

Resource Summary Report

Generated by [NIF](#) on Aug 12, 2026

GENIE3

RRID:SCR_000217

Type: Tool

Proper Citation

GENIE3 (RRID:SCR_000217)

Resource Information

URL: <https://github.com/vahuynh/dynGENIE3>

Proper Citation: GENIE3 (RRID:SCR_000217)

Description: An algorithm for the inference of gene regulatory networks from expression data.

Abbreviations: GENIE3

Resource Type: software resource

Defining Citation: [PMID:20927193](#)

Keywords: javascript, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: GENIE3

Resource ID: SCR_000217

Alternate IDs: biotools:genie3, OMICS_01683

Alternate URLs: <https://bio.tools/genie3>

Old URLs: <http://www.montefiore.ulg.ac.be/~huynh-thu/software.html>

Record Creation Time: 20220129T080200+0000

Record Last Update: 20260808T185716+0000

Ratings and Alerts

No rating or validation information has been found for GENIE3.

No alerts have been found for GENIE3.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Yabaji SM, et al. (2025) Lipid peroxidation and type I interferon coupling fuels pathogenic macrophage activation causing tuberculosis susceptibility. *eLife*, 14.

Wang W, et al. (2024) Identification of hypoxic macrophages in glioblastoma with therapeutic potential for vasculature normalization. *Cancer cell*, 42(5), 815.

Tasis A, et al. (2024) Single-Cell Analysis of Bone Marrow CD8+ T Cells in Myeloid Neoplasms Reveals Pathways Associated with Disease Progression and Response to Treatment with Azacitidine. *Cancer research communications*, 4(12), 3067.

Li CY, et al. (2022) The sage genome provides insight into the evolutionary dynamics of diterpene biosynthesis gene cluster in plants. *Cell reports*, 40(7), 111236.

Cebrian-Silla A, et al. (2021) Single-cell analysis of the ventricular-subventricular zone reveals signatures of dorsal and ventral adult neurogenesis. *eLife*, 10.

Dibaeinia P, et al. (2020) SERGIO: A Single-Cell Expression Simulator Guided by Gene Regulatory Networks. *Cell systems*, 11(3), 252.

Kang Y, et al. (2018) NetProphet 2.0: mapping transcription factor networks by exploiting scalable data resources. *Bioinformatics (Oxford, England)*, 34(2), 249.

Desai JS, et al. (2017) Improving Gene Regulatory Network Inference by Incorporating Rates of Transcriptional Changes. *Scientific reports*, 7(1), 17244.

Hu Y, et al. (2016) A machine learning approach for the identification of key markers involved in brain development from single-cell transcriptomic data. *BMC genomics*, 17(Suppl 13), 1025.

Huynh-Thu VA, et al. (2010) Inferring regulatory networks from expression data using tree-based methods. *PloS one*, 5(9).