

# Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

## 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

**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:** 20260801T190425+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 [RRID](#) .

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) VirSorter: mining viral signal from microbial genomic data. *PeerJ*, 3, e985.

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

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