

Fasta Uploader- User Manual

Definition:

The fasta uploader is a tool used for batch processing files and accompanying metadata set to repositories via Application Programming Interface (API).

Purpose:

The purpose of the document is to define the use of fasta uploader and processing of the files in fasta uploader.

Procedure:

Go to [fasta uploader](#) in GitHub and download the zip file

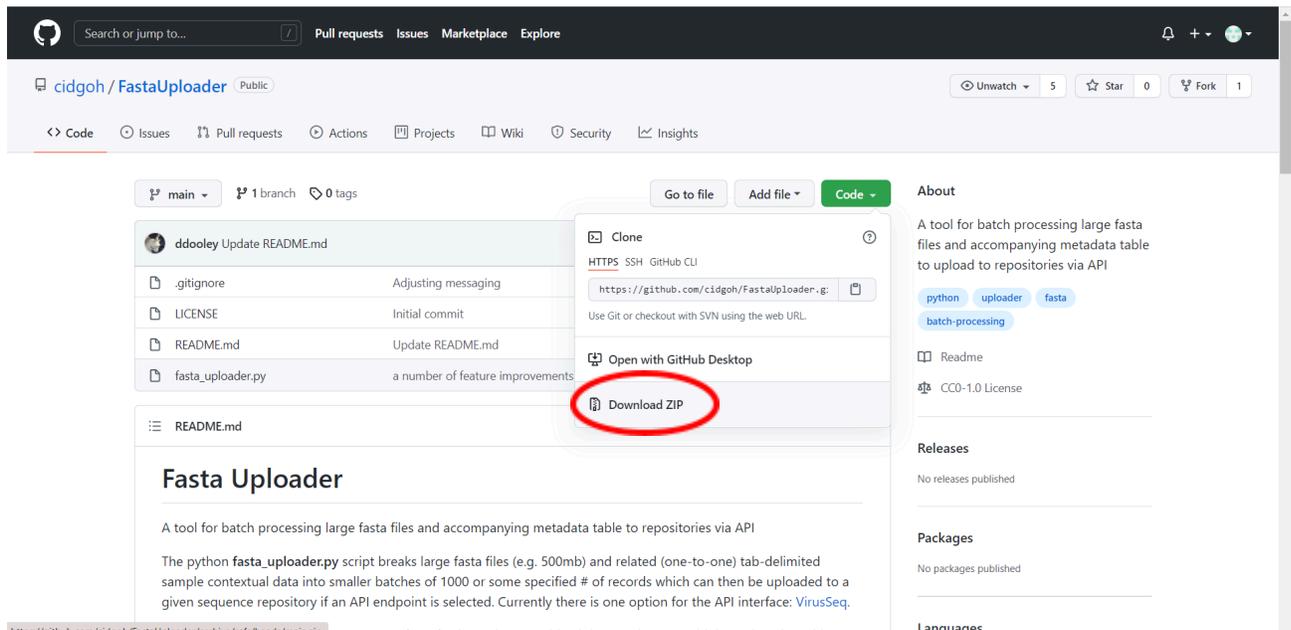


Figure 1

Install biopython

Install requests

- Save the metadata and fasta files to the fasta uploader folder

-f fasta file name for instance test.fasta

-m metadata file name for instance test.tsv

-k metadata field name to match to fasta record identifier for VirusSeq data portal “fasta header name”

-b batch number for instance 100

-a target API to send data too. A batch submission job will be initiated for it. Default it’s “VirusSeq_Portal”

-u an API user token is required for API access

Note: Occasionally there will be a lag to connect with the API after certain updates or fixes to the Virusseq data portal, please contact Scott Cain (scott@scottcain.net), OICR.

Appendix:

Revision History

Version	Date	Writer	Description of Change
1.0	November 01, 2021	Nithu Sara John and Damion Dooley	Created