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Brain tumour extraction from multi-modality Magnetic Resonance images using Support Vector Machine models

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Abstract— Segmentation of images holds an important position in the area of image processing. It becomes more important while typically dealing with medical images where pre-surgery and post surgery decisions are required for the purpose of initiating and speeding up the recovery process The Computer aided detection of abnormal growth of tissues is primarily motivated by the necessity of achieving maximum possible accuracy. Manual segmentation of these abnormal tissues cannot be compared with modern day's high speed computing machines, which enable us to visually observe the volume and location of unwanted tissues. In MRI images, the task of labelling voxels according to their tissue type which include White Matter (WM), Grey Matter (GM), Cerebrospinal Fluid (CSF) and sometimes pathological tissues like tumour etc. This paper describes an efficient method for automatic brain tumour segmentation for the extraction of tumour tissues from MR images. The method combines Multi-Modality Magnetic Resonance Images and Support Vector Machine Models. The conventional structural MR modalities are combined with diffusion tensor imaging data to create an integrated multimodality profile for brain tumours. A wavelet based texture feature set is derived. The optimal texture features are extracted from normal and tumour regions by using spatial gray level dependence method (SGLDM). These features are given as input to the SVM classifier for further analysis.

Keywords: *Brain tumours, tissue classification, multimodal MRI data, Support Vector Machine, Classifiers.*

1. INTRODUCTION

The developments in the application of information technology have completely changed the world. The obvious reason for the introduction of computer systems is: reliability, accuracy, simplicity and ease of use. Besides, the customization and optimization features of a computer system stand among the major driving forces in adopting and subsequently strengthening the computer aided systems. In medical imaging, an image is captured, digitized and processed for doing segmentation and for extracting important information. Manual segmentation is an alternate method for segmenting an image. Additionally, manual segmentation process requires at least three hours completing the task. According to the traditional methods for measuring tumour volumes are not reliable and are error sensitive.

Brain tumour is an abnormal mass of tissue in which cells grow and multiply uncontrollably, seemingly unchecked by the mechanisms that control normal cells. Brain tumours can be primary or metastatic, and either malignant or benign. A metastatic brain tumour is a cancer that has spread from Elsewhere in the body to the brain. The image on a display contains the 3 brightness levels Red(R), Green (G), &Blue (B). Each of these are represented by the decimal values from 0-255(that is binary 0000 0000-1111 1111). Because there are 8 bits in the binary representation of the Gray level, this imaging method is called 8-bit gray scale.

1.1 Multi - Modality Magnetic Resonance Images

In heterogeneous, comprising enhancing and non-enhancing tumour tissue types and edema, rendering the transition from tumour to healthy tissue gradual. This paper aims at creating tissue profiles that identify different tumour components, edema and healthy tissue using a combination Of several structural MR modalities and diffusion tensor MRI. While clinical decisions on tumour treatments rely, in

part, on radiological evaluation of structural images, such as Fluid Attenuated Inversion Recovery (FLAIR) and T1-weighted MR images, to obtain estimates of tumour, edema and healthy tissue, that may be later dependent, several automated methods of tumour segmentation [1-4] have produced promising results mostly in differentiating tumour and normal tissue based on the traditional T1 and/or T2 MR modalities. In this paper, we seek to address and alleviate these issues by combining structural MRI and DTI images into

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a multimodality tissue profile, which paves the way for classifying healthy and tumour tissues, followed by a categorization of brain tissue into more specific classes of enhancing tumour (ET), non-enhancing tumour (NET), edema, white matter (WM), gray matter (GM) and cerebrospinal fluid (CSF). The proposed brain tissue classification framework incorporates intensities from each modality into an appearance signature.

Diffusion tensor imaging (DTI) is important when a tissue, such as the neural axons of white matter in the brain or musclefibre in the heart, has an internal fibrous structure analogous to the anisotropy of some crystals. Water will then diffuse more rapidly in the direction aligned with the internal structure, and more slowly as it moves perpendicular to the preferred direction. This also means that the measured rate of diffusion will differ depending on the direction from which an observer is looking.

The contributions of this work are: 1) creation of a multimodality tumour profile by integrating DTI images with conventional structural images, using tumour data from several patients 2) Investigation of the potential of this multi-modal classification in differentiating edema from the tumour components. Accurate and consistent tumour classification results for several tumour brains illustrate the robustness of our framework, and suggest potential applications in assessing tumour growth and in computer-guided surgery.

1.2 Support Vector Machine

Brain tumours can have a variety of shapes and sizes; it can appear at any location and in different image intensities. Brain tumours can be benign or malignant. Low grade Gliomas and Meningiomas, which are benign tumours, represent the most common type of brain tumour. Many techniques have been reported for classification of brain tumours in MR images, most notably, support vector machine (SVM) neural network , knowledge based techniques , expectation–maximization (EM) algorithms and Fuzzy c-means (FCM) clustering. An SVM is a machine learning system developed using statistical learning theories to classify data points into two classes. Notably, SVM models have been applied extensively for classification, image recognition and bioinformatics. SVM's are suggested to show their superior performance and feasibility in the classification of brain tissues in classical maximum-likelihood methods.

2. TYPES OF TISSUE

With the aim of distinguishing between healthy tissue and Tumour components, our classification strategy defines 6 types of tissue classes: tumour (ET and NET), healthy tissues (WM, GM and CSF), and edema. Based on expert-defined training samples, classifiers were trained for each of the tissue types using information from a single patient or by pooling training data from several patients leading to intra- and interpatient framework and were applied to new data from the same or another patient. Details of our framework are provided below.

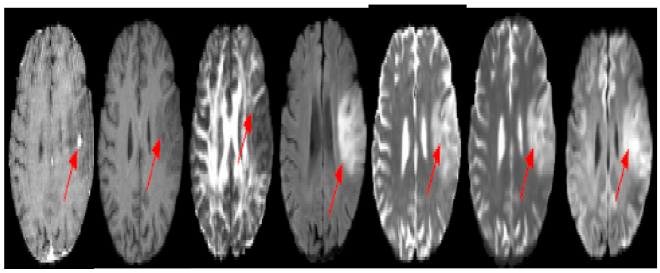

Figure 1. A representative slice from each of the seven MR modalities used in creating the multimodality tissue profile.

2.1 MR Acquisition

For creating our multi-modality profile, we use seven MR images: five structural MR acquisition protocols, namely, B0, Diffusion Weighted Images (DWI), Fluid-Attenuated Inversion Recovery (FLAIR), T1-weighted, and gadolinium enhanced T1-weighted (GAD), and two scalar maps computed from the DTI, namely, Fractional Anisotropy (FA) and Apparent Diffusion Coefficient (ADC).[2]

2.2 Preprocessing

Prior to creating the intensity features from these images, the images are skull stripped and Gaussian smoothed using FSL. Then, for each patient, all the modalities are rigidly co registered to the T1-weighted image using FSL's registration algorithm, called FLIRT. It may be noted that as the feature vectors are created by fusing information across modalities from within the same patient, rigid registration suffices between the modalities. In order to combine training samples from different patients, the images of the same modality are histogram matched across all patients.[3]

2.3 Classes of training samples

In order to train a robust classifier for each tissue class, we require samples of ET, NET and edema based on expert knowledge. Training samples for each of these classes were conservatively identified by a neuro-radiologist (SKL) typically using the FLAIR and GAD-T1 images. Edema is very difficult, if possible at all, to define with high confidence, because it is often mixed with infiltrating tumour. In defining edema, our neuro-radiologist selected regions that based on the inspection of several MR modalities like GAD (for enhancing tumour) and FLAIR (for determining tumour

boundaries). This was combined with implicit spatial knowledge about proximity of abnormal tissue to tumour, which would be identified as edema. Training samples for the healthy tissue (WM, GM and CSF) classes were defined using segmentation. Furthermore, to avoid bias in the training phase, the number of voxels selected in each WM/GM/CSF sub-region is set equal to the average number of samples in enhancing, non-enhancing and edema classes.

2.4 Feature Vector

The feature vector for each voxel x, where I is 3D image volume. These feature vectors are defined at each voxel in the training samples. In order to voxels are stacked into a long vector (35 dimensional), It is used as a feature vector.

2.5 Classifier Construction

We construct two kinds of classifiers: 1) Intra-patient classifier: classifier is built using only half of each patient's expert defined training sample, then tested on the remaining half and 2) Inter-patient classifier: the classifier is trained and tested on separate datasets. Because our database is quite limited at this point, we used leave-one-out cross validation mechanism. At the outset, it may be said that intra-patient classification is good in cases for which conservative training samples can be identified on the patient. Inter-patient classification addresses new cases for which no training data is available. Fig.2. a representative slice from each of the seven MR modalities used in creating the multimodality tissue profile. These have been rigidly co-registered to the T1 image of the patient. From left to right, the images are GAD, T1, FA, FLAIR, ADC, B0 and DWI. We use red arrows to stress tissue differences across the MR modalities.

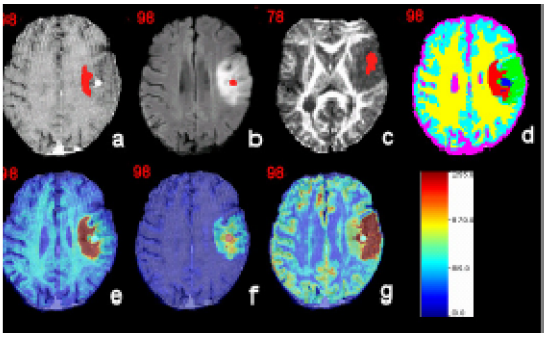

Figure.2 Intra-patient Segmentation

Intra-patient classification:
We use the Quadratic Discriminate Analysis (QDA) method, to design discriminate functions for each of the 6 tissue classes. By computing the mean and the covariance matrix over the feature vectors of the training samples for the 6 tissue classes, we obtain a Quadratic Discriminant function [8] for each tissue class that we refer to as the respective *tissue class classifier*. This discriminant evaluated at each voxel, provides the posterior probability of that voxel belonging to one of the 6 classes of ET, NET, edema, WM, GM and CSF. This produces a voxel-wise probability map for each brain, one pertaining to each of the 6 tissue classes. These discriminant values are normalized for visualization purposes. In addition, we can obtain hard segmentation by assigning the voxel to the class having the highest discriminant value, among the six classes. By assuming multivariate Gaussian distribution, the discriminant function can be computed efficiently and provides fast and efficient classification. The classifiers were trained on half of the training regions for that patient and tested on the remaining half.

Inter-patient classification:
Classification of tumour and healthy tissue of a patient has a high accuracy in our framework when tested on that same subject. While useful for individual patient analysis and for treatment planning, such a profile can only be applied to current and perhaps future scans of that patient only, owing to the fact that the profile will not be able to capture the variability across patients. Indeed, these intra-patients classifiers typically fail on new patients, owing to the tumour variability. This motivated the definition of classifiers for tissue types, using training data from many different patients, incorporated into an Support Vector Machine (SVM)-based framework. In this case, we combine training samples from across subjects, to obtain a more generalizable tissue classification. We design an SVM based classifier for all the 6 tissue classes by taking training samples from all the patients [9]. Due to the high variability across individuals, Quadratic Discriminant classification with their multinomial assumption does not provide adequate classification. We define classifiers, one pertaining to each of healthy (WM, GM and CSF combined), ET, NET and edema, in a one-versus-all framework. As SVM classifiers are tolerant to high variability, a single class for healthy tissue suffices and in addition, data from several patients can be combined to Obtain robust classifiers. Responses from the classifiers are Combined into a voting framework to obtain tissue classification. The classifiers are validated using a leave one- Out mechanism on the patients, that is, classifiers were trained using training samples from all patients except one, which was used for testing.

3. CLASSIFICATION USING SVM

Support Vector Machine (SVM) is a powerful supervised classifier and accurate learning technique that has been introduced in 1995. It is derived from the statistical theory

developed by Vapnick in 1982. It yields successful classification results in various application domains, e.g. medical diagnosis. Support Vector Machine (SVM) is based on the structural risk minimization principle from the statistical learning theory. Its kernel is to control the empirical risk and classification capacity in order to maximize the margin between the classes and minimize the true costs. A support vector machine searches an optimal separating hyper-plane between members and non-members of a given class in a high dimension feature space.

The inputs to the SVM algorithm are the feature subset selected using GA during data pre-processing step and extracted using the SGLDM method. In our method, the two classes are normal or abnormal brain. Then classification procedure continues to divide the abnormal brain into malignant and benign tumours; each Subject is represented by a vector in all images. There are many common kernel functions,

Such as:

- Linear: xi·xj,
- Polynomial of degree d: (xi·xj + 1) d,
- Radial basis function (RBF):

Among these kernel functions, a radial basis function proves to be useful, due to the fact the vectors are nonlinearly mapped to a very high dimension feature space. The optimal values of constants γ and C are determined, where γ is the width of the kernel function and C is the error/trade-off parameter that adjusts the importance of the separation error in the creation of the separation surface. We perform the classification for the MRI dataset with (γ, C) varying along a grid. SVM-based classification takes N training samples, trains the classifier on N-1 samples, then uses the remaining one sample to test. This procedure is repeated until all N samples have been used as the test sample. The performance of the classification for a given value (γ, C) is evaluated by computing the accuracy across all subjects.

Results and Discussion: Our proposed hybrid techniques are implemented on a real human brain dataset. The input dataset consist in 83 images: 29 images are normal, 22 malignant tumours suffering from a low grade Glioma, Meningioma and 32 benign tumours suffering from a Bronchogenic Carcinoma, Glioblastoma multiform, Sarcoma and Grade IV tumours. These normal and pathological benchmark images used for classification, are axial, T2-weighted of 256×256 sizes and acquired at several positions of the Trans axial planes. These images were collected from the Harvard Medical School website. We have considered that all images belonging to seven persons (four men and three women). Their ages vary between 22 and 81 years. The determination of MR tumour type, which can be achieved by the histopathological analysis of biopsies, was considered as the gold standard for the classification of images. A typical representative MR image of normal, benign and malignant tumour is shown in Figure features are also extracted for the performance of our method. This yields a total of 44 features including the mean and the range.

Due to the small size of the dataset, the SVM classifier is employed. In the classification step we choose the RBF kernel due to the fact that many studies have demonstrated that the preferable choice is RBF, and the technique used to fix its optimal parameters is a grid search using a cross-validation. Cross-validation method with 5 folders is used.

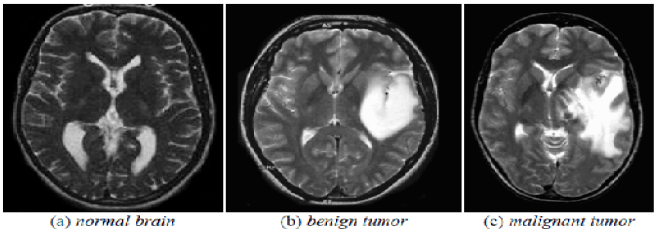

Figure 3. Three T2 weighted MR images in axial plane (a) Normal brain (b) benign tumour (c) malignant tumour

4. CONCLUSION

This study applied a multivariate nonlinear classification Scheme to the problem of soft tissue segmentation in brain Tumour patients. It combines conventional structural MRI with DTI, and used them to train classifiers for the tumour types of enhancing and non-enhancing tumour, edema and healthy tissue. The accurate distinction of the tumour tissue from healthy tissue as shown in Figs.3a, 3b, 3c. Indicates that the framework can be useful in integrating multi-modality information into a combined profile and its classification. The hard segmentation as well as the probability maps can potentially provide a better understanding of the spatial distribution of healthy tissue, tumour and edema, thereby assisting in treatment or surgical planning. In the future, we plan to incorporate texture information into our features to distinguish between high grade and low grade tumours. In addition, we propose to build a two stage framework, in which SVM classification is combined with Quadratic Discriminant based classification to obtain a better tumour profile. The paper developed a hybrid technique with normal and benign or malignant classes. Our medical decision making system is designed by the wavelet transform (WT), genetic algorithm (GA) and supervised learning methods (SVM). The proposed approach gives very promising results in the physician to make the final decision. The proposed classification distinguishes the healthy and pathological brain. The benefit of the system is to assist algorithm to find an efficient mode

for classification of the human brain as normal or abnormal (benign and malignant tumour) with high sensitivity, specificity and accuracy rates. The performance of this study appears some advantages of this technique: it is accurate, robust easy to operate, non-invasive and inexpensive. The approach is limited by the fact that it necessitates fresh training each time whenever there is a change in image database.

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