Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

StemID

RRID:SCR_017242
Type: Tool

Proper Citation

StemID (RRID:SCR_017242)

Resource Information

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

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Description: Algorithm for derivation of cell lineage trees based on RaceID2 results and predicts multipotent cell identites. StemID2 is algorithm for identification of lineage trees based on RaceID3 analysis. Used for better understanding of differentiation dynamics in variety of systems. Written in R computing language.

Synonyms: StemID2

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

Defining Citation: PMID:27345837

Keywords: derivation, cell, linage, tree, predict, multipotent, identity, dynamic

Funding: DON Foundation ;
Dutch Diabetes Research Foundation ;
European Research Council ;
Nederlandse Organisatie voor Wetenschappelijk Onderzoek

Availability: Free, Available for download, Freely available

Resource Name: StemID

Resource ID: SCR_017242

Alternate URLs: https://github.com/dgrun/RaceID3_StemID2, https://github.com/dgrun/RaceID3_StemID2_package

Record Creation Time: 20220129T080334+0000

Record Last Update: 20260905T132821+0000

Ratings and Alerts

No rating or validation information has been found for StemID.

No alerts have been found for StemID.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Henon C, et al. (2024) Single-cell multiomics profiling reveals heterogeneous transcriptional programs and microenvironment in DSRCTs. Cell reports. Medicine, 5(6), 101582.

Wang X, et al. (2024) MarsGT: Multi-omics analysis for rare population inference using single-cell graph transformer. Nature communications, 15(1), 338.

Wang S, et al. (2024) scSID: A lightweight algorithm for identifying rare cell types by capturing differential expression from single-cell sequencing data. Computational and structural biotechnology journal, 23, 589.

Wang X, et al. (2023) MarsGT: Multi-omics analysis for rare population inference using single-cell graph transformer. bioRxiv : the preprint server for biology.

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

Rosales-Alvarez RE, et al. (2023) VarID2 quantifies gene expression noise dynamics and unveils functional heterogeneity of ageing hematopoietic stem cells. Genome biology, 24(1), 148.

Yan R, et al. (2022) Discovery of Muscle-Tendon Progenitor Subpopulation in Human Myotendinous Junction at Single-Cell Resolution. Research (Washington, D.C.), 2022, 9760390.

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

Zhang F, et al. (2022) FitDevo: accurate inference of single-cell developmental potential using sample-specific gene weight. Briefings in bioinformatics, 23(5).

Molenaar B, et al. (2021) Single-cell transcriptomics following ischemic injury identifies a role for B2M in cardiac repair. Communications biology, 4(1), 146.

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

Honkoop H, et al. (2019) Single-cell analysis uncovers that metabolic reprogramming by ErbB2 signaling is essential for cardiomyocyte proliferation in the regenerating heart. eLife, 8.