

Resource Summary Report

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[hierfstat](#)

RRID:SCR_022021

Type: Tool

Proper Citation

hierfstat (RRID:SCR_022021)

Resource Information

URL: <https://cran.r-project.org/package=hierfstat>

Proper Citation: hierfstat (RRID:SCR_022021)

Description: Software R package for estimation and tests of hierarchical F statistics.Used to estimate hierarchical F-statistics from haploid or diploid genetic data with any numbers of levels in hierarchy.Intended for analysis of population structure using genetic markers.

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

Defining Citation: [DOI:10.1093/genetics/144.4.1933](https://doi.org/10.1093/genetics/144.4.1933), [DOI:10.1534/genetics.116.198424](https://doi.org/10.1534/genetics.116.198424)

Keywords: estimation and tests of hierarchical F statistics, haploid or diploid genetic data, analysis of population structure, genetic markers

Availability: Free, Available for download, Freely available

Resource Name: hierfstat

Resource ID: SCR_022021

Alternate URLs: <https://github.com/jgx65/hierfstat>

License: GPL-3

Record Creation Time: 20220421T050138+0000

Record Last Update: 20260813T055226+0000

Ratings and Alerts

No rating or validation information has been found for hierfstat.

No alerts have been found for hierfstat.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Pereus D, et al. (2026) Genetic metrics decode Plasmodium falciparum diversity: complexity of infection, parasite connectivity, and transmission intensity in Mainland Tanzania's diverse regions. *Frontiers in genetics*, 17, 1695073.

Weir BS, et al. (2026) Allelic association analyses: estimation recommendations. *Genetics*, 233(2).

Adhikari L, et al. (2026) Dissecting the population structure, diversity and genetic architecture of rust resistance in wild emmer wheat (*Triticum turgidum* subsp. *dicoccoides*). *BMC genomics*, 27(1).

Garrett MJ, et al. (2025) Genetic Variation and Metapopulation Structure Inform Recovery Goals in a Threatened Species. *Genes*, 16(6).

Arbizu CI, et al. (2025) Genotyping by sequencing reveals the genetic diversity and population structure of Peruvian highland maize races. *Frontiers in plant science*, 16, 1526670.

Pickett BD, et al. (2022) Genome assembly of the roundjaw bonefish (*Albula glossodonta*), a vulnerable circumtropical sportfish. *GigaByte (Hong Kong, China)*, 2022, gigabyte44.

Hernandez-Castro LE, et al. (2022) Population genomics and geographic dispersal in Chagas disease vectors: Landscape drivers and evidence of possible adaptation to the domestic setting. *PLoS genetics*, 18(2), e1010019.

Purfield DC, et al. (2017) The distribution of runs of homozygosity and selection signatures in six commercial meat sheep breeds. *PloS one*, 12(5), e0176780.

Mousset M, et al. (2016) Lower selfing rates in metalicolous populations than in non-metallicolous populations of the pseudometallophyte *Noccaea caerulea* (Brassicaceae) in Southern France. *Annals of botany*, 117(3), 507.

Hasbún R, et al. (2016) Using Genome-Wide SNP Discovery and Genotyping to Reveal the Main Source of Population Differentiation in *Nothofagus dombeyi* (Mirb.) Oerst. in Chile. *International journal of genomics*, 2016, 3654093.

Zhao F, et al. (2015) Detection of selection signatures in dairy and beef cattle using high-density genomic information. *Genetics, selection, evolution : GSE*, 47(1), 49.