Microstructure model selection in fetal diffusion MRI

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Background

Diffusion MRI is sensitive to the microstructural and microcirculatory properties of tissue, and is emerging as a promising tool for diagnosis and monitoring of the mother and fetus during pregnancy. However, this is a relatively new application, and there has been little diffusion MRI model development compared to other organs, such as the brain. Consequently, the best models for quantitative assessment of pregnancy-specific tissue structures – such as the placenta, uterine wall, and fetal organs – are not known.

In this project, you will fit a variety of models to diffusion MRI scans acquired during pregnancy, and quantify which models best describe the data within distinct tissue regions.

Associated publications: https://onlinelibrary.wiley.com/doi/abs/10.1002/mrm.27036
https://www.sciencedirect.com/science/article/pii/S1053811911011566

Prerequisites: Basic MATLAB

Code

You can download the code from https://github.com/PaddySlator/summer-school-project.

Microstructural models for diffusion MRI

[Note: This is a sort of "cheat sheet". I've tried to (hopefully!) give you enough knowledge to complete the project without having to look at the papers above. If you want to learn more you can look at those in more detail later.]

A diffusion MRI (dMRI) scan is a series of images with varying diffusion weighting. The diffusion weighting can be described by the gradient table. This is a table with each row corresponding to a single dMRI volume. The rows are as follows – [gx gy gz b], where gx, gy, gz are the gradient strengths in the x, y, and z directions, and b is the b-value. So in

We can analyse dMRI data using a wide variety of microstructural models. The simplest and most well-known is the apparent diffusion coefficient (ADC) model. This model relates the observed signal (S) to the b-values with a simple exponential decay function.

$$S(b) = S0 \exp(-b D)$$

where S0 is the signal with no diffusion weighting (b-value = 0), b is the b-value, and D is the apparent diffusion coefficient.

We often normalize the image so that the b=0 volumes equal 1. This accounts for different T2-weighting in the b=0 images. In the project, we use normalized dMRI data, so the fitted values you get for S0 will be around 1.

However, the ADC has many flaws. For one it doesn't account for the contribution to the signal from different tissue compartments with vastly different diffusivities. For example,

water within perfusing blood diffuses much faster than water within tissue. Models which do account for this are called multi-compartment models. The intravoxel incoherent motion (IVIM) model is one example. This is given by

$$\mathrm{S(b)} = \mathrm{S0}[\mathrm{f}\exp(-\mathrm{bD_p}) + (1-\mathrm{f})\exp(-\mathrm{bD})]$$

where f is the perfusion fraction and D_p is the pseudo-diffusivity. The first term is associated with perfusing blood, and the second term with diffusion in tissue. D_p is larger than D, so the first term describes the signal attenuation at lower b-values, and the second term at higher b-values.

We could also model the effects of three compartments with separate diffusivities on the signal with a tri-exponential model, given by

$$\mathrm{S(b)} = \mathrm{S0}[f_1\exp(-\mathrm{bD_1}) + f_2\exp(-\mathrm{b}D_2) + (1-f_1-f_2)\exp(-\mathrm{b}D_3)]$$

Model fitting

We fit microstructural models to the data using maximum log-likelihood estimation assuming Rician noise. The log-likelihood of the Rician distribution is

$$\ln\hat{L} = \sum_{i=1}^{N} \ln S_i - 2\ln\sigma - \frac{S_i^2 + \tilde{S}_i^2}{2\sigma^2} + \ln I_0\left(\frac{S_i\tilde{S}_i}{\sigma^2}\right)$$

where $\widetilde{S_i}$ are the measured signals, S_i are the model predicted signals, σ is the standard deviation on the real and imaginary parts of the signal, and I_0 is the modified Bessel function of the first kind. We will use the matlab function fmincon to fit the models to the data, using the negation of the log-likelihood as the objective function (since fmincon is a function minimizer).

Model selection

We will calculate the Bayesian information criterion (BIC) model selection statistic. This is given by

$$\mathrm{BIC} = -2\ln\hat{L} + k\ln n$$

where $\ln\hat{L}$ is the maximised value of the log-likelihood, k is the number of model parameters and n is the number of observations (i.e. the total number of dMRI volumes). The model with the lowest BIC value best explains the data, i.e., provides the best tradeoff between model complexity and goodness of fit. Additionally, the strength of preference between a pair of models (1 and 2) can be assessed with

$$\Delta\mathrm{BIC} = \mathrm{BIC_1} - \mathrm{BIC_2}$$

A ΔBIC of 10 or more implies “decisive” preference for the model with lower BIC (see Kass and Raftery (1995), J. Am Stat Assoc.).

Bonus section - Anisotropic models

So far, we have only used the b-value in our models – discounting the effect of gradient direction on the dMRI signal. Some tissue types (e.g. white matter, muscle) have a coherent orientation, and therefore the dMRI is anisotropic – the signal attenuation depends on the gradient direction. A simple anisotropic is the diffusion tensor model (i.e. DTI)

$$\mathrm{S(b,G)} = \mathrm{S0}\ \exp(-\mathrm{bG^T}\mathbf{D}\mathrm{G})$$

where **D** is a six-parameter diffusion tensor, and G=[gx gy gz] is the diffusion gradient direction.

A simple example of a multi-compartment microstructural model which also accounts for anisotropy is stick-ball

$$\mathrm{S(b,G)} = \mathrm{S0}[\mathrm{f}\exp\left(-\mathrm{b}\ \mathrm{D_p}\ (\mathrm{n}.\mathrm{G})^2\right) + (1-\mathrm{f})\exp(-\mathrm{bD})]$$

Here n is the fibre direction, which defines the orientation of the "stick" compartment. It is usually parameterised by angles θ and φ as follows: $\mathrm{n} = (\cos\phi\sin\theta, \sin\phi\sin\theta, \cos\theta)$.