Resource Summary Report

Generated by kravitz2 on Jul 31, 2026

Indelible

RRID:SCR_016163
Type: Tool

Proper Citation

Indelible (RRID:SCR_016163)

Resource Information

URL: http://abacus.gene.ucl.ac.uk/software/indelible/

Proper Citation: Indelible (RRID:SCR_016163)

Description: Software that generates nucleotide, amino acid and codon sequence data by simulating insertions and deletions (indels) as well as substitutions. It is used for biological sequence simulation of multi-partitioned nucleotide, amino-acid, or codon data sets through the processes of insertion, deletion, and substitution in continuous time.

Resource Type: simulation software, software resource, software application

Defining Citation: PMID:19423664

Keywords: indel, insertion, deletion, biological, sequence, simulation, multi-partitioned, nucleotide, amio-acid, codon, data, set, insertion, deletion, substitution, continous, time, non-homogeneous, non-stationary, phylogeny, simulator, evolution

Funding: EPSRC/MRC Doctoral Training Centre studentship ;
BBSRC

Availability: Free, Available for download

Resource Name: Indelible

Resource ID: SCR_016163

Alternate IDs: OMICS_15369

Alternate URLs: https://sources.debian.org/src/indelible/

License: GNU GPL v3

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260731T042959+0000

Ratings and Alerts

No rating or validation information has been found for Indelible.

No alerts have been found for Indelible.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 23 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Redelings BD, et al. (2024) Insertions and Deletions: Computational Methods, Evolutionary Dynamics, and Biological Applications. Molecular biology and evolution, 41(9).

Zhai Y, et al. (2024) ReAlign-N: an integrated realignment approach for multiple nucleic acid sequence alignment, combining global and local realignments. NAR genomics and bioinformatics, 6(4), lqae170.

Zhai Y, et al. (2024) TPMA: A two pointers meta-alignment tool to ensemble different multiple nucleic acid sequence alignments. PLoS computational biology, 20(4), e1011988.

Leal JL, et al. (2023) Phylogenetic Analysis of Allotetraploid Species Using Polarized Genomic Sequences. Systematic biology, 72(2), 372.

Zhao H, et al. (2021) Global Landscape of Clostridioides Difficile Phylogeography, Antibiotic Susceptibility, and Toxin Polymorphisms by Post-Hoc Whole-Genome Sequencing from the MODIFY I/II Studies. Infectious diseases and therapy, 10(2), 853.

Wang W, et al. (2021) Build a better bootstrap and the RAWR shall beat a random path to your door: phylogenetic support estimation revisited. Bioinformatics (Oxford, England), 37(Suppl_1), i111.

Lucaci AG, et al. (2021) Extra base hits: Widespread empirical support for instantaneous multiple-nucleotide changes. PloS one, 16(3), e0248337.

Penev PI, et al. (2021) TwinCons: Conservation score for uncovering deep sequence similarity and divergence. PLoS computational biology, 17(10), e1009541.

Criscuolo A, et al. (2020) On the transformation of MinHash-based uncorrected distances into proper evolutionary distances for phylogenetic inference. F1000Research, 9, 1309.

Goremykin V, et al. (2019) A Novel Test for Absolute Fit of Evolutionary Models Provides a Means to Correctly Identify the Substitution Model and the Model Tree. Genome biology and evolution, 11(8), 2403.

Bigot T, et al. (2019) Simulation data for the estimation of numerical constants for approximating pairwise evolutionary distances between amino acid sequences. Data in brief, 25, 104212.

Donath A, et al. (2018) Split-inducing indels in phylogenomic analysis. Algorithms for molecular biology : AMB, 13, 12.

Solis-Reyes S, et al. (2018) An open-source k-mer based machine learning tool for fast and accurate subtyping of HIV-1 genomes. PloS one, 13(11), e0206409.

Jones BR, et al. (2018) Phylogenetic approach to recover integration dates of latent HIV sequences within-host. Proceedings of the National Academy of Sciences of the United States of America, 115(38), E8958.

McCloskey RM, et al. (2017) A model-based clustering method to detect infectious disease transmission outbreaks from sequence variation. PLoS computational biology, 13(11), e1005868.

Rivera-Rivera CJ, et al. (2016) LS??: A Method for Improving Phylogenomic Inferences When Evolutionary Rates Are Heterogeneous among Taxa. Molecular biology and evolution, 33(6), 1625.

Poon AF, et al. (2016) Impacts and shortcomings of genetic clustering methods for infectious disease outbreaks. Virus evolution, 2(2), vew031.

Poon AF, et al. (2015) Phylodynamic Inference with Kernel ABC and Its Application to HIV Epidemiology. Molecular biology and evolution, 32(9), 2483.

Parks M, et al. (2015) Impacts of low coverage depths and post-mortem DNA damage on variant calling: a simulation study. BMC genomics, 16(1), 19.

Diekmann Y, et al. (2015) Gene Tree Affects Inference of Sites Under Selection by the Branch-Site Test of Positive Selection. Evolutionary bioinformatics online, 11(Suppl 2), 11.