

Resource Summary Report

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QIIME: VIROME comparinator tool diversity metrics

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Protocol Information

URL: <https://dx.doi.org/10.17504/protocols.io.ec9baz6>

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Summary: Viral Informatics Resource for Metagenome Exploration (VIROME) is a bioinformatics pipeline that classifies viral metagenome sequences after searching against annotated reference sequence databases (i.e., UniRef, SEED, ACLAME, COG, GO, KEGG, and PhageSEED) and a custom environmental database, Metagenomes Online (MgOI). VIROME's compare tool allows users to compare any number of metagenomes to one another by generating a Biological Observation Matrix (biom) file that contain counts of occurrences of custom observations (comparison metrics), and a mapping text file that provides per-sample metadata (library IDs and descriptions). Quantitative Insights Into Microbial Ecology (QIIME) is an open-source software pipeline that allows users to interpret raw sequencing data and create graphical displays to interact with the data. QIIME is modular, providing users with the flexibility to select and integrate various applications. While QIIME has many capabilities and online tutorials, this SOP is limited to the steps a user will take to use VIROME's compare tool output (biom and mapping files) to explore composition (what is in a sample), alpha-diversity (diversity within a sample), and beta-diversity (comparison of diversity between samples). This SOP generally follows guidance in online tutorials but with modifications unique to the VIROME Comparinator output analysis.

Affiliations: University of Delaware

External URL: <http://virome.dbi.udel.edu>

Version: 1

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