Resource Summary Report

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RaceID

RRID:SCR_017045
Type: Tool

Proper Citation

RaceID (RRID:SCR_017045)

Resource Information

URL: https://github.com/dgrun/RaceID

Proper Citation: RaceID (RRID:SCR_017045)

Description: Algorithm for identification of rare and abundant cell types from single cell transcriptome data. Based on transcript counts obtained with unique molecular identifies. Used for discovering rare cell types and corresponding marker genes in healthy and diseased organs. Operating system Unix/Linux, Mac OS, Windows.

Synonyms: RaceID3, RaceID2

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

Defining Citation: PMID:26287467, PMID:27345837

Keywords: inference, cell, type, single, RNAseq, data, sequencing, rare, abundant, transcriptome, marker, gene, organ

Funding: European Research Council Advanced grant ;
Nederlandse Organisatie voor Wetenschappelijk Onderzoek Vici award

Availability: Free, Available for download, Freely available

Resource Name: RaceID

Resource ID: SCR_017045

Alternate IDs: OMICS_12591, SCR_017243

Alternate URLs: https://rdrr.io/cran/RaceID/, https://github.com/dgrun/RaceID3_StemID2

Record Creation Time: 20220129T080333+0000

Record Last Update: 20250508T065744+0000

Ratings and Alerts

No rating or validation information has been found for RaceID.

No alerts have been found for RaceID.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Galbo PM, et al. (2024) Functional Contribution and Clinical Implication of Cancer-Associated Fibroblasts in Glioblastoma. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(4), 865.

Yu V, et al. (2023) Differential CpG methylation at Nnat in the early establishment of beta cell heterogeneity. bioRxiv : the preprint server for biology.

Pérez-Mojica JE, et al. (2023) Single-embryo RNA sequencing for continuous and sex-specific gene expression analysis on Drosophila. STAR protocols, 4(3), 102535.

Yang CH, et al. (2022) Independent phenotypic plasticity axes define distinct obesity sub-types. Nature metabolism, 4(9), 1150.

Zhang L, et al. (2022) Digital Cell Atlas of Mouse Uterus: From Regenerative Stage to Maturational Stage. Frontiers in genetics, 13, 847646.

Sankowski R, et al. (2021) Commensal microbiota divergently affect myeloid subsets in the mammalian central nervous system during homeostasis and disease. The EMBO journal, 40(23), e108605.

Fa B, et al. (2021) GapClust is a light-weight approach distinguishing rare cells from voluminous single cell expression profiles. Nature communications, 12(1), 4197.

Patra D, et al. (2020) Site-1 protease ablation in the osterix-lineage in mice results in bone

marrow neutrophilia and hematopoietic stem cell alterations. Biology open, 9(6).

Grün D, et al. (2020) Revealing dynamics of gene expression variability in cell state space. Nature methods, 17(1), 45.

Peyvandipour A, et al. (2020) Identification of cell types from single cell data using stable clustering. Scientific reports, 10(1), 12349.

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

Ouadah Y, et al. (2019) Rare Pulmonary Neuroendocrine Cells Are Stem Cells Regulated by Rb, p53, and Notch. Cell, 179(2), 403.

Boulais PE, et al. (2018) The Majority of CD45- Ter119- CD31- Bone Marrow Cell Fraction Is of Hematopoietic Origin and Contains Erythroid and Lymphoid Progenitors. Immunity, 49(4), 627.