Resource Summary Report

Generated by NIF on Apr 19, 2025

Hadoop-BAM

RRID:SCR_005516
Type: Tool

Proper Citation

Hadoop-BAM (RRID:SCR_005516)

Resource Information

URL: http://sourceforge.net/projects/hadoop-bam/

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Description: A Java library for the manipulation of files in common bioinformatics formats using the Hadoop MapReduce framework with the Picard SAM JDK, and command line tools similar to SAMtools. The file formats currently supported are BAM, SAM, FASTQ, FASTA, QSEQ, BCF, and VCF.

Abbreviations: Hadoop-BAM

Resource Type: software toolkit, software library, software resource

Defining Citation: PMID:22302568

Keywords: mapreduce/hadoop, java, next generation sequencing data, cloud

Funding:

Availability: MIT License

Resource Name: Hadoop-BAM

Resource ID: SCR_005516

Alternate IDs: OMICS_01051

Record Creation Time: 20220129T080230+0000

Record Last Update: 20250419T055015+0000

Ratings and Alerts

No rating or validation information has been found for Hadoop-BAM.

No alerts have been found for Hadoop-BAM.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Wiewiórka M, et al. (2023) Cloud-native distributed genomic pileup operations. Bioinformatics (Oxford, England), 39(1).

Maarala AI, et al. (2021) Distributed hybrid-indexing of compressed pan-genomes for scalable and fast sequence alignment. PloS one, 16(8), e0255260.

Tahir M, et al. (2020) A Fast and Scalable Workflow for SNPs Detection in Genome Sequences Using Hadoop Map-Reduce. Genes, 11(2).

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

Decap D, et al. (2017) Halvade-RNA: Parallel variant calling from transcriptomic data using MapReduce. PloS one, 12(3), e0174575.

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

Decap D, et al. (2015) Halvade: scalable sequence analysis with MapReduce. Bioinformatics (Oxford, England), 31(15), 2482.