1 import java.io.\*;  
 2 import java.lang.\*;  
 3 import java.util.\*;  
 4   
 5 public class DNA {  
 6 public static void main(String[] args) {  
 7 Scanner scanner = new Scanner(System.in);  
 8 System.out.println("This program reports information about DNA");  
 9 System.out.println("nucleotide sequences that may encode proteins.");  
 10 System.out.print("Input file name? ");  
 11 String fileName = scanner.next();  
 12 System.out.print("Output file name? ");  
 13 String fileName2 = scanner.next();  
 14 File fileIn = new File(fileName);  
 15 File fileOut = new File(fileName2);  
 16 readData(fileIn, fileOut);  
 17 }  
 18   
 19 public static void readData(File fileIn, File fileOut) {  
 20 String[] regionName = new String[9];  
 21 String[] nucleotides = new String[9];  
 22   
 23 try {  
 24 Scanner in = new Scanner(fileIn);  
 25 int counter = 0;  
 26 int i = 0;  
 27 int j = 0;  
 28   
 29 while (in.hasNextLine()) {  
 30 if (counter % 2 == 0) {  
 31 regionName[i] = in.nextLine();  
 32 i++;  
 33 } else {  
 34 nucleotides[j] = in.nextLine();  
 35 j++;  
 36 }  
 37 counter++;  
 38 }  
 39   
 40 in.close();  
 41 } catch (FileNotFoundException e) {  
 42 e.printStackTrace();  
 43 }  
 44   
 45 readyData(regionName, nucleotides, fileOut);  
 46 }  
 47   
 48 public static void readyData(String[] regionName, String[] nucleotides, File fileOut) {  
 49 String printStuff = "";  
 50 for (int i = 0; i < regionName.length; i++) {  
 51 String nucs = nucleotides[i];  
 52   
 53 // Puts all the nucleotides in an array  
 54 int stopper = nucs.length() / 3;  
 55 String[] nucPrint = new String[stopper];  
 56 for (int j = 0; j <= stopper - 1; j++) {  
 57 nucPrint[j] = nucs.substring(0, 3);  
 58 nucs = nucs.substring(3, nucs.length());  
 59 }  
 60 double totalMass = 0;  
 61 double[] mass = new double[4];  
 62 double[] values = {135.128, 111.103, 151.128, 125.107};  
 63 double junk = 100.0;  
 64 int[] counter = new int[4];  
 65 int useless = 0;  
 66 String isIt = "NO";  
 67 for (int j = 0; j < nucPrint.length; j++) {  
 68 for (int k = 0; k < 3; k++) {  
 69 char letter = nucPrint[j].toLowerCase().charAt(k);  
 70 if (letter == 'a') {  
 71 counter[0]++;  
 72 } else if (letter == 'c') {  
 73 counter[1]++;  
 74 } else if (letter == 'g') {  
 75 counter[2]++;  
 76 } else if (letter == 't') {  
 77 counter[3]++;  
 78 } else {  
 79 useless++;  
 80 }  
 81 }  
 82 }  
 83 for (int j = 0; j < 4; j++) {  
 84 mass[j] = counter[j] \* values[j];  
 85 }  
 86   
 87 for (double j : mass) {  
 88 totalMass += j;  
 89 }  
 90 totalMass += useless \* junk;  
 91 for (int j = 0; j < 4; j++) {  
 92 mass[j] = Math.round(((counter[j] \* values[j]) / totalMass) \* 1000.0) / 10.0;  
 93 }  
 94   
 95 if (nucPrint.length >= 5) {  
 96 isIt = "YES";  
 97 }  
 98 printStuff += "Region Name: " + regionName[i] + "\n";  
 99 printStuff += "Nucleotides: " + nucleotides[i].toUpperCase() + "\n";  
100 printStuff += "Nuc. Counts: " + Arrays.toString(counter) + "\n";  
101 printStuff += "Total Mass%: " + Arrays.toString(mass) + " of " + (Math.round(totalMass \* 10.0) / 10.0) + "\n";  
102 printStuff += "Codons List: " + Arrays.toString(nucPrint).toUpperCase() + "\n" + "\n";  
103 printStuff += "Is Protein?: " + isIt + "\n" + "\n";  
104 }  
105   
106 printData(printStuff, fileOut);  
107 }  
108   
109 public static void printData(String stuffPrint, File fileOut) {  
110 try {  
111 PrintStream printStream = new PrintStream(fileOut);  
112 printStream.print(stuffPrint);  
113 printStream.close();  
114 } catch (FileNotFoundException e) {  
115 e.printStackTrace();  
116 }  
117 }  
118 }  
119