MATLAB code documentation: "Penumbra quantification from MR SWI-DWI mismatch and its comparison with MR ASL PWI-DWI mismatch in patients with acute ischemic stroke"

IIT Delhi

Indian Institute of Technology Delhi

Code prepared by:

Rupsa Bhattacharjee, Dr. Anup Singh, et.al.

MedImg Group,

Center for Biomedical Engineering (CBME) IIT Delhi

This code sharing module is prepared for Research usage strictly

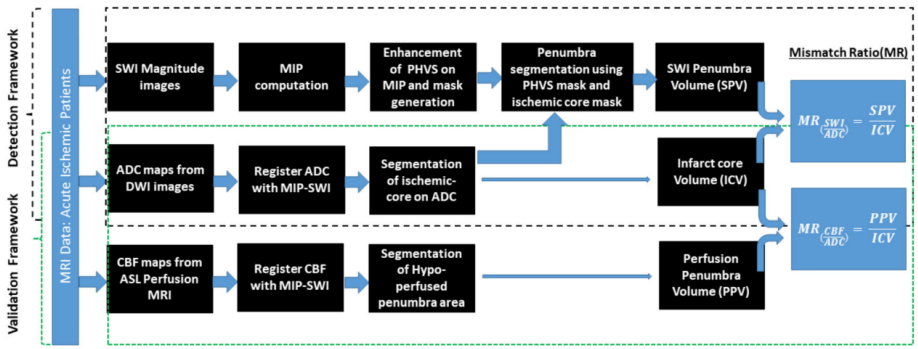


FIGURE 1 Flowchart of proposed methodology for penumbra quantification from MR SWI-DWI mismatch and its comparison with MR ASL PWI-DWI mismatch

Block A: Preprocessing: Read the data, resize, register (Line: 3-255) : Descriptions and examples given for small segments of the block

1st Segment (Line 6 -24)

Description: **(Alternatively, use lab-specific data reading practices)**

i) Insert the folder location where the DICOM data is stored.
ii) Enter the total number of slices/images for all the four sequences: SWI, pCASL (PWI/CBF), ADC and FLAIR.
iii) Select all the DICOM Images from each of the respective folders.
iv) Define the resolution of SWI. We have worked with 1008 X 1008.

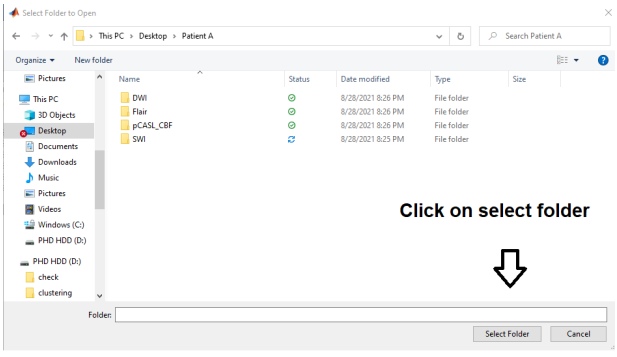
```
%% Informations about the Input Data

InputDir = uigetdir('Select patient data folder'); %% Insert the folder location, where the DICOM data is kept
cd(InputDir)

SliceTotalSWI = input('Total Number of Slices in SWI =   '); %Input the total number of slices/images in SWI sequence, example n = 130/140/150
SliceTotalpCASL = input('Total Number of Slices in pCASL =   '); %Input the total number of slices/images in pCASL sequence, example n = 14
SliceTotalDWI = input('Total Number of Slices in ADC =   '); %Input the total number of slices/images in ADC sequence, example n = 25
SliceTotalFLAIR = input('Total Number of Slices in Flair =   '); %Input the total number of slices/images in FLAIR sequence, example n = 25


%%Select all the dicom images from each of the folders
[filenameSWI_mag, pathnameSWI_mag] = uigetfile('multiselect', 'on', '*.*','select SWI mag images');
[filenamepCASL, pathnamepCASL] = uigetfile('multiselect', 'on', '*.*','select 3D ASL images');
[filenameADC, pathnameADC] = uigetfile('multiselect', 'on', '*.*','select ADC images');
[filenameFLAIR, pathnameFLAIR] = uigetfile('multiselect', 'on', '*.*','select FLAIR images');

%%Resolutions of SWI images (In our case this is 1008 X 1008), can be
%%modified as per input data.
H =1008; H_SWI = 1008; W =1008; W_SWI = 1008;
```

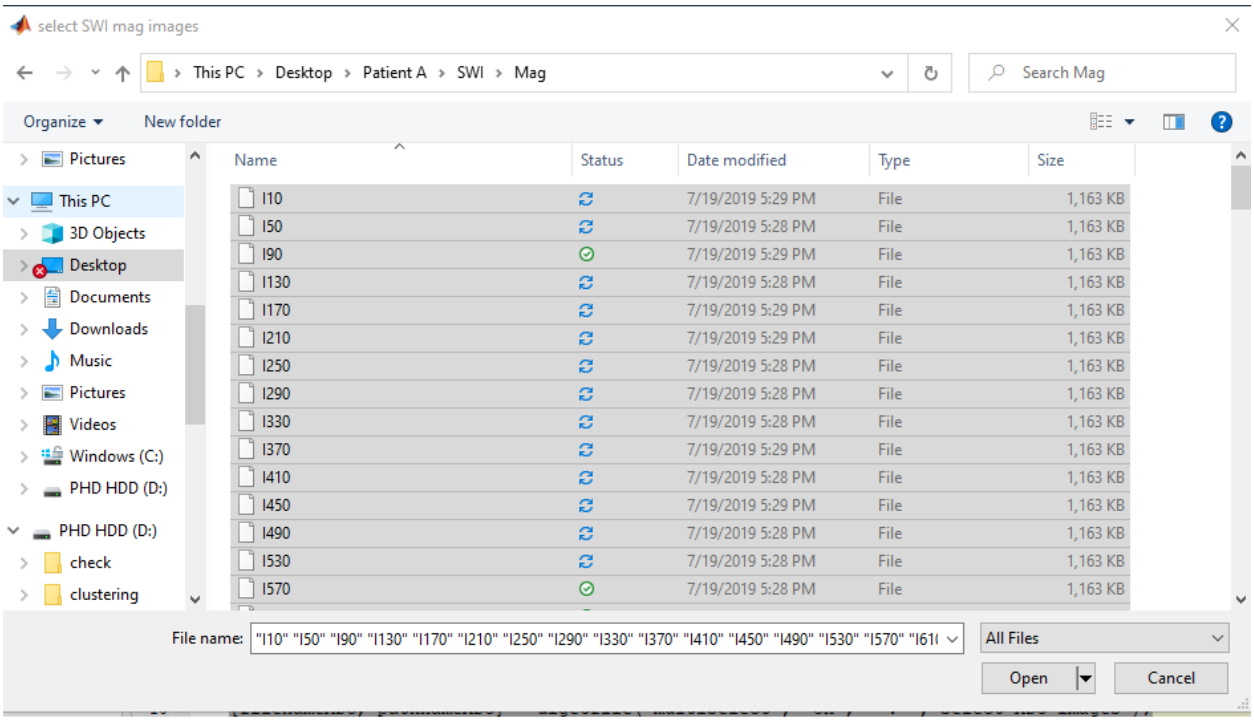


Click on select folder

⇩

```
Total Number of Slices in SWI =   145
Total Number of Slices in pCASL =   14
Total Number of Slices in ADC =   25
Total Number of Slices in Flair =   25
```

Enter in Command window



Use Ctrl + A and select all the slices/images in each of the four sequence folders

2nd Segment (Line 25 – 83)

Description:

i) Read the input data from location previously specified.
ii) Run either of the modules depending on whether the data is in Enhanced DICOM Format or Classic DICOM format
iii) Define the Starting and ending slice range: where the diffusion restriction is seen on ADC (Ex: 10 to 19 in given example)
iv) Define the Starting and ending slice range: where the Hypo-perfusion is seen on ASL_CBF
v) Define the Starting and ending slice range: where the PHVS is seen on SWI
vi) Define the Starting and ending slice range: where the Abnormality is seen on FLAIR

```
%% READ the Input Data
%%IF Dicom datasets are ENHANCED DICOM: Run this module
SI_SWI_mag1  = double(dicomread(fullfile(pathnameSWI_mag,filenameSWI_mag)));
SI_pCASL1  = double(dicomread(fullfile(pathnamepCASL,filenamepCASL)));
SI_ADC1 = double(dicomread(fullfile(pathnameADC,filenameADC)));
SI_FLAIR1 = double(dicomread(fullfile(pathnameFLAIR,filenameFLAIR)));
for i=1:(SliceTotalSWI)
    SI_SWI_mag(:,:,i)  = SI_SWI_mag1(:,:,:,i);
end

for i=1:SliceTotalpCASL
    SI_pCASL(:,:,i)  = SI_pCASL1(:,:,:,i);
end

for i=1:SliceTotalDWI
    SI_ADC(:,:,i)  = SI_ADC1(:,:,:,i);
end

for i=1:SliceTotalFLAIR
    SI_FLAIR(:,:,i)  = SI_FLAIR1(:,:,:,i);
end
```

For Enhanced DICOM

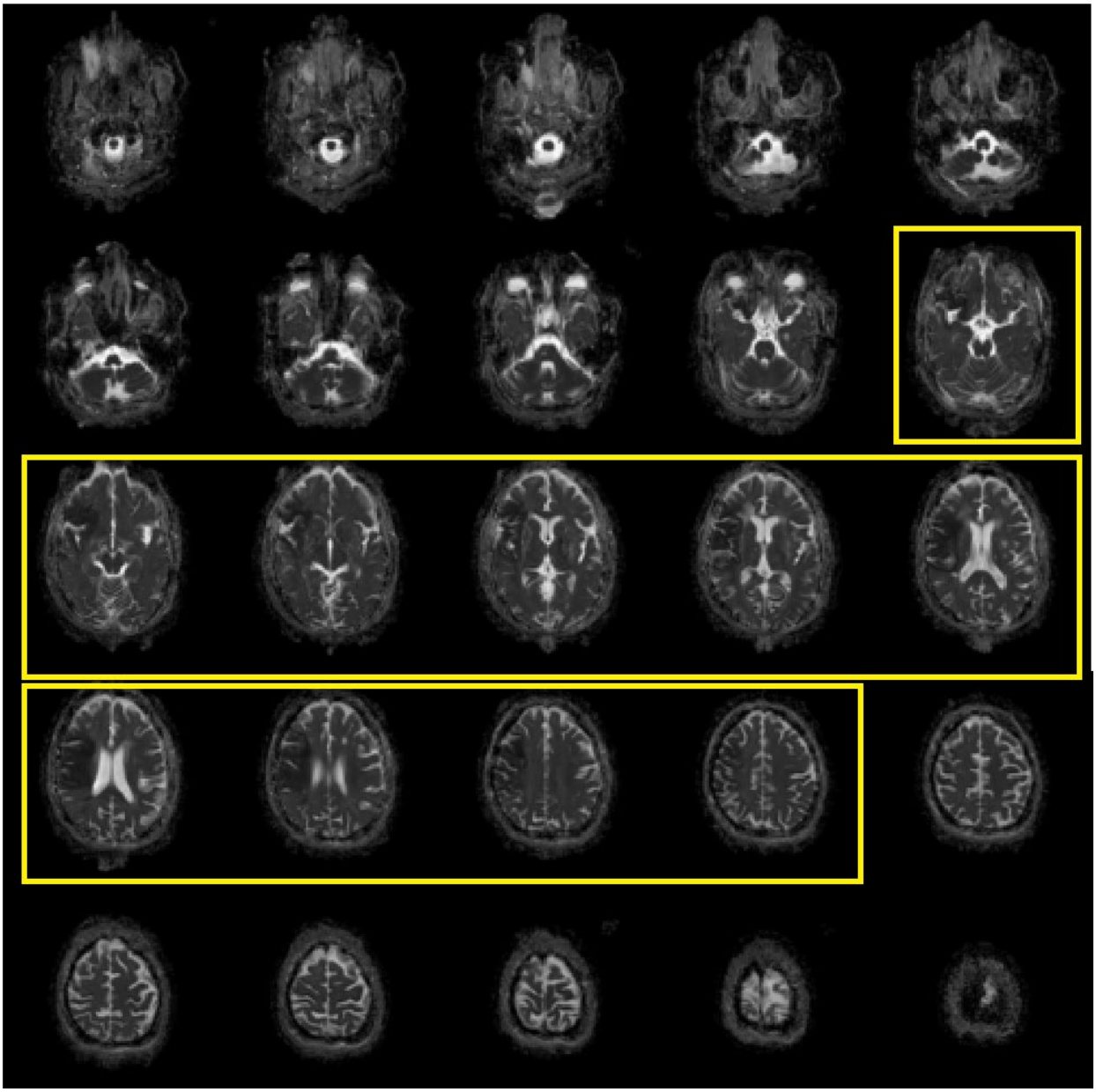
```
%%IF Dicom datasets are CLASSIC DICOM: Run this module
for i=1:SliceTotalSWI
    SI_SWI_mag(:,:,i)  = double(dicomread(fullfile(pathnameSWI_mag,filenameSWI_mag(i))));
end

for i=1:SliceTotalpCASL
    SI_pCASL(:,:,i)  = double(dicomread(fullfile(pathnamepCASL,filenamepCASL(i))));
end

for i=1:SliceTotalDWI
    SI_ADC(:,:,i)  = double(dicomread(fullfile(pathnameADC,filenameADC(i))));
end

for i=1:SliceTotalFLAIR
    SI_FLAIR(:,:,i)  = double(dicomread(fullfile(pathnameFLAIR,filenameFLAIR(i))));
end
```

For Classic DICOM



Example : Slice number 10 to 19 shows Diffusion restriction

3rd Segment (Line 84 – 255)

Description: **Run the modules/lines, no inputs required, change values as necessary**

i) Resize ADC , FLAIR & 3D pCASL images as per SWI resolution (Highest matrix size)
ii) Create sub-matrix of ADC FLAIR & 3D pCASL images, containing only relevant abnormal slices (Rest of them are not taken into consideration)
iii) Create MIP (minimum intensity projection for SWI) for every 6 slices. In this code, SWI is of 1 mm slice thickness, rest sequences (ADC, FLAIR, pCASL) are of 6 mm slice thickness. Hence

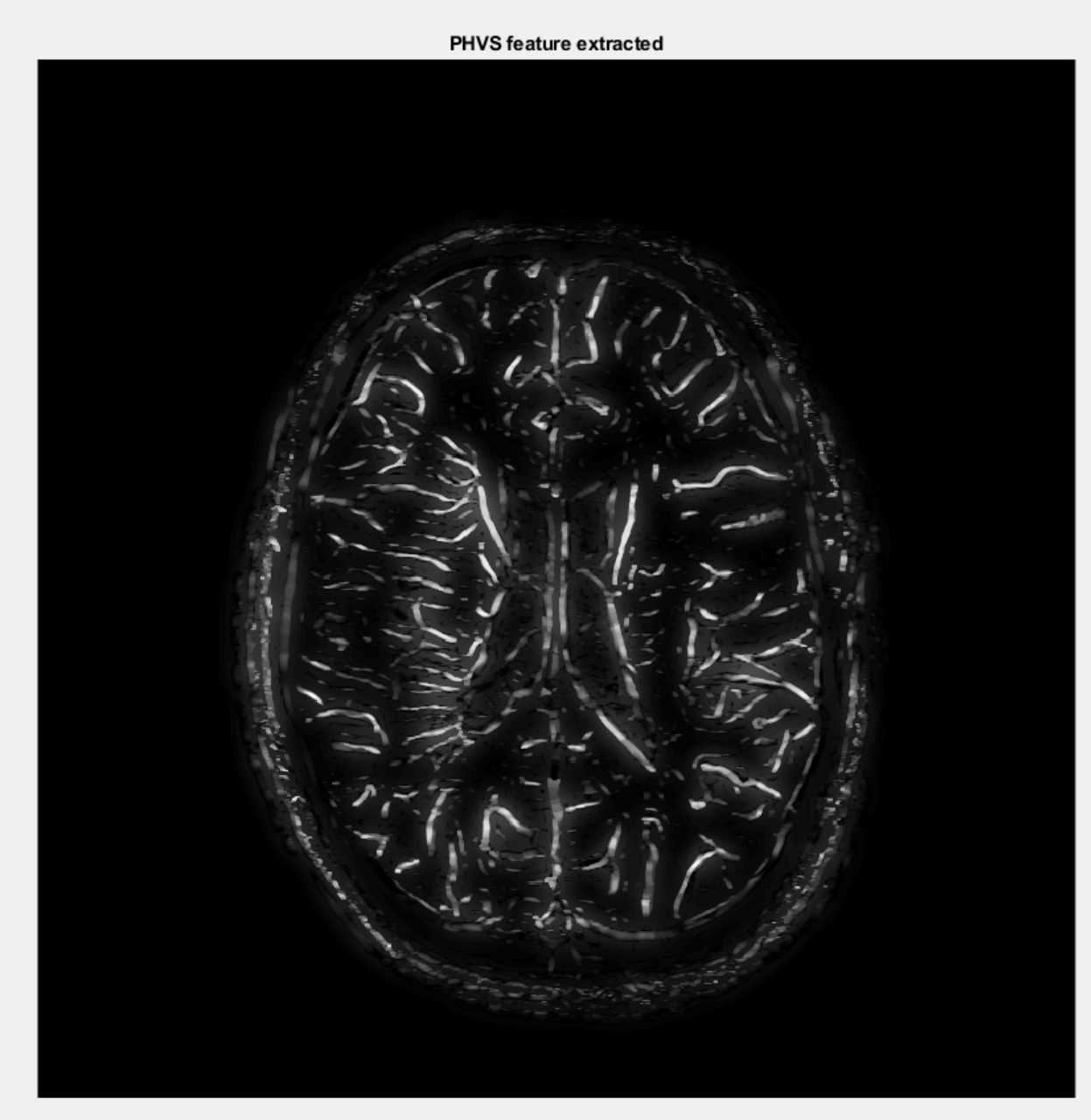
the MIP is created for every 6 SWI slices, to match the rest. This can be modified as per user-specific sequence parameters.

iv) Registration of ADC, FLAIR and ASL with SWI MIP

Block B: Enhancement of PHVS Features (Line: 256-306)

Description: **Run the modules/lines, no inputs required, change values if necessary**

i) Frangi 2D Filter implementation on SWI MIP
ii) Frangi 3D implementation on SWI MIP
iii) Frangi 2D and 3D Combination and Top Hat Morphological transformation
iv) Gaussian Filter + Morphological Dilation
v) Final PHVS feature extracted image is generated



Block C: Penumbra Probability mask creation and automatic segmentation of SWI Penumbra (Line: 309-368)

Description: **Run the modules/lines, change values if necessary**

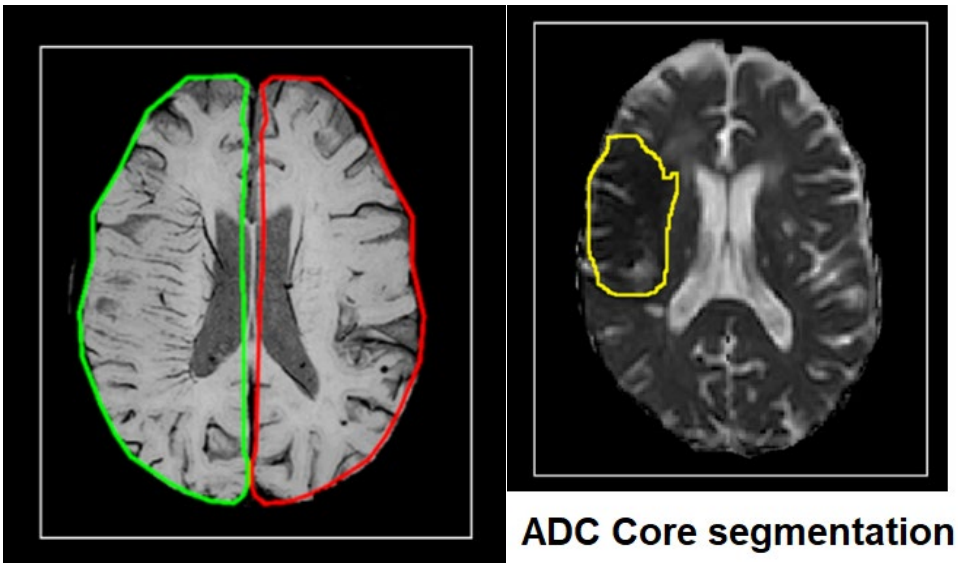
i) Mark the Stroke occurring hemisphere (SOH) & Contralateral Normal appearing hemisphere (CNAH) on SWI MIP images (Each MIP Slice)

ii) Multiplying the ROI's to PHVS feature images

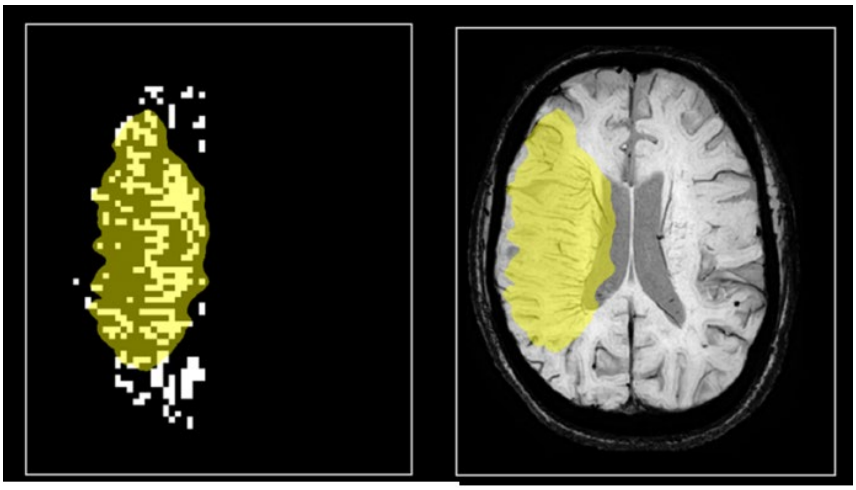
iii) ADC Core segmentation: We have automatized upon human threshold, observed, and reported. Can be manually segmented or changed as per animal models. This core mask works as a seed point.

iv) Binarize, vessel density maps and automatize using functions

v) SWI_penumbra is the final segmented BW mask.



ADC Core segmentation



SWI_Penumbra mask, overlaid on SWI MIP

Block D: Volumes and Mismatch ratios calculation (Line: 369-461)

Description: **Run the modules/lines, change values if necessary**

- Final output values are **Volumes :** ICV_in_ml, PPV_in_ml, SPV_in_ml, FLV_in_ml, **Ratios:** Mismatch_Ratio_SWI_ADC, Mismatch_Ratio_pCASL_ADC, Mismatch_Ratio_FLAIR_ADC

- For our study, FOV was fixed at 230 X 230. If the FOVs are changed for any sequence, accordingly those values need to be updated in this section.
- For our study, slice thickness and gaps were fixed at 6 mm and 0 mm respectively. If these values are changed for any sequence, accordingly those values need to be updated in this section.

If you use the framework, please cite the following Reference:

[1] R. Bhattacharjee, R. K. Gupta, B. Das, V. K. Dixit, P. Gupta, and A. Singh, "Penumbra quantification from MR SWI-DWI mismatch and its comparison with MR ASL PWI-DWI mismatch in patients with acute ischemic stroke," *NMR Biomed.*, no. December 2020, pp. 1–15, 2021, doi: 10.1002/nbm.4526.

Contact Details: For any further clarifications, please contact:

- **Rupsa Bhattacharjee, rupsa.bhattacharjee1@gmail.com, +91-8800172999**
- **Dr. Anup Singh, Anup.Singh@cbme.iitd.ac.in, +91-7042311855**