Drexel-Email-ID: _____ Name: _____ Expected Course Grade: _____

BIOMED 201 - Programming & Modeling for BME

Final Exam, 2011.12.01, 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 10 questions in this exam. Turn in Questions 1-7 before you start working on Questions 8-10. Submit your programs for Questions 8-10 on BBVista, in addition to turning in your paper exam.

Q1 (5 pts). *Indexing.* Let **A** be a matrix of any size. Write a single statement that will assign into B, the odd rows of A. e.g., if A is a 5x4 matrix, B will become a 3x4 matrix containing the 1st, 3rd, and 5th rows of A. Your code should work for any sized matrix A. Do not use loops.

```
B = A(1:2:end, :)
```

Q2 (5 pts). *Linear Indexing.* If matrix **M** has 5 rows and 7 columns, **M(4,3)** can equivalently be expressed as **M(x)**. What is the value of **x**?

```
14
```

Q4 (5 pts). *Logical Indexing.* Let **M** be a matrix of any size. Replace each element of M that is divisible by 3 with its square-root. Do not use loops.

```
I = mod(M,3)==0;

M(I) = M(I).^.5
```

Q5 (5 pts). *structs.* Fill in the blanks in the output. *Hint:* If **A** is a struct, there is a difference between **A.B** and **A.(B)**

```
>> points = struct( 'x', 1, 'y', 3);
>> points(2) = struct( 'x', 2, 'y', 4);
>> x='y';
>> disp( sum( [ points.(x) ] ) )

    7
```

Q6 (10 pts). *cells*. Fill in the blanks in the outputs below.

```
>> m = { 'a', 1:100; 7:8, 'hello'; 9, [ ] }
>> size(m)

   3   2

>> size( m(2) )

   1   1

>> size( m{2} )

   1   2
```

Q7 (10 pts). *string functions*. Fill out the outputs below.

```
>> disp( strcmp('flow crow','ow') )

     0

>> disp( strcmpi({'a','b','A','b'},'a') )

     1     0     1     0

>> disp( strfind('flow crow','ow') )

     3     8

>> disp( strrep('flow crow','ow','y') )

fly cry
```

Drexel-Email-ID: _____ Name: _____ Expected Course Grade: _____

I have neither given nor received aid on this examination.

Time of submission: _____

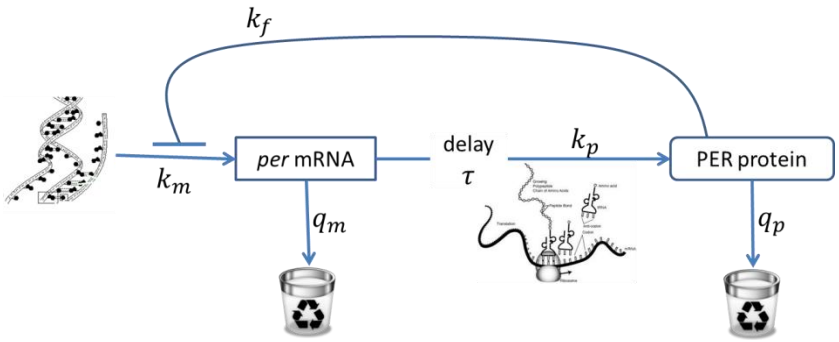
Signed: _____

Q8 (20 pts). *strings, file IO.* Write a function **filegrep(file, needle)** that takes a file name **file** and a string **needle**, and returns the number of times the string appears in the file. Perform a case-insensitive (i.e. ignore the case) search in the file.

```
>> filegrep('adventure1.txt','the')
ans =
    31
>> filegrep('adventure1.txt','ThE')
ans =
    31
>> filegrep('adventure1.txt','holmes')
ans =
     3
>> filegrep('adventure1.txt','Sherlock Holmes')
ans =
     1
>> filegrep('adventure1.txt','orange')
ans =
     0
>> filegrep('c:/windows/notepad.exe','privilege')
ans =
     2
```

Q9 (20 pts). *data analysis.* Write a matlab function **crps_gettopmirnas(k)**, that returns a k-by-2 cell array of top-k most significantly differentially expressed miRNAs, with the first column containing mirna names, and the second column contains the p-value for each miRNA obtained from a ttest2(), comparing the miRNA levels between CRPS patients and controls. The returned list of miRNAs should be sorted by their p-values (i.e., the most significantly differentially expressed miRNA has smallest p-value and should be listed in the first row). If a value for **k** is not given, use k=5. Write below, the name of the most significantly differentially expressed miRNA.

Q10 (20 pts). Many organisms, including animals, plants, and cyanobacteria undergo 24 circadian hour rhythms in their physiology and behavior. This rhythm is observed even in constant dark conditions and is guided by internal molecular oscillators. The intracellular circadian rhythm is believed to be a result of the time delay in protein production and the negative feedback loops causing auto-inhibition of gene expression. This phenomena is illustrated in the following simplified model (Schepper et al., J of Neuroscience, 1999, 19:40-47) for expression of the period gene *per* in Drosophila.



The system above can be mathematically modeled using the following two differential equations that calculate the rate of change in the concentrations of *per* mRNA (**M**) and PER protein (**P**).

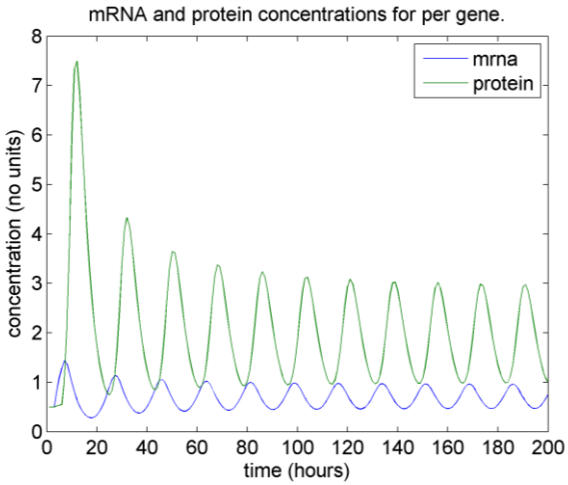
$$\frac{\delta M}{\delta t} = \frac{k_m}{1 + \left(\frac{P}{k_f}\right)^2} - q_m M$$

$$\frac{\delta P}{\delta t} = k_p M_{t-\tau}^3 - q_p P$$

where $\mathrm{k_m}$ is mRNA transcription rate, $\mathrm{k_p}$ is rate of translation from mRNA to protein, $\mathrm{q_m}$ is mRNA degradation rate, $\mathrm{q_p}$ is protein degradation rate, $\mathrm{k_f}$ is a scaling factor for the auto-inhibition of transcription by the protein, and τ is the time delay for production of protein. All rates are in $hour^{-1}$ and the time delay is in $hours$. In order to simulate this model, we will take $\Delta t = 1hour$, and we will consider only integer values of the time delay τ. The concentrations of M and P in time step $t+1$ can be written as:

$$M_{t+1} = M_t + \frac{k_m}{1 + \left(\frac{P_t}{k_f}\right)^2} - q_m M_t$$

$$P_{t+1} = P_t + k_p M_{t-\tau}^3 - q_p P_t$$



Write a script **bioclock.m** that simulates the concentrations of M and P for the first 200 time steps. Use the following parameter values: $k_m = 1, k_p = 1, k_f = 1, q_m = 0.21, q_p = 0.21, \tau = 4$. Use initial concentrations: $M_1 = 0.5$ and $P_1 = 0.5$, and assume that the concentrations of mRNA and protein do not change for the first τ steps. Plot the mRNA and protein concentrations over time, as shown on the right. Remember to add axes labels, title, and legend to your figure.