* Marineomics as a resource
* Ancient DNA specific might be better for this workshop
  + Angsd for SNP calling
  + Create a tutorial
  + Paleomix pipeline for ancient dna- map your reads to reference genomes
  + Low coverage whole genomes or mtDNA genomes? GUIs to use for mtDNA
* Stephen- paleomix pipeline tutorial
* Melina- angsd, look into Rstudiocloud type thing
* mtDNA- Melina?
* Trees mtDNA? SNPs? Low coverage WGS?
* Docker
* EAGER
* Check out survey and edit list of bioinformatic pipelines!!
  + Stacks
  + Angsd
  + Paleomix
  + Conda
  + Bash/Command line
  + I would remove Astral, uparse, mothur, qiime2