113-1 MATLAB Midterm Exam

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Please follow the instructions and upload **three m-files**, including **midterm_1.m, midterm_2.m, midterm_3.m**, to the **Midterm** folder in the E3 system. Please have a copy of all files and bring them to the classroom next week for correction.

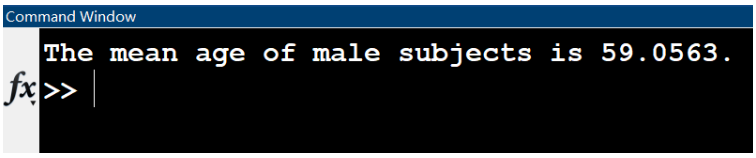
1. Program Debug (25 points)

Note: Please open the **Debug.m** file in the **MImaterials_midterm** directory and follow the steps below to debug the script. Please save the debugged file as **midterm_1.m**.

Steps:

(1) Please correct one error of **xlsread** INPUTS on Line 6. (5 points)
(2) Please correct one error on Line 10 to find male subjects. (5 points)
(3) Please correct one error on Line 12 to get all data (all columns) for male subjects. (5 points)
(4) Please correct two errors on Line 20. (10 points)

Once all the errors are corrected, you should be able to see the output message in the Command Window, as shown in **Figure 1**.



```
The mean age of male subjects is 59.0563.
>>
```

Figure 1

2. Fill in Program –DICOM Anonymization（匿名化）(35 points)

Note: Anonymization of DICOM images can protect patient privacy. In this topic, please follow the steps below to rewrite the specific headers within the DICOM files (**MImaterials_midterm\data2**). Please open the **Fillin.m** file in the **MImaterials_midterm** directory and follow the steps below to fill in your codes. Please save the script as **midterm_2.m**.

(1) Please use **for-loop** to get all the headers by **dicominfo** for all the 23 DICOM files and store them in the variable ***info***. (5 points)
(2) Please use **for-loop** to read images by **dicomread** for all the 23 DICOM files and store them in the variable ***img***. (5 points) (5 points)
(3) Please use **for-loop** to rewrite the field values under the ***info*** as follows (15 points),
  - ✓ Rewrite the value of **PatientID** field as a string of Patient#1;
  - ✓ Rewrite the value of **PatientName.FamilyName** field as a string of Patient#1;
  - ✓ Rewrite the value of **PatientBirthDate** field as a string of 20241107.

(4) Please use **for-loop** with **dicomwrite** to create 23 anonymous DICOM files. Please add the prefix 'new_' to the original file names. (10 points)
HINT: dicomwrite(*img*, 'FILENAME', ***info***)

3. Image ROI and Tumor-to-Normal Tissue (T/N) Ratio (40 points)

Note: Positron Emission Tomography (PET, 正子放射斷層攝影) with radioactive tracers can be used to assess tumor uptake for a molecule. We can draw regions of interest (ROI) for the tumor area and the normal tissue to measure tumor uptake. In this topic, please follow the steps below to accomplish the process and calculate the T/N ratio. Please save the script as **midterm_3.m**.

Steps:

(1) Please load **PETandMRI.mat** file within the **MImaterials_midterm\data3** folder. (5 points) You should be able to see two variables within the Workspace, ***MRIimg*** and ***PETimg***.

(2) Please use **montage** function to display image slices #47 to #62 of ***MRIimg*** in one figure (as shown in **Figure 2**). Please set up the **'Displayrange'** between 0 and 1. (5 points)
HINT: help **montage** % for further information

(3) Please use **montage** function to display image slices #47 to #62 of ***PETimg*** in another figure (as shown in **Figure 3**). Please set up the **'Displayrange'** between 0 and 3. (5 points)

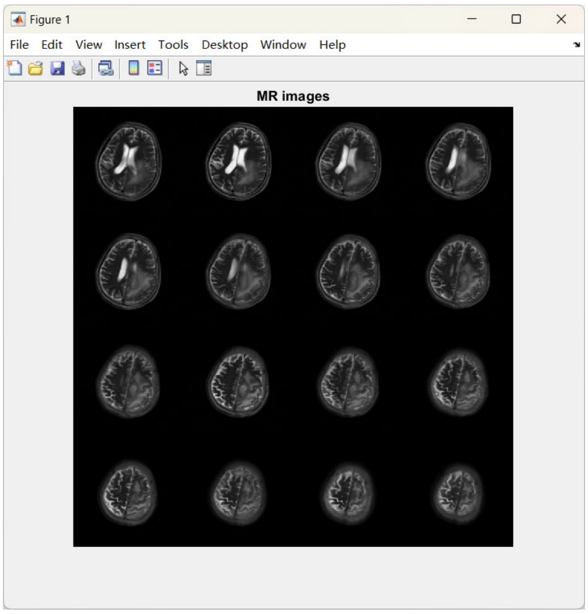


Figure 2

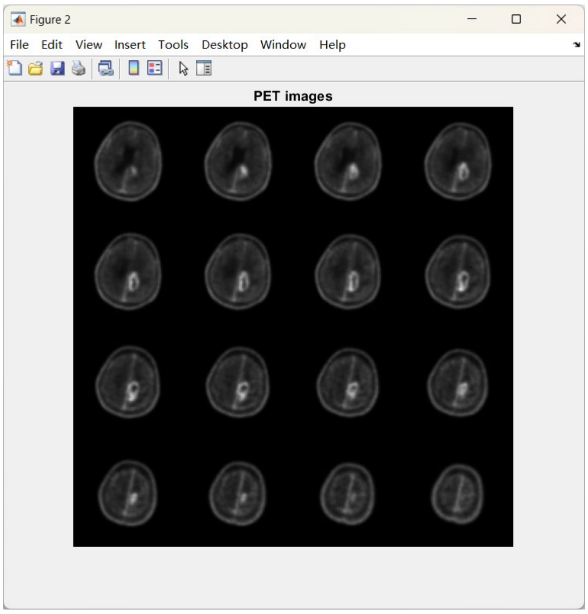


Figure 3

(4) Please open a new figure and use **imshow** to display image slice #54 of PETimg. Please set the **'Border'** property to 'tight' and the **'InitialMagnification'** property to 500 (as shown in **Figure 4**). (5 points)

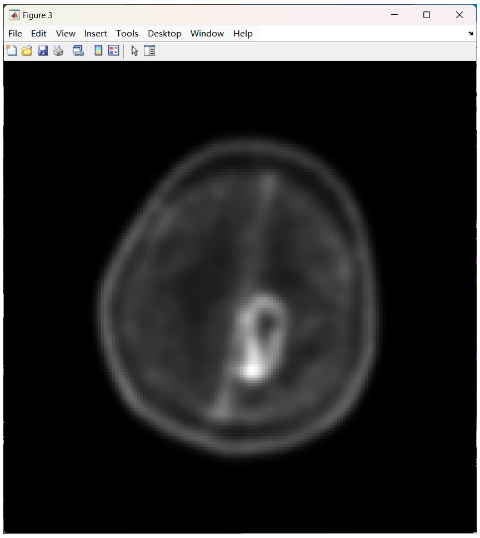


Figure 4

(5) Please use **<u>drawassisted</u>** function to draw the tumor ROI. Please name the ROI variable as ***tumorROI***. Please set the field **'Label'** of ***tumorROI*** to 'tumor' and the field **'Color'** to 'red' (**Figure 5**). (5 points)

HINT1: help **drawassisted** % for further information

HINT2: ***tumorROI*** = **drawassisted**;

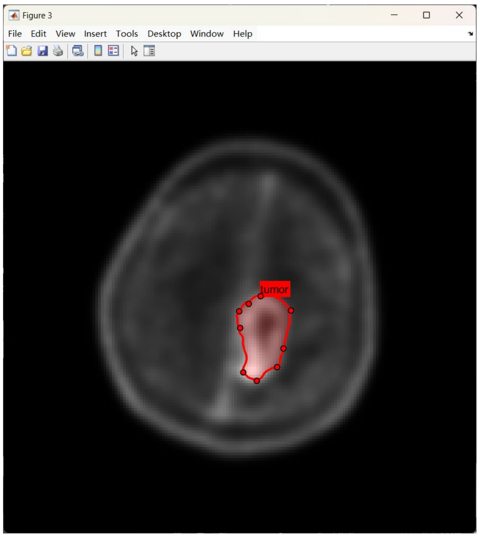
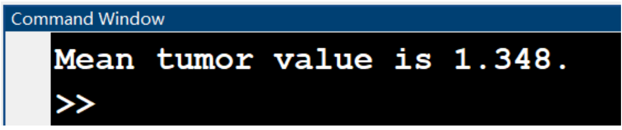


Figure 5

(6) Please calculate the mean value of the PET image within the tumor ROI (assign the value to variable ***tumorValue***) and use the **fprintf** function to display the value in the Comment Window (**Figure 6**). (5 points)

Note: The mean value would change depending on the tumor ROI.

HINT: tumorMask = tumorROI.createMask;   % create binary mask from ***tumorROI***



```
Mean tumor value is 1.348.
>>
```

Figure 6

(7) Please repeat Steps (5) and (6) to create another ROI for normal tissue (variable name: ***normalROI***, **Figure 7**) and print out the mean value within this ROI (assign the value to variable ***normalValue***, **Figure 8**). Please set the field **'Label'** of ***normalROI*** to 'normal' and the field **'Color'** to 'blue'. (5 points)

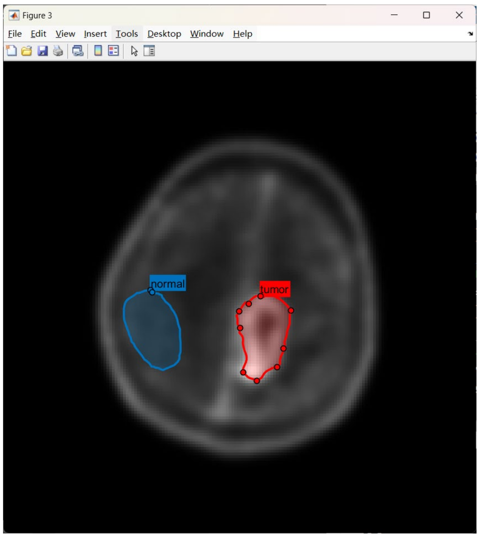
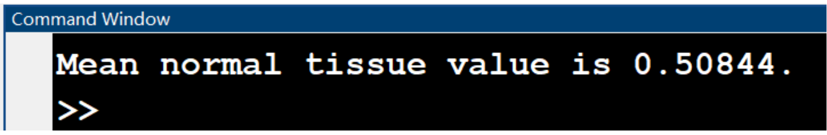


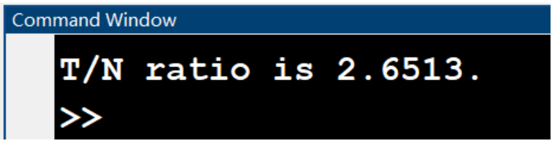
Figure 7



```
Mean normal tissue value is 0.50844.
>>
```

Figure 8

(8) Calculate the T/N ratio based on the ***tumorValue*** and ***normalValue***, and print the result in the Commend Window (as shown in **Figure 9**). (5 points)



```
T/N ratio is 2.6513.
>>
```

Figure 9