

Resource Summary Report

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SCDE

RRID:SCR_015952

Type: Tool

Proper Citation

SCDE (RRID:SCR_015952)

Resource Information

URL: <http://hms-dbmi.github.io/scde/index.html>

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Description: Software package that implements a set of statistical methods for analyzing single-cell RNA-seq data, including differential expression analysis (Kharchenko et al.) and pathway and geneset overdispersion analysis (Fan et al.)

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

Defining Citation: [PMID:24836921](#)

Keywords: statistic, single, cell, rna, seq, rnaseq, differential, analysis, pathway, gene, geneset, dispersion, overdispersion, bayesian, expression, magnitude

Funding: NIA K25 AG037596;
NIDDK R01 DK050234;
NHLBI R01 HL097794;
Leukemia and Lymphoma Research UK ;
Leukemia and Lymphoma Society

Availability: Free, Available for download

Resource Name: SCDE

Resource ID: SCR_015952

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260804T043630+0000

Ratings and Alerts

No rating or validation information has been found for SCDE.

No alerts have been found for SCDE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 32 mentions in open access literature.

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

Arya A, et al. (2025) Navigating single-cell RNA-sequencing: protocols, tools, databases, and applications. Genomics & informatics, 23(1), 13.

Yang J, et al. (2025) MARTRE family proteins negatively regulate CCR4-NOT activity to protect poly(A) tail length and promote translation of maternal mRNA. Nature communications, 16(1), 248.

Quah HS, et al. (2023) Single cell analysis in head and neck cancer reveals potential immune evasion mechanisms during early metastasis. Nature communications, 14(1), 1680.

Loukas I, et al. (2023) Selective advantage of epigenetically disrupted cancer cells via phenotypic inertia. Cancer cell, 41(1), 70.

Brombin A, et al. (2022) Tfap2b specifies an embryonic melanocyte stem cell that retains adult multifate potential. Cell reports, 38(2), 110234.

Raz AA, et al. (2021) Planarian stem cells specify fate yet retain potency during the cell cycle. Cell stem cell, 28(7), 1307.

Faure L, et al. (2020) Single cell RNA sequencing identifies early diversity of sensory neurons forming via bi-potential intermediates. Nature communications, 11(1), 4175.

Zou C, et al. (2020) Reduction of mNAT1/hNAT2 Contributes to Cerebral Endothelial Necroptosis and A?? Accumulation in Alzheimer's Disease. Cell reports, 33(10), 108447.

Weinberger M, et al. (2020) Functional Heterogeneity within the Developing Zebrafish Epicardium. Developmental cell, 52(5), 574.

Calgaro M, et al. (2020) Assessment of statistical methods from single cell, bulk RNA-seq, and metagenomics applied to microbiome data. Genome biology, 21(1), 191.

Johansson JA, et al. (2020) PRL3-DDX21 Transcriptional Control of Endolysosomal Genes Restricts Melanocyte Stem Cell Differentiation. Developmental cell, 54(3), 317.

Mizrak D, et al. (2020) Single-Cell Profiling and SCOPE-Seq Reveal Lineage Dynamics of Adult Ventricular-Subventricular Zone Neurogenesis and NOTUM as a Key Regulator. *Cell reports*, 31(12), 107805.

Li A, et al. (2019) IL-33 Signaling Alters Regulatory T Cell Diversity in Support of Tumor Development. *Cell reports*, 29(10), 2998.

Weng Q, et al. (2019) Single-Cell Transcriptomics Uncovers Glial Progenitor Diversity and Cell Fate Determinants during Development and Gliomagenesis. *Cell stem cell*, 24(5), 707.

Teo YV, et al. (2019) Notch Signaling Mediates Secondary Senescence. *Cell reports*, 27(4), 997.

Chen G, et al. (2019) Single-Cell RNA-Seq Technologies and Related Computational Data Analysis. *Frontiers in genetics*, 10, 317.

Leng L, et al. (2019) Single-Cell Transcriptome Analysis of Uniparental Embryos Reveals Parent-of-Origin Effects on Human Preimplantation Development. *Cell stem cell*, 25(5), 697.

Stuart HT, et al. (2019) Distinct Molecular Trajectories Converge to Induce Naive Pluripotency. *Cell stem cell*, 25(3), 388.

Pang B, et al. (2019) Single-cell RNA-seq reveals the invasive trajectory and molecular cascades underlying glioblastoma progression. *Molecular oncology*, 13(12), 2588.

Mizrak D, et al. (2019) Single-Cell Analysis of Regional Differences in Adult V-SVZ Neural Stem Cell Lineages. *Cell reports*, 26(2), 394.