**MATLAB For Scientists**

**HW3**

**Instructions**

* Complete each question below in an **individual** script. Each individual script should be named according to: HW#Q#\_script.m, where <#> indicates the corresponding HW number or question. These are the scripts that will be considered for grading.
* Scripts should contain appropriate headers as specified in class.
* Submit all files (**including** the provided data, but **excluding** any tables/files that are saved as a result of the HW question) as a compressed .zip folder with the name **<HW#\_studentID.zip>.**
* Each script **must** run entirely through without error. If you did not finish part of a question, comment it out so it runs.
* Suppress all intermediate outputs other than your answer to the question; only the answer should display on the command line.
* Absolutely no hard coding beyond the minimum specified.
* **Everything must be commented. Uncommented codes get zero credit!**

**Problems**

**Question 1 (2 pt)**

Write a script that performs the following MATLAB operations:

* 1. Create a 3x5 matrix of random numbers using the function rand and assign it to a variable called mat. Perform each of the following operations on the original mat:
     1. Delete the entire 3rd row, and display the size of the remaining matrix in a complete sentence
     2. Add a new row of all zeros to the bottom of the matrix and display the size of the resulting matrix in a complete sentence
     3. Display the sum of all values in the matrix that are *greater than* 0.5 in a complete sentence
     4. Display the syntax you would use to replace all values in columns 2, 3 and 4, with the number 6
  2. You are given two matrices, A and B, below. In the following parts, the final answer should print to the command line (e.g., don’t use disp)

Define A and B manually, and perform the following operations:

* + 1. Use logical indexing to print the elements in A that are less than 1
    2. Use find to print the elements in B that are less than 1
    3. Create a new matrix that is the same size as A and B, and contains a logical 1 where A *and* B are *both* *less than* 1, and a logical 0 otherwise. Use this matrix to print all elements of A where A and B are both less than 1.

**Question 2 (4 pt)**

Microtiter plates are arrays (grids) of wells that are often used to grow cells. These plates commonly come in arrays of 8x12 (96-well plates), 6x8 (48-well plates), or 6x4 (24-well plates). Microtiter plates suffer from edge effects, meaning the cells located in wells around the edge of the plate don’t grow the same as those located in the center of the plate. For this reason, all edge wells are typically filled with water during the experiment, and removed from any downstream analysis. Write a script that does the following:

* Imports the microplate file HW3Q2\_microplate96.mat (which contains a matrix representing a 96-well microplate such that each value corresponds to fluorescence intensity of cells in each well)
* Removes all values corresponding to wells located on the “edge” of the plate (i.e., 1st row, 8th row, 1st column, and 12th column)
* Displays the total *number* of remaining elements on the command line in a complete sentence

**Question 3 (2 pt))**

West Nile Virus (WNV) is the leading cause of mosquito-borne disease in the continental US. 1 in 5 people infected develop fever and other positive symptoms. The file HW3Q3\_WNV\_per\_year.mat reports the mean WNV cases in California from 2006-2019 per year. Using this data, write a script that does the following:

* Creates a new vector that consists of the same WNV data excluding all data from years where the number of WNV cases were either under 100 or greater than 700
* Saves this filtered data, along with the original data, to a new .mat file with the name WNV\_per\_year\_updated.mat.

**Question 4 (4 pt)**

A new drug is being tested on efficacy against colon cancer cells. The drug, called SOL147, was incubated with the cell line HCT116 at different concentrations: 0mM, 50mM, 100mM, 300mM, and 500mM. Cell viability was measured daily over the course of 5 days, and reported as % survival. The file HW3Q4\_sol147.mat contains a matrix called survival. In this matrix, every row corresponds to a different day, starting at day 0 in the first row, and ending at day 5 in the last row; every column corresponds to a different drug concentration, starting with 0mM in the left most column, and ending with 500mM in the right most column. Write a script that does the following:

* Loads in the data
* Creates one vector containing only the data corresponding to treatment with 500mM, a second matrix containing the remaining data, and a vector called day that corresponds to the days of treatment (defined using any method of your choice; full credit for answers that do not hard code values)
* Saves a new .mat file called sol147\_new that contains the control data, the treatment data, and the days vector

**Question 5 (4 pt)**

The SOL147 experiment was conducted 3 independent times. The replicates are named HW3Q5\_sol147\_rep2.mat and HW3Q5\_sol147\_rep3.mat, along with the original replicate sol147.mat. Use these three files to write a script that does the following:

* Loads in all three datasets without overwriting data stored in each
* Defines a matrix consisting of cell viability on the **first** day of treatment for all three replicates (e.g., a combined matrix where the rows are replicates and the columns are treatment conditions)
* Saves this matrix, and all three original matrices, in a new .mat file called sol147\_combined.mat