



UNIVERSITY OF
CAMBRIDGE



A2 MEDICAL IMAGING COURSEWORK PRESENTATION

P. Antonopoulos (pa517@cam.ac.uk)

Contents

Module 1 – PET-CT
Image
Reconstruction

Module 2 – MRI
Image Denoising

Module 3 – CT
Image Segmentation
and Classification

Introduction

Processing medical images is important because it helps...

- To see inside the body
- Diagnose diseases
- To plan treatments

But it is complex because medical images can be...

- Collected from different devices with different methods
- Affected by noise and artefacts

Introduction

A typical procedure to process medical images consists of:



Image Reconstruction

- Going from raw data to an interpretable image



Image Denoising

- Removing noise and/or artefacts from the image



Image Segmentation & Classification

- Segmenting the region of interest and classifying tumours

Module 1 – PET-CT Image Reconstruction

When reconstructing an image, we start with a sinogram

- This is a collection of x-ray measurements at different angles

We use the Beer-Lambert equation

- This describes how radiation is absorbed by tissue

We can reconstruct the image using different methods

- Direct methods (FBP)
- Iterative algorithms (SIRT, OS-SART, MLEM, OSEM)

Module 1 – Methodology

First clean up sinograms by removing noise



```
graph TD; A[First clean up sinograms by removing noise] --> B[Attenuate correct the PET sinogram<br/>• Trial direct method and iterative algorithms to reconstruct the CT image (tune necessary hyperparameters)<br/>• Resize the CT image and use it to correct the PET sinogram]; B --> C[Reconstruct the PET image using the corrected sinogram];
```

Attenuate correct the PET sinogram

- Trial direct method and iterative algorithms to reconstruct the CT image (tune necessary hyperparameters)
- Resize the CT image and use it to correct the PET sinogram

Reconstruct the PET image using the corrected sinogram

Module 1 – Results I

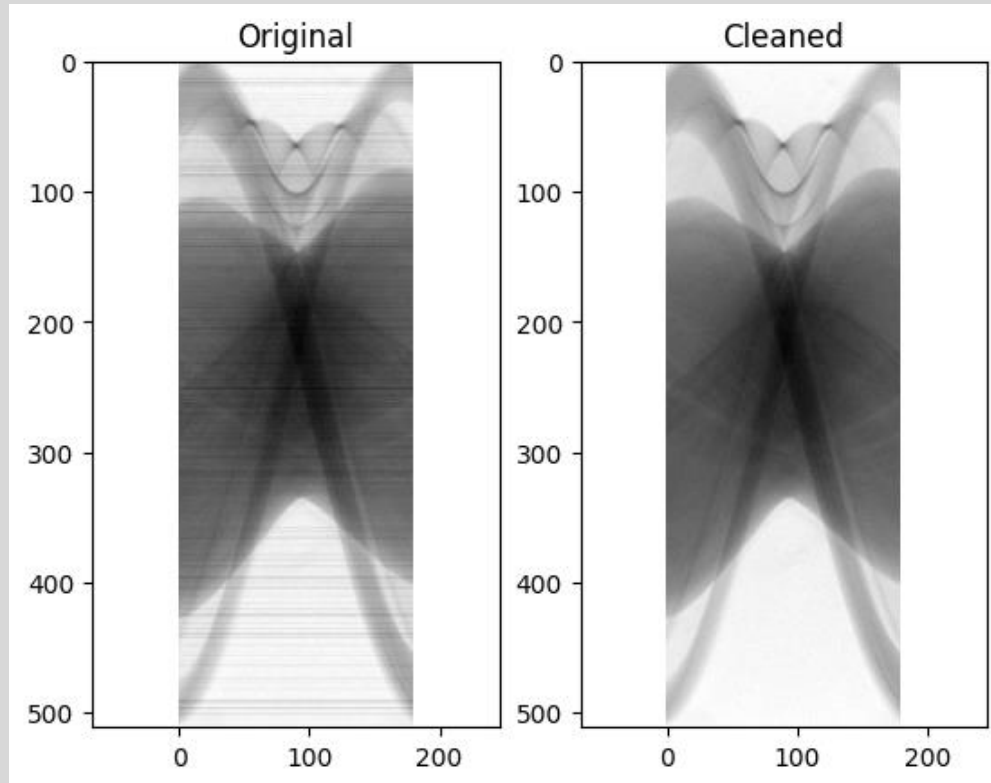


Figure 1: Original and cleaned CT sinograms

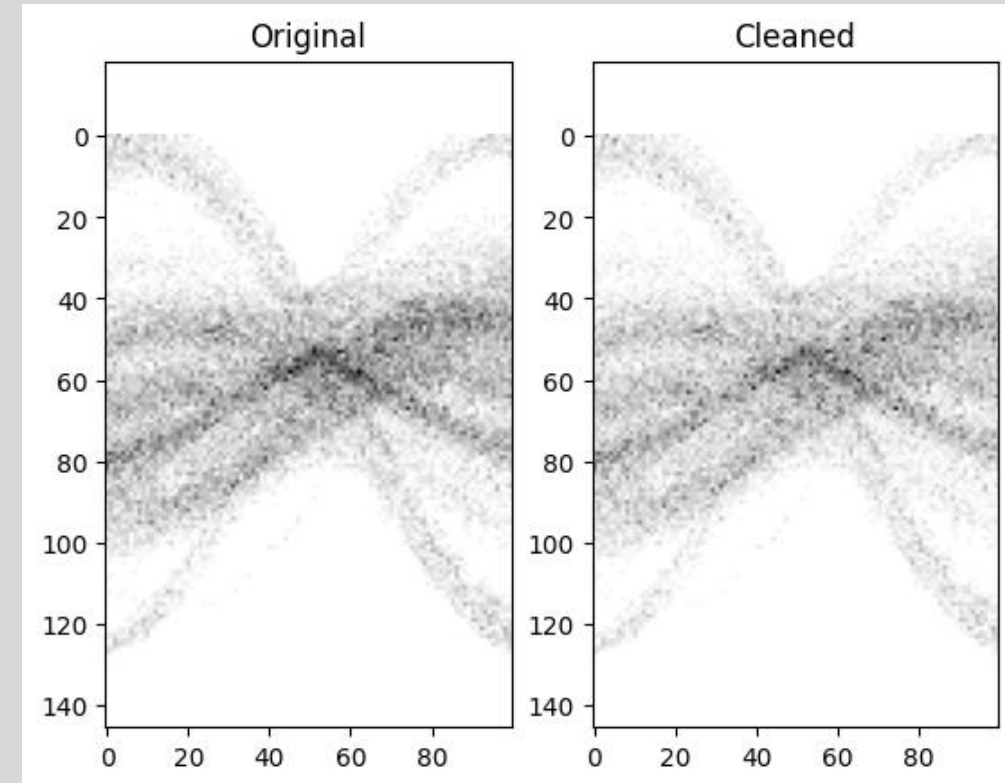


Figure 2: Original and cleaned PET sinograms

Module 1 – Results II

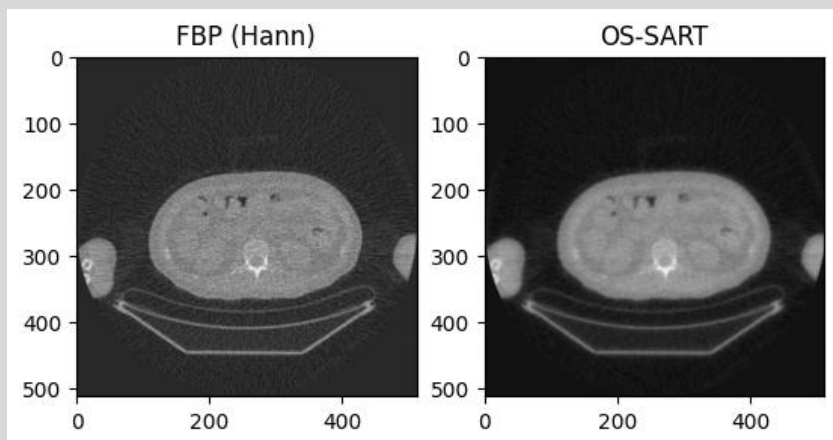


Figure 3: Direct method (FBP) vs OS-SART iterative algorithm

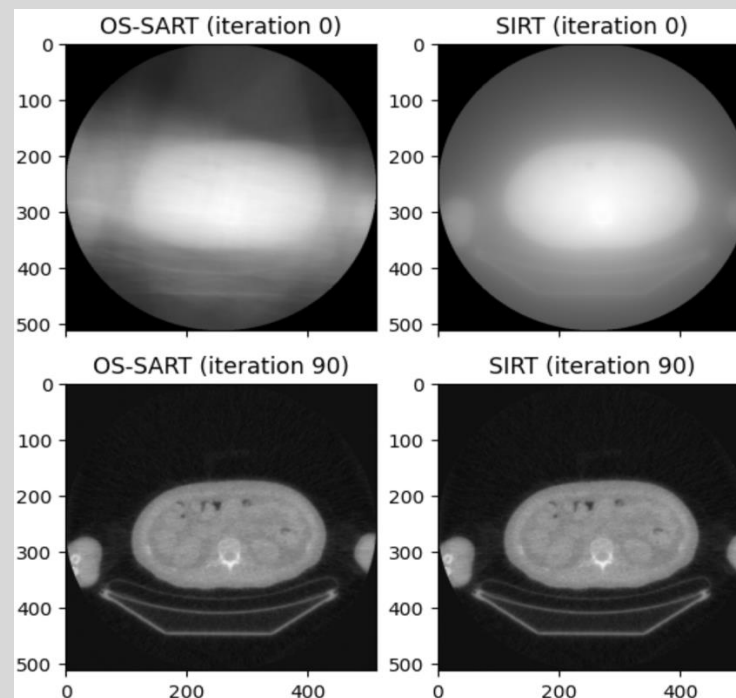


Figure 4: OS-SART vs SIRT iterative algorithm

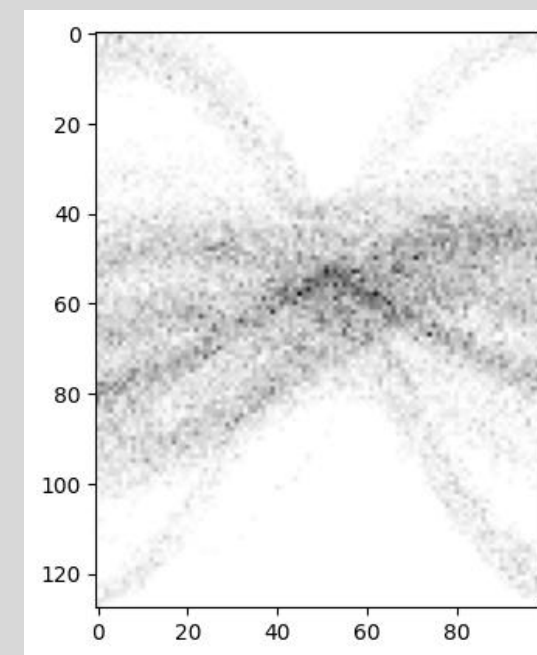


Figure 5: Attenuated corrected PET sinogram

Module 1 – Results III

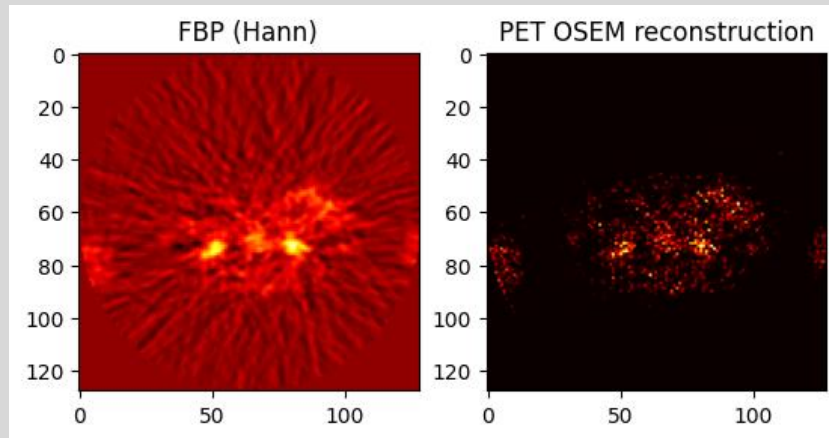


Figure 6: FBP vs OSEM iterative algorithm using corrected PET sinogram

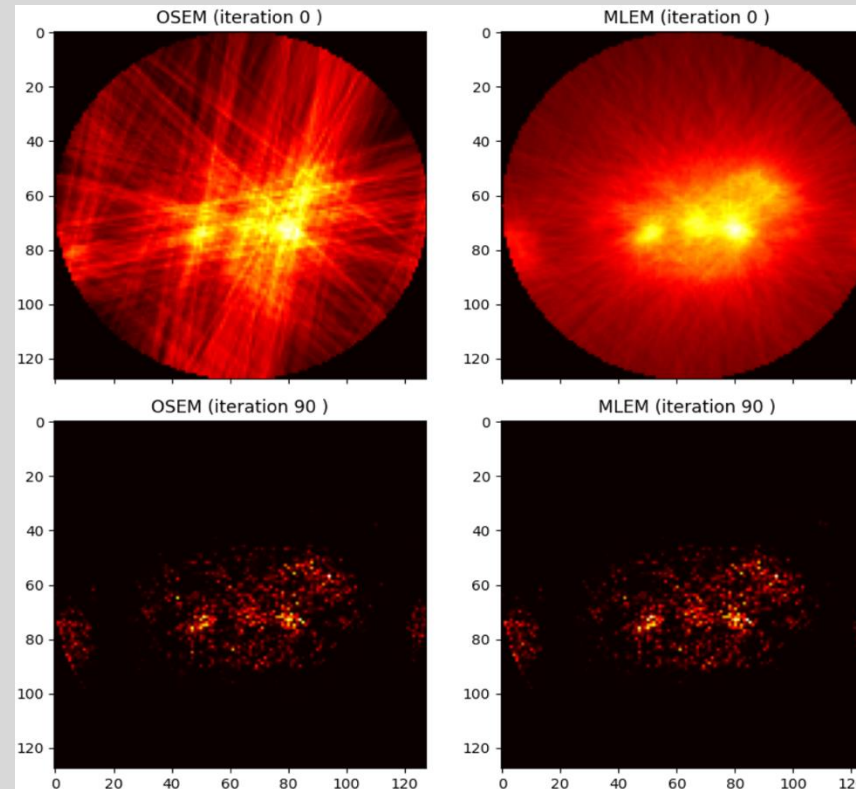


Figure 7: OSEM vs MLEM iterative algorithm

Module 1 – Observations and Conclusions

After tuning hyperparameters, OS-SART could produce a better image than FBP

OS-SART is much faster than SIRT due to it using subsets of angles

For PET images, OSEM is faster than MLEM and both are better than FBP

Functional (PET) and structural (CT) images can be combined (Figure 8)

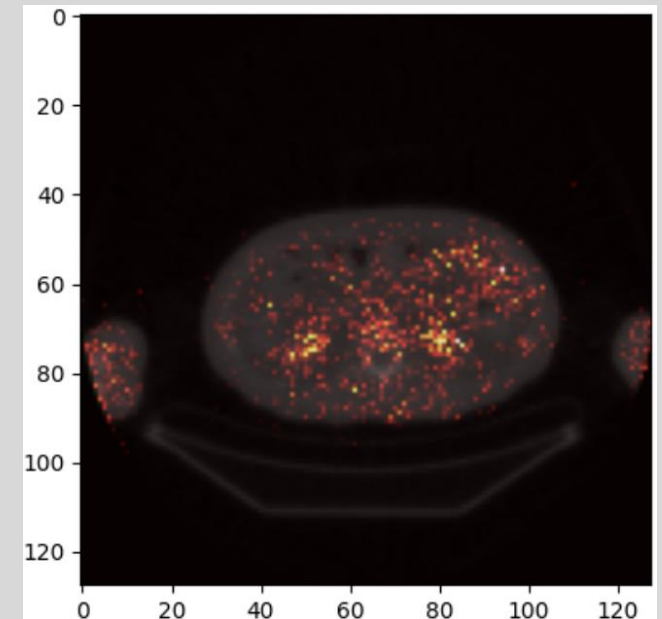


Figure 8: Overlaid PET and CT

Module 2 – MRI Image Denoising

MRI uses coils to collect data

- Separate data from each coil at different locations
- The different images from each coil must be combined into a single image

MRI data is complex

- Due to an amplitude and phase component of signal

Denoise the images using filters

- From the skimage/scipy Python libraries
- Manually defined and used with the convolution theorem

Module 2 – Methodology

Get a combined image from all coils

- Apply Fourier Transform to the complex data from each coil to get an image
- Combine the images by summing their squared magnitudes

Denoise the coil images

- Using the Wavelet, Bilateral, Gaussian and Butterworth filters

Recreate a new combined image

- Using the best performing denoising method (Butterworth filter) and the convolution theorem

Module 2 – Results I

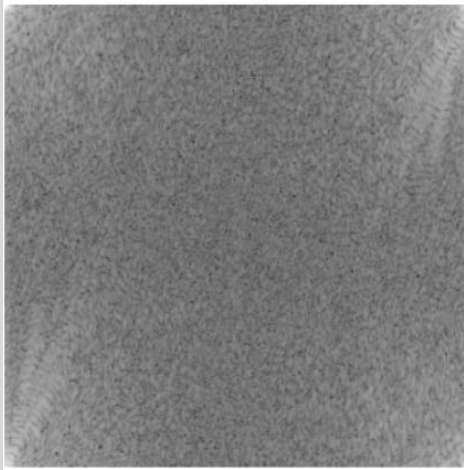


Figure 9: Magnitude of the complex data from the first coil

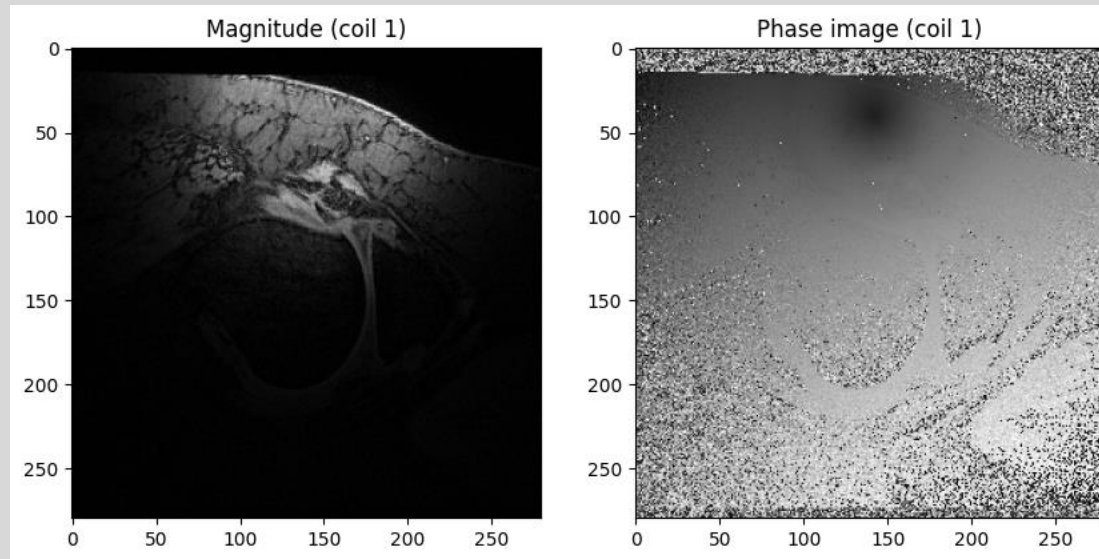


Figure 10: Magnitude and phase of the image space data of the first coil

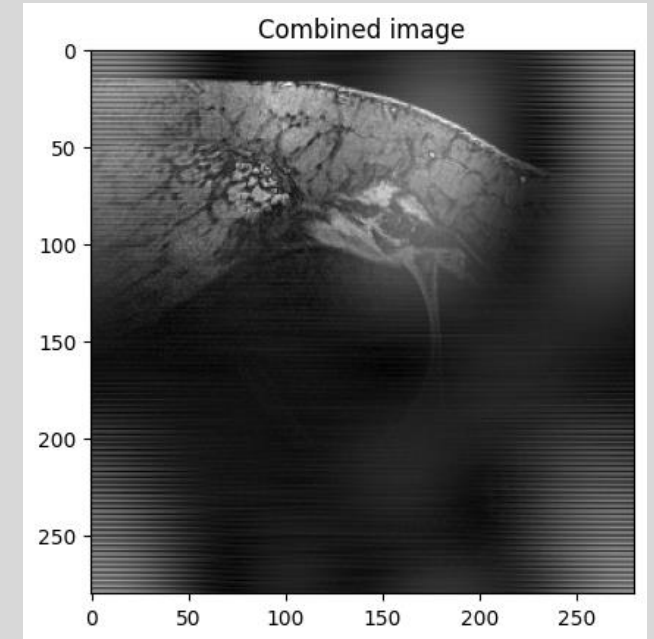


Figure 11: Sum – squared combined magnitude image from all coils

Module 2 – Results II

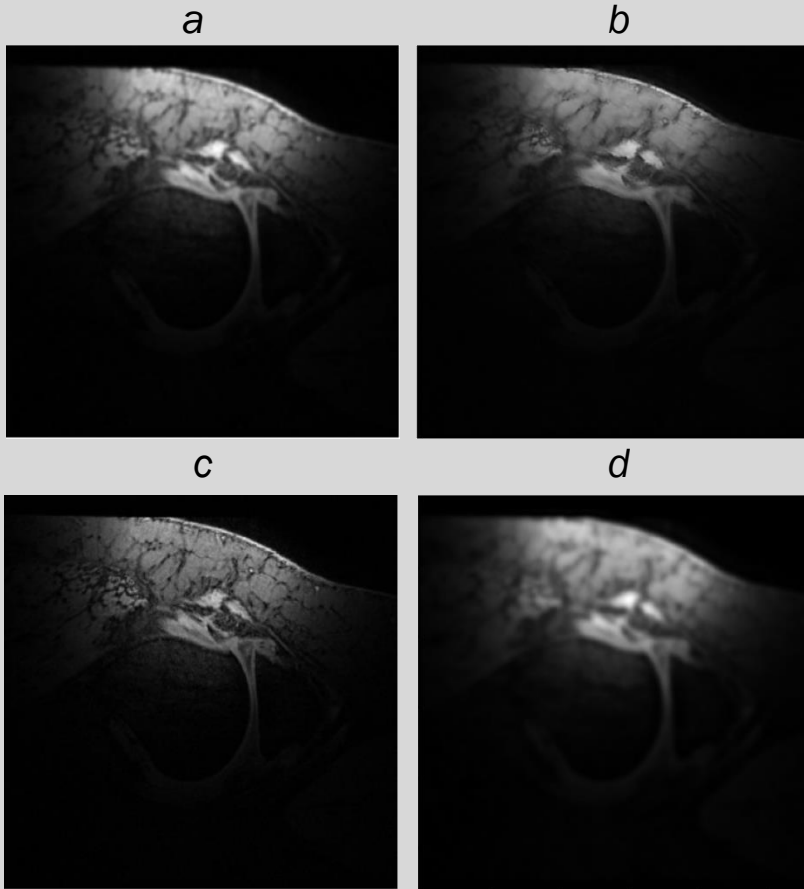


Figure 12: (a) Gaussian filtered image, (b) Bilateral method, (c) Wavelet method, (d) Butterworth method. All magnitude of image space data from coil 1

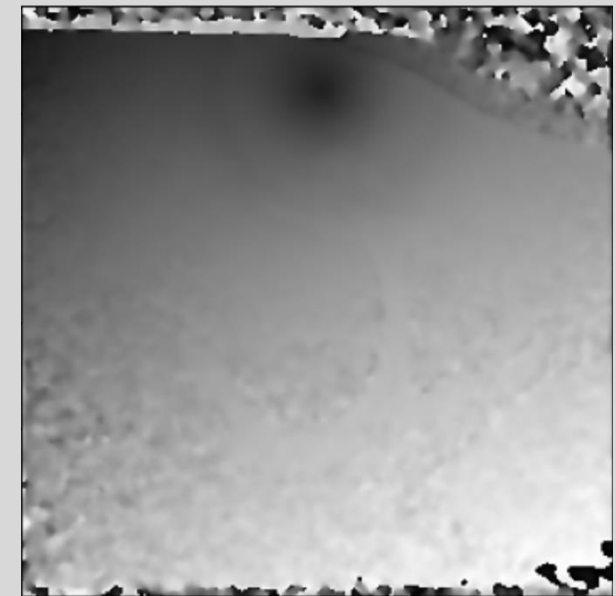


Figure 13: Butterworth filtered phase image

Module 2 – Results III

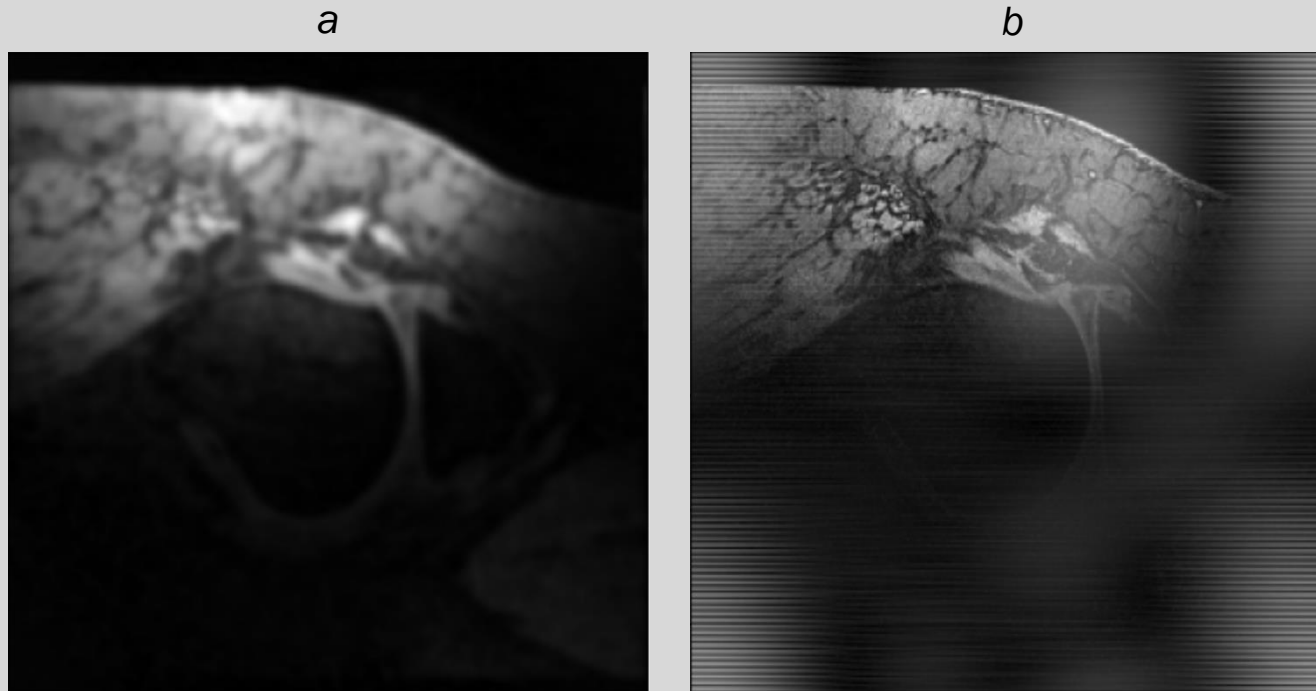


Figure 14: (a) Combined image using the Butterworth filter, (b) Original combined image

Module 2 – Observations and Conclusions

Denoising the images using the Butterworth filter appear to improve the combined image

Can tune the Butterworth filter's hyperparameters to further improve image quality

Alternatively, excluding seemingly erroneous coils also yields a decent image (Figure 15)

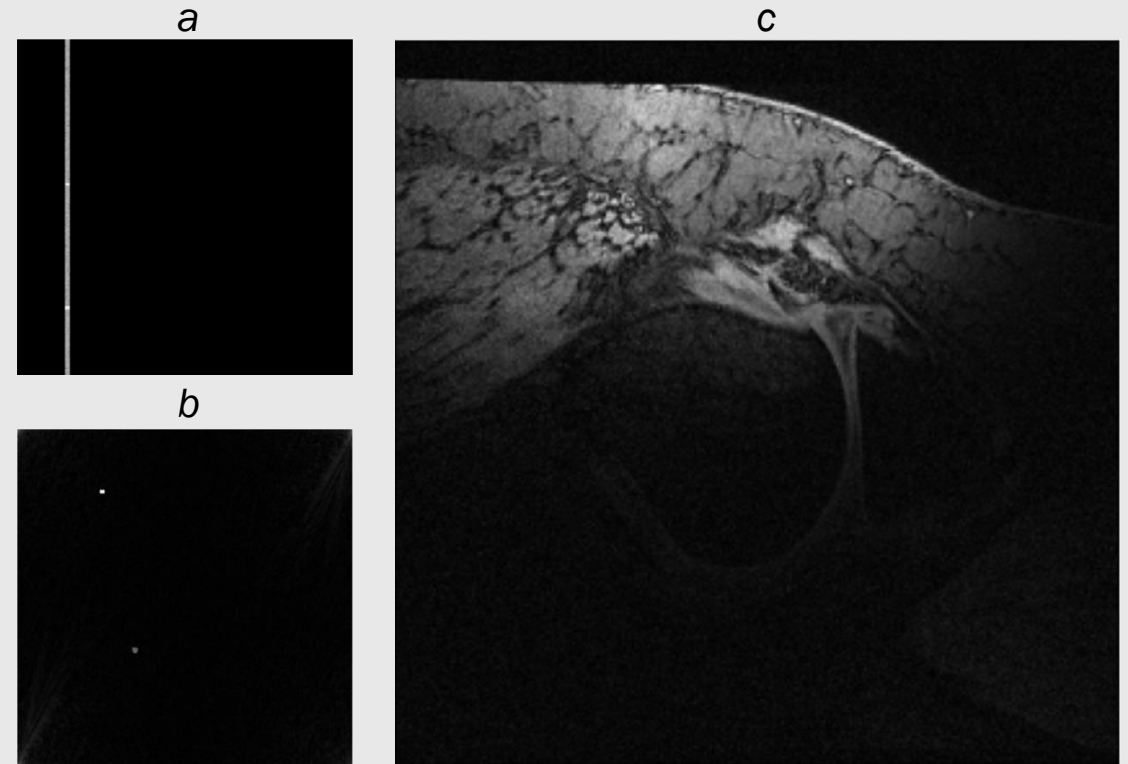


Figure 15: (a, b) Magnitude of complex data from coil 4 & 6, (c) Combined image excluding these coils

Module 3 – CT Image Segmentation and Classification

CT scan images were stored as NIfTI files

- Image and true tumour segmentations loaded using Python libraries such as SimpleITK
- Alternative file format for CT images can be used (DICOM)

Tumours can be segmented in CT scan images

- Using simple methods such as a threshold algorithm based on pixel intensities
- Using more sophisticated methods such as Machine Learning

Histogram-based radiomic features can be used to classify tumours

- Examples include Energy, Mean Absolute Deviation (MAD), and Uniformity

Module 3 – Methodology

Create a sub-volume of each image which contains the tumour

- Convert the images and true segmentation to numpy arrays
- Use the true segmentations to index the image to obtain the sub-volume

Segment the sub-volumes using a thresholding algorithm

- Implement a thresholding algorithm that retains only the pixels whose intensities fall within the min and max intensity values of the tumour region
- Compare the results of this algorithm with the true segmentations

Classify the malignant and benign tumours

- Determine the radiomic feature values for each patient's tumour and use these for classification

Module 3 – Results I

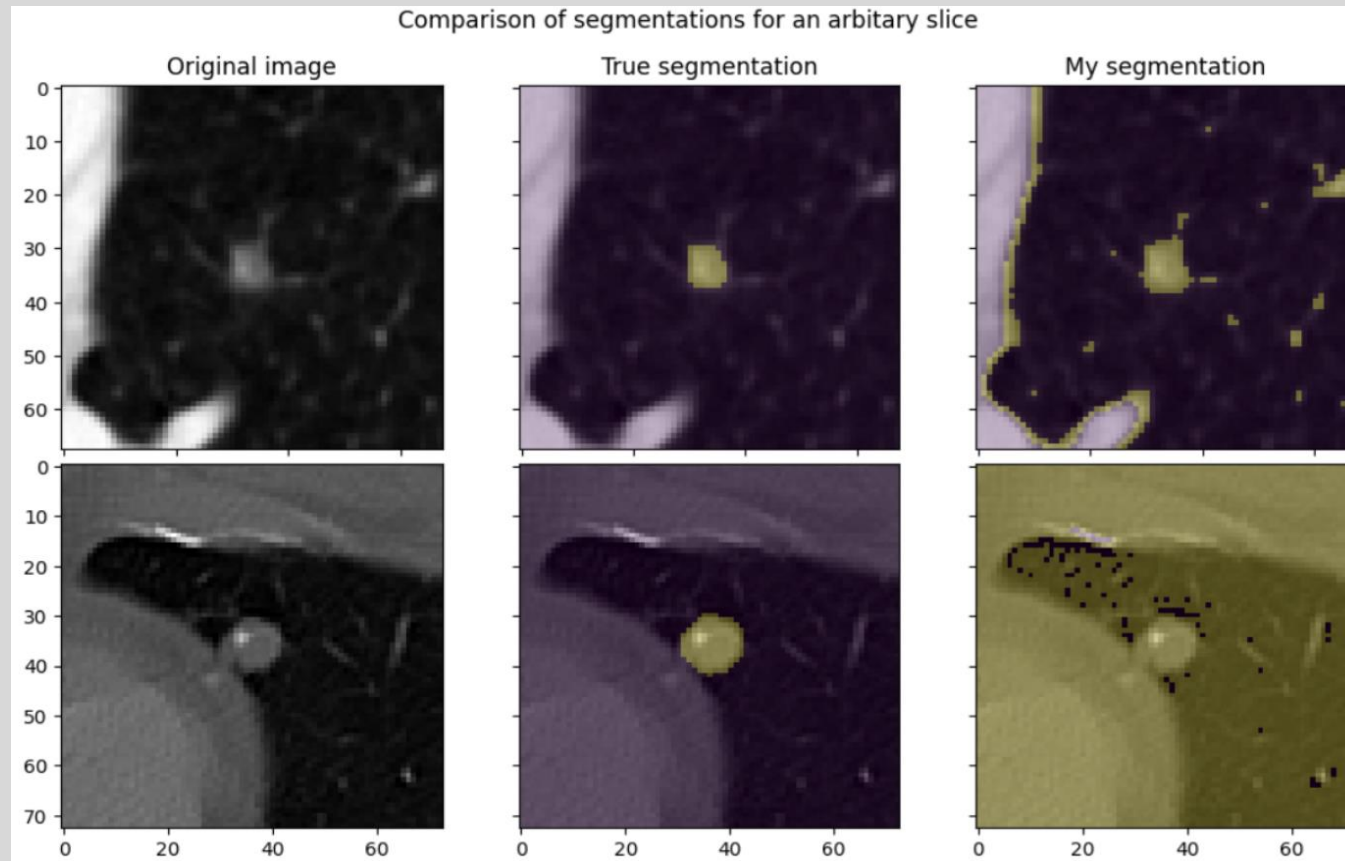


Figure 16: A decent (top) and poor (bottom) example of the thresholding algorithm's performance

Module 3 – Results II

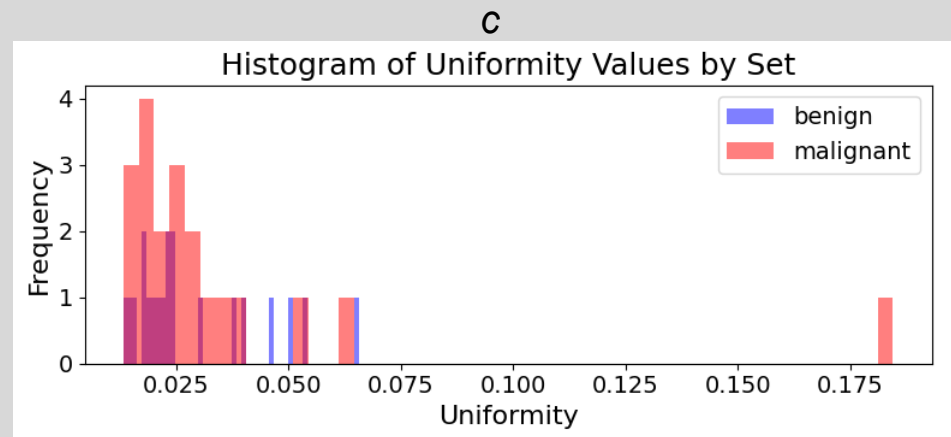
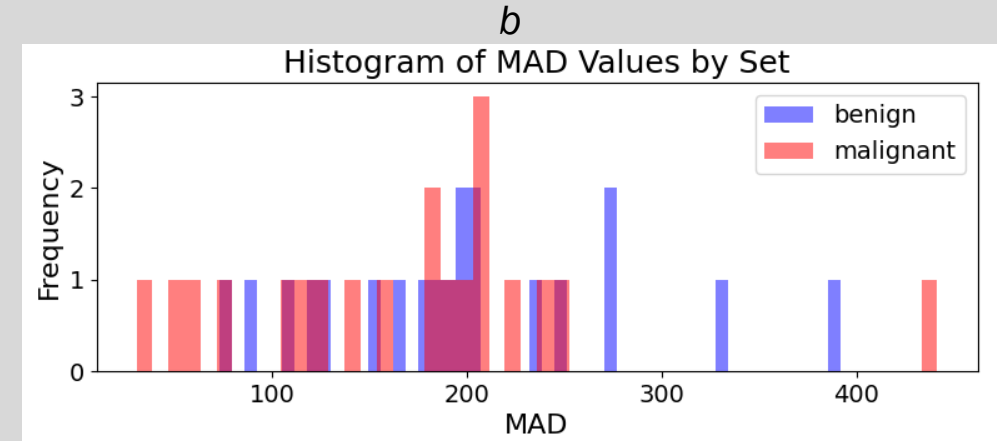
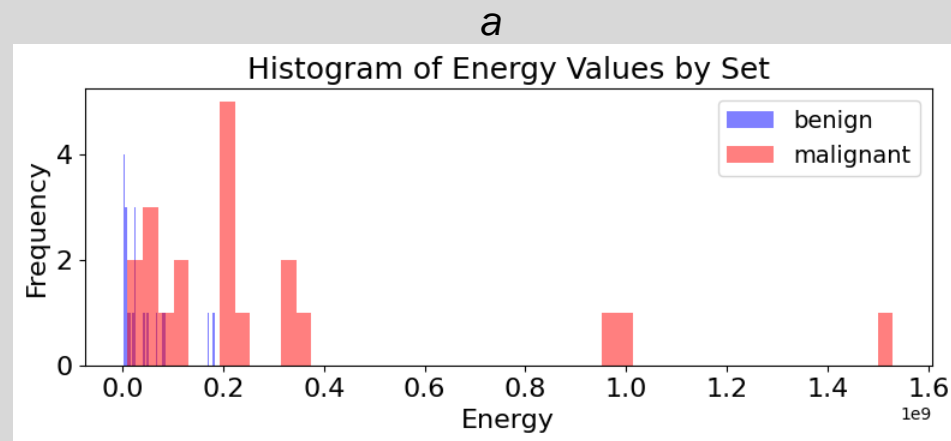


Figure 17: (a, b, c) Histograms of the Energy, Mean Absolute Deviation (MAD), and Uniformity radiomic features

Module 3 – Results III

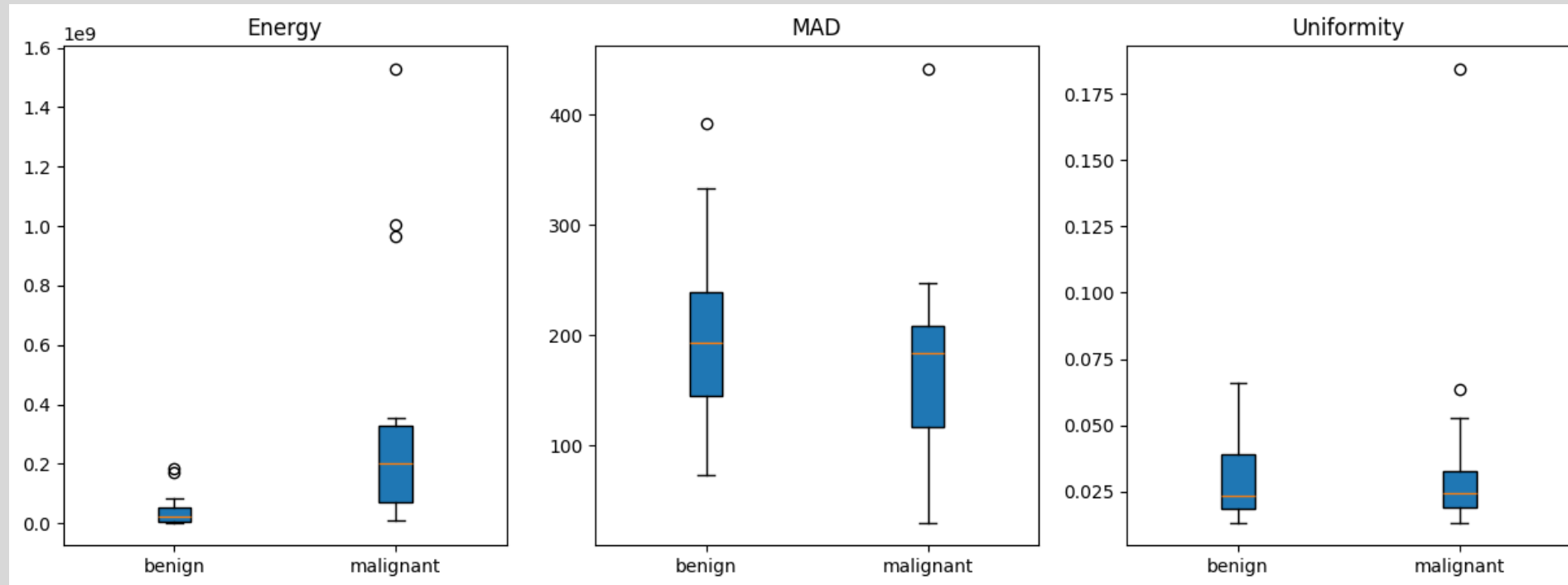


Figure 18: Box-plots of the Energy, Mean Absolute Deviation (MAD), and Uniformity radiomic features

Module 3 – Observations and Conclusions

The performance of the thresholding algorithm's segmentations are mixed

- Could be improved using a more sophisticated method such as Machine Learning

The malignant and benign radiomic feature histograms are all relatively overlapped

- No clear separation that can be used for classification

However, the box-plots suggest the Energy feature can be used for classification

- The Energy feature's plot shows a separation between benign and malignant tumours

Summary

We have gone through the main stages of processing medical images

- Reconstruction
- Denoising
- Segmentation and Classification

We have seen these stages in two different contexts

- (PET)-CT
- MRI

For further details, please consult the coursework report and GitLab repository

- Thank you for listening!