Bayesian reconstruction of low resolution magnetic resonance imaging modalities

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1 Introduction

Magnetic Resonance Imaging (MRI) data are available in a large variety of modalities that individually can provide anatomical, metabolic, physiological, and functional descriptions of the brain. Structural MRI (sMRI) is now standard for the diagnosis of soft tissue injury, especially for delineation of anatomical features in the brain. Unfortunately, although most Magnetic Resonance (MR) modalities have great potential for aiding clinical applications including diagnosis and surgical intervention, some are not attainable with the high signal-to-noise ratio (SNR) of sMRI, and hence are necessarily acquired at low spatial resolution. This research aims to utilise information from the high SNR modality of sMRI in order to boost the effective resolution of lower SNR MRI modalities.

sMRI of the brain provides high resolution maps of signal intensity contrasts between different types of tissue, such as grey matter (neuronal cell bodies), white matter (axons) and cerebro-spinal fluid. The segmented sMRI maps are here employed as prior information to enable improved resolution reconstruction of lower resolution MRI modalities such as: Perfusion Imaging for measuring blood flow, Magnetic Resonance Spectroscopy Imaging (MRSI) for measuring metabolite levels and Diffusion Tensor Imaging (DTI) for measuring water diffusion in tissue.

2 General model formulation

In order to obtain locational information in MRI, linear magnetic field gradients are applied in the x (k_x) and y (k_y) directions so that the frequency (or phase) of the observed MRI signal is effectively encoded to provide spatial information.

A simplified general format for MRI data takes the following form: data is obtained at individual points in k-space [or frequency space] (k_x, k_y) where each k-space point corresponds to a particular setting of the magnetic field gradients. MRI data is acquired in k-space so that the observed data is:

$$d[k_x, k_y] = s[k_x, k_y] + \epsilon[k_x, k_y] \tag{1}$$

where $\epsilon[k_x, k_y] \sim N(0, \sigma^2)$.

The k-space signal, $s(k_x, k_y)$ comprises complex amplitude data summed over all the locations in the image corresponding to the k-space point (k_x, k_y):

$$s[k_x, k_y] = \sum_{p=1}^{P} \sum_{q=1}^{Q} \int_{y[q]-\frac{1}{2}}^{y[q]+\frac{1}{2}} \int_{x[p]-\frac{1}{2}}^{x[p]+\frac{1}{2}} A[x, y] \exp\left\{2\pi i \left[k_x x/P + k_y y/Q\right]\right\} dxdy \tag{2}$$

where, $s[k_x, k_y]$ is the 'true' signal at point (k_x, k_y) in k-space, $p = 1, \ldots, P$ and $q = 1, \ldots, Q$ are the sets of values for the co-ordinates (p, q) of pixel locations matched to the resolution of the high resolution sMRI, and the $A[p, q]$ terms are the signal amplitudes for the pixels (p, q), i.e. the unknown parameters of interest in image (Euclidean) space.

Making the assumption that the signal is constant within each pixel in image space at the high resolution of the sMRI, the analytic solution to the integral (2) is:

$$s[k_x, k_y] = \frac{\sin(\pi k_x/P)}{\pi k_x/P} \frac{\sin(\pi k_y/Q)}{\pi k_y/Q} \sum_{p=1}^{P} \sum_{q=1}^{Q} A[p, q] \exp\{2\pi i [k_x p/P + k_y q/Q]\} \qquad (3)$$

(Note that the integral can be analytically obtained when each $A[p, q]$ is defined by a polynomial surface and this property is later exploited in order to fit a continuous spline surface to the signal in MRSI analysis.)

3 The likelihood

The likelihood adopted relates the low-resolution imaging modality's signal (observed in k/frequency-space) to the map to be reconstructed in standard image space (e.g., Miller and Schaewe 1995) and takes the form:

$$\begin{aligned} \pi(d|s) &\propto \exp\left\{ -\frac{1}{\sigma 2} \sum_{(k_x,k_y)} |d[k_x, k_y] - s[k_x, k_y]|^2 \right\} \\ &= \exp\left\{ -\frac{1}{\sigma 2} \sum_{(k_x,k_y)} \left| d[k_x, k_y] - \frac{\sin(\pi k_x/P)}{\pi k_x/P} \frac{\sin(\pi k_y/Q)}{\pi k_y/Q} \times \right. \right. \\ &\qquad \left. \left. \sum_{p=1}^{P} \sum_{q=1}^{Q} A_1[p, q] \exp\{2\pi i [k_x p/P + k_y q/Q]\} \right|^2 \right\} \qquad (1) \end{aligned}$$

This has complicated dependence structure, therefore to aid posterior optimisastion algorithms (e.g. Geman and Geman,1984) the model is expanded to

$$\sum_{(p,q)} z[p, q, k_x, k_y] = s[k_x, k_y] + \epsilon[k_x, k_y]$$

The $z[p, q, k_x, k_y]$ terms can be considered as missing (unobservable) data. Each $z[p, q, k_x, k_y]$ is the contribution of data from the point (k_x, k_y) in k-space $(d[k_x, k_y])$ to the amplitude $(A[p, q])$ at pixel (p, q).

4 Incorporating prior information

The prior information incorporated into the model is based on knowledge of tissue type obtained from segmented sMRIs. Regularity conditions are incorporated via Markov random field priors applied within each tissue type (i.e. the objective is to smooth within each of CSF, grey and white matter, but to reduce the penalty for discontinuities in amplitude when they occur across boundaries. Further, regions outside the brain have intensities set to zero.

The prior distribution is defined by a modified intrinsic Gaussian Markov random field model (e.g., Besag and Kooperberg, 1995) at the spatial resolution of the sMRI:

$$\pi(A) \propto \exp\left\{ -\frac{1}{2\tau_1 2}\left[\sum_{<(p,q),(p',q')>} \left(I_{M_{\{(p,q),(p',q')\}}} + \delta I_{N_{\{(p,q),(p',q')\}}} \right) (A[p,q] - A[p',q'])\, 2 \right] \right\}$$

subject to A being constrained to zero outside of the brain.

The sum over $< (p,q),(p',q') >$ is the sum over all pairs of 'neighbouring' pixels (p,q) and (p',q'). The functions $I_{M_{\{(p,q),(p',q')\}}}$ and $I_{N_{\{(p,q),(p',q')\}}}$ are indicator functions for matching and non-matching pairs of tissue type respectively. The parameter δ describes the relative smoothing for non-matching neighbours as compared to matching neighbours with $0 \leq \delta < 1$. Allowing $\delta > 0$ helps prevent undesirable edge effects at the boundaries of tissue type within the brain. The overall effect of this prior model is to encourage smoothness within homogeneous tissue type while allowing jumps when crossing tissue type boundaries.

In simulation studies we observed that optimisations of the ensuing posterior distribution provided much improved reconstructions over those obtained using standard discrete Fourier transform methods. The Bayesian reconstruction provided solutions that better resembled the true map, with much reduced Gibbs ringing and noise.

5 Application to specific MRI modalities

Arterial spin labeled (ASL) perfusion MRI

ASL perfusion MRI, which uses blood water as an endogenous tracer for cerebral blood flow, suffers from poor SNR, because labeled blood water is only a tiny fraction of the overall MRI water signal from the brain. ASL perfusion MRI is typically acquired at a resolution of several millimeters, compared to 1mm for sMRI, therefore lacking anatomical specificity. Moreover, since perfusion of grey matter is usually 2-3 times higher than perfusion of white matter, poor spatial resolution introduces a bias towards lower perfusion values along grey/white matter boundaries because of grey/white matter partial volumes. Therefore, accuracy in measuring regional brain perfusion should increase with better spatial resolution. The proposed method in this paper is directly applicable in its simple form described above to this data.

MRSI

MRSI, which detects certain brain metabolites, suffers from poor SNR because most brain metabolites are of the order of 10^{-5} less concentrated than water. Spatial resolution of MRSI is therefore, similar to ASL perfusion, in the range of several millimeters to a centimeter.

A further difficulty when dealing with MRSI data is the increased dimensionality of the problem. There is a time component to the data so that the signal becomes $s[k_x, k_y, t]$ and the brain metabolites contribute separate signals (at different frequencies) so that there are m metabolites amplitudes $A_m[x,y]$ that need to be separated.

Although this model can readily be extended to deal with MRSI data by adding in the temporal decay components for the separate metabolite components, the size of the problem is not currently computationally tractable. The proposed method to address this issue is to first generate a nonuniform multi-resolution pixel grid from the high resolution segmented image by optimising a combined entropy (favouring tissue homogeneity in pixels) and complexity (penalizing against high resolution in homogeneous pixels) function on the generated voxel grid.

Then in each voxel a spline function for each metabolite is fit to the data. Splines constitute an appropriate choice for a number of reasons, chief among them 1) that they have been shown to be optimal interpolation functions over a broad range of medical imaging modalities (Meijering, 2000) and 2) the ability to obtain analytic (though fairly complicated) functions in k-space, mentioned above, to fit directly to the data, avoiding the well known and problematic FFT artifacts.

DTI

DTI, which can probe the directional diffusivity of tissue water, reflecting ultra-structural tissue properties, also suffers from low SNR, because diffusion in the presence of a magnetic field gradient attenuates the MRI signal. In addition, to determine the spatial anisotropy of diffusion, measurements have to be repeated along multiple unique gradient directions, which markedly prolongs acquisition time. Therefore, limiting spatial resolution for DTI acquisition not only helps to increase SNR, but also to shorten scan time. This model allows the acquisition of DTI at lower spatial resolution in order to gain SNR and scan time, while recovering spatial information from the segmented sMRI. For DTI, the signal is extended to include a diffusion gradient, i.e. the signal is now $s[k_x, k_y, k_d]$ where k_d is the diffusion gradient, and the signal amplitude $A[x, y]$ becomes a tensor matrix at (x, y). The modelling extensions required here are predominantly related to the prior distribution and centre on setting up the neighbourhood relationships for the tensor elements in neighbouring voxels.

A recently developed simulation program that allows for the detailed specification of anatomical models will allow us to test various prior distributions in known models containing multiple local diffusion tensors and neighbourhood dependency structures.

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