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/

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 Name: Seq-Gen

Proper Citation: Seq-Gen (RRID:SCR_014934)

Resource Type: Resource, software resource, software application, simulation software

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

Resource ID: SCR_014934

Parent Organization: University of Edinburgh; Scotland; United Kingdom

Funding Agency: BBSRC, Fogarty, The Royal Society, Wellcome Trust

Availability: Available for download

Website Status: Last checked up

Mentions Count: 104
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 104 mentions in open access literature.

**Listed below are recent publications.** The full list is available at FDI Lab - SciCrunch Infrastructure.


Duchene S, et al. (2018) Inferring demographic parameters in bacterial genomic data using...
Bayesian and hybrid phylogenetic methods. BMC evolutionary biology, 18(1), 95.


