**BIO609**: Part 2, exercise solutions

 **Exercise 5: handling RNA-seq data**

#!/bin/bash  
for i in {1..10}  
do  
 wget [https://bioinfo.evolution.uzh.ch/share/bio609/dicty/sample${i}.fastq.gz](https://bioinfo.evolution.uzh.ch/share/bio609/dicty/sample$%7Bi%7D.fastq.gz)  
done

 **Exercise 6: map the RNA-seq data to the reference genome**

We will now try to use STAR and map our 10 samples of RNA-seq data to the reference genome. First, you need to create an "index" for the dd.fasta reference genome. You can do this with:

mkdir **istar** # folder for genome index  
STAR --runMode genomeGenerate --genomeDir **istar** --genomeFastaFiles **dd.fasta**

The command should take around 1-2 minutes to finish. The index is now stored in the folder **istar**.

Then you can write a script to map the RNA-seq data to the reference genome using the newly created index above.

An example command to map sample1 would be:

#!/bin/bash  
for i in {1..10}  
do  
 STAR --genomeDir istar --readFilesIn sample${i}.fastq.gz --readFilesCommand zcat

mv Aligned.out.sam sample${i}.sam

samtools view -S -b sample${i}.sam > sample${i}.bam

samtools sort sample${i}.bam -o sample${i}.bam

samtools index sample${i}.bam

rm sample${i}.sam

done

 **Exercise 7: download genome annotation in GFF format and count reads aligned to genes**

#!/bin/bash  
for i in {1..10}  
do  
 htseq-count -f bam sample${i}.bam dd.gtf > sample${i}.tab

done

**\*** **Exercise 8: combine gene expression tables into one single table**

awk 'NF > 1{ a[$1] = a[$1]"\t"$2} END {for( i in a ) print i a[i]}' \*.tab > samples.tab