How to submit RNA-Seq and BS-Seq data to GEO?

1. Create an NCBI account http://www.ncbi.nlm.nih.gov/sites/myncbi/

2. Link NCBI account to GEO http://www.ncbi.nlm.nih.gov/geo/submitter/

3. Create a folder on your server containing all the raw and/or processed files to be submitted

4. Fill in the metadata sheet http://www.ncbi.nlm.nih.gov/geo/info/examples/seq_template_v2.1.xls (*How to fill? Refer to examples on the same sheet*)

5. How to submit? http://www.ncbi.nlm.nih.gov/geo/info/seq.html

6. Linux/Unix: try 'ncftp'.

> **1.Connect to the server:**
> ncftp ftp://geo:33%259uyj_fCh%3FM16H@ftp-private.ncbi.nlm.nih.gov/fasp/
>
> **2.Set buffer size (recommended for faster transfer):**
> set so-bufsize 33554432
>
> **3.Transfer an entire directory (named using your GEO username) plus content using:**
> put -R GEOusername_directory
>
> For example:
>
> - To submit RNA-Seq and BS-Seq files, we submit the BAM files of RNA-Seq and BS-Seq data. BAM files are considered raw files.
>
>   (My NCBI id is moloyandri@gmail.com and I created a folder moloyandri in the SAL server containing BAM files of all samples)
> - Go to command line, login to your account on the server, create the folder with files to be submitted.
> - Filenames should match the list on the metadata sheet
>
>   moloya@SAL:~$ tmux a (*maintains an uninterrupted session for data uploading into GEO server*)
>
>   moloya@SAL :~$ ncftp ftp://geo:33%259uyj_fCh%3FM16H@ftp-private.ncbi.nlm.nih.gov/fasp/ (*Connects to ncftp server into the fasp directory*)
>
>   moloya@SAL :~$ set so-bufsize 33554432
>
>   moloya@SAL :~$ put –R moloyandri (*files in the folder moloyandri start uploading to GEO server*)
>
> - Once the files are uploaded mail the GEO curator (geo@ncbi.nlm.nih.gov) regarding your submission, mention the list of files, sizes of each and expected release date, username, directory where the files are added (*eg.* fasp/moloyandri).