Resource Summary Report

Generated by dkNET on May 1, 2025

biobambam

RRID:SCR_003308
Type: Tool

Proper Citation

biobambam (RRID:SCR_003308)

Resource Information

URL: https://github.com/gt1/biobambam

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Description: Software tools for read pair collation based algorithms on BAM files including * bamcollate2: reads BAM and writes BAM reordered such that alignment or collated by query name * bammarkduplicates: reads BAM and writes BAM with duplicate alignments marked using the BAM flags field * bammaskflags: reads BAM and writes BAM while masking (removing) bits from the flags column * bamrecompress: reads BAM and writes BAM with a defined compression setting. This tool is capable of multi-threading. * bamsort: reads BAM and writes BAM resorted by coordinates or query name * bamtofastq: reads BAM and writes FastQ; output can be collated or uncollated by query name

Resource Type: software resource, data processing software, software application

Defining Citation: DOI:10.1186/1751-0473-9-13

Keywords: standalone software, bio.tools

Funding:

Availability: GNU General Public License, v3

Resource Name: biobambam

Resource ID: SCR_003308

Alternate IDs: biotools:biobambam, OMICS_04664

Alternate URLs: https://bio.tools/biobambam, https://sources.debian.org/src/biobambam2/

Record Creation Time: 20220129T080218+0000

Record Last Update: 20250501T080554+0000

Ratings and Alerts

No rating or validation information has been found for biobambam.

No alerts have been found for biobambam.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 50 mentions in open access literature.

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

Smirnov P, et al. (2024) Multi-omic and single-cell profiling of chromothriptic medulloblastoma reveals genomic and transcriptomic consequences of genome instability. Nature communications, 15(1), 10183.

Tang Z, et al. (2024) Longitudinal integrative cell-free DNA analysis in gestational diabetes mellitus. Cell reports. Medicine, 5(8), 101660.

Fukumoto T, et al. (2024) Steroids-producing nodules: a two-layered adrenocortical nodular structure as a precursor lesion of cortisol-producing adenoma. EBioMedicine, 103, 105087.

Mentzer AJ, et al. (2024) High-resolution African HLA resource uncovers HLA-DRB1 expression effects underlying vaccine response. Nature medicine, 30(5), 1384.

Borowsky A, et al. (2024) Tumor microenvironmental determinants of high-risk DCIS progression. Research square.

Neumann J, et al. (2023) Disrupted Ca2+ homeostasis and immunodeficiency in patients with functional IP3 receptor subtype 3 defects. Cellular & molecular immunology, 20(1), 11.

Claeys A, et al. (2023) Benchmark of tools for in silico prediction of MHC class I and class II genotypes from NGS data. BMC genomics, 24(1), 247.

Giannakopoulou E, et al. (2023) A T cell receptor targeting a recurrent driver mutation in FLT3 mediates elimination of primary human acute myeloid leukemia in vivo. Nature cancer,

4(10), 1474.

Napolitano S, et al. (2023) Antitumor Efficacy of Dual Blockade with Encorafenib + Cetuximab in Combination with Chemotherapy in Human BRAFV600E-Mutant Colorectal Cancer. Clinical cancer research : an official journal of the American Association for Cancer Research, 29(12), 2299.

Shiraishi Y, et al. (2023) Precise characterization of somatic complex structural variations from tumor/control paired long-read sequencing data with nanomonsv. Nucleic acids research, 51(14), e74.

Gilly A, et al. (2022) Gene-based whole genome sequencing meta-analysis of 250 circulating proteins in three isolated European populations. Molecular metabolism, 61, 101509.

Valls-Margarit J, et al. (2022) GCAT|Panel, a comprehensive structural variant haplotype map of the Iberian population from high-coverage whole-genome sequencing. Nucleic acids research, 50(5), 2464.

Criscione SW, et al. (2022) The landscape of therapeutic vulnerabilities in EGFR inhibitor osimertinib drug tolerant persister cells. NPJ precision oncology, 6(1), 95.

Wong JKL, et al. (2022) Association of mutation signature effectuating processes with mutation hotspots in driver genes and non-coding regions. Nature communications, 13(1), 178.

Gomes NL, et al. (2022) Contribution of Clinical and Genetic Approaches for Diagnosing 209 Index Cases With 46,XY Differences of Sex Development. The Journal of clinical endocrinology and metabolism, 107(5), e1797.

Fujii Y, et al. (2021) Molecular classification and diagnostics of upper urinary tract urothelial carcinoma. Cancer cell, 39(6), 793.

Aslam M, et al. (2021) Putative second hit rare genetic variants in families with seemingly GBA-associated Parkinson's disease. NPJ genomic medicine, 6(1), 2.

Steinberg J, et al. (2021) A molecular quantitative trait locus map for osteoarthritis. Nature communications, 12(1), 1309.

Srivastava A, et al. (2021) Whole Genome Sequencing Prioritizes CHEK2, EWSR1, and TIAM1 as Possible Predisposition Genes for Familial Non-Medullary Thyroid Cancer. Frontiers in endocrinology, 12, 600682.

Serres-Armero A, et al. (2021) Copy number variation underlies complex phenotypes in domestic dog breeds and other canids. Genome research, 31(5), 762.