Resource Summary Report

Generated by NIF on Apr 20, 2025

SVMerge

RRID:SCR_004777
Type: Tool

Proper Citation

SVMerge (RRID:SCR_004777)

Resource Information

URL: http://svmerge.sourceforge.net/

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Description: Software pipeline to detect structural variants (SVs) by integrating calls from several existing SV callers, which are then validated and the breakpoints refined using local de novo assembly. The output is in BED format allowing for easy downstream analysis or viewing in a genome browser. It is modular and extensible allowing new callers to be incorporated as they become available.

Abbreviations: SVMerge

Synonyms: SVMerge - Enhanced structural variant and breakpoint detection

Resource Type: software resource

Defining Citation: PMID:21194472

Keywords: structural variant, breakpoint, bio.tools

Funding:

Resource Name: SVMerge

Resource ID: SCR_004777

Alternate IDs: biotools:svmerge, OMICS_00325

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

Record Creation Time: 20220129T080226+0000

Record Last Update: 20250420T014236+0000

Ratings and Alerts

No rating or validation information has been found for SVMerge.

No alerts have been found for SVMerge.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Chen Y, et al. (2024) Structural variations in livestock genomes and their associations with phenotypic traits: a review. Frontiers in veterinary science, 11, 1416220.

Xu L, et al. (2023) Long-read sequencing identifies novel structural variations in colorectal cancer. PLoS genetics, 19(2), e1010514.

Du X, et al. (2022) Robust Benchmark Structural Variant Calls of An Asian Using State-of-the-art Long-read Sequencing Technologies. Genomics, proteomics & bioinformatics, 20(1), 192.

Wagner J, et al. (2022) Benchmarking challenging small variants with linked and long reads. Cell genomics, 2(5).

Lemay MA, et al. (2022) Combined use of Oxford Nanopore and Illumina sequencing yields insights into soybean structural variation biology. BMC biology, 20(1), 53.

Zhang JY, et al. (2021) Using de novo assembly to identify structural variation of eight complex immune system gene regions. PLoS computational biology, 17(8), e1009254.

Xiaoli L, et al. (2021) Detection of genomic structure variants associated with wrinkled skin in Xiang pig by next generation sequencing. Aging, 13(22), 24710.

Bhattacharya S, et al. (2021) nanotatoR: a tool for enhanced annotation of genomic structural variants. BMC genomics, 22(1), 10.

Ma Z, et al. (2021) High-quality genome assembly and resequencing of modern cotton

cultivars provide resources for crop improvement. Nature genetics, 53(9), 1385.

Bujaldon S, et al. (2020) The BF4 and p71 antenna mutants from Chlamydomonas reinhardtii. Biochimica et biophysica acta. Bioenergetics, 1861(4), 148085.

Dharanipragada P, et al. (2018) iCopyDAV: Integrated platform for copy number variations-Detection, annotation and visualization. PloS one, 13(4), e0195334.

Dowell R, et al. (2016) Genome characterization of the selected long- and short-sleep mouse lines. Mammalian genome : official journal of the International Mammalian Genome Society, 27(11-12), 574.

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. Database : the journal of biological databases and curation, 2015.

Keane TM, et al. (2014) Identification of structural variation in mouse genomes. Frontiers in genetics, 5, 192.

Perdigão J, et al. (2014) Unraveling Mycobacterium tuberculosis genomic diversity and evolution in Lisbon, Portugal, a highly drug resistant setting. BMC genomics, 15(1), 991.