

Resource Summary Report

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QuasiRecomb

RRID:SCR_008812

Type: Tool

Proper Citation

QuasiRecomb (RRID:SCR_008812)

Resource Information

URL: <https://github.com/armintoeper/QuasiRecomb/releases>

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Description: A jumping hidden Markov model that describes the generation of the viral quasispecies and a method to infer its parameters by analysing next generation sequencing data.

Abbreviations: QuasiRecomb

Synonyms: QuasiRecomb - Probabilistic inference of viral Quasispecies

Resource Type: software resource

Defining Citation: [PMID:23383997](#)

Keywords: haplotype, next-generation sequencing, virus, parameter, bio.tools

Resource Name: QuasiRecomb

Resource ID: SCR_008812

Alternate IDs: OMICS_00229, biotools:quasirecomb

Alternate URLs: <https://bio.tools/quasirecomb>

Record Creation Time: 20220129T080249+0000

Record Last Update: 20260912T195709+0000

Ratings and Alerts

No rating or validation information has been found for QuasiRecomb.

No alerts have been found for QuasiRecomb.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 33 mentions in open access literature.

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

Abdullah SMU, et al. (2026) Linkage-aware inference of fitness from short-read time-series genomic data. bioRxiv : the preprint server for biology.

Walker MR, et al. (2025) Temporal dynamics of viral fitness and the adaptive immune response in HCV infection. eLife, 13.

Dong X, et al. (2025) Using minor variant genomes and machine learning to study the genome biology of SARS-CoV-2 over time. Nucleic acids research, 53(4).

Tsai YY, et al. (2024) The molecular epidemiology of a dengue virus outbreak in Taiwan: population wide versus infrapopulation mutation analysis. PLoS neglected tropical diseases, 18(6), e0012268.

Fuhrmann L, et al. (2024) V-pipe 3.0: a sustainable pipeline for within-sample viral genetic diversity estimation. GigaScience, 13.

Dong X, et al. (2023) Analysis of SARS-CoV-2 Population Genetics from Samples Associated with Huanan Market and Early Cases Identifies Substitutions Associated with Future Variants of Concern. Viruses, 15(8).

Dong X, et al. (2023) Linked Mutations in the Ebola Virus Polymerase Are Associated with Organ Specific Phenotypes. Microbiology spectrum, 11(2), e0415422.

Caraballo Cortés K, et al. (2023) T-Cell Exhaustion in HIV-1/Hepatitis C Virus Coinfection Is Reduced After Successful Treatment of Chronic Hepatitis C. Open forum infectious diseases, 10(11), ofad514.

Richner J, et al. (2023) SARS-CoV-2 Bottlenecks and Tissue-Specific Adaptation in the Central Nervous System. Research square.

Samer S, et al. (2022) Blockade of TGF- β signaling reactivates HIV-1/SIV reservoirs and immune responses in vivo. JCI insight, 7(21).

Watson RJ, et al. (2021) Dose-Dependent Response to Infection with Ebola Virus in the Ferret Model and Evidence of Viral Evolution in the Eye. Journal of virology, 95(24), e0083321.

Bosworth A, et al. (2021) Analysis of an Ebola virus disease survivor whose host and viral markers were predictive of death indicates the effectiveness of medical countermeasures

and supportive care. *Genome medicine*, 13(1), 5.

Deng ZL, et al. (2021) Evaluating assembly and variant calling software for strain-resolved analysis of large DNA viruses. *Briefings in bioinformatics*, 22(3).

Serrão de Andrade AA, et al. (2021) Testing the genomic stability of the Brazilian yellow fever vaccine strain using next-generation sequencing data. *Interface focus*, 11(4), 20200063.

Afridi SQ, et al. (2021) Prolonged norovirus infections correlate to quasispecies evolution resulting in structural changes of surface-exposed epitopes. *iScience*, 24(7), 102802.

Scutari R, et al. (2021) Impact of Analytical Treatment Interruption on Burden and Diversification of HIV Peripheral Reservoir: A Pilot Study. *Viruses*, 13(7).

Al Khatib HA, et al. (2020) Inter- Versus Intra-Host Sequence Diversity of pH1N1 and Associated Clinical Outcomes. *Microorganisms*, 8(1).

Andreu-Moreno I, et al. (2020) Collective Viral Spread Mediated by Virion Aggregates Promotes the Evolution of Defective Interfering Particles. *mBio*, 11(1).

Dong X, et al. (2020) Variation around the dominant viral genome sequence contributes to viral load and outcome in patients with Ebola virus disease. *Genome biology*, 21(1), 238.

Wille M, et al. (2020) Evolutionary genetics of canine respiratory coronavirus and recent introduction into Swedish dogs. *Infection, genetics and evolution : journal of molecular epidemiology and evolutionary genetics in infectious diseases*, 82, 104290.