Resource Summary Report

Generated by NIF on Apr 22, 2025

EASYPOP

RRID:SCR_008961
Type: Tool

Proper Citation

EASYPOP (RRID:SCR_008961)

Resource Information

URL: https://www.unil.ch/dee/en/home/menuinst/softwares--dataset/softwares/easypop.html

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Description: Software application allowing to simulate population genetics datasets. It allows generating genetic data for haploid, diploid, and haplodiploid organisms under a variety of mating systems. It includes various migration and mutation models. Output can be generated for the FSTAT, GENEPOP, and ARLEQUIN genetic analysis packages. (entry from Genetic Analysis Software)

Abbreviations: EASYPOP

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, ms-windows, (95/98/nt/2000/xp), macos, (x)

Funding:

Resource Name: EASYPOP

Resource ID: SCR_008961

Alternate IDs: nlx_154012

Old URLs: http://www.unil.ch/dee/page36926_fr.html

Record Creation Time: 20220129T080250+0000

Record Last Update: 20250421T053707+0000

Ratings and Alerts

No rating or validation information has been found for EASYPOP.

No alerts have been found for EASYPOP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Parreira BR, et al. (2025) Effects of Social Structure on Effective Population Size Change Estimates. Evolutionary applications, 18(1), e70063.

Erdman B, et al. (2024) Complications of Estimating Hatchery Introgression in the Face of Rapid Divergence: A Case Study in Brook Trout (Salvelinus fontinalis). Evolutionary applications, 17(12), e70026.

Ackiss AS, et al. (2020) Genotyping-by-sequencing illuminates high levels of divergence among sympatric forms of coregonines in the Laurentian Great Lakes. Evolutionary applications, 13(5), 1037.

Miller JM, et al. (2020) The influence of a priori grouping on inference of genetic clusters: simulation study and literature review of the DAPC method. Heredity, 125(5), 269.

Monette K, et al. (2020) Inferring responses to climate warming from latitudinal pattern of clonal hybridization. Ecology and evolution, 10(1), 307.

Sethuraman A, et al. (2018) Estimating Genetic Relatedness in Admixed Populations. G3 (Bethesda, Md.), 8(10), 3203.

Kuismin MO, et al. (2017) CONE: Community Oriented Network Estimation Is a Versatile Framework for Inferring Population Structure in Large-Scale Sequencing Data. G3 (Bethesda, Md.), 7(10), 3359.

Pelletier A, et al. (2017) Determining causes of genetic isolation in a large carnivore (Ursus americanus) population to direct contemporary conservation measures. PloS one, 12(2), e0172319.

Gracianne C, et al. (2016) Temporal sampling helps unravel the genetic structure of naturally occurring populations of a phytoparasitic nematode. 2. Separating the relative effects of gene flow and genetic drift. Evolutionary applications, 9(8), 1005.

Rojas-Hernandez N, et al. (2016) Highly Connected Populations and Temporal Stability in Allelic Frequencies of a Harvested Crab from the Southern Pacific Coast. PloS one, 11(11), e0166029.

Ascensão F, et al. (2016) Disentangle the Causes of the Road Barrier Effect in Small Mammals through Genetic Patterns. PloS one, 11(3), e0151500.

Kvistad L, et al. (2015) Very Low Population Structure in a Highly Mobile and Wide-Ranging Endangered Bird Species. PloS one, 10(12), e0143746.

Guildea C, et al. (2015) Introgression threatens the survival of the critically endangered freshwater crayfish Cherax tenuimanus (Decapoda: Parastacidae) in the wild. PloS one, 10(3), e0121075.

Carvajal-Rodríguez A, et al. (2010) Simulation of genes and genomes forward in time. Current genomics, 11(1), 58.

Liu Y, et al. (2008) A survey of genetic simulation software for population and epidemiological studies. Human genomics, 3(1), 79.