Resource Summary Report

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POLYMUTT

RRID:SCR_002051
Type: Tool

Proper Citation

POLYMUTT (RRID:SCR_002051)

Resource Information

URL: http://genome.sph.umich.edu/wiki/Polymutt

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Description: Software program that implemented a likelihood-based framework for calling single nucleotide variants and detecting de novo point mutation events in families for next-generation sequencing data. The program takes as input genotype likelihood format (GLF) files which can be generated following the Creation of GLF files instruction and outputs the result in the (VCF) format. The variant calling and de novo mutation detection are modelled jointly within families and can handle both nuclear and extended pedigrees without consanguinity loops. The input is a set of GLF files for each of family members and the relationships are specified through the .ped file. (entry from Genetic Analysis Software)

Abbreviations: Polymutt

Synonyms: POLYmorphism and de novo MUTaTion call in families with sequencing data

Resource Type: software resource, software application

Defining Citation: PMID:23055937

Keywords: gene, genetic, genomic, next-generation sequencing, mutation, de novo point mutation, single nucleotide variant

Availability: Free, Available for download, Freely available

Resource Name: POLYMUTT

Resource ID: SCR_002051

Alternate IDs: OMICS_00088, nlx_154539

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260808T190451+0000

Ratings and Alerts

No rating or validation information has been found for POLYMUTT.

No alerts have been found for POLYMUTT.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Yan Q, et al. (2016) The impact of genotype calling errors on family-based studies. Scientific reports, 6, 28323.

Li B, et al. (2015) Leveraging Identity-by-Descent for Accurate Genotype Inference in Family Sequencing Data. PLoS genetics, 11(6), e1005271.

Huang YS, et al. (2015) Sequencing strategies and characterization of 721 vervet monkey genomes for future genetic analyses of medically relevant traits. BMC biology, 13, 41.