Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 16, 2025

Strelka

RRID:SCR_005109
Type: Tool

Proper Citation

Strelka (RRID:SCR_005109)

Resource Information

URL: http://bioinformatics.oxfordjournals.org/content/early/2012/05/10/bioinformatics.bts271.full.pdf

Proper Citation: Strelka (RRID:SCR_005109)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on March 7,2024. Software for somatic single nucleotide variant (SNV) and small indel detection from sequencing data of matched tumor-normal samples. The method employs a novel Bayesian approach which represents continuous allele frequencies for both tumor and normal samples, whilst leveraging the expected genotype structure of the normal. This is achieved by representing the normal sample as a mixture of germline variation with noise, and representing the tumor sample as a mixture of the normal sample with somatic variation. A natural consequence of the model structure is that sensitivity can be maintained at high tumor impurity without requiring purity estimates. The method has superior accuracy and sensitivity on impure samples compared to approaches based on either diploid genotype likelihoods or general allele-frequency tests.

Abbreviations: Strelka

Resource Type: commercial organization, software resource

Defining Citation: PMID:22581179, PMID:30013048

Keywords: single nucleotide variant, indel, somatic snv, next-generation sequencing, bio.tools

Related Condition: Cancer, Tumor, Normal

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Strelka

Resource ID: SCR_005109

Alternate IDs: biotools:strelka

Alternate URLs: https://bio.tools/strelka, https://github.com/Illumina/strelka/, https://sources.debian.org/src/strelka/

Record Creation Time: 20220129T080228+0000

Record Last Update: 20250411T054951+0000

Ratings and Alerts

No rating or validation information has been found for Strelka.

No alerts have been found for Strelka.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 230 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Hao W, et al. (2025) Advances in predicting breast cancer driver mutations: Tools for precision oncology (Review). International journal of molecular medicine, 55(1).

Martins Rodrigues F, et al. (2025) Germline predisposition in multiple myeloma. iScience, 28(1), 111620.

Lee D, et al. (2025) Increased local DNA methylation disorder in AMLs with DNMT3A-destabilizing variants and its clinical implication. Nature communications, 16(1), 560.

Kasikova L, et al. (2024) Tertiary lymphoid structures and B cells determine clinically relevant T cell phenotypes in ovarian cancer. Nature communications, 15(1), 2528.

Aghova T, et al. (2024) Diagnostic challenges in complicated case of glioblastoma. Pathology oncology research : POR, 30, 1611875.

Das A, et al. (2024) Combined Immunotherapy Improves Outcome for Replication-Repair-Deficient (RRD) High-Grade Glioma Failing Anti-PD-1 Monotherapy: A Report from the International RRD Consortium. Cancer discovery, 14(2), 258.

Li W, et al. (2024) PBRM1 presents a potential ctDNA marker to monitor response to neoadjuvant chemotherapy in cervical cancer. iScience, 27(3), 109160.

Larkin J, et al. (2024) Nilotinib in KIT-driven advanced melanoma: Results from the phase II single-arm NICAM trial. Cell reports. Medicine, 5(3), 101435.

Li GX, et al. (2024) Comprehensive proteogenomic characterization of rare kidney tumors. Cell reports. Medicine, 5(5), 101547.

Blanco-Heredia J, et al. (2024) Converging and evolving immuno-genomic routes toward immune escape in breast cancer. Nature communications, 15(1), 1302.

Dopeso H, et al. (2024) Genomic and epigenomic basis of breast invasive lobular carcinomas lacking CDH1 genetic alterations. NPJ precision oncology, 8(1), 33.

Schott CR, et al. (2024) Osteosarcoma PDX-Derived Cell Line Models for Preclinical Drug Evaluation Demonstrate Metastasis Inhibition by Dinaciclib through a Genome-Targeted Approach. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(4), 849.

Park J, et al. (2024) DeepSomatic: Accurate somatic small variant discovery for multiple sequencing technologies. bioRxiv : the preprint server for biology.

Watkins JA, et al. (2024) Introduction and impact of routine whole genome sequencing in the diagnosis and management of sarcoma. British journal of cancer, 131(5), 860.

Ijaz J, et al. (2024) Haplotype-specific assembly of shattered chromosomes in esophageal adenocarcinomas. Cell genomics, 4(2), 100484.

Sosinsky A, et al. (2024) Insights for precision oncology from the integration of genomic and clinical data of 13,880 tumors from the 100,000 Genomes Cancer Programme. Nature medicine, 30(1), 279.

Klein K, et al. (2024) A lineage-specific STAT5BN642H mouse model to study NK-cell leukemia. Blood, 143(24), 2474.

Sveen A, et al. (2024) Evolutionary mode and timing of dissemination of high-grade serous carcinomas. JCI insight, 9(3).

Titmuss E, et al. (2024) Exploration of Germline Correlates and Risk of Immune-Related Adverse Events in Advanced Cancer Patients Treated with Immune Checkpoint Inhibitors. Current oncology (Toronto, Ont.), 31(4), 1865.

Mo CK, et al. (2024) Tumour evolution and microenvironment interactions in 2D and 3D space. Nature, 634(8036), 1178.