Resource Summary Report

Generated by NIF on Apr 27, 2025

JointSNVMix

RRID:SCR_006804
Type: Tool

Proper Citation

JointSNVMix (RRID:SCR_006804)

Resource Information

URL: http://compbio.bccrc.ca/software/jointsnvmix/

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Description: Software that implements a probabilistic graphical model to analyze sequence data from tumor / normal pairs. The model draws statistical strength by analysing both genome jointly to more accurately classify germline and somatic mutations. It effectively reduces false positive somatic mutation predictions in tumour-normal pair sequencing data. It is highly recommended to post-process results with mutationSeq in order to filter technical artifacts.

Abbreviations: JointSNVMix

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

Defining Citation: PMID:22285562

Keywords: tumor, cancer, normal, somatic mutation, mutation

Funding:

Availability: GNU General Public License, v3, Registration required

Resource Name: JointSNVMix

Resource ID: SCR_006804

Alternate IDs: OMICS_00085

Record Creation Time: 20220129T080238+0000

Record Last Update: 20250426T055904+0000

Ratings and Alerts

No rating or validation information has been found for JointSNVMix.

No alerts have been found for JointSNVMix.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Krull JE, et al. (2024) Follicular lymphoma B cells exhibit heterogeneous transcriptional states with associated somatic alterations and tumor microenvironments. Cell reports. Medicine, 5(3), 101443.

Bohannan ZS, et al. (2019) Calling Variants in the Clinic: Informed Variant Calling Decisions Based on Biological, Clinical, and Laboratory Variables. Computational and structural biotechnology journal, 17, 561.

Sun Z, et al. (2017) Indel detection from RNA-seq data: tool evaluation and strategies for accurate detection of actionable mutations. Briefings in bioinformatics, 18(6), 973.

Bohnert R, et al. (2017) Comprehensive benchmarking of SNV callers for highly admixed tumor data. PloS one, 12(10), e0186175.

Reuter JA, et al. (2016) Simul-seq: combined DNA and RNA sequencing for whole-genome and transcriptome profiling. Nature methods, 13(11), 953.

Li Y, et al. (2015) MixClone: a mixture model for inferring tumor subclonal populations. BMC genomics, 16 Suppl 2(Suppl 2), S1.

Ryland GL, et al. (2015) Mutational landscape of mucinous ovarian carcinoma and its neoplastic precursors. Genome medicine, 7(1), 87.

Denroche RE, et al. (2015) A cancer cell-line titration series for evaluating somatic classification. BMC research notes, 8, 823.

Ha G, et al. (2012) Integrative analysis of genome-wide loss of heterozygosity and

monoallelic expression at nucleotide resolution reveals disrupted pathways in triple-negative breast cancer. Genome research, 22(10), 1995.