Resource Summary Report

Generated by dkNET on Apr 29, 2025

NeSSM

RRID:SCR_011941
Type: Tool

Proper Citation

NeSSM (RRID:SCR_011941)

Resource Information

URL: http://cbb.sjtu.edu.cn/~ccwei/pub/software/NeSSM.php

Proper Citation: NeSSM (RRID:SCR_011941)

Description: A Next-Generation Sequencing Simulator for Metagenomics.

Abbreviations: NeSSM

Resource Type: software resource

Keywords: bio.tools

Funding:

Resource Name: NeSSM

Resource ID: SCR_011941

Alternate IDs: OMICS_01510, biotools:nessm

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

Record Creation Time: 20220129T080307+0000

Record Last Update: 20250420T014602+0000

Ratings and Alerts

No rating or validation information has been found for NeSSM.

No alerts have been found for NeSSM.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Song K, et al. (2021) Reads Binning Improves the Assembly of Viral Genome Sequences From Metagenomic Samples. Frontiers in microbiology, 12, 664560.

Xi W, et al. (2019) Using QC-Blind for Quality Control and Contamination Screening of Bacteria DNA Sequencing Data Without Reference Genome. Frontiers in microbiology, 10, 1560.

Song K, et al. (2019) Reads Binning Improves Alignment-Free Metagenome Comparison. Frontiers in genetics, 10, 1156.

Qiao Y, et al. (2018) MetaBinG2: a fast and accurate metagenomic sequence classification system for samples with many unknown organisms. Biology direct, 13(1), 15.

Roux S, et al. (2017) Benchmarking viromics: an in silico evaluation of metagenome-enabled estimates of viral community composition and diversity. PeerJ, 5, e3817.

Ren J, et al. (2017) VirFinder: a novel k-mer based tool for identifying viral sequences from assembled metagenomic data. Microbiome, 5(1), 69.

Randle-Boggis RJ, et al. (2016) Evaluating techniques for metagenome annotation using simulated sequence data. FEMS microbiology ecology, 92(7).

Lin YC, et al. (2015) A New Binning Method for Metagenomics by One-Dimensional Cellular Automata. International journal of genomics, 2015, 197895.

Roux S, et al. (2015) Viral dark matter and virus-host interactions resolved from publicly available microbial genomes. eLife, 4.

Roux S, et al. (2015) VirSorter: mining viral signal from microbial genomic data. PeerJ, 3, e985.

Jia B, et al. (2013) NeSSM: a Next-generation Sequencing Simulator for Metagenomics. PloS one, 8(10), e75448.