

Resource Summary Report

Generated by [PRECISE-TBI](#) on Jul 29, 2026

TooManyCells

RRID:SCR_025328

Type: Tool

Proper Citation

TooManyCells (RRID:SCR_025328)

Resource Information

URL: <https://github.com/GregorySchwartz/too-many-cells>

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Description: Software suite of tools, algorithms, and visualizations focusing on relationships between cell clades. This includes new ways of clustering, plotting, choosing differential expression comparisons. Identifies and visualizes relationships of single-cell clades.

Resource Type: software toolkit, source code, software resource

Defining Citation: [PMID:32123397](#)

Keywords: Spectral clustering, radial tree, visualization, cell clades,

Funding: NCI T32 CA009140;
NCI R01 CA215518;
NHLBI R01 HL145754;
Sloan Foundation ;
NCI R01 CA230800

Availability: Free, Available for download, Freely available

Resource Name: TooManyCells

Resource ID: SCR_025328

Alternate URLs: <https://gregoryschwartz.github.io/too-many-cells/>

Record Creation Time: 20240515T053238+0000

Record Last Update: 20260729T044619+0000

Ratings and Alerts

No rating or validation information has been found for TooManyCells.

No alerts have been found for TooManyCells.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Li X, et al. (2025) The Dynamically Evolving Cell States and Ecosystem from Benign Nevi to Melanoma. Clinical cancer research : an official journal of the American Association for Cancer Research, 31(12), 2478.

Prompsy P, et al. (2024) IDclust: Iterative clustering for unsupervised identification of cell types with single cell transcriptomics and epigenomics. NAR genomics and bioinformatics, 6(4), lqae174.

Mongia A, et al. (2024) AnnoSpat annotates cell types and quantifies cellular arrangements from spatial proteomics. Nature communications, 15(1), 3744.

Sun Y, et al. (2024) Hierarchical marker genes selection in scRNA-seq analysis. PLoS computational biology, 20(12), e1012643.