

Resource Summary Report

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kb_python

RRID:SCR_018213

Type: Tool

Proper Citation

kb_python (RRID:SCR_018213)

Resource Information

URL: https://github.com/pachterlab/kb_python

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Description: Software Python package that wraps kallisto and bustools single-cell RNA-seq workflow. Used for single-cell RNA-seq pre-processing. Simplifies downloading and running of kallisto and bustools programs. Consists of kb ref and kb count commands. kb ref builds or downloads species specific index for pseudo alignment of reads and must be run prior to kb count and it runs kallisto index. kb count runs kallisto and bustools programs and is used for pre-processing of data from variety of single-cell RNA-seq technologies, and for number of different workflows (e.g. production of gene count matrices, RNA velocity analyses, etc.).

Resource Type: software resource, software toolkit

Defining Citation: [DOI:10.1038/nbt.3519](https://doi.org/10.1038/nbt.3519), [DOI:10.1101/673285](https://doi.org/10.1101/673285)

Keywords: Wrapper, single cell RNA seq, pre-processing, species specific index, pseudo alignment, read, gene count matrice, RNA velocity analysis, data

Availability: Free, Available for download, Freely available

Resource Name: kb_python

Resource ID: SCR_018213

License: BSD 2-Clause "Simplified" License

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260912T200255+0000

Ratings and Alerts

No rating or validation information has been found for kb_python.

No alerts have been found for kb_python.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Hotz M, et al. (2026) Single-cell analyses identify independent aging processes that compete to determine cellular fate in budding yeast. *Proceedings of the National Academy of Sciences of the United States of America*, 123(11), e2534452123.

Jones MG, et al. (2024) Spatiotemporal lineage tracing reveals the dynamic spatial architecture of tumor growth and metastasis. *bioRxiv : the preprint server for biology*.

Wang W, et al. (2024) Single-cell analysis of tumor microenvironment and cell adhesion reveals that interleukin-1 beta promotes cancer cell proliferation in breast cancer. *Animal models and experimental medicine*, 7(5), 617.

Sullivan DK, et al. (2024) kallisto, bustools, and kb-python for quantifying bulk, single-cell, and single-nucleus RNA-seq. *bioRxiv : the preprint server for biology*.

Wang Y, et al. (2024) Identification of JUN gene and cellular microenvironment in response to PD-1 blockade treatment in lung cancer patients via single-cell RNA sequencing. *Aging*, 16(12), 10348.

Booeshaghi AS, et al. (2024) Quantifying orthogonal barcodes for sequence census assays. *Bioinformatics advances*, 4(1), vbad181.

Millet A, et al. (2024) An exhausted-like microglial population accumulates in aged and APOE4 genotype Alzheimer's brains. *Immunity*, 57(1), 153.

Luebbert L, et al. (2023) Efficient and accurate detection of viral sequences at single-cell resolution reveals novel viruses perturbing host gene expression. *bioRxiv : the preprint server for biology*.

Ivanova EN, et al. (2023) mRNA COVID-19 vaccine elicits potent adaptive immune response without the acute inflammation of SARS-CoV-2 infection. *iScience*, 26(12), 108572.

Gorin G, et al. (2023) Studying stochastic systems biology of the cell with single-cell genomics data. *Cell systems*, 14(10), 822.

Morabito S, et al. (2023) hdWGCNA identifies co-expression networks in high-dimensional transcriptomics data. *Cell reports methods*, 3(6), 100498.

Qiu X, et al. (2022) Mapping transcriptomic vector fields of single cells. *Cell*, 185(4), 690.

Qiu C, et al. (2022) Systematic reconstruction of cellular trajectories across mouse embryogenesis. *Nature genetics*, 54(3), 328.

He D, et al. (2022) Alevin-fry unlocks rapid, accurate and memory-frugal quantification of single-cell RNA-seq data. *Nature methods*, 19(3), 316.

Booeshaghi AS, et al. (2021) Isoform cell-type specificity in the mouse primary motor cortex. *Nature*, 598(7879), 195.

Liu N, et al. (2021) Single-cell analysis of COVID-19, sepsis, and HIV infection reveals hyperinflammatory and immunosuppressive signatures in monocytes. *Cell reports*, 37(1), 109793.

Shainer I, et al. (2021) Choice of pre-processing pipeline influences clustering quality of scRNA-seq datasets. *BMC genomics*, 22(1), 661.

Ren X, et al. (2021) COVID-19 immune features revealed by a large-scale single-cell transcriptome atlas. *Cell*, 184(7), 1895.