Resource Summary Report

Generated by NIF on Apr 27, 2025

TempEst

RRID:SCR_017304
Type: Tool

Proper Citation

TempEst (RRID:SCR_017304)

Resource Information

URL: https://beast.community/tempest

Proper Citation: TempEst (RRID:SCR_017304)

Description: Software tool for investigating temporal signal and clocklikeness of molecular phylogenies. Used for visualization and analysis of temporally sampled sequence data to assess whether there is sufficient temporal signal in data to proceed with phylogenetic molecular clock analysis, and to identify sequences whose genetic divergence and sampling date are incongruent. Not available for downloading as of August 8, 2019.

Synonyms: Path-O-Gen, tempest

Resource Type: data processing software, data analysis software, software toolkit, software resource, software application

Defining Citation: DOI:doi.org/10.1093/ve/vew007

Keywords: temporal, signal, clocklikeness, molecular, phylogeny, visualization, analysis, temporally, sampled, sequenced, data, identify, genetic, incongruent

Funding: EU Seventh Framework Programme ;
ERC Grant

Availability: Restricted

Resource Name: TempEst

Resource ID: SCR_017304

Old URLs: http://tree.bio.ed.ac.uk/software/tempest/

Record Creation Time: 20220129T080334+0000

Record Last Update: 20250426T060623+0000

Ratings and Alerts

No rating or validation information has been found for TempEst.

No alerts have been found for TempEst.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 123 mentions in open access literature.

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

Zamunér CFC, et al. (2025) Evolution and spread of Xanthomonas citri subsp. citri in the São Paulo, Brazil, citrus belt inferred from 758 novel genomes. Microbial genomics, 11(1).

Fernandez JE, et al. (2024) Time-calibrated phylogenetic and chromosomal mobilome analyses of Staphylococcus aureus CC398 reveal geographical and host-related evolution. Nature communications, 15(1), 5526.

Rojas A, et al. (2024) Characterization of Dengue Virus 4 Cases in Paraguay, 2019-2020. Viruses, 16(2).

Flores RA, et al. (2024) Genetic Characterization and Phylogeographic Analysis of the First H13N6 Avian Influenza Virus Isolated from Vega Gull in South Korea. Viruses, 16(2).

da Costa Castilho M, et al. (2024) Evidence of Zika Virus Reinfection by Genome Diversity and Antibody Response Analysis, Brazil. Emerging infectious diseases, 30(2), 310.

Lu L, et al. (2024) West Nile virus spread in Europe: Phylogeographic pattern analysis and key drivers. PLoS pathogens, 20(1), e1011880.

Haga IR, et al. (2024) Sequencing and Analysis of Lumpy Skin Disease Virus Whole Genomes Reveals a New Viral Subgroup in West and Central Africa. Viruses, 16(4).

Cella E, et al. (2024) Streptococcus pneumoniae serotype 3 population structure in the era of conjugate vaccines, 2001-2018. Microbial genomics, 10(3).

Katahira K, et al. (2024) Mobile genetic element-driven genomic changes in a community-associated methicillin-resistant Staphylococcus aureus clone during its transmission in a regional community outbreak in Japan. Microbial genomics, 10(7).

Chem YK, et al. (2024) Molecular epidemiology of dengue in Malaysia: 2015-2021. Frontiers in genetics, 15, 1368843.

White RT, et al. (2024) Rapid identification and subsequent contextualization of an outbreak of methicillin-resistant Staphylococcus aureus in a neonatal intensive care unit using nanopore sequencing. Microbial genomics, 10(7).

Godwe C, et al. (2024) Phylogenetic evidence of extensive spatial mixing of diverse HIV-1 group M lineages within Cameroon but not between its neighbours. Virus evolution, 10(1), veae070.

Jaton J, et al. (2024) Research Note: Characterization and phylodynamic analysis of new infectious bursal disease virus variants circulating in Argentina. Poultry science, 103(6), 103623.

Yu D, et al. (2024) The origin, dissemination, and molecular networks of HIV-1 CRF65_cpx strain in Hainan Island, China. BMC infectious diseases, 24(1), 269.

Ba X, et al. (2024) Global emergence of a hypervirulent carbapenem-resistant Escherichia coli ST410 clone. Nature communications, 15(1), 494.

Goya S, et al. (2024) Standardized Phylogenetic Classification of Human Respiratory Syncytial Virus below the Subgroup Level. Emerging infectious diseases, 30(8), 1631.

Li X, et al. (2024) The evolutionary and transmission dynamics of HIV-1 CRF08_BC. PloS one, 19(9), e0310027.

Li YT, et al. (2024) From emergence to endemicity of highly pathogenic H5 avian influenza viruses in Taiwan. Nature communications, 15(1), 9348.

Moraes MM, et al. (2024) Spatiotemporal Dynamics of SARS-CoV-2 Variants During the First Year of the Pandemic Highlight the Earlier Emergence of the Zeta Variant of Interest in Brazil. Pathogens (Basel, Switzerland), 13(12).

Feng Y, et al. (2023) An integrated nationwide genomics study reveals transmission modes of typhoid fever in China. mBio, 14(5), e0133323.