Resource Summary Report

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Slingshot

RRID:SCR_017012
Type: Tool

Proper Citation

Slingshot (RRID:SCR_017012)

Resource Information

URL: https://github.com/kstreet13/slingshot

Proper Citation: Slingshot (RRID:SCR_017012)

Description: Software R package for identifying and characterizing continuous developmental trajectories in single cell data. Cell lineage and pseudotime inference for single-cell transcriptomics.

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

Defining Citation: PMID:29914354

Keywords: identify, characterize, continuous, developmental, trajectory, single, cell, data, lineage, pseudotime, inference, transcriptomic

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California Institute of Regenerative Medicine

Availability: Free, Available for download, Freely available

Resource Name: Slingshot

Resource ID: SCR_017012

Record Creation Time: 20220129T080333+0000

Record Last Update: 20250524T060727+0000

Ratings and Alerts

No rating or validation information has been found for Slingshot.

No alerts have been found for Slingshot.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 65 mentions in open access literature.

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

Wang K, et al. (2025) Exploring the Role of Ccn3 in Type III Cell of Mice Taste Buds. Journal of neurochemistry, 169(1), e16291.

Spildrejorde M, et al. (2024) Citalopram exposure of hESCs during neuronal differentiation identifies dysregulated genes involved in neurodevelopment and depression. Frontiers in cell and developmental biology, 12, 1428538.

Ko KD, et al. (2024) A deep learning adversarial autoencoder with dynamic batching displays high performance in denoising and ordering scRNA-seq data. iScience, 27(3), 109027.

Devakinandan GVS, et al. (2024) Single-cell transcriptomics of vomeronasal neuroepithelium reveals a differential endoplasmic reticulum environment amongst neuronal subtypes. eLife, 13.

Wang H, et al. (2024) Deciphering deep-sea chemosynthetic symbiosis by single-nucleus RNA-sequencing. eLife, 12.

Gonzalez Galofre ZN, et al. (2024) Runx1+ vascular smooth muscle cells are essential for hematopoietic stem and progenitor cell development in vivo. Nature communications, 15(1), 1653.

Roet JEG, et al. (2024) Human lymph node fibroblastic reticular cells maintain heterogeneous characteristics in culture. iScience, 27(7), 110179.

Nath S, et al. (2024) Interaction between subventricular zone microglia and neural stem cells impacts the neurogenic response in a mouse model of cortical ischemic stroke. Nature

communications, 15(1), 9095.

Wang XD, et al. (2024) Integrated transcriptomic analysis reveals evolutionary and developmental characteristics of tendon ossification in teleost. BMC biology, 22(1), 304.

Fetit R, et al. (2024) Characterizing Neutrophil Subtypes in Cancer Using scRNA Sequencing Demonstrates the Importance of IL1?/CXCR2 Axis in Generation of Metastasis-specific Neutrophils. Cancer research communications, 4(2), 588.

Ko KD, et al. (2024) A deep learning framework for denoising and ordering scRNA-seq data using adversarial autoencoder with dynamic batching. STAR protocols, 5(2), 103067.

Reyes JM, et al. (2024) Hematologic DNMT3A reduction and high-fat diet synergize to promote weight gain and tissue inflammation. iScience, 27(3), 109122.

Hu R, et al. (2024) Expanding GABAergic Neuronal Diversity in iPSC-Derived Disease Models. bioRxiv : the preprint server for biology.

Patir A, et al. (2024) Phenotypic and spatial heterogeneity of brain myeloid cells after stroke is associated with cell ontogeny, tissue damage, and brain connectivity. Cell reports, 43(5), 114250.

Zhang Q, et al. (2023) Single-cell sequencing identifies differentiation-related markers for molecular classification and recurrence prediction of PitNET. Cell reports. Medicine, 4(2), 100934.

Fang S, et al. (2023) Computational Approaches and Challenges in Spatial Transcriptomics. Genomics, proteomics & bioinformatics, 21(1), 24.

Lin Z, et al. (2023) Tissue-embedded stretchable nanoelectronics reveal endothelial cell-mediated electrical maturation of human 3D cardiac microtissues. Science advances, 9(10), eade8513.

Lamarthée B, et al. (2023) Transcriptional and spatial profiling of the kidney allograft unravels a central role for FcyRIII+ innate immune cells in rejection. Nature communications, 14(1), 4359.

Chen W, et al. (2023) A single-cell landscape of pre- and post-menopausal high-grade serous ovarian cancer ascites. iScience, 26(10), 107712.

Abdel-Hafiz HA, et al. (2023) Single-cell profiling of murine bladder cancer identifies sex-specific transcriptional signatures with prognostic relevance. iScience, 26(9), 107703.