

BIOMED 201 - Programming & Modeling for BME

Final Exam, 2012.06.12, 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 ProgrammingBank, 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**, every third column of **A**. e.g., if **A** is a 4x9 matrix, **B** will become a 4x3 matrix containing the 1st, 4th, and 7th columns of **A**. Your code should work for any sized matrix **A**. Do not use loops.

```
B = A(:, 1:3:end)
```

Q2 (5 pts). *Linear Indexing.* Let matrix **M** be a square matrix of **R** rows and **R** columns. Write a single statement that sets the diagonal elements of **M** to zero. Diagonal elements are defined as **M(i,i)**, where **i=1,2...R**. Do not use loops.

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

Q3 (5 pts). *Logical Indexing.* Let **A** be a matrix of any size. Write a single statement that will assign into **B**, the columns of **A** whose sum is zero. e.g., if **A** is [2 -3 4; -4 4 6; 3 -1 1], **B** will be [-3; 4; -1], which is the only column of **A** whose sum is zero. Your code should work for any sized matrix **A**. Do not use loops.

```
B = A(:, sum(A)==0)
```

Q4 (5 pts). *structs.* Fill in the blanks in the output.

```
>> points = struct('a', {1 2 5}, 'b', {3 4 7}, 'c', {5 10 15});
>> disp(sum([points.(char('a'+1)) ] ) )
```

```
14
```

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

```
>> m = { 'a' 1:2 {7:8} ; 'hello' 9 [ ] }
>> size(m)

2 3
>> size( m(2) )

1 1
>> size( m{2} )

1 5
>> [ m{3} m{5}{1} ]

1 2 7 8
```

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

```
>> disp( strcmp('flow', char('gmpx'-1)) )

1
>> disp( find( strcmpi({'flow','crow','ow','bow'}, 'ow') ) )

3
>> s='flow crow'; disp( s(strfind(s,'cr'):end) )

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

fly cry
```

I have neither given nor received aid on this examination.

Time of submission: _____

Signed: _____

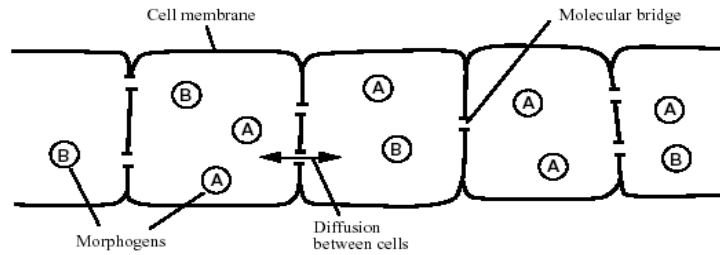
Q8 (20 pts). *data analysis.* Write a matlab function **crps_pvalue(factor)**, that takes a string factor and returns the p-value of the difference of that factor between CRPS patients and controls. Fill in the blanks in the following output.

```
>> disp( crps_pvalue( 'mir-223' ) )  
    0.1541  
>> disp( crps_pvalue( 'mir-191' ) )
```

Q9 (20 pts). *strings, file IO.* Write a function **decryptstory(file, code)** that takes a file name **file** and an integer **code** returns the decrypted contents of the file. Assume the file has been encrypted by shifting each letter by **code** according to its alphabetical order. E.g., encrypting 'applez' by code=2 would result in 'crrngb'. Notice that if adding the code results in a letter passed 'z', you wrap around and continue from 'a' (thus, 'z'+2 gives 'b').

```
>> decryptstory('secretstory.txt',1)  
ans =  
  
adventure i. a scandal in bohemia  
  
i.  
  
to sherlock holmes she is always the woman. i have seldom heard  
him mention her under any other name. in his eyes she eclipses  
and predominates the whole of her sex. it was not that he felt  
any emotion akin to love for irene adler. all emotions, and that  
  
...[the rest of the output is not shown]
```

Q10 (20 pts). Reaction and diffusion of a few substances (morphogens) can generate a vast number of patterns seen in developmental biology. In this problem, we will consider a 1-dimensional arrangement of N cells and the reaction-diffusion of 2 morphogens **A** and **B**, as illustrated below. You will simulate the reaction-diffusion of **A** and **B** over T discrete time steps.



Concentrations of A and B at each time point are calculated from their concentrations at previous time point. Furthermore, the concentrations in the i^{th} cell depend on the concentrations in its neighbor cells. The change in concentrations of A and B are described by the following formulas:

$$\Delta a_i = D_a(a_{i+1} + a_{i-1} - 2a_i) + k(16 - a_i b_i)$$

$$\Delta b_i = D_b(b_{i+1} + b_{i-1} - 2b_i) + k(a_i b_i - b_i - \beta_i)$$

Where a_i , b_i , and β_i are the concentrations of the morphogens A and B and a substrate β in the i^{th} cell; D_a and D_b are the diffusion rates of the morphogens, and k is the reaction rate.

Write a function `reaxdiff1d.m` that takes N and T as input and simulates the reaction-diffusion of A and B. Use the following values for constants: $D_a = 0.25$, $D_b = 0.0625$, $k = 0.003125$. The initial values of a_i and b_i in all of the N cells is 4. The initial values of β_i should be random numbers between 12 and 12.05. Assume that a_1 , b_1 , a_N , and b_N do not change during the entire simulation (i.e., you only need to update concentrations of cells 2 to $N-1$). Your function should plot the final concentrations of A and B on the same plot, as shown in the following example. Your plot should contain the title, axis labels, and legend. Note that, since the values of β_i are set randomly, your simulation may provide a different plot than shown below.

