Resource Summary Report

Generated by NIF on Apr 8, 2025

LIGER

RRID:SCR_018100
Type: Tool

Proper Citation

LIGER (RRID:SCR_018100)

Resource Information

URL: https://bioinformaticshome.com/tools/rna-seq/descriptions/LIGER.html

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Description: Software R package for integrating and analyzing multiple single-cell datasets. It relies on integrative non-negative matrix factorization to identify shared and dataset-specific factors. Used for analysis of multiple scRNA-seq data sets.

Synonyms: Linked Inference of Genomic Experimental Relationships

Resource Type: software resource, software application, data analysis software, data processing software

Defining Citation: PMID:31178122

Keywords: Single cell genomic, data integration, dataset, cell identity, integrative analysis, gene regulation, disease state, scRNA seq analysis, shared factor among data set,

Funding: NIH

Availability: Free, Available for download, Freely available

Resource Name: LIGER

Resource ID: SCR_018100

Alternate URLs: https://github.com/MacoskoLab/liger

License: GNU GPL v3

Record Creation Time: 20220129T080338+0000

Record Last Update: 20250407T220443+0000

Ratings and Alerts

No rating or validation information has been found for LIGER.

No alerts have been found for LIGER.

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.

Gao C, et al. (2024) Integrating single-cell multimodal epigenomic data using 1D-convolutional neural networks. bioRxiv : the preprint server for biology.

Agrawal A, et al. (2024) NiCo identifies extrinsic drivers of cell state modulation by niche covariation analysis. Nature communications, 15(1), 10628.

Wang S, et al. (2024) 3D reconstruction of the mouse cochlea from scRNA-seq data suggests morphogen-based principles in apex-to-base specification. Developmental cell, 59(12), 1538.

O'Toole SM, et al. (2023) Molecularly targetable cell types in mouse visual cortex have distinguishable prediction error responses. Neuron, 111(18), 2918.

Widmer FC, et al. (2022) NMDA receptors in visual cortex are necessary for normal visuomotor integration and skill learning. eLife, 11.

Osorno T, et al. (2022) Candelabrum cells are ubiquitous cerebellar cortex interneurons with specialized circuit properties. Nature neuroscience, 25(6), 702.

Larouche JA, et al. (2021) Murine muscle stem cell response to perturbations of the neuromuscular junction are attenuated with aging. eLife, 10.

Yao Z, et al. (2021) A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. Nature, 598(7879), 103.

Li G, et al. (2021) ExpressHeart: Web Portal to Visualize Transcriptome Profiles of Non-

Cardiomyocyte Cells. International journal of molecular sciences, 22(16).

van Dijk D, et al. (2018) Recovering Gene Interactions from Single-Cell Data Using Data Diffusion. Cell, 174(3), 716.