Resource Summary Report

Generated by Kravitz on Sep 10, 2026

GASV

RRID:SCR_000061
Type: Tool

Proper Citation

GASV (RRID:SCR_000061)

Resource Information

URL: http://code.google.com/p/gasv/

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Description: Software tool for identifying structural variants (SVs) from paired-end sequencing data.GASV distribution includes three components that are typically run in succession: the BAM file of unique paired-read mappings is processed; structural variants are identified by clustering discordant fragments; and a probabilistic algorithm improves the specificity of GASV predictions.

Abbreviations: GASV

Synonyms: Geometric Analysis of Structural Variants

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

Defining Citation: PMID:19477992

Keywords: paired-end sequencing data, structural variant, probabilistic algorithm, discordant fragment, bio.tools

Funding: ADVANCE Program at Brown University ;
Burroughs Wellcome Fund ;
Department of Defense Breast Cancer Research ;
NSF 0548311

Availability: Free, Available for download, Freely available

Resource Name: GASV

Resource ID: SCR_000061

Alternate IDs: biotools:gasv, OMICS_01352

Alternate URLs: http://compbio.cs.brown.edu/projects/gasv/, https://bio.tools/gasv

License URLs: https://code.google.com/projecthosting/terms.html

Record Creation Time: 20220129T080159+0000

Record Last Update: 20260905T132410+0000

Ratings and Alerts

No rating or validation information has been found for GASV.

No alerts have been found for GASV.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Magris G, et al. (2019) Genetic, epigenetic and genomic effects on variation of gene expression among grape varieties. The Plant journal : for cell and molecular biology, 99(5), 895.

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

Zhuang J, et al. (2014) TEMP: a computational method for analyzing transposable element polymorphism in populations. Nucleic acids research, 42(11), 6826.

Zhao M, et al. (2013) Computational tools for copy number variation (CNV) detection using next-generation sequencing data: features and perspectives. BMC bioinformatics, 14 Suppl 11(Suppl 11), S1.