

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 application, simulation software, software resource

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 158 mentions in open access literature.

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

Ivan J, et al. (2026) Selecting a Window Size for Phylogenomic Analyses of Whole Genome Alignments Using AIC. Systematic biology, 75(1), 100.

Lewnard JA, et al. (2026) Extensive cryptic circulation sustains mpox among men who have sex with men. Nature communications, 17(1).

Kolbow N, et al. (2026) SNaQ.jl: Improved scalability for level-1 phylogenetic network inference. Bioinformatics (Oxford, England), 42(6).

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.

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.

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.

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.

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

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.

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.

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.