

Resource Summary Report

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Tangram

RRID:SCR_006152

Type: Tool

Proper Citation

Tangram (RRID:SCR_006152)

Resource Information

URL: <https://github.com/jiantao/Tangram>

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Description: A C / C++ command line toolbox for structural variation (SV) detection that reports mobile element insertions (MEI). It takes advantage of both read-pair and split-read algorithms and is extremely fast and memory-efficient. Powered by the Bamtools API, it can call SV events on multiple BAM files (a population) simultaneously to increase the sensitivity on low-coverage dataset.

Resource Type: software resource, software toolkit

Defining Citation: [PMID:25228379](#)

Keywords: standalone software, c, c++

Availability: MIT License

Resource Name: Tangram

Resource ID: SCR_006152

Alternate IDs: OMICS_05785

Record Creation Time: 20220129T080234+0000

Record Last Update: 20260725T191236+0000

Ratings and Alerts

No rating or validation information has been found for Tangram.

No alerts have been found for Tangram.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 61 mentions in open access literature.

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

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

Klein D, et al. (2025) Mapping cells through time and space with moscot. *Nature*, 638(8052), 1065.

Zhang Y, et al. (2025) Cancer therapy resistance from a spatial-omics perspective. *Clinical and translational medicine*, 15(7), e70396.

Zhang L, et al. (2025) Mature tertiary lymphoid structures linked to HPV status and anti-PD-1 based chemoimmunotherapy response in head and neck squamous cell carcinoma. *Oncoimmunology*, 14(1), 2528109.

Holm Nygaard A, et al. (2025) Patterning effects of FGF17 and cAMP on generation of dopaminergic progenitors for cell replacement therapy in Parkinson's disease. *Stem cells (Dayton, Ohio)*, 43(3).

Aggarwal B, et al. (2025) CellSP: Module discovery and visualization for subcellular spatial transcriptomics data. *bioRxiv : the preprint server for biology*.

Pareja-Lorente E, et al. (2025) Systematic assessment of microenvironment-dependent transcriptional patterns and intercellular communication. *Genome biology*, 26(1), 193.

Li T, et al. (2025) Computational pathology annotation enhances the resolution and interpretation of breast cancer spatial transcriptomics data. *NPJ precision oncology*, 9(1), 310.

Sunil HS, et al. (2025) TMPRSS11B promotes an acidified microenvironment and immune suppression in squamous lung cancer. *EMBO reports*, 26(24), 6346.

Noor H, et al. (2025) Response to Antiangiogenic Therapy Is Associated with AIMP Protein Family Expression in Glioblastoma and Lower-Grade Gliomas. *Cancer research communications*, 5(9), 1651.

Chen W, et al. (2025) A visual-omics foundation model to bridge histopathology with spatial transcriptomics. *Nature methods*, 22(7), 1568.

Huang R, et al. (2025) Single-cell and spatiotemporal profile of ovulation in the mouse ovary. *PLoS biology*, 23(6), e3003193.

Kaul D, et al. (2025) Astrocytic glutamate regulation is shaped by adversity and glucocorticoid signalling. *bioRxiv : the preprint server for biology*.

Chu C, et al. (2025) Immunoregulatory Roles of Tumor-Originated Pericytes Identified by Single-Cell Analysis in Glioblastoma. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(47), e11856.

Zhao J, et al. (2025) Enhancing Spatial Transcriptomics via Spatially Constrained Matrix Decomposition with EDGES. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(42), e08346.

Haviv D, et al. (2025) The covariance environment defines cellular niches for spatial inference. *Nature biotechnology*, 43(2), 269.

Elison W, et al. (2025) Single cell multiomics reveals drivers of metabolic dysfunction-associated steatohepatitis. *medRxiv : the preprint server for health sciences*.

Liao L, et al. (2025) SC2Spa: a deep learning based approach to map transcriptome to spatial origins at cellular resolution. *BMC bioinformatics*, 26(1), 148.

Aggarwal B, et al. (2025) CellSP enables module discovery and visualization for subcellular spatial transcriptomics data. *Communications biology*, 8(1), 1528.

Li H, et al. (2025) Cell2Spatial is a computational framework that maps single cells to spatial transcriptomic spots to reconstruct tissue architecture. *PLoS biology*, 23(11), e3003477.