

Resource Summary Report

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Weighted Gene Co-expression Network Analysis

RRID:SCR_003302

Type: Tool

Proper Citation

Weighted Gene Co-expression Network Analysis (RRID:SCR_003302)

Resource Information

URL: <http://www.genetics.ucla.edu/labs/horvath/CoexpressionNetwork/>

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Description: Software R package for weighted correlation network analysis. WGCNA is also available as point-and-click application. Unfortunately this application is not maintained anymore. It is known to have compatibility problems with R-2.8.x and newer, and the methods it implements are not all state of the art., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: WGCNA

Synonyms: WGCNA: an R package for weighted correlation network analysis

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

Defining Citation: [PMID:19114008](#)

Keywords: gene, co-expression, analysis, network, bio.tools, bio.tools

Funding: NCI P50CA092131;
NIDA 1R01DA030913-01;
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NIAID U19 AI063603-01

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Weighted Gene Co-expression Network Analysis

Resource ID: SCR_003302

Alternate IDs: nif-0000-31889, biotools:crosslinkwgcn

Alternate URLs:

<http://labs.genetics.ucla.edu/horvath/htdocs/CoexpressionNetwork/Rpackages/WGCNA/#citation>,
<https://bio.tools/crosslinkwgcna>

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Ratings and Alerts

No rating or validation information has been found for Weighted Gene Co-expression Network Analysis.

No alerts have been found for Weighted Gene Co-expression Network Analysis.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1860 mentions in open access literature.

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

Wagoner ZW, et al. (2025) Systems immunology analysis of human immune organoids identifies host-specific correlates of protection to different influenza vaccines. *Cell stem cell*, 32(4), 529.

Krueger ME, et al. (2025) Comparative analysis of Parkinson's and inflammatory bowel disease gut microbiomes reveals shared butyrate-producing bacteria depletion. *NPJ Parkinson's disease*, 11(1), 50.

Wang X, et al. (2025) Integrative machine learning and transcriptomic analysis identifies key molecular targets in MNPN-associated oral squamous cell carcinoma pathogenesis. *Frontiers in bioinformatics*, 5, 1664576.

Miao P, et al. (2025) Potential role of immune-related LncRNAs in prognosis of hepatocellular carcinoma: an integrative study. *Discover oncology*, 16(1), 1661.

Mitsuyasu Barbosa B, et al. (2025) Deciphering the Heterogeneity of Pancreatic Cancer: DNA Methylation-Based Cell Type Deconvolution Unveils Distinct Subgroups and Immune Landscapes. *Epigenomes*, 9(3).

Babygirija R, et al. (2025) Restriction of individual branched-chain amino acids has distinct effects on the development and progression of Alzheimer's disease in 3xTg mice. *bioRxiv* : the preprint server for biology.

Zhang N, et al. (2025) Biohacking agarwood: the impact of fire drills and brine on endophytes and metabolites of *Aquilaria sinensis*. *BMC plant biology*, 25(1), 555.

Cao J, et al. (2025) Identification of mitochondrial function and programmed cell death associated key biomarkers and the circRNA-miRNA-mRNA regulatory network in systemic lupus erythematosus. *Frontiers in molecular biosciences*, 12, 1586294.

Wang J, et al. (2025) A multi-omic approach implicates novel protein dysregulation in post-traumatic stress disorder. *Genome medicine*, 17(1), 43.

Mitchell DV, et al. (2025) *ndufs2*^{-/-} zebrafish have impaired survival, neuromuscular activity, morphology, and one-carbon metabolism treatable with folic acid. *bioRxiv* : the preprint server for biology.

Geng F, et al. (2025) Genome Assembly and Winged Fruit Gene Regulation of Chinese Wingnut: Insights from Genomic and Transcriptomic Analyses. *Genomics, proteomics & bioinformatics*, 22(6).

Jiang L, et al. (2025) Elucidation of the key flavonol biosynthetic pathway in golden Camellia and its application in genetic modification of tomato fruit metabolism. *Horticulture research*, 12(2), uhae308.

Li M, et al. (2025) Integrated analysis of M2 macrophage-related gene prognostic model and single-cell sequence to predict immunotherapy response in lung adenocarcinoma. *Frontiers in genetics*, 16, 1519677.

Du L, et al. (2025) Integrating machine learning with mendelian randomization for unveiling causal gene networks in glioblastoma multiforme. *Discover oncology*, 16(1), 38.

Li X, et al. (2025) A comprehensive analysis to reveal the underlying molecular mechanisms of natural killer cell in thyroid carcinoma based on single-cell RNA sequencing data. *Discover oncology*, 16(1), 44.

Huang G, et al. (2025) Salidroside sensitizes Triple-negative breast cancer to ferroptosis by SCD1-mediated lipogenesis and NCOA4-mediated ferritinophagy. *Journal of advanced research*, 74, 589.

Li Y, et al. (2025) Identification and multi-omics analysis of essential coding and long non-coding genes in colorectal cancer. *Biochemistry and biophysics reports*, 41, 101938.

Chang Q, et al. (2025) Identification of a novel prognostic and therapeutic prediction model in clear cell renal carcinoma based on Renin-angiotensin system related genes. *Frontiers in endocrinology*, 16, 1521940.

Yang P, et al. (2025) Multiomic Analysis Provided Insights into the Responses of Carbon Sources by Wood-Rotting Fungi *Daldinia carpinicola*. *Journal of fungi (Basel, Switzerland)*, 11(2).

Sheikh SI, et al. (2025) A shared gene but distinct dynamics regulate mimicry polymorphisms in closely related species. *bioRxiv* : the preprint server for biology.