

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

BBKNN

RRID:SCR_022807

Type: Tool

Proper Citation

BBKNN (RRID:SCR_022807)

Resource Information

URL: <https://bbknn.readthedocs.io/en/latest/>

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Description: Software to identify each cell's top neighbours in each batch separately instead of entire cell pool with no accounting for batch. Nearest neighbours for each batch are then merged to create final list of neighbours for cell. Aligns batches in a quick and lightweight manner.

Synonyms: Batch Balanced KNN

Resource Type: software resource, software application

Keywords: Aligns batches, nearest neighbours for each batch, identify each cell's top neighbours, each batch separately,

Availability: Free, Available for download, Freely available

Resource Name: BBKNN

Resource ID: SCR_022807

Alternate URLs: <https://github.com/Teichlab/bbknn/blob/master/docs/index.rst>,
<https://github.com/Teichlab/bbknn>

License: MIT License

Record Creation Time: 20220929T050157+0000

Record Last Update: 20260731T043119+0000

Ratings and Alerts

No rating or validation information has been found for BBKNN.

No alerts have been found for BBKNN.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Messingschlager M, et al. (2025) DNA methylation changes during acute COVID-19 are associated with long-term transcriptional dysregulation in patients' airway epithelial cells. EMBO molecular medicine, 17(5), 923.

Liu YT, et al. (2025) Immune-featured stromal niches associate with response to neoadjuvant immunotherapy in oral squamous cell carcinoma. Cell reports. Medicine, 6(3), 102024.

Nehar-Belaid D, et al. (2025) SARS-CoV-2 induced immune perturbations in infants vary with disease severity and differ from adults' responses. Nature communications, 16(1), 4562.

Johansen VBI, et al. (2025) Regulation of LEAP2 by insulin and glucagon in mice and humans. Cell reports. Medicine, 6(3), 101996.

Balderson B, et al. (2025) Systematic analysis of the transcriptional landscape of melanoma reveals drug-target expression plasticity. Briefings in functional genomics, 24.

Feng JX, et al. (2025) Single-cell lineage tracing identifies hemogenic endothelial cells in the adult mouse bone marrow. bioRxiv : the preprint server for biology.

Li YS, et al. (2025) Cellular dynamics in cerebrospinal fluid unveils the key regulators of intracranial response to immune checkpoint inhibitors in NSCLC brain metastases. Journal for immunotherapy of cancer, 13(11).

Klughammer J, et al. (2024) A multi-modal single-cell and spatial expression map of metastatic breast cancer biopsies across clinicopathological features. Nature medicine, 30(11), 3236.

Yang X, et al. (2024) Integrated multiomic analysis reveals disulfidptosis subtypes in glioblastoma: implications for immunotherapy, targeted therapy, and chemotherapy. Frontiers in immunology, 15, 1362543.

Chen DG, et al. (2024) Integrative systems biology reveals NKG2A-biased immune responses correlate with protection in infectious disease, autoimmune disease, and cancer. Cell reports, 43(3), 113872.

Chiou KL, et al. (2023) A single-cell multi-omic atlas spanning the adult rhesus macaque brain. *Science advances*, 9(41), eadh1914.

Neirijnck Y, et al. (2023) Single-cell transcriptomic profiling redefines the origin and specification of early adrenogonadal progenitors. *Cell reports*, 42(3), 112191.

Wiedemann J, et al. (2023) Differential cell composition and split epidermal differentiation in human palm, sole, and hip skin. *Cell reports*, 42(1), 111994.