Resource Summary Report

Generated by NIF on Sep 1, 2026

Halvade Somatic

RRID:SCR_021771
Type: Tool

Proper Citation

Halvade Somatic (RRID:SCR_021771)

Resource Information

URL: https://bitbucket.org/dries_decap/halvadeforspark/

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Description: Software implements germline and somatic variant calling pipelines based on best practices pipelines from Broad Institute using Spark framework. Produces VCF output file which contains single nucleotide polymorphisms (SNPs) and short insertions and deletions (indels) when supported by used tools. Program requires Spark on either local cluster with one or more nodes, Amazon EMR cluster or Docker image to run.

Synonyms: Halvade for Spark

Resource Type: software resource

Keywords: somatic variant, GATK, Halvade, VCF output file, germline, somatic variant calling, Spark framework

Availability: Free, Available for download, Freely available

Resource Name: Halvade Somatic

Resource ID: SCR_021771

License: GPL 3.0

Record Creation Time: 20220129T080357+0000

Record Last Update: 20260829T182718+0000

Ratings and Alerts

No rating or validation information has been found for Halvade Somatic.

No alerts have been found for Halvade Somatic.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Decap D, et al. (2022) Halvade somatic: Somatic variant calling with Apache Spark. GigaScience, 11(1).