

Resource Summary Report

Generated by [kravitz2](#) on Jul 30, 2026

MP-EST

RRID:SCR_012145

Type: Tool

Proper Citation

MP-EST (RRID:SCR_012145)

Resource Information

URL: <https://code.google.com/p/mp-est/>

Proper Citation: MP-EST (RRID:SCR_012145)

Description: Software that can consistently estimate the topology and branch lengths (in coalescent units) of the species tree. Although the pseudo-likelihood is derived from coalescent theory, and assumes no gene flow or horizontal gene transfer (HGT), the MP-EST method is robust to a small amount of HGT in the dataset. In addition, increasing the number of genes does not increase the computational time substantially. The MP-EST method is fast for analyzing datasets that involve a large number of genes but a moderate number of species.

Synonyms: Maximum Pseudo-likelihood Estimate of the Species Tree (MP-EST), Maximum Pseudo-likelihood for Estimating Species Trees

Resource Type: software resource

Defining Citation: [PMID:20937096](#)

Keywords: standalone software, web app

Availability: GNU General Public License, v2

Resource Name: MP-EST

Resource ID: SCR_012145

Alternate IDs: OMICS_06053

Record Creation Time: 20220129T080308+0000

Record Last Update: 20260725T190732+0000

Ratings and Alerts

No rating or validation information has been found for MP-EST.

No alerts have been found for MP-EST.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Jiang Z, et al. (2024) Gene flow and an anomaly zone complicate phylogenomic inference in a rapidly radiated avian family (Prunellidae). *BMC biology*, 22(1), 49.

Xiong H, et al. (2022) Species Tree Estimation and the Impact of Gene Loss Following Whole-Genome Duplication. *Systematic biology*, 71(6), 1348.

Flouri T, et al. (2022) Bayesian Phylogenetic Inference using Relaxed-clocks and the Multispecies Coalescent. *Molecular biology and evolution*, 39(8).

Kozak KM, et al. (2021) Rampant Genome-Wide Admixture across the Heliconius Radiation. *Genome biology and evolution*, 13(7).

Campbell MA, et al. (2020) Addressing incomplete lineage sorting and paralogy in the inference of uncertain salmonid phylogenetic relationships. *PeerJ*, 8, e9389.

Cloutier A, et al. (2019) Whole-Genome Analyses Resolve the Phylogeny of Flightless Birds (Palaeognathae) in the Presence of an Empirical Anomaly Zone. *Systematic biology*, 68(6), 937.

Feng C, et al. (2019) Multiple convergent events created a nominal widespread species: *Triplophysa stoliczkae* (Steindachner, 1866) (Cobitoidea: Nemacheilidae). *BMC evolutionary biology*, 19(1), 177.

Pan H, et al. (2019) High-coverage genomes to elucidate the evolution of penguins. *GigaScience*, 8(9).

Wang K, et al. (2018) Incomplete lineage sorting rather than hybridization explains the inconsistent phylogeny of the wisent. *Communications biology*, 1, 169.

Qiu H, et al. (2016) Red Algal Phylogenomics Provides a Robust Framework for Inferring Evolution of Key Metabolic Pathways. *PLoS currents*, 8.

Burri R, et al. (2015) Linked selection and recombination rate variation drive the evolution of the genomic landscape of differentiation across the speciation continuum of *Ficedula* flycatchers. *Genome research*, 25(11), 1656.

Colombo M, et al. (2015) Diversity and disparity through time in the adaptive radiation of Antarctic notothenioid fishes. *Journal of evolutionary biology*, 28(2), 376.

Zimmermann T, et al. (2014) BBKA: Improving the scalability of *BEAST using random binning. *BMC genomics*, 15 Suppl 6(Suppl 6), S11.