Semi-automatic segmentation of bony lesions from diffusion weighted MRI to assess disease burden and quantify response using Markov random fields

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Introduction: The use of diffusion weighted imaging (DWI) in oncology is gaining popularity for detection of disease. A combination of low diffusion coefficients (ADC) and long T_2 values in tumours means that signal from suspect malignancies in fat suppressed images acquired at high b-values is hyper-intense compared to normal background tissues. Employing whole body diffusion-weighted MR imaging with background suppression (DWIBS) enables visual localization of metastases throughout the body [1]. Although this method has shown great promise for staging disease and for monitoring treatment effects, data processing and interpretation of these large volume sets remains a major challenge and clinicians are typically required to provide qualitative assessment and/or assess the changes in a target lesions by manually defining regions of interest (ROIs). Here we provide a semi-automatic method for defining suspect regions in DWIBS data sets using Markov random field models (MRFs) and assess the utility of this technique for providing whole body tumour volume estimates.

Methods:

Segmentation- An illustration for the segmentation scheme is presented in Figure 1. The input is a set of acquired b-value images and the corresponding ADC maps. The user is initially presented with a window containing a maximum-intensity projection of computed DWI data at an arbitrary, usually high b-value (typically b > 1000 s/mm^2) as calculated from the acquired DWI images (typically b < 1000 s/mm^2). A threshold is then visually modified to separate background from disease signals. The use of computed DWI has been studied in previous reports and has shown improved background signal suppression [2]. Once the starting threshold has been defined the following MRF posterior is maximized using the iterated conditional modes (ICM) algorithm [3]:

$$P(x_i \mid y_i, x_{\partial i}) \propto P(y_i \mid x_i) P(x_i \mid x_{\partial i})$$

where x_i represents the label at voxel i (0 or 1 representing background or disease respectively), y_i represents the computed signal at i and ∂i symbolises the neighbourhood of i (we use a second order neighbourhood in the axial plane and a first order neighbourhood in the inferior-superior direction due to anisotropic voxel shape). Models for the conditional probability $P(x_i|x_{\partial i})$ may take various forms but we have chosen the Ising model [4], which incorporates a parameter β to represent the attraction for neighboring pixels to have the same label. We use β=1 but further optimization may be required for specific disease conditions. The form of $P(y_i|x_i)$ depends on the imaging model and is largely used to include noise. Unfortunately, the exact form is intractable for computed imaging but we have found an approximation that works well for segmentation purposes. Background signal, $P(y_i|x_i = 0)$, is modelled by a Rayleigh distribution, whose parameters are re-calculated at each iteration of the ICM algorithm. Disease signal, $P(y_i|x_i = 1)$, is then modeled by a uniform distribution whose amplitude equals $P(y_i|x_i = 0)$ at the starting threshold value. We have performed convergence tests on the suggested procedure and found good convergence after 3 iterations of ICM algorithm. ***Image acquisition***- DWIBS imaging was performed on a 1.5T MR imaging system (Avanto, Siemens Healthcare, Erlangen, Germany) using a repetition time of 14000ms, echo time of 67/68ms, matrix size of 128x104x150/128x104x200, slice thickness of 5mm, receiver bandwidth of 1628 Hz/pixel, 6 signal averages, STIR fat suppression with an inversion time of 180 ms and an imaging field of view set to 430x430 mm^2. Images were acquired at b = 50/800 s mm^{-2} (pre-treatment) and b = 50/900 s mm^{-2} (post-treatment). ***Analysis***- This segmentation scheme was applied to a female patient diagnosed with extensive bony metastases from primary breast cancer. Images were taken 9 weeks apart both before and after treatment with chemotherapy and bisphosponates. Segmentation was used to evaluate treatment response through volumetric tumour burden estimates (shown in ml above figure 1 and 2).

Figure 1

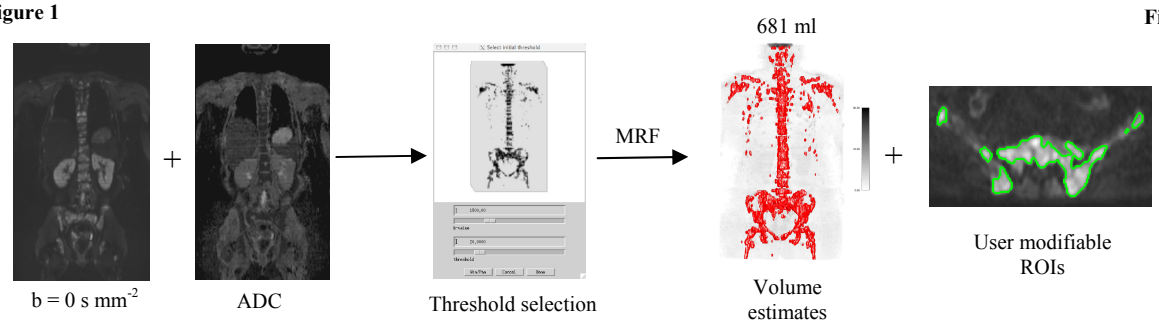

Figure 2

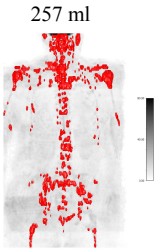

Figure 1: A schematic demonstrating the processing pipeline of the proposed segmentation algorithm. Computed DWI is used to provide users with an increased degree of freedom over the choice of viewing b-value used when producing the initial threshold selection. In this case the b-value was chosen to be 1500 s/mm^2 and the threshold to be 20. The resulting segmentation results can be viewed as an entire volume overlain on top of a maximum-intensity projection, or as individual ROIs that can be modified by the user. **Figure 2:** Segmentation results for the same patient shown in figure 1 after treatment using the same initial b-value and threshold.

Results: Figure 1 and 2 demonstrate the segmentation results of the patient before and after treatment respectively. Visually there is a clear reduction in the extent of disease as determined using this segmentation procedure. This is reflected by total bone marrow tumour volume estimates of 681ml and 257ml before and after treatment respectively. The time taken to perform such a routine requires ~4 minutes on a standard PC (2.4 GHz dual core processor), vastly reducing the processing time to provide whole body regions of interest.

Conclusion: The large amount of data obtained in whole body diffusion weighted imaging can be difficult to analyze. Although the image contrast can provide exquisite qualitative information on the location and extent of disease; detailed, quantifiable analysis of all suspect lesions remains a major challenge. Typically, a representative target lesion is chosen from the data to perform quantitative assessment of the disease, such as ADC value or lesion diameter, but this ignores other lesions where treatment response may be different. Here we have proposed a simple, fast and semi-automatic method of obtaining whole body regions of interest in DWI, using markov random field models. This method holds promise for providing estimates of tumour volume throughout the body, which is a useful biomarker for monitoring treatment. Changes in whole body tumour ADC values can also be used to monitor therapy response in the segmented volumes provided adequate registration between data sets can be achieved. There is a need to demonstrate the utility of this method on a larger patient cohort. However, there is potential for this technique to provide clinicians with a powerful tool for evaluating therapy response of the whole body metastatic tumour burden in an objective way via tumour volume and ADC changes.

References: [1] Takahara *et al*., Radiat Med 2004; 22(4):275-282, [2] Blackledge *et al*., Proc 18th Annual Meeting ISMRM 2010, [3] Besag, J. R. Statist. Soc. B 1986; 48(3):259-302, [4] Ising, Z. Phys. 1925; 31:253:258

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