Resource Summary Report

Generated by NIF on Apr 8, 2025

BIRDSUITE

RRID:SCR_001794
Type: Tool

Proper Citation

BIRDSUITE (RRID:SCR_001794)

Resource Information

URL: https://www.broadinstitute.org/birdsuite/birdsuite

Proper Citation: BIRDSUITE (RRID:SCR_001794)

Description: Open-source set of tools to detect and report SNP genotypes, common Copy-Number Polymorphisms (CNPs), and novel, rare, or de novo CNVs in samples processed with the Affymetrix platform. While most of the components of the suite can be run individually (for instance, to only do SNP genotyping), the Birdsuite is especially intended for integrated analysis of SNPs and CNVs.

Abbreviations: Birdsuite

Resource Type: software resource, software application

Defining Citation: PMID:18776909

Keywords: gene, genetic, genomic, snp, genotype, copy number polymorphism, copy number variant, affymetrix

Funding:

Availability: Open unspecified license

Resource Name: BIRDSUITE

Resource ID: SCR_001794

Alternate IDs: OMICS_00705, nlx_154245

Record Creation Time: 20220129T080209+0000

Record Last Update: 20250404T060047+0000

Ratings and Alerts

No rating or validation information has been found for BIRDSUITE.

No alerts have been found for BIRDSUITE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 40 mentions in open access literature.

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

Romdhane L, et al. (2024) Ethnic and functional differentiation of copy number polymorphisms in Tunisian and HapMap population unveils insights on genome organizational plasticity. Scientific reports, 14(1), 4654.

Pagadala M, et al. (2023) Germline modifiers of the tumor immune microenvironment implicate drivers of cancer risk and immunotherapy response. Nature communications, 14(1), 2744.

Shi M, et al. (2022) Genetic Architecture of Plasma Alpha-Aminoadipic Acid Reveals a Relationship With High-Density Lipoprotein Cholesterol. Journal of the American Heart Association, 11(11), e024388.

Balagué-Dobón L, et al. (2022) Fully exploiting SNP arrays: a systematic review on the tools to extract underlying genomic structure. Briefings in bioinformatics, 23(2).

Ozcan Z, et al. (2022) Chromosomal imbalances detected via RNA-sequencing in 28 cancers. Bioinformatics (Oxford, England), 38(6), 1483.

Rong Y, et al. (2021) DDRS: Detection of drug response SNPs specifically in patients receiving drug treatment. Computational and structural biotechnology journal, 19, 3650.

Romdhane L, et al. (2021) A map of copy number variations in the Tunisian population: a valuable tool for medical genomics in North Africa. NPJ genomic medicine, 6(1), 3.

Toh C, et al. (2021) Genetic risk score for ovarian cancer based on chromosomal-scale length variation. BioData mining, 14(1), 18.

Hubbard L, et al. (2021) Rare Copy Number Variants Are Associated With Poorer Cognition in Schizophrenia. Biological psychiatry, 90(1), 28.

Fan X, et al. (2021) Accucopy: accurate and fast inference of allele-specific copy number alterations from low-coverage low-purity tumor sequencing data. BMC bioinformatics, 22(1), 23.

Schmitz-Abe K, et al. (2020) Homozygous deletions implicate non-coding epigenetic marks in Autism spectrum disorder. Scientific reports, 10(1), 14045.

Dai JY, et al. (2020) DNA methylation and cis-regulation of gene expression by prostate cancer risk SNPs. PLoS genetics, 16(3), e1008667.

Merino J, et al. (2020) Interaction Between Type 2 Diabetes Prevention Strategies and Genetic Determinants of Coronary Artery Disease on Cardiometabolic Risk Factors. Diabetes, 69(1), 112.

Fortin JP, et al. (2019) Multiple-gene targeting and mismatch tolerance can confound analysis of genome-wide pooled CRISPR screens. Genome biology, 20(1), 21.

Lee AS, et al. (2019) Rare mutations in the complement regulatory gene CSMD1 are associated with male and female infertility. Nature communications, 10(1), 4626.

Cheng L, et al. (2019) Integration of genomic copy number variations and chemotherapy-response biomarkers in pediatric sarcoma. BMC medical genomics, 12(Suppl 1), 23.

Zhang X, et al. (2019) Genome-wide Burden of Rare Short Deletions Is Enriched in Major Depressive Disorder in Four Cohorts. Biological psychiatry, 85(12), 1065.

Gusev A, et al. (2019) A transcriptome-wide association study of high-grade serous epithelial ovarian cancer identifies new susceptibility genes and splice variants. Nature genetics, 51(5), 815.

, et al. (2019) CAG Repeat Not Polyglutamine Length Determines Timing of Huntington's Disease Onset. Cell, 178(4), 887.

Bycroft C, et al. (2019) Patterns of genetic differentiation and the footprints of historical migrations in the Iberian Peninsula. Nature communications, 10(1), 551.