User-ID:	Name:
----------	-------

BIOMED 201 - Programming & Modeling for BME

Midterm Exam, 2012.11.06, Instructor: Ahmet Sacan

Sign the honor code below. No credit will be given for the exam without a signed pledge.

I have neither given nor received aid on this examination.

Signed:

There are 9 questions in this exam. <u>Turn in Questions 1-8 before you start working on Questions 9-10</u>. Submit your programs for Questions 9-10 on ProgrammingBank, in addition to turning in your paper exam. Sign off your submission before exiting the room.

Q1 (5 pts). *Indexing.* Let **A** be a square matrix with **R** rows. Write a single statement that will set the diagonal elements of A to zero. Do not use loops.

```
A(1:R+1:end)=0
```

Q2 (5 pts). *Creating vectors.* Fill in the blanks below with what Matlab would display for the given expression.

```
>> [ [5:3] 1 [2:4] repmat([1 2],1,2) ]
ans =
    1 2 3 4 1 2 1 2
```

Q3 (5 pts). Binary and hexadecimal numbers. In the first box below, write down the binary representation of the decimal number 256. In the second box, write down the hexadecimal representation of the decimal number 256.

```
10000000
```

0x**100**

User-ID: _____ Name: ____

scope. Fill in the blanks in the output.

Q5 (5 pts). *Indexing*. Let M be a matrix with 100 rows and 200 columns. M(12345) can equivalently be expressed as M(x,y). What is the value of y?

```
function y = orange(x)

y = x + 5;
```

124

Q6 (5 pts). Vectorizing code, element-wise operations, logical indexing. Let **X,Y,Z,M** be column matrices with the same size. Rewrite the for loop below without any using loops. You may define additional variables.

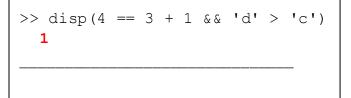
```
for i=1:numel(X)
  if (X(i)<Y(i)) && ...
    (X(i)^2+Y(i)^2 ==Z(i)*Z(i))
  M(i) = X(i)/Y(i);
  else
  M(i) = X(i)*Y(i);
  end; end</pre>
I = (X<Y) & (X.^2+Y.^2==Z.^2);
  M(I) = X(I)./Y(I);
  M(~I) = X(~I).*Y(~I);</pre>
```

Q7 (10 pts). *Nested for loops.* Fill in the blanks in the output below.

```
>> x = zeros(2,0);
>>  for a = [ 0 5 ]
     for b = [10 20]
>>
       x(end:-1:1,end+1:end+2) = [ab;a+1b+1];
>>
>>
     end
>> end
>> disp ( x )
    1
         11
                     21
                           6
                                11
                                       6
                                            21
    0
         10
                0
                     20
                           5
                                10
                                       5
                                            20
```

Q8 (10 pts). Operator precedence, logic. Fill in the blanks in the outputs below.

```
>> x=20;
>> disp( -3 <= x <= 3 )
1
```



User-ID: _____ Name: ____

```
>> X=randi(2,1,10)-1;
>> disp(all(x) && ~any(x))
0
```

```
>> x=[0 0 1 1]; y=[0 1 0 1];
>> disp(xor(x,y) & xor(~x,y))
0 0 0 0
```

I have neither given nor received aid on this examination.

Time of submission:

Signed:

Q9 (25 pts). Selection statements, loops or vectorized code. Write a function **getaframe(R,C,s)** that takes the number of rows and columns and returns a character matrix that has the shape of a rectangular frame. The frame will be drawn using the third input s, and the inner part will be filled in with blank space, as shown below. Assume that R and C are positive integers and that s is a single character.

```
>> getaframe(6,5,'*')
ans =

****

* *

* *

* *

* *
```

Q10 (25 pts). *Loops or vectorized code.* Write a function **reverse complement dna(s)** that takes a strand of DNA and returns its reverse complement and the number of hydrogen bonds formed between the two strands. Consider the following single-stranded DNA, written from 5' end to the 3' end: 5'-ATGCATGGC-3'

The complementary strand of the above DNA segment can be written by replacing A with T, T with A, G with C, and C with G.

```
3'-TACGTACCG-5'
```

The reverse complement is than obtained by writing the complementary strand from 5' end to 3' end: 5'-GCCATGCAT-3'

The complementarity of the nucleotides is determined by the hydrogen bonds formed between the nucleotides. There are two hydrogen bonds between A and T, and there are three hydrogen bonds

between C and G. In the following double-stranded DNA,

5'-ATGCATGGC-3'

3'-TACGTACCG-5'

complementary bases form a total of 23 hydrogen bonds.

NOTE: Do not use functions from the bioinformatics toolbox to solve this problem.

```
>> [rc,bonds] =
reversecomplementdna('ATGCATGGC')
rc =
GCCATGCAT

bonds =
   23
```