Resource Summary Report

Generated by dkNET on Sep 16, 2026

Dawg

RRID:SCR_016068
Type: Tool

Proper Citation

Dawg (RRID:SCR_016068)

Resource Information

URL: http://scit.us/projects/dawg

Proper Citation: Dawg (RRID:SCR_016068)

Description: Software application to simulate the evolution of recombinant DNA sequences in continuous time based on the robust general time reversible model with gamma and invariant rate heterogeneity and a novel length-dependent model of gap formation. The application accepts phylogenies in Newick format and can return the sequence of any node, allowing for the exact evolutionary history to be recorded at the discretion of users.

Abbreviations: Dawg

Synonyms: Dawg: DNA assembly with gaps

Resource Type: data analysis software, data processing software, sequence analysis software, simulation software, software application, software resource

Defining Citation: PMID:16306390

Keywords: simulate, evolution, recombinant, DNA, sequences, history, assembly, gaps

Availability: Free, Available for download

Resource Name: Dawg

Resource ID: SCR_016068

Alternate URLs: https://github.com/reedacartwright/dawg

License: GPL-2.0

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260912T195834+0000

Ratings and Alerts

No rating or validation information has been found for Dawg.

No alerts have been found for Dawg.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 18 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET .

Lees JA, et al. (2018) Evaluation of phylogenetic reconstruction methods using bacterial whole genomes: a simulation based study. Wellcome open research, 3, 33.

Ashkenazy H, et al. (2017) SpartaABC: a web server to simulate sequences with indel parameters inferred using an approximate Bayesian computation algorithm. Nucleic acids research, 45(W1), W453.

Ezawa K, et al. (2016) Characterization of multiple sequence alignment errors using complete-likelihood score and position-shift map. BMC bioinformatics, 17, 133.

Ezawa K, et al. (2016) General continuous-time Markov model of sequence evolution via insertions/deletions: local alignment probability computation. BMC bioinformatics, 17(1), 397.

Weatherly DB, et al. (2016) Recombination-driven generation of the largest pathogen repository of antigen variants in the protozoan Trypanosoma cruzi. BMC genomics, 17(1), 729.

Schwartz RS, et al. (2015) A composite genome approach to identify phylogenetically informative data from next-generation sequencing. BMC bioinformatics, 16, 193.

Wheeler WC, et al. (2015) Phylogenetic network analysis as a parsimony optimization problem. BMC bioinformatics, 16, 296.

Thiergart T, et al. (2014) Concatenated alignments and the case of the disappearing tree. BMC evolutionary biology, 14, 266.

Varón A, et al. (2013) Local search for the generalized tree alignment problem. BMC bioinformatics, 14, 66.

Lücking R, et al. (2011) PICS-Ord: unlimited coding of ambiguous regions by pairwise identity and cost scores ordination. BMC bioinformatics, 12, 10.

O'Connor T, et al. (2010) Analysis of long branch extraction and long branch shortening. BMC genomics, 11 Suppl 2(Suppl 2), S14.

Li H, et al. (2010) Fast and accurate long-read alignment with Burrows-Wheeler transform. Bioinformatics (Oxford, England), 26(5), 589.

Dwivedi B, et al. (2009) Phylogenetic inference under varying proportions of indel-induced alignment gaps. BMC evolutionary biology, 9, 211.

Fletcher W, et al. (2009) INDELible: a flexible simulator of biological sequence evolution. Molecular biology and evolution, 26(8), 1879.

Yang K, et al. (2008) Performance comparison between k-tuple distance and four model-based distances in phylogenetic tree reconstruction. Nucleic acids research, 36(5), e33.

Sinha S, et al. (2007) MORPH: probabilistic alignment combined with hidden Markov models of cis-regulatory modules. PLoS computational biology, 3(11), e216.

Huang W, et al. (2007) Phylogenetic simulation of promoter evolution: estimation and modeling of binding site turnover events and assessment of their impact on alignment tools. Genome biology, 8(10), R225.

Cartwright RA, et al. (2006) Logarithmic gap costs decrease alignment accuracy. BMC bioinformatics, 7, 527.