Resource Summary Report

Generated by NIF on Aug 31, 2026

VariantMaster

RRID:SCR_000569
Type: Tool

Proper Citation

VariantMaster (RRID:SCR_000569)

Resource Information

URL: http://sourceforge.net/projects/variantmaster/

Proper Citation: VariantMaster (RRID:SCR_000569)

Description: Software program that extracts causative variants in familial and sporadic genetic diseases. The algorithm takes into account predicted variants (SNPs and indels) in affected individuals or tumor samples and utilizes the row (BAM) data to robustly estimate the conditional probability of segregation in a family, as well as the probability of it being de novo or somatic. In familial cases, various modes of inheritance are considered: X-linked, autosomal dominant, and recessive (homozygosity or compound heterozygosity). Moreover, it integrates phenotypes and genotypes, and employs Annovar to produce additional information as allelic frequencies in general population and damaging scores.

Abbreviations: VariantMaster

Synonyms: VariantMaster - Extract causative variants for monogenic and sporadic genetic diseases

Resource Type: software resource

Defining Citation: PMID:24389049

Keywords: unix/linux, clinical, genetics, high throughput sequencing, monogenic disease, variant, snp, indel

Related Condition: Genetic disease, Tumor

Availability: Free, Available for download, Freely available,

Resource Name: VariantMaster

Resource ID: SCR_000569

Alternate IDs: OMICS_02261

Record Creation Time: 20220129T080202+0000

Record Last Update: 20260829T182027+0000

Ratings and Alerts

No rating or validation information has been found for VariantMaster.

No alerts have been found for VariantMaster.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We have not found any literature mentions for this resource.