

# Resource Summary Report

Generated by [Kravitz](#) on Sep 17, 2026

## SplitsTree

RRID:SCR\_014734

Type: Tool

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### Proper Citation

SplitsTree (RRID:SCR\_014734)

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### Resource Information

**URL:** <http://www.splitstree.org/>

**Proper Citation:** SplitsTree (RRID:SCR\_014734)

**Description:** Application that uses molecular sequence data to compute unrooted phylogenetic networks. Given an alignment of sequences, a distance matrix, or a set of trees, the program will compute a phylogenetic tree or network using methods such as split decomposition, neighbor-net, consensus network, super networks methods or methods for computing hybridization or simple recombination networks., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

**Synonyms:** SplitsTree3, SplitsTree4

**Resource Type:** data analysis software, data processing software, data visualization software, software application, software resource

**Keywords:** sequence data, unrooted phylogenetic network, phylogenetic network, phylogeny, data analysis software, data visualization software, software

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** SplitsTree

**Resource ID:** SCR\_014734

**Record Creation Time:** 20220129T080322+0000

**Record Last Update:** 20260912T195821+0000

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### Ratings and Alerts

No rating or validation information has been found for SplitsTree.

No alerts have been found for SplitsTree.

## Data and Source Information

**Source:** [SciCrunch Registry](#)

## Usage and Citation Metrics

We found 1361 mentions in open access literature.

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

Guo Y, et al. (2025) Genomic characterization of multidrug-resistant tuberculosis in Shanghai, China: antibiotic resistance, virulence and transmission. JAC-antimicrobial resistance, 7(3), dlaf064.

Jia M, et al. (2025) Molecular and Morphological Evidence Reveals Four New Neocosmospora Species from Dragon Trees in Yunnan Province, China. Journal of fungi (Basel, Switzerland), 11(8).

Šmíd J, et al. (2025) Phylogeny and systematics of Arabian lacertids from the Mesalina guttulata species complex (Squamata, Lacertidae), with the description of a new species. BMC zoology, 10(1), 11.

Marshall VA, et al. (2025) Kaposi Sarcoma-Associated Herpesvirus Sequencing in People Living With HIV in the Southern United States Reveals Subtype Diversity and Multiple Infections. Journal of medical virology, 97(7), e70467.

Kotov AA, et al. (2025) A phylogeographic pattern of the trans-Palaeartic littoral water flea Pleurotus truncatus (O.F. Müller, 1785) (Cladocera: Chydoridae). PeerJ, 13, e19355.

Van Borm S, et al. (2025) Genesis and Spread of Novel Highly Pathogenic Avian Influenza A(H5N1) Clade 2.3.4.4b Virus Genotype EA-2023-DG Reassortant, Western Europe. Emerging infectious diseases, 31(6), 1100.

De-Kayne R, et al. (2025) Incomplete recombination suppression fuels extensive haplotype diversity in a butterfly colour pattern supergene. PLoS biology, 23(2), e3003043.

Roca-Grande J, et al. (2025) Genomic characterization of invasive Neisseria meningitidis in Spain (2011/12-2022/23): expansion of clonal complex 213 and the potential threat to 4CMenB vaccine strain coverage. Emerging microbes & infections, 14(1), 2482696.

Chang CY, et al. (2025) Chromosome number variation and phylogenetic divergence of East Asian Cirsium sect. Onotrophe subsect. Nipponocirsium (Compositae), with a new species from Taiwan. Botanical studies, 66(1), 8.

Abad R, et al. (2025) Outbreak of invasive meningococcal disease caused by a meningococcus serogroup B expressing a rare porA genosubtype (19-54, 15), Spain, March to April 2024. Euro surveillance : bulletin European sur les maladies transmissibles = European communicable disease bulletin, 30(44).

Berg R, et al. (2025) Peripheral Budding Following Range Expansion Explains Diversity and Distribution of One-Sided Livebearing Fish. Molecular ecology, 34(16), e70023.

Kurilenko V, et al. (2025) Description and Genome-Based Analysis of *Vibrio chaetopteri* sp. nov., a New Species of the Mediterranei Clade Isolated from a Marine Polychaete. *Microorganisms*, 13(3).

Ahmadpour A, et al. (2025) Morphological and phylogenetic analyses of *Bipolaris* species associated with Poales and Asparagales host plants in Iran. *Frontiers in cellular and infection microbiology*, 15, 1520125.

Shazib SUA, et al. (2025) Phylogeny and species delimitation of ciliates in the genus *Spirostomum* (class Heterotrichea) using single-cell transcriptomes. *BMC ecology and evolution*, 25(1), 17.

Shen Z, et al. (2025) Genomic DNA barcodes provide novel insights into species delimitation in the complex *Camellia* sect. *Thea* (Theaceae). *BMC plant biology*, 25(1), 570.

Gomes F, et al. (2025) Long-term maintenance of a Deltacoronavirus infecting multiple bird species in Antarctica. *Microbiology spectrum*, 13(8), e0268824.

Dufresnes C, et al. (2025) Speciation and historical invasions of the Asian black-spined toad (*Duttaphrynus melanostictus*). *Nature communications*, 16(1), 298.

Schmidt SA, et al. (2025) Diversity on a small scale: phylogeography of the locally endemic dwarf succulent genus *Oophytum* (Aizoaceae) in the Knersvlakte of South Africa. *Annals of botany*, 135(4), 735.

Coomber AL, et al. (2025) A pangenome analysis reveals the center of origin and evolutionary history of *Phytophthora infestans* and 1c clade species. *PloS one*, 20(1), e0314509.

Johannesman A, et al. (2025) Phages carry orphan antitoxin-like enzymes to neutralize the DarTG1 toxin-antitoxin defense system. *Nature communications*, 16(1), 1598.