

Resource Summary Report

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scvi-tools

RRID:SCR_026673

Type: Tool

Proper Citation

scvi-tools (RRID:SCR_026673)

Resource Information

URL: <https://scvi-tools.org/>

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Description: Software Python library for deep probabilistic analysis of single-cell and spatial omics data. Used for probabilistic modeling and analysis of single-cell omics data, built on top of PyTorch and AnnData.

Synonyms: single-cell variational inference tools

Resource Type: data processing software, software toolkit, data analysis software, source code, software resource, software library, software application

Defining Citation: [PMID:35132262](#)

Keywords: probabilistic analysis, single-cell omics data, spatial omics data,

Funding: NIGMS R35GM124916;
Chan-Zuckerberg Foundation ;
NHGRI T32HG000047

Availability: Free, Available for download, Freely available

Resource Name: scvi-tools

Resource ID: SCR_026673

Alternate URLs: <https://github.com/scverse/scvi-tools>

License: BSD-3-Clause

Record Creation Time: 20250328T060315+0000

Record Last Update: 20260731T043217+0000

Ratings and Alerts

No rating or validation information has been found for scvi-tools.

No alerts have been found for scvi-tools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 31 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Chen Y, et al. (2025) UCS: A Unified Approach to Cell Segmentation for Subcellular Spatial Transcriptomics. *Small methods*, 9(5), e2400975.

Yu H, et al. (2025) PerturbNet predicts single-cell responses to unseen chemical and genetic perturbations. *Molecular systems biology*, 21(8), 960.

Plummer D, et al. (2025) A comprehensive benchmark of single-cell Hi-C embedding tools. *Nature communications*, 16(1), 9119.

Tian A, et al. (2025) Divergence in cellular markers observed in single-cell transcriptomics datasets between cultured primary trabecular meshwork cells and tissues. *Scientific data*, 12(1), 264.

Chen M, et al. (2025) SMOPCA: spatially aware dimension reduction integrating multi-omics improves the efficiency of spatial domain detection. *Genome biology*, 26(1), 135.

Siegel SJ, et al. (2025) Graft-versus-host disease prophylaxis shapes T cell biology and immune reconstitution after hematopoietic cell transplant. *medRxiv : the preprint server for health sciences*.

Nadig A, et al. (2025) Consequences of training data composition for deep learning models in single-cell biology. *bioRxiv : the preprint server for biology*.

Furudate K, et al. (2025) Spatial colocalization and molecular crosstalk of myofibroblastic CAFs and tumor cells shape lymph node metastasis in oral squamous cell carcinoma. *PLoS genetics*, 21(9), e1011791.

Liu Z, et al. (2025) Viral-Track integrated single-cell RNA-sequencing reveals HBV lymphtropism and immunosuppressive microenvironment in HBV-associated hepatocellular carcinoma. *Communications biology*, 8(1), 1030.

Arya A, et al. (2025) Navigating single-cell RNA-sequencing: protocols, tools, databases, and applications. *Genomics & informatics*, 23(1), 13.

Hatkevich T, et al. (2025) Gonadal sex and temperature independently influence germ cell differentiation and meiotic progression in *Trachemys scripta*. *Proceedings of the National Academy of Sciences of the United States of America*, 122(1), e2413191121.

Deng K, et al. (2025) ImageDoubler: image-based doublet identification in single-cell sequencing. *Nature communications*, 16(1), 21.

Li CY, et al. (2025) Benchmarking single-cell cross-omics imputation methods for surface protein expression. *Genome biology*, 26(1), 46.

Simon CS, et al. (2025) Suppression of ERK signalling promotes pluripotent epiblast in the human blastocyst. *Nature communications*, 16(1), 6922.

Zhou T, et al. (2025) stTransfer enables transfer of single-cell annotations to spatial transcriptomics with single-cell resolution. *Cell reports methods*, 5(11), 101205.

Feng JX, et al. (2025) Single-cell lineage tracing identifies hemogenic endothelial cells in the adult mouse bone marrow. *bioRxiv : the preprint server for biology*.

Guan X, et al. (2025) Integrated multi-omics profiling to establish an IGFBP-based prognostic score for pancreatic ductal adenocarcinoma: unraveling prognostic biomarkers, immune microenvironment crosstalk, and therapeutic implications. *Frontiers in immunology*, 16, 1600527.

Zampieri C, et al. (2025) The urokinase receptor/uPAR is a major effector of p53 gain-of-function mutations in gemcitabine-treated pancreatic ductal adenocarcinoma. *The Journal of biological chemistry*, 301(9), 110561.

Shah VS, et al. (2025) Single cell profiling of human airway identifies tuft-ionocyte progenitor cells displaying cytokine-dependent differentiation bias in vitro. *Nature communications*, 16(1), 5180.

Boyeau P, et al. (2025) Deep generative modeling of sample-level heterogeneity in single-cell genomics. *Nature methods*, 22(11), 2264.