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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. **Turn in Questions 1-8 before you start working on Questions 9-10.** 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
```

```
0x100
```

```
>> x=5; y=10;  
>> y=apple(x); x=orange(x);  
>> [x y]  
ans =  
    10    20
```

Q4 (5 pts). *Variable*

```
function x = apple( x )  
y = x+3;  
x = 2 * orange(x);
```

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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;
```

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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
```

```
I = (X<Y) & (X.^2+Y.^2==Z.^2);  
M(I) = X(I)./Y(I);  
M(~I) = X(~I).*Y(~I);
```

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) = [ a b; a+1 b+1 ];  
>>     end  
>> end  
>> disp ( x )  
    1    11    1    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
```

```
>> disp(4 == 3 + 1 && 'd' > 'c')  
1
```

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```
>> 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 =

*****
*      *
*      *
*      *
*      *
*****
```

```
>> getaframe(5,15,'/')
ans =

//////////////////
/                  /
/                  /
/                  /
//////////////////
```

Q10 (25 pts). *Loops or vectorized code.* Write a function **reversecomplementdna(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 then 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.

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

bonds =
    23
```

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