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, particularly in the brain. The primary objective of DTI is to estimate the diffusion tensor D∈R^(3×3) 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. 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. 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. 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

## 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 38–42 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 (MD) and fractional anisotropy (FA).

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.