

Resource Summary Report

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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: data processing software, software application, software resource

Defining Citation: [PMID:29608555](#)

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

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: 20260905T133053+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 17 mentions in open access literature.

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

Sollier E, et al. (2025) Enhancer Hijacking Discovery in Acute Myeloid Leukemia by Pyjacker Identifies MNX1 Activation via Deletion 7q. *Blood cancer discovery*, 6(4), 343.

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).

Fan X, et al. (2024) scGraphformer: unveiling cellular heterogeneity and interactions in scRNA-seq data using a scalable graph transformer network. *Communications biology*, 7(1), 1463.

Lan W, et al. (2024) scMoMtF: An interpretable multitask learning framework for single-cell multi-omics data analysis. *PLoS computational biology*, 20(12), e1012679.

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) CXCR4^{high} 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.