Resource Summary Report

Generated by dkNET on May 18, 2025

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

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

Funding:

Availability: Free, Available for download, Freely available

Resource Name: igraph for R

Resource ID: SCR_021238

Record Creation Time: 20220129T080354+0000

Record Last Update: 20250517T060431+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 45 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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.

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.

Rizos I, et al. (2023) Beyond the limits of the unassigned protist microbiome: inferring large-scale spatio-temporal patterns of Syndiniales marine parasites. ISME communications, 3(1), 16.

Cheah M, et al. (2023) Integrin-Driven Axon Regeneration in the Spinal Cord Activates a Distinctive CNS Regeneration Program. The Journal of neuroscience : the official journal of the Society for Neuroscience, 43(26), 4775.

Hoyd R, et al. (2023) Exogenous Sequences in Tumors and Immune Cells (Exotic): A Tool for Estimating the Microbe Abundances in Tumor RNA-seq Data. Cancer research communications, 3(11), 2375.

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.

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.

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.

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.

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

Yang Y, et al. (2022) SC-MEB: spatial clustering with hidden Markov random field using empirical Bayes. Briefings in bioinformatics, 23(1).

Kim EY, et al. (2022) Transcriptome-wide changes in gene expression, splicing, and lncRNAs in response to a live attenuated dengue virus vaccine. Cell reports, 38(6), 110341.