

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

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: 20260821T194101+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 407 mentions in open access literature.

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

Yuan X, et al. (2026) Genetic Adaptation of Mesorhizobium Symbionts Associated With Caragana in Northern China Deserts. Ecology and evolution, 16(2), e73134.

She Q, et al. (2026) Rapid dissemination of Staphylococcus aureus in the neonatal intensive care unit is associated with invasive infection. Nature communications, 17(1).

Ko S, et al. (2026) Genome co-adaptation and the evolution of methicillin resistant Staphylococcus aureus. Genome biology, 27(1).

Yin Z, et al. (2026) Insights into novel diagnostic assay development, antimicrobial resistance, and pathogenicity in Proteus mirabilis through pan-genome analysis. Applied and environmental microbiology, 92(3), e0189825.

Zhang T, et al. (2026) Genomic survey uncovers the emergence of a multidrug-resistant dominant lineage in Proteus mirabilis populations. npj antimicrobials and resistance, 4(1).

Yu XA, et al. (2026) Genome-wide sweeps create ecological units in the human gut microbiome. Nature, 655(8121), 202.

Yoshizawa S, et al. (2026) One Health genomic insights into environmental and animal reservoirs of community-associated Clostridioides difficile in Japan. Applied and environmental microbiology, 92(6), e0039726.

Sharma P, et al. (2026) Putative azithromycin resistance mutations in Chlamydia trachomatis are globally distributed but arose before azithromycin was discovered. Antimicrobial agents and chemotherapy, 70(3), e0170825.

Griffin A, et al. (2026) Transport of the abundant intestinal amino acid glutamine by the enteric pathogen Campylobacter jejuni occurs via GutA (Cj0903), an AGCS family transporter. Microbiology (Reading, England), 172(1).

Hariharan J, et al. (2026) Biogeographical and phylogenetic constraints on horizontal gene transfer and genome evolution in *Streptomyces*. *Microbiology spectrum*, 14(2), e0295825.

Zhang X, et al. (2026) Within-host diversity and phased variant analysis reveal structures and recombination of *Helicobacter pylori* subpopulations in stomach. *GigaScience*, 15.

Chen D, et al. (2026) Analysis of mobile genetic elements carrying *mcr* genes in clinical *Leclercia* spp. isolates. *BMC microbiology*, 26(1).

Yano H, et al. (2026) Giant linear plasmids in *Mycobacterium avium* harbour a tRNA array unit. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 33(1).

Bull EM, et al. (2026) Pathological convergence of a bacterial plant pathogen is associated with the horizontal transfer of an effector-containing mobile element. *BMC genomics*, 27(1).

Mota-Merlo M, et al. (2026) Diversity of enzymes for exopolysaccharide synthesis in the fructophilic honeybee symbiont *Apilactobacillus kunkeei*. *BMC microbiology*, 26(1), 62.

Fang C, et al. (2026) Fourteen-year genomic surveillance of pediatric invasive *Streptococcus pneumoniae*: genomic and pan-genomic characterization. *BMC microbiology*, 26(1).

Rouxel C, et al. (2026) Exploration of geographical population structure of *Anaplasma phagocytophilum*: Insights from 12 newly sequenced European human and bovine genome assemblies. *Current research in parasitology & vector-borne diseases*, 9, 100393.

Monteith W, et al. (2026) Everything is everywhere but *Escherichia coli* adapts to different niches. *The ISME journal*, 20(1).

Webster J, et al. (2026) Buscogeny: A BUSCO leveraged phylogenomic tree builder. *International microbiology : the official journal of the Spanish Society for Microbiology*, 29(2), 255.

Maldonado N, et al. (2026) A matched case-control study on *Escherichia coli* factors contributing to sepsis and septic shock in bacteraemic patients. *Communications medicine*, 6(1), 104.