Resource Summary Report

Generated by dkNET on May 20, 2025

DistMap

RRID:SCR_005473
Type: Tool

Proper Citation

DistMap (RRID:SCR_005473)

Resource Information

URL: http://code.google.com/p/distmap/

Proper Citation: DistMap (RRID:SCR_005473)

Description: A user-friendly software pipeline designed to map short reads in a MapReduce framework on a local Hadoop cluster. It is designed to be easily implemented by researchers who do not have expert knowledge of bioinformatics. As it does not have any dependencies, it provides full flexibility and control to the user. The user can use any version of a compatible mapper and any reference genome assembly. There is no need to maintain the mapper, reference or DistMap source code on each of the slaves (nodes) in the Hadoop cluster, making maintenance extremely easy.

Abbreviations: DistMap

Resource Type: software resource

Defining Citation: PMID:24009693

Keywords: mapreduce/hadoop, command line, hadoop cluster, next-generation sequencing, bio.tools

Funding:

Availability: GNU General Public License, v3

Resource Name: DistMap

Resource ID: SCR_005473

Alternate IDs: OMICS_00660, biotools:distmap

Alternate URLs: https://bio.tools/distmap

Record Creation Time: 20220129T080230+0000

Record Last Update: 20250519T203402+0000

Ratings and Alerts

No rating or validation information has been found for DistMap.

No alerts have been found for DistMap.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 22 mentions in open access literature.

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

Yu Y, et al. (2024) Spatial and temporal gene expression patterns during early human odontogenesis process. Frontiers in bioengineering and biotechnology, 12, 1437426.

Vahid MR, et al. (2023) High-resolution alignment of single-cell and spatial transcriptomes with CytoSPACE. Nature biotechnology, 41(11), 1543.

Langmüller AM, et al. (2023) The genomic distribution of transposable elements is driven by spatially variable purifying selection. Nucleic acids research, 51(17), 9203.

Christodoulaki E, et al. (2022) Natural variation in Drosophila shows weak pleiotropic effects. Genome biology, 23(1), 116.

Hu H, et al. (2022) Dental niche cells directly contribute to tooth reconstitution and morphogenesis. Cell reports, 41(10), 111737.

Everetts NJ, et al. (2021) Single-cell transcriptomics of the Drosophila wing disc reveals instructive epithelium-to-myoblast interactions. eLife, 10.

Kim J, et al. (2021) Single-cell transcriptomics: a novel precision medicine technique in nephrology. The Korean journal of internal medicine, 36(3), 479.

Gupta S, et al. (2020) Feature Selection for Topological Proximity Prediction of Single-Cell

Transcriptomic Profiles in Drosophila Embryo Using Genetic Algorithm. Genes, 12(1).

Zand M, et al. (2020) Spatial mapping of single cells in the Drosophila embryo from transcriptomic data based on topological consistency. F1000Research, 9, 1014.

Zhao X, et al. (2020) Evaluation of single-cell classifiers for single-cell RNA sequencing data sets. Briefings in bioinformatics, 21(5), 1581.

Bonda U, et al. (2020) 3D Quantification of Vascular-Like Structures in z Stack Confocal Images. STAR protocols, 1(3), 100180.

Waylen LN, et al. (2020) From whole-mount to single-cell spatial assessment of gene expression in 3D. Communications biology, 3(1), 602.

Mazzucco R, et al. (2020) Long-Term Dynamics Among Wolbachia Strains During Thermal Adaptation of Their Drosophila melanogaster Hosts. Frontiers in genetics, 11, 482.

Tanevski J, et al. (2020) Gene selection for optimal prediction of cell position in tissues from single-cell transcriptomics data. Life science alliance, 3(11).

Loher P, et al. (2020) Machine Learning Approaches Identify Genes Containing Spatial Information From Single-Cell Transcriptomics Data. Frontiers in genetics, 11, 612840.

Expósito RR, et al. (2018) HSRA: Hadoop-based spliced read aligner for RNA sequencing data. PloS one, 13(7), e0201483.

Barghi N, et al. (2017) Drosophila simulans: A Species with Improved Resolution in Evolve and Resequence Studies. G3 (Bethesda, Md.), 7(7), 2337.

Tobler R, et al. (2017) High rate of translocation-based gene birth on the Drosophila Y chromosome. Proceedings of the National Academy of Sciences of the United States of America, 114(44), 11721.

Kofler R, et al. (2016) The impact of library preparation protocols on the consistency of allele frequency estimates in Pool-Seq data. Molecular ecology resources, 16(1), 118.

Yu P, et al. (2016) Single-cell Transcriptome Study as Big Data. Genomics, proteomics & bioinformatics, 14(1), 21.