

Resource Summary Report

Generated by [RRID](#) on Aug 13, 2026

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 processing software, data analysis software, software resource, software application

Defining Citation: [PMID:22285562](#)

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

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: 20260813T054934+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 10 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Karasozen Y, et al. (2025) Low-Allele-Frequency Somatic Variants in a Cohort of Sporadic Saccular "Berry" Cerebral Aneurysms. *Journal of the American Heart Association*, 14(18), e032483.

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.

Bohannon 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.

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

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

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.