

Resource Summary Report

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Clonalframe

RRID:SCR_016060

Type: Tool

Proper Citation

Clonalframe (RRID:SCR_016060)

Resource Information

URL: <http://www.xavierdidelot.xtreemhost.com/clonalframe.htm>

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Description: Software package for the inference of bacterial microevolution using multilocus sequence data. It is used to identify the clonal relationships between the members of a sample, while also estimating the chromosomal position of homologous recombination events that have disrupted the clonal inheritance.

Synonyms: ClonalFrameML

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

Defining Citation: [DOI:10.1534/genetics.106.063305](https://doi.org/10.1534/genetics.106.063305)

Keywords: analysis, sequence, inference, bacteria, microevolution, multilocus, clonal, sample, chromosome, homologous, recombination, disrupted, inheritance, DNA, genome

Funding: Wellcome Trust

Availability: Free, Available for download

Resource Name: Clonalframe

Resource ID: SCR_016060

Alternate IDs: OMICS_14623

Alternate URLs: <https://github.com/xavierdidelot/ClonalFrameML>,
<https://sources.debian.org/src/clonalframe/>

License: GNU General Public License

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260729T044404+0000

Ratings and Alerts

No rating or validation information has been found for Clonalframe.

No alerts have been found for Clonalframe.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 379 mentions in open access literature.

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

Unitt A, et al. (2025) Neisseria gonorrhoeae LIN codes provide a robust, multi-resolution lineage nomenclature. eLife, 14.

Narechania A, et al. (2025) What Do We Gain When Tolerating Loss? The Information Bottleneck Wrings Out Recombination. Molecular biology and evolution, 42(3).

Kim M, et al. (2025) Genomics and physiological characterizations of an acidotolerant nitrite-oxidizing Nitrospira enriched from freshwater pond. Applied and environmental microbiology, 91(10), e0152225.

Mechai S, et al. (2025) Genetic landscape of Borrelia burgdorferi sensu stricto in Canada: a study of genetic diversity. Scientific reports, 15(1), 40954.

Yassine I, et al. (2025) Investigating the population structure of Moraxella catarrhalis using a cgMLST scheme and LIN code system. Nature communications, 16(1), 9137.

Kaestli M, et al. (2025) High genomic diversity of Vibrio parahaemolyticus from underexplored tropical northern Australia: a baseline for future surveillance. Microbial genomics, 11(10).

Labbe F, et al. (2025) Genomic footprint of a shared Type 5 prophage in "Candidatus Liberibacter asiaticus" and "Candidatus Liberibacter africanus," two destructive bacterial pathogens of citrus Huanglongbing. Applied and environmental microbiology, 91(11), e0107225.

Lamberte LE, et al. (2025) Staphylococcus haemolyticus is a reservoir of antibiotic resistance genes in the preterm infant gut. Gut microbes, 17(1), 2519700.

Harada S, et al. (2025) Genomic epidemiology and antimicrobial resistance of Corynebacterium macclintockiae, the predominant species of human pathogens within the

Corynebacterium jeikeium complex. Journal of clinical microbiology, 63(8), e0050025.

Serna C, et al. (2025) Global dissemination of npmA mediated pan-aminoglycoside resistance via a mobile genetic element in Gram-positive bacteria. Nature communications, 16(1), 6360.

Krause AL, et al. (2025) Comparative and functional genomic analysis of foreign DNA defense mechanisms in *Enterococcus faecium*. Microbiology spectrum, 13(8), e0028925.

Zhao M, et al. (2025) Characterization of *Pseudomonas alliivorans* strains isolated from Georgia, USA: insights into genomic diversity and pathogenicity in onions. Applied and environmental microbiology, 91(12), e0164325.

Hale OF, et al. (2025) Elevated rates and biased spectra of mutations in anaerobically cultured lactic acid bacteria. mBio, 16(12), e0305425.

Timilsina S, et al. (2025) Diversification of an emerging bacterial plant pathogen; insights into the global spread of *Xanthomonas euvesicatoria* pv. *perforans*. PLoS pathogens, 21(4), e1013036.

Swali P, et al. (2025) Ancient *Borrelia* genomes document the evolutionary history of louse-borne relapsing fever. Science (New York, N.Y.), 388(6749), eadr2147.

Aoki K, et al. (2025) Tracking Antimicrobial Resistant Organisms Timely: a workflow validation study for successive core-genome SNP-based nosocomial transmission analysis. JAC-antimicrobial resistance, 7(3), dlaf069.

Kahn AK, et al. (2025) A pathogen of good taste: genetics of a bacterial host jump of the plant pathogen *Xylella fastidiosa* from coffee to wine grapes. Microbial genomics, 11(7).

Yassine I, et al. (2025) Understanding the population structure of *Moraxella catarrhalis* using core genome multilocus sequence typing (cgMLST) and a life identification number (LIN) code classification system. bioRxiv : the preprint server for biology.

Yang Q, et al. (2025) Bacterial genome-wide association studies: exploring the genetic variation underlying bacterial phenotypes. Applied and environmental microbiology, 91(6), e0251224.

Tu S, et al. (2025) Unveiling the emergence of community-acquired methicillin-resistant *Staphylococcus aureus* (CA-MRSA) in Chinese hospitals with remarkable genetic diversity: a multicenter molecular epidemiological investigation. Microbiology spectrum, 13(12), e0339524.