Resource Summary Report

Generated by RRID on Apr 28, 2025

fineSTRUCTURE

RRID:SCR_018170
Type: Tool

Proper Citation

fineSTRUCTURE (RRID:SCR_018170)

Resource Information

URL: http://paintmychromosomes.com/

Proper Citation: fineSTRUCTURE (RRID:SCR_018170)

Description: Software tool as algorithm for identifying population structure using dense sequencing data. Can perform model based Bayesian clustering on large datasets, including full resequencing data.

Synonyms: FineSTRUCTURE version 2

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

Keywords: Identifying population structure, dense sequencing data, Bayesian clustering, large dataset, data, analysis, bio.tools

Funding:

Availability: Free, Available for download, Freely available

Resource Name: fineSTRUCTURE

Resource ID: SCR_018170

Alternate IDs: biotools:finestructure

Alternate URLs: https://bio.tools/finestructure

Record Creation Time: 20220129T080339+0000

Record Last Update: 20250428T054117+0000

Ratings and Alerts

No rating or validation information has been found for fineSTRUCTURE.

No alerts have been found for fineSTRUCTURE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 22 mentions in open access literature.

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

Henschel A, et al. (2024) Human migration from the Levant and Arabia into Yemen since Last Glacial Maximum. Scientific reports, 14(1), 31704.

Howard-McCombe J, et al. (2023) Genetic swamping of the critically endangered Scottish wildcat was recent and accelerated by disease. Current biology : CB, 33(21), 4761.

Ladner JT, et al. (2022) The population genetics of the causative agent of snake fungal disease indicate recent introductions to the USA. PLoS biology, 20(6), e3001676.

Cumer T, et al. (2022) Landscape and Climatic Variations Shaped Secondary Contacts amid Barn Owls of the Western Palearctic. Molecular biology and evolution, 39(1).

Zhang Z, et al. (2022) The Tibetan-Yi region is both a corridor and a barrier for human gene flow. Cell reports, 39(4), 110720.

You Y, et al. (2022) Genomic differentiation within East Asian Helicobacter pylori. Microbial genomics, 8(2).

Zhao Z, et al. (2022) Protocol to analyze population structure and migration history based on human genome variation data. STAR protocols, 4(1), 101928.

Capodiferro MR, et al. (2021) Archaeogenomic distinctiveness of the Isthmo-Colombian area. Cell, 184(7), 1706.

van Hal SJ, et al. (2021) The global dissemination of hospital clones of Enterococcus faecium. Genome medicine, 13(1), 52.

Muñoz-Ramirez ZY, et al. (2021) A 500-year tale of co-evolution, adaptation, and virulence:

Helicobacter pylori in the Americas. The ISME journal, 15(1), 78.

Whiting JR, et al. (2021) Drainage-structuring of ancestral variation and a common functional pathway shape limited genomic convergence in natural high- and low-predation guppies. PLoS genetics, 17(5), e1009566.

Joseph SJ, et al. (2021) Comparative Genomic and Transcriptomic Analysis of Naegleria fowleri Clinical and Environmental Isolates. mSphere, 6(4), e0063721.

Almarri MA, et al. (2021) The genomic history of the Middle East. Cell, 184(18), 4612.

Flores-Bello A, et al. (2021) Genetic origins, singularity, and heterogeneity of Basques. Current biology : CB, 31(10), 2167.

Paim TDP, et al. (2020) Genomic Breed Composition of Selection Signatures in Brangus Beef Cattle. Frontiers in genetics, 11, 710.

Paim TDP, et al. (2020) Dynamics of genomic architecture during composite breed development in cattle. Animal genetics, 51(2), 224.

Cui Y, et al. (2020) The landscape of coadaptation in Vibrio parahaemolyticus. eLife, 9.

Easton A, et al. (2020) Molecular evidence of hybridization between pig and human Ascaris indicates an interbred species complex infecting humans. eLife, 9.

Byrne RP, et al. (2020) Dutch population structure across space, time and GWAS design. Nature communications, 11(1), 4556.

Serra-Vidal G, et al. (2019) Heterogeneity in Palaeolithic Population Continuity and Neolithic Expansion in North Africa. Current biology : CB, 29(22), 3953.