MXB201 Technical Report

Amber Xie,

Anish Kamalakkannan

Charlie McBride

Jean Warren Bulacan

01/06/2025

Table of Contents

[1 Introduction 2](#_Toc199700800)

[2 Part I: Diffusion Tensor Fitting in MRI 2](#_Toc199700801)

[2.1 Issues with Bad or Invalid Data 5](#_Toc199700802)

[3 Part II: Feature Extraction 6](#_Toc199700803)

[3.1 Motivation 6](#_Toc199700804)

[3.2 Mathematical foundation 6](#_Toc199700805)

[3.3 Eigenfaces 7](#_Toc199700806)

[3.4 Projection onto subspaces 8](#_Toc199700807)

[3.5 Moustache detector 8](#_Toc199700808)

[3.6 Relevance 9](#_Toc199700809)

[4 Conclusion 10](#_Toc199700810)

[5 References 10](#_Toc199700811)

# Introduction

This report investigates two linear algebra-based approaches to modelling and interpreting high-dimensional image data. The report is divided into two sections corresponding to these tasks, outlining the methods used, results, and relevant visualisations.

Part I focuses on processing diffusion-weighted MRI scans: a common medical imaging technique used to examine soft tissue structures such as the brain. This is done to estimate the diffusion tensor at each voxel. By modelling signal attenuation as an exponential function of gradient direction and tensor components, an overdetermined linear system is formed and solved using least squares. From the estimated tensor, derived quantities such as mean diffusivity, fractional anisotropy, and principal diffusion direction are computed and visualised.

Part II examines a dataset of 1000 greyscale facial images. The reduced singular value decomposition is applied to extract eigenfaces, allowing dimensionality reduction and image reconstruction. These coordinates are used for basic feature classification, demonstrated through detecting the presence of a moustache. In the context of MRI scans, this process can be used for various functions, including the recognition of “biomarkers” to aid in identifying neurodegenerative diseases or tumours.

# Part I: Diffusion Tensor Fitting in MRI

Diffusion Tensor Imaging (DTI) is an MRI-based neuroimaging technique designed to quantify the diffusivity of water molecules within biological tissues (Jiang et al., 2006), particularly in the brain. The primary objective of DTI is to estimate the diffusion tensor at each voxel in the scan, providing insights into the microstructural organisation and integrity of neural tissue (Jiang et al., 2006).

The physical basis of MRI relies on the nuclear spin properties of hydrogen protons, which possess a magnetic moment that aligns with an externally applied magnetic field (Elster, 2019). When subjected to a carefully tuned radiofrequency pulse, these aligned protons are excited and begin to precess around the direction of the magnetic field. As they relax back to their equilibrium state, they send out signals that are detected by the MRI scanner.

In DTI, magnetic field gradients are applied in multiple directions, and the resulting changes in signal attenuation caused by the directional diffusion of water, are used to infer the components of the diffusion tensor (Jiang et al., 2006; Elster, 2019). This tensor captures the three-dimensional pattern of water diffusion within the brain, allowing for reconstruction of meaningful clinical indicators such as mean diffusivity and fractional anisotropy.

The acquired MRI signal under diffusion weighting decays exponentially according to:

Where:

is the baseline signal obtained without diffusion sensitisation,

is a constant scalar known as the diffusion weighting factor, and

is the normalised gradient direction vector.

To estimate these tensor components, multiple MRI signals are recorded with gradient pulses applied in various directions , typically using 30 to 64 different directions to ensure robust estimates (Jiang et al., 2006). The signal relationship, transformed via logarithms, becomes a linear equation:

Given the symmetric nature of the diffusion tensor , there are only six independent tensor components that must be estimated at each voxel, which is

For a single gradient direction this gives a linear equation in the six unknowns:

Rearranging terms yields an overdetermined linear system, with n diffusion directions ( one obtains

Where:

is the 6-component vector of unknown tensor elements ,

is the matrix composed of known gradient directions,

and is the vector of measured log-signal ratios .

A voxel-wise solution is obtained via:

Jiang et al. (2006) recommend solving this overdetermined system using the pseudo-inverse, although in practice, computational tools such as MATLAB's backslash operator offer equivalent solutions and improved numerical stability.

Re-insert into the symmetric matrix , then obtain

* Mean diffusivity
* Fractional anisotropy from the eigenvalues
* Principal diffusion direction: eigenvector of tractography

Quantitative maps derived from the eigenvalues and eigenvectors of the fitted diffusion tensor (Elster, 2019) are shown in Figures 1 to 3. Together they summarise both the magnitude and directional anisotropy of diffusion across the brain.

A close-up of a brain

AI-generated content may be incorrect.

Figure 1:Axial slice of mean diffusivity computed from the provided DTI dataset (partI.m).

This image estimates the overall magnitude of water diffusion in each voxel. Bright zones along the ventricles and cortical CSF spaces indicate unrestricted diffusion, whereas darker regions in compact white-matter tracts show more restricted motion; Intermediate shades correspond to grey matter.

A close-up of a brain scan

AI-generated content may be incorrect.

Figure 2: Axial fractional anisotropy map derived from the eigenvalues of the fitted diffusion tensor (partI.m).

The brightness in FA map represents directional preference of diffusion. High-contrast white ridges trace coherent white-matter bundles such as the corpus callosum and internal capsule. Grey matter and cerebrospinal fluid appear much darker because diffusion there is nearly the same in all directions (low anisotropy).

A close-up of a colorful brain

AI-generated content may be incorrect.

Figure 3: Colour-encoded principal diffusion direction map generated using the calculated eigenvectors (partI.m)

In the principal diffusion direction map, voxel hue denotes dominant fibre orientation, red for mediolateral, green for anteroposterior, and blue for super-inferior trajectories. Whereas luminance scales with fractional anisotropy, rendering highly anisotropic voxels bright and isotropic voxels dark.

## Issues with Bad or Invalid Data

In practical DTI data collection, issues such as patient movement, scanner instabilities, or physiological artifacts often yield corrupted or unreliable signals. Such issues are critical because diffusion tensors calculated from corrupted data can significantly bias estimates of diffusivity and diffusion anisotropy, subsequently impacting clinical interpretations and diagnostic accuracy (Jiang et al., 2006).

These invalid data points generally manifest as negative values after logarithmic transformation which are not physically meaningful, or as aberrantly low signal intensities. Hence, these data points require careful management.

In the provided MATLAB code, corrupted data are handled by firstly explicitly checking for negative or zero signals prior to logarithmic transformation (lines 38 to 42 in the file “partI.m”) also by skipping computations entirely for affected voxels, ensuring they do not compromise the tensor estimation.

This explicit handling is justified because including corrupted data in the least-squares estimation would disproportionately influence results, cause erroneous tensor representations and reduce the reliability of derived scalar metrics like mean diffusivity and fractional anisotropy.

In summary, by identifying and explicitly excluding invalid data, the accuracy and robustness of diffusion tensor estimates are maintained, ensuring reliable clinical and research outcomes.

# Part II: Feature Extraction

## Motivation

A significant use case for MRI is the identification of neurodegenerative diseases and/or tumours within the brain. MRI scans produce enormous amounts of data which can be extremely difficult to analyse manually. As such, a combination of mathematical and machine learning techniques are often employed in conjunction to aid such analysis. We will demonstrate one of the common mathematical techniques used within this field. For practicality’s sake, black and white images of human faces will be used as a demonstrative proxy for MRI brain scans. Where while in the latter context, we would be interested in identifying tumours and/or biomarkers of disease, in the context of our proxy we will simply be attempting to detect moustaches. In a real implementation, machine learning would most likely be used in conjunction with the mathematical technique explained below, however since we will be mainly focusing on the mathematics, our detector will be highly rudimentary at best and will not rely on any machine learning techniques. It should be noted that although our chosen proxy is two dimensional while MRI data is three dimensional, extending the maths to three dimensions is extremely simple.

## Mathematical foundation

Say we have a set of black and white images of human faces denoted as matrices . Our goal is to use this data to derive some method for identifying moustaches within the images. The matrices are first vectorized, i.e., their columns are stacked on top of one another to form vectors:

where . The resultant vectors are then stacked column-wise to form a matrix containing the data from all images:

We will identify the “average face” by taking the column-wise mean of :

This can be used to mean centre :

where is a column vector of ones. We will now consider the reduced singular value decomposition of :

where , and . This can be visualised as follows:

where , and and denote the columns of and respectively. The RHS can be rearranged to form a sum of rank one matrices:

Since by their construction we have that , we also have that . As such, we can see that the relative contribution of each matrix towards the reconstruction of is determined solely by the value of . Since , it can be deduced that said contribution monotonically decreases as increases. It turns out that in most instances this happens very quickly. As such, can often be very well approximated by

where or even . Returning to matrix format this can be expressed as

where , and . From this we can write an equation for the column of :

where is the row of or more intuitively the column of .

## Eigenfaces

The columns of are called eigenfaces. They represent the principal components or features of the data. More specifically they are the vectors that minimise total squared reconstruction error,

or equivalently,

for . To be very clear, when we use a rank approximation, is just the first columns of . If the system is underdetermined, that is, , then is simply the minimum-norm solution among all valid orthonormal bases. Eigenfaces can be visualised by de-vectorizing the columns of and viewing the resulting matrices as images. The eigenface of is given by:

When visualised, eigenfaces often take the form of ghostly human faces, each representing different ways in which the faces in the dataset deviate from the mean face. The span of a set of eigenfaces is called a -dimentional eigenface space.

## Projection onto subspaces

Recall that:

Let . This enables the expression above to be rewritten as:

Having done this one can clearly see that is simply the coordinate vector of with respect to the basis . Note that is simply a projection of onto the lower rank bearing basis , i.e.:

Now let’s say we have some vectorized image and we want to find its closest representation with respect to the basis . To do this we would first have to mean centre the image:

We would then find the projection of onto with respect to . Since is orthonormal, said projection is given by:

This can then be expressed in terms of the standard basis as follows:

Adding the mean returns a vectorized approximation of the original image:

It is fairly easy to see that is essentially just a vector of the amounts of each of the eigenfaces present in the mean centred image. As we will see, this particular result is what makes this method so useful.

## Moustache detector

With the mathematical background out of the way, we will now explain how this technique was used this to create a rudimentary moustache detector. For our detector we set . This decision was made based on the following graph:

A graph of a number of values

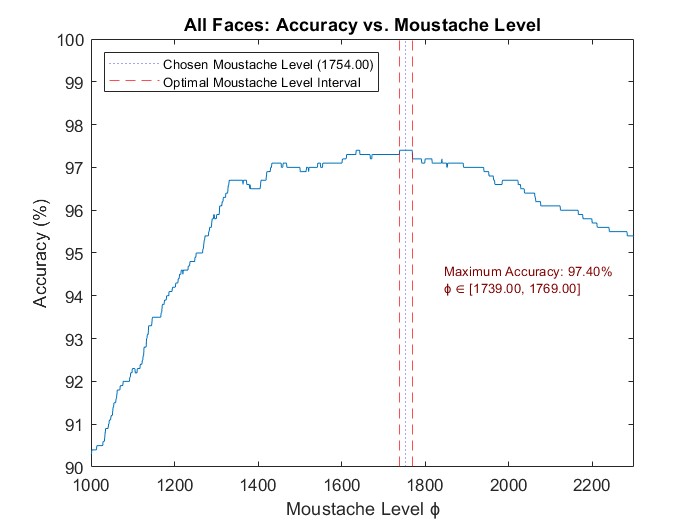
AI-generated content may be incorrect.

As can be seen, singular values fall away very rapidly. Singular value 47 was the first to drop below five figures. Singular value 47 was also visually the approximate point at which we deemed the computational cost to outweigh the increase in detector accuracy. It is important to note that this choice is entirely subjective. Upon visual inspection of the eigenfaces we were able to see that the 13th eigenface, , clearly corresponded to the feature of interest, a moustache. Recall that for some mean centred vectorized image we have that it’s projection onto in terms of given by is essentially just a vector of the amounts of each of the eigenfaces present in . As such, since corresponds to moustaches, we can simply observe the magnitude of the 13th element of , i.e., , to gauge the amount of variation from the mean face explainable by a moustache. With this logic in mind, we found and subsequently for . We then set about finding a suitable moustache detection threshold that best made true the statement

for .

This was achieved by numerically solving the following maximisation problem:

where the square brackets are the Iverson brackets. The results can be seen in the following graph:



As such we set . While the graph would seem to suggest that for the given choice of , the detector boasts an exceptional degree of accuracy, namely 97.4%, it is important to recognise that this accuracy reading is going to be high by construction as we are testing against the data on which the detector was trained and optimised for. As such, the detector is likely to exhibit a lower degree of accuracy when tested against unseen data. Unfortunately, we do not have a validation set upon which to perform such a test however the exceptional accuracy of the detector given the training data probably does suggests at least some degree of model utility.

## Relevance

While moustache detection is admittedly rather trivial, the identification of disease is most certainly not. In the context of MRI, a large dataset of MRI scan data for both diseased and healthy brains could be broken down into its features using the same mathematical technique detailed above. Assuming the data are labelled, a relatively simple machine learning model could be trained to pick up on features indicative of disease. This could then be used to identify such features in new scans by projecting said scans onto the feature-space and having the model interpret the resulting vector/s. Such a model would have enormous potential to speed and/or increase the accuracy of diagnosis of brain conditions.

# Conclusion

The report has presented the mathematical foundations for fitting the diffusion tensor using diffusion-weighted MRI data. It highlighted the importance of solving an overdetermined least-squares problem, as well as the importance of managing invalid data, ensuring accurate and robust diffusion tensor estimation. Properly addressing these concerns regarding data quality ensures validity and enhances the reliability of derived diffusion metrics, reinforcing the utility of diffusion tensor imaging for both diagnostic and research applications.

We then demonstrated how SVD based feature extraction can be used in conjunction with either manual or machine learning based principal component analysis to identify indicators of disease within MRI scans. This was demonstrated through the proxy of a fully functional moustache detector which was shown to exhibit some degree of model utility. This has significant implications for the identification of neurodegenerative diseases and/or tumours within the brain where early and accurate diagnosis can have a huge impact on survivability.

# References

Allen, D. E. (2019). *Diffusion tensor imaging*. MRIquestions. <https://mriquestions.com/dti-tensor-imaging.html>

Jiang, H., Van Zijl, P. C., Kim, J., Pearlson, G. D., & Mori, S. (2006). DtiStudio: resource program for diffusion tensor computation and fiber bundle tracking. *Computer Methods and Programs in Biomedicine, 81*(2), 106–116. <http://individual.utoronto.ca/ktaylor/DTIstudio_mori2006.pdf>

Lee, K. C., Ho, J., & Kriegman, D. J. (2005). *The Extended Yale Face Database B*. UCSD Computer Vision. <http://vision.ucsd.edu/~iskwak/ExtYaleDatabase/ExtYaleB.html>