

# Resource Summary Report

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## 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 [NIF](#) .

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.

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).

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

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.

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.

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.

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.

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.

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.

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).

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.

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

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.

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).

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

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.

Calchi AC, et al. (2025) Diversity of *Cytauxzoon* spp. (Piroplasmida: Theileriidae) in Wild Felids from Brazil and Argentina. *Pathogens (Basel, Switzerland)*, 14(2).

Xia X, et al. (2025) Structural Variations Associated with Adaptation and Coat Color in Qinghai-Tibetan Plateau Cattle. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(31), e03258.

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

Li J, et al. (2025) ?Species of *Diaporthe* (Diaporthaceae, Diaporthales) associated with *Alnus nepalensis* leaf spot and branch canker diseases in Xizang, China. *MycKeys*, 116, 185.