Assignment 2

- Log into the server at IP 168.123.185.34
- Perform a BLAST search of the Acropora genes fasta file against the nucleotide (nt) database located in /usr/local/databases/ncbi (you may want to use screen to run your analysis)
- Run the BLAST search on 2 cores (CPUs/threads) and only retain the best hit of the BLAST search (hint: look into the maximum targets option of BLAST)
- Use scp to copy your BLAST results from the server to your local computer
- Filter the output to retain BLAST hits with an e-value ≤ 0.01 and only keep those hits that contain species of the genus Acropora – you may use a combination of Linux tools (eg, grep) and modified Python scripts from the course github page to accomplish the filtering task

Submit your work to me via email, as a tar archive using *tar cvzf* to create a *tar.gz* file (see command line reference on the github page).

Place all commands you used to run the analysis in a text file and include any script you used to process the data. Also include the BLAST output file into your tar archive.