Name: _____________________________
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Honor code acknowledgment (signature) _____________________________

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The method `dimerOccurrences` below returns the number of occurrences of a specific dimer (two-nucleotide strand) in dna; it works correctly. For example, if `ds` is an object/instance of the class `DNAStuff` then

```java
int x = ds.dimerOccurrences("AGTCCGATCGCGAT", "CG");
int y = ds.dimerOccurrences("AGTCCGATCGAG", "AG");
```

gives x the value 3 and y the value 1. You’ll be asked to write code based on `dimerOccurrences`. We’re assuming an ORF of 1, i.e., we’re starting with the first character.

```java
public class DNAStuff {
    public int dimerOccurrences(String dna, String dimer){
        int count = 0;
        for(int k=0; k < dna.length()-1; k+=2){
            String sub = dna.substring(k,k+2);
            if (dimer.equals(sub)){
                count = count+1;
            }
        }
        return count;
    }
}
```

**Part A (2 points)**

Why does the loop use `k < dna.length()-1` instead of `k < dna.length()` in the loop-guard shown above?

**Part B (2 points)**

Why does the code use `.equals` instead of `==` in comparing dimers?
Part C (8 points)
Complete the method `maxDimer` that returns the dimer that occurs most frequently in a strand of DNA. The call below should return "CG" since that dimer occurs more frequently than any other.

```java
ds.maxDimer("AGTCCGATCGCGAT")
```

You may call `dimerOccurrences` in the code you write, both that method and `maxDimer` are in the same class: DNAStuff.

```java
public class DNAStuff {
    public int dimerOccurrences(String dna, String dimer) {
        // as shown above, not repeated
    }
    
    /**
     * Returns the dimer that occurs with maximal frequency in parameter dna
     * @param dna is a string with only chars 'A', 'G', 'T', 'C'
     * @return the maximally occurring dimer in dna
     */
    public String maxDimer(String dna) { 
        
    }
}
```
Part D (8 points) The molecular weight of a strand of DNA is calculated by the following formula (this is the real formula) where \( n_A \) is the number of occurrences of (A) Adenine, \( n_T \) is the number of (T) Thymine occurrences, and so on.

\[
18.02 + (n_A \times 313.21) + (n_T \times 288.20) + (n_G \times 329.21) + (n_C \times 289.19)
\]

Write the method `molecularWeight` that returns the molecular weight of a strand of DNA. The parameter `strand` will contain only the characters 'A', 'T', 'C', and 'G'.

```java
class DNAStuff {
    /**
     * Returns the molecular weight of a strand of DNA based on the standard formula.
     * @param strand is dna (all chars are 'A', 'G', 'T', 'C') whose weight is returned
     * @return the weight of strand
     */
    public double molecularWeight(String strand) {
```

}