🌐 Downloading Viral Metagenome Data

🔖 In 1 collection

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ABSTRACT

Downloading reads from the Ocean Sampling Day (2014) using fastq-dump, a tool from the SRA toolkit implemented in Cyverse.

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PROTOCOL CITATION

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COLLECTIONS ⓘ

📋 **Processing a Viral Metagenome Using iVirus**

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LICENSE

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49417

PARENT PROTOCOLS

Part of collection
Processing a Viral Metagenome Using iVirus

GUIDELINES

Follow along and learn how to process a viral metagenome!

MATERIALS TEXT

To run this protocol, users must first register for Cyverse account. All data (both inputs and outputs) are available within Cyverse's data store at /iplant/home/shared/iVirus/ExampleData/

BEFORE STARTING

To run this protocol, users must first [register](#) for Cyverse account. All data (both inputs and outputs) are available within Cyverse's data store at /iplant/home/shared/iVirus/ExampleData/

Getting Started

1   This is the very first step in downloading reads from [Ocean Sampling Day (2014)](#). If you navigate through their wiki and other documentation, you can find the SRA associated with this dataset: ERR771003.
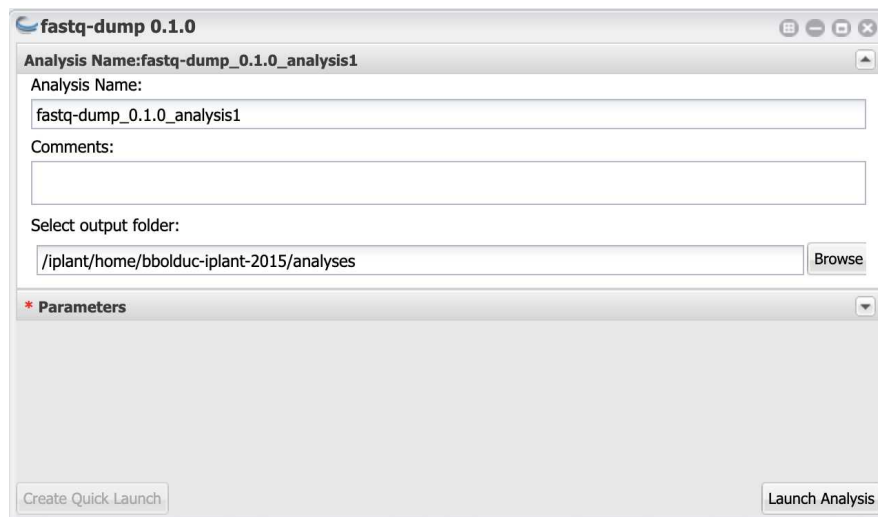
There are a lot of ways to download this data and get it on CyVerse. The following are a few ways:

- Download the data from SRA manually and then use [Cyberduck](#), follow CyVerse's Cyberduck [instructions](#).
- Download the data from SRA manually and then upload via [iCommands](#).

For this, we'll use the FASTQ-dump tool available from the SRA, which is also available on CyVerse.

Download from SRA

2   Open FASTQ-dump

3   Specify the SRA accession

4 Launch Analysis

Run the job!

5 After the job finishes, you'll have a directory with two important files, ERR771003_1.fastq and ERR771003_2.fastq.

You can use these files directly in the next step, or compress them if you want to save disk space.