

**DIFFUSION TENSOR IMAGING FOR BRAIN DATA SETS****S. Athersh¹**

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ABSTRACT: Diffusion tensor imaging (DTI) is a technique which estimates the location, orientation and anisotropy of the brain's white matter tracts. The paper analyses the difficulties faced in the classical Euclidean approach and proposes a new analysing technique known as non-Euclidean approach for identifying the tumour affected brain by comparing with the healthy brain, the diffusion tensor image measurements are taken from the voxels. The log Euclidean method is used to calculate DTI measurements.

Keywords: DTI, Voxels, non-Euclidean, log-Euclidean, Covariance Matrix.

I.INTRODUCTION

Brain tumour is the growth of the abnormal cells within the brain. They can be either cancerous or non-cancerous and can be classified as primary or secondary. A primary brain tumour originates in your brain. Many primary brain tumours are benign. A secondary brain tumour, occurs another organ cancer cells, such as lung or breast spread to brain. They can develop from your: brain cells the membranes that surround your brain, which are called meninges nerve cells glands. Primary tumours can be benign or cancerous. The most common types of brain tumours found in adults are gliomas and meningiomas. Treatment for brain tumours depends on several factors including the type, location and size of the tumour as well as the patient's age and general health. Treatment methods differ for children and adults. Brain tumours are treated with surgery, radiation therapy and chemotherapy. Various imaging techniques are used for the detection of brain tumour. Several drawbacks of histology-based imaging techniques include .1. invasive. 2.labor-intensive and destructive nature makes it a non-ideal choice for examining the entire brain or for performing quantitative three-dimensional analyses. Magnetic Resonance imaging technique diagnose or monitor treatment for a variety of conditions within the chest, abdomen and pelvis. It is non-invasive, three-dimensional, and requires as little as a few minutes to characterize the entire brain anatomy. RI methods including DTI (Diffusion tensor imaging) are potentially powerful probes for characterizing and analysing the effects of disease and aging on microstructure. The applications of DTI are growing because the technique is highly sensitive to variations at the cellular and micro-structural level.

II.PREVIOUS WORKS

A simple and effective Riemannian framework for DTI calculus proposed by Vincent Arsigny et al., is presented in paper [2] where this paper is focused mainly on the interpolation and the regularization of tensors. New algorithms and recent developments for calculating a mean covariance matrix where data are assumed to be covariance matrices is introduced in the paper titled Non-Euclidean statistics for covariance matrices, with applications to diffusion tensor imaging [6] written by Ian L. Dryden et al., They have given new algorithms for calculation of covariance matrices that are rooted in shape analysis. areas, including modelling longitudinal data.

Analysis of some of the recent growth in the estimation of covariance matrices when the number of variables is large compared to the number of observations is mentioned in the paper written by Jushan Bai et al., in their paper Estimating High Dimensional Covariance Matrices and its Applications [7]. They mainly concentrated in GMM (generalized method of moments estimation). In the paper "Diffusion Tensor Imaging of the Brain" by Andrew L. Alexander et al., [9] they described DTI as the Influential method for describing changes in tissue microstructure linked to brain disorders. The inadequacy of pathologic specificity of scalar DTI is also mentioned for blind diagnosis. They also discussed about white matter tracks detection, diffusion spectrum imaging and models. The poor understanding between the connectivity of functional areas of the human brain is discussed In the paper titled "Diffusion MRI of Complex Neural Architecture" written by David S. Tuch et al., [10]. They claimed this ability of q-ball imaging to find solution for the complex intravoxel fiber architecture removes an important obstacle to map neural connectivity in the human brain noninvasively. Their imaging is based on the Funk-Radon transform reconstruction, generally called as spherical Radon transform. They went on to show that QBI technique is better than DTI in several ways using experimental images.

Lawrence R. Frank in his paper titled "Characterization of Anisotropy in High Angular Resolution Diffusion-Weighted MRI" has employed group theory to the problem of characterizing the diffusion measured in high angular resolution MR

experiments. This led to a natural representation of the local diffusion in terms of spherical harmonics. In this illustration, it is proved that isotropic diffusion, anisotropic diffusion from a single fiber, and anisotropic diffusion from multiple fiber directions fall into distinct and separable channels.

This decomposition can be calculated for any voxel without any prior information by a spherical harmonic transform, and for distinct cases the magnitude and orientation of the local diffusion may be arrived at. Furthermore, non-diffusion-related irregularities produced by experimental artifacts fall into channels dissimilar from the fiber channels, thereby allowing their separation and a subsequent reduction in noise from the restored fibers. In the case of a single fiber, the algorithm reduced identically to the standard diffusion tensor method.

In their paper titled "Detection and Modelling of non-Gaussianity in MR Diffusion Imaging" by D. C. Alexander et al., a technique that is used for modelling the profile of the ADC over the sphere is proposed which handles the higher order, non-Gaussian effects that can happen at, for example, intersections of different tissue types or white matter fibre tracts.

When higher order effects are important, the common diffusion tensor model for the ADC profile was unsuitable, since it assumed of an underlying Gaussian diffusion process. A sequence of models of growing complexity was obtained by truncating the spherical harmonic expansion of the ADC calculations at several orders. Additionally, a method was described for selection of the most suitable of these models, to explain the data adequately and without overfitting. The combined process can be used to classify the profile at each voxel as isotropic, anisotropic Gaussian or non-Gaussian.

They have described approaches for modelling and detection of higher order ADC (apparent diffusion coefficient) profiles and presented that such profiles can be observed in standard clinical DW-MR data. The SH (spherical harmonic) series up to order 8 was fit to samples of the ADC profile in each voxel, which provides a sequence of models of increasing complexity. A series of ANOVA (analysis of variance) tests were used to find the simplest of these models that adequately describes the data.

Their procedure was applied to human brain data collected with parameters typical of those used in clinical scanners and performed to classify isotropic and anisotropic regions correctly as order 0 and order 2, respectively. Numerous regions the pons, the optic radiation and the corona radiation, were found reliably to contain a sizable proportion of order 4 models.

III.METHODOLOGY

3.1. Diffusion Tensor Imaging

The diffusion of water molecules to generate contrast in MR images is performed using Diffusion weighted magnetic resonance imaging.

To measure diffusion using MRI, magnetic field gradients are employed to create an image that is sensitized to diffusion in a direction. By repeating this process of diffusion weighting in multiple directions, a three-dimensional diffusion model (the tensor) can be estimated. In simplified terms, diffusion imaging works by introducing extra gradient pulses whose effect "cancels out" for stationary water molecules, and causes a random phase shift for molecules that diffuse. Due to their random phase, signal from diffusing molecules is lost. This loss of signal creates darker voxels (volumetric pixels). This means that white matter fiber tracts parallel to the gradient direction will appear dark in the diffusion-weighted image for that direction. The decreased signal (S_k) is compared to the original signal (S_0) to calculate the diffusion tensor (D) by solving the Stejskal-Tanner equation. This equation describes how the signal intensity at each voxel decreases in the presence of Gaussian diffusion:

$$S_k = S_0 e^{-\mathbf{g}_k^T \mathbf{D} \mathbf{g}_k}$$

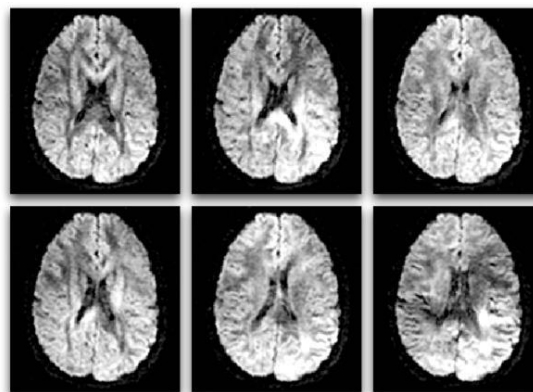


Figure.1 Six diffusion-weighted images (the minimum number required for tensor calculation).

S_0 is the original image intensity at the voxel (measured with no diffusion-sensitizing gradient) and S_k is the intensity measured after the application of the k th diffusion-sensitizing gradient in the (unit) direction $\hat{\mathbf{g}}_k$. The product $\mathbf{g}_k^T \mathbf{D} \mathbf{g}_k$ represents the diffusion coefficient (diffusivity) in direction $\hat{\mathbf{g}}_k$. Note that because the complete set of diffusion-weighted images is used (giving many values for S_k and $\hat{\mathbf{g}}_k$), this is a system of equations that is solved for D,

the diffusion tensor. To calculate the 6 independent numbers in the 3x3 symmetric matrix D, at least 7 images are needed: 6 diffusion-weighted images from 6 gradient directions (giving 6 values for S_k) plus one baseline image (giving S_0). But in clinical research today a higher number of images are almost always used. The above system of equations can be solved via the least squares method at each voxel.

In Diffusion MRI, the water molecules at a voxel diffuse concurring to a multivariate Gaussian model centred on the voxel and with covariance matrix 2D. The displacement of a water molecule $\mathbf{x} \in \mathbb{R}^3$ has probability density function

$$f(\mathbf{x}) = \frac{1}{(2\pi)^{\frac{3}{2}} |2\mathbf{D}|^{\frac{1}{2}}} \exp\left(-\frac{1}{2} \mathbf{x}^T (2\mathbf{D})^{-1} \mathbf{x}\right) \quad (1)$$

where D is the diffusion tensor (a 3x3 symmetric positive semi-definite real matrix). The diffusion tensor is calculated at each voxel in the brain, and is found by fitting a physically motivated model on measurements from the Fourier transform of the molecule displacements [14].

The eigen-system of the diffusion tensor contributes a key role in Diffusion MRI. Three eigenvectors V_1, V_2 and V_3 and their consequent positive eigenvalues λ_1, λ_2 and λ_3 (in decreasing order) overlap with the main diffusion directions and associated diffusion strengths, respectively. Specifically, the principal eigenvector V_1 , corresponding to the largest eigenvalue λ_1 , is aligned with the dominant fibre orientation at the voxel. The eigen-system also provides a visualisation method in the form of a diffusion ellipsoid for D (see Figure 1a) with principal axes given by the eigenvectors and lengths of axes proportional to $\sqrt{\lambda_i}, i=1, 2, 3$. The point that water molecular diffusion wishes to follow the orientation of fibres causes diffusion directional dependence (anisotropy). FA is one of the most popular anisotropy measures (see Figure2b) and the definition is

$$FA = \left(\sqrt{3 \sum_{i=1}^3 (\lambda_i - \bar{\lambda})^2} \right) / \left(\sqrt{2 \sum_{i=1}^3 \lambda_i^2} \right)$$

Where $\bar{\lambda}$ is the arithmetic mean of Eigen values? FA ranges from 0 for complete isotropy to 1 for linear anisotropy. There is an increasing need to develop processing tools for diffusion tensor data.

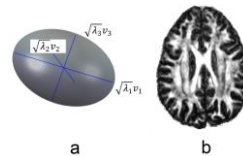


Figure 2. (a) Diffusion ellipsoid, (b) FA map

3.2 Euclidean Method to Valuing Mean Covariance Matrices

By considering an example of N covariance matrices (symmetric and positive semi-definite k x k matrices) S_1, \dots, S_N . For diffusion tensor data, $k = 3$. We presume that the S_i are independent and identically distributed (id.) from a distribution with mean T. The normal approach to estimate the mean covariance matrix is to assume a scaled Wishart distribution for the sample covariance matrices, and then the maximum likelihood estimator (mle) of the population covariance matrix is the arithmetic mean of the sample covariance matrices. This result can also be found if using a least squares approach by minimising the sum of square Euclidean distances. The Euclidean distance between two covariance matrices is given by

$$d_E(S_1, S_2) = \| S_1 - S_2 \|, \quad (2)$$

where $\|A\| = \sqrt{\text{trace}\{A^T A\}}$ is the Euclidean norm (also known as the Frobenius norm) Then the least squares estimator is given by

$$\hat{T}_E = \arg \inf_T d_E(S_i, T)^2 = \frac{1}{N} \sum_{i=1}^N S_i. \quad (3)$$

However the space of covariance matrices is certainly not Euclidean. By means of the arithmetic mean of the sample to estimate the population mean may not be suitable for covariance matrix data.

3.3 Non-Euclidean Calculations of Mean Covariance Matrix

As the space of covariance matrices is non-Euclidean, there is increasing need to use non-Euclidean metrics to evaluate the mean covariance matrix. It is first necessary to define what is meant by a mean covariance matrix in a non-Euclidean space. Let $f(S)$ be a probability density function of a covariance matrix S on a Riemannian metric space. The Fréchet mean is defined as

$$T = \arg \inf_T \frac{1}{2} \int d(S, T)^2 f(S) dS, \quad (4)$$

where $d(\cdot)$ is a non-Euclidean distance. For a sample of N covariance matrices S_1, \dots, S_N , the sample Fréchet mean is given by finding

$$\hat{T} = \arg \inf_T \sum_{i=1}^N d(S_i, T)^2. \quad (5)$$

In the following section, we will be discussing about one non-Euclidean distance metric called log-Euclidean.

IV. CONCLUSION AND FUTURE WORK

The paper is based on the identification of tumour affected brain using non-Euclidean approach that involves evaluation of mean covariance matrix. The comparison between the Euclidean and Non-Euclidean approach has been analysed. In Future work, the 3D view of brain will be analysed by Tractography. The fiber counts to be measured and comparison between the healthy and affected brain will be charted.

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