ABPG2014 **L10** HOMEWORK EXPLANATIONS.

Your homework will be to work with AverageMutual\_Information program (AvMutInfo\_ABPG2014.txt) via a command line on Mac computer.

Step-by-step instructions:

1. copy the program (AvMutInfo\_ABPG2014.txt) onto the Desktop of your MAC computer.
2. Copy two files (“long\_human\_exons30” and “human\_introns\_ABPG2014”) containing fasta-formated exon and intron sequences written as a simple text (not **.doc** file) .
3. Open Application folder on Mac, then go to Utilities folder, then click on TERMINAL program
4. In a command line type **cd** [enter]
5. In a command line type **cd Desktop** [enter]
6. In a command line type **ls** [enter]
7. This command shows all files in your current directory (Desktop). You should see three files that you downloaded into this place (desktop).
8. Change the extension name of your program from **.txt** to **.pl.** In order to do so, type in a command line:

**mv AvMutInfo\_ABPG2014.txt AvMutInfo\_ABPG2014.pl**

1. OPTIONAL: You can view the content of your files using unix command “**more**”. In order to do so, type in a command line:

**more yourfilename** [enter] (yourfilename is the name of the file with your sequence. To scroll down page press space-bar key; to quit reading mode and return to a command line press ‘**q**’

1. In a command line type **perl AvMutInfo\_ABPG2014.pl** [enter] (see instructions for the command line.
2. Follow the instructions and type the proper command line. For example, **perl AvMutInfo\_ABPG2014.pl**  **human\_introns\_ABPG2014** **out\_name 60** [enter]
3. Follow the instructions on the video demonstration to run **AvMutInfo\_ABPG2014.pl** program on exons and introns for three sets of cutoff parameter 60, 120, and 180 (nucleotides).

Your HOMEWORK for L10 is to compare the distribution of AMI-values in exons vs introns for three settings of cutoff parameter (60, 120 and 180). Email to me your observations and conclusions.