Dear Students,

I am forwarding to you the link to our ABPG+BRIM lecture #5.

Just a few comments:

>90% of Bioinformatics projects is performed on computers with UNIX or LINUX operating systems. Today’s LAB was a demonstration of how to process FASTQ files into SAM, BAM, and VCF formats. It was done on my LINUX workstation, which we call “intron2”.

For several of you it is the first experience with processing data using command line in UNIX/LINUX computers. Yet remember that almost all supercomputers use UNIX/LINUX. Finally, every spring I teach Introduction to Bioinformatics Computation course, which is programming in Perl. I start this course with studying LINUX. Now you have a better understanding why I think LINUX is important.

However, programming in Perl is possible in every operating system (Microsoft PC, MAC, or UNIX/LINUX)

<https://echo360.org/media/9731c988-0e14-40dd-ac5e-83bd3eda0b64/public>

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