

Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 14, 2025

BayeScan

RRID:SCR_022018

Type: Tool

Proper Citation

BayeScan (RRID:SCR_022018)

Resource Information

URL: <http://cmpg.unibe.ch/software/BayeScan/index.html>

Proper Citation: BayeScan (RRID:SCR_022018)

Description: Software tool to identify candidate loci under natural selection from genetic data, using differences in allele frequencies between populations.

Resource Type: data analysis software, software application, software resource, data processing software

Defining Citation: [DOI:10.1534/genetics.108.092221](https://doi.org/10.1534/genetics.108.092221), [DOI:10.1111/j.1365-294X.2010.04820.x](https://doi.org/10.1111/j.1365-294X.2010.04820.x), [DOI:10.1111/j.1365-294X.2011.05015.x](https://doi.org/10.1111/j.1365-294X.2011.05015.x)

Keywords: identify candidate loci under natural selection, genetic data, differences in allele frequencies between populations

Funding: University of Bern Research Foundation ;
Swiss National Science Foundation

Availability: Free, Available for Download, Freely available

Resource Name: BayeScan

Resource ID: SCR_022018

Record Creation Time: 20220421T050138+0000

Record Last Update: 20250412T060426+0000

Ratings and Alerts

No rating or validation information has been found for BayeScan.

No alerts have been found for BayeScan.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 74 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Torrado H, et al. (2025) Evolutionary Genomics of Two Co-occurring Congeneric Fore Reef Coral Species on Guam (Mariana Islands). *Genome biology and evolution*, 17(1).

Worthington BM, et al. (2024) Serological evidence of sarbecovirus exposure along Sunda pangolin trafficking pathways. *BMC biology*, 22(1), 274.

Bruno S, et al. (2024) Validation of selection signatures for coat color in the Podolica Italiana gray cattle breed. *Frontiers in genetics*, 15, 1453295.

Rengefors K, et al. (2024) Population genomic analyses reveal that salinity and geographic isolation drive diversification in a free-living protist. *Scientific reports*, 14(1), 4986.

Vangestel C, et al. (2024) Chromosomal inversions from an initial ecotypic divergence drive a gradual repeated radiation of Galápagos beetles. *Science advances*, 10(22), eadk7906.

Russo A, et al. (2024) Genome of the early spider-orchid *Ophrys sphegodes* provides insights into sexual deception and pollinator adaptation. *Nature communications*, 15(1), 6308.

Vásquez C, et al. (2023) Natural mega disturbances drive spatial and temporal changes in diversity and genetic structure on the toadfish *Aphos porosus*. *Scientific reports*, 13(1), 13902.

Zhou C, et al. (2023) Genetic structure of an endangered species *Ormosia henryi* in southern China, and implications for conservation. *BMC plant biology*, 23(1), 220.

Sun Y, et al. (2023) Population Genomic Analyses Suggest a Hybrid Origin, Cryptic Sexuality, and Decay of Genes Regulating Seed Development for the Putatively Strictly Asexual *Kingdonia uniflora* (Circaceasteraceae, Ranunculales). *International journal of molecular sciences*, 24(2).

Silliman K, et al. (2023) Epigenetic and Genetic Population Structure is Coupled in a Marine Invertebrate. *Genome biology and evolution*, 15(2).

Lindstedt C, et al. (2022) The impact of life stage and pigment source on the evolution of novel warning signal traits. *Evolution; international journal of organic evolution*, 76(3), 554.

Kiani M, et al. (2022) ddRAD Sequencing Identifies Pesticide Resistance-Related Loci and Reveals New Insights into Genetic Structure of *Bactericera cockerelli* as a Plant Pathogen Vector. *Insects*, 13(3).

Farhadi A, et al. (2022) Genome-wide SNPs in the spiny lobster *Panulirus homarus* reveal a hybrid origin for its subspecies. *BMC genomics*, 23(1), 750.

Chou CH, et al. (2022) Patterns of genetic variation and QTLs controlling grain traits in a collection of global wheat germplasm revealed by high-quality SNP markers. *BMC plant biology*, 22(1), 455.

Hoey JA, et al. (2022) Genetic decline and recovery of a demographically rebuilt fishery species. *Molecular ecology*, 31(22), 5684.

Pickett BD, et al. (2022) Genome assembly of the roundjaw bonefish (*Albula glossodonta*), a vulnerable circumtropical sportfish. *GigaByte (Hong Kong, China)*, 2022, gigabyte44.

Teske PR, et al. (2021) The sardine run in southeastern Africa is a mass migration into an ecological trap. *Science advances*, 7(38), eabf4514.

Schwabl P, et al. (2021) Colonization and genetic diversification processes of *Leishmania infantum* in the Americas. *Communications biology*, 4(1), 139.

McLean-Rodríguez FD, et al. (2021) Genetic diversity and selection signatures in maize landraces compared across 50 years of in situ and ex situ conservation. *Heredity*, 126(6), 913.

Bootsma ML, et al. (2021) The ghosts of propagation past: haplotype information clarifies the relative influence of stocking history and phylogeographic processes on contemporary population structure of walleye (*Sander vitreus*). *Evolutionary applications*, 14(4), 1124.