

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

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:crosslinkwgcna

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 [ASWG](#) .

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.