

Resource Summary Report

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scVelo

RRID:SCR_018168

Type: Tool

Proper Citation

scVelo (RRID:SCR_018168)

Resource Information

URL: <https://github.com/theislab/scvelo>

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Description: Software package for estimating and analyzing RNA velocities in single cells using dynamical modeling. RNA Velocity using dynamical modeling.

Synonyms: scvelo, single-cell RNA Velocity generalized to transient cell states

Resource Type: software resource, software toolkit

Keywords: RNA veloscity, analysis, single cell, dynamic modeling, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: scVelo

Resource ID: SCR_018168

Alternate IDs: biotools:scVelo

Alternate URLs: <https://scvelo.readthedocs.io/>, <https://bio.tools/scVelo>

License: BSD 3-Clause "New" or "Revised" License

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260725T191303+0000

Ratings and Alerts

No rating or validation information has been found for scVelo.

No alerts have been found for scVelo.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 199 mentions in open access literature.

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

Burgos-Ruiz AM, et al. (2026) A single-cell multiomics roadmap of zebrafish spermatogenesis reveals regulatory principles of male germline formation. *Molecular systems biology*, 22(1), 42.

Song X, et al. (2025) Spatial and single-cell transcriptomics reveal cellular heterogeneity and a novel cancer-promoting Treg cell subset in human clear-cell renal cell carcinoma. *Journal for immunotherapy of cancer*, 13(1).

Nakano K, et al. (2025) Colorectal cancer cell line-derived organoid model with stem cell properties captures the regrowing state of residual cancer cells after neoadjuvant chemotherapy. *Cell death discovery*, 11(1), 282.

Ji P, et al. (2025) Single-cell delineation of the microbiota-gut-brain axis: Probiotic intervention in Chd8 haploinsufficient mice. *Cell genomics*, 5(2), 100768.

Yu S, et al. (2025) Single-cell RNA sequencing uncovers cellular heterogeneity of granulosa cells and provides a signature for follicular development in chicken. *Poultry science*, 104(9), 105430.

Wang K, et al. (2025) Ontogeny Dictates Oncogenic Potential, Lineage Hierarchy, and Therapy Response in Pediatric Leukemia. *bioRxiv : the preprint server for biology*.

Ninni A, et al. (2025) MACanalyzeR scRNAseq analysis tool reveals PPAR⁺ HIGH/GDF15⁺ lipid-associated macrophages facilitate thermogenic expansion in BAT. *Nature communications*, 16(1), 5063.

Bui HV, et al. (2025) White and brown adipose tissue share a convergent fibro-adipogenic progenitor population. *EMBO reports*, 26(22), 5612.

Cheng M, et al. (2025) PHLOWER leverages single-cell multimodal data to infer complex, multi-branching cell differentiation trajectories. *Nature methods*, 22(11), 2328.

Wen X, et al. (2025) Deciphering splicing heterogeneity at single-cell resolution by SCSES. *Nature communications*, 16(1), 9459.

Moshkelgosha S, et al. (2025) Emergence of a senescent and inflammatory pulmonary CD4⁺ T cell population prior to lung allograft failure. *Science advances*, 11(12), eadp9052.

Ramezankhani R, et al. (2025) Identification of Cell Fate Determining Transcription Factors for Generating Brain Endothelial Cells. *Stem cell reviews and reports*, 21(3), 744.

Mugisha S, et al. (2025) S100A8/A9 innate immune signaling as a distinct mechanism driving progression of smoking-related breast cancers. *Oncogene*, 44(15), 1051.

Wang S, et al. (2025) Inhibition of soluble epoxide hydrolase confers neuroprotection and restores microglial homeostasis in a tauopathy mouse model. *Molecular neurodegeneration*, 20(1), 44.

Ge M, et al. (2025) TIVelo: RNA velocity estimation leveraging cluster-level trajectory inference. *Nature communications*, 16(1), 6258.

Hua Y, et al. (2025) SeuratExtend: streamlining single-cell RNA-seq analysis through an integrated and intuitive framework. *GigaScience*, 14.

Kang RB, et al. (2025) Human pancreatic β -cell heterogeneity and trajectory inference analyses reveal SMOC1 as a β -cell dedifferentiation gene. *Nature communications*, 16(1), 8434.

Shi Y, et al. (2025) Mechanisms of tumor persistence in metastatic melanoma following successful immunotherapy. *bioRxiv* : the preprint server for biology.

Xiao Y, et al. (2025) Tracking single-cell evolution using clock-like chromatin accessibility loci. *Nature biotechnology*, 43(5), 784.

Chen Y, et al. (2025) Spatial transcriptomics combined with single-nucleus RNA sequencing reveals glial cell heterogeneity in the human spinal cord. *Neural regeneration research*, 20(11), 3302.