

Resource Summary Report

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igraph for R

RRID:SCR_021238

Type: Tool

Proper Citation

igraph for R (RRID:SCR_021238)

Resource Information

URL: <https://igraph.org/r/>

Proper Citation: igraph for R (RRID:SCR_021238)

Description: Software R package of igraph network analysis library.

Synonyms: rigraph, R/igraph

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

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

Availability: Free, Available for download, Freely available

Resource Name: igraph for R

Resource ID: SCR_021238

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260903T235710+0000

Ratings and Alerts

No rating or validation information has been found for igraph for R.

No alerts have been found for igraph for R.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 68 mentions in open access literature.

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

Di Marco N, et al. (2026) Decoding the evolution of melodic and harmonic structure of Western music through the lens of network science. *Scientific reports*, 16(1).

Shendye N, et al. (2026) β -adrenergic receptors modulate CA1 population coding and synaptic plasticity during cumulative spatial memory formation and updating. *Scientific reports*, 16(1).

Liu H, et al. (2026) Vaginal microbiota transfer ameliorates cesarean-associated neurodevelopmental deficits in mice via N-bc2S1P synthesis on neonatal skin. *Cell host & microbe*, 34(5), 942.

Hilgart E, et al. (2026) DNA Methylation Stochasticity Is Linked to Transcriptional Variability and Convergent Epigenetic Disruption across Genetic Subtypes of Acute Myeloid Leukemia. *Cancer research*, 86(13), 3325.

Siu JHY, et al. (2025) Early lymph node T follicular helper cell signalling hub drives influenza vaccine response in an ancestrally diverse cohort. *EBioMedicine*, 122, 106036.

Kuett L, et al. (2025) Distant Metastases of Breast Cancer Resemble Primary Tumors in Cancer Cell Composition but Differ in Immune Cell Phenotypes. *Cancer research*, 85(1), 15.

Riley S, et al. (2025) TMT-based quantitative proteomic assessment of *Vicia sativa* induced neurotoxicity by β -cyano-L-alanine and β -glutamyl- β -cyano-L-alanine in SH-SY5Y cells. *Scientific reports*, 16(1), 510.

Borrell LR, et al. (2025) Functional brain network correlates of cardiorespiratory fitness and moderation by depression symptoms. *Brain structure & function*, 230(6), 85.

Gonzalez-Lozano MA, et al. (2025) EndoMAP.v1 charts the structural landscape of human early endosome complexes. *Nature*, 643(8070), 252.

Ali M, et al. (2025) Multi-cohort cerebrospinal fluid proteomics identifies robust molecular signatures across the Alzheimer disease continuum. *Neuron*, 113(9), 1363.

Levé M, et al. (2025) Metabolomics and metagenomics in mice reveal the role of the gut microbiota in tryptophan metabolism. *iScience*, 28(11), 113751.

Paloviita P, et al. (2025) Integrated transcriptomic analysis reveals metabolic remodeling and gene expression networks related to human 8-cell-stage embryo-like cells. *Cell reports*, 45(1), 116748.

Khemka N, et al. (2024) Integrative network analysis of miRNA-mRNA expression profiles during epileptogenesis in rats reveals therapeutic targets after emergence of first spontaneous seizure. *Scientific reports*, 14(1), 15313.

Chia KS, et al. (2024) The N-terminal domains of NLR immune receptors exhibit structural and functional similarities across divergent plant lineages. *The Plant cell*, 36(7), 2491.

Wang X, et al. (2024) A Social Network Analysis of a Multi-sector Service System for Intimate Partner Violence in a Large US City. *Journal of prevention* (2022), 45(3), 357.

Fuchs Wightman F, et al. (2024) Influence of RNA circularity on Target RNA-Directed MicroRNA Degradation. *Nucleic acids research*, 52(6), 3358.

Karri K, et al. (2023) Dysregulation of murine long noncoding single-cell transcriptome in nonalcoholic steatohepatitis and liver fibrosis. *RNA* (New York, N.Y.), 29(7), 977.

Anderson AG, et al. (2023) A single-cell trajectory atlas of striatal development. *Scientific reports*, 13(1), 9031.

Weeks K, et al. (2023) Characterization of microbiomic and geochemical compositions across the photosynthetic fringe. *Frontiers in microbiology*, 14, 1176606.

Klonizakis A, et al. (2023) SEGCOND predicts putative transcriptional condensate-associated genomic regions by integrating multi-omics data. *Bioinformatics* (Oxford, England), 39(1).