

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 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 application, software resource

Defining Citation: [PMID:19423664](#)

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

Funding: BBSRC ;
EPSRC/MRC Doctoral Training Centre studentship

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: 20260905T132804+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 24 mentions in open access literature.

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

Flom LT, et al. (2026) Characterization of Neuronal Ensembles in a Model of Dual-Reward Conditioned Place Preference. *eNeuro*, 13(6).

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.

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

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.

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.