Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 24, 2025

estMOI

RRID:SCR_006192
Type: Tool

Proper Citation

estMOI (RRID:SCR_006192)

Resource Information

URL: http://pathogenseq.lshtm.ac.uk/estmoi

Proper Citation: estMOI (RRID:SCR_006192)

Description: A per-based software to estimate multiplicity of infection (MOI) in parasite genomic sequence data. It is primarily developed to address the limitations of current laboratory (PCR) based estimates of multiplicity using high throughput sequence data. It requires a BAM (alignment output of short reads to the reference genome), VCF (a file with information on variant calls) and FASTA (reference genome) files. # Short reads are aligned to a reference genome using BWA, BOWTIE, SMALT or other short read aligners to generate a BAM file. # Single Nucleotide Polymorphisms (SNPs) are then identified using SAMTools/BCFtools and stored in the VCF format. # The reference FASTA file is expected to be indexed using "samtools faidx" to generate a *.fai file. estMOI generates files containing MOI estimates for each SNP combinations (file with name *.log) and a summary for all chromosomes (file with name *.txt).

Abbreviations: estMOI

Synonyms: estMOI - Estimating multiplicity of infection using parasite deep sequencing data

Resource Type: software resource

Defining Citation: PMID:24443379

Keywords: multiplicity of infection, parasite, genome, high throughput sequencing, single nucleotide polymorphism, chromosome

Funding:

Availability: Free, Public

Resource Name: estMOI

Resource ID: SCR_006192

Alternate IDs: OMICS_02240

Record Creation Time: 20220129T080234+0000

Record Last Update: 20250420T014316+0000

Ratings and Alerts

No rating or validation information has been found for estMOI.

No alerts have been found for estMOI.

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 FDI Lab - SciCrunch.org.

Ibrahim A, et al. (2024) Genome sequencing of Plasmodium malariae identifies continental segregation and mutations associated with reduced pyrimethamine susceptibility. Nature communications, 15(1), 10779.

Turkiewicz A, et al. (2023) Population genetic analysis of Plasmodium knowlesi reveals differential selection and exchange events between Borneo and Peninsular sub-populations. Scientific reports, 13(1), 2142.

De Meulenaere K, et al. (2023) A new Plasmodium vivax reference genome for South American isolates. BMC genomics, 24(1), 606.

Berger DJ, et al. (2022) Genomic evidence of contemporary hybridization between Schistosoma species. PLoS pathogens, 18(8), e1010706.

Deelder W, et al. (2021) Using deep learning to identify recent positive selection in malaria parasite sequence data. Malaria journal, 20(1), 270.

Tichkule S, et al. (2021) Comparative genomics revealed adaptive admixture in

Cryptosporidium hominis in Africa. Microbial genomics, 7(1).

Shah Z, et al. (2020) Optimization of parasite DNA enrichment approaches to generate whole genome sequencing data for Plasmodium falciparum from low parasitaemia samples. Malaria journal, 19(1), 135.

Brashear AM, et al. (2019) A glance of the blood stage transcriptome of a Southeast Asian Plasmodium ovale isolate. PLoS neglected tropical diseases, 13(11), e0007850.

Benavente ED, et al. (2019) Whole genome sequencing of amplified Plasmodium knowlesi DNA from unprocessed blood reveals genetic exchange events between Malaysian Peninsular and Borneo subpopulations. Scientific reports, 9(1), 9873.

Benavente ED, et al. (2018) Global genetic diversity of var2csa in Plasmodium falciparum with implications for malaria in pregnancy and vaccine development. Scientific reports, 8(1), 15429.