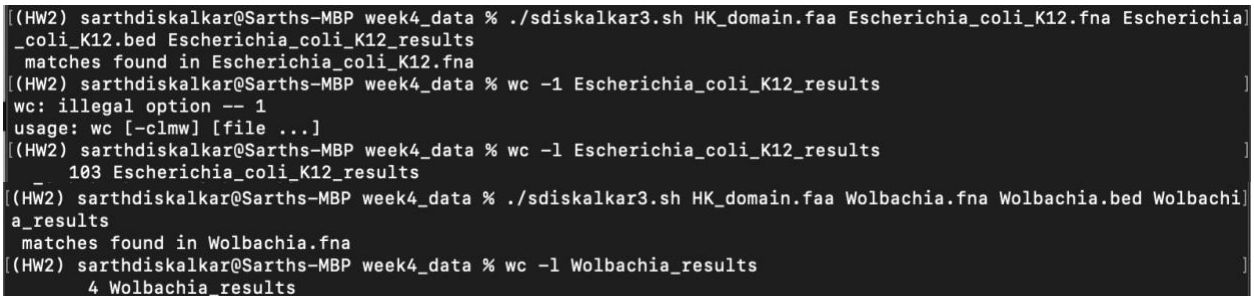
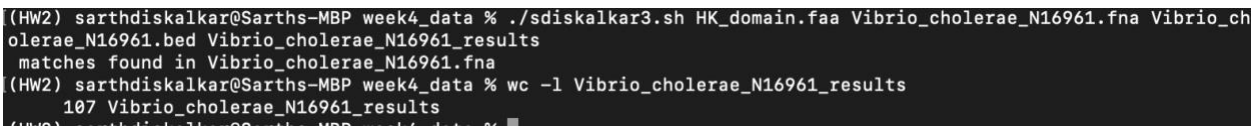
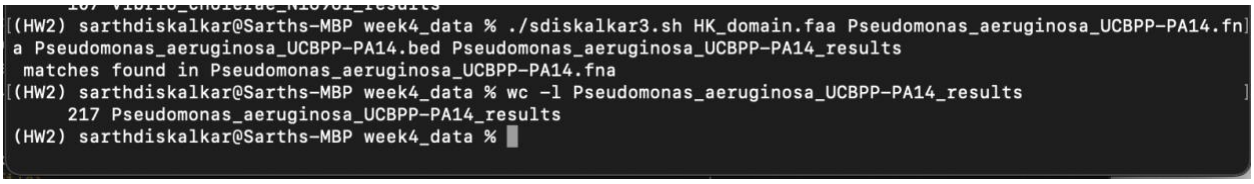
Instructions

1. Find putative homologs of query amino acid sequences in FASTA format (same as last week's instruction - i.e., what your current script does)
2. Use Bash loops and Bash conditional statements (no Python!) to identify which genes in a BED file contain the identified homologous histidine kinase domains. (Hint: if a gene contains a domain, then the location of the domain will be entirely within the boundaries of the gene)
3. Write an output file containing the unique gene names which your script identified as containing predicted HK domains.

Usage of your script should be: `homolog_identify.sh <query.faa> <subject.fna> <bedfile> <outfile>`







Script is attached in canvas.