**Biocomputing Bioinformatics Project Plan**

Brett, Seth and Stephanie

Seth:

* Upload BLAST hits for each of 6 transcripts in uniquetranscripts.fasta to repo
* Upload a table with top hit for each of the 6 transcripts (low E, 100% identity)
* Upload a fasta file for each of the six unique transcripts with 10 protein sequences in each file.

Stephanie:

* Make a bash script that generates HMM models for 6 transcripts and 4 RNAseq files and HMMsearches 4 RNAseq files for each of 6 HMM protein models

Brett:

* Graph expression levels of proteins in RNAseq files
* Qualitatively compare to Kuhns & Pluznick 2017 paper
* Short Answer question 1

In group meeting on Monday 12/3 during regular Biocomputing class time

* Short Answer question 2
  + Use HMM script Stephanie is making