MXB201 Group Project

Introduction

Magnetic resonance imaging or MRI is a non-invasive medical imaging procedure that utilizes a magnetic field and radio waves to produce images of the body's interior (Victoria State Government, 2014). The scan is useful in investigating and aiding in identification of soft tissue conditions such as tumours or brain disorders (Victoria State Government, 2014). When a patient is placed in an MRI machine, the hydrogen protons in the water in the soft tissue of the patient reacts with the magnetic field, sending out a response in the MRI radio waves, which is measured by the coil of the MRI (Mayo Clinic, 2021). The response locations are then mapped via computer software to produce the desired images (Broadhouse, 2019).

This report focuses on two aspects of MRI - diffusion tensor imaging of the brain and facial feature extraction. Both of these aspects have been analysed using MATLAB software. The diffusion tensor imaging is investigated in part 1 and facial feature extraction is discussed in part 2. These aspects have been vital in the age of modern medicine and assist in everyday real-world situations.

Part I

MRI diffusion tensor imaging is a specific type of imaging procedure where the different sequences of adiabatic radio frequency (RF) pulses and gradients are measured at each voxel (Moroney, 2022). These pulses and gradients are analysed to determine certain properties of the tissue, with diffusion weighted MRI, the property being analysed is the diffusivity of water molecules in the soft tissue (Moroney, 2022). The signal utilizes a diffusion tensor D [mm2/s], which expresses the rate at which water molecules spread out or diffuse over a surface area (Moroney, 2022). This diffusion tensor is expressed as a 3x3 symmetric positive definite matrix:

$$D = \begin{bmatrix} D_{xx} & D_{xy} & D_{xz} \\ D_{xy} & D_{yy} & D_{yz} \\ D_{xz} & D_{yz} & D_{zz} \end{bmatrix}$$

The equation of the signal is expressed as an exponential decay (Jiang, et al. 2006):

$$S = S_0 \exp(-bgTDg)$$

Where S0 is the signal obtained without the diffusion sensitising gradient vector, g (Moroney, 2022). b is a parameter called a diffusion-weighting factor, which has been set at 1000 [s/mm2] (Moroney, 2022). By taking the logarithm of both sides of this equation:

$$\log\frac{S}{S_0} = -bgTDg$$

Then dividing through by -b:

$$\frac{\log\frac{S}{S_0}}{-b} = -bgTDg$$

As D is a symmetric positive definite matrix, there are only six independent elements, thus:

$$D = \begin{bmatrix} D_{xx} & D_{yy} & D_{zz} & D_{xy} & D_{xz} & D_{yz} \end{bmatrix}^T$$

(Jiang, et al. 2006). The diffusion tensor can be now calculated via solving an over-determined linear equation system through least squares regression (Jiang, et al. 2006):

$$A\overline{D} = B$$

The mathematical problem of fitting the diffusion tensor arises from the data received from the MRI machine. The output image is 115x90, meaning there are 115x90 voxel per image (Jiang, et al. 2006).

Issues that arose throughout analysing the data and creating the algorithm were negative values occurring in the B-vector. This effected the results of matrix D, eigenvalues and was evident that it had a large impact as the fractional anisotropy value was greater than 1. As it is proven that the fractional anisotropy value can only range between 0 and 1, the vector needed to be limited to only positive values, as there are no negative values of fractional anisotropy. A 'for' loop was created for the vector and the absolute value of the vector was taken and divide by 2 to give the positive value within reason. Hence, the issue with the negative values was mitigated.

Invalid data provided issues when forming the fractional anisotropy map. When using the algorithm to create the fractional anisotropy map, the initial system had several values of NaN, not a number, in the system which would not allow the algorithm to perform correctly. To mitigate this situation an extra line of code was created. This code would register every value of NaN and change the value to 0 which allowed the algorithm to function smoothly and create a more accurate dataset.

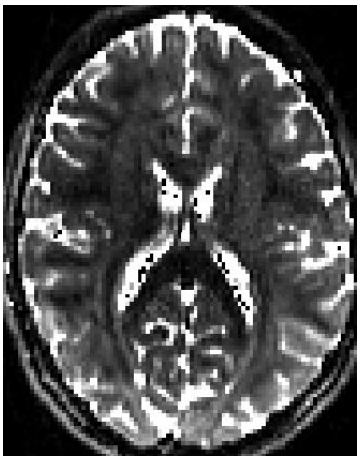

Figure 1: Mean Diffusivity Map

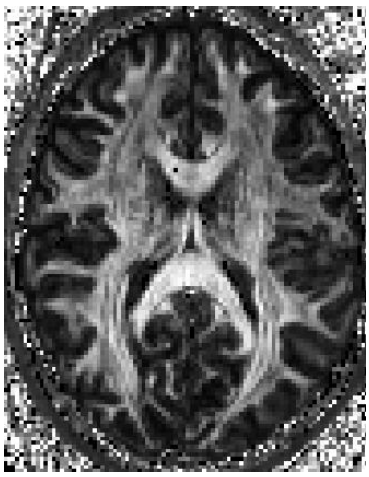

Figure 2: Fractional Anisotropy Map

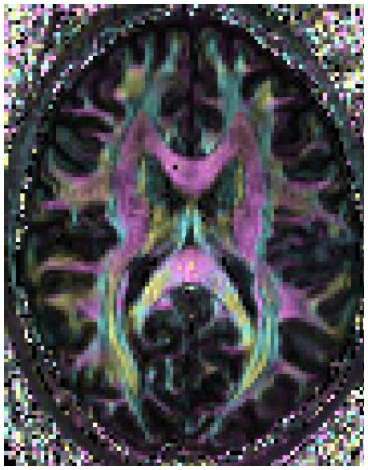

Figure 3: Principal Diffusion Direction Map

Modifications and improvements that could be implemented into this system are incorporating a fibre tracking map into the code. This would allow the process to analysis multiple slices of the brain as well as multiple patients at the same time. Also, the fibre tracking map would display a 3D image of the entire brain instead of a single slice which would be useful in locating the defective or damaged area within the brain. It is conceptually a continuous tracking map that is composed from the user applying the seed voxels in a selected section of the brain which will automate the trajectories of fibres entering and exiting that part of the brain. The primary eigenvector will follow on to the next eigenvector and continue doing until a change in trajectory which will point in the direction of a new eigenvector (Allen D. Elster, 2019).

Part 2

This section aims to create a program that determines whether or not a face has a moustache. Advanced linear algebra techniques and concepts will be utilized in MATLAB to make the program. An eigenface is the measure of the variability between images in a set of images. In other words, it's a measure of how close a face is to the average face of every face in the set of images. This will be extremely useful as a face with a moustache is different from the “average” face and can be used to determine the faces with moustaches. To generate the eigenfaces for the given data set, first the images need to be converted into matrices. This can be done by reading the pgm images and converting them into double values, giving a 192x168 matrix for each face. These matrices are turned into a left-hand side vector of size 32256x1 and are then combined into a singular matrix. To then calculate the mean, face all the rows will be averaged and combined into one mean face vector, which when converted back into a matrix will show us the mean face. Then, by mean centring the faces, by subtracting the mean face from each column of our matrix that constructed our mean face, a new matrix is a made which is a measure of how each face differs from the mean face. Then by simply using singular value decomposition, the left singular vectors are a collection of all the eigenfaces for the set of images.

Figure 4: Mean Face Classification

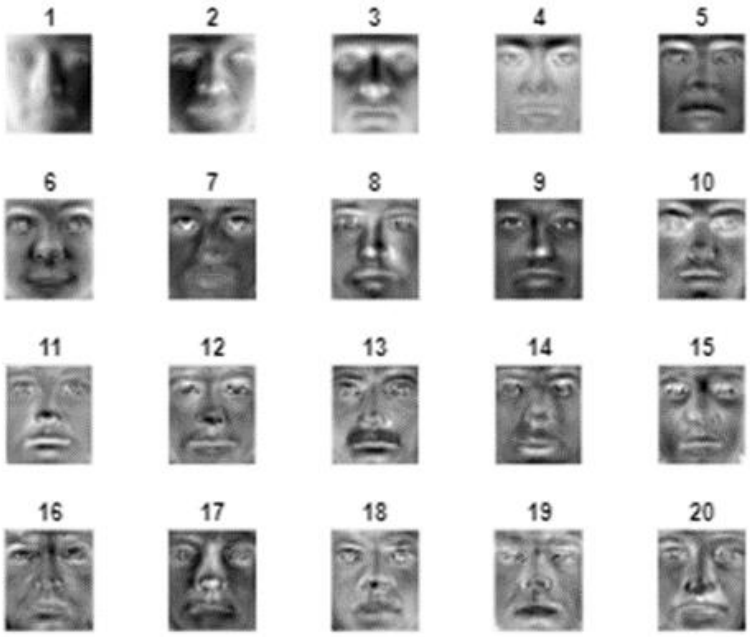

Figure 5: Eigenfaces from 1 to 20

Seeing as the singular values in Sigma decay rapidly, meaning there is little variance between eigen faces, using linear combinations of the first v eigenfaces, where v<N, a good reconstruction of each face in the data set can be achieved. This means that each face would correspond to a v-dimensional coordinate vector and in turn, be its projection onto the "eigenface space". To create a moustache detector the program needs to project the face onto the eigenface space and collect its v-dimensional coordinate vector. If the projection created primarily is made of an eigenface that has a moustache, it's safe to assume that the face has a moustache on it. Since our 13th eigenface has a moustache, we will use that as our eigenface to compare against. For our function if the projected face is made up of 6% or more of this eigenface the function will return that it has a moustache otherwise it will return that it does not.

After showing that coordinate vectors can be used to create a machine that can determine features on a face, it can also be said that the same techniques can be utilized in MRI scans. Like a

moustache, there are subtle differences in MRI brain scans between a healthy and unhealthy brain. The differences, although hard to see to an untrained eye, are there and can potentially be recognised by a computer program using linear algebra techniques. For example, there are cloudy white spots and outlines on an MRI scan of a brain with a tumour or Multiple Sclerosis. These "biomarkers" can be identified by a program using SVD and identifying distinguishable characteristics that differ from a healthy MRI scan. The ability of such a program would be to diagnose a patient almost instantaneously and could recommend new patients to medical professionals for intervention sooner. Furthermore, as more MRI scans enter the data set of healthy and unhealthy brains, the program would only get more accurate over time. The system could also be improved by specificity, as in having separate coordinate vectors for each possible diagnosis e.g., strokes, tumors, lupus etc. Using such a system would greatly improve the digital health space and help people around the world immensely.

Conclusion

Magnetic resonance imaging, also known as MRI, is a medical imaging process that uses radiology techniques to form scans and pictures of the body. Mostly used for scanning organs, the MRI scan can also be used in tissue and bone scans and is used to identify illnesses. Using various advanced linear algebra techniques and concepts, an MRI image can be produced and analysed. Using different radio frequencies, the pulses and gradient responses of the water in the tissue are recorded. This is called diffuser weighted MRI and analysing these responses can determine a patient's diagnosis. As seen in part one, using linear algebra techniques, the diffusion and diffusion direction maps can be created and greatly aid in identifying illnesses in the patient's brain. Using similar linear algebra techniques, a program can be created to identify illnesses in the brain. Using the methodology in Part 2, showing the steps and methods to make a program that can identify key differences in a face, the same principles can be applied to an MRI scan. Having a program be able to identify illnesses in the brain through analysing a patient's brain and comparing it to a known healthy brain would help save countless lives. Being able to read large numbers of MRI scans quickly and effectively would help in intervening sooner.

Conclusively, this report outlined the methods used to extract the information obtained from magnetic resonance imaging and ways to analyse the images presented. This was done using various advanced linear algebra techniques and concepts and can be implemented into real world scenarios.

Github, Video and Collaboration

Part1: https://github.com/JamesKosiol/MXB201

Part2: https://github.com/JamesKosiol/MXB201

Chat logs: https://github.com/Rentneg/MXB201/blob/main/MXB201%20-%20Text%20Channel%20(1).pdf

We ended up just sharing files and recommendations through discord which the chat logs have been provided for in the above repository. This includes any files and links that were shared during discussions. We weren't able to figure out how to use Github and its repositories but this is our attempt.

References

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