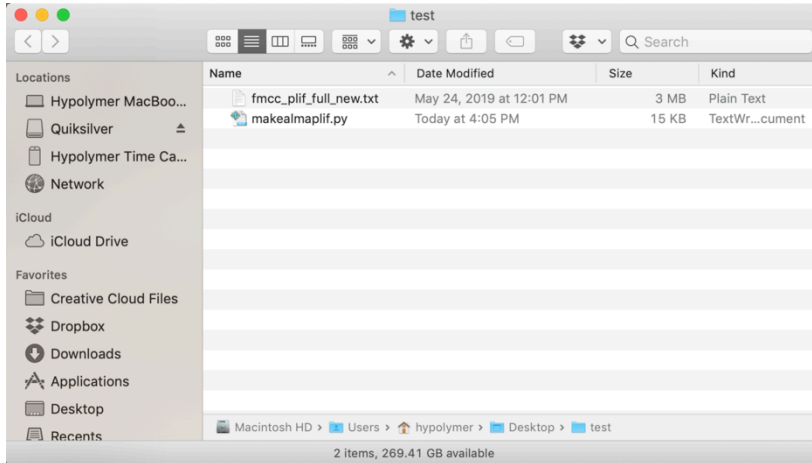


Instructions for the Alma patron data transformer Python script

On a Mac or Linux environment, have the Python script file in the same directory as the patron data file

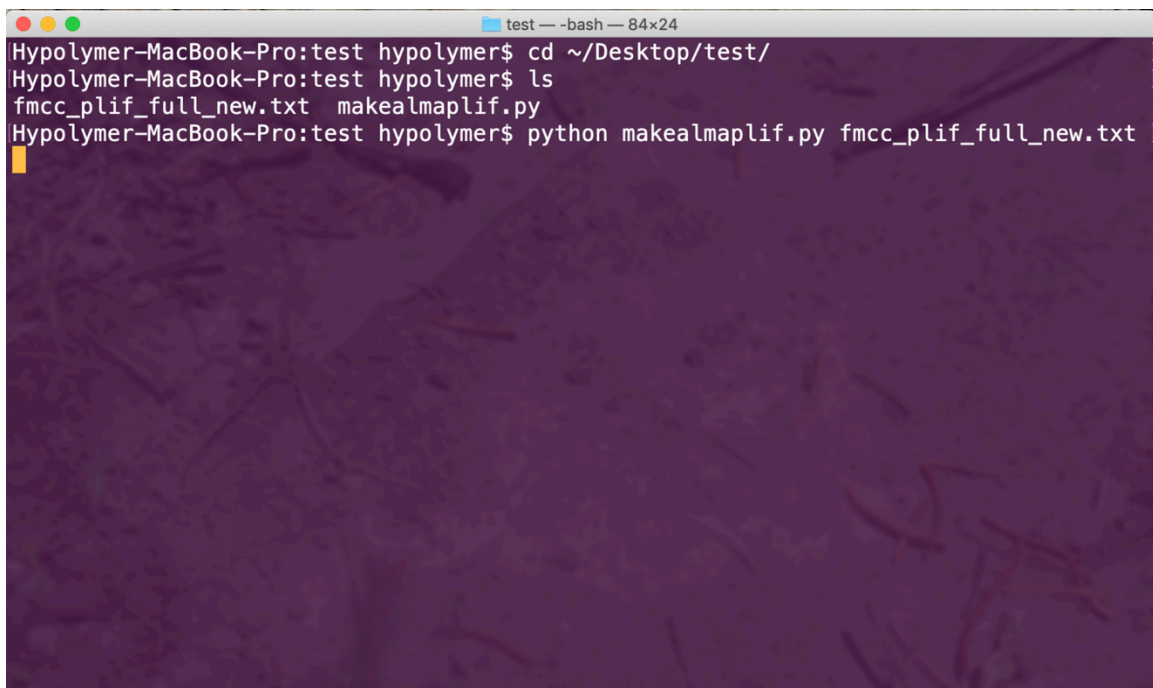


Open Terminal and navigate to the directory containing the patron data file and the Python file by using the 'cd' command (e.g., `cd ~/Desktop/test`)

Once you are in the directory with the patron file and the Python script, type:

```
python makealmaplif.py fmcc_plif_full_new.txt
```

[python][script to run][file to run the script on]



Once you type the command and hit enter, some confirmation information will appear letting you know how many records were processed and what the file name of the .zip folder is:

```
Hypolymer-MacBook-Pro:test hypolymer$ cd ~/Desktop/test/
Hypolymer-MacBook-Pro:test hypolymer$ ls
fmcc_plif_full_new.txt  makealmaplif.py
Hypolymer-MacBook-Pro:test hypolymer$ python makealmaplif.py fmcc_plif_full_new.txt
#
#
#
Congratulations!
You just completed processing 1,358 patron records
A .zip file has been created with the filename: Alma_XML_user_export_20190618_161746.zip
The .zip file is ready to be uploaded to the Alma SFTP server
Hypolymer-MacBook-Pro:test hypolymer$
```

When you go to the directory now, you'll see the new .zip folder that was created. This .zip folder contains the XML file that has the schema for Alma's patron loader. You'll use this .zip folder to upload to Alma through the SFTP server.

