Welcome to CyVerse
QIIME 2™ is a next-generation microbiome bioinformatics platform that is extensible, free, open source, and community developed.

- Automatically track your analyses with decentralized data provenance — no more guesswork on what commands were run!
- Interactively explore your data with beautiful visualizations that provide new perspectives.
- Easily share results with your team, even those members without QIIME 2 installed.
- Plugin-based system — your favorite microbiome methods all in one place.

In this quick start, we will show you how to launch JupyterLab-QIIME2 VICE app in DE
Prerequisites

2.1 Downloads, access, and services

In order to complete this tutorial you will need access to the following services/software:

<table>
<thead>
<tr>
<th>Prerequisite</th>
<th>Preparation/Notes</th>
<th>Link/Download</th>
</tr>
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<tbody>
<tr>
<td>CyVerse account</td>
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2.2 Platform(s)

We will use the following CyVerse platform(s):

<table>
<thead>
<tr>
<th>Platform</th>
<th>Interface</th>
<th>Link</th>
<th>Platform Documentation</th>
<th>Learning Docs</th>
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<tbody>
<tr>
<td>Discovery Environment</td>
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2.3 Input and example data

In order to complete this quickstart you will need to have the following inputs prepared.
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<td>Sequencing reads</td>
<td>FastQ</td>
<td>Any sequencing reads in FastQ format will work. They do not need to be pre-processed. They may also be compressed (e.g. fastq.gz)</td>
<td>gut microbiome (iplantcollaborative &gt; example_data &gt; qiime2 and select gut-microbiome folder)</td>
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1. Login to the CyVerse and view the App.
2. Under “Parameters” for ‘Input folder’ or ‘Input files’, click Browse, then navigate to and select one or more FastQ files to analyze; Then click OK.

   **Note:** To use our example data, navigate to Community Data > iplantcollaborative > example_data > qiime2 and select gut-microbiome folder.

4. Click **Launch Analysis**. You will receive a notification that the job has been submitted and running with the “Access your running analysis here”.

5. Clicking on the “Access your running analysis” will open the JupyterLab-QIIME2 in another tab in the browser after a brief building phase.

   **Note:** You will be asked to authenticate again to the JupyterLab with your CyVerse username and password

6. You will see the input data under “vice” folder of the JupyterLab. Now you can upload your own Jupyter Notebook or create one using one of the available kernels

   **Warning:** Do not create or store any outputs inside the input folder (gut-microbiome) as those outputs are not brought back after the analysis

7. Finally, once you finish analysis, navigate to the DE tab, select the Analysis window and select the analysis, click “save and complete analysis”. Upon clicking complete analysis, the analysis will be completed and all the outputs will be brought back to the analysis folder.

   **Note:** UPDATE: Newest version QIIME-2019.10
The latest version (currently v2019.10 as of 11/8/2019) for QIIME2 in VICE has the capabilities for in-line visualizations in the jupyter notebook.

Simply import the qiime2 module into the python notebook:

```python
import qiime2
```

And use the following command to view your .qzv files in-line with your jupyter notebook:

```python
qiime2.Visualizations.load('demux.qzv')
```

This provides all of the perks of using view.qiime2.org to visualize your .qzv files, but you don’t need to change tabs. Additionally, everything is kept in the notebook which can be used as a lab notebook or for reproducibility.

**IMPORTANT:** Save all needed output files in the vice directory. Files not in the vice directory will not be retained in your data store analyses folder.

• Full materials for the webinar is available here
• See the original JupyterLab quick start
• See the original qiime2.org for how to run qiime2 analysis
• Contact CyVerse support by clicking the intercom button on the page.

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• Send feedback: Tutorials@CyVerse.org
4.1 Goals

QIIME 2™ is a next-generation microbiome bioinformatics platform that is extensible, free, open source, and community developed.

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