

Resource Summary Report

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

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

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: 20260729T044451+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 23 mentions in open access literature.

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

Liu S, et al. (2025) Origin and de novo domestication of sweet orange. *Nature genetics*, 57(3), 754.

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.

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

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.

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).

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.

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.

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

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

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.

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

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

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.