Resource Summary Report

Generated by NIF on Sep 15, 2026

GenGIS

RRID:SCR_001465
Type: Tool

Proper Citation

GenGIS (RRID:SCR_001465)

Resource Information

URL: https://github.com/beiko-lab/gengis

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Description: A bioinformatics application that allows users to combine digital map data with information about biological sequences collected from the environment. It provides a 3D graphical interface in which the user can navigate and explore the data, as well as a Python interface that allows easy scripting of statistical analyses using the Rpy libraries.

Resource Type: software resource

Defining Citation: PMID:23922841

Keywords: standalone software

Funding: Genome Atlantic ;
Genome Canada ;
Biomonitoring 2.0 Project ;
Dalhousie Centre for Comparative Genomics and Evolutionary Bioinformatics ;
Tula Foundation ;
Natural Sciences and Engineering Research Council of Canada ;
Dalhousie Faculty of Computer Science

Availability: Free, Available for download, Freely available

Resource Name: GenGIS

Resource ID: SCR_001465

Alternate IDs: OMICS_04013

Alternate URLs: http://kiwi.cs.dal.ca/GenGIS/

License: GNU General Public License, v3

Record Creation Time: 20220129T080207+0000

Record Last Update: 20260912T195526+0000

Ratings and Alerts

No rating or validation information has been found for GenGIS.

No alerts have been found for GenGIS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 38 mentions in open access literature.

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

Klesser R, et al. (2024) Ice cage: new records and cryptic, isolated lineages in wingless snow flies (Diptera, Limoniidae: Chionea spp.) in German lower mountain ranges. Die Naturwissenschaften, 111(2), 15.

Wang X, et al. (2024) Barley farmland harbors a highly homogeneous soil bacterial community compared to wild ecosystems in the Qinghai-Xizang Plateau. Frontiers in microbiology, 15, 1418161.

Yang L, et al. (2023) Phylogeography and ecological niche modeling implicate multiple microrefugia of Swertia tetraptera during quaternary glaciations. BMC plant biology, 23(1), 450.

Vélez JM, et al. (2021) Phylogenetic diversity of 200+ isolates of the ectomycorrhizal fungus Cenococcum geophilum associated with Populus trichocarpa soils in the Pacific Northwest, USA and comparison to globally distributed representatives. PloS one, 16(1), e0231367.

Ellepola G, et al. (2021) Molecular species delimitation of shrub frogs of the genus Pseudophilautus (Anura, Rhacophoridae). PloS one, 16(10), e0258594.

Magalhães KX, et al. (2021) Phylogeography of Baryancistrus xanthellus (Siluriformes: Loricariidae), a rheophilic catfish endemic to the Xingu River basin in eastern Amazonia. PloS one, 16(8), e0256677.

Guo W, et al. (2021) Contrasting Phylogeographic Patterns in Lumnitzera Mangroves Across the Indo-West Pacific. Frontiers in plant science, 12, 637009.

Coscolla M, et al. (2021) Phylogenomics of Mycobacterium africanum reveals a new lineage and a complex evolutionary history. Microbial genomics, 7(2).

Werth S, et al. (2021) Deep divergence between island populations in lichenized fungi. Scientific reports, 11(1), 7428.

Mao TR, et al. (2021) Evolution in Sinocyclocheilus cavefish is marked by rate shifts, reversals, and origin of novel traits. BMC ecology and evolution, 21(1), 45.

Tan W, et al. (2020) Soil bacterial diversity correlates with precipitation and soil pH in long-term maize cropping systems. Scientific reports, 10(1), 6012.

Nikolic N, et al. (2020) Connectivity and population structure of albacore tuna across southeast Atlantic and southwest Indian Oceans inferred from multidisciplinary methodology. Scientific reports, 10(1), 15657.

Le MH, et al. (2020) Structure and membership of gut microbial communities in multiple fish cryptic species under potential migratory effects. Scientific reports, 10(1), 7547.

Zhou J, et al. (2020) Wine Terroir and the Soil Bacteria: An Amplicon Sequencing-Based Assessment of the Barossa Valley and Its Sub-Regions. Frontiers in microbiology, 11, 597944.

Vuji? A, et al. (2020) Revision of the Merodon serrulatus group (Diptera, Syrphidae). ZooKeys, 909, 79.

Stapleton PJ, et al. (2019) Evaluating the use of whole genome sequencing for the investigation of a large mumps outbreak in Ontario, Canada. Scientific reports, 9(1), 12615.

Vandelannoote K, et al. (2019) Mycobacterium ulcerans Population Genomics To Inform on the Spread of Buruli Ulcer across Central Africa. mSphere, 4(1).

Hwang EY, et al. (2019) Genetic Diversity and Phylogenetic Relationships of Annual and Perennial Glycine Species. G3 (Bethesda, Md.), 9(7), 2325.

Vuji? A, et al. (2018) Revision of the Palaearctic species of the Merodon desuturinus group (Diptera, Syrphidae). ZooKeys(771), 105.

Mercante JW, et al. (2018) Genomic heterogeneity differentiates clinical and environmental subgroups of Legionella pneumophila sequence type 1. PloS one, 13(10), e0206110.