

Resource Summary Report

Generated by [dkNET](#) on Aug 30, 2026

TIGRESS

RRID:SCR_011977

Type: Tool

Proper Citation

TIGRESS (RRID:SCR_011977)

Resource Information

URL: <http://cbio.ensmp.fr/~ahaury/svn/dream5/html/index.html>

Proper Citation: TIGRESS (RRID:SCR_011977)

Description: Software providing a scoring technique for stability selection, which improves the performance of feature selection with LARS. TIGRESS can be run online through the GenePattern platform (GP-DREAM, <http://dream.broadinstitute.org>).

Abbreviations: TIGRESS

Synonyms: Trustful Inference of Gene REGulation using Stability Selection, TIGRESS: Trustful Inference of Gene REGulation using Stability Selection

Resource Type: software resource

Defining Citation: [PMID:23173819](#)

Keywords: matlab

Resource Name: TIGRESS

Resource ID: SCR_011977

Alternate IDs: OMICS_01687

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260829T182413+0000

Ratings and Alerts

No rating or validation information has been found for TIGRESS.

No alerts have been found for TIGRESS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Mbebi AJ, et al. (2023) Gene regulatory network inference using mixed-norms regularized multivariate model with covariance selection. PLoS computational biology, 19(7), e1010832.

Hillerton T, et al. (2022) Fast and accurate gene regulatory network inference by normalized least squares regression. Bioinformatics (Oxford, England), 38(8), 2263.

Schubert M, et al. (2020) Gene networks in cancer are biased by aneuploidies and sample impurities. Biochimica et biophysica acta. Gene regulatory mechanisms, 1863(6), 194444.

Yang P, et al. (2019) Core transcriptional signatures of phase change in the migratory locust. Protein & cell, 10(12), 883.

Wang H, et al. (2018) Genome-wide RNAseq study of the molecular mechanisms underlying microglia activation in response to pathological tau perturbation in the rTg4510 tau transgenic animal model. Molecular neurodegeneration, 13(1), 65.

Siahpirani AF, et al. (2017) A prior-based integrative framework for functional transcriptional regulatory network inference. Nucleic acids research, 45(4), e21.

Thiagarajan R, et al. (2017) The feasibility of genome-scale biological network inference using Graphics Processing Units. Algorithms for molecular biology : AMB, 12, 8.

Ruyssinck J, et al. (2016) Netter: re-ranking gene network inference predictions using structural network properties. BMC bioinformatics, 17, 76.

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.