

Resource Summary Report

Generated by [NIF](#) on Sep 18, 2026

CytoSPACE

RRID:SCR_027634

Type: Tool

Proper Citation

CytoSPACE (RRID:SCR_027634)

Resource Information

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

Proper Citation: CytoSPACE (RRID:SCR_027634)

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, software resource, source code

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 ;
Donald E. and Delia B. Baxter Foundation ;
NCI R00CA187192;
NCI R01CA255450;
NCI R21CA238971;
Norwegian Cancer Society ;
Virginia and D. K. Ludwig Fund for Cancer Research

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: 20260912T200532+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 [NIF](#).

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.