

## BIOMED 201 - Programming & Modeling for BME

Final Exam, 2015.06.04, 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 (20 pts).** *Strings, File, Loops.* Write a function `geneid2speciesname(gid,gidfile,taxonfile)` that takes a gene id `gid`, a file `gidfile` that maps gene ids to species ids, and a file `taxonfile` that maps species ids to species names. Both files are tab delimited and the first line contains the column names. In your function, you will first map the given gene id to the species id using the `gidfile`, and then map the species id you found to the species name using the `taxonfile`. Your function needs to return the species name found. You can download sample `gidfile` and `taxonfile` from: <http://sacan.biomed.drexel.edu/ftp/bmeprog/gidfile.txt> and <http://sacan.biomed.drexel.edu/ftp/bmeprog/taxonfile.txt>

Assume that the files given in the input arguments always exist (so you don't need to check for existence), but can have other names than shown here. You also do not need to download these files within your code.

```
>> disp(geneid2speciesname(3893,'gidfile.txt','taxonfile.txt'))
Saccharomyces cerevisiae
>> disp(geneid2speciesname(33470,'gidfile.txt','taxonfile.txt'))
Homo sapiens
>> disp(geneid2speciesname(40549,'gidfile.txt','taxonfile.txt'))
Plasmid ColE9-J
```

**Q7 (30 pts).** *Loops.* In this problem, you will simulate an experiment where bacteria are being grown on a grid-based maze. Write a function `bacteriamaze(m,T)` that takes an initial maze configuration `m`, and a total time `T` hours. In the maze configuration, the walls of the maze where bacteria cannot grow are represented with '#'; the locations that the bacteria are currently growing on are represented with 'B'; and the bacteria-free locations are represented with '\_'. Assume that the boundaries of the maze will always have walls, ensuring the bacteria cannot move out of the maze. After each hour, the bacteria in each location replicate and move to all the neighboring cells (including diagonals). Your function needs to simulate the experiment for `T` hours, and return the resulting maze configuration.

```
>> disp( bacteriamaze(['#####'; '#__B__#'; '#B__##_#'; '#####_#'; ...
'#_#____#'; '#####'], 1)

#####
#BBBB__#
#BBB##_#
####_#
#_#_#_#
#####
```

ID (e.g., as3344): \_\_\_\_\_ Name: \_\_\_\_\_ Expected Course LetterGrade (5pts): \_\_\_\_\_

**Q1 (10 pts).** *Vectorized code.* Let  $n$  be a positive integer. Write a single statement to assign into  $s$  the value of the following sum. Do not use loops.

$$s = 1^{-n} + 2^{-n+1} + 3^{-n+2} + \dots + (n-1)^{-2} + n^{-1}$$

`s =`

**Q2 (10 pts).** *Logical Indexing.* Fill in the output below.

```
>> m = [ 1 2 3; 2 3 1 ]; Iwall=m==2; m=m+10; m(Iwall)=2;
>> disp( m )
```

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

```
>> s='blue,3,56,orange,28,92'; I=strfind(s,',');
>> disp( s(I(3)-1:I(4)) )
```

**Q4 (10 pts).** *structs, dynamic field names, indexing.* What is the value of  $s$  after the following statements? Circle the correct choice.

```
>> p=struct('a', {3 5 7 11 13 17 19 23},'b',{29 31 37 41 43 47 53 59});
>> s=sum([p(mod([p.(char('a'+1))],10)==3).a ] );
```

(A) 0    (B) 3    (C) 32    (D) 39    (E) 96    (F) 131    (G) 135

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

```
>> cats={'name' 'breed' 'age' 'weight'
'Fluffy' 'Angora' 3 10
'Puffy' 'Persian' 5 9
'Kitty' 'Siamese' 1 5
'Tiger' 'Angora' 7 11
'Patches' 'Manx' 12 13
'Pumpkin' 'Persian' 16 7 };
>> disp( cats{ strcmp(cats(:,1),'Tiger'), 3 } )

_____  

>> disp( mean( [ cats{ strcmp(cats(:,2),'Persian'), 4 } ] ) )

_____  

>> disp( cats( ...
strcmp(cats(:,1),'Patches')|strcmp(cats(:,1),'Pumpkin'), 2)' )

_____
```