```
Program  = cop2270pgm4f
COP 2270 - C FOR ENGINEERS
Professor: Michael Robinson
e-mail   : michael.robinson@fiu.edu
Web Page : www.cs.fiu.edu/~mrobi002/teaching


Insert the following section in your program
/*********************************************************************
Author:        Your Name
Course:        COP 2270 t/th 12:30PM-01:50PM
Professor:     Michael Robinson
Program #:     Program cop2270pgm4f
Due Date:      ??/??/2012

Certification:
I hereby certify that this work is my own and none of it is the work of any other person.



.........{                                  }..........
*********************************************************************/
```

Worth 2 points
- Assign your name to a char data type
- Using the loop of you choice in one line print the vowels in your name ONLY
  and in another line your name WITHOUT vowels

Worth 5 points
- Download the file called 1200.dna from:
  http://users.cis.fiu.edu/~mrobi002/downloads/samples/1200.dna
  - open this file.
  - load it into a one dimension array or a String, your choice
    this file contains nueclotides/bases/letters in it such as a, c, g, t, and others.
  - Find out the total amount of neuclotides UPPER and LOWER cases a, how many c, how many g, how many t
    and how many all others are in this file.
    Make sure to test for upper and lower cases of each a,c,g,t, and others base.
  - Print the first and the last neuclodide in the file, and using the ceil() method print the one
    exactly in the middle of the file

Worth 3 points
- Download the file called pa01Probes.dna from:
  http://users.cis.fiu.edu/~mrobi002/downloads/samples/pa01Probes.dna
  - open this file.
  - this file contains sequences of length 5 each
    find out how many sequences there are
    find out which sequences have duplicates, if any
    find out if these sequences are sorted, HINT : swap