CSC 314**, Bioinformatics Lab #2B Name:\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

**DNA and Complementary Base Pairing**

DNA is a double stranded molecule composed of complementary base pairs. If the sequence of one strand is known, the *complementary sequence* (***complement***) can be determined based on the following rules: adenine (A) binds with thymine (T) and vice-versa; and cytosine (C) binds with guanine (G) and vice-versa.

If a sequence is read from its 5' to 3' end, its ***reverse***is the same sequence read from its 3' to 5' end (and vice-versa). A sequence and its complement are also *anti-parallel* (they go in opposite directions)

The ***reverse-complement*** of a DNA sequence is the reverse of its complement (or, equivalently, the complement of its reverse).

1. Find the specified sequences based on the sequence below. Note that your answers must include labels for the 5’ and 3’ ends. This is the **original** sequence:

5'-GTTACC-3'

1. Find the reverse of the *original* sequence
2. Find the complement of the *original* sequence
3. Find the reverse-complement of the *original* sequence
4. If the original sequence (5'-GTTACC-3’) was an RNA sequence instead of a DNA sequence, what would its sequence be?
5. Complete the Lab 2B Python Jupyter Notebook that prompts the user to enter a sequence, formats the sequence for invalid characters, outputs the sequence and is length, and finds the complement, reverse-complement, and determines whether the sequence contains a *start codon*.
6. Respond to the questions posted on Piazza, related to the Implications of Cheap Genomic Sequencing.

***Note: You may use your grace period for questions 1 and 2 but you must respond on Piazza by the due date.***