

Resource Summary Report

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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., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Resource Type: software resource

Defining Citation: [PMID:22025480](#)

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

Availability: Free, Available for download, Freely available

Resource Name: PoPoolation2

Resource ID: SCR_003284

Alternate IDs: OMICS_05824

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260912T195555+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 242 mentions in open access literature.

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

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

Liu Z, et al. (2025) The fourspine stickleback (*Apeltes quadracus*) has an XY sex chromosome system with polymorphic inversions on both X and Y chromosomes. *PLoS genetics*, 21(5), e1011465.

Pinseel E, et al. (2025) Genome-Wide Adaptation to a Complex Environmental Gradient in a Keystone Phytoplankton Species. *Molecular ecology*, 34(13), e17817.

Kouamo MFM, et al. (2025) Allelic variation in a cluster of epsilon glutathione S-transferase genes contributes to DDT and pyrethroid resistance in the major African malaria vector *Anopheles funestus*. *BMC genomics*, 26(1), 452.

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.

Kraft DW, et al. (2025) Global stock structure of the Silky shark (*Carcharhinus falciformis*, *Carcharhinidae*) assessed with high-throughput DNA sequencing. *PeerJ*, 13, e19493.

Hearn J, et al. (2025) Over-expression and increased copy numbers of a cytochrome P450 and two UDP-glucuronosyltransferase genes in macrocyclic lactone resistant *Psoroptes ovis* of cattle. *PLoS pathogens*, 21(7), e1012963.

Schäfer M, et al. (2025) Aphid herbivory on macrophytes drives adaptive evolution in an aquatic community via indirect effects. *Proceedings of the National Academy of Sciences of the United States of America*, 122(34), e2502742122.

López ME, et al. (2025) Dynamic Outlier Slicing Allows Broader Exploration of Adaptive Divergence: A Comparison of Individual Genome and Pool-Seq Data Linked to Humic Adaptation in Perch. *Molecular ecology*, 34(4), e17659.

Haberkorn C, et al. (2025) Chromosome-scale genome assembly of the bed bug *Cimex lectularius* sheds light on a key insecticide resistance locus. *G3 (Bethesda, Md.)*, 15(9).

Brennan RS, et al. (2025) Complementary genetic and epigenetic changes facilitate rapid adaptation to multiple global change stressors. *Proceedings of the National Academy of Sciences of the United States of America*, 122(29), e2422782122.

Cao LJ, et al. (2025) Recurrent mutations drive the rapid evolution of pesticide resistance in the two-spotted spider mite *Tetranychus urticae*. *eLife*, 14.

Mathieu-Bégné E, et al. (2025) Genetic basis of resistance in hosts facing alternative infection strategies by a virulent bacterial pathogen. *G3 (Bethesda, Md.)*, 15(3).

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.

Forde S, et al. (2025) Management and conservation implications of cryptic population substructure for two commercially exploited fishes (*Merluccius* spp.) in southern Africa. *Molecular ecology resources*, 25(5), e13820.

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) Molecular dissection of laboratory contamination between two schistosome populations. *Parasites & vectors*, 17(1), 528.

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

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.