**January 2nd, 2020**

**Non-common processes note**

I have some non-common processes and I do need to document the SOP for easy access

1. Accessing the windows machine as aa-account

NIH IT support number:  866-319-4357

Go to websie: priv.nih.gov and get the password

1. Strayer University IT support: 866-610-8123 (Snowman2019!!)

**January 3rd, 2020**

**Found out an error in exomeSeq project**

I miss a variant in mouse Entpd4 gene, it turns out there are multiple regions with mm10 genome build.

BWA gives “MAQ 0” for alignment to multiple places: <https://www.biostars.org/p/83364/>

Therefore, my “bq20” criteria excludes reads with multiple locations

**To work with this, I need to retain multiple placement**

An Indian guy from Guangzhou Medical University has a post: <https://www.researchgate.net/post/How_to_derive_multiple_mapped_reads_from_a_SAM_file>

Get FLAG meeting here: <http://broadinstitute.github.io/picard/explain-flags.html>

I used BWA mem alignment, now i have reads with MAPQ 0 that i would like to extract into a new sam or bam file. Do you know if it is possible to do that with Samtools or another tool?

Untill now i tried:

samtools view -bSq 1 input.sam > output.bam

which filter out all reads with mapping quality lower then 1, but i would like to extract them to a new sam/bam file and work on them.