

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

Defining Citation: [PMID:19114008](#)

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

Funding: NCI P50CA092131;
NIDA 1R01DA030913-01;
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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 [NIF](#) .

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

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.

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.

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).

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.

Tian L, et al. (2025) Interactions between NAD⁺ metabolism and immune cell infiltration in ulcerative colitis: subtype identification and development of novel diagnostic models. *Frontiers in immunology*, 16, 1479421.

Liu X, et al. (2025) The evolution, variation and expression patterns of the annexin gene family in the maize pan-genome. *Scientific reports*, 15(1), 5711.

- 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.
- Sheikh SI, et al. (2025) A shared gene but distinct dynamics regulate mimicry polymorphisms in closely related species. *bioRxiv : the preprint server for biology*.
- 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.
- Lin D, et al. (2025) Huafengdan Inhibits Glioblastoma Cell Growth and Mobility by Acting on PLA2 and CAV1 Targets. *Pharmaceuticals (Basel, Switzerland)*, 18(3).
- Wang N, et al. (2025) Neuronal ABCA7 deficiency aggravates mitochondrial dysfunction and neurodegeneration in Alzheimer's disease. *Alzheimer's & dementia : the journal of the Alzheimer's Association*, 21(3), e70112.
- Yang L, et al. (2025) Comprehensive integration of diagnostic biomarker analysis and immune cell infiltration features in sepsis via machine learning and bioinformatics techniques. *Frontiers in immunology*, 16, 1526174.
- 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).
- Wen X, et al. (2025) Integrated Metabolomic and Transcriptomic Analyses Reveal the Potential Molecular Mechanism Underlying Callus Browning in *Paeonia ostii*. *Plants (Basel, Switzerland)*, 14(4).
- Wu R, et al. (2025) Activation of endogenous full-length utrophin by MyoAAV-UA as a therapeutic approach for Duchenne muscular dystrophy. *Nature communications*, 16(1), 2398.
- Hu Y, et al. (2025) Rapid and Effective Neuronal Conversion of Human Glioblastoma In Vitro and In Vivo Using Potent Small Molecules. *Cell proliferation*, 58(8), e70013.
- Meng T, et al. (2025) Bioinformatics insights into mitochondrial and immune gene regulation in Alzheimer's disease. *European journal of medical research*, 30(1), 89.
- 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.
- Zhao H, et al. (2025) New insights into the salt-responsive regulation in eelgrass at transcriptional and post-transcriptional levels. *Frontiers in plant science*, 16, 1497064.