Resource Summary Report

Generated by dkNET on May 22, 2025

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

Defining Citation: DOI:10.1534/genetics.106.063305

Keywords: analysis, sequence, inference, bacteria, microevolution, multilocus, clonal, sample, chromosome, homologuous, 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: 20250522T061020+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 125 mentions in open access literature.

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

Yu Z, et al. (2024) Multilocus sequence typing and antibiotic resistance of Aeromonas isolated from freshwater fish in Hebei Province. PloS one, 19(3), e0298745.

Nong Y, et al. (2024) Emergence and clonal expansion of a qacA-harbouring sequence type 45 lineage of methicillin-resistant Staphylococcus aureus. Communications biology, 7(1), 349.

Fillo S, et al. (2021) Extensive Genome Exploration of Clostridium botulinum Group III Field Strains. Microorganisms, 9(11).

Gupta M, et al. (2021) Are ecological communities the seat of endosymbiont horizontal transfer and diversification? A case study with soil arthropod community. Ecology and evolution, 11(21), 14490.

Tseng SP, et al. (2020) Evidence for Common Horizontal Transmission of Wolbachia among Ants and Ant Crickets: Kleptoparasitism Added to the List. Microorganisms, 8(6).

Wang W, et al. (2019) Incomplete lineage sorting and introgression in the diversification of Chinese spot-billed ducks and mallards. Current zoology, 65(5), 589.

González-Torres P, et al. (2019) Impact of Homologous Recombination on the Evolution of Prokaryotic Core Genomes. mBio, 10(1).

Kajtoch ?, et al. (2019) Using host species traits to understand the Wolbachia infection distribution across terrestrial beetles. Scientific reports, 9(1), 847.

Lorenzo-Carballa MO, et al. (2019) Widespread Wolbachia infection in an insular radiation of damselflies (Odonata, Coenagrionidae). Scientific reports, 9(1), 11933.

Bai X, et al. (2019) Molecular Characterization and Comparative Genomics of Clinical Hybrid Shiga Toxin-Producing and Enterotoxigenic Escherichia coli (STEC/ETEC) Strains in Sweden. Scientific reports, 9(1), 5619.

Zhao Z, et al. (2019) Comparative genomics reveal pathogenicity-related loci in Pseudomonas syringae pv. actinidiae biovar 3. Molecular plant pathology, 20(7), 923.

Liu Z, et al. (2019) New Insight into the Evolution of Symbiotic Genes in Black Locust-Associated Rhizobia. Genome biology and evolution, 11(7), 1736.

Terán LC, et al. (2018) Phylogenomic Analysis of Lactobacillus curvatus Reveals Two Lineages Distinguished by Genes for Fermenting Plant-Derived Carbohydrates. Genome biology and evolution, 10(6), 1516.

Mahony AA, et al. (2018) Vancomycin-resistant Enterococcus faecium sequence type 796 - rapid international dissemination of a new epidemic clone. Antimicrobial resistance and infection control, 7, 44.

Rendueles O, et al. (2018) Genetic exchanges are more frequent in bacteria encoding capsules. PLoS genetics, 14(12), e1007862.

Li Z, et al. (2018) Investigation of genetic diversity and epidemiological characteristics of Pasteurella multocida isolates from poultry in southwest China by population structure, multi-locus sequence typing and virulence-associated gene profile analysis. The Journal of veterinary medical science, 80(6), 921.

González-Torres P, et al. (2018) Genome Variation in the Model Halophilic Bacterium Salinibacter ruber. Frontiers in microbiology, 9, 1499.

Bai X, et al. (2018) Identification and pathogenomic analysis of an Escherichia coli strain producing a novel Shiga toxin 2 subtype. Scientific reports, 8(1), 6756.

Hossain ZZ, et al. (2018) Transmission and Toxigenic Potential of Vibrio cholerae in Hilsha Fish (Tenualosa ilisha) for Human Consumption in Bangladesh. Frontiers in microbiology, 9, 222.

Seth-Smith HMB, et al. (2017) European Chlamydia abortus livestock isolate genomes reveal unusual stability and limited diversity, reflected in geographical signatures. BMC genomics, 18(1), 344.