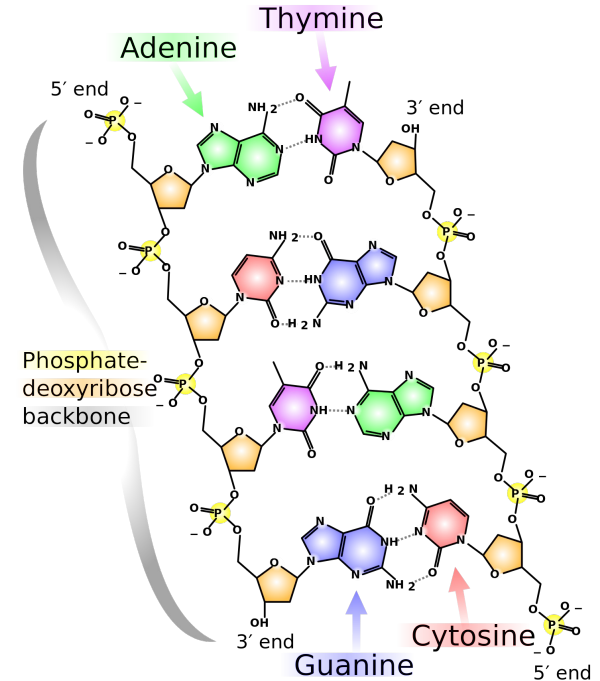


String Coding



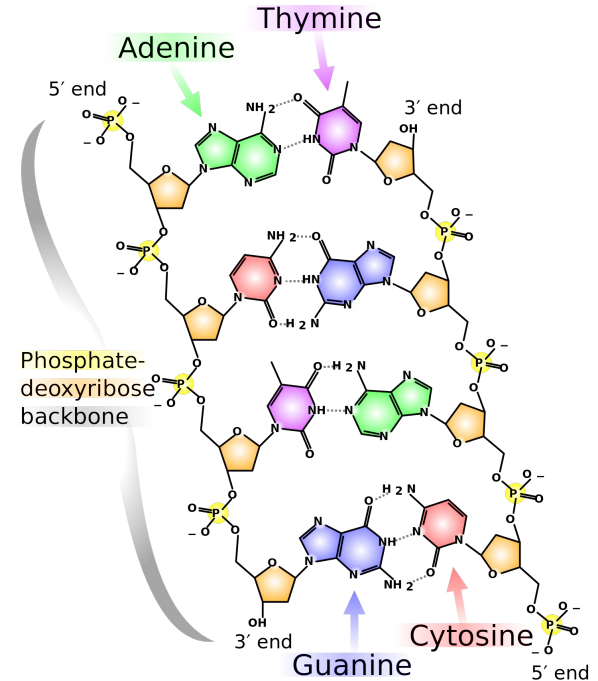
Part 1: Counting Base Pairs

- Scan in a string (using `fgets()`) consisting of C, G, A, and T
- Print out the number of C's, G's, A's and T's as output



Part 2: Analyzing GC Content

- Using your count from part one, calculate the percentage of the string that consists of G's or C's.
 - If the GC content is $> 60\%$, print “extron”
 - If the GC content is $< 50\%$, print “intron”
 - Else, print that the purpose is unknown



Part 3: Reverse Complement

- When copied, DNA is flipped ($A \rightarrow T$, $T \rightarrow A$, $C \rightarrow G$, $G \rightarrow C$) AND reversed, becoming a *reverse complement*. In addition to the information printed in Parts 1 and 2, print the reverse complement of the scanned DNA string.

- Example:
 - Normal: AAAACCGGT
 - RC: TCCGGTTTT

