Resource Summary Report

Generated by <u>NIF</u> on May 16, 2025

PoPoolation2

RRID:SCR_003284 Type: Tool

Proper Citation

PoPoolation2 (RRID:SCR_003284)

Resource Information

URL: https://code.google.com/p/popoolation2/

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Description: Software to compare allele frequencies for SNPs between two or more populations and to identify significant differences. PoPoolation2 requires next generation sequencing data of pooled genomic DNA (Pool-Seq). It may be used for measuring differentiation between populations, for genome wide association studies and for experimental evolution.

Resource Type: software resource

Defining Citation: PMID:22025480

Keywords: standalone software, next generation sequencing, population genetics, population genomics, statistics, toolkit, population

Funding:

Availability: New BSD License

Resource Name: PoPoolation2

Resource ID: SCR_003284

Alternate IDs: OMICS_05824

Record Creation Time: 20220129T080218+0000

Record Last Update: 20250420T014139+0000

Ratings and Alerts

No rating or validation information has been found for PoPoolation2.

No alerts have been found for PoPoolation2.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 230 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>NIF</u>.

Wang G, et al. (2025) Molecular and Biochemical Mechanisms of Scutellum Color Variation in Bactrocera dorsalis Adults (Diptera: Tephritidae). Insects, 16(1).

Veregge M, et al. (2025) Virulence is not directly related to strain success in planta in Clavibacter nebraskensis. mSystems, 10(1), e0135524.

Kaur A, et al. (2025) Navigating Host Immunity and Concurrent Ozone Stress: Strain-Resolved Metagenomics Reveals Maintenance of Intraspecific Diversity and Genetic Variation in Xanthomonas on Pepper. Evolutionary applications, 18(1), e70069.

Eynard SE, et al. (2025) Sequence-Based Multi Ancestry Association Study Reveals the Polygenic Architecture of Varroa destructor Resistance in the Honeybee Apis mellifera. Molecular ecology, 34(3), e17637.

Garcia EM, et al. (2024) Phase variable colony variants are conserved across Gardnerella spp. and exhibit different virulence-associated phenotypes. mSphere, 9(7), e0045024.

Jutzeler KS, et al. (2024) Molecular dissection of laboratory contamination between two schistosome populations. Parasites & vectors, 17(1), 528.

Salamon M, et al. (2024) Limited Migration From Physiological Refugia Constrains the Rescue of Native Gastropods Facing an Invasive Predator. Evolutionary applications, 17(10), e70004.

Lin L, et al. (2024) Transposable elements impact the population divergence of rice blast fungus Magnaporthe oryzae. mBio, 15(5), e0008624.

Jutzeler KS, et al. (2024) Rapid phenotypic and genotypic change in a laboratory schistosome population. bioRxiv : the preprint server for biology.

Moulistanos A, et al. (2024) Genomic Signatures of Domestication in European Seabass

(Dicentrarchus labrax L.) Reveal a Potential Role for Epigenetic Regulation in Adaptation to Captivity. Ecology and evolution, 14(12), e70512.

Corral-Lopez A, et al. (2024) Functional convergence of genomic and transcriptomic architecture underlies schooling behaviour in a live-bearing fish. Nature ecology & evolution, 8(1), 98.

Bett VK, et al. (2024) Chromosome-Level Assembly of Artemia franciscana Sheds Light on Sex Chromosome Differentiation. Genome biology and evolution, 16(1).

Errbii M, et al. (2024) Causes and consequences of a complex recombinational landscape in the ant Cardiocondyla obscurior. Genome research, 34(6), 863.

Hoang KL, et al. (2024) Incomplete immunity in a natural animal-microbiota interaction selects for higher pathogen virulence. Current biology : CB, 34(6), 1357.

Jeffery NW, et al. (2024) Variation in genomic vulnerability to climate change across temperate populations of eelgrass (Zostera marina). Evolutionary applications, 17(4), e13671.

Jia P, et al. (2024) Evolution and Genetic Differentiation of Pleurotus tuoliensis in Xinjiang, China, Based on Population Genomics. Journal of fungi (Basel, Switzerland), 10(7).

Woronowicz KC, et al. (2024) Phylogenomic analysis of the Lake Kronotskoe species flock of Dolly Varden charr reveals genetic and developmental signatures of sympatric radiation. bioRxiv : the preprint server for biology.

You S, et al. (2024) Thermal acclimation uncovers a simple genetic basis of adaptation to high temperature in a cosmopolitan pest. iScience, 27(3), 109242.

Muharromah AF, et al. (2024) Fine-scale adaptive divergence and population genetic structure of Aedes aegypti in Metropolitan Manila, Philippines. Parasites & vectors, 17(1), 233.

?ížková D, et al. (2024) Convergence of gut phage communities but not bacterial communities following wild mouse bacteriophage transplantation into captive house mice. The ISME journal, 18(1).