Resource Summary Report

Generated by dkNET on Apr 22, 2025

NGSadmix

RRID:SCR_003208
Type: Tool

Proper Citation

NGSadmix (RRID:SCR_003208)

Resource Information

URL: http://www.popgen.dk/software/index.php/NgsAdmix

Proper Citation: NGSadmix (RRID:SCR_003208)

Description: A tool for finding admixture proportions from next generation sequencing (NGS) data that is based on genotype likelihoods. It is a multithreaded c/c++ program.

Abbreviations: NGSadmix

Resource Type: software resource

Defining Citation: PMID:24026093

Keywords: next generation sequencing, admixture proportion, admixture, genotype, c, c++, admixture, association study, population structure, resequencing

Funding:

Availability: Acknowledgement requested

Resource Name: NGSadmix

Resource ID: SCR_003208

Alternate IDs: OMICS_01553

Record Creation Time: 20220129T080217+0000

Record Last Update: 20250420T014137+0000

Ratings and Alerts

No rating or validation information has been found for NGSadmix.

No alerts have been found for NGSadmix.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 105 mentions in open access literature.

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

van Elst T, et al. (2025) Integrative taxonomy clarifies the evolution of a cryptic primate clade. Nature ecology & evolution, 9(1), 57.

Aichelman HE, et al. (2025) Cryptic coral diversity is associated with symbioses, physiology, and response to thermal challenge. Science advances, 11(3), eadr5237.

Kontou D, et al. (2025) Adaptation in a keystone grazer under novel predation pressure. Proceedings. Biological sciences, 292(2039), 20241935.

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.

Knief U, et al. (2024) Evolution of Chromosomal Inversions across an Avian Radiation. Molecular biology and evolution, 41(6).

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

Caesar L, et al. (2024) Metagenomic analysis of the honey bee queen microbiome reveals low bacterial diversity and Caudoviricetes phages. mSystems, 9(2), e0118223.

Quiroga-Carmona M, et al. (2024) Species limits and hybridization in Andean leaf-eared mice (Phyllotis). bioRxiv : the preprint server for biology.

Hekimo?lu O, et al. (2024) High Crimean-Congo hemorrhagic fever incidence linked to greater genetic diversity and differentiation in Hyalomma marginatum populations in Türkiye. Parasites & vectors, 17(1), 477.

Mukogawa B, et al. (2024) The Varroa paradox: infestation levels and hygienic behavior in feral scutellata-hybrid and managed Apis mellifera ligustica honey bees. Scientific reports,

14(1), 1148.

Kessler C, et al. (2024) Genomic Analyses Capture the Human-Induced Demographic Collapse and Recovery in a Wide-Ranging Cervid. Molecular biology and evolution, 41(3).

Weatherup EF, et al. (2024) Co-phylogeographic structure in a disease-causing parasite and its oyster host. Parasitology, 151(7), 671.

Wimalarathna NA, et al. (2024) Genetic diversity and population structure of Piper nigrum (black pepper) accessions based on next-generation SNP markers. PloS one, 19(6), e0305990.

Wang X, et al. (2024) Persistent Gene Flow Suggests an Absence of Reproductive Isolation in an African Antelope Speciation Model. Systematic biology, 73(6), 979.

Moran PA, et al. (2024) Whole-Genome Resequencing Reveals Polygenic Signatures of Directional and Balancing Selection on Alternative Migratory Life Histories. Molecular ecology, 33(23), e17538.

Blom MPK, et al. (2024) Hybridization in birds-of-paradise: Widespread ancestral gene flow despite strong sexual selection in a lek-mating system. iScience, 27(7), 110300.

Gose MA, et al. (2024) Population genomics of the white-beaked dolphin (Lagenorhynchus albirostris): Implications for conservation amid climate-driven range shifts. Heredity, 132(4), 192.

Przelomska NAS, et al. (2024) Morphometrics and Phylogenomics of Coca (Erythroxylum spp.) Illuminate Its Reticulate Evolution, With Implications for Taxonomy. Molecular biology and evolution, 41(7).

Sirsi S, et al. (2024) Using genome-wide data to ascertain taxonomic status and assess population genetic structure for Houston toads (Bufo [=?Anaxyrus] houstonensis). Scientific reports, 14(1), 3306.

Jourdain E, et al. (2024) Social and genetic connectivity despite ecological variation in a killer whale network. Proceedings. Biological sciences, 291(2021), 20240524.