Resource Summary Report

Generated by NIF on May 21, 2025

ngsTools

RRID:SCR_005489
Type: Tool

Proper Citation

ngsTools (RRID:SCR_005489)

Resource Information

URL: https://github.com/mfumagalli/ngsTools

Proper Citation: ngsTools (RRID:SCR_005489)

Description: A collection of software programs for population genetics analyses from NGS (Next-Generation Sequencing) data, taking into account its statistical uncertainty. The methods implemented in these programs do not rely on SNP (Single Nucleotide Polymorphism) or genotype calling, and are particularly suitable for low sequencing depth data.

Abbreviations: ngsTools

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

Defining Citation: PMID:24458950

Keywords: java, next-generation sequencing, population, genetics, bio.tools

Funding:

Availability: GNU General Public License, v3, Acknowledgement requested

Resource Name: ngsTools

Resource ID: SCR_005489

Alternate IDs: OMICS_02248, biotools:ngstools

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

Record Creation Time: 20220129T080230+0000

Record Last Update: 20250519T203403+0000

Ratings and Alerts

No rating or validation information has been found for ngsTools.

No alerts have been found for ngsTools.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 51 mentions in open access literature.

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

Marr MM, et al. (2025) Genomic Insights Into Red Squirrels in Scotland Reveal Loss of Heterozygosity Associated With Extreme Founder Effects. Evolutionary applications, 18(1), e70072.

Gutiérrez-Guerrero YT, et al. (2024) Across two continents: The genomic basis of environmental adaptation in house mice (Mus musculus domesticus) from the Americas. PLoS genetics, 20(7), e1011036.

Howe NS, et al. (2024) Genomic evidence for domestication selection in three hatchery populations of Chinook salmon, Oncorhynchus tshawytscha. Evolutionary applications, 17(2), e13656.

Unneberg P, et al. (2024) Ecological genomics in the Northern krill uncovers loci for local adaptation across ocean basins. Nature communications, 15(1), 6297.

Ketchum RN, et al. (2024) Rapid speciation in the holopelagic ctenophore Mnemiopsis following glacial recession. bioRxiv : the preprint server for biology.

Sin SYW, et al. (2024) Genetic Basis and Evolution of Structural Color Polymorphism in an Australian Songbird. Molecular biology and evolution, 41(3).

Gustafsson M, et al. (2024) Unlocking the secret life of blue mussels: Exploring connectivity in the Skagerrak through biophysical modeling and population genomics. Evolutionary applications, 17(5), e13704.

Black AN, et al. (2024) Rapid vertebrate speciation via isolation, bottlenecks, and drift. Proceedings of the National Academy of Sciences of the United States of America, 121(22), e2320040121.

Folkertsma R, et al. (2024) Genomic signatures of climate adaptation in bank voles. Ecology and evolution, 14(3), e10886.

Pokharel K, et al. (2023) Whole-genome sequencing provides novel insights into the evolutionary history and genetic adaptation of reindeer populations in northern Eurasia. Scientific reports, 13(1), 23019.

Provost K, et al. (2022) The Genomic Landscapes of Desert Birds Form over Multiple Time Scales. Molecular biology and evolution, 39(10).

de Jager D, et al. (2021) High diversity, inbreeding and a dynamic Pleistocene demographic history revealed by African buffalo genomes. Scientific reports, 11(1), 4540.

Ferris KG, et al. (2021) The genomics of rapid climatic adaptation and parallel evolution in North American house mice. PLoS genetics, 17(4), e1009495.

Choi JY, et al. (2020) Divergent Selection and Primary Gene Flow Shape Incipient Speciation of a Riparian Tree on Hawaii Island. Molecular biology and evolution, 37(3), 695.

Gómez-Bahamón V, et al. (2020) Speciation Associated with Shifts in Migratory Behavior in an Avian Radiation. Current biology : CB, 30(7), 1312.

Hou Z, et al. (2020) Genetic architecture, demographic history, and genomic differentiation of Populus davidiana revealed by whole-genome resequencing. Evolutionary applications, 13(10), 2582.

Jia H, et al. (2020) Genome resequencing reveals demographic history and genetic architecture of seed salinity tolerance in Populus euphratica. Journal of experimental botany, 71(14), 4308.

Rose NH, et al. (2020) Climate and Urbanization Drive Mosquito Preference for Humans. Current biology : CB, 30(18), 3570.

Hou Z, et al. (2020) Population Genomics Reveals Demographic History and Genomic Differentiation of Populus davidiana and Populus tremula. Frontiers in plant science, 11, 1103.

Trier C, et al. (2020) Next-generation sequencing of newborn screening genes: the accuracy of short-read mapping. NPJ genomic medicine, 5, 36.