ABPG2014 **L4** HOMEWORK DEMO.

Your homework will be to work with three MRI programs via a command line on Mac computer.

Step-by-step instructions:

1. copy three programs (SRI\_analyzer.pl SRI\_generator.pl MRI\_analyzer.pl) on the Desktop of your MAC computer.
2. Copy your fasta-formated promoter sequence written as a simple text (.**txt** and not **.doc** file) from previous lectures.
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. In a command line type **more yourfilename** [enter] (yourfilename is the name of the file with your sequence.
8. To scroll down page press space bar key; to quit reading mode and return to a command line press ‘**q**’
9. In a command line type **perl SRI\_analyzer.pl** [enter] (see instructions for the command line.
10. Follow the instructions and type the proper command line. For example, **perl SRI\_analyzer.pl** **yourfilename** **outputfilename 5** [enter]
11. Follow the instructions on the video demonstration to run SRI\_generator.pl and MRI\_analyzer.pl programs.

Your HOMEWORK is to compare the number of MRI regions in your sequence and in your randomized file. Email to me these numbers.