Resource Summary Report

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ShoRAH

RRID:SCR_005211
Type: Tool

Proper Citation

ShoRAH (RRID:SCR_005211)

Resource Information

URL: http://www.bsse.ethz.ch/cbg/software/shorah

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Description: A software package that allows for inference about the structure of a population from a set of short sequence reads as obtained from ultra-deep sequencing of a mixed sample. The package contains programs that support mapping of reads to a reference genome, correcting sequencing errors by locally clustering reads in small windows of the alignment, reconstructing a minimal set of global haplotypes that explain the reads, and estimating the frequencies of the inferred haplotypes.

Abbreviations: ShoRAH

Synonyms: Short Reads Assembly into Haplotypes, ShoRAH - Short Reads Assembly into Haplotypes

Resource Type: software resource

Defining Citation: PMID:21521499

Keywords: linux, mac os x, windows, next-generation sequencing, c++, python, perl, structure, population, short sequence read, haplotype, bio.tools

Funding:

Availability: GNU General Public License, v3

Resource Name: ShoRAH

Resource ID: SCR_005211

Alternate IDs: biotools:shorah, OMICS_00231

Alternate URLs: https://bio.tools/shorah

Record Creation Time: 20220129T080229+0000

Record Last Update: 20250410T065236+0000

Ratings and Alerts

No rating or validation information has been found for ShoRAH.

No alerts have been found for ShoRAH.

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 FDI Lab - SciCrunch.org.

Sutcliffe SG, et al. (2024) Tracking SARS-CoV-2 variants of concern in wastewater: an assessment of nine computational tools using simulated genomic data. Microbial genomics, 10(5).

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

Fuhrmann L, et al. (2024) VILOCA: sequencing quality-aware viral haplotype reconstruction and mutation calling for short-read and long-read data. NAR genomics and bioinformatics, 6(4), lqae152.

Höfler T, et al. (2024) Evolutionary Dynamics of Accelerated Antiviral Resistance Development in Hypermutator Herpesvirus. Molecular biology and evolution, 41(7).

Woodford L, et al. (2022) Quantitative and Qualitative Changes in the Deformed Wing Virus Population in Honey Bees Associated with the Introduction or Removal of Varroa destructor. Viruses, 14(8).

Posada-Céspedes S, et al. (2021) V-pipe: a computational pipeline for assessing viral genetic diversity from high-throughput data. Bioinformatics (Oxford, England), 37(12), 1673.

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

Morga B, et al. (2021) Genomic Diversity of the Ostreid Herpesvirus Type 1 Across Time and Location and Among Host Species. Frontiers in microbiology, 12, 711377.

Trinks J, et al. (2020) The genetic variability of hepatitis B virus subgenotype F1b precore/core gene is related to the outcome of the acute infection. Virus research, 277, 197840.

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.

Gaube G, et al. (2020) Characterization of HIV-1 diversity in various compartments at the time of primary infection by ultradeep sequencing. Scientific reports, 10(1), 2409.

Kobayashi K, et al. (2020) Heparan sulfate attachment receptor is a major selection factor for attenuated enterovirus 71 mutants during cell culture adaptation. PLoS pathogens, 16(3), e1008428.

Janiak M, et al. (2019) Hepatitis C virus (HCV) genotype 1b displays higher genetic variability of hypervariable region 1 (HVR1) than genotype 3. Scientific reports, 9(1), 12846.

Walker MR, et al. (2019) Clearance of hepatitis C virus is associated with early and potent but narrowly-directed, Envelope-specific antibodies. Scientific reports, 9(1), 13300.

Henningsson R, et al. (2019) DISSEQT-DIStribution-based modeling of SEQuence space Time dynamics. Virus evolution, 5(2), vez028.

Hathaway NJ, et al. (2018) SeekDeep: single-base resolution de novo clustering for amplicon deep sequencing. Nucleic acids research, 46(4), e21.

Steyer A, et al. (2018) Intrahost Norovirus Evolution in Chronic Infection Over 5 Years of Shedding in a Kidney Transplant Recipient. Frontiers in microbiology, 9, 371.

Caraballo Cortes K, et al. (2018) Next-generation sequencing analysis of a cluster of hepatitis C virus infections in a haematology and oncology center. PloS one, 13(3), e0194816.

Esposito I, et al. (2018) Prevalence and Factors Related to Natural Resistance-Associated Substitutions to Direct-Acting Antivirals in Patients with Genotype 1 Hepatitis C Virus Infection. Viruses, 11(1).

Parameswaran P, et al. (2017) Intrahost Selection Pressures Drive Rapid Dengue Virus Microevolution in Acute Human Infections. Cell host & microbe, 22(3), 400.