source code:

DARWIN-Whole Genome Alignment workflow

fasta_dict = read_fasta(fasta_file)
fastq_dict = read_fastq(fastq_file)
filtered_fasta_dict = filter_fasta(fasta_dict, min_length, max_length,
min_length_fraction, max_length_fraction)
filtered_fastq_dict = filter_fastq(fastq_dict, min_quality, max_quality)
write_output(filtered_fasta_dict, filtered_fastq_dict, output_file)

