# Resource Summary Report

Generated by NIF on May 23, 2025

# 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:** software application, data processing software, software resource, data analysis software

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

**Funding:**

**Availability:** Free, Available for download, Freely available

**Resource Name:** MetaNeighbor

**Resource ID:** SCR_016727

**Alternate URLs:** https://github.com/maggiecrow/MetaNeighbor, https://github.com/gillislab/MetaNeighbor

**License:** MIT License

**Record Creation Time:** 20220129T080332+0000

**Record Last Update:** 20250523T055216+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 37 mentions in open access literature.

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

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.

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

Totty MS, et al. (2024) Transcriptomic diversity of amygdalar subdivisions across humans and nonhuman primates. bioRxiv : the preprint server for biology.

Hruska-Plochan M, et al. (2024) A model of human neural networks reveals NPTX2 pathology in ALS and FTLD. Nature, 626(8001), 1073.

Nardone S, et al. (2024) A spatially-resolved transcriptional atlas of the murine dorsal pons at single-cell resolution. Nature communications, 15(1), 1966.

Bai Y, et al. (2024) A single-cell transcriptomic study of heterogeneity in human embryonic tanycytes. Scientific reports, 14(1), 15384.

Huang Y, et al. (2024) Discovery of an unconventional lamprey lymphocyte lineage highlights divergent features in vertebrate adaptive immune system evolution. Nature communications, 15(1), 7626.

Loh L, et al. (2024) Unraveling the phenotypic states of human innate-like T cells: Comparative insights with conventional T cells and mouse models. Cell reports, 43(9), 114705.

Passalacqua MJ, et al. (2024) Coexpression enhances cross-species integration of single-cell RNA sequencing across diverse plant species. Nature plants, 10(7), 1075.

Ricker CA, et al. (2024) Historical perspective and future directions: computational science in

immuno-oncology. Journal for immunotherapy of cancer, 12(1).

Singh PNP, et al. (2024) Transcription factor dynamics, oscillation, and functions in human enteroendocrine cell differentiation. Cell stem cell, 31(7), 1038.

Nardone S, et al. (2023) A spatially-resolved transcriptional atlas of the murine dorsal pons at single-cell resolution. bioRxiv : the preprint server for biology.

Loh L, et al. (2023) Unraveling the Phenotypic States of Human innate-like T Cells: Comparative Insights with Conventional T Cells and Mouse Models. bioRxiv : the preprint server for biology.

Li J, et al. (2023) Integrated multi-omics single cell atlas of the human retina. Research square.

Liu D, et al. (2023) Characterization of human pluripotent stem cell differentiation by single-cell dual-omics analyses. Stem cell reports, 18(12), 2464.

Roig Adam A, et al. (2023) Transcriptional diversity in specific synaptic gene sets discriminates cortical neuronal identity. Biology direct, 18(1), 22.

Jung M, et al. (2023) Cross-species transcriptomic atlas of dorsal root ganglia reveals species-specific programs for sensory function. Nature communications, 14(1), 366.

Yoon SH, et al. (2023) Molecular traces of Drosophila hemocytes reveal transcriptomic conservation with vertebrate myeloid cells. PLoS genetics, 19(12), e1011077.

Zhong J, et al. (2023) Multi-species atlas resolves an axolotl limb development and regeneration paradox. Nature communications, 14(1), 6346.

Suresh H, et al. (2023) Comparative single-cell transcriptomic analysis of primate brains highlights human-specific regulatory evolution. Nature ecology & evolution, 7(11), 1930.