BIOMED 201 - Programming & Modeling for BME

Final Exam, 2014.06.10, 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 **8 questions** in this exam. <u>Turn in your paper exam before you start working on Questions 7-8</u>. Submit your programs for Questions 7-8 on ProgrammingBank.*

Q7 (25 pts). *Data analysis.* Write a function **xls_diffcorr(xlfile,var1,var2,targetvar)** that reads the data contained in an Excel file **xlfile** and returns the correlation between the difference in values of **var1** and **var2** and the **targetvar** values. The first row of the Excel file is a header row containing the names of each data column. Each of the **var1**, **var2**, and **targetvar** is a string that refers to a data column. Perform case insensitive comparison when determining the column number from the variable name. A sample Excel file is available from **http://sacan.biomed.drexel.edu/ftp/bmeprog/crps_data.xlsx**

```
>> disp( xls_diffcorr('crps_data.xlsx','il-4','TNFa','pain') )
    0.1654
```

Q8 (25 pts). *Strings, File, Loops.* ChIP-seq is used to identify genomic segments bound by transcription factors. In a ChIP-seq experiment, you obtain the chromosome regions that the transcription factor FoxA is binding. Write a Matlab function **locationtogenes(chr,start,finish,genefile)** that takes a chromosome name, the start and finish of the chromosome region in base pairs, and a gene-location file; and determines which genes are located in that region. The gene-location file is a tab-delimited text file where each line contains chromosome-start-finish-genename. Find the genes whose position overlaps with the input range. Return these genes as a cell array. If no genes are found in an input range, return an empty cell array. An example gene-location file can be downloaded from **http://sacan.biomed.drexel.edu/ftp/bmeprog/genelocs_sample.txt**

```
>> disp(locationtogenes('chr1',59000000,59247000,'genelocs_sample.txt'))
    'JUN'
>> disp(locationtogenes('chr1',50000000,100000000,'genelocs_sample.txt'))
    'RP4-784A16.2'    'MRPL37'    'JUN'    'LRRC8C'
```

ID (e.g., as3344): _____________ Name: ______________________ Expected Course LetterGrade (5pts): ____

Q1 (10 pts). *Logical Indexing*. Let **A** be a cell array of gene names and let **B** and **C** be numerical vectors representing the expression levels of these genes in the brain and kidney, respectively. Write a single statement that will assign into **D** the names of the genes whose expression in brain is at least twice as it is in kidney. Do not use loops.

```
D =
```

Q2 (10 pts). *Vectorized code*. Let **n** be a positive integer and **X** be the vector **1:n**. Write a single statement to assign into **s** the value of the following sum. Do not use loops.

$$s = 1 + \frac{1}{2^2} + \frac{1}{3^3} + \cdots + \frac{1}{n^n}$$

```
s =
```

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

```
>> fs={'a','x','t'};
>> p=struct('a',{3 5},'x',{[20 40]},'t',7);
>> disp( [ p.a  p(1).a  p(1).(fs{1}) p.x  p.t ] )


   ____________________________________________________________
```

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

```
>> m={[1 5] {1 5} 'orange'; 1:5 {1:5} {'orange'}};
>> disp([numel(m(1)) numel(m(2)) numel(m(3)) numel(m(4))  numel(m(5)) numel(m(6))])


________________________________
>> disp([numel(m{1}) numel(m{2}) numel(m{3}) numel(m{4})  numel(m{5})  numel(m{6})])


________________________________
```

Q5 (10 pts). *string functions, indexing*. Fill in the outputs below.

```
>> vars = {'gender' 'weight' 'bmi'};
>> data=[1 120 13; 1 130 16; 2 150 20; 1 210 30; 3 190 25; 2 230 35];
>> disp( data(:, strcmp(vars,'bmi'))' );


__________________________________________________
>> disp( data(data(:,1)==2, strcmp(vars,'bmi'))' );


__________________________________________________
```

Q6 (Extra 5 pts). Circle True if the following statement evaluates to true, otherwise circle False.

True / False

"I have already filled out the course survey" OR "I plan to fill out the course survey" OR "I do not plan to fill out the course survey."