Resource Summary Report

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NPSV

RRID:SCR_020984
Type: Tool

Proper Citation

NPSV (RRID:SCR_020984)

Resource Information

URL: https://github.com/mlinderm/npsv

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Description: Software Python tool for standalone genotyping of deletion and insertion structural variants in short read whole genome sequencing data. Implements machine learning based approach for SV genotyping that employs NGS simulation to model the combined effects of the genomic region, sequencer and alignment pipeline.

Synonyms: Non-Parametric Structural Variant Genotyper, Non-Parametric Structural Variant genotyper

Resource Type: software resource, software application, simulation software

Keywords: WGS data, short read, whole genome sequencing data, standalone genotyping, insertion structural variants, deletion structural variants, structural variants, SV genotyping, NGS simulation

Funding:

Availability: Free, Available for download, Freely available

Resource Name: NPSV

Resource ID: SCR_020984

License: MIT License

Record Creation Time: 20220129T080353+0000

Record Last Update: 20250501T081533+0000

Ratings and Alerts

No rating or validation information has been found for NPSV.

No alerts have been found for NPSV.

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 FDI Lab - SciCrunch.org.

Linderman MD, et al. (2021) NPSV: A simulation-driven approach to genotyping structural variants in whole-genome sequencing data. GigaScience, 10(7).