

Resource Summary Report

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MetaNeighbor

RRID:SCR_016727

Type: Tool

Proper Citation

MetaNeighbor (RRID:SCR_016727)

Resource Information

URL: <https://www.bioconductor.org/packages/release/bioc/html/MetaNeighbor.html>

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Description: Software package to assess cell type identity using both functional and random gene sets. Used for single cell replicability analysis to quantify cell type replicability across datasets using neighbor voting.

Resource Type: data analysis software, data processing software, software application, software resource

Keywords: quantify, cell, type, replicability, dataset, access, cell, type, identity, functional, random, gene

Availability: Free, Available for download, Freely available

Resource Name: MetaNeighbor

Resource ID: SCR_016727

Alternate URLs: <https://github.com/maggiecrow/MetaNeighbor>,
<https://github.com/gillislabs/MetaNeighbor>

License: MIT License

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260821T194056+0000

Ratings and Alerts

No rating or validation information has been found for MetaNeighbor.

No alerts have been found for MetaNeighbor.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 58 mentions in open access literature.

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

Schmitz MT, et al. (2026) A consensus spinal cord cell type atlas across mouse, macaque, and human. bioRxiv : the preprint server for biology.

Liu H, et al. (2026) Cochlear nucleus spatial transcriptomes of normal and hearing loss mice reveal a critical role of Spp1 in bushy cells. Cell research, 36(7), 531.

Chen L, et al. (2026) Construction of a Multitissue Cell Atlas Reveals Cell-Type-Specific Regulation of Molecular and Complex Phenotypes in Pigs. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(8), e04961.

Cheng J, et al. (2026) Single-cell atlas reveals cellular heterogeneity and BMP5-mediated regulation of adipogenic differentiation in sheep adipose tissue. Communications biology, 9(1).

Venkatesan S, et al. (2026) Cell type-agnostic transcriptomic signatures enable uniform comparisons of neural maturation. PLoS biology, 24(4), e3003757.

Li X, et al. (2026) A spatiotemporal atlas of cerebrovascular development in zebrafish. Nature communications, 17(1).

Yao X, et al. (2026) Unveiling the early defense response dynamics in grapevines against Plasmopara viticola by single-cell transcriptomics. Genome biology, 27(1), 43.

Kim H, et al. (2026) MAPseq2: a sensitive barcoded connectomics method. bioRxiv : the preprint server for biology.

Zhao B, et al. (2026) Comparative Single-Cell Transcriptomic Atlas Reveals the Genetic Regulation of Reproductive Traits. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(17), e17633.

Tian Y, et al. (2025) The Transcriptomic Signature of Donkey Ovarian Tissue Revealed by Cross-Species Comparative Analysis at Single-Cell Resolution. Animals : an open access journal from MDPI, 15(12).

Feng X, et al. (2025) Cortical arealization of interneurons defines shared and distinct molecular programs in developing human and macaque brains. Nature communications, 16(1), 672.

Han B, et al. (2025) A multi-tissue single-cell expression atlas in cattle. Nature genetics, 57(10), 2546.

Werner JM, et al. (2025) The misplaced mouse Pax6 interneuron subclass: A cross-species transcriptomic reassignment. *bioRxiv : the preprint server for biology*.

Gavriouchkina D, et al. (2025) A single-cell atlas of the bobtail squid visual and nervous system highlights molecular principles of convergent evolution. *Nature ecology & evolution*, 9(7), 1245.

Xiong LL, et al. (2025) A Single-Nucleus Transcriptomic Atlas Reveals Cellular and Genetic Characteristics of Alzheimer's-Like Pathology in Aging Tree Shrews. *MedComm*, 6(4), e70114.

Zhao B, et al. (2025) Integrative single-cell transcriptomics of sheep ovarian development reveals dynamic transcriptional programs relevant to reproductive traits. *iScience*, 28(5), 112422.

Johansen NJ, et al. (2025) Cross-species consensus atlas of the primate basal ganglia. *bioRxiv : the preprint server for biology*.

Tian Y, et al. (2025) Revealing the Transcriptional and Metabolic Characteristics of Sebocytes Based on the Donkey Cell Transcriptome Atlas. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(16), e2413819.

Alkaslasi MR, et al. (2025) The transcriptional response of cortical neurons to concussion reveals divergent fates after injury. *Nature communications*, 16(1), 1097.

Fiorini MR, et al. (2025) Neural networks reveal novel gene signatures in Parkinson disease from single-nuclei transcriptomes. *NPJ Parkinson's disease*, 11(1), 304.