Resource Summary Report

Generated by dkNET on May 19, 2025

Scmap

RRID:SCR_017338
Type: Tool

Proper Citation

Scmap (RRID:SCR_017338)

Resource Information

URL: https://github.com/hemberg-lab/scmap

Proper Citation: Scmap (RRID:SCR_017338)

Description: Software tool for unsupervised projection of single cell RNA-seq data. Used for projecting cells from scRNA-seq data set onto cell types or individual cells from other experiments.

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

Defining Citation: PMID:29608555

Keywords: Unsupervised, projection, single, cell, RNA-seq, data

Funding:

Availability: Free, Available for download, Freely available

Resource Name: Scmap

Resource ID: SCR_017338

Alternate URLs: http://bioconductor.org/packages/scmap/, https://www.sanger.ac.uk/science/tools/scmap

License: GNU GPLv3

Record Creation Time: 20220129T080334+0000

Record Last Update: 20250519T204537+0000

Ratings and Alerts

No rating or validation information has been found for Scmap.

No alerts have been found for Scmap.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Zheng C, et al. (2024) scNovel: a scalable deep learning-based network for novel rare cell discovery in single-cell transcriptomics. Briefings in bioinformatics, 25(3).

Liu C, et al. (2023) Multi-task learning from multimodal single-cell omics with Matilda. Nucleic acids research, 51(8), e45.

Cheng Y, et al. (2023) A scalable sparse neural network framework for rare cell type annotation of single-cell transcriptome data. Communications biology, 6(1), 545.

Wang J, et al. (2022) CXCR4high megakaryocytes regulate host-defense immunity against bacterial pathogens. eLife, 11.

Brombin A, et al. (2022) Tfap2b specifies an embryonic melanocyte stem cell that retains adult multifate potential. Cell reports, 38(2), 110234.

Mancio-Silva L, et al. (2022) A single-cell liver atlas of Plasmodium vivax infection. Cell host & microbe, 30(7), 1048.

Xie B, et al. (2021) Automatic cell type identification methods for single-cell RNA sequencing. Computational and structural biotechnology journal, 19, 5874.

Xu Y, et al. (2021) Single-cell transcriptome analysis reveals the dynamics of human immune cells during early fetal skin development. Cell reports, 36(6), 109524.

Zhang Y, et al. (2021) SSBER: removing batch effect for single-cell RNA sequencing data. BMC bioinformatics, 22(1), 249.

Andreatta M, et al. (2021) Interpretation of T cell states from single-cell transcriptomics data using reference atlases. Nature communications, 12(1), 2965.

Rohlenova K, et al. (2020) Single-Cell RNA Sequencing Maps Endothelial Metabolic

Plasticity in Pathological Angiogenesis. Cell metabolism, 31(4), 862.

Kalucka J, et al. (2020) Single-Cell Transcriptome Atlas of Murine Endothelial Cells. Cell, 180(4), 764.

Tan Y, et al. (2019) SingleCellNet: A Computational Tool to Classify Single Cell RNA-Seq Data Across Platforms and Across Species. Cell systems, 9(2), 207.

Huang L, et al. (2017) A genome-wide SNP-based genetic map and QTL mapping for agronomic traits in Chinese cabbage. Scientific reports, 7, 46305.