

# Step by Step Tutorial: Cyverse and Qiime2 for Parkinson's Mouse microbiome tutorial.

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This tutorial is a series of steps on how to set up a Cyverse account and to setup analyses for Qiime2.

CyVerse provides life scientists with powerful computational infrastructure to handle huge datasets and complex analyses, thus enabling data-driven discovery.

CyVerse was originally created by the National Science Foundation in 2008 with the name iPlant Collaborative to serve U.S. plant science communities. From its inception, iPlant quickly grew into a mature organization providing powerful resources and offering scientific and technical support services to researchers nationally and internationally. In 2015, iPlant was rebranded to CyVerse to emphasize an expanded mission to serve all life sciences as our cyberinfrastructure is germane to all life sciences disciplines.

Please visit <https://cyverse.org/about> for more information.

## Step 1. Creating a Cyverse Account

Visit the Cyverse webpage: <https://cyverse.org/> and click on the 'Register' link (Figure 1).

Once you have clicked in the "Register" link there will be a welcome sign on your screen (Figure 2).

You will need to fill all the relevant data in their form (Figure 3).

## Step 2. Login to Cyverse and open the Discovery Environment

Once you have set up your Cyverse account, login with your credentials (Figure 4).

In the home page, please LAUNCH your Discovery Environment by clicking the 'launch' link (Figure 5).

## Step 3. Open the Apps icon and search for Qiime2 (2018.11)

Once you are in the Discovery Environment click on the APP icon in the top left of your screen. In the new window search for "Qiime2" applications (Figure 6). Select the "JupyterLab-Qiime2-2018.11" application in a purple icon, developed by Upendra Kumar (Figure 6).

## Step 4. Select the input data and output folder

Once the application is opened, you can rename your analysis, select the folder to save the output. Under the "parameters" tab select the input folder, which path is: Shared With Me/njbayonav/Qiime2\_Class\_2020/Parkinson\_Mouse/

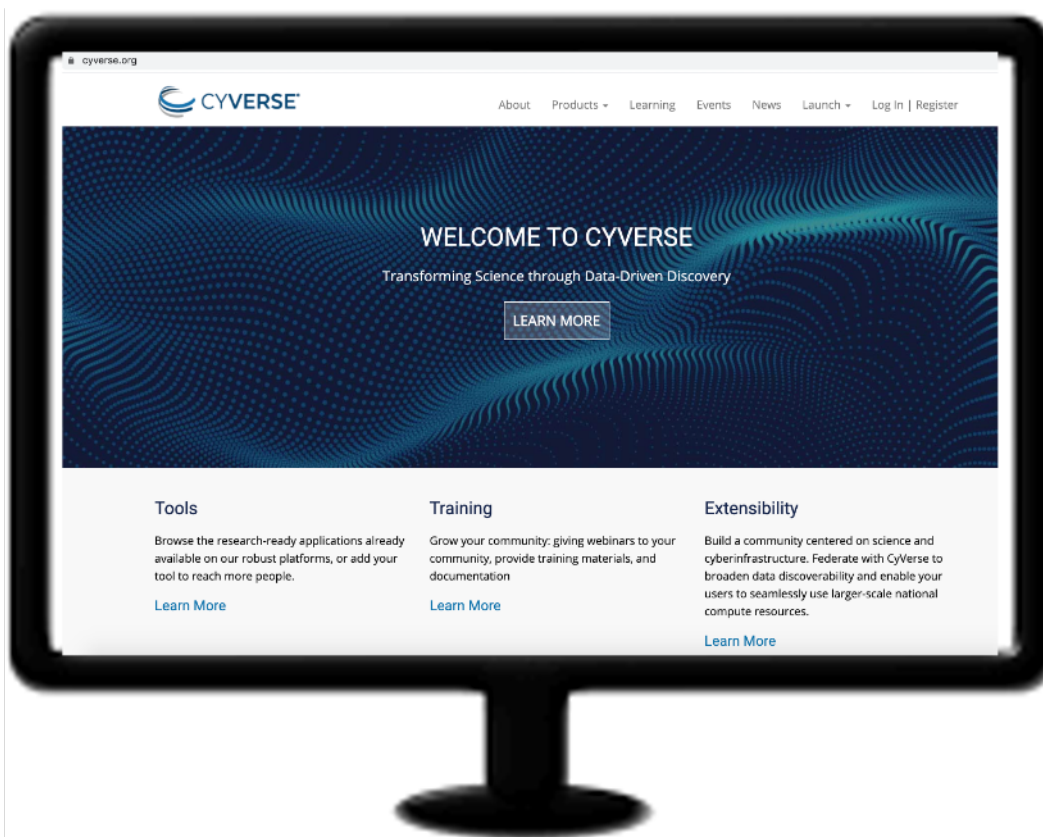


Figure 1: Cyverse webpage



Figure 2: Welcome to Cyverse



Figure 3: Registration form

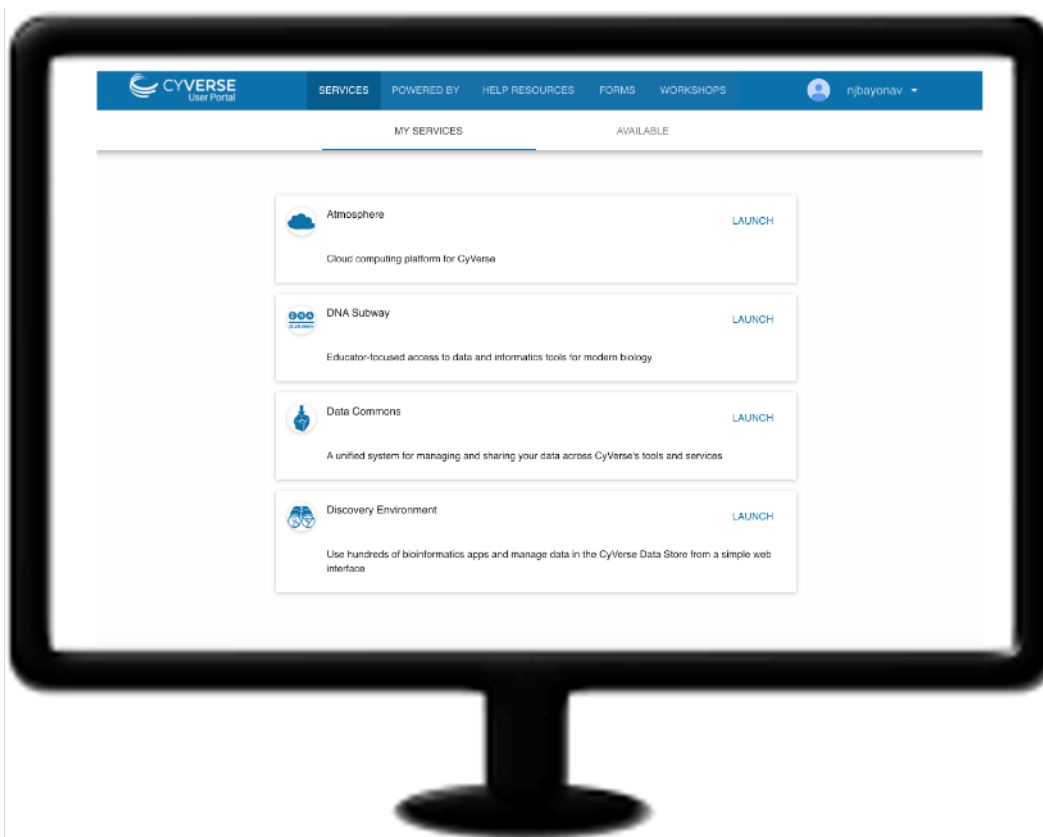


Figure 4: Login in



Figure 5: Launch Discovery Environment

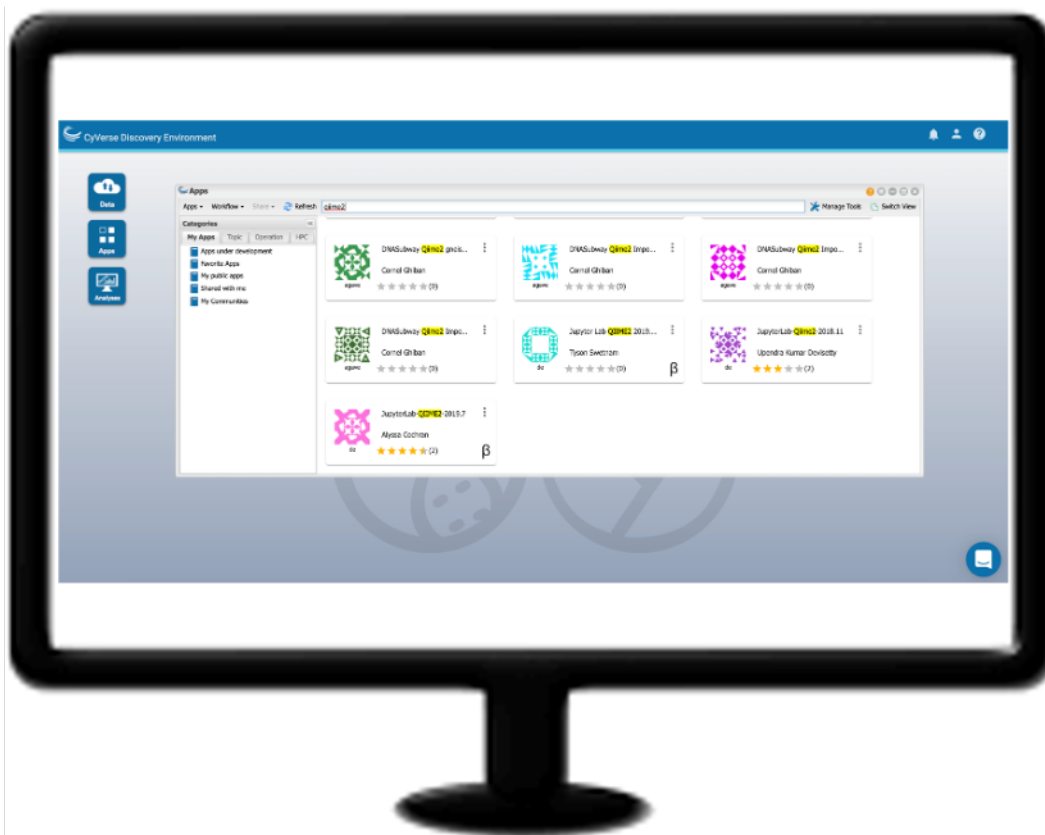


Figure 6: Qiime 2 app

(Figure 7).

NOTE: If you don't have access to this folder, please send me an email to [njbayonav@gmail.com](mailto:njbayonav@gmail.com) with your Cyverse username and I will share it with you. Otherwise you could upload the relevant data specified below, available in my Github tutorial page to your Cyverse Data folder.

Please make sure you have selected the folder (not any file within the folder). Once you have selected the folder click OK.

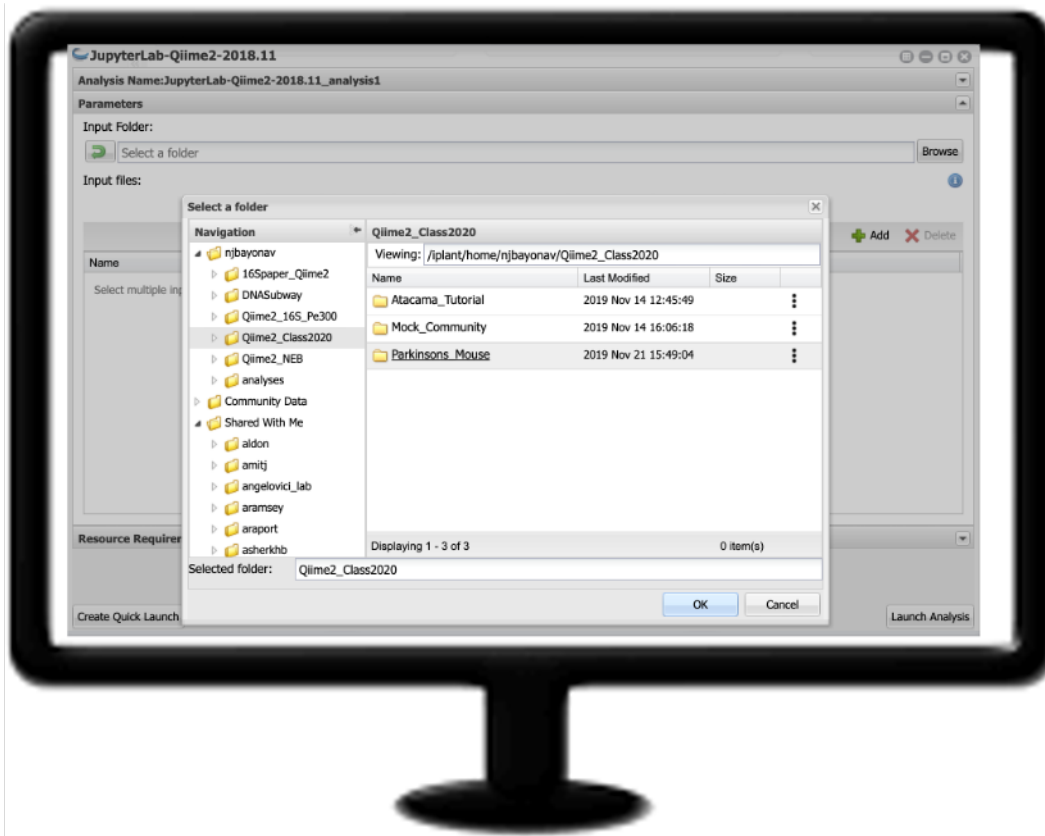


Figure 7: Selecting input folder

## Step 5. We are ready to launch the analysis!

Once you have named the analysis and selected your input and output folders, click LAUNCH ANALYSIS. You will get a notification under the bell on the top right of your Discovery environment. You can access to your analysis by clicking the link under notifications (Figure 8) or clicking on the ANALYSES icon.

You will have a new window open in your browser with an icon indicating your app is launching (Figure 9).

Once the app is launched, in the new window you will have a left pane with two directories, a central pane with access to create jupyter notebooks, terminal, or R code, among others (Figure 10).

Within the vice directory, you will find our Parkinson\_Mouse folder (Figure 11). Open the Parkinson Mouse folder, here you will be able to locate the following: > 1. fastqs folder: containing the sequencing data needed for the tutorial. > 2. gg\_13\_8\_otus: Greengenes V. 13.8 database to use as reference for taxonomic assignment. > 3. Qiime2\_Parkinson's\_Mouse.ipynb: Jupyter notebook to run Qiime2 in the Parkinson's Mouse dataset. > 4. manifest file: Manifest file with sample IDs and read orientation of the sequencing





Figure 8: Notification of your analysis

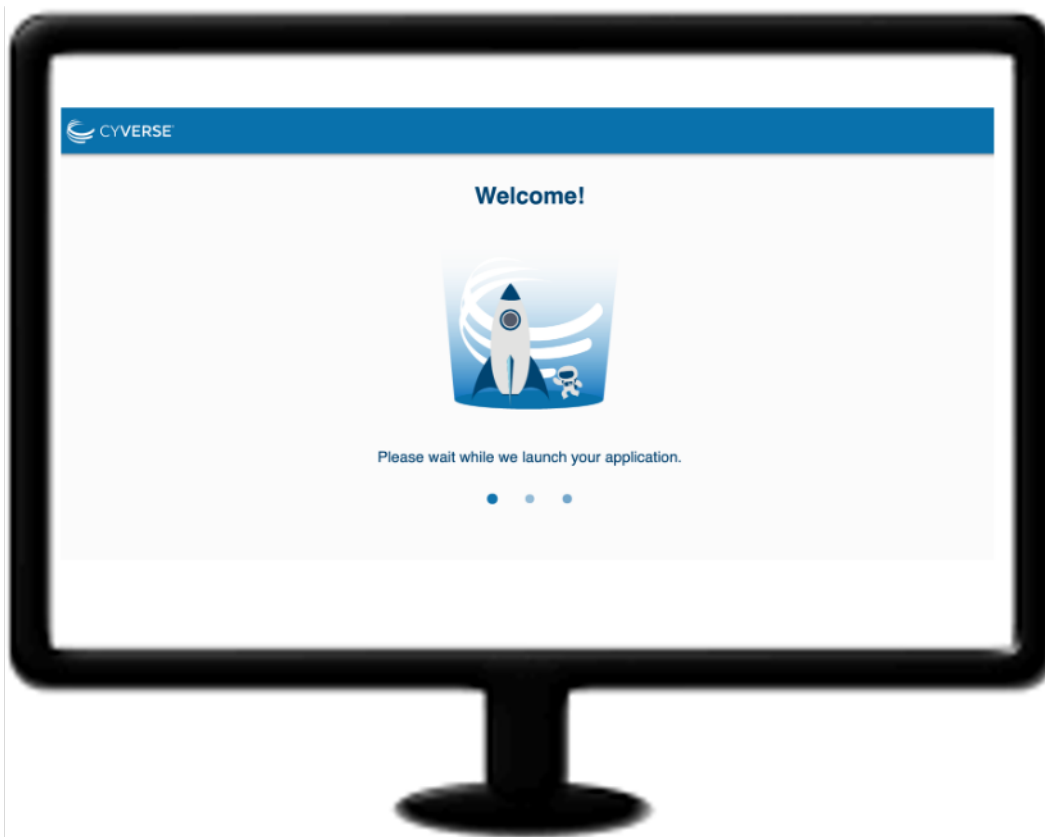


Figure 9: Launch App

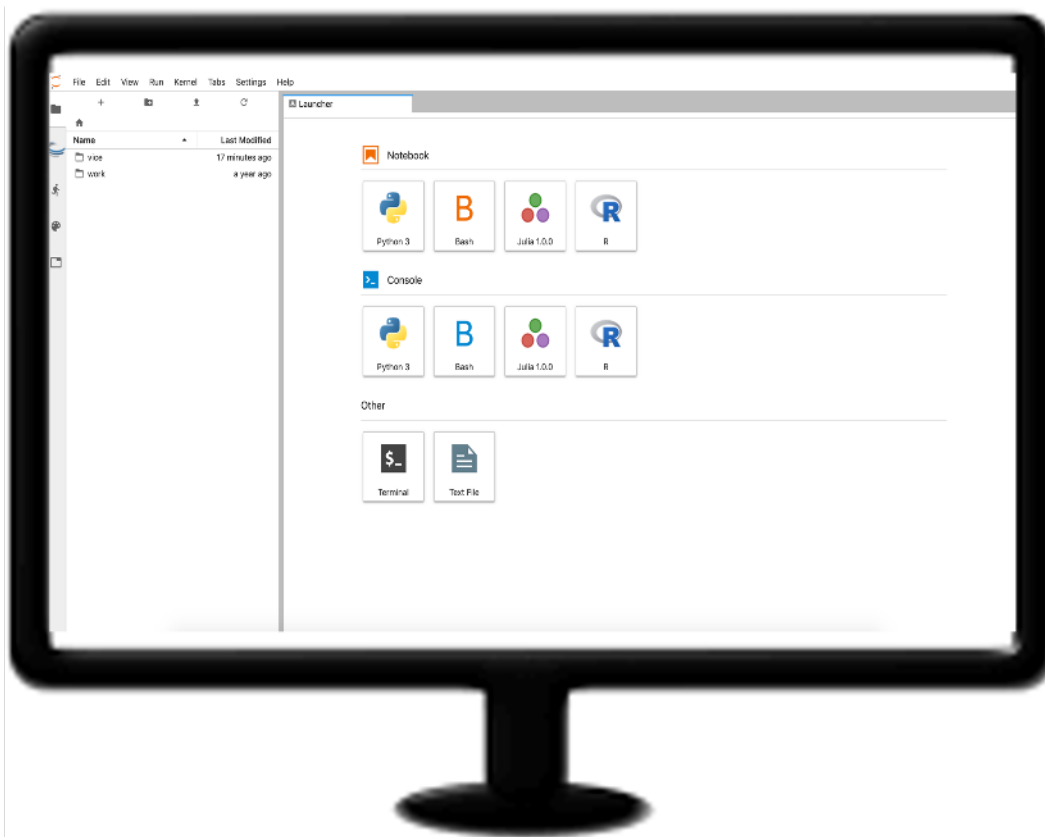


Figure 10: Application launched

file. > NOTE: This manifest file needs to be updated by the user where the path is replaced with the **absolute** path to the vice folder that contains the fastqs (/home/jovyan/vice/Parkinson\_Mouse/fastqs/). > 5. metadata\_map\_file.tsv: Metadata file containing categorical and numerical information for each sample. > 6. tree.qza: Artifact object of a phylogenetic tree estimated.

Please open the jupyter notebook file, and we are ready to start! (Figure 11).

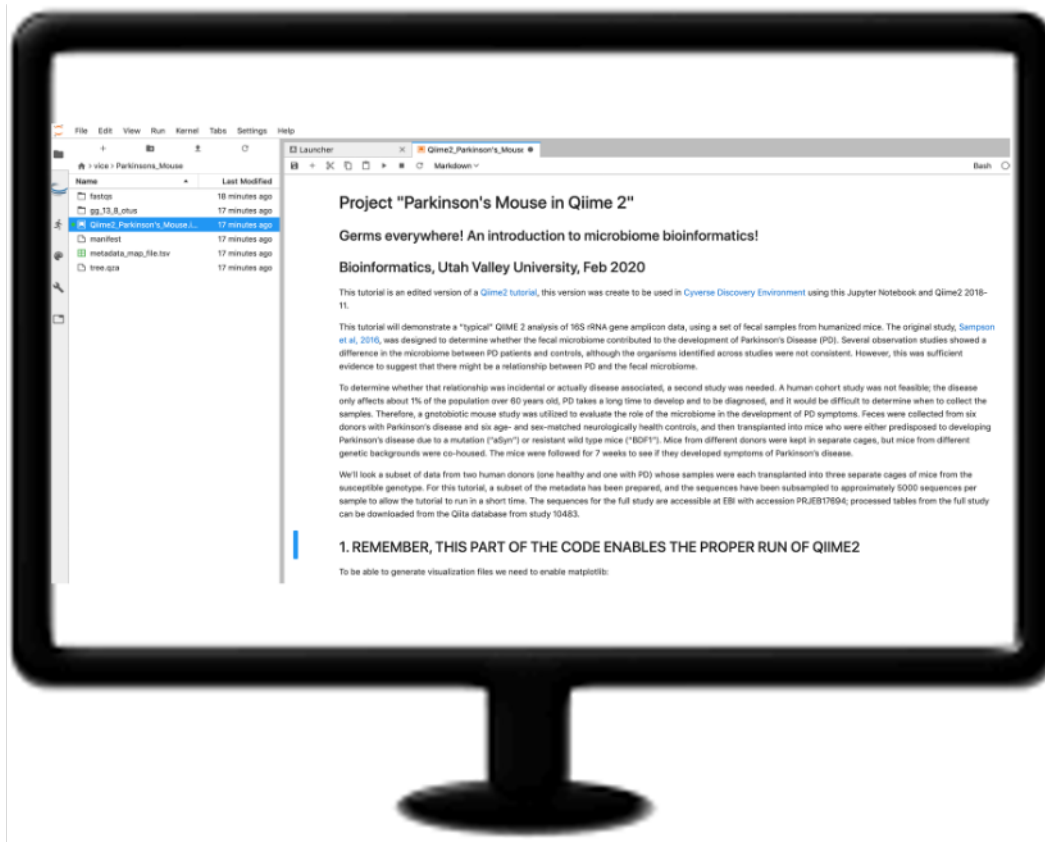


Figure 11: Jupyter Notebook