

1. Using python write a tool which generates a random subsampling tool for sequences. Given a FASTA sequence database file, which has 100,000 sequences, generate a new file which is a random subset these sequences selecting only 10% of them. Make this 10% an option in the program so it is easy to change to 20%, etc.

See the script 'rand_shuffle_seqs.py' in the homework template

2. Run RNAseq analysis to compute the gene expression for two experiments. We will use data from this paper on light induction in bacterium *Prochlorococcus*

See this paper:

- Thompson et al. PLoS One 2016; 11(10): e0165375 doi: 10.1371/journal.pone.0165375
- Here is a view of the sequencing data. All data are on cluster in this folder `/bigdata/gen220/shared/projects/HW4/hw4_template`

Also you can get it from the web directly yourself. <https://www.ebi.ac.uk/ena/data/view/PRJNA315575>

The data for one timepoint: 0hrs light

Go and get the fastq files to process - see the download script

Light 0hr

- 0hr_1.fastq.gz
- 0hr_2.fastq.gz

The data for another timepoints: 4hrs light

The fastq files to process

- 4hr_1.fastq.gz
- 4hr_2.fastq.gz

Here is the *Prochlorococcus marinus* subsp. *pastoris* str. CCMP1986 genome: GCF_000011465.1. The RefSeq for this genome is at that link.

Can be obtained from this link

And the GFF

- Use Hisat2, samtools, and stringtie to generate a table of expression for these two experiments
- Write a python script that will generate a report with 5 columns of data. Gene Name, Chromosome, Start, End, Strand, Gene Length, FPKM exp1, FPKM exp 2
- Using R or other tools, make these plots
 - Plot gene expression from exp1 vs gene expression of exp 2
 - Plot gene length vs expr1 expression (FPKM). Is there a relationship?

- Plot gene location vs expr2 (FPKM). Is there any relationship?
- print a list of genes which are > 2 fold higher in the 4hr time point?