./blastn -query ./week1\_query.fa -db nr -remote -outfmt "6 sseqid sseq" -evalue .0001 -num\_alignments 1000 -out 1000\_homologs

./01-tsv\_to\_fasta 1000\_homologs > 1000\_homologs.fasta

transeq 1000\_homologs.fasta pep\_1000\_homolog.fa

mafft pep\_1000\_homolog.fa > alignment\_pep\_1000\_homolog.fa

./02-peptide\_to\_nucleotide 1000\_homologs.fasta alignment\_pep\_1000\_homolog.fa | less –S

./03-dN\_dS nucleotide\_sequence\_withgaps.fa