

Resource Summary Report

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igraph

RRID:SCR_019225

Type: Tool

Proper Citation

igraph (RRID:SCR_019225)

Resource Information

URL: <https://cran.r-project.org/web/packages/igraph/>

Proper Citation: igraph (RRID:SCR_019225)

Description: Software package for graphs and network analysis. Provides functions for generating random and regular graphs, graph visualization, centrality methods and much more. Can be programmed in R, Python, Mathematica, C/C Plus Plus.

Synonyms: igraph 0.8.4, igraph 1.2.6

Resource Type: software toolkit, software resource, data visualization software, data processing software, network graph visualization software, software application, data analysis software, network analysis software

Keywords: Graphs analysis, network analysis, generating graph function, graph visualization

Availability: Free, Available for download, Freely available

Resource Name: igraph

Resource ID: SCR_019225

Alternate URLs: <https://igraph.org/>, <https://github.com/igraph/igraph/releases/tag/0.8.4>

License: GPL v3

Record Creation Time: 20220129T080344+0000

Record Last Update: 20260803T040807+0000

Ratings and Alerts

No rating or validation information has been found for igrph.

No alerts have been found for igrph.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 354 mentions in open access literature.

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

Viana J, et al. (2026) Molecular hydrogen and kidney diseases: a scoping review based on scientometry and data analytics. *Medical gas research*, 16(2), 161.

Bui HV, et al. (2025) White and brown adipose tissue share a convergent fibro-adipogenic progenitor population. *EMBO reports*, 26(22), 5612.

Watt AE, et al. (2025) Parameters for one health genomic surveillance of *Escherichia coli* from Australia. *Nature communications*, 16(1), 17.

Yulug B, et al. (2025) Multi-omics characterization of improved cognitive functions in Parkinson's disease patients after the combined metabolic activator treatment: a randomized, double-blinded, placebo-controlled phase II trial. *Brain communications*, 7(1), fcae478.

Bai X, et al. (2025) Microbiome profiling reveals gut bacterial species associated with rapid lung function decline in people with HIV. *Frontiers in immunology*, 16, 1555441.

Perkins SA, et al. (2025) Heterogeneous constraint and adaptation across the malaria parasite life cycle. *bioRxiv : the preprint server for biology*.

Rodríguez-Herrera J, et al. (2025) A computational Evo-Devo approach for elucidating the roles of PLETHORA transcription factors in regulating root development. *PloS one*, 20(7), e0327511.

Wang T, et al. (2025) Metabolomics analysis and mRNA/miRNA profiling reveal potential cardiac regulatory mechanisms in Yili racehorses under different training regimens. *PloS one*, 20(7), e0322468.

Weidner L, et al. (2025) T-cell repertoire correlates with cytokine imbalance in multiple sclerosis patients. *Frontiers in immunology*, 16, 1604452.

Toya R, et al. (2025) Risk of multidrug resistance in *Escherichia coli* associated with routine antimicrobial prophylaxis on pig farms. *npj antimicrobials and resistance*, 3(1), 59.

de Mendonça Fernandes GM, et al. (2025) Epitranscriptomic analysis reveals clinical and molecular signatures in glioblastoma. *Acta neuropathologica communications*, 13(1), 74.

Smith AH, et al. (2025) Social Network Analysis of Secure Text Messaging Metadata During Clinical Deterioration in an Inpatient Children's Hospital Setting. *Journal of medical systems*, 49(1), 116.

Gupta C, et al. (2025) Network-based drug repurposing for psychiatric disorders using single-cell genomics. *Cell genomics*, 5(11), 101003.

Cano-Argüelles AL, et al. (2025) Protocol to study the impact of breast cancer on colonization resistance of mouse microbiota using network node manipulation. *STAR protocols*, 6(1), 103618.

Arthur TD, et al. (2025) Multiomic QTL mapping reveals phenotypic complexity of GWAS loci and prioritizes putative causal variants. *Cell genomics*, 5(3), 100775.

Hsiao MH, et al. (2025) Molecular Display of the Animal Meta-Venome for Discovery of Novel Therapeutic Peptides. *Molecular & cellular proteomics : MCP*, 24(2), 100901.

Siam MHB, et al. (2025) CAFE: an integrated web app for high-dimensional analysis and visualization in spectral flow cytometry. *Bioinformatics (Oxford, England)*, 41(6).

Hansel-Fröse AFF, et al. (2025) Petri net modeling and simulation of post-transcriptional regulatory networks of human embryonic stem cell (hESC) differentiation to cardiomyocytes. *Journal of integrative bioinformatics*, 22(1).

Tuechler N, et al. (2025) Dynamic multi-omics and mechanistic modeling approach uncovers novel mechanisms of kidney fibrosis progression. *Molecular systems biology*, 21(8), 1030.

Isshiki M, et al. (2025) Genetic disease risks of under-represented founder populations in New York City. *PLoS genetics*, 21(6), e1011755.