

Processing a Viral Metagenome Using iVirus

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Abstract

A collection of protocols designed to guide the user in processing a viral metagenome from raw sequence data to assembly, and subsequent analysis. The user uses *actual* reads from <u>Ocean Sampling Day (2014)</u> and processes them entirely within Cyverse, a NSF-supported cyberinfrastructure.

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Collection

PROTOCOLS

1. Assembling Viral Metagenomic Data with SPAdes (Cyverse)

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2. <u>Identifying Viral Sequences Using VirSorter (Cyverse)</u>

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3. Preparing Data for vContact from Proteins (Cyverse)

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4. Applying vContact to Viral Sequences and Visualizing the Output (Cyverse)

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