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Abstract

The presented method addresses the problem of multi-spectral image segmentation through use of a model which takes into account the physical process of the medical image formation. In particular the method addresses the problem of partial volumes of tissues being present in a single voxel due to imaging process. The partial volume effect is evident at tissue boundaries and not accounting for it results in tissue misclassification. Multiple images of different modalities are used to improve segmentation, as better tissue separation can be achieved in a higher dimensional space. The parameters of the multi-dimensional model of pure tissues and their mixtures are iteratively adjusted using an Expectation Maximisation (EM) optimisation technique. Bayes theory is used to generate probability maps for each segmented tissue which estimates the most likely *tissue volume fraction* within each voxel as opposed to previous approaches which attempt to compute how likely a certain grey level would be generated by a particular tissue class.

1 Introduction

The physical processes underlying medical imaging equipment such as computed tomography (CT) and magnetic resonance imaging (MRI) result in the production images in which the contrast mechanism is based on a physical property of the tissues such as X-Ray attenuation or proton density. Accurate segmentation of images offers the opportunity to produce parametric images of tissue type (i.e. grey matter, white matter, tumour etc.) that are more relevant to clinical investigation. Once the images are segmented and tissue models obtained they can be used for extraction of tissue boundaries or volume rendering for visualisation purposes. Derived 3D models of scanned anatomy can then be applied to pre-operative planning, surgical rehearsal and training [1].

A common approach for medical image segmentation involves modelling only pure tissue intensity distributions. However, in a significant proportion of clinical data a mixture of tissues can be present in any given voxel. The data cannot be analysed as simply the competing interpretation of mutually exclusive hypotheses. Accurate interpretation of the data requires that partial volume distributions must be modelled [2]. Knowledge of the physics of image formation in a wide variety of medical image data allows us to conclude that partial volume distributions for paired tissue combinations can be modelled as a linear process. Relative fractions of different tissues contribute proportionately to the intensity in a given voxel [3]. It will be shown in this paper that this assumption can be tested easily on candidate data sets by forming scatter plots of data from pairs of images. We define a computational approach to model these partial volume distributions. As in other work, the Expectation Maximisation (EM) algorithm [4, 5] is utilised for the estimation of parameters of the multi-dimensional models. In addition we extended the EM approach for terms which describe both the pure and partial volume tissues. The conventional interpretation of this algorithm is as a system for estimating unseen variables. Used here it should simply be interpreted as an efficient way of fitting a density model to a multi-dimensional data set.

The devised method is based on Bayesian probability theory which obtains conditional probabilities for a particular tissue type given the data based on the probability density functions of the image intensity distribution. Derived conditional probabilities provide the answer to the question of how likely it is that a certain grey level was generated by a particular part of the model. The statistical separability of tissues will seldom be adequate for individual image types but can be improved by the use of multiple spatially co-registered images that are chosen to decorrelate the statistical distributions of individual tissues in the tissue space. The use of multi-spectral data also allows estimation of partial volume effects based on observed expected intensity values for pure tissues.

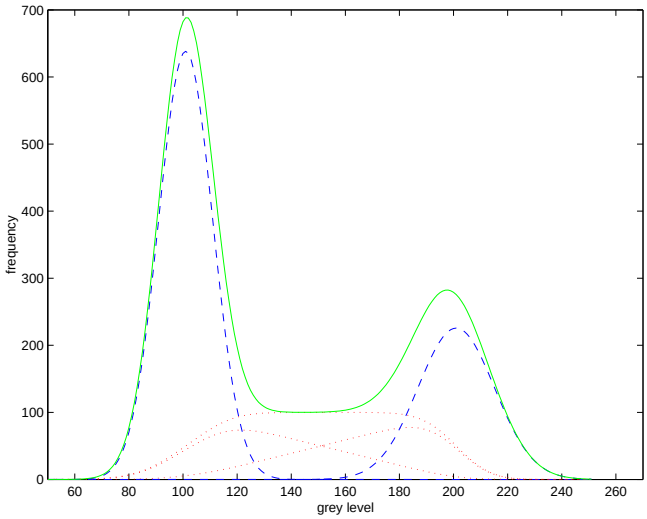


Figure 1: Pure tissues have Gaussian distribution (*blue dashed line*); Mixtures of tissues take form of triangular distribution convolved with Gaussian (*dotted red line*); The resulting distribution for a particular tissue is sum of two distributions (*solid green line*)

2 Segmentation Method Outline

The pure tissues have been modelled using a Gaussian distribution, while mixtures of tissues take the form of a triangular distribution convolved with a Gaussian (see Fig. 1).

The multi-dimensional Gaussian distributions model the effects of both inherent tissue variability and measurement noise. A multi-variate Gaussian distribution for multi-dimensional data $\mathbf{g}$ for each pure tissue t is defined as

$$d_t(\mathbf{g}) = \alpha_t e^{-\frac{1}{2}(\mathbf{g}-\mathbf{M_t})^T C_t (\mathbf{g}-\mathbf{M_t})}$$

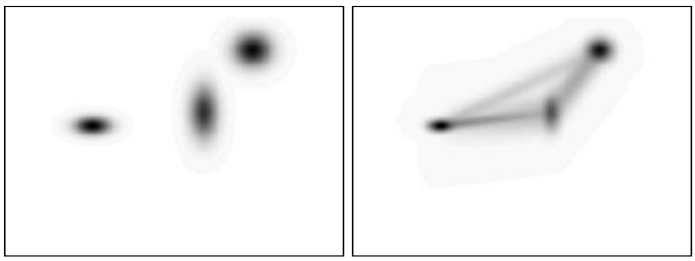
where:
$\mathbf{M_t}$ is a mean tissue vector
C_t is an inverse of covariance matrix
α_t is a constant which gives unit normalisation

In [2] partial volume distributions were modelled as a uniform (1D) distribution convolved with a fixed point spread function. This model is valid for an equal prior probability of all possible partial volumes. In our approach, using an assumption of a linear image formation process, this partial volume distribution can be thought of as being composed of two triangular distributions convolved with a Gaussian ($T_{ts}(\mathbf{g}) + T_{st}(\mathbf{g})$), where $T_{ts}(\mathbf{g})$ is the local density estimate for tissue t generated by a partial voluming process with tissue s. This model can take a range of different forms depending upon the level of measurement noise and tissue variability. Assuming that tissue variability is more significant than the measurement processes, multi-dimensional partial volume distributions can be modelled along the line between two pure tissue means $\mathbf{M_t}$ and $\mathbf{M_s}$

$$d_{ts}(\mathbf{g}) = \beta_{ts} T_{ts}(h) e^{-\frac{1}{2} N(\mathbf{g})^{\mathbf{T}} \mathbf{C_h} \mathbf{N}(\mathbf{g})}$$

where the parameters for the given data $\mathbf{g}$ are:
h is a fractional distance between two centres of distribution $[0 < h < 1]$
$h = (\mathbf{g} - \mathbf{M_s})^T C_h (\mathbf{M_t} - \mathbf{M_s}) / |(\mathbf{M_t} - \mathbf{M_s})^T C_h (\mathbf{M_t} - \mathbf{M_s})|$
C_h is an inverse covariance matrix: $C_h = C_t h + C_s (1 - h)$
$T_{ts}(h)$ is the 1D partial volume triangular distribution
$N(\mathbf{g})$ is the normal distance of $\mathbf{g}$ from the line between two centres of distribution
β_{ts} is a constant which gives unit normalisation

As the definitions of h and C_h are dependent the first two steps of this process must be performed as an iterated closest point algorithm. The partial volume distribution is calculated as a product of Gaussian function for normal distance $N(\mathbf{g})$ from two distribution centres and 1D partial volume triangular distribution $T_{ts}(h)$. Examples of the



(a) (b)

Figure 2: An example of distributions generated from the model for two images (a) Pure tissue distributions (b) Combined distributions of pure tissues and partial volumes between centres of pure tissues

types of distributions obtained from the model parameters of two images for pure tissue and their partial volumes are shown in Figure 2.

It can be seen that pure tissue distribution models take the form of nearly circular features, while the partial volumes are shown as elongated structures between centres of distributions. The scatter plots of pairs of images had shown that the combined pure and mixture of tissues model is in good agreement with real data.

3 Model Parameter Estimation

Parameters of the model can be iteratively estimated using the Expectation Maximisation (EM) approach [4] [6]. EM is used to estimate the parameters by maximising the likelihood of the data distribution. This involves first getting from the likelihood distributions defined above to a probability of a given tissue proportion given the data $P(t|\mathbf{g_v})$. The conditional probability of a grey level being due to a certain mechanism n (either a pure or mixture tissue component) can be calculated using Bayes theory

$$P(n|\mathbf{g}) = \frac{d_n(\mathbf{g})f_n}{f_0 + \sum_t d_t(\mathbf{g})f_t + \sum_t \sum_s d_{ts}(\mathbf{g})f_{ts}}$$

where f_n, f_0, f_t and f_{ts} are effectively "priors", expressed here as frequencies (i.e. number of voxels) which belong to a particular tissue type, pure tissues or partial volumes. Unknown tissues are accounted for in the Bayesian formulation by including a fixed extra term f_o for infrequently occurring outlier data [7] in total probability which enables separation of pathological tissues.

The EM approach has been applied for the estimation of model parameters for pure and mixture tissues, (f_t, f_{ts}), mean $(\mathbf{G_t})$ and covariance matrices (C_t) which take the form

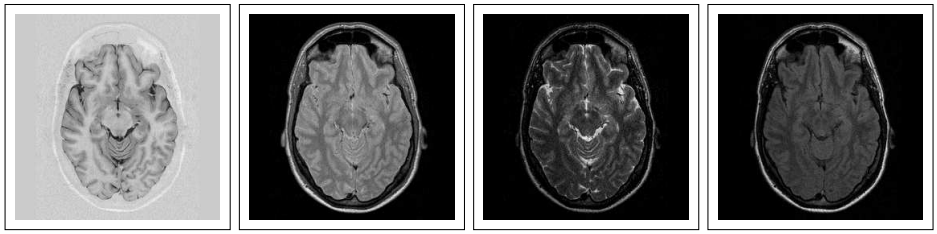
$$f'_t = \sum_v^V P(t|\mathbf{g}_v) \qquad and \qquad f'_{ts} = f'_{st} = \frac{1}{2}\sum_v^V P(ts|\mathbf{g}_v) + P(st|\mathbf{g}_v)$$

$$G'_t = \frac{1}{V}\sum_v^V P(t|\mathbf{g}_v)\mathbf{g}_v \qquad and \qquad {C'}_t^{-1} = \frac{1}{V}\sum_v^V P(t|\mathbf{g}_v)(\mathbf{g}_v - \mathbf{G_t}) \otimes (\mathbf{g}_v - \mathbf{G_t})^T$$

By using this representation it is possible to obtain the most probable volumetric measurement V_t for each tissue t given the observed data $\mathbf{g_v}$ in voxel V

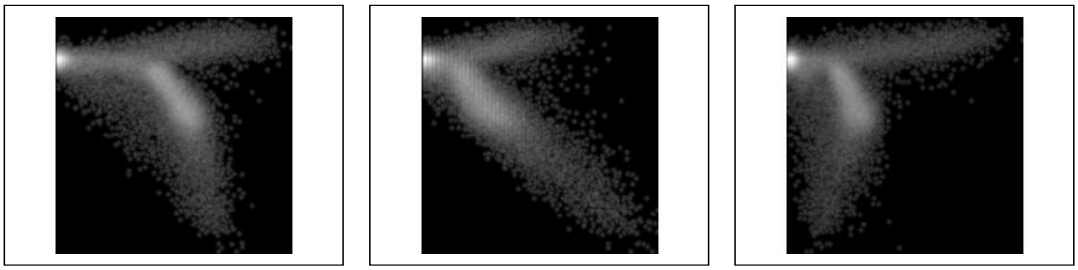
$$V_t(\mathbf{g_v}) = P(t|\mathbf{g_v}) + \sum_t P(ts|\mathbf{g_v})$$

The **Expectation** step recalculates multi-dimensional probability density, while the **Maximisation** step involves re-estimation of model parameters in a maximum likelihood (i.e. least squares) manner. The method is guaranteed to converge [8], but suffers the same problems of all such optimisation techniques. In particular, it can converge to a local minimum and can also be badly affected by outliers. Therefore, it is necessary to be able to derive initial estimates of parameters in such way that the assumed density model corresponds well to the true distribution of the data. It is therefore important that all aspects of the multi-dimensional distribution are modelled. The problem of outliers shows itself in density estimation problems as data points which are well away from the expected



(a) (b) (c) (d)

Figure 3: Image Sequences : (a) IRTSE (b) VE(PD) (c) VE(T2) (d) FLAIR



(a) (b) (c)

Figure 4: Scatter plots : (a) IRTSE and VE(PD) (b) IRTSE and VE(T2) (c) IRTSE and FLAIR

distribution. One way to deal with this is to use an outlier class. However, partial voluming produces data which lies between pure tissue regions and can occur in such quantities that this approach is not sufficient to solve the problem. The problem is likely to worsen with the use of multi-dimensional data as the pure tissue distributions become more separated in the space.

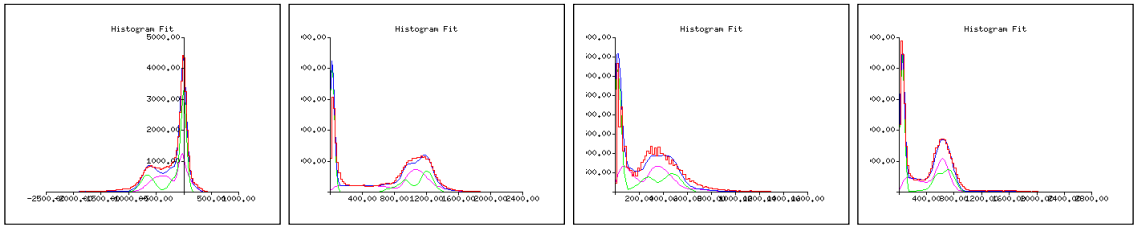
4 Segmentation Results

The devised algorithm has been implemented and tested on a number of co-registered MRI brain images of different modalities chosen for their good tissue separation and availability in a clinical environment. These images, variable echo proton density and T2 (VE (PD) and VE (T2)), inversion recovery turbo spin-echo (IRTSE) and FLAIR are shown in Fig. 3.

Selected images provide a good separation between air and bone, fat, soft tissue (such as skin and muscle), cerebro-spinal fluid (CSF), grey matter (GM), and white matter (WM). Voxel dimensions in acquired images are 0.89 x 0.89 x 3.5 mm^3. The greater the thickness of the slice the better the signal to noise ratio in the data, but the problem of partial voluming increases as there is a higher chance of a tissue boundary passing through a voxel. This in turn makes quantitative measurement of the data more difficult.

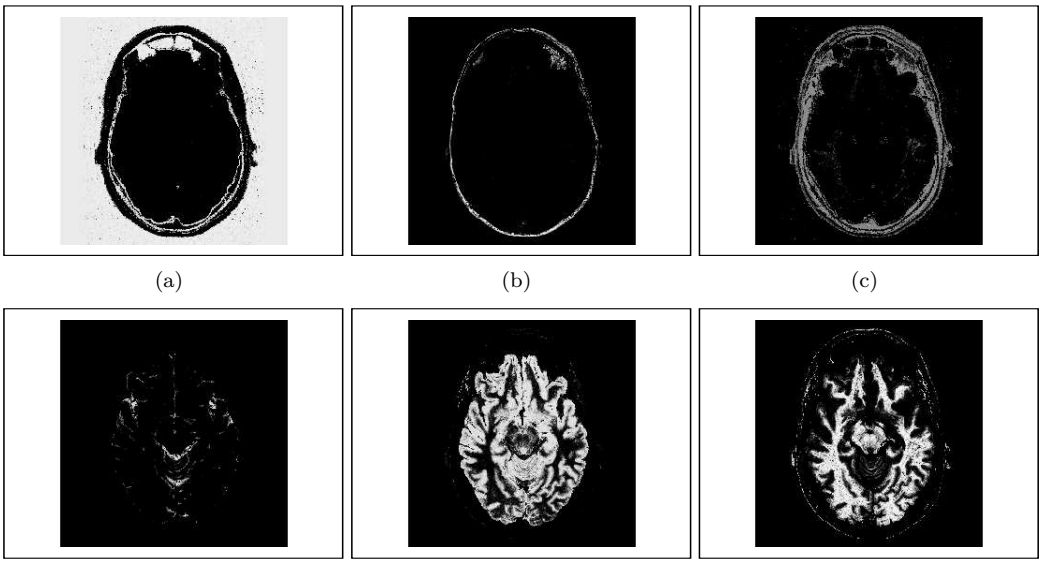
As previously discussed, the segmentation method is based on the assumption that the contribution to the intensity in any pixel is proportional to the relative fractions of each tissue within a voxel. For this to be true the partial volumes of tissues have to lie between centres of corresponding intensity distributions. To make sure that this condition has been met, for these data types, scatter plots have been generated for pairs of the acquired test images. The result can be seen in Fig. 4, which clearly demonstrates partial volume effects as elongated structures. Pure tissues form compact (nearly circular) features.

Prior to multi-spectral segmentation stage the data sets had to be co-registered, and variations in local image intensity due to artefacts of the imaging process had to be corrected [9]. The initial values of parameters were estimated from the images and stored in the file. Multi-spectral segmentation was then performed for six different tissue classes on four images (i.e. in four dimensions) by applying expectation and maximisation steps in turns. It has been found that the algorithm converges within 10 iteration steps. Figure 5 illustrates the resulting distribution models obtained after ten iteration of EM algorithm for each dimension. It can be seen that the model is in good agreement with data and that a partial volume model accounts for almost half of data present, hence emphasising the importance of inclusion of that part of a model.



(a) (b) (c) (d)

Figure 5: Histogram (stepped line) and corresponding model (solid line) plots for each image: (a) IRTSE (b) VE(PD) (c) VE(T2) (d) FLAIR



(a) (b) (c)

(d) (e) (f)

Figure 6: Probability maps for: (a) Bone and air (b) Fat (c) Soft tissue (d) CSF (e) GM (f) WM

The resulting Bayesian probability maps are generated for each tissue type and can be seen in Fig. 6.

The probability maps range from 0 to 1 and can be used for boundary location extraction (e.g. 0.5 probability point represents the boundary location between two tissues) or volume rendering.

5 Conclusion

The multi-dimensional image segmentation with partial voluming discussed in this paper provides a novel way for more accurate segmentation of medical images of different modalities. It has been found that half of the data we observed is due to the partial voluming, which is mainly result of the slice thickness. The presented method enables the identification of pathological tissue which rely on accurate statistical identification of normal tissues sufficient to allow confident identification of pathological areas as statistical outliers. This assumes the contribution of data from multiple spectra (images) and the proper treatment of partial volume effects to provide adequate confidence for the identification of normal tissues. Furthermore, inclusion of a partial volume model leads to better visual appearance of segmented tissues as voxels are not simply classified as a single tissue, which causes artifacts at tissue boundaries. This in turn enables creation of better geometric models to be used in simulation and visualisation stages of medical data. In addition to MRI data segmentation the method will be further implemented and tested on CT and MRA data to obtain better separation of bone and blood vessels. This method can be applied on any sequence of images for which the linearity assumption holds.

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