Day 1)

-part 3) advanced\_exercise1: nucleotide diversity

Day2)

-part 1) advanced\_exercise1: calculate genome size and GC content

advanced\_exercise2: read form FASTQ flie (total read, avg length, gc conten)

-part2) exercise2: (func) read in aligned FASTA file and compute nucleotide diversity

-part3) advanced\_exercise1: load FASTA, count and display segregating sites

-part4) advanced\_exercise1: compute nucleotide diversity, segregating sites, Tajimas D -Part5) exercise1: compute pi Tajimas D for multiple files (sys, glob, os)

Day3)

-part1) exercise1: compute nucleotide diversity with VCF format