

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

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: 20260729T044508+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 51 mentions in open access literature.

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

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.

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.

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.

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.

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.

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

Scherngell T, et al. (2023) The geographical dynamics of global R&D collaboration networks in robotics: Evidence from co-patenting activities across urban areas worldwide. *PloS one*, 18(4), e0281353.

Shang J, et al. (2023) DM-MOGA: a multi-objective optimization genetic algorithm for identifying disease modules of non-small cell lung cancer. *BMC bioinformatics*, 24(1), 13.

Karri K, et al. (2023) TCDD dysregulation of lncRNA expression, liver zonation and intercellular communication across the liver lobule. *bioRxiv : the preprint server for biology*.

Haubrich J, et al. (2023) Network-level changes in the brain underlie fear memory strength. *eLife*, 12.

Szebényi K, et al. (2023) A human proteogenomic-cellular framework identifies KIF5A as a modulator of astrocyte process integrity with relevance to ALS. *Communications biology*, 6(1), 678.

Planchais C, et al. (2023) HIV-1 treatment timing shapes the human intestinal memory B-cell repertoire to commensal bacteria. *Nature communications*, 14(1), 6326.