

Tumor Detection In Brain Images Via Distributed Estimation

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Abstract— The aim of this paper is to introduce a scheme for tumor detection and segmentation in medical images. We consider MRI brain image. Automatic segmentation of brain image is done. In abnormality detection, we match vector with the probability distribution obtained from normal data, it is marked as anomalous if it is different. If data is large it is not possible to estimate probability density function. So we take every image as partition. Block wise separation of the image is performed. Here we calculate parameters like eigenvalue, eigenvector, energy, maximum likelihood for each block. The concave likelihood function estimate abnormality for each block based on a distributed estimation algorithm. The likelihood function contains a model and data. Based on the parameters value tumor is detected and tumor is segmented based on expectation maximization algorithm. This kind of method is used for automatic brain pathology segmentation, such as simulated brain infarction and dysplasia, real lesions in diabetes patients. Harlick features which is a statistical parameter can be estimated and the type of tumor can be classified using artificial neural networks.

Keywords— Anomaly detection, brain pathology, image segmentation, Distributed Estimation

1. INTRODUCTION

Recent developments in Technology find vast application in medical images. The collection of data of same kind allows construction and exploitation of application-specific statistical models which optimally summarizes knowledge. The models can be incorporated into framework for anomaly detection. The methods developed for segmenting anomalies, use labeled samples to characterize the abnormal objects. Supervised anomaly detection techniques require a data set that has been labeled as "normal" and "abnormal" and involves training a classifier (the key difference to many other problems is the inherent unbalanced nature of outlier detection). Semi-supervised anomaly detection techniques construct a model representing normal behavior from a given normal training data set, and then testing the likelihood of a test instance to be generated by the learnt model. Supervised method may be unsuccessful due to unbalanced data. Semi-Supervised method model a normal data and then using a distance measure and thresholding to find abnormality. The present approach goes beyond abnormality, it not only characterize normal or abnormal, but locates part of abnormality. And the approach is generic, it does not make assumption about shape or intensity profile of the abnormality. In abnormality detection,

we match vector with the probability distribution obtained from normal data, it is marked as anomalous if it is different. If data is large it is not possible to estimate probability density function. So we take every image as partition. Block wise separation of the image is performed.

Medical imaging is the technique and process used to create images of the human body for clinical purposes or medical science. Research into the application and interpretation of medical images is usually the preserve of radiology and the medical sub-discipline relevant to medical condition or area of medical science under investigation. Many of the techniques developed for medical imaging also have scientific and industrial applications. MRI provides good contrast between soft tissues of the body, which makes it especially useful in imaging the brain, muscles, the heart, and cancers compared with other medical imaging techniques such as computed tomography (CT) or X-rays.

2. IMAGE SEGMENTATION

Image segmentation plays a crucial role in many medical imaging applications by automating or facilitating the delineation of anatomical structures and other regions of interest. Diagnostic imaging is an invaluable tool in medicine today. Magnetic

resonance imaging (MRI), computed tomography (CT), digital mammography, and other imaging modalities provide an effective means for noninvasively mapping the anatomy of a subject. These technologies have greatly increased knowledge of normal and diseased anatomy for medical research and are a critical component in diagnosis and treatment planning. In particular, computer algorithms for the delineation of anatomical structures and other regions of interest are a key component in assisting and automating specific radiological tasks.

The algorithms, called image segmentation algorithms, play a vital role in numerous biomedical imaging applications such as the quantification of tissue volumes, diagnosis, localization of pathology, study of anatomical structure, treatment planning, partial volume correction of functional imaging data and computer integrated surgery. It becomes more important while typically dealing with medical images, magnetic resonance (MR) imaging offers more accurate information for medical examination than other medical images such as X-ray, ultrasonic and CT images.

3. BRAIN TUMOR

Tumor segmentation from MRI data is an important, but time consuming task performed manually by medical experts when compared with modern day's high speed computing machines which enable us to visually observe the volume and location of unwanted tissues. One of the reasons behind the inferior segmentation efficiency is the presence of artifacts in the MR images.

The tumor type and behavior determine radiographic appearance. Depending on the primary proliferating cell, benign skull tumors can be any of the following: Bone forming, Cartilage forming, Tumors of connective tissue, Histiocytic tumors, Tumors of blood or blood vessel origin. Other types, including fibrous dysplasia, Paget disease or epidermoid, dermoid or aneurysmal bone cysts. Tumors of the skull are uncommon lesions that are not reported systematically in the medical

literature. Therefore, assessing their true incidence and consequences to the health of the general population is difficult. Recent diagnostic advances have made such lesions easier to recognize, and new skull-base surgery techniques have provided access to previously inoperable skull tumors.

3.2 Current Methods In Medical Image Processing

There is currently no single segmentation method that yields acceptable results for every medical image. Methods do exist that are more general and can be applied to a variety of data. For increasing computational efficiency, multiscale processing and parallelizable methods such as neural networks appear to be promising approaches. Computational efficiency will be particularly important in real-time processing applications

Automatic brain tumor segmentation from MR images is a difficult task that involves various disciplines covering pathology, MRI physics, radiologist's perception, and image analysis based on intensity and shape. There are many issues and challenges associated with brain tumor segmentation. Brain tumors may be of any size, may have a variety of shapes, may appear at any location, and may appear in different image intensities. Some tumors also deform other structures and appear together with edema that changes intensity properties of the nearby region. For many human experts, manual segmentation is a difficult and time consuming task, which makes an automated brain tumor segmentation method desirable. There are many possible applications of an automated method, it can be used for surgical planning, treatment planning, and vascular analysis.

4. METHODOLOGY

The automated tumor segmentation method that we have developed is composed of three major stages, as shown in Fig.2. First, image is divided in to blocks. For each block we are finding parameters values such as eigen value, eigen vector, mean ,principal component analysis, entropy by means of distributed estimation and Tumor is

detected, second, tumor is segmented by means of expectation maximization. Third, stages of tumor are to be classified.

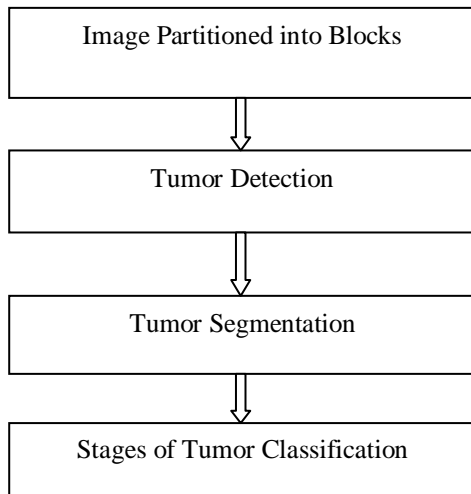


Fig 1: Tumor Segmentation Steps

4.1 Estimated distribution algorithm:

EDAs belong to the class of evolutionary algorithms. The main difference between EDAs and most conventional evolutionary algorithms is that evolutionary algorithms generate new candidate solutions using an implicit distribution defined by one or more variation operators, whereas EDAs use an explicit probability distribution encoded by a Bayesian network, a multivariate normal distribution, or another model class. Similarly as other evolutionary algorithms, EDAs can be used to solve optimization problems defined over a number of representations from vectors to LISP style S expressions, and the quality of candidate solutions is often evaluated using one or more objective functions.

The general procedure of an EDA is outlined in the following:

1. $t = 0$
2. initialize model $M(0)$ to represent uniform distribution over admissible solutions
3. while (termination criteria not met)

1. $P =$ generate $N > 0$ candidate solutions by sampling $M(t)$
2. $F =$ evaluate all candidate solutions in P
3. $M(t+1) =$ adjust model $(P, F, M(t))$
4. $t = t + 1$

Estimation of distribution algorithm: For each iteration i , a random draw is performed for a population P in a distribution. The distribution parameters PDe are then estimated using the selected points PS . The illustrated example optimizes a continuous objective function $f(X)$ with a unique optimum O . The sampling (following a normal distribution N) concentrates around the optimum as one goes along unwinding algorithm.

4.2 Expectation Maximization:

Expectation-maximization (EM) algorithm is an iterative method for finding maximum likelihood or maximum a posteriori (MAP) estimates of parameters in statistical models, where the model depends on unobserved latent variables. The EM iteration alternates between performing an expectation (E) step, which creates a function for the expectation of the likelihood evaluated using the current estimate for the parameters, and maximization (M) step, which computes parameters maximizing the expected log-likelihood found on the E step. These parameter-estimates are then used to determine the distribution of the latent variables in the next E step.

The EM algorithm is used to find the maximum likelihood parameters of a statistical model in cases where the equations cannot be solved directly. Typically these models involve latent variables in addition to unknown parameters and known data observations. That is, either there are missing values among the data, or the model can be formulated more simply by assuming the existence of additional unobserved data points

An Artificial Neural Network, often just called a neural network, is a mathematical model inspired by biological neural networks. A neural network consists of an interconnected group of artificial

neurons, and it processes information using a connectionist approach to computation. In most cases a neural network is an adaptive system that changes its structure during a learning phase. Neural networks are used to model complex relationships between inputs and outputs or to find patterns in data. With the help of feed forward back propagation algorithm ,tumor classified as initial and final stages.

5. IMPLEMENTATION

Thus the image is converted to grayscale and image partitioned in to blocks. Each block undergoes estimation. Parameters of normal brain blocks are calculated. Parameters of tumor brain image is also calculated.

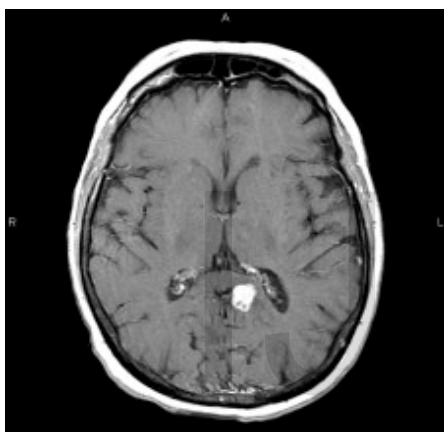


Fig 2:Brain Tumor Image

With Maximum likelihood ratio Parameters values are compared and tumor part is detected. With the help of EM algorithm tumor is segmented.

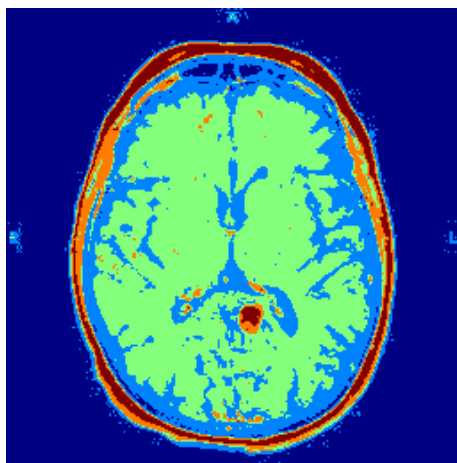


Fig 3:Segmented Tumor

Stages of tumor such as initial and final tumor stage classified using artificial neural network. This can be performed well by MATLAB software.

6. CONCLUSIONS

Any MRI brain input image can be taken and tested for abnormality. The present approach find application in medical imaging, the approach is generic ,any type of MRI brain tumor image is tested and identified. Thus the tumor is detected and segmented and stages of tumor is classified effectively.

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