**RNASeq analysis (using Ubuntu Linux)**

**How to run bowtie Aligner?**

* CD to bowtie folder and issue commands as under
  + extract bowtie\_0.12.7-1\_amd64.deb with command

**sudo dpkg –i extract filename.deb**

* + build indexes against which the alignments will be done

**bowtie-build transcripts.txt my-indexes**

#whatever you name it

* + Align the reads with indexes and store them in file alignments.sam

**bowtie my-indexes mu1.txt > mu1.sam** # will align mu1 reads to reference (transcripts) and store it to file mu1.sam or whatever name you give it

**bowtie my-indexes mu1.txt # writes results on screen**

**Get read counts while using counter script (python code) ‘getCountMatrix.py’ as;**

You must place the aligned bowtie outputs (mu1.sam and mu2.sam) in a folder called **bowtieOutputs**

Make sure that the **getCountMatrix.py**, **GeneIDs.txt** and **outputs folder** are in the same folder. CD to that folder, while opening the terminal in Ubuntu.

Issue the following command;

**python getCounts.py**

You will find the read counts in the file ‘countMatrix.txt’.

Recheck some random gene counts and confirm it with actual sam output file.