Resource Summary Report

Generated by NIF on May 24, 2025

GASVPro

RRID:SCR_005259
Type: Tool

Proper Citation

GASVPro (RRID:SCR_005259)

Resource Information

URL: http://compbio.cs.brown.edu/projects/gasv/

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Description: Software tool combining both paired read and read depth signals into probabilistic model which can analyze multiple alignments of reads. Used to find structural variation in both normal and cancer genomes using data from variety of next-generation sequencing platforms. Used to predict structural variants directly from aligned reads in SAM/BAM format.Combines read depth information along with discordant paired read mappings into single probabilistic model two common signals of structural variation. When multiple alignments of read are given, GASVPro utilizes Markov Chain Monte Carlo procedure to sample over the space of possible alignments.

Abbreviations: GASVPro

Synonyms: GASVPro: Geometric Analysis of Structural Variants

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

Defining Citation: PMID:22452995

Keywords: structural variation, genome, genomics, alignment, sequencing, variant, variation, detection, dna, paired, end, read, sequence

Funding: NHGRI R01 HG5690;
Burroughs Wellcome Career Award at the Scientific Interface

Availability: Free, Available for download, Freely available

Resource Name: GASVPro

Resource ID: SCR_005259

Alternate IDs: OMICS_00317

Alternate URLs: http://code.google.com/p/gasv/downloads/list

License: GNU GPL v3

Record Creation Time: 20220129T080229+0000

Record Last Update: 20250524T060034+0000

Ratings and Alerts

No rating or validation information has been found for GASVPro.

No alerts have been found for GASVPro.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Smith SD, et al. (2017) Lightning-fast genome variant detection with GROM. GigaScience, 6(10), 1.

Fève K, et al. (2017) Identification of a t(3;4)(p1.3;q1.5) translocation breakpoint in pigs using somatic cell hybrid mapping and high-resolution mate-pair sequencing. PloS one, 12(11), e0187617.

Xia LC, et al. (2016) A genome-wide approach for detecting novel insertion-deletion variants of mid-range size. Nucleic acids research, 44(15), e126.

Hilker R, et al. (2016) ReadXplorer 2-detailed read mapping analysis and visualization from one single source. Bioinformatics (Oxford, England), 32(24), 3702.

Salo OV, et al. (2015) Genomic mutational analysis of the impact of the classical strain improvement program on ?-lactam producing Penicillium chrysogenum. BMC genomics, 16, 937.

Pirooznia M, et al. (2015) Whole-genome CNV analysis: advances in computational approaches. Frontiers in genetics, 6, 138.

Scozzari R, et al. (2014) An unbiased resource of novel SNP markers provides a new chronology for the human Y chromosome and reveals a deep phylogenetic structure in Africa. Genome research, 24(3), 535.

Gilly A, et al. (2014) TE-Tracker: systematic identification of transposition events through whole-genome resequencing. BMC bioinformatics, 15(1), 377.