Volume 5, Issue 6, June 2015 ISSN: 2277 128X
International Journal of Advanced Research in Computer Science and Software Engineering
Research Paper
Available online at: www.ijarcsse.com

MRI Tissue Segmentation and Elimination of Corruption in MRI Images

[1]Prajwal Rao K J, [2]Jyothi K S, [3]Rashmi C R
[1]PG Student, [2]Associate Professor, [3]Assistant Professor
[1, 2, 3] Dept of CSE, CIT Gubbi, Tumkur, Mysore, India

Abstract-A new energy minimization method is proposed in this paper for the estimation of bias field and segmentation of MR images. The energy minimization takes the full advantage of the decomposition of MR images into two multiplicative components, which are true image that describes a physical property of the tissues and the bias field that accounts for the intensity inhomogeneity, and their respective spatial properties. Estimation of Bias Field and segmentation of tissues are achieved simultaneously by energy minimization process. The bias field is continuously adjusted by using efficient matrix computations, which are verified to be numerically stable by matrix analysis. More significantly, the energy in our formulation is convex in each of its variables, which indications the robustness of the proposed energy minimization algorithm. We have also introduced edge detection known as canny edge detection which shows the image edge preciously and also the energy graph for energy minimization in this paper.

Keywords: MRI Brain segmentation, Intensity inhomogeneity, Bias field estimation, Bias field correction.

I. INTRODUCTION

Image processing

Image processing is any form of signal processing for which the input is an image, such as a photograph or video frame, the output may be either an image or a set of characteristics or parameters related to the image.

Applications of image processing

- In the field of medicine, such as: radiology.
- Digital art: graphic designing and animation.
- Meteorology: detect and predict weather patterns.
- Law enforcement: digital photo processing in traffic control systems, etc.,

Image segmentation

Image segmentation is one of the most important tasks in medical image analysis and is often the first and the most critical step in many clinical applications. In brain MRI analysis, image segmentation is commonly used for measuring and visualizing the brain's anatomical structures, for analysing brain changes, for delineating pathological regions, and for surgical planning and image-guided interventions. In the last few decades, various segmentation techniques of different accuracy and degree of complexity have been developed and reported in the literature.

Image segmentation is a tool in medical image processing and is used in various applications. For example, in medical imaging filed is used to detect multiple sclerosis lesion quantification, surgical planning, conduct surgery simulations, locate tumours and other pathologies, measure tissue volumes, brain MRI segmentation, study of anatomical structure etc.

The goal of image segmentation is to divide an image into a set of semantically meaningful, homogeneous, and non-overlapping regions of similar attributes such as intensity, depth, colour, texture. The segmentation results are either an image of labels identifying each homogeneous region or a set of counters which describe the region boundaries.

Some of the segmentation methods are threshold, clustering methods, compression-based methods, histogram-based methods, edge detection, dual clustering method, region-growing method, partial differential equation-based methods, parametric methods, level set methods, fast marching methods, graph partitioning methods, Markov random fields, supervised image segmentation using MRF and MAP, model-based segmentation, one-dimensional hierarchical signal segmentation.

Magnetic Resonance Image [MRI]

MRI is a tomographic or medical imaging technique used in radiology that produces images of internal physical and chemical characteristics of an object from externally measured nuclear magnetic resonance (NMR) signals. MRI scanners use magnetic fields and radio waves to form images of the body. The technique is widely used in hospitals for medical diagnosis, staging of disease and follow-up without exposure to ionizing radiation.

MRI has a wide range of applications in medical diagnosis and over 25,000 scanners are estimated to be in use worldwide. MRI has an impact on diagnosis and treatment in many specialists although the effect on improved health outcomes is uncertain.

Bias Field

A bias field is a low frequency smooth undesirable signal that corrupts MRI images because of the in homogeneities in the magnetic fields of the MRI machine. Bias field blurs images and thus decreases the high frequency contents of the image such as edges and contours and changes the intensity values of image pixels so that the same tissue has different grey level distribution across the image. A low level difference will not have great influence on clinical diagnosis. Still it degrades the performance of image processing algorithms such as segmentation and classification or any algorithm that is based on the assumption of spatial invariance of the processed image [1]. A pre-processing step is needed to correct for the effect of bias field before doing segmentation or classification.

MRI Segmentation

MRI Segmentation is a main technique to differentiate abnormal and normal tissue in MR image data. In general, MRI segmentation is not a trivial task, because acquired MR images are imperfect and are often corrupted by noise and other image artifacts. The diversity of image processing applications has led to progress of various methods for image segmentation. This is for the reason that there is no particular technique that can be suitable for all images, nor are all methods equally good for a specific type of image. For example, some of the methods use only the gray level histogram [2], while some integrate spatial image information to be robust for noisy environments. Some methods use probabilistic or fuzzy set theoretic [2] approaches, while some additionally integrate prior knowledge (specific image formation model, e.g., MRI brain atlas) to further improve segmentation performance.

However, most of the segmentation methods developed for one class of images can be easily applied or extended to a different class of images. For example, the theory of graph cuts [2], although firstly developed for binary images, can be modified and used for MRI segmentation of the brain tissue. Also, unsupervised fuzzy clustering [2] has been successfully applied in different areas such as remote sensing, geology, and medical, biological, and molecular imaging.

Some of the MRI segmentation methods are edge detection, boundary tracing, thresholding, seed-growing, template models, random field, mean-shift, histogram thresholding, graph cuts segmentation, Fuzzy connectivity, Optimal single and multiple surface segmentation, K-means Clustering, etc.

II. RELATED WORK

An HMRF-EM Algorithm for Partial Volume Segmentation of Brain MRI

The Hidden Markov Random Field (HMRF) model, which represents a stochastic process generated by a Markov Random Field whose state sequence cannot be observed directly but which can be indirectly estimated through observations, has been successfully applied on segmenting piecewise constant images, especially for human brain MR images we extend this model, and its associated expectation-maximization (EM) algorithm from dealing only with discrete class labels to working with continuous vectors. In particular, the problem of partial volume effect classification of images is addressed. In this method, the underlying partial volume classification, as well as its interaction with the observed image intensities, is modelled as a spatially correlated hidden Markov random field, with parameters estimated through an EM algorithm. A deterministic annealing algorithm is then used to obtain the optimal solution; this method is shown to work both for multi-spectral data (where a unique solution exists) and for data with insufficient spectral channels (where only an ‘optimal’ solution can be obtained). Quantitative evaluations are presented to examine the accuracy and the repeatability of this algorithm.

Drawbacks:

- This approach has established a solid computational framework for PVE classification for multi-tissue and multi-spectral MR data.
- The least-square estimation of the mean matrix may be difficult to solve given the size of the equation and the presence of noise.
- The assumption of an equal covariance matrix for all classes may not be valid given that some tissue types, such as CSF, normally have much larger variations than others.
- This method can only be used for multi-spectral data sets which are not always available.

An Adaptive Fuzzy C-Means Algorithm for Improving MRI Segmentation

The new fuzzy c-means method for improving the magnetic resonance imaging (MRI) segmentation. The method called “possiblistic fuzzy c-means (PFCM)” which hybrids the fuzzy c-means (FCM) and possiblistic c-means (PCM) functions. It is realized by modifying the objective function of the conventional PCM algorithm with Gaussian exponent weights to produce memberships and possibilities simultaneously, along with the usual point prototypes or cluster centres for each cluster. The membership values can be interpreted as degrees of possibility of the points belonging to the classes, *i.e*., the compatibilities of the points with the class prototypes. For that, this algorithm is capable to avoid various problems of existing fuzzy clustering methods that solve the defect of noise sensitivity and overcomes the coincident clusters problem of PCM. The efficiency of the algorithm is demonstrated by extensive segmentation experiments by applying them to the challenging applications: grey matter/white matter segmentation in magnetic resonance image (MRI) datasets and by comparison with other state of the art algorithms.

Drawbacks:
- Increase the computational time, complexity and introducing unwanted smoothing
- MRIs segmentation algorithms had suppressed the impact of noise and intensity inhomogeneity to some extents; these algorithms still produce misclassified small regions.
- The problems of over-segmentation and sensitivity to noise are still the challenge.
- FCM and PCM are also very sensitive to initialization and sometimes coincident clusters will occur.
- Moreover, coincident clusters may occur during fuzziness processes which can affect the final segmentation.

The EM Algorithm

The EM Algorithm is a general method of finding the maximum-likelihood estimate of the parameters of an underlying distribution from a given data set when the data is incomplete or has missing values.

There are two main applications of the EM algorithm. The first occurs when the data indeed has missing values, due to problems with or limitations of the observation process. The second occurs when optimizing the likelihood function is analytically intractable but when the likelihood function can be simplified by assuming the existence of and values for additional but missing (or hidden) parameters.

The latter application is more common in the computational pattern recognition community.

Drawbacks:
- The method requires estimating threshold and does not produce accurate results most of the time.
- The details of the EM steps required to compute the given quantities are very dependent on the particular application so they are not discussed when the algorithm is presented in this abstract form.

K-means Clustering

K-means is the unsupervised algorithms that solve clustering problem. The procedure for K-means clustering algorithm is simple and easy way to segment the image using basic knowledge of cluster value. In K-means initially randomly define k centroids. The selection of this k centroid is placed in cunning way because different location makes different clustering. So, better is to place centroid value will be as much as far away from each other. Secondly calculate distance between each pixel to selected cluster centroid. Each pixel compares with k clusters centroids and finding distance using distance formula. If the pixel has shortest distance among all, than it is move to particular cluster. Repeat this process until all pixel compare to cluster centroids. The process continues until some convergence criteria are met.

Fuzzy C-means Clustering

Fuzzy C-means is an overlapping clustering technique. One pixel value depending on two or more clusters centers. It is also called soft clustering method. One of the most widely used fuzzy clustering algorithms is the Fuzzy C-means (FCM) algorithm (Bezdek 1981)[6]. The FCM algorithm is partition of n element X={x_1,…,x_n} into a collection of C-fuzzy clusters with respect to below given criteria.[4] It is based on minimization of the following objective function:

$$J=\sum_{i=1}^{N}\sum_{j=1}^{c} u_{ij}^{m}\,|x_i - y_i|^2$$

Where,
m = level of fuzziness and real number greater than 1.
U_{ij}= degree of membership of x_i in the cluster $c_{j.}$
x = data value.

Fuzzy C-means is a popular method for medical image Segmentation but it only considers image intensity thereby creating unsatisfactory results in noisy images. A bunch of algorithms are proposed to make FCM robust against noise and in homogeneity but it's still not perfect.

III. EXISTING SYSTEM

The diversity of image processing applications has led to development of various segmentation techniques of different accuracy and degree of complexity. The intensity of brain tissue is one of the most important features for MRI segmentation. However, when intensity values are corrupted by MRI artefacts such as image, noise, partial volume effect (PVE), and bias field effect, intensity-based segmentation algorithms will lead to wrong results. After MRI acquisition several pre-processing steps are necessary to prepare MR images for segmentation. The most important steps include MRI bias field correction, image registration [3] (in the case of multimodal image analysis), and removal of non-brain tissue (also called a brain extraction).

The bias field, also called intensity inhomogeneity, is a low-frequency spatially varying MRI artefact causing a smooth signal intensity variation within tissue of the same physical properties. The bias field arises from spatial inhomogeneity of the magnetic field, variations in the sensitivity of the reception coil, and the interaction between the magnetic field and the human body. The bias field dependent on the strength of the magnetic field.

The **simplified multiplicative model** [3] is used currently in most state-of-the-art bias correction methods to represent the bias field. However in reality there are certain limitations to the correctness of this model. Even though the model is consistent with the variations arising from the sensitivity of the receiver coil, the relationship between the measured and true intensities in MRI is more complicated.

In the literature, various methods have been proposed to correct the bias field in MRI. One of the earliest methods proposed to correct the bias field is based on the manual labelling of the brain tissue voxels, which are then used to reconstruct the bias field in form of a parametric surface. The main disadvantage of this surface fitting method is the need for manual interaction. The bias field can be also estimated and corrected by using low-pass filtering [3], but this approach can introduce additional artefacts in the image because it also removes the low-frequency component of the true image data.

Both the surface fitting method and the low-pass method can be improved and made fully automatic if they are coupled with automatic segmentation of the brain [3].

Other approaches for the bias field correction include minimizing the image entropy [3], fitting the histogram of the local neighbourhood to global histogram of the image [3], maximizing the high-frequency content of the image [3], and using a registered template image [3].

Image registration is a necessary step for the inclusion of probabilistic atlases as a prior knowledge of the brain anatomy into the segmentation method. A probabilistic atlas is often used to initialize and constrain the segmentation process. The prior knowledge of the brain anatomical structures can increase the robustness and accuracy of a segmentation method.

IV. PROPOSED SYSTEM

The proposed method jointly performs bias field estimation and the tissue membership functions in an energy minimization process to optimize two multiplicative intrinsic components of an MR image, the bias field that accounts for the intensity inhomogeneity and the true image that characterizes a physical property of the tissues. The spatial properties of these two components are fully reflected in their representations and the proposed energy minimization formulation.

Advantages of proposed method over the current method:

- It is robust, accurate and efficient than the current method.
- It can be applied to higher field (e.g. 7 T) MRI scanners; the intensity inhomogeneity has more complicated profiles than 1.5 T and 3 T MR Images.
- It is numerical stable in computation of the bias field.
- Doesn’t require much time as for the simplified multiplicative model.

V. METHODOLOGY

3.1 System Architecture

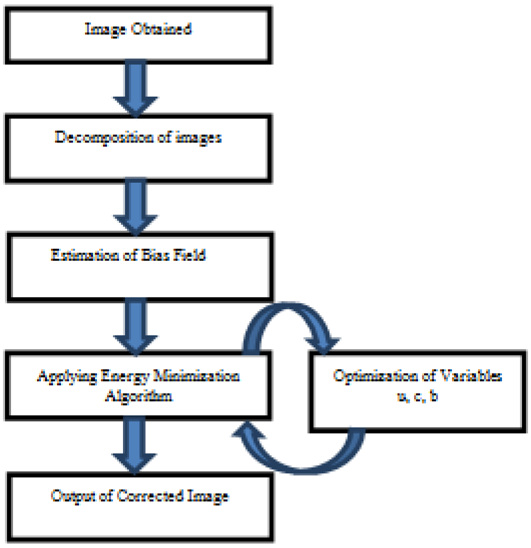

Fig 1: System Architecture

The system architecture represents the flow of process carried out during the execution of project. It gives the indication of working of whole system. It deals with the flow of chief component which are used in working of system.

In the above flow-diagram, the variable u indicates member functions, c indicates constants and b indicates bias field.

3.2 Energy minimization

The energy minimization can be accomplished by alternately minimizing $F_q(u, c, w)$ with respect to each of its variables given the other two fixed[4]. The minimization of $F_q(u, c, w)$ with respect to each of its variables is described below.

3.2.1 Optimization of c

For fixed w and u = $(u_1, \cdots, u_N)^T$, the energy F(u, c, w) is minimized with respect to the variable c. It is easy to show that F(u, c, w) is minimized by c=$\hat{c}$=$(\widehat{c1},\ldots\ldots,\widehat{cn})^T$

With $\widehat{ci} = \frac{\int \Omega^{I(x)b(x)u_i^q(x)}\, dx}{\int \Omega^{b^2(x)u_i^q(x)}\, dx}$

3.2.2 Optimization of w and bias field estimation

For fixed c and u, we minimize the energy F(u, c, w) with respect to the variable w. This can be achieved by solving the equation $\frac{\partial F}{\partial w}$ = 0.It is easy to show that

$\frac{\partial F}{\partial w}$ =-2v+2Aw.

Where v is an M-dimensional column vector given by

v = $\int_\Omega G(x)I(x)\sum_{i=1}^{N} c_i^2\, u_i^q(x)$ dx

Where A is an M × M matrix

A = $\int_\Omega G(x)G^T(x)\sum_{i=1}^{N} c_i^2\, u_i^q(x)$

3.2.3 Optimization of u

We first consider the case of q > 1. For fixed c and w, we minimize the energy F(u, c, w) subject to the constraint that u ∈U. It can be shown that F(u, c, w) is minimized at u = $\hat{u}$ = $(\hat{u}_1,\ldots\ldots,\hat{u}_N)^T$, given by

$\hat{u}_i(x) = \frac{(\delta i(x))^{\frac{1}{1-q}}}{\sum_{j=1}^{N}(\delta i(x))^{\frac{1}{1-q}}}$

Where $\delta_i(x)=|I(x) - wTG(x)Ci|^2$

For q = 1, it can be shown that the minimizer $(\hat{u}_1,\ldots\ldots,\hat{u}_N)^T$ is given by $i \neq i_{min}(x)$

$\hat{u}_i(x)= \begin{cases} 1 & i = imin(x) \\ 0 & i \neq imin(x) \end{cases}$

Where $i_{min}(x)=arg_i^{min}$ $\{\delta_i(I(x))\}$

3.3 Decomposition of MR images

From the formation of MR images, it has been generally accepted that an MR image I can be modelled as

$$I(x) =b(x)\, J(x) =n(x) \qquad (1)$$

Where I(x) is the intensity of the observed image at voxel x, J(x) is the true image, b(x) is the bias field that accounts for the intensity inhomogeneity in the observed image, and n(x) is preservative noise with zero-mean. The bias field b is expected to be smoothly varying. The true image J characterizes a physical property of the tissues being imaged, which ideally take a definite value for the voxels within the same type of tissue. Therefore, we assume that J(x) is approximately a constant ci for all point x in the i-thtissue[5]. In this paper, we consider (1) as a decomposition of the MR image I into two multiplicative components b and J and additive zero-mean noise n. From this perspective, we formulate bias field estimation and tissue segmentation as an energy minimization problem of seeking optimal decomposition of the image I into two multiplicative components b and J. We refer to the bias field b and the true image J as intrinsic components of the observed MR image I. In the context of computer vision, an observed image of a scene has a similar decomposition as in (1). An observed image I can be decomposed as I = RS with two multiplicative components: the reflectance image R and the illumination image S.

3.4 Representations of multiplicative intrinsic components

To effectively use the properties of the bias field b and true image J, we need suitable mathematical representation and description of the bias field and true image. In our method, the bias field is represented by a linear combination of a given set of smooth basis functions $g_1,\ldots,g_M$, which ensures the smoothly varying property of the bias field. Theoretically, a function can be estimated by a linear combination of a number of basis functions up to arbitrary accuracy, given a sufficiently large number M of the basis functions. In the applications of 1.5 T and 3 T MRI data, we use 20 polynomials of the first three degrees as the basis functions. The estimation of the bias field is performed by discovery the optimal coefficients $w_1,\ldots,w_M$ in the linear combination b(x) = $\sum_K^M 1 w_k g_k$. We represent the coefficients $w_1,\ldots,w_M$ by a column vector w = $(w_1, \cdots, w_M)^T$, where T is the transpose operator. The basis functions $g_1(x),\ldots,g_M(x)$ are represented by a column vector valued function G(x) = $(g1(x), \cdots, g_M(x))^T$. Thus, the bias field b(x) can be expressed in the following vector form

$$b(x) = W^T G(x) \qquad (2)$$

The above vector representation will be used in our projected energy minimization method for bias field estimation, which permits us to use efficient vector and matrix computations to calculate the optimal bias field derived from the energy minimization problem.

The piecewise approximately constant property of the true image J can be stated more specifically as follows. We assume that there are N types of tissues in the image domain Ω. The true image J(x) is approximately a constant ci for x in the i-th tissue. We denote by Ωi the region where the i-th tissue is situated. Each section (tissue) Ωi can be represented by its membership function u_i[5]. In the ideal case where every voxel contains only one type of tissue, the membership function ui is a binary membership function, with $u_i(x) = 1$ for $x \in \Omega_i$ and $u_i(x) = 0$ for $x \notin \Omega_i$. In reality, one voxel may contain more than one type of tissues due to the partial volume effect, especially at the interface between neighbouring tissues. In this case, the N tissues can be represented by fuzzy membership functions $u_i(x)$ that take values between 0 and 1 and satisfy$\sum_i^N = 1u_i(x) = 1$. The value of the fuzzy membership function $u_i(x)$ can be interpreted as the percentage of the i-th tissue within the voxel x. Such membership functions $u_1,\ldots,u_N$ can be represented by a column vector valued function $u = (u_1,\ldots,u_N)^T$, where T is the transpose operator.
Given the membership functions ui and constants c_i, the true image J can be approximated by

$$J(x) = \sum_{i=1}^{N} c_i u_i(x) \qquad (3)$$

In the case that the membership functions ui are binary functions, the function in (3) is a piecewise constant function, with $J(x) = c_i$ for $x \in \Omega_i$. The binary membership functions $u_1,\ldots,u_N$ represent a hard segmentation result, and the corresponding regions $\Omega_1,\ldots,\Omega_N$ form a partition of the image domain Ω, such that $U_i^N=1\Omega_i = \Omega$ and $\Omega_i \cap \Omega_j = \emptyset$. More generally, fuzzy membership functions $u_1,\ldots,u_N$ with values between 0 and 1 represent a soft segmentation result. Based on the image model (1), we propose an energy minimization method for simultaneous bias field estimation and tissue segmentation. The result of tissue segmentation is given by the membership function $u = (u_1,\ldots,u_N)$. The estimated bias field b is used to generate the bias field corrected image, which is computed as I/b.

3.4 Edge Detection

Edge detection is the title for a group of mathematical methods whose objective is at identifying points in digital image at which the image brightness varies sharply.The points at which image brightness varies sharply are typically structured into a set of curved line segments termed *edges.*

There are many methods to perform edge detection. However, the most may be grouped into two categories, gradient and Laplacian. The gradient method identifies the edges by looking for the maximum and minimum in the first derivative of the image. The Laplacian method searches for zero crossings in the second derivative of the image to find edges.

The method which we use to detect edge detection is canny edge detection.The Canny edge detector is a very popular and effective edge feature detector that is used as a pre-processing step in many computer vision algorithms. It is a multi-step detector which performs smoothing and filtering, non-maxima suppression, followed by a connected-component analysis stage to detect edges, while suppressing non edge filter responses.
The Canny Edge Detection Algorithm has the following steps.
Step 1: Smooth the image with a Gaussian filter.
Step 2: Compute the gradient magnitude and orientation using finite-difference approximations for the partial derivatives.
Step 3: Apply nonmaxima suppression to the gradient magnitude, Use the double thresholding algorithm to detect and link edges.
Canny edge detector approximates the operator that optimizes the product of signal-to-noise ratio and localization. It is generally the first derivative of a Gaussian. For example, in our case study shown the shark type is identified in Fig 2 (a) and (b).

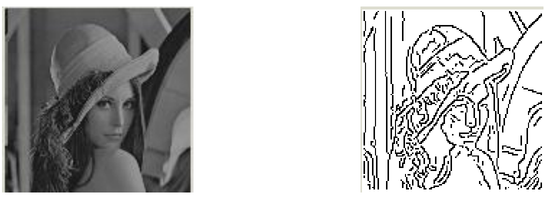

Fig2 (a): original image Fig2 (b): Image with edge Detected

VI. RESULT

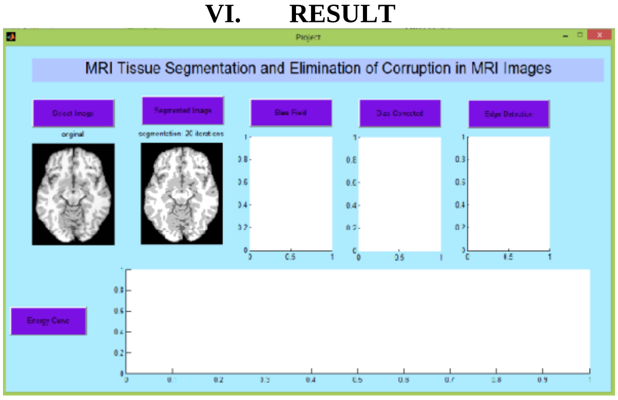

Fig 3: Selected original image and segmented image

In the above Fig3 we have selected an image and the next image is the segmented image with 20 iteration.

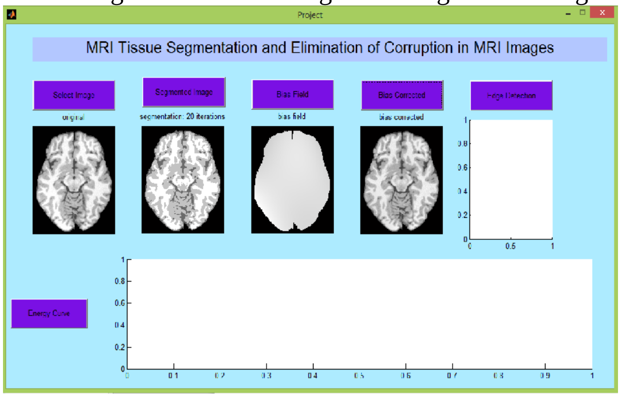

Fig 4: Bias Field and Bias Corrected Image

In the above Fig4 we shown the original image, segmented image and bias field which is extracted from the original image and the next is the bias corrected image of the original image.

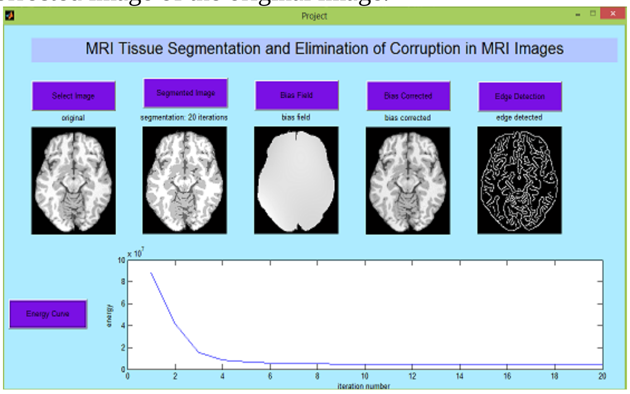

Fig5: Edge Detected Image and Energy Curve

In the above Fig5 we show the original image, segmented image, bias field, bias corrected field and also the edge detection we have used the canny edge detection and the last step is the energy curve.

VII. CONCLUSION

In this paper we have proposed a new energy minimization method for the estimation of bias field and segmentation of MR Images. We have derived efficient energy minimization scheme for the computation of bias field by calculus of matrix and vector and also used matrix analysis to verify the numerical stability of the computation for the optimization of the bias field. For the detection of edges of MR Images we have used an edge detection algorithm

ACKNOWLEDGMENT

We are grateful to express sincere thanks to our faculties who gave support and special thanks to our department for providing facilities that were offered to us for carrying out this paper.

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