

Resource Summary Report

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GRNBoost2

RRID:SCR_025614

Type: Tool

Proper Citation

GRNBoost2 (RRID:SCR_025614)

Resource Information

URL: <https://academic.oup.com/bioinformatics/article/35/12/2159/5184284>

Proper Citation: GRNBoost2 (RRID:SCR_025614)

Description: Algorithm for regulatory network inference using gradient boosting, based on GENIE3 architecture. Used for inference of gene regulatory networks.

Synonyms: GRNBoost, Gene Regulatory Network Boost

Resource Type: software application, software resource

Defining Citation: [PMID:30445495](#)

Keywords: GRN, Gene Regulatory Network, inference of gene regulatory networks,

Availability: Free, Freely available

Resource Name: GRNBoost2

Resource ID: SCR_025614

Alternate URLs: <https://arboreto.readthedocs.io/en/latest/>,
<https://github.com/aertslab/GRNBoost>

Record Creation Time: 20240815T053252+0000

Record Last Update: 20260810T040917+0000

Ratings and Alerts

No rating or validation information has been found for GRNBoost2.

No alerts have been found for GRNBoost2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Lind??n M, et al. (2026) REACTOR: REgulon Activity analysis and Comparison Tool for single-cell transcriptOmics Research. Bioinformatics (Oxford, England), 42(5).

Schmitt AM, et al. (2026) Spatially-resolved subtype progression reveals metabolic vulnerabilities in pancreatic ductal adenocarcinoma. Molecular cancer, 25(1).

Zhou B, et al. (2025) Single-cell RNA sequencing reveals altered immune and stromal landscape in primary and liver metastasis of gastric cancer. Biochemistry and biophysics reports, 43, 102163.

Sheng K, et al. (2025) Deciphering the generation of heterogeneity in esophageal squamous cell carcinoma metastasis via single-cell multiomics analysis. Journal of translational medicine, 23(1), 148.

Chen J, et al. (2025) CD146+ CAFs mediate immunosuppression in gastric cancer via COL4A1: potential therapeutic targets. Journal for immunotherapy of cancer, 13(12).

Lou P, et al. (2025) Single-cell sequencing reveals a senescent immune landscape in bone marrow lesions inducing articular cartilage damage in osteoarthritis. Bone research, 13(1), 94.

Yang S, et al. (2025) Hypoxia-associated genes as predictors of outcomes in gastric cancer: a genomic approach. Frontiers in immunology, 16, 1553477.

Huang K, et al. (2025) Biomni: A General-Purpose Biomedical AI Agent. bioRxiv : the preprint server for biology.

Du M, et al. (2024) Unraveling the dynamic transcriptomic changes during the dimorphic transition of *Talaromyces marneffei* through time-course analysis. Frontiers in microbiology, 15, 1369349.

Lu Y, et al. (2022) A single-cell atlas of the multicellular ecosystem of primary and metastatic hepatocellular carcinoma. Nature communications, 13(1), 4594.

van Wyk R, et al. (2021) MALBoost: a web-based application for gene regulatory network analysis in *Plasmodium falciparum*. Malaria journal, 20(1), 317.