Hendry lab server: cbsuhendry.tc.cornell.edu

* Hosted by the BIOHPC
* Log-on: ssh [NETID]@cbsuhendry.tc.cornell.edu
* Home directory: /home/hendrylab/[NETID]
  + We typically use the home storage for long term storage of sequencing/data/analysis files.
  + Data should be stored there until it is published and available on GenBank.
* Any processes that you run should be run on files that are on the server, not on the cloud.
  + You can make yourself a work folder in the workdir: /local/workdir/[NAME] (for example) and copy files for your projects there.
* All of the programs hosted by the biohpc can be run in the normal way when you are logged into the server.
  + For quick maximium likelihood trees, I would tend to use FastTree or IQTree.
  + For alignment, I like MAFFT.