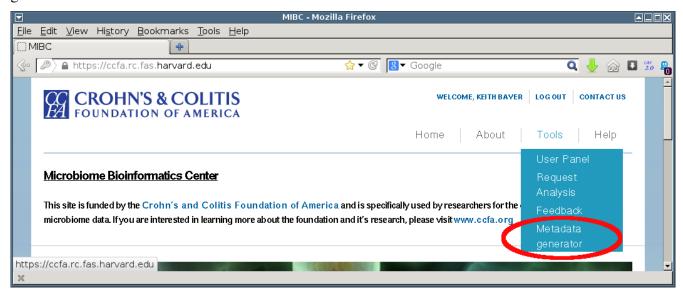
Metadata procedure for CCFA Microbiome Initiative Bioinformatics Center

Introduction

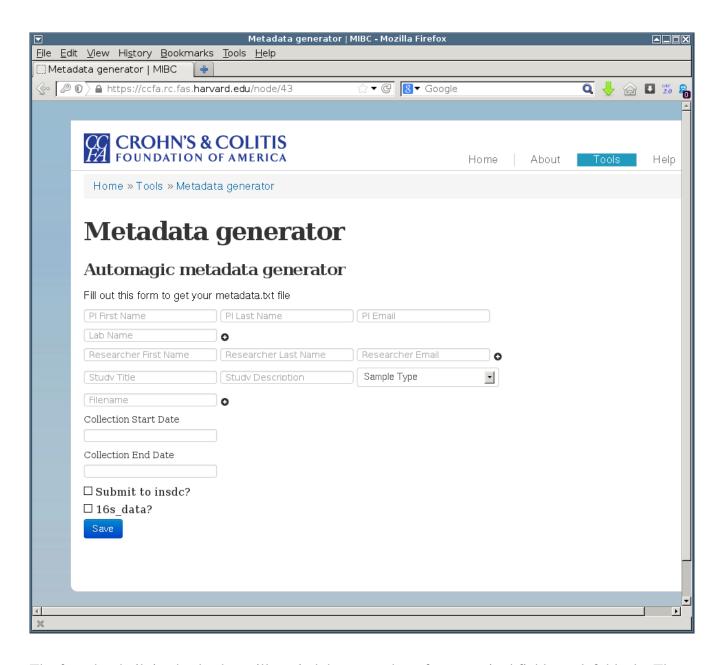
This document guides researchers through creating a Metadata.txt file. This file contains information regarding the all of the files uploaded to the researchers project directory. It is used to automatically check the syntax of the files contained in the project directory and for notification of potential issues requiring manual intervention (via email to the researcher).

Metadata Generator

To help with this process, a form has been created which will ask for all the necessary information and generate the Metadata.txt file. To access the generator, select the Tools menu and click on 'Metadata generator'.

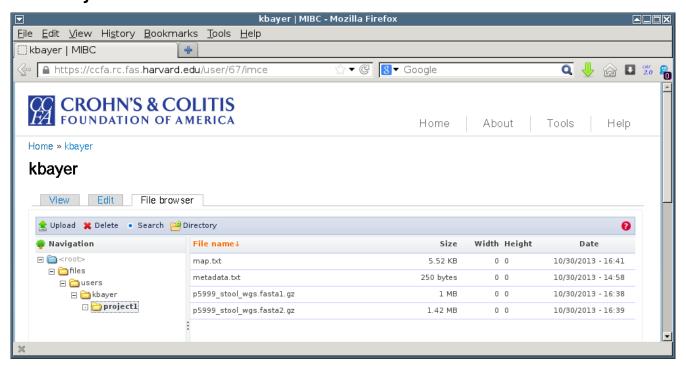


This brings up the generator page.



The form has built in checks that will remind the researcher of any required fields are left blank. The researcher email will be used for correspondance while checking syntax of all uploaded files into the project directory. After filling in the form, a 'Save' button at the bottom will generate the metadata.txt file and ask to store it on the researchers local computer. This file *must* then be uploaded to the project directory using either the Web UI or Secure FTP as described in the <u>Data Upload.pdf</u> guide.

Directory Structure



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

- Sample data file(s)
- metadata.txt file
- map.txt file

The map.txt file type is described in the following document:

• Sample Metadata https://ccfa.rc.fas.harvard.edu/docs/Map_txt.pdf