

ID (e.g., ab1234): _____ Name: _____ Expected Course Grade (+5pts): _____

BMES201 - Programming & Modeling for BME | Final, 2016.06.03, Instructor: Ahmet Sacan

Turn in your exam paper before you start working on programming questions. Submit your code for Questions 7 and 8 on ProgrammingBank. Sign the sign-out sheet before leaving the room.

Q1 (10 pts). *Vectorized code.* Let **C** and **r** be real numbers, and **n** a positive integer. Write a single statement to assign into **P**, the value of the following sum. Do not use loops.

$$P = C + C(1+r) + C(1+r)^2 + C(1+r)^3 + \dots + C(1+r)^n$$

```
P = C * sum( (1+r) .^(0:n) )
```

Q2 (10 pts). *Logical Indexing.* Consider the matrix **m** shown as a table below. Fill in the output below.

8	6	7	16	13
14	1	20	16	15
4	2	1	4	16
15	17	9	10	6
1	14	8	9	14

```
>> disp( m(logical([0 1 0 1 0]),[1 end]) );
```

```
14    15
15     6
```

Q3 (10 pts). *Strings.* Fill in the output below.

```
>> s='apple,orange,banana,cherry,berry';
>> I=strfind(s,',' );
>> disp( s( I(2)+1:I(3)-1 ) )
banana
```

Q4 (10 pts). *Loops, min.* What is the value of **s** after the following statements?

```
v=[11 14 18 20 11 3 2 6 17 6];
s=0;
for i=1:2;
    [x,I]=min(v);
    v(I)=[];
    s = s+I; end
```

- (A) [] (B) 0 (C) 1
(D) 2 (E) 3 (F) 5
(G) 8 (H) 13 (I) 18
(D) 55 (E) 36 (C) 108

ID (e.g., ab1234): _____ Name: _____

Q5 (10 pts). *structs, indexing.* What is the value of **s** after the following statements?

```
p=struct('a', {1 2}, 'b', [5 10], 'c', 7);  
s=sum([ p.(char('a'+1)) ] )
```

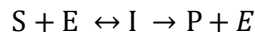
- (A) 0 (B) 3 (C) 5 (D) 6 (E) 15 (F) 17 (G) 25 (H) 30 (I) 36

Q6 (10 pts). *Cells, indexing.* What is the value of **v** after the following statements?

```
gender={'m' 'f' 'M' 'm' 'f' };  
data=[5 7 1 9 2; 2 3 8 6 4];  
I=strcmpi(gender, 'm');  
v = data(2,~I)
```

- (A) 0 (B) 1 (C) [] (D) [5 1 9] (E) [7 2] (F) [2 8 6] (G) [3 4]
(H) [5 1 9; 2 8 6] (I) [7 2; 3 4] (J) [5 7 1 9 2; 2 3 8 6 4] (K) 47

Q7 Programming (20 pts). Consider the following enzymatic reaction:



where E is the enzyme, S is the substrate, I is the enzyme-substrate intermediate complex, and P is the product. The change in concentrations of these four species per second can be described by the following differential equations:

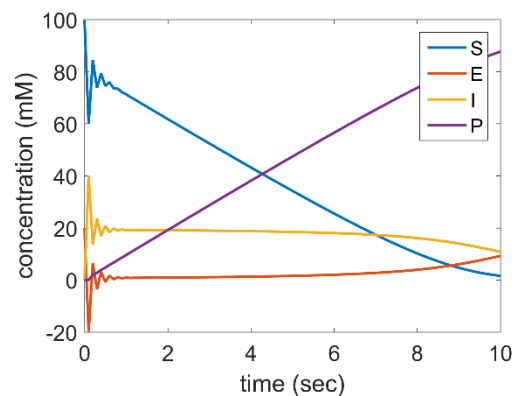
$$\Delta S = -k_1ES + k_2I$$

$$\Delta E = -k_1ES + k_2I + k_3I$$

$$\Delta I = k_1ES - k_2I - k_3I$$

$$\Delta P = k_3I$$

where concentrations are in mM, and reaction rates are given per second. Write a function **[T Y] = enzymesimulation(Y0, K, deltat, totaltime)** that takes in the initial concentrations of **S, E, I, P** in a 1x4 vector **Y0**; the reaction rates **k1, k2, and k3** in a 1x3 vector **K**; the length of each simulation time step **deltat**; and duration of the entire simulation **totaltime**. Return the time vector **T** as a single column vector (from time=0 up to time=**totaltime**, with time step of **deltat**); and the concentrations of the four species throughout the simulation as a 4-column matrix **Y**. Also plot the concentrations of the species across the simulation. If **deltat** is not provided, use **deltat=0.1** sec; if **totaltime** is not provided, use **totaltime=10** secs. Note that some of the concentrations may become negative, which is unrealistic, but we don't attempt to fix that in this model.



```
>> [T Y]=enzymesimulation([100 20 0 0], [0.2 0.1 0.5], 0.1, 0.4)
```

```
>> [T Y] % Showing T and Y together for brevity.
```

```
ans =
```

```
      0  100.0000   20.0000         0         0  
  0.1000   60.0000  -20.0000   40.0000         0  
  0.2000   84.4000    6.4000   13.6000    2.0000  
  0.3000   73.7328   -3.5872   23.5872    2.6800  
  0.4000   79.2586    3.1179   16.8821    3.8594
```

Q8 Programming (20 pts). *File I/O, strings.* Identifier and name conversion is one of the common tasks in Bioinformatics. In this problem, you will write a function **symbol=geneid2symbol_xml(id,filename)** that will

ID (e.g., ab1234): _____ Name: _____

return the symbol of a gene, given its GeneID, looked up from a given file. Each line in the file contains information about a gene, where each information field is formatted as <fieldname>fieldvalue</fieldname>. For example, the gene with ID 5961937 is given on a single line as (the textbox below uses line-wrapping):

```
<gene> <taxid>33</taxid> <geneid>5961937</geneid> <symbol>pMF1.23</symbol>
<description>hypothetical protein</description> </gene>
```

Download and use the sample file available from <http://sacan.biomed.drexel.edu/ftp/bmeprog/geneinfo.xml>. You should manually download this file (either using your browser or `urlwrite()` in command window); do not try to download the file within your function. If filename is not given, use `geneinfo.xml` by default. If it is given (may be different than `geneinfo.xml`), use the filename provided as input. The gene id input to your function can be a string or a number.

```
>> disp(geneid2symbol_xml(1246500,'geneinfo.xml'))
repA1
>> disp(geneid2symbol_xml('4362664','geneinfo.xml'))
Ip21p11
```