Resource Summary Report

Generated by NIF on May 19, 2025

ARACNE

RRID:SCR_002180
Type: Tool

Proper Citation

ARACNE (RRID:SCR_002180)

Resource Information

URL: http://wiki.c2b2.columbia.edu/califanolab/index.php/Software/ARACNE

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Description: An algorithm, using microarray expression profiles, to scale up to the complexity of regulatory networks in mammalian cells, yet general enough to address a wider range of network deconvolution problems. This method uses an information theoretic approach to eliminate the vast majority of indirect interactions typically inferred by pairwise analysis.

Abbreviations: ARACNE

Synonyms: Algorithm for the Reconstruction of Accurate Cellular Networks

Resource Type: software resource, software application

Defining Citation: PMID:16723010

Keywords: cellular network, cellular, network, microarray, expression profile, deconvolution, regulatory network

Funding:

Resource Name: ARACNE

Resource ID: SCR_002180

Alternate IDs: OMICS_01851

Record Creation Time: 20220129T080212+0000

Record Last Update: 20250519T204858+0000

Ratings and Alerts

No rating or validation information has been found for ARACNE.

No alerts have been found for ARACNE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 145 mentions in open access literature.

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

Yu Q, et al. (2025) Causal genes identification of giant cell arteritis in CD4+?Memory t cells: an integration of multi-omics and expression quantitative trait locus analysis. Inflammation research : official journal of the European Histamine Research Society ... [et al.], 74(1), 3.

Khayer N, et al. (2025) A dynamic co-expression approach reveals Gins2 as a potential upstream modulator of HNSCC metastasis. Scientific reports, 15(1), 3322.

Galindez G, et al. (2024) Inference of differential gene regulatory networks using boosted differential trees. Bioinformatics advances, 4(1), vbae034.

Logan R, et al. (2024) Sex-specific Concordance of Striatal Transcriptional Signatures of Opioid Addiction in Human and Rodent Brains. Research square.

Song KJ, et al. (2024) Proteogenomic analysis reveals non-small cell lung cancer subtypes predicting chromosome instability, and tumor microenvironment. Nature communications, 15(1), 10164.

Fiorentino J, et al. (2024) Prediction of protein-RNA interactions from single-cell transcriptomic data. Nucleic acids research, 52(6), e31.

Anglada-Girotto M, et al. (2024) Disentangling the splicing factor programs underlying complex molecular phenotypes. bioRxiv : the preprint server for biology.

Moakley DF, et al. (2024) Reverse engineering neuron type-specific and type-orthogonal splicing-regulatory networks using single-cell transcriptomes. bioRxiv : the preprint server for biology.

Katebi A, et al. (2024) Data-driven modeling of core gene regulatory network underlying leukemogenesis in IDH mutant AML. NPJ systems biology and applications, 10(1), 38.

Suda N, et al. (2024) ?-cell Jagged1 is sufficient but not necessary for islet Notch activity and insulin secretory defects in obese mice. Molecular metabolism, 81, 101894.

Mallawaarachchi S, et al. (2024) Detecting co-selection through excess linkage disequilibrium in bacterial genomes. NAR genomics and bioinformatics, 6(2), lqae061.

Olascoaga S, et al. (2024) Gene co-expression networks reveal sex-biased differences in musculoskeletal ageing. Frontiers in aging, 5, 1469479.

Ager CR, et al. (2024) Neoadjuvant androgen deprivation therapy with or without Fc-enhanced non-fucosylated anti-CTLA-4 (BMS-986218) in high risk localized prostate cancer: a randomized phase 1 trial. medRxiv : the preprint server for health sciences.

Fu J, et al. (2024) Plasticity of intragraft alloreactive T cell clones in human gut correlates with transplant outcomes. The Journal of experimental medicine, 221(1).

Mansoor S, et al. (2024) Comparative transcriptomic analysis of the nodulation-competent zone and inference of transcription regulatory network in silicon applied Glycine max [L.]-Merr. Roots. Plant cell reports, 43(7), 169.

Velazquez-Caldelas TE, et al. (2024) Coordinated inflammation and immune response transcriptional regulation in breast cancer molecular subtypes. Frontiers in immunology, 15, 1357726.

Innocenti G, et al. (2024) Real-time identification of epistatic interactions in SARS-CoV-2 from large genome collections. Genome biology, 25(1), 228.

Krull JE, et al. (2024) Follicular lymphoma B cells exhibit heterogeneous transcriptional states with associated somatic alterations and tumor microenvironments. Cell reports. Medicine, 5(3), 101443.

Ho NCW, et al. (2024) Bioengineered Hydrogels Recapitulate Fibroblast Heterogeneity in Cancer. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(20), e2307129.

Valenti G, et al. (2024) Regulatory network analysis of Dclk1 gene expression reveals a tuft cell-ILC2 axis that inhibits pancreatic tumor progression. bioRxiv : the preprint server for biology.