

Resource Summary Report

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PoPoolation

RRID:SCR_003495

Type: Tool

Proper Citation

PoPoolation (RRID:SCR_003495)

Resource Information

URL: <http://code.google.com/p/popoolation/>

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Description: A collection of tools to facilitate population genetic studies of next generation sequencing data from pooled individuals. It builds upon open source tools (bwa, samtools) and uses standard file formats (gtf, sam, pileup) to ensure a wide compatibility. PoPoolation allows to calculate Tajima's Pi, Watterson's Theta and Tajima's D for reference sequences using a sliding window approach. Alternatively these population genetic estimators may be calculated for a set of genes (provided as gtf). One of the main challenges in population genomics is to identify regions of interest on a genome wide scale. PoPoolation will greatly aid this task by allowing a fast and user friendly analysis of NGS data from DNA pools.

Abbreviations: PoPoolation

Resource Type: software resource

Defining Citation: [PMID:21253599](#)

Keywords: population genetics, next generation sequencing, sliding window, genome, bio.tools

Availability: Acknowledgement requested

Resource Name: PoPoolation

Resource ID: SCR_003495

Alternate IDs: OMICS_04414, biotools:popoolation

Alternate URLs: <https://bio.tools/popoolation>

Record Creation Time: 20220129T080219+0000

Ratings and Alerts

No rating or validation information has been found for PoPoolation.

No alerts have been found for PoPoolation.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 139 mentions in open access literature.

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

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

Schmidt TL, et al. (2025) Populations of the Australian Saltmarsh Mosquito *Aedes vigilax* Vary Between Panmixia and Temporally Stable Local Genetic Structure. *Evolutionary applications*, 18(6), e70119.

Pereira P, et al. (2025) Adaptation to Freshwater in Allis Shad Involved a Combination of Genomic and Epigenomic Changes. *Journal of molecular evolution*, 93(3), 406.

Ho TAT, et al. (2025) Gene Flow Disruption and Population Declines in a Soil Arthropod in Fragmented Habitats. *Molecular ecology*, 34(23), e17820.

Almojil D, et al. (2025) The two sub-genomes of the allotetraploid frog *Xenopus laevis* are evolving under similar selective pressure in extant populations. *BMC genomics*, 26(1), 887.

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.

Lucek K, et al. (2025) Genomic implications of the repeated shift to self-fertilization across a species' geographic distribution. *The Journal of heredity*, 116(1), 43.

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

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.

Ríos N, et al. (2025) Transcriptomic Divergence and Associated Markers Between Genomic Lineages of Silver Catfish (*Rhamdia quelen*). *Ecology and evolution*, 15(3), e71021.

Steward RA, et al. (2024) Genetic constraints in genes exhibiting splicing plasticity in facultative diapause. *Heredity*, 132(3), 142.

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

Marques J, et al. (2024) Long-term blood-free rearing of *Anopheles* mosquitoes with no effect on fitness, *Plasmodium* infectivity nor microbiota composition. *Scientific reports*, 14(1), 19473.

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.

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

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*.

Angst P, et al. (2024) Genome-Wide Allele Frequency Changes Reveal That Dynamic Metapopulations Evolve Differently. *Molecular biology and evolution*, 41(7).

Ord J, et al. (2023) High Nucleotide Diversity Accompanies Differential DNA Methylation in Naturally Diverging Populations. *Molecular biology and evolution*, 40(4).

Díaz F, et al. (2023) Transcriptional misexpression in hybrids between species linked by gene flow is associated with patterns of sequence divergence. *Genome biology and evolution*, 15(5).

Huang G, et al. (2023) Balancing selection on an MYB transcription factor maintains the twig trichome color variation in *Melastoma normale*. *BMC biology*, 21(1), 122.