Resource Summary Report

Generated by kravitz2 on Aug 1, 2026

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

Proper Citation: MetaNeighbor (RRID:SCR_016727)

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 processing software, data analysis 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/gillislab/MetaNeighbor

License: MIT License

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260801T042801+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 49 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

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.

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).

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.

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.

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.

Yan H, et al. (2025) A single-cell rice atlas integrates multi-species data to reveal cis-regulatory evolution. Nature plants, 11(10), 2050.

Bhattacharya S, et al. (2025) Intestinal secretory differentiation reflects niche-driven phenotypic and epigenetic plasticity of a common signal-responsive terminal cell. Cell stem cell, 32(6), 952.

Fisher J, et al. (2024) Cortical somatostatin long-range projection neurons and interneurons exhibit divergent developmental trajectories. Neuron, 112(4), 558.

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.

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.

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

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.