

BIOMED 201 - Programming & Modeling for BME

Final Exam, 2014.12.08, 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 **7 questions** in this exam. Turn in your paper exam before you start working on Questions 6-7. Submit your programs for Questions 6-7 on ProgrammingBank.

Q6 (30 pts). *Loops.* Write a function **b=wsmooth(a)** that takes a vector **a** of length $n \geq 2$ and employs a weighted moving average smoothing and returns the resulting vector **b**. The first and last elements of **a** remain unchanged; the rest of the elements are smoothed as shown below.

$$\begin{aligned} b_1 &= a_1 \\ b_2 &= \frac{a_1}{4} + \frac{a_2}{2} + \frac{a_3}{4} \\ b_3 &= \frac{a_2}{4} + \frac{a_3}{2} + \frac{a_4}{4} \\ b_4 &= \frac{a_1}{4} + \frac{a_2}{2} + \frac{a_3}{4} \\ &\dots \\ b_{n-1} &= \frac{a_{n-2}}{4} + \frac{a_{n-1}}{2} + \frac{a_n}{4} \\ b_n &= a_n \end{aligned}$$

```
>> disp(wsmooth([4 2 4]))
     4     3     4

>> disp(wsmooth([4 2 2 4]))
     4.0000     2.5000     2.5000     4.0000

>> disp(wsmooth(1:8))
     1     2     3     4     5     6     7     8

>> disp(wsmooth([5 5 5 5 5 5]))
     5     5     5     5     5     5
```

Q7 (20 pts). *Strings, File, Loops.* Identifying the proteins a drug binds to is useful for determining its side-effects and for finding other diseases the drug can be used for. Drugbank is a database that collects information about drugs and their target proteins. In this problem, you will write a function that uses a Drugbank text file and returns a list of proteins that a drug binds to. An example Drugbank file can be downloaded from http://sacan.biomed.drexel.edu/ftp/bmeprog/drugbank_targets_sample.csv. The drugbank file is a comma separated file, where the first row is the header row, and each of the other rows contains information on a protein and lists the drugs it binds to. For each protein, the numerical drug ids are represented by a 7-character string with a prefix of 'DB' and separated by semicolons. Write a function **drug2ptns(drugid,file)** that takes a drug id and a drugbank file and returns all the protein ids the drug is listed to bind, as a cell array of strings. The drug id given to your function can be either a string with the 'DB' prefix, or a number.

```
>> disp(drug2ptns('DB00117','drugbank_targets_sample.csv'))
     'P19113'

>> disp(drug2ptns('DB00114','drugbank_targets_sample.csv'))
     'P19113'     'P06737'

>> disp(drug2ptns('DB00303','drugbank_targets_sample.csv'))
     'P45059'

>> disp(drug2ptns(117,'drugbank_targets_sample.csv'))
     'P19113'
```

Q1 (10 pts). *Base conversion.* Write the decimal number **65** in **binary** and in **base-5**.

binary: 1000001	In base 5: 230
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Q2 (10 pts). *Vectorized code.* Let **n** be an even number. Write a single statement to assign into **s** the value of the following sum. Do not use loops.

$$s = 1 - 2 + 3 - 4 + \dots + (n - 1) - n$$

s = **sum((1:2:n-1) - (2:2:n))**

Q3 (10 pts). *structs, indexing.* Fill in the output below.

```
>> p=struct('a', {3 5 7 11 13 17}, 'b', {19 23 29 31 37 41});
>> disp( [p( mod([p.a],5)==2).b ] )
```

29 41

Q4 (10 pts). *cells.* Fill in the output below.

```
>> m={ [1 5] {1 10}; 1:20 {1:30} };
>> disp([numel(m(1:3)) numel(m{1}) numel(m{2}) numel(m{end}) numel(m{end}{1})])
```

3 2 20 1 30

Q5 (10 pts). *cells, indexing.* Fill in the output below.

```
>> s='mouse';
>> dict={'human',3; 'mouse',7; 'fruitfly',11};
>> I=strcmp(dict(:,1),s);
>> dict{I,2} = dict{I,2} +1;
>> disp([ dict{:,2} ]);
```

3 8 11
