Section 2

BIODESIGN LABORATORY

Plate reader analysis using NEMO

Part 1

Plate reformatting

Generated: 09/05/2023

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Aim:
Reformat the kinetics data from the plate reader to make it useful for any further required analysis.

Introduction:
In order to analyse the data we need to reformat the data file that is generated by the plate reader. We have used : **Plate Reader EnSight Multimode Plate Reader (LOCATION SW511 L5-2419 (QM Elizabeth Li)).**
Data file is a csv file that records absorbance results, then fluorescence and finally luminescence results. Plate repeat numbers correspond to the cycle number or time points. This SOP guides you to reformat the data using the script accessible in the share folder.
Prerequisite:

1) Shared pathway to be used for Data processing
2) Connect to nemo on Terminal:

   ssh -Y your_name@login.nemo.thecrick.org

3) Copy the template folder with scripts from the share folder to your user folder:

   cp -rp /camp/lab/debenedictise/home/shared/microplatereader_template

/camp/lab/debenedictise/home/users/your_name/your_folder_name

4) Put your plate reader output data under your_folder_name as a csv file (your_csv_file.csv) and your plate content information as Manifest.csv. For this you can use any of these two methods:

   Method 1:

   Open another Terminal window (not connected to nemo) and use scp command on your terminal to transfer your csv file to nemo:

   scp -rp '/Users/path_to_your_file/your_csv_file.csv'

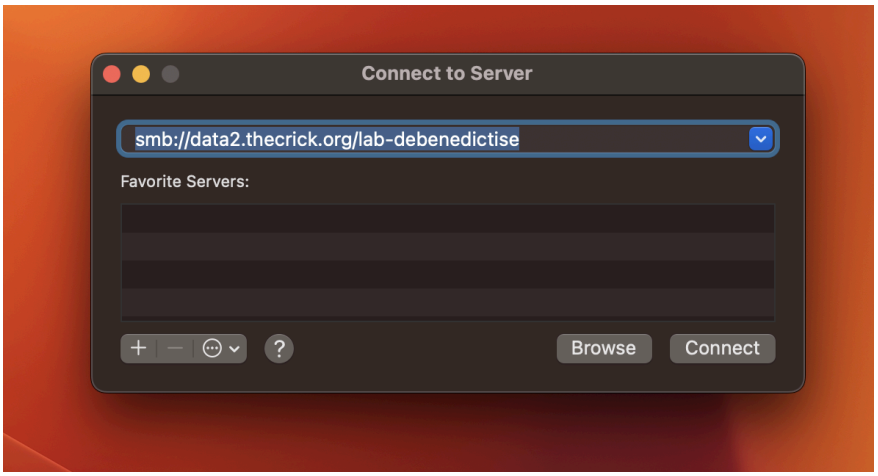
   your_name@login.nemo.thecrick.org:/camp/lab/debenedictise/home/users/your_name/your_folder_name/.

scp -rp '/Users/path_to_your_file/Manifest.csv' your_name@login.nemo.thecrick.org:/camp/lab/debenedictise/home/users/your_name/your_folder_name/.

Method 2:

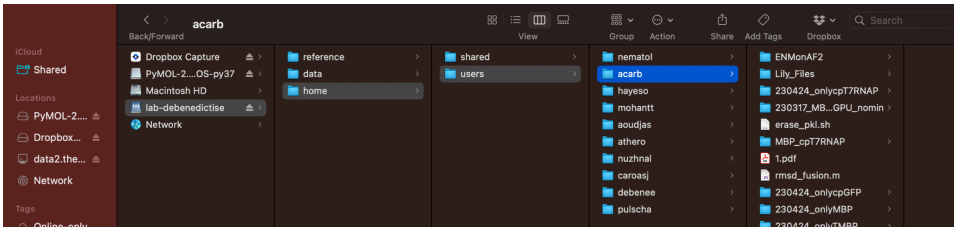
Use smb file transfer which treats nemo as an external memory drive on your computer.

a. Press [command + K] when Finder is open or Finder>Go>Network. The following screen will appear. Write the address as given and click *Connect.*



b. Type your username and password for Crick (nemo)

c. Once connected you will see the folders:



d. Drag your file into the your_folder_name/ under lab-debenedictise/home/user/your_name

5) Now you have both your csv file to be formatted and analysed, and the required formatting and analysis scripts in your_folder_name/.

6) Go back to Terminal with nemo connected and go to your folder including the csv and script files with the following command:

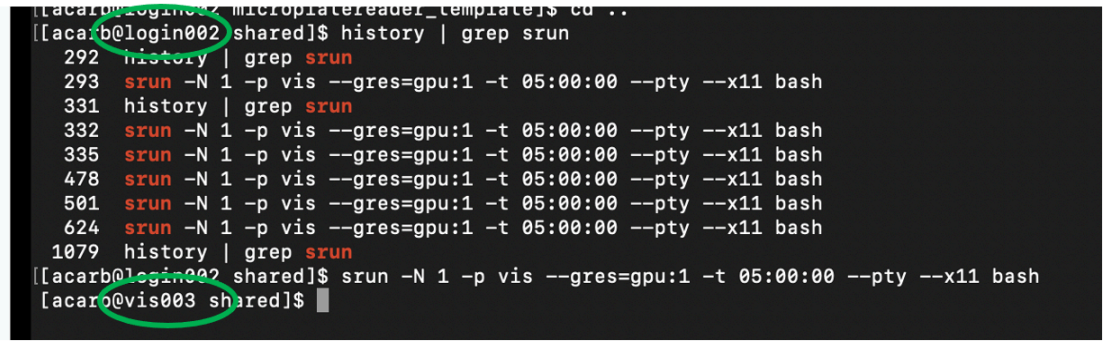
```
cd /camp/lab/debenedictise/home/users/your_name/your_folder_name/
```

7) To perform calculations, we need to go to vis partition (has more computational capacity) instead of login, with:

```
srun -N 1 -p vis --gres=gpu:1 -t 05:00:00 --pty --x11 bash
```

For x11 to work, XQuartz must be downloaded on your computer if you are using Mac:

https://www.xquartz.org/



- Now you are ready to go :) Call function callreader.sh to format the csv file:

  ```
  ./callreader.sh your_csv_file.csv
  ```

- This will create two separate folders for Fluorescence and Luminescence with the exact names, both including OD data. You can use the formatted csv files (*20200530_erika_taga_00001_reader_plate_1_kinetic_supp_abs.csv* for OD and *20200530_erika_taga_00001_reader_plate_1_kinetic_supp_3_high.csv* for Fluorescence or Luminescence, depending on the parent folder) under

these folders directly for your own analysis or continue with Erika's analysis with the following:

- Go to Fluorescence folder

  ```
  cd Fluorescence
  ```

- Call analysis function

  ```
  ./callanalysis.sh
  ```

- Repeat these two steps for Luminescence