

Resource Summary Report

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Monocle2

RRID:SCR_016339

Type: Tool

Proper Citation

Monocle2 (RRID:SCR_016339)

Resource Information

URL: <http://cole-trapnell-lab.github.io/monocle-release/docs/>

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Description: Software package for analyzing single cell gene expression, classifying and counting cells, performing differential expression analysis between subpopulations of cells, and reconstructing cellular trajectories. Works well with very large single-cell RNA-Seq experiments containing tens of thousands of cells or more. Used in computational analysis of gene expression data in single cell gene expression studies to profile transcriptional regulation in complex biological processes and highly heterogeneous cell populations.

Synonyms: Monocle 2

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

Defining Citation: [PMID:24658644](#)

Keywords: analysis, heterogeneous, population, single, cell, gene, expression, data, large, single-cell RNA-Seq, transcriptional, regulation, heterogen

Funding Agency: NIH , Alfred P. Sloan Foundation Research Fellowship

Availability: Free, Available for download, Freely available

Resource Name: Monocle2

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Ratings and Alerts

No rating or validation information has been found for Monocle2.

No alerts have been found for Monocle2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 116 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Hong YK, et al. (2024) TEM1/endosialin/CD248 promotes pathologic scarring and TGF- β activity through its receptor stability in dermal fibroblasts. *Journal of biomedical science*, 31(1), 12.

Zhang J, et al. (2024) Single-cell transcriptome sequencing reveals aberrantly activated inter-tumor cell signaling pathways in the development of clear cell renal cell carcinoma. *Journal of translational medicine*, 22(1), 37.

Zheng Q, et al. (2024) Single-cell landscape identifies the immunophenotypes and microenvironments of HBV-positive and HBV-negative liver cancer. *Hepatology communications*, 8(2).

Cui YH, et al. (2024) Exploration of neuron heterogeneity in human heart failure with dilated cardiomyopathy through single-cell RNA sequencing analysis. *BMC cardiovascular disorders*, 24(1), 86.

Ghasemi DR, et al. (2024) Compartments in medulloblastoma with extensive nodularity are connected through differentiation along the granular precursor lineage. *Nature communications*, 15(1), 269.

Bhat GP, et al. (2024) Structured wound angiogenesis instructs mesenchymal barrier compartments in the regenerating nerve. *Neuron*, 112(2), 209.

Sun Y, et al. (2024) Integrated multi-omics profiling to dissect the spatiotemporal evolution of metastatic hepatocellular carcinoma. *Cancer cell*, 42(1), 135.

Jin X, et al. (2023) Single-cell transcriptomic analysis of tumor heterogeneity and intercellular networks in human urothelial carcinoma. *Chinese medical journal*, 136(6), 690.

Wu F, et al. (2023) A CCL2+DPP4+ subset of mesenchymal stem cells expedites aberrant formation of creeping fat in humans. *Nature communications*, 14(1), 5830.

Jiang X, et al. (2023) A differentiation roadmap of murine placentation at single-cell

resolution. *Cell discovery*, 9(1), 30.

Zhang Y, et al. (2023) Integrated transcriptome study of the tumor microenvironment for treatment response prediction in male predominant hypopharyngeal carcinoma. *Nature communications*, 14(1), 1466.

Fan Y, et al. (2023) Single-cell analysis reveals region-heterogeneous responses in rhesus monkey spinal cord with complete injury. *Nature communications*, 14(1), 4796.

Lin P, et al. (2023) Spatially multicellular variability of intervertebral disc degeneration by comparative single-cell analysis. *Cell proliferation*, 56(10), e13464.

Huang D, et al. (2023) A single-nucleus transcriptomic atlas of primate testicular aging reveals exhaustion of the spermatogonial stem cell reservoir and loss of Sertoli cell homeostasis. *Protein & cell*, 14(12), 888.

Chen H, et al. (2023) IFN γ Transcribed by IRF1 in CD4⁺ Effector Memory T Cells Promotes Senescence-Associated Pulmonary Fibrosis. *Aging and disease*, 14(6), 2215.

Wang L, et al. (2023) Single-nucleus and bulk RNA sequencing reveal cellular and transcriptional mechanisms underlying lipid dynamics in high marbled pork. *NPJ science of food*, 7(1), 23.

Dou X, et al. (2023) Upregulated CD8⁺ MAIT cell differentiation and KLRD1 gene expression after inactivated SARS-CoV-2 vaccination identified by single-cell sequencing. *Frontiers in immunology*, 14, 1174406.

Zou R, et al. (2023) Single-cell transcriptomics reveals zinc and copper ions homeostasis in epicardial adipose tissue of heart failure. *International journal of biological sciences*, 19(13), 4036.

Xia Y, et al. (2023) Spatial single cell analysis of tumor microenvironment remodeling pattern in primary central nervous system lymphoma. *Leukemia*, 37(7), 1499.

Wang D, et al. (2023) Assessing the effects of aging on the liver endothelial cell landscape using single-cell RNA sequencing. *Hepatology communications*, 7(2), e0021.