

Resource Summary Report

Generated by T1D on Aug 2, 2026

Gephi

RRID:SCR_004293

Type: Tool

Proper Citation

Gephi (RRID:SCR_004293)

Resource Information

URL: <http://gephi.org/>

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Description: Open-source software for network visualization and analysis helping data analysts to intuitively reveal patterns and trends, highlight outliers and tells stories with their data. It uses a 3D render engine to display large graphs in real-time and to speed up the exploration. Gephi combines built-in functionalities and flexible architecture to: explore, analyze, spatialize, filter, cluterize, manipulate and export all types of networks. Gephi runs on Windows, Linux and Mac OS X. Gephi is based on a visualize-and-manipulate paradigm which allow any user to discover networks and data properties. Moreover, it is designed to follow the chain of a case study, from data file to nice printable maps. It is open-source and free (GNU General Public License). Applications: * Exploratory Data Analysis: intuition-oriented analysis by networks manipulations in real time. * Link Analysis: revealing the underlying structures of associations between objects, in particular in scale-free networks. * Social Network Analysis: easy creation of social data connectors to map community organizations and small-world networks. * Biological Network analysis: representing patterns of biological data. * Poster creation: scientific work promotion with hi-quality printable maps. Gephi 0.7 architecture is modular and therefore allows developers to add and extend functionalities with ease. New features like Metrics, Layout, Filters, Data sources and more can be easily packaged in plugins and shared. The built-in Plugins Center automatically gets the list of plugins available from the Gephi Plugin portal and takes care of all software updates. Download, comment, and rate plugins provided by community members and third-party companies, or post your own contributions!

Abbreviations: Gephi

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

Keywords: network, visualization, visual analytics, exploratory data analysis, graph, analysis, open source, plugin, filter, cluter, manipulate, export

Availability: GNU General Public License

Resource Name: Gephi

Resource ID: SCR_004293

Alternate IDs: nlx_31183

Record Creation Time: 20220129T080223+0000

Record Last Update: 20260801T190824+0000

Ratings and Alerts

No rating or validation information has been found for Gephi.

No alerts have been found for Gephi.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3059 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Parween S, et al. (2026) Host genome and bacterial taxa shape the Arabidopsis seed microbiome. EMBO reports, 27(1), 122.

Garc??a JF, et al. (2026) Intraspecies sequence-graph analysis of the Phytophthora theobromicola genome reveals a dynamic structure and variable effector repertoires. G3 (Bethesda, Md.), 16(1).

Ajaz S, et al. (2026) Maximum entropy networks show that plant-arbuscular mycorrhizal fungi associations are anti-nested and modular. The New phytologist, 249(1), 460.

Yun Y, et al. (2026) Gut microbiome plasticity explains the altitudinal distribution pattern and adaptability in a small mammal species (Apodemus draco). Microbiology spectrum, 14(1), e0238825.

Han P, et al. (2026) Integrated multi-omics reveals microbial and metabolic mechanisms driving enhanced fermentation quality in cigar tobacco leaves with exogenous additives. Bioresources and bioprocessing, 13(1), 2.

Long Y, et al. (2026) Interactions between phytoplankton and bacterioplankton communities in Caohai plateau lake, revealed by environmental DNA metagenomics. BMC microbiology, 26(1), 4.

Erginkaya M, et al. (2025) A competitive disinhibitory network for robust optic flow processing in Drosophila. Nature neuroscience, 28(6), 1241.

Goldmann U, et al. (2025) Data- and knowledge-derived functional landscape of human solute carriers. *Molecular systems biology*, 21(6), 599.

Zhang P, et al. (2025) Network analysis of headache diagnoses using international classification of headache disorders, 3rd edition. *Frontiers in neurology*, 16, 1526037.

Guo BC, et al. (2025) Deciphering Plant NLR Genomic Evolution: Synteny-Informed Classification Unveils Insights into TNL Gene Loss. *Molecular biology and evolution*, 42(2).

Han D, et al. (2025) Multi-omics approach reveals the impact of prognosis model-related genes on the tumor microenvironment in medulloblastoma. *Frontiers in oncology*, 15, 1477617.

Sun Y, et al. (2025) Plants Drive Microbial Biomass and Composition but Not Diversity to Promote Ecosystem Multifunctionality in Karst Vegetation Restoration. *Microorganisms*, 13(3).

Hou Z, et al. (2025) Differentiated response mechanisms of soil microbial communities to nitrogen deposition driven by tree species variations in subtropical planted forests. *Frontiers in microbiology*, 16, 1534028.

Xiang M, et al. (2025) Grazing Intensity Modifies Soil Microbial Diversity and Their Co-Occurrence Networks in an Alpine Steppe, Central Tibet. *Microorganisms*, 13(1).

Wang Z, et al. (2025) Compositional shifts and co-occurrence patterns of topsoil bacteria and micro-eukaryotes across a permafrost thaw gradient in alpine meadows of the Qilian Mountains, China. *Applied and environmental microbiology*, 91(3), e0195524.

Zhang Y, et al. (2025) High-throughput single-cell sequencing of activated sludge microbiome. *Environmental science and ecotechnology*, 23, 100493.

Shi M, et al. (2025) Salt stress alters the selectivity of mature pecan for the rhizosphere community and its associated functional traits. *Frontiers in plant science*, 16, 1473473.

Yang X, et al. (2025) Differences in rhizospheric microbial communities between cultivated and wild endangered *Glyptostrobos pensilis*. *Frontiers in microbiology*, 16, 1548836.

Yang B, et al. (2025) The efficacy and safety of fecal microbiota transplantation in the treatment of sarcopenia: a retrospective study. *Journal of translational medicine*, 23(1), 645.

Qi B, et al. (2025) Graph Representation Learning for the Prediction of Medication Usage in the UK Biobank Based on Pharmacogenetic Variants. *Bioengineering (Basel, Switzerland)*, 12(6).