

Tutorial for CyVerse

By now, you should have received your sequences from the sequencing center. The next step is to analyze your sequences. You will be performing sequence analysis with applications available in CyVerse, a web-based platform that allows you to access computational tools for microbiome analysis.

Before getting started, you must first create a CyVerse account and upload your sequence files into CyVerse's file management system known as the Data Store. Along with your sequences, you must upload a metadata file, which is an additional file that you must create and upload to the CyVerse's data store.

Goal:

In this tutorial, you will learn how to:

- Create a CyVerse account
- Upload your sequence files into the CyVerse Data Store

Create a CyVerse Account for your group

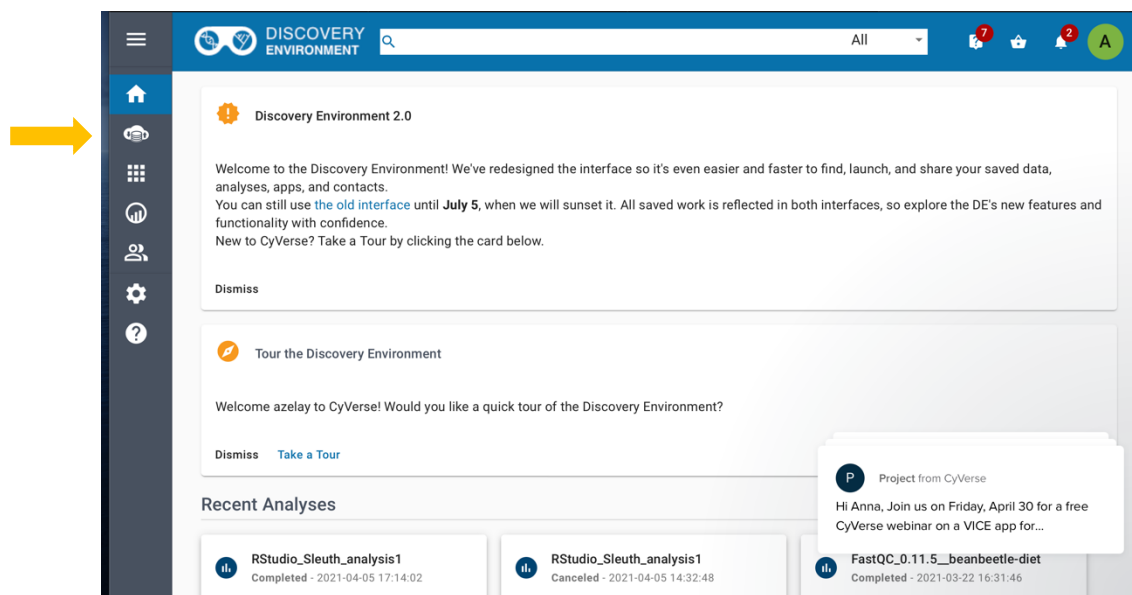
1. Go to <https://user.cyverse.org/register>.
 - a. *Note: To avoid glitches, the Chrome browser is recommended.*
2. Fill in the requested information for one of the members of your group to create your group account. Making sure to use your university email address.
3. An email will be sent to the university address of the member who input their information. This email will contain a link to confirm that the email address used was valid. Check your email and follow the steps contained in the email to confirm your address.
4. Once you confirm your email address, you will be directed to create a password for your new group account.

Upload files into CyVerse Data Store

Before we go over the process of uploading files, first make sure you have all the appropriate data files in the proper format.

- You should have received a folder containing two (2) fastq.gz files for each of your samples. For each sample the two files should look something like this:
 - SampleID_S#_L001_R1_001.fastq.gz
 - SampleID_S#_L001_R2_001.fastq.gz
 - *Note: Each sample will be numbered uniquely with S#. A sample number was assigned to each sample during the sequencing process.*
 - *Verify that you have two (2) fastq.gz files for EVERY sample*
- Once you have all of your files, you are ready to upload them into the data store

1. Open a web browser and go to <https://de.cyverse.org/de/>
2. Click on log in with your CyVerse ID
3. Log in using your CyVerse ID
4. You will then enter the CyVerse Discovery Environment 2.0. This is an area that can store files and documents for you to use within CyVerse. To upload your sequence files and metadata file, click on the Data icon, which can be found in the navigation bar on the left.



Note: This tutorial was created using MacOS High Sierra version 10.13.6 and Microsoft Office Suite Version 16.26. Steps may vary depending on OS and Microsoft Office versions used

NSF-Bean Beetle Microbiome Project Summer 2021

5. Clicking this icon will take you to your data folder. Your page will initially be empty as you do not have any data yet.
6. To create a new folder where you will store your sequences, click on the `Folder` button on the upper right hand corner.
7. A new box will appear. Type in the name of what you would like your folder to be called. Here, I am naming my new file `Beetle_Diet_Microbiome`. Then click `Create`.
8. After clicking `OK`, you should see your new folder appear on the screen. Click on it to enter the folder.
9. Click on the folder to open it. It will be empty at first.
10. To upload data from your local computer, you can click on the `Upload`. A drop down menu will provide options for where you would like to upload data from. To upload from your local computer, click on `Browse Local`
11. A new window will appear that will show you files from your local computer. Navigate to the files you'd like to upload, select, and upload the files.
12. You will now see your files in your folder. If you do not see them, refresh you're your page by clicking on the `Refresh` button.
13. If you have more files to upload, repeat the upload process until all your files have been uploaded.
14. Once you have successfully uploaded all of your files. You can now log out from CyVerse, or simply close your browser.

You can now proceed to the next tutorial **DNA Subway Purple Line Tutorial**

This tutorial was developed by Anna Zelaya, PhD for the Bean Beetle Microbiome Project, supported by National Science Foundation Grants, DUE-1821533, and DUE-1821184 to Morehouse College and Emory University, Atlanta, Georgia, USA. Any opinions, findings, and conclusions or recommendations expressed in this material are those of the authors and do not necessarily reflect the views of the National Science Foundation, Emory University, or Morehouse College.

Note: This tutorial was created using MacOS High Sierra version 10.13.6 and Microsoft Office Suite Version 16.26. Steps may vary depending on OS and Microsoft Office versions used