

Resource Summary Report

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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: 20260801T190130+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 [dkNET](#) .

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.

Klessner 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.

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.

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

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

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.

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

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.

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.

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.

Vujić 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.

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

Sathkumara HD, et al. (2018) Clinical, Bacteriologic, and Geographic Stratification of Melioidosis Emerges from the Sri Lankan National Surveillance Program. *The American journal of tropical medicine and hygiene*, 98(2), 607.