Resource Summary Report

Generated by dkNET on May 24, 2025

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 trajcectories. 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 application, software toolkit, data analysis software, data processing software, software resource

Defining Citation: PMID:24658644

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

Funding: NIH DP2 HD088158;
Alfred P. Sloan Foundation Research Fellowship

Availability: Free, Available for download, Freely available

Resource Name: Monocle2

Resource ID: SCR_016339

Record Creation Time: 20220129T080330+0000

Record Last Update: 20250524T060705+0000

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 151 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Ren C, et al. (2025) Single-Cell Insights Into Cellular Response in Abdominal Aortic Occlusion-Induced Hippocampal Injury. CNS neuroscience & therapeutics, 31(1), e70154.

Lu L, et al. (2025) A Single-Cell Atlas of Crab Ovary Provides New Insights Into Oogenesis in Crustaceans. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(2), e2409688.

Zeng J, et al. (2025) CancerSCEM 2.0: an updated data resource of single-cell expression map across various human cancers. Nucleic acids research, 53(D1), D1278.

Yang J, et al. (2024) A new exploration: characterization of the differentiation trajectory of prostate cancer cells. Discover oncology, 15(1), 426.

Lu H, et al. (2024) Aging hallmarks of the primate ovary revealed by spatiotemporal transcriptomics. Protein & cell, 15(5), 364.

Yang Y, et al. (2024) Prognostic heterogeneity of Ki67 in non-small cell lung cancer: A comprehensive reappraisal on immunohistochemistry and transcriptional data. Journal of cellular and molecular medicine, 28(14), e18521.

Scatolin GN, et al. (2024) Single-cell transcriptional landscapes of bovine peri-implantation development. iScience, 27(4), 109605.

Huang J, et al. (2024) Granulocyte colony stimulating factor promotes scarless tissue regeneration. Cell reports, 43(10), 114742.

Cao C, et al. (2024) CXCR4 orchestrates the TOX-programmed exhausted phenotype of CD8+ T cells via JAK2/STAT3 pathway. Cell genomics, 4(10), 100659.

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

Wang H, et al. (2024) Single-cell analysis reveals a subpopulation of adipose progenitor cells that impairs glucose homeostasis. Nature communications, 15(1), 4827.

Cao C, et al. (2024) Elucidating the changes in the heterogeneity and function of radiation-induced cardiac macrophages using single-cell RNA sequencing. Frontiers in immunology, 15, 1363278.

Liu F, et al. (2024) Single-cell transcriptome sequencing reveals SPP1-CD44-mediated macrophage-tumor cell interactions drive chemoresistance in TNBC. Journal of cellular and molecular medicine, 28(13), e18525.

Zhou M, et al. (2024) Single-Cell Transcriptomic Analysis Reveals Dynamic Cellular Processes in Corneal Epithelium During Wound Healing in Cynomolgus Monkeys. Investigative ophthalmology & visual science, 65(11), 43.

Huang Y, et al. (2024) Discovery of an unconventional lamprey lymphocyte lineage highlights divergent features in vertebrate adaptive immune system evolution. Nature communications, 15(1), 7626.

Luo M, et al. (2024) Integrated single-cell and spatial transcriptomics reveal microenvironment disruptions by androgen in mouse ovary. iScience, 27(10), 111028.

Ma D, et al. (2024) Multi-omics-driven discovery of invasive patterns and treatment strategies in CA19-9 positive intrahepatic cholangiocarcinoma. Journal of translational medicine, 22(1), 1031.

Li Z, et al. (2024) Dietary caloric restriction protects experimental autoimmune uveitis by regulating Teff/Treg balance. iScience, 27(12), 111279.

Li R, et al. (2024) Spatial transcriptome profiling identifies DTX3L and BST2 as key biomarkers in esophageal squamous cell carcinoma tumorigenesis. Genome medicine, 16(1), 148.

Chen S, et al. (2024) Myeloid-Mas Signaling Modulates Pathogenic Crosstalk among MYC+CD63+ Endothelial Cells, MMP12+ Macrophages, and Monocytes in Acetaminophen-Induced Liver Injury. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(16), e2306066.