

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 resource, software toolkit

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: 20260801T191106+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 239 mentions in open access literature.

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

Wu D, et al. (2025) Phylogeographic history of Parthenocissus (Vitaceae) in North America based on chloroplast and nuclear DNA sequences. *Frontiers in plant science*, 16, 1521784.

Bui TTH, et al. (2025) Preliminary detection of haemoplasma in Thai cat blood samples using universal primers: identifying 'Candidatus Mycoplasma haemominutum' and closely related species. *Journal of feline medicine and surgery*, 27(5), 1098612X251335211.

El Fahime E, et al. (2025) Moroccan genome project: genomic insight into a North African population. *Communications biology*, 8(1), 584.

Brocklebank JW, et al. (2025) Maternal origins and genetic diversity of Sabahan swamp buffalo using mitochondrial cytochrome b gene. *Scientific reports*, 15(1), 33685.

Kumar P, et al. (2025) Genetic structuring and estimation of reproductive adults in *Onchocerca volvulus*: A genome-wide analysis across hosts and regions. *PLoS neglected tropical diseases*, 19(7), e0013221.

Dos Santos MC, et al. (2025) Does viral circulation in slums have a global impact? The lesson learned from SARS-CoV-2 circulation in Complexo de favelas da Maré, Rio de Janeiro, Brazil. *Frontiers in microbiology*, 16, 1483895.

Xiao R, et al. (2025) Phylogeographic and genetic insights into *Sinonychia martensi*: an endemic cave-dwelling harvestman in Beijing. *BMC ecology and evolution*, 25(1), 5.

Zhang Q, et al. (2025) Multi-centric origins and gene flow shape the diversity of α -thalassemia mutations in Southern East Asia. *Nature communications*, 16(1), 10220.

Millanes AM, et al. (2025) Different Patterns of Frequency, Lichen Specificity and Thallus Location Between the Yeast and Filamentous Phases of Two Lichen-Inhabiting Basidiomycetes. *Environmental microbiology*, 27(11), e70203.

Gao S, et al. (2025) Genetic diversity and structure of Mongolian gazelle (*Procapra gutturosa*) in fragmented habitats. *BMC genomics*, 26(1), 1152.

- Mulko M, et al. (2025) Taxonomic reassessment of captive sugar gliders using genetic analyses and complementary acoustic data. *Scientific reports*, 15(1), 45082.
- Arce LF, et al. (2025) Genetic diversity of *Diectophyme renale* in Southern South America. *Parasitology*, 152(8), 776.
- Ochoa-Zavala M, et al. (2025) Mitochondrial DNA patterns describe the evolutionary history of the bonnethead shark *Sphyrna tiburo* (Linneus 1758) complex in the western Atlantic Ocean. *Journal of fish biology*, 106(2), 403.
- Hayakawa T, et al. (2025) Genome-scale evolution in local populations of wild chimpanzees. *Scientific reports*, 15(1), 548.
- Moudgil AD, et al. (2025) Mitochondrial genetic markers based phylogenetic analyses of *Hyalomma dromedarii* Koch, 1844 (Acari: Ixodidae). *Journal, genetic engineering & biotechnology*, 23(1), 100460.
- Castex C, et al. (2025) Genetic characterization of the bat and human lineages of the common bed bug (*Cimex lectularius*) at a local scale. *Parasitology*, 152(5), 510.
- Khan J, et al. (2025) Phylogeographic Patterns and Genetic Diversity of *Anopheles stephensi*: Implications for Global Malaria Transmission. *Tropical medicine and infectious disease*, 10(4).
- Lu K, et al. (2025) Characterization of Spectrin Family Genes and Their Evolutionary Roles in Domestication and Breeding of the Silkworm *Bombyx mori*. *Insects*, 16(6).
- Park K, et al. (2025) Discovery and genomic characterization of Ulleung virus harbored by *Crocidura utsuryoensis* on Ulleung Island in Republic of Korea. *Scientific reports*, 15(1), 21748.
- Horikoshi RJ, et al. (2025) Population genetic structure and demographic of *Spodoptera eridania* (Lepidoptera: Noctuidae), an emerging soybean pest in Brazil. *Journal of insect science (Online)*, 25(5).