Resource Summary Report

Generated by dkNET on Apr 29, 2025

SoftSearch

RRID:SCR_006683
Type: Tool

Proper Citation

SoftSearch (RRID:SCR_006683)

Resource Information

URL: https://code.google.com/p/softsearch/

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Description: A sensitive structural variant (SV) detection software tool for Illumina paired-end next-generation sequencing data. It simultaneously utilizes soft-clipping and read-pair strategies for detecting SVs to increase sensitivity. Soft clips are proxies for split-reads that indicate part of the read maps to the reference genome, but the other part is not localized at the same place (e.g. breakpoint spanning reads). Discordant read-pairs refer to a read and its mate, where the insert size is greater (or less than) the expected distribution of the dataset ? or ? where the mapping orientation of the reads is unexpected (e.g. both on the same strand). SoftSearch looks for areas with soft-clipping in the genome that have discordant read pairs supporting the anomaly. Once areas with both these conditions are identified, the read and mate information is extracted directly from the BAM file containing the discordant reads, obviating the need for time-consuming and error-prone complex alignment strategies. Only a small number of soft-masked bases discordant read-pairs are necessary to identify an SV, which on their own would not be sufficient to make an SV call, thus highlighting SoftSearch?s improved sensitivity. SoftSearch is well suited to be ?plugged in? to most sequence analysis workflows, since it requires standard file inputs, such as a BAM file using almost any aligner and a reference genome FASTA file. Because SoftSearch requires soft-masked bases, the only requirement is that the aligner must have this functionality, which is usually turned on by default by many standard aligners (e.g. BWA, Novoalign, etc).

Abbreviations: SoftSearch

Synonyms: SoftSearch - Detecting Structural Variations Using Split Reads and Discordant Read Pairs

Resource Type: software resource

Keywords: illumina, structural variant, next-generation sequencing, perl, academic

Funding:

Availability: GNU General Public License, v2

Resource Name: SoftSearch

Resource ID: SCR_006683

Alternate IDs: OMICS_00322

Record Creation Time: 20220129T080237+0000

Record Last Update: 20250420T014341+0000

Ratings and Alerts

No rating or validation information has been found for SoftSearch.

No alerts have been found for SoftSearch.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Wu L, et al. (2022) Exon skipping caused by a complex structural variation in SH2D1A resulted in X-linked lymphoproliferative syndrome type 1. Molecular genetics & genomic medicine, 10(3), e1873.

Jia L, et al. (2020) intansv: an R package for integrative analysis of structural variations. PeerJ, 8, e8867.

Nguyen HT, et al. (2016) SRBreak: A Read-Depth and Split-Read Framework to Identify Breakpoints of Different Events Inside Simple Copy-Number Variable Regions. Frontiers in genetics, 7, 160.

Hart SN, et al. (2016) VCF-Miner: GUI-based application for mining variants and annotations

stored in VCF files. Briefings in bioinformatics, 17(2), 346.

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