

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

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: 20260731T042958+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 [dkNET](#) .

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.

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

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.

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.

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

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.

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).

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.

Li X, et al. (2025) Molecular insights into the persistence and co-occurrence of two different carbapenem-resistant *Pseudomonas aeruginosa* lineages within a hospital setting. *Microbiology spectrum*, 13(10), e0043325.

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*.

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.

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

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.