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 intererest 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

Funding:

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

Record Last Update: 20250410T065011+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 131 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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.

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.

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.

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.

Jeffery NW, et al. (2024) Variation in genomic vulnerability to climate change across

temperate populations of eelgrass (Zostera marina). Evolutionary applications, 17(4), e13671.

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

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.

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

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.

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).

Rimbault M, et al. (2023) Contrasting Evolutionary Patterns Between Sexual and Asexual Lineages in a Genomic Region Linked to Reproductive Mode Variation in the pea aphid. Genome biology and evolution, 15(9).

Chen Y, et al. (2023) The mutational signatures of poor treatment outcomes on the drug-susceptible Mycobacterium tuberculosis genome. eLife, 12.

Barata C, et al. (2023) Selection on the Fly: Short-Term Adaptation to an Altered Sexual Selection Regime in Drosophila pseudoobscura. Genome biology and evolution, 15(7).

Zarate D, et al. (2023) Seasonal variation in defense behavior in European and scutellata-hybrid honey bees (Apis mellifera) in Southern California. Scientific reports, 13(1), 12790.

Flury JM, et al. (2023) Potential Contribution of Ancient Introgression to the Evolution of a Derived Reproductive Strategy in Ricefishes. Genome biology and evolution, 15(8).

DiVito Evans A, et al. (2023) Histone methylation regulates reproductive diapause in Drosophila melanogaster. PLoS genetics, 19(9), e1010906.

Li Z, et al. (2023) The pig pangenome provides insights into the roles of coding structural variations in genetic diversity and adaptation. Genome research, 33(10), 1833.

Langmüller AM, et al. (2023) The genomic distribution of transposable elements is driven by spatially variable purifying selection. Nucleic acids research, 51(17), 9203.