

Resource Summary Report

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CytoSPACE

RRID:SCR_027634

Type: Tool

Proper Citation

CytoSPACE (RRID:SCR_027634)

Resource Information

URL: <https://cytospace.stanford.edu/>

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Description: Software tool for assigning single cells from scRNA-seq to spatial transcriptomics coordinates via optimization framework. Supports high-resolution cell/spot alignment, capacity-constrained/domain-aware placement, and outputs per-cell/per-spot assignments and probabilities for downstream visualization and analysis. Used for optimal mapping of scRNA-seq data to spatial transcriptomics data.

Resource Type: software application, source code, software resource

Defining Citation: [PMID:36879008](#)

Keywords: Optimal mapping of scRNA-seq data to spatial transcriptomics data, assigning single cells from scRNA-seq, spatial transcriptomics coordinates, optimization framework, mapping, scRNA-seq data, spatial transcriptomics data,

Funding: American Association for Cancer Research ;
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NCI R01CA255450;
NCI R00CA187192;
NCI R21CA238971;
Virginia and D. K. Ludwig Fund for Cancer Research ;
Donald E. and Delia B. Baxter Foundation

Availability: Free, Available for download, Freely available

Resource Name: CytoSPACE

Resource ID: SCR_027634

Alternate URLs: <https://github.com/digitalcytometry/cytospace>

License URLs: <https://github.com/digitalcytometry/cytospace?tab=License-1-overfile#readme>

Record Creation Time: 20251108T062234+0000

Record Last Update: 20260817T040737+0000

Ratings and Alerts

No rating or validation information has been found for CytoSPACE.

No alerts have been found for CytoSPACE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Zhang W, et al. (2026) Non-invasive profiling of the tumour microenvironment with spatial ecotypes. Nature, 654(8120), 1076.

Bourgain-Chang E, et al. (2026) Reconstructing single-cell resolution from spatial transcriptomics with CellRefiner. Nature communications, 17(1).

Wang R, et al. (2026) Constructing the spatiotemporal atlas of single-cell lineage trajectories in stereotypic biological structures. iScience, 29(1), 114307.

Martin PCN, et al. (2025) Multi-scale and multi-context interpretable mapping of cell states across heterogeneous spatial samples. Nature communications, 16(1), 7814.

Chen S, et al. (2025) Multi-omic and spatial analysis of mouse kidneys highlights sex-specific differences in gene regulation across the lifespan. Nature genetics, 57(5), 1213.

Baldassari S, et al. (2025) Single-cell genotyping and transcriptomic profiling of mosaic focal cortical dysplasia. Nature neuroscience, 28(5), 964.

Wang L, et al. (2025) Inference of cell-type composition and single-cell spatial maps from spatial transcriptomics data with SWOT. Communications biology, 8(1), 1611.

Vahid MR, et al. (2023) High-resolution alignment of single-cell and spatial transcriptomes with CytoSPACE. Nature biotechnology, 41(11), 1543.

Wang M, et al. (2021) Identification of Potential Bioactive Ingredients and Mechanisms of the Guanxin Suhe Pill on Angina Pectoris by Integrating Network Pharmacology and Molecular Docking. Evidence-based complementary and alternative medicine : eCAM,

2021, 4280482.

Martín-Gálvez D, et al. (2017) Genome variation and conserved regulation identify genomic regions responsible for strain specific phenotypes in rat. *BMC genomics*, 18(1), 986.