

Resource Summary Report

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Conos

RRID:SCR_026381

Type: Tool

Proper Citation

Conos (RRID:SCR_026381)

Resource Information

URL: <https://github.com/kharchenkolab/conos>

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Description: Software R package for joint analysis of multiple single-cell RNA-seq datasets. Used to wire together large collections of single-cell RNA-seq datasets, which allows for both identification of recurrent cell clusters and propagation of information between datasets in multi-sample or atlas-scale collections.

Resource Type: source code, software toolkit, software resource

Defining Citation: [DOI:10.1038/s41592-019-0466-z](https://doi.org/10.1038/s41592-019-0466-z)

Keywords: joint analysis of multiple single-cell RNA-seq datasets, multiple single-cell RNA-seq datasets, identification of recurrent cell clusters, propagation of information between datasets, multi-sample, atlas-scale collections,

Funding: NHLBI R01HL131768;
NSF ;
Zimin Foundation

Availability: Free, Available for download, Freely available

Resource Name: Conos

Resource ID: SCR_026381

License: GNU GPL v3

Record Creation Time: 20250206T060329+0000

Record Last Update: 20260729T044637+0000

Ratings and Alerts

No rating or validation information has been found for Conos.

No alerts have been found for Conos.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Jelcic I, et al. (2025) T-bet+ CXCR3+ B cells drive hyperreactive B-T cell interactions in multiple sclerosis. Cell reports. Medicine, 6(3), 102027.

Wu SY, et al. (2025) Targeting tumor-intrinsic BCL9 reverses immunotherapy resistance by eliciting macrophage-mediated phagocytosis and antigen presentation. Nature communications, 16(1), 10039.

Mei S, et al. (2025) Single-Cell and Spatial Transcriptomics Reveal a Tumor-Associated Macrophage Subpopulation that Mediates Prostate Cancer Progression and Metastasis. Molecular cancer research : MCR, 23(7), 653.

Lau KEH, et al. (2024) Differential microRNA editing may drive target pathway switching in human temporal lobe epilepsy. Brain communications, 6(1), fcad355.

Hirz T, et al. (2023) Dissecting the immune suppressive human prostate tumor microenvironment via integrated single-cell and spatial transcriptomic analyses. Nature communications, 14(1), 663.

Krivanek J, et al. (2020) Dental cell type atlas reveals stem and differentiated cell types in mouse and human teeth. Nature communications, 11(1), 4816.