Resource Summary Report

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Bis-SNP

RRID:SCR_005439
Type: Tool

Proper Citation

Bis-SNP (RRID:SCR_005439)

Resource Information

URL: http://epigenome.usc.edu/publicationdata/bissnp2011/

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Description: A software package based on the Genome Analysis Toolkit (GATK) map-reduce framework for genotyping and accurate DNA methylation calling in bisulfite treated massively parallel sequencing (Bisulfite-seq, NOMe-seq, RRBS and any other bisulfite treated sequencing) with Illumina directional library protocol. It contains the following key features: * Call and summarize methylation of any cytosine context provided (CpG, CHH, CHG, GCH et.al.); * Work for single end and paired-end data; * Accurtae variant detection. Enable base quality recalibration and indel calling in bisulfite sequencing; * Based on Java map-reduce framework, allow multi-thread computing. Cross-platform; * Allow multiple output format, detailed VCF files, CpG haplotype reads file for mono-allelic methylation analysis, simplified bedGraph, wig and bed format for visualization in UCSC genome broswer and IGV browser. BisSNP uses bayesian inference with locus specific methylation probabilities and bisulfite conversion rate of different cytosine context(not only CpG, CHH, CHG in Bisulfite-seq, but also GCH et.al. in other bisulfite treated sequencing) to determine genotypes and methylation levels simultaneously.

Abbreviations: Bis-SNP

Synonyms: Bis-SNP - A bisulfite space genotyper & methylation caller, Bis-SNP - A bisulfite space genotyper and methylation caller

Resource Type: software resource

Defining Citation: PMID:22784381

Keywords: bio.tools

Funding:

Resource Name: Bis-SNP

Resource ID: SCR_005439

Alternate IDs: biotools:bis-snp, OMICS_00591

Alternate URLs: https://bio.tools/bis-snp

Record Creation Time: 20220129T080230+0000

Record Last Update: 20250420T014251+0000

Ratings and Alerts

No rating or validation information has been found for Bis-SNP.

No alerts have been found for Bis-SNP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 48 mentions in open access literature.

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

Liu Y, et al. (2024) FinaleMe: Predicting DNA methylation by the fragmentation patterns of plasma cell-free DNA. bioRxiv : the preprint server for biology.

Liu Y, et al. (2024) FinaleMe: Predicting DNA methylation by the fragmentation patterns of plasma cell-free DNA. Nature communications, 15(1), 2790.

Furrer R, et al. (2023) Molecular control of endurance training adaptation in male mouse skeletal muscle. Nature metabolism, 5(11), 2020.

Cheung WA, et al. (2023) Direct haplotype-resolved 5-base HiFi sequencing for genome-wide profiling of hypermethylation outliers in a rare disease cohort. Nature communications, 14(1), 3090.

Wang W, et al. (2022) Genomic imprinting-like monoallelic paternal expression determines

sex of channel catfish. Science advances, 8(51), eadc8786.

Zhou X, et al. (2022) CRAG: de novo characterization of cell-free DNA fragmentation hotspots in plasma whole-genome sequencing. Genome medicine, 14(1), 138.

Laplana M, et al. (2022) Differentially methylated regions within lung cancer risk loci are enriched in deregulated enhancers. Epigenetics, 17(2), 117.

Liang J, et al. (2021) A new approach to decode DNA methylome and genomic variants simultaneously from double strand bisulfite sequencing. Briefings in bioinformatics, 22(6).

Domin A, et al. (2021) The Identification of a Novel Fucosidosis-Associated FUCA1 Mutation: A Case of a 5-Year-Old Polish Girl with Two Additional Rare Chromosomal Aberrations and Affected DNA Methylation Patterns. Genes, 12(1).

Rodger EJ, et al. (2021) Comparison of Global DNA Methylation Patterns in Human Melanoma Tissues and Their Derivative Cell Lines. Cancers, 13(9).

Han T, et al. (2021) An epigenetic basis of inbreeding depression in maize. Science advances, 7(35).

Orjuela S, et al. (2020) DAMEfinder: a method to detect differential allele-specific methylation. Epigenetics & chromatin, 13(1), 25.

Allum F, et al. (2019) Dissecting features of epigenetic variants underlying cardiometabolic risk using full-resolution epigenome profiling in regulatory elements. Nature communications, 10(1), 1209.

Schulze KV, et al. (2019) Novel parent-of-origin-specific differentially methylated loci on chromosome 16. Clinical epigenetics, 11(1), 60.

Li G, et al. (2019) Joint profiling of DNA methylation and chromatin architecture in single cells. Nature methods, 16(10), 991.

Müller F, et al. (2019) RnBeads 2.0: comprehensive analysis of DNA methylation data. Genome biology, 20(1), 55.

Yang Y, et al. (2019) Developmental atlas of the RNA editome in Sus scrofa skeletal muscle. DNA research : an international journal for rapid publication of reports on genes and genomes, 26(3), 261.

Lu T, et al. (2019) Whole-genome bisulfite sequencing in systemic sclerosis provides novel targets to understand disease pathogenesis. BMC medical genomics, 12(1), 144.

Jiao J, et al. (2019) Genetic and epigenetic characteristics in ovarian tissues from polycystic ovary syndrome patients with irregular menstruation resemble those of ovarian cancer. BMC endocrine disorders, 19(1), 30.

Nordström KJV, et al. (2019) Unique and assay specific features of NOMe-, ATAC- and DNase I-seq data. Nucleic acids research, 47(20), 10580.