Resource Summary Report

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Monocle3

RRID:SCR_018685
Type: Tool

Proper Citation

Monocle3 (RRID:SCR_018685)

Resource Information

URL: https://cole-trapnell-lab.github.io/monocle3/

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Description: Software analysis toolkit for single cell RNA-seq. Used for single cell RNA-Seq experiments. Unsupervised algorithm that increases temporal resolution of transcriptome dynamics using single-cell RNA-Seq data collected at multiple time points.

Synonyms: Monocle, Monocle 3

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

Defining Citation: PMID:24658644

Keywords: Data analysis, singel cell RNAseq data, single cell RNAseq experiment, transcriptome dynamics

Funding: NIH Office of the Director DP2 OD00667;
NIGMS P01 GM099117;
NIH Office of the Director DP2 0D008514;
NHGRI P50 HG006193;
Single Cell Genomics initiative

Availability: Free, Available for download, Freely available

Resource Name: Monocle3

Resource ID: SCR_018685

Alternate URLs: https://github.com/cole-trapnell-lab/monocle3

License: MIT License

Record Creation Time: 20220129T080341+0000

Record Last Update: 20250330T061801+0000

Ratings and Alerts

No rating or validation information has been found for Monocle3.

No alerts have been found for Monocle3.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 205 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Lv Y, et al. (2025) CD14loCD301b+ macrophages gathering as a proangiogenic marker in adipose tissues. Journal of lipid research, 66(1), 100720.

Jin W, et al. (2025) Bayesian-optimized deep learning for identifying essential genes of mitophagy and fostering therapies to combat drug resistance in human cancers. Journal of cellular and molecular medicine, 29(2), e18254.

Montagne JM, et al. (2025) CD137 agonism enhances anti-PD1 induced activation of expanded CD8+ T cell clones in a neoadjuvant pancreatic cancer clinical trial. iScience, 28(1), 111569.

Masuda K, et al. (2025) Distinct CD8+ T-cell types Associated with COVID-19 Severity in Unvaccinated HLA-A2+ Patients. bioRxiv : the preprint server for biology.

Liu Y, et al. (2025) Differential transcriptomic profiling of lipid metabolism and collagen remodeling in fast- and slow-twitch skeletal muscles in aging. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 39(2), e70335.

Lee LR, et al. (2025) Glutathione accelerates the cell cycle and cellular reprogramming in plant regeneration. Developmental cell.

Su Y, et al. (2024) Distribution-Agnostic Deep Learning Enables Accurate Single-Cell Data

Recovery and Transcriptional Regulation Interpretation. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(16), e2307280.

Sun Y, et al. (2024) Single-cell transcriptomic analyses of tumor microenvironment and molecular reprograming landscape of metastatic laryngeal squamous cell carcinoma. Communications biology, 7(1), 63.

Lian W, et al. (2024) Single-cell sequencing reveals increased LAMB3-positive basal keratinocytes and ZNF90-positive fibroblasts in autologous cultured epithelium. Communications biology, 7(1), 79.

Wang L, et al. (2024) Sorafenib inhibits ossification of the posterior longitudinal ligament by blocking LOXL2-mediated vascularization. Bone research, 12(1), 24.

Scarfò R, et al. (2024) CD32 captures committed haemogenic endothelial cells during human embryonic development. Nature cell biology, 26(5), 719.

Yi N, et al. (2024) Functional variation among mesenchymal stem cells derived from different tissue sources. PeerJ, 12, e17616.

Duan J, et al. (2024) LoRA-TV: read depth profile-based clustering of tumor cells in single-cell sequencing. Briefings in bioinformatics, 25(4).

Croizer H, et al. (2024) Deciphering the spatial landscape and plasticity of immunosuppressive fibroblasts in breast cancer. Nature communications, 15(1), 2806.

Mozin E, et al. (2024) Dystrophin deficiency impairs cell junction formation during embryonic myogenesis from pluripotent stem cells. iScience, 27(7), 110242.

Zhi M, et al. (2024) Elucidation of the pluripotent potential of bovine embryonic lineages facilitates the establishment of formative stem cell lines. Cellular and molecular life sciences : CMLS, 81(1), 427.

Perrin S, et al. (2024) Single-nucleus transcriptomics reveal the differentiation trajectories of periosteal skeletal/stem progenitor cells in bone regeneration. eLife, 13.

Zhao F, et al. (2024) Integrated single-cell transcriptomic analyses identify a novel lineage plasticity-related cancer cell type involved in prostate cancer progression. EBioMedicine, 109, 105398.

Cao L, et al. (2024) From single-cell to spatial transcriptomics: decoding the glioma stem cell niche and its clinical implications. Frontiers in immunology, 15, 1475235.

Yao J, et al. (2024) Integration of multi-omics data revealed the orphan CpG islands and enhancer-dominated c is-regulatory network in glioma. iScience, 27(10), 110946.