Look at Brittany's blastn output. I also ran with -outfmt 7. Compare outputs. Look at default output and go over alignment components and what is reported in output. See if they can figure out how his could be used to annotate genes.

Brittany help Alethea execute blast using new instructions, which is the same as last week except with different sequences, and you need to make a blast database.

(I deleted one, so Brittany will do one and Alethea will do one.)

Then Alethea launch a job of 1 assembly to each of the databases using the appropriate program.

(scafs blastn 2 CDS,

scafs blastx 2 faa,

scafs tblastx 2 faa)