**Programming Assignment – 1**

**Deadline:**

Using C/C++/Java/Perl/Python:

1. (a) Write a program to generate a restriction map for a specific RE, EcorI in the given DNA sequence (File: *ecoli\_11kb.txt*). Output the positions of the restriction recognition sites for EcorI. Use Rebase (Mapper) to confirm your predictions.

(b) Write a program to identify restriction recognition sites in a given DNA sequence. Deadline: 23rd Aug

1. Write a program to reverse, complement, and reverse complement a DNA sequence. Output mRNA sequence for the corresponding DNA sequence. (File: take a gene sequence)
2. Write a program to change format of a DNA sequence: from Fasta format to Flat file format and vice versa. (File: take any gene sequence)
3. Write a script to parse the features table from a GenBank file. (File: FJ959345; NM\_175762) Deadline: 30th Aug
4. It is assumed that A = T and G = C in a genome. Compute G+C content, (G+C)/(A+T+G+C), deviation from A = T, (A-T)/(A+T) and deviation from G = C, (G-C)/(G+C) to confirm. Use a non-overlapping sliding window of size 50Kb. [Hint use some bacterial genome] Deadline: 6th Sept