

Resource Summary Report

Generated by [RRID](#) on Aug 5, 2026

GENEPOP

RRID:SCR_009194

Type: Tool

Proper Citation

GENEPOP (RRID:SCR_009194)

Resource Information

URL: <http://wbiomed.curtin.edu.au/genepop/>

Proper Citation: GENEPOP (RRID:SCR_009194)

Description: Population genetic data analysis software package. Used to perform exact Hardy Weinberg Equilibrium test. Used for population differentiation and for genotypic disequilibrium among pairs of loci. Computes estimates of F-statistics, null allele frequencies, allele size-based statistics for microsatellites, etc. and performs analyses of isolation by distance from pairwise comparisons of individuals or population samples., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: Genepop

Synonyms: genepop'007

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

Defining Citation: [PMID:21585727](#)

Keywords: Population, differentiation, genetic, data, analysis, Hardy Weinberg Equilibrium test, statistics, genotyping, disequilibrium, pair, loci, allele, frequency

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: GENEPOP

Resource ID: SCR_009194

Alternate IDs: nlx_154337

Alternate URLs: <https://kimura.univ-montp2.fr/~rousset/Genepop.htm>, <https://cran.r-project.org/web/packages/genepop/index.html>

License: CeCILL licence

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260805T044219+0000

Ratings and Alerts

No rating or validation information has been found for GENEPOP.

No alerts have been found for GENEPOP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2266 mentions in open access literature.

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

Yang H, et al. (2025) Population Genetics of *Haliotis discus hannai* in China Inferred Through EST-SSR Markers. *Genes*, 16(1).

Karaiskou N, et al. (2025) Grey Partridge (*Perdix perdix*) Introductions: Genetic Survey on Wild and Captive Populations at the Edges of the Range. *Ecology and evolution*, 15(3), e71122.

Areb E, et al. (2025) Functional and Genetic Insights into the Role of the NR4A1 Gene in the Litter Size of the Shaanbei White Cashmere Goat. *Animals : an open access journal from MDPI*, 15(12).

Martínez P, et al. (2025) Screening a new European hake (*Merluccius merluccius*) chromosome-level genome assembly suggests an XX/XY sex-determining system driven by the SRY-box transcription factor 3 (*sox3*). *G3 (Bethesda, Md.)*, 15(8).

Rueger T, et al. (2025) No evidence for kin selection as an explanation for social group formation in clown anemonefish. *Behavioral ecology : official journal of the International Society for Behavioral Ecology*, 36(4), araf075.

Mavrych V, et al. (2025) Genetic structure of different ethnic populations at the frontotemporal dementia risk loci. *PloS one*, 20(8), e0329809.

Bekkevold D, et al. (2025) Genetic Recovery of Two Wild Seatrout Populations Following Long-Term Stocking With Non-Native Conspecifics. *Molecular ecology*, 34(17), e70036.

Perez-Bello P, et al. (2025) DdRAD sequencing of the endangered species *Primula Palinuri* Petagna reveals high levels of inter-population diversity. *Scientific reports*, 15(1), 15245.

Soresinetti L, et al. (2025) The genetic trail of the invasive mosquito species *Aedes koreicus* from the east to the west of Northern Italy. *PLoS neglected tropical diseases*, 19(3), e0012945.

Lawrence AJ, et al. (2025) Maintenance of Genetic Diversity Despite Population Fluctuations in the Lesser Prairie-Chicken (*Tympanuchus pallidicinctus*). *Ecology and evolution*, 15(1), e70879.

Ronchetti F, et al. (2025) The Significance of Genetic Relatedness and Nest Sharing on the Worker-Worker Similarity of Gut Bacterial Microbiome and Cuticular Hydrocarbon Profile in a Sweat Bee. *Ecology and evolution*, 15(6), e71519.

Cordonnier M, et al. (2025) Frequent Queen Replacement and Presence of Unrelated Queens in Colonies of a Functionally Monogynous Ant Species. *Ecology and evolution*, 15(5), e71133.

Shen-Tu XL, et al. (2025) Size-Dependent Genetic Erosion due to Human Logging and Conservation Recommendation for an Endangered Yew (*Taxus fuana*) in Tibet, China. *Ecology and evolution*, 15(7), e71844.

Yovogan B, et al. (2025) Impact of dual active ingredients long-lasting insecticidal nets on the genetic structure of insecticide resistant populations of *Anopheles gambiae* in Southern Benin. *Malaria journal*, 24(1), 72.

Godina E, et al. (2025) Prediction of success in sports based on assumed individual genetic predisposition: lack of association with the C > T variant in the ACTN3 gene. *Journal of physiological anthropology*, 44(1), 6.

Umbrello L, et al. (2025) Noninvasive sampling reveals landscape genetic structure in the threatened ghost bat (*Macroderma gigas*) in an ore-rich region of Western Australia. *The Journal of heredity*, 116(4), 453.

Lee J, et al. (2025) Tracking genetic diversity in amur tigers: a long-term study using microsatellites in Southwest Primorye, Russia. *Molecular biology reports*, 52(1), 264.

Riccioni G, et al. (2025) Genetic structure and historical demography of inland wetland fish using the endangered Lisbon arched-mouth nase as a case-study. *Scientific reports*, 15(1), 22998.

Sambade IM, et al. (2025) Signatures of Selection for Resistance/Tolerance to *Perkinsus olseni* in Grooved Carpet Shell Clam (*Ruditapes decussatus*) Using a Population Genomics Approach. *Evolutionary applications*, 18(5), e70106.

Lamperty T, et al. (2025) Defaunation Increases Clustering and Fine-Scale Spatial Genetic Structure in a Small-Seeded Palm Despite Remaining Small-Bodied Frugivores. *Molecular ecology*, 34(2), e17620.