

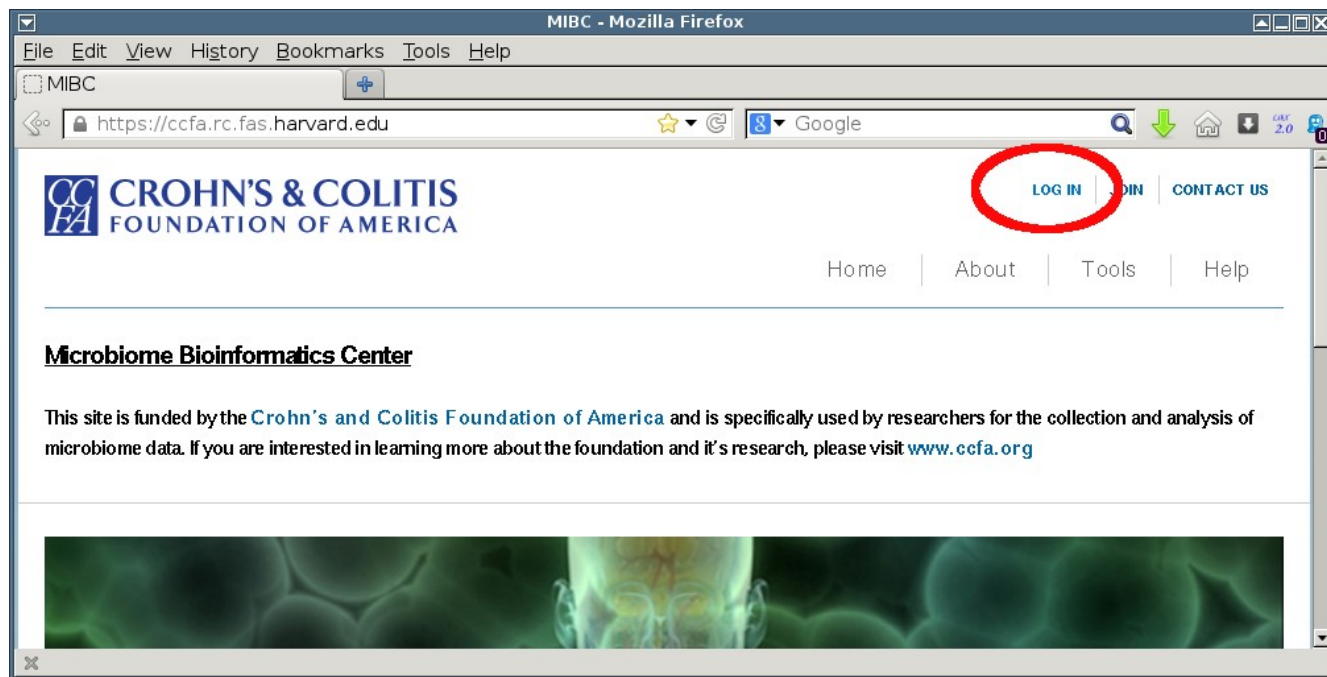
# Data Upload Procedure for CCFA Microbiome Initiative Bioinformatics Center

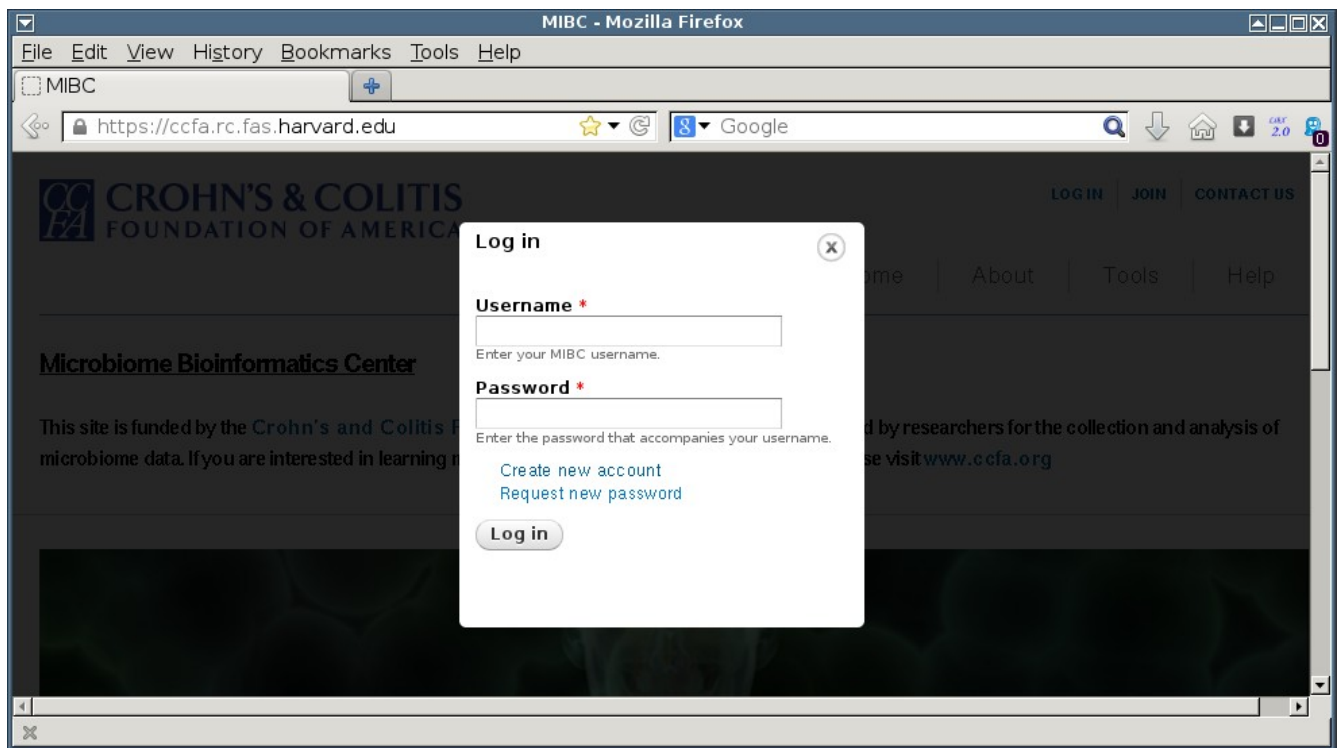
## Introduction

This document guides researchers through uploading data to the site. Currently, there are two ways to do so: via the Web UI and via Secure FTP. After registering for an account, either method can be used to upload data.

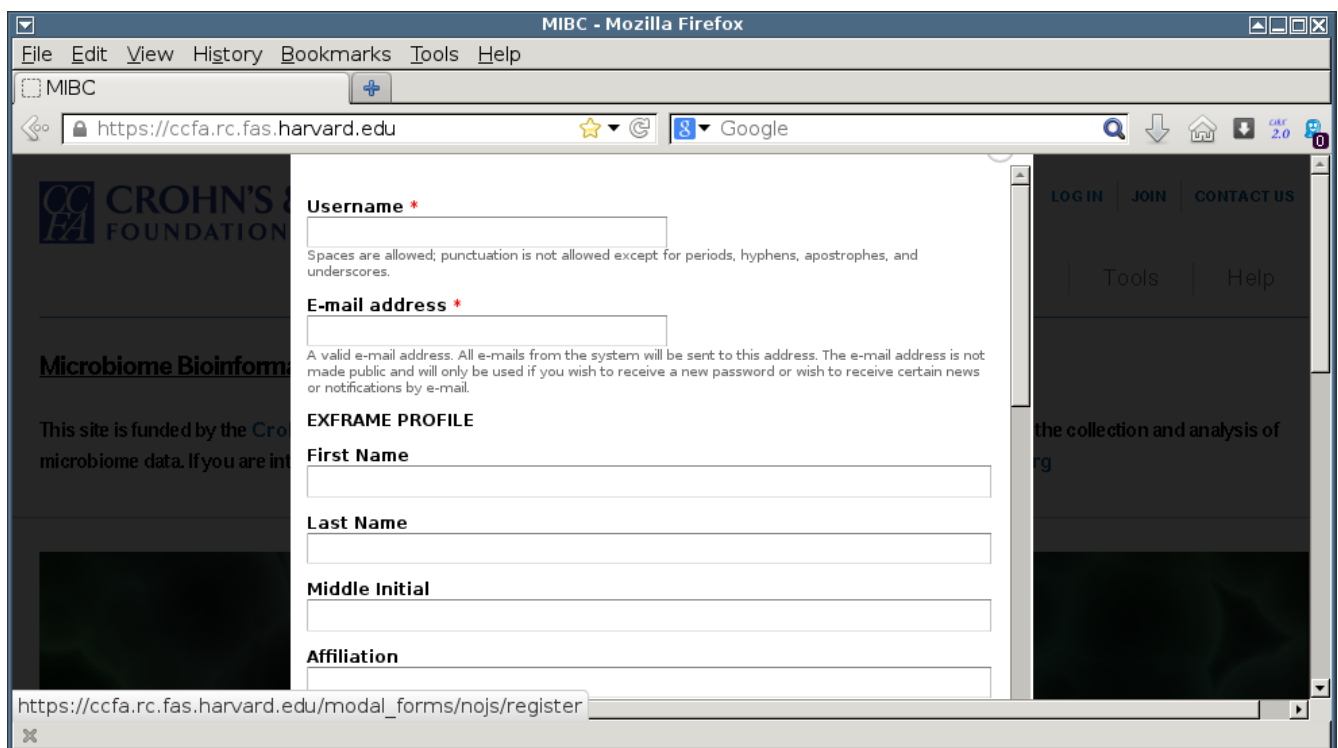
## Create Account

Via the web browser, researchers can register for an account by using the web form here: [https://ccfa.rc.fas.harvard.edu/modal\\_forms/nojs/register](https://ccfa.rc.fas.harvard.edu/modal_forms/nojs/register) or via the LOG IN link in the upper right hand corner of the page.





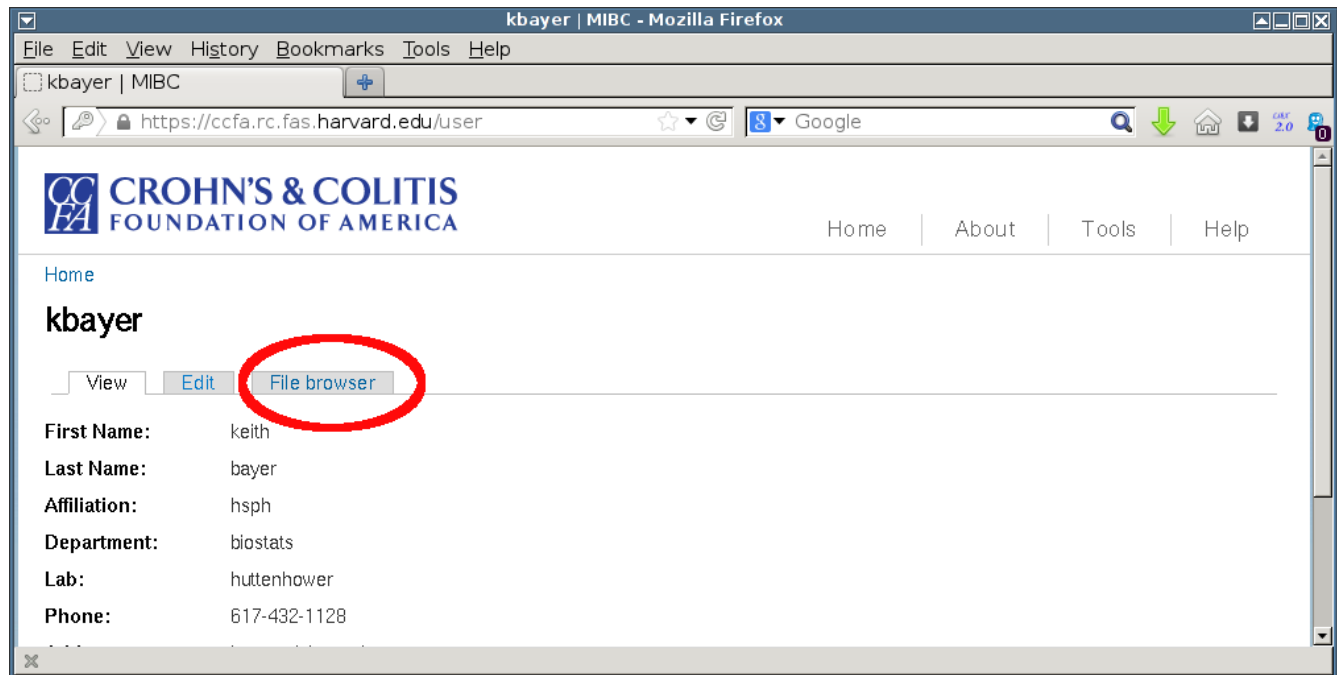
Select the link to 'Create new Account', fill in the form, and submit it. We'll create the account and email you with your account details.



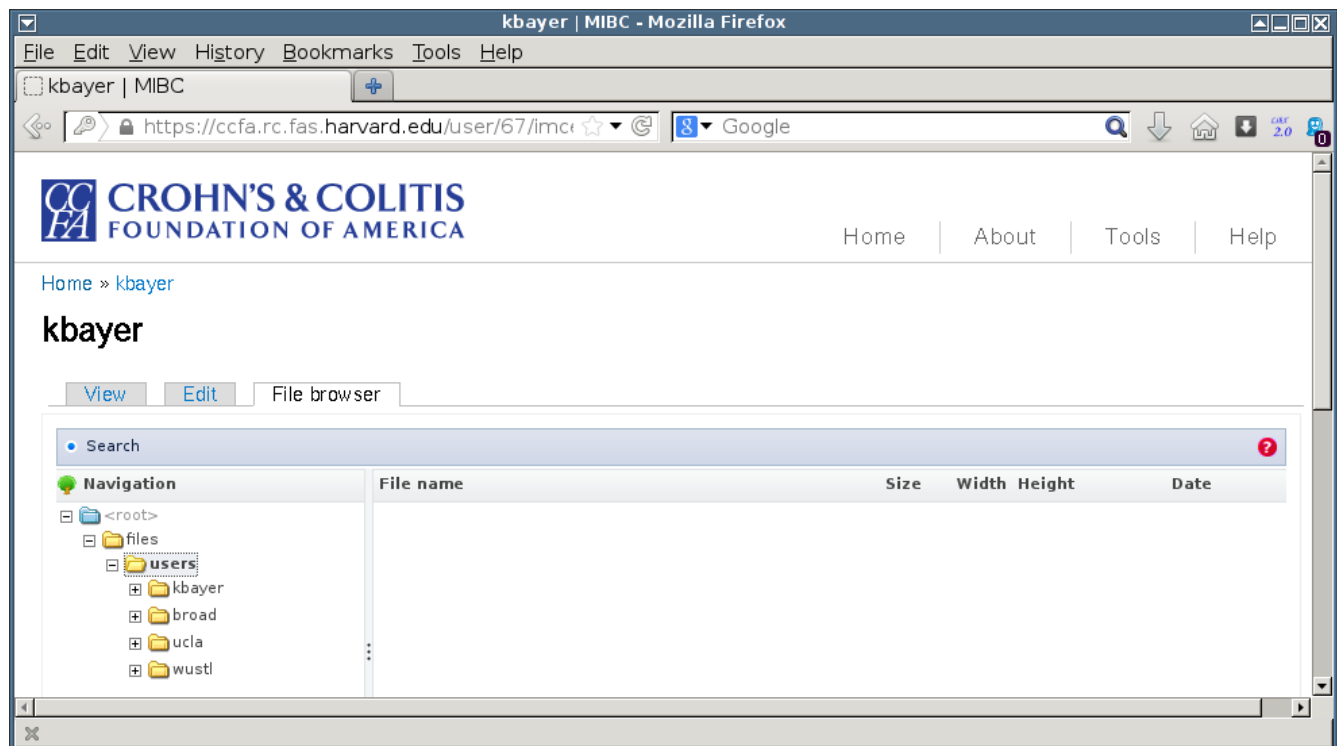
After the form is submitted, we will create an account and email the researcher via the given email address.

## Using the Web UI

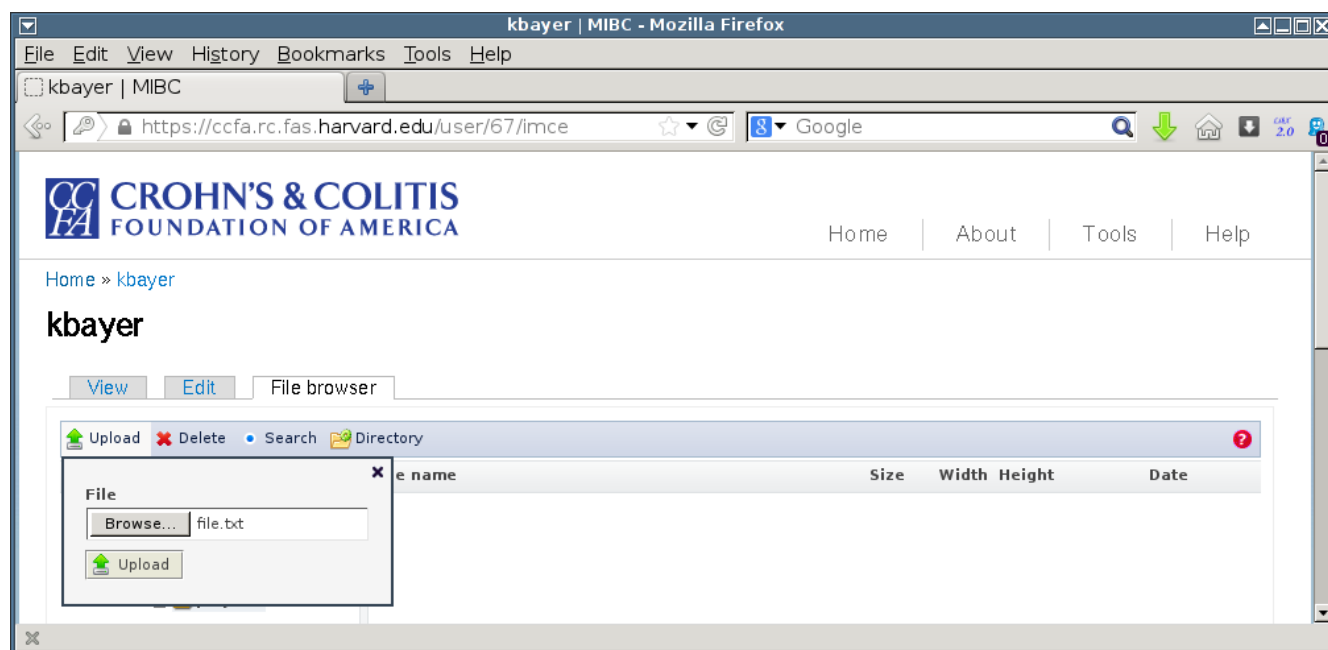
After registration, login to <https://ccfa.rc.fas.harvard.edu> and navigate under Tools / User Panel which will bring up a list of options. Select 'File browser'.



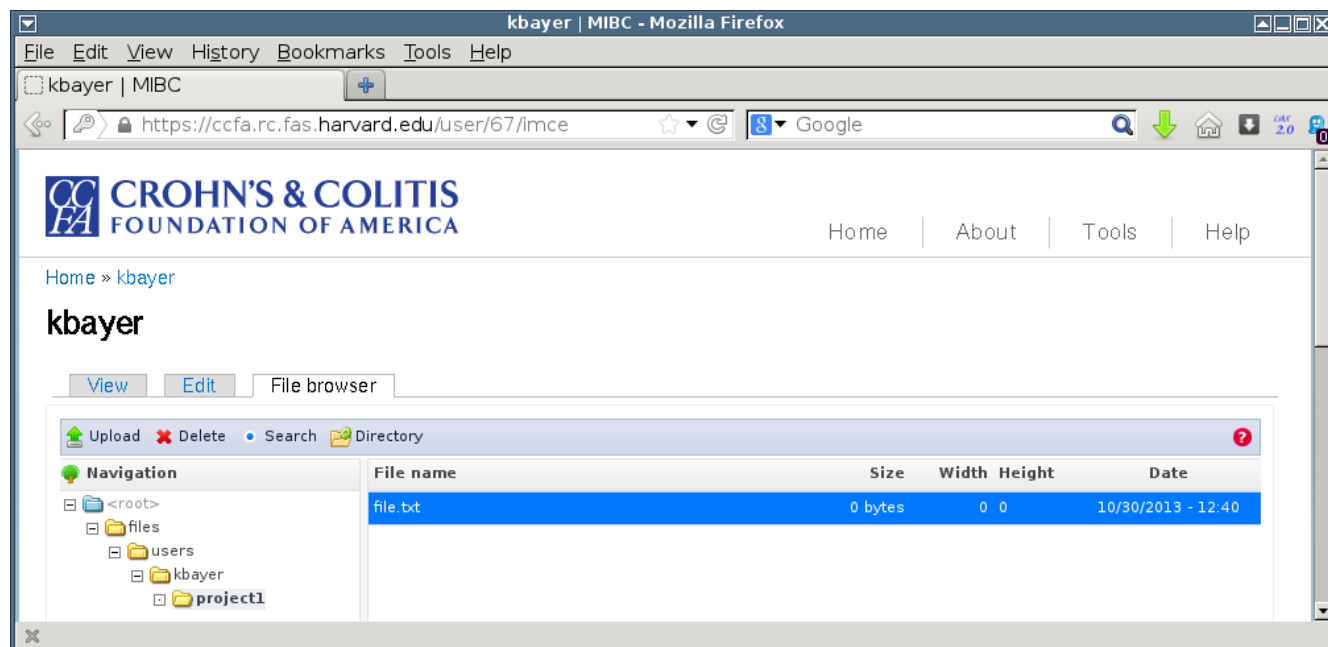
The File Browser will present a list of folders for the researcher:



Directories / Folders can be created under the researchers home directory (/files/users/'researcher') via the 'Directory' option located in the tool bar above the files. Use the 'Upload' option to upload individual files. Click on the browse button and select a local file to upload. Hit submit to transfer the file to the MIBC.



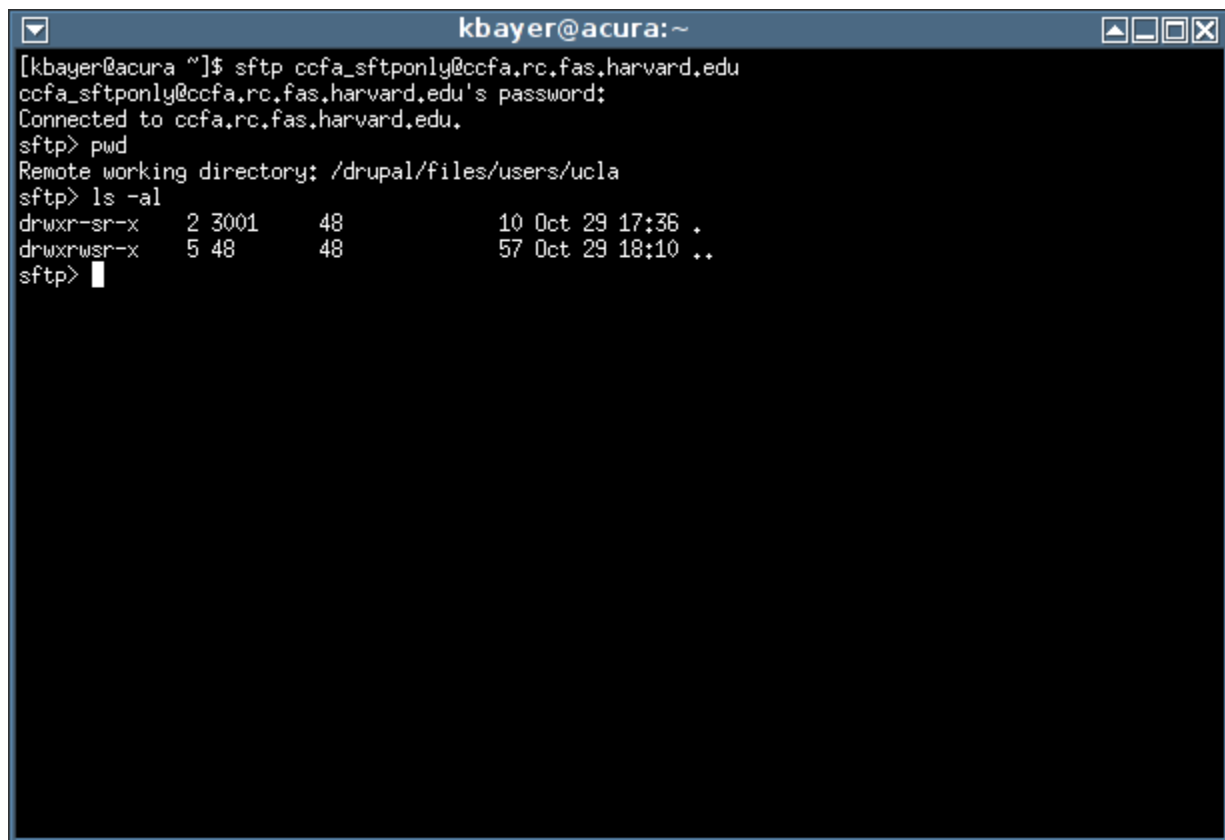
After the transfer, the Web UI File Browser should update to display the file.



## Using Secure FTP

Via Secure FTP, users can directly login to [ccfa.rc.fas.harvard.edu](https://ccfa.rc.fas.harvard.edu) to transfer files. To use secure ftp for Windows clients, a free secure client [WinSCP](#) can be installed and used for transfer. Guides for

both [installation](#) and [use](#) are available at the [WinSCP site](#). For Mac and Linux/Unix clients, sftp or scp can be used and is natively installed by most distributions.

A terminal window titled 'kbayer@acura: ~' with standard window controls. The terminal shows an sftp session with the following text:

```
[kbayer@acura ~]$ sftp ccfa_sftponly@ccfa.rc.fas.harvard.edu
ccfa_sftponly@ccfa.rc.fas.harvard.edu's password:
Connected to ccfa.rc.fas.harvard.edu.
sftp> pwd
Remote working directory: /drupal/files/users/ucla
sftp> ls -al
drwxr-sr-x  2 3001  48          10 Oct 29 17:36 .
drwxrwsr-x  5  48    48          57 Oct 29 18:10 ..
sftp> █
```

*Illustration 1: Command Line sftp on Linux*

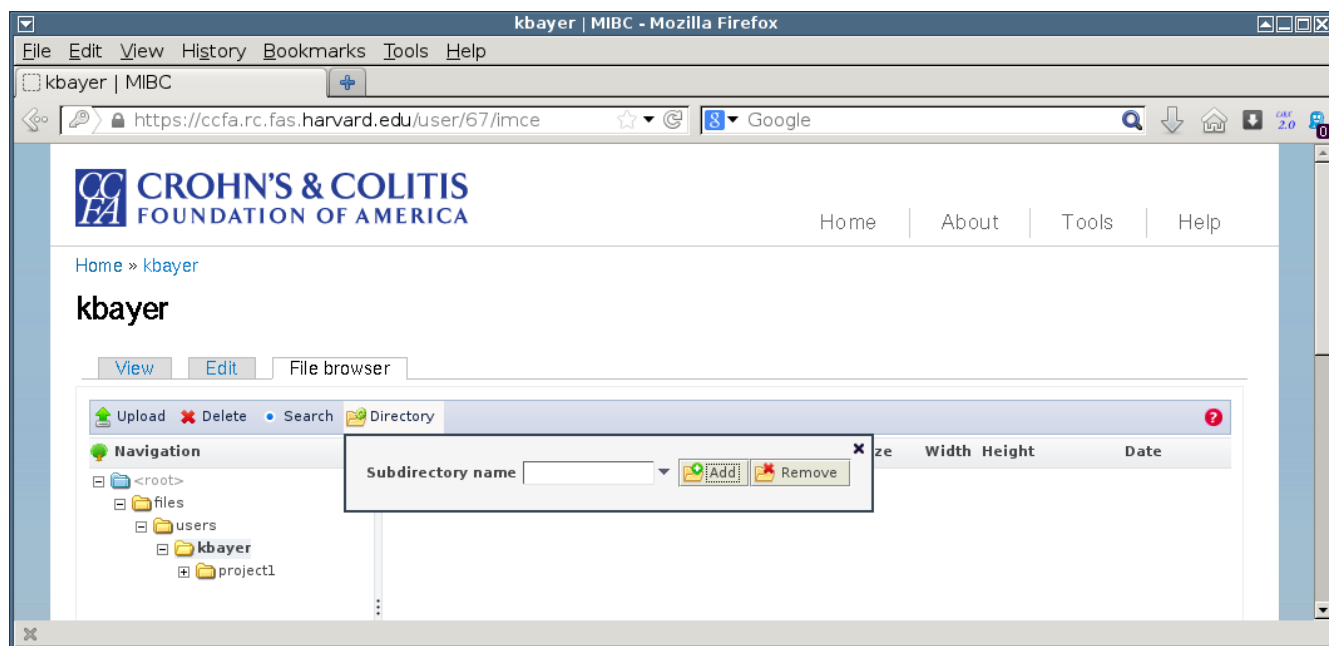
A list of command available via sftp can be found by typing '?' or help. Folders can be created by using the 'mkdir' command. Files can be uploaded using the 'put' command (and retrieved from the server using the 'get' command). Multiple files can be uploaded via a single command by using a wildcard symbol '\*'. For example:

```
sftp> put sample_data*
```

will upload all files beginning with 'sample\_data' in your current directory.

## Content

Under the user directory (e.g. /files/users/wustl/ ), one or more project folders should be created via either the file browser 'Directory' option or via sftp's internal mkdir command. The folder structure would then look like this:



Inside each project folder, the researcher ***must*** upload three types of files:

- Sample file(s)
- Metadata file
- Map.txt file(s)

Each of the file types are described in the following documents:

- Study Metadata <https://ccfa.rc.fas.harvard.edu/docs/Metadata.pdf>
- Sample Metadata [https://ccfa.rc.fas.harvard.edu/docs/Map\\_txt.pdf](https://ccfa.rc.fas.harvard.edu/docs/Map_txt.pdf)