Resource Summary Report

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QuRe

RRID:SCR_005209
Type: Tool

Proper Citation

QuRe (RRID:SCR_005209)

Resource Information

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

Proper Citation: QuRe (RRID:SCR_005209)

Description: A software program for viral quasispecies reconstruction, specifically developed to analyze long read (>100 bp) next-generation sequencing (NGS) data. The software performs alignments of sequence fragments against a reference genome, finds an optimal division of the genome into sliding windows based on coverage and diversity and attempts to reconstruct all the individual sequences of the viral quasispecies--along with their prevalence--using a heuristic algorithm, which matches multinomial distributions of distinct viral variants overlapping across the genome division. QuRe comes with a built-in Poisson error correction method and a post-reconstruction probabilistic clustering, both parameterized on given error rates in homopolymeric and non-homopolymeric regions.

Abbreviations: QuRe

Synonyms: qure - software for viral quasispecies reconstruction from next-gen seq. data

Resource Type: software resource

Keywords: next-generation sequencing, virus, long read, reconstruction

Funding:

Resource Name: QuRe

Resource ID: SCR_005209

Alternate IDs: OMICS_00230

Record Creation Time: 20220129T080229+0000

Record Last Update: 20250410T065236+0000

Ratings and Alerts

No rating or validation information has been found for QuRe.

No alerts have been found for QuRe.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 6 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Cevallos C, et al. (2020) Longitudinal characterization of HIV-1 pol-gene in treatment-naïve men-who-have-sex-with-men from acute to chronic infection stages. Heliyon, 6(12), e05679.

Correa-Fiz F, et al. (2020) Porcine circovirus 2 (PCV2) population study in experimentally infected pigs developing PCV2-systemic disease or a subclinical infection. Scientific reports, 10(1), 17747.

González R, et al. (2019) Mutagenesis Scanning Uncovers Evolutionary Constraints on Tobacco Etch Potyvirus Membrane-Associated 6K2 Protein. Genome biology and evolution, 11(4), 1207.

Correa-Fiz F, et al. (2018) Porcine circovirus 2 (PCV-2) genetic variability under natural infection scenario reveals a complex network of viral quasispecies. Scientific reports, 8(1), 15469.

Ogishi M, et al. (2015) Deconvoluting the composition of low-frequency hepatitis C viral quasispecies: comparison of genotypes and NS3 resistance-associated variants between HCV/HIV coinfected hemophiliacs and HCV monoinfected patients in Japan. PloS one, 10(3), e0119145.

Poh WT, et al. (2013) Viral quasispecies inference from 454 pyrosequencing. BMC bioinformatics, 14, 355.