TO DO:

-write first part of first script (download GB genomes) to a new file, for efficiency

-run first part of first script to download GB genomes

-write ordering test code

-write gb\_file code, or code that makes ‘fake’ genomes by replacing Columbia NTs with CVI and LER snp

- take from synced file (you’ll have to pull out section specific to making a snp genome) and save this to a separate file

\*not to be confused with a To Do Set