% created in January 2021, by Ho Nhu Y Nguyen

This dataset contains the data used in the article: "Reflection artifact identification in photoacoustic imaging using multi-wavelength excitation".
https://doi.org/10.1364/BOE.9.004613

- Data files of the phantom experiments:

phantom_#3_20170329_140337.rfe

phantom#2_3.5%intralipid20%_20172620_132602.rfe

- Data files of the *in vivo* experiment:

finger_movie_20170505_110511.rfe

- Data files of the Δz study: all other .rfe files with a deltaZ prefix in the file name.

- Script.zip contains the Matlab scripts used in this work and the use of these scripts are described below.

1. Matlab script

This part will be about the Matlab script used for this work.

1.1. With segmentation

Run the script "Script\ process_data_v2.m" for processing raw data files (phantom and in vivo). In this script, important support functions are listed as the following:
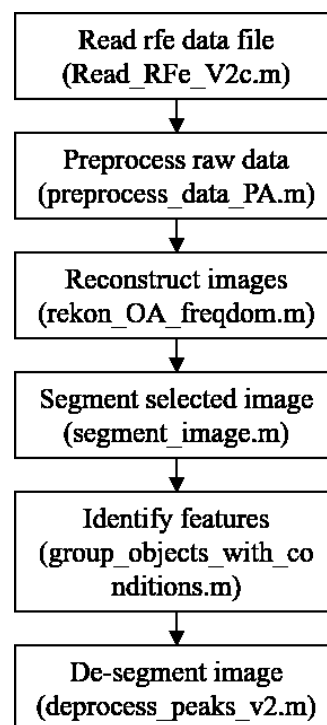
In this script, the segmentation step is called at:

```
Objects = segment_image(clearestImg, Settings);
```
It is already mentioned in the paper that the segmentation threshold is selected half of the Matlab calculated threshold. But you might change the threshold depending on your purpose. In "segment_image.m"

```matlab
[~, threshold] = edge(clearestImg(Settings.cutOffIdx1+1:end-
Settings.cutOffHalfIdx-1,:), 'sobel'); % find a threshold for defining
                                        % edge of Objects using sobel
objectsEdge = edge(clearestImg,'sobel', threshold*0.5); % detect Objects
edge
```
"threshold*0.5" is where you modify the threshold.

All information of the segmented features is stored in Objects. You might want to get the spectral response of features which is in Objects.objPxlValueWavelength. For example: Objects.objPxlValueWavelength(:, 100) to have the spectral response of feature 100.

You might need to change the Δz_{min} which is in "process_data_v2.m" at:

```matlab
Cond.zDistanceThreshold = 1.7; % the distance threshold along depth between
the
                        % absorber and the reflection to define if it is
                        % the reflection [mm]
```
The rest of the script is explained with comments.

1.2. Without segmentation

Run the script "Script\process_data_no_segmentation_v3.m". Keep in mind that Δz_{min} was 2 mm. To modify this, change the command at:

```matlab
depthThreshold = floor(2/sampleDepth);
```
2 is 2 mm in this command.

If you want to see the correlation coefficient map at a certain pixel then put a bug after the command

```matlab
curMask = curMask & corrMask;
```
Set a condition for that bug as iScan = (iRow-1)*64+iCol. For example, in this paper, I plotted a correlation coefficient map of a skin pixel (row=163, column=30). Then iScan=(163-1)*64+30=10398.

When the script hits the bug, `corrMask` is the correlation coefficient map. But you need to reshaped it as:

```matlab
corrMask = reshape(corrMask, nCols, nRows);
```
It is now ready to use `imagesc(corrMask)`.

The rest is explained with comments.

1.3. Δz_{min}

Run the script "Script\correlation_coefficient_vs_depth.m".

This script will call "process_data_v2.m" as a function. Therefore:

- uncomment "function [Settings, Data, Objects, rekon, crossCor] = process_data_v2(file)"
- uncomment "[Settings, Data] = Read_RFe_V2c(file, 0, 0);"
- comment "[Settings, Data] = Read_RFe_V2c('P:\TNW\BMPI\Users\Ho Nhu Y Nguyen\Published papers\RA artifact reduction using multi-wavelength excitation\data ', 0, 0);"

Undo those above steps when you don't need to use it as a function.

Select all data files for this analysis once.

When the script is running, it will ask to put in the feature number of the 2 suture wires. Give it correct feature numbers. Refer to "medium spectrum.fig" for the absorption spectrum of the medium in this experiment.