

Resource Summary Report

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POPART

RRID:SCR_021924

Type: Tool

Proper Citation

POPART (RRID:SCR_021924)

Resource Information

URL: <http://popart.otago.ac.nz/>

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Description: Software package that provides implementation of haplotype network methods, phylogeographic visualisation tools and standard statistical tests, together with publication ready figure production. Population genetics software. Used to understand evolutionary relationships among populations.

Abbreviations: PopART

Synonyms: Population Analysis with Reticulate Trees

Resource Type: software toolkit, software resource

Defining Citation: [DOI:10.1111/2041-210X.12410](https://doi.org/10.1111/2041-210X.12410)

Keywords: population genetics, evolutionary relationships among populations

Funding: Allan Wilson Centre Imaging Evolution Initiative

Availability: Free, Available for download, Freely available

Resource Name: POPART

Resource ID: SCR_021924

Alternate URLs: <https://github.com/jessicawleigh/popart-current>

License: Lesser GNU Public License

Record Creation Time: 20220421T050137+0000

Record Last Update: 20260819T044524+0000

Ratings and Alerts

No rating or validation information has been found for POPART.

No alerts have been found for POPART.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 320 mentions in open access literature.

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

Han ACN, et al. (2026) ?A new species of the *Amyntas corticis* group with support from mitogenomic data and a new record of *Metaphire agrestis* (Goto & Hatai, 1899) (Oligochaeta, Megascolecidae) in northeastern China. *ZooKeys*, 1266, 231.

Bulanawichit W, et al. (2026) Molecular detection and genetic diversity of hemotropic *Mycoplasma* species in synanthropic rodents across Thailand. *Current research in parasitology & vector-borne diseases*, 9, 100370.

Godinez CJP, et al. (2026) Phylogeny and Genetic Diversity of Philippine Mallard Ducks Based on the Mitochondrial DNA D-loop Region. *The journal of poultry science*, 63, 2026012.

Liang XY, et al. (2026) Ancient mitogenomes reveal the genetic relationship among extinct and extant water buffaloes. *iScience*, 29(7), 116354.

Fakhfakh SEA, et al. (2026) Whole Genome Characterization of Lumpy Skin Disease Virus and Bovine Papular Stomatitis Virus Detected in Cattle During the 2024-2025 Outbreaks in Tunisia. *Viruses*, 18(6).

Owaresat JK, et al. (2026) Genetic diversity, phylogeography, population structure, and demographic history of wild *Catla catla* at a transboundary scale across South Asia revealed by Mitochondrial COI sequences. *PloS one*, 21(2), e0341820.

Naik VCB, et al. (2026) Genetic structure and haplotype diversity in Indian populations of brown plant hopper, *Nilaparvata lugens* stal using mtCOI. *Scientific reports*, 16(1), 2971.

Valenzuela-Turner C, et al. (2026) Across the Arctic: Mitogenomic Phylogeny of Arctic Foxes (*Vulpes lagopus*) Reveals Several New Matriline and Illuminates the Colonization History of the Icelandic Population. *Genes*, 17(2).

Vermaak A, et al. (2026) Three new species of *Macvicaria* Gibson & Bray, 1982 (Digenea: Opecoelidae) infecting *Diplodus* spp. (Teleostei, Sparidae) from South Africa and Namibia. *Systematic parasitology*, 103(4).

Koç-?nak N, et al. (2026) Insecticide resistance level and geographical distribution of target-site mutations in field collections of the house fly (*Musca domestica*) from Türkiye. *Ecotoxicology* (London, England), 35(5).

Blaschikoff L, et al. (2026) Genomic Variation and Population Structure of Portuguese Native Dog Breeds. *Animal genetics*, 57(3), e70144.

Ssenkuba F, et al. (2026) Invaders taking over-Mollusc faunal change in volcanic barrier lakes of the Albertine Rift biodiversity hotspot. *PloS one*, 21(6), e0352648.

Nicolas LA, et al. (2026) Parallel clines of chromosomal inversion frequencies in seaweed flies are associated with thermal variation. *Heredity*, 135(3), 162.

Tomarovsky AA, et al. (2026) Genomics of Sable (*Martes zibellina*) × Pine Marten (*Martes martes*) Hybridization. *Genome biology and evolution*, 18(3).

Chai MJ, et al. (2026) Data collected in a citizen scientist study uncover a new species record of *Phoxinus* minnow for Austria. *Environmental monitoring and assessment*, 198(4).

Kullan ARK, et al. (2026) Genetic diversity of mitochondrial DNA D-loop sequences in UAE native chickens. *Poultry science*, 105(6), 106748.

Hashemzadeh Segherloo I, et al. (2026) New Insights Into the Biogeography of Six Garra Species (Teleostei: Cyprinidae) in the Persian Gulf Basin. *Ecology and evolution*, 16(4), e73463.

Fakoya AO, et al. (2026) HapAsmbl: A reference-aided pipeline for assembling haplotypes in Nanopore amplicon sequence data of polymorphic populations. *Applications in plant sciences*, 14(3), e70062.

Luu AH, et al. (2026) Adaptive radiation and structural tailoring of the Vietnamese Blec2 immunogenetic reservoir. *Frontiers in genetics*, 17, 1819401.

El-Barasi OM, et al. (2026) Genetic taxonomical study of the families squalidae and squatinidae with the first mediterranean record of *Squalus mitsukurii* and the first libyan record of *Squalus megalops*. *Open veterinary journal*, 16(2), 817.