Resource Summary Report

Generated by dkNET on May 8, 2025

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) simutaneously to increase the sensitivity on low-coverage dataset.

Resource Type: software toolkit, software resource

Defining Citation: PMID:25228379

Keywords: standalone software, c, c++

Funding:

Availability: MIT License

Resource Name: Tangram

Resource ID: SCR_006152

Alternate IDs: OMICS_05785

Record Creation Time: 20220129T080234+0000

Record Last Update: 20250508T065031+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 41 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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

Li K, et al. (2024) stDiff: a diffusion model for imputing spatial transcriptomics through single-cell transcriptomics. Briefings in bioinformatics, 25(3).

Kueckelhaus J, et al. (2024) Inferring histology-associated gene expression gradients in spatial transcriptomic studies. Nature communications, 15(1), 7280.

Nelson ED, et al. (2024) An integrated single-nucleus and spatial transcriptomics atlas reveals the molecular landscape of the human hippocampus. bioRxiv: the preprint server for biology.

Duan Z, et al. (2024) iMIRACLE: an Iterative Multi-View Graph Neural Network to Model Intercellular Gene Regulation from Spatial Transcriptomic Data. Proceedings of the ... ACM International Conference on Information & Knowledge Management. ACM International Conference on Information and Knowledge Management, 2024, 538.

Hao M, et al. (2024) STEM enables mapping of single-cell and spatial transcriptomics data with transfer learning. Communications biology, 7(1), 56.

Dimitrov D, et al. (2024) LIANA+ provides an all-in-one framework for cell-cell communication inference. Nature cell biology, 26(9), 1613.

Blampey Q, et al. (2024) Sopa: a technology-invariant pipeline for analyses of image-based spatial omics. Nature communications, 15(1), 4981.

Wu Y, et al. (2024) A spatiotemporal transcriptomic atlas of mouse placentation. Cell discovery, 10(1), 110.

Zeng Y, et al. (2024) Imputing spatial transcriptomics through gene network constructed from

protein language model. Communications biology, 7(1), 1271.

Qiu C, et al. (2024) A single-cell time-lapse of mouse prenatal development from gastrula to birth. Nature, 626(8001), 1084.

Shi Y, et al. (2024) Decoding the spatiotemporal regulation of transcription factors during human spinal cord development. Cell research, 34(3), 193.

Fu YC, et al. (2024) scHolography: a computational method for single-cell spatial neighborhood reconstruction and analysis. Genome biology, 25(1), 164.

Swain AK, et al. (2024) SpatialPrompt: spatially aware scalable and accurate tool for spot deconvolution and domain identification in spatial transcriptomics. Communications biology, 7(1), 639.

Chang Y, et al. (2024) Graph Fourier transform for spatial omics representation and analyses of complex organs. Nature communications, 15(1), 7467.

Zhang Y, et al. (2023) Reference-based cell type matching of in situ image-based spatial transcriptomics data on primary visual cortex of mouse brain. Scientific reports, 13(1), 9567.

Li X, et al. (2023) STellaris: a web server for accurate spatial mapping of single cells based on spatial transcriptomics data. Nucleic acids research, 51(W1), W560.

Huang X, et al. (2023) Single-cell, whole-embryo phenotyping of mammalian developmental disorders. Nature, 623(7988), 772.

Sun ED, et al. (2023) TISSUE: uncertainty-calibrated prediction of single-cell spatial transcriptomics improves downstream analyses. bioRxiv: the preprint server for biology.

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