**Documentation** (*Updated: 10/16/2014*)

* Added /note to the result (10\_16\_2014\_mikehostisonote.txt)
* 04072014fastafull.fas contains the full fasta file (MikeTaylor + BLAST + GenBank)
  + It also includes the whole genome & haven’t been separated yet

\* Currently developing the script to separate the file into large sequences and < 2000

fastaextract.pl -> extracts 16S

* Need to reprogram it so that the non-16S descriptions will be in a separate file