bruijn graphs. *BMC bioinformatics*, 24(1), 235.

Asar Y, et al. (2023) Evaluating the Accuracy of Methods for Detecting Correlated Rates of Molecular and Morphological Evolution. *Systematic biology*, 72(6), 1337.

Luo A, et al. (2023) Impacts of Taxon-Sampling Schemes on Bayesian Tip Dating Under the Fossilized Birth-Death Process. *Systematic biology*, 72(4), 781.