# Image Segmentation and Classification of MRI Brain Tumor Based on Cellular Automata and Neural Networks

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## Abstract

This paper proposes segmentation of MRI brain tumor using cellular automata and classification of tumors using Gray level Co-occurrence matrix features and artificial neural network. In this technique, cellular automata (CA) based seeded tumor segmentation method on magnetic resonance (MR) images, which uses volume of interest (VOI) and seed selection. Seed based segmentation is performed in the image for detecting the tumor region and then highlighting the region with help of level set method. The brain images are classified into three stages that are normal, benign and malignant. For this non knowledge based automatic image classification, image texture features and Artificial Neural Network are employed. The conventional method for medical resonance brain images classification and tumors detection is by human inspection. Decision making was performed in two stages: feature extraction using Gray level Co-occurrence matrix and the classification using Radial basis function which is the type of ANN. The performance of the ANN classifier was evaluated in terms of training performance and classification accuracies. Artificial Neural Network gives fast and accurate classification than other neural networks and it is a promising tool for classification of the tumors.

*Keywords: Segmentation, Classification, Probabilistic Neural Networks, Growcut Algorithm, Grey level Co-occurence. Run length matrix.*

## 1. INTRODUCTION

Segmentation and Classification of brain tissues in gray matter[1] ,white matter[2] ,and tumor[3] on medical images is not only of high interest in serial treatment monitoring of "disease burden" in oncologic imaging, but also gaining popularity with the advance of image guided surgical approaches. Interactive algorithms have become popular for image segmentation problem in recent years. Graph based seeded segmentation framework has been generalized such that random walker (RW) [13], shortest paths, and power watersheds[14] have been interpreted as special cases of a general seeded segmentation algorithm, which solves a minimization problem involving a graph's edge weights constrained by adjacent vertex variables or probabilities. Although it was reported that the shortest paths and RW produce relatively more seed-dependent results, it can be argued that the global minimum of an image segmentation energy is worth as good as the

ability of its energy to capture underlying statistics of images, and a local minimum may produce a solution closer to the ground truth than that of a global minimum. Hence, with good prior information provided as in the case of a seeded image segmentation problem, efficiently finding.

Deformable registration of brain images with tumor to the population atlas is an extremely challenging problem and still an active research area due to intensity variations around the tumor mainly caused by edema/infiltration, and the tumor mass effect, which also deforms the healthy tissue morphology [8]. In some studies, affine registration has been used for this purpose, however misalignment issues arise, especially where there is a large deformation of the brain structures [5], [9].

On the other hand, cellular automata (CA) algorithm motivated biologically from bacteria growth and competition, is based on a discrete dynamic system defined on a lattice, and Iteratively propagates the system states via local transition rules. It was first used by Vezhnevets *et al.* (Grow-cut) for image segmentation, which showed the potential of the CA algorithm on generic medical image problems. However, Grow-cut was not designed for specific structures, such as tumors, which display heterogeneous content such as necrotic and enhancing tissue. Moreover, anatomic structures typically have relatively smooth boundaries, however, Grow-cut tends to produce irregular and jagged surface results, and only an *ad hoc* way of smoothing was introduced.

In this paper, we re-examine the CA algorithm to establish the connection of the CA-based segmentation to the graph-theoretic methods to show that the iterative CA framework solves the shortest path problem with a proper choice of the transition rule and Neural network for classification of the normal and abnormal image.

## 2. RELATED WORK

Segmentation refers to the process of partitioning a digital image into multiple regions (sets of pixels). The goal of segmentation is to simplify and/or change the

representation of an image into something that is more meaningful and easier to analyze. Image segmentation is typically used to locate objects and boundaries (lines, curves, etc.) in images.

## 2.1 Gray Level Co Occurrence Matrix (GLCM)

A glcm is found by calculating how often a pixel with the intensity (gray-level) value i occurs in a specific spatial relationship to a pixel with the value j. Each element (i,j) in the resultant glcm is simply the sum of the number of times that the pixel with value i occurred in the specified spatial relationship to a pixel with value j in the input image. The number of gray levels in the image determines the size of the GLCM .

## 2.2 Cellular Automata In Image Segmentation

A cellular automata is basically a computer algorithm that is discrete in space and time and operates on a lattice of cells [6]. Since it was first proposed by Von Neumann and Ulam [4], Cellular Automata has attracted researchers from various fields in both physical and social sciences because of its simplicity, and potential in modeling complex systems [11].

Each individual cell is in a specific state and changes synchronously depending on the states of some neighbors as determined by a local update rule [12]. They are parallel, local and homogeneous since the state of any cell depends only on the states of the local neighbors at the previous time step and the update rules are same for every cell.

Although the usual definition for "Cellular Automata" is in favour of a finite state set (discrete and bounded), continuous state sets in which the states are real numbers are also used in CA literature under the name "Continuous CA" or "Coupled Map Lattices" Grow-cut method uses a continuous state cellular automata to interactively label images using user supplied seeds. The cells are corresponding to image pixels, and the feature vector is RGB or gray scale intensities.

The Grow-cut algorithm is equivalent to the Belman-Ford algorithm, which calculates the shortest paths on a weighted graph [16]. However, there, the motivation and emphasis was on fast hardware implementation of the CA algorithms, due both increasing availability of low-cost graphical hardware (GPUs), and CA algorithm's suitability to run on parallel processors.

## 2.3 Probabilistic Neural Network (PNN)

Performance of the PNN classifier was evaluated in terms of training performance and classification accuracies. Probabilistic Neural Network gives fast and accurate classification and is a promising tool for classification of the tumors. Existing weights will never be alternated but only new vectors are inserted into weight matrices when training. So it can be used in real-time. Since the training and running procedure can be implemented by matrix manipulation, the speed of PNN is very fast. The network classifies input vector into a specific class because that class has the maximum probability to be correct. In this paper, the PNN has three layers: the Input Layer, Radial Basis Layer and the Competitive layer. Radial Basis Layer evaluates vector distances between input vector and row weight vectors in weight matrix These distances are scaled by Radial Basis Function nonlinearly. Competitive Layer finds the shortest distance among them, and thus finds the training pattern closest to the input pattern based on their distance.

# 3. PROPOSED METHOD

The Grow cut is an interactive segmentation algorithm which uses CA as an image model. A cellular automata is basically a computer algorithm that is discrete in space and time and operates on a lattice of cells. Each individual cell is in a specific state and changes synchronously depending on the states of some neighbours as determined by a local update rule. The local neighbours at the previous time step and the update rules are same for every cell.

## 3.1 Automatic Seed Point Selection

Seed point selection will be done in the cropped tumor image. This will be done by using Grey Level Co-occurrence Matrix (GLCM). Texture feature of the image will be extracted by using GLCM. Energy and Entropy are two features taken from the tumor image. Run length features are based on computation of continuous probability of the length and gray level of the primitive in the texture.

The selection of seed pixel from co-occurrence features, we can check whether the selected seed pixel belongs to abnormal region or not. This can be checked by calculating the Run length features. The long run length emphasis is high for homogeneous region and low for non homogeneous region and the run length non uniformity is low for homogeneous and high for non homogeneous. A Co-Occurrence Matrix (COM) is square matrices of relative frequencies $P(i, j, d, \Theta)$ with which two neighbouring pixels separated by distance d at orientation occur in the image, one with gray level i and the other with gray level j.

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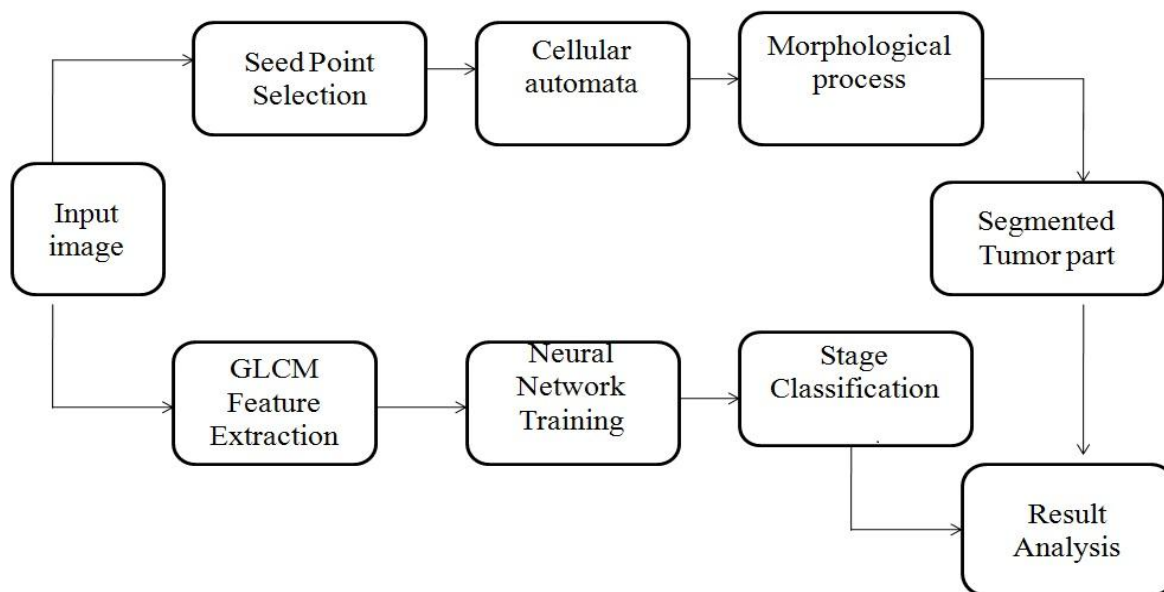**ISSN: 2320 - 8791**
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Fig. 1 Steps of the proposed tumor segmentation and classification method.

A Co Occurrence Matrix is therefore a square matrix that has the size of the largest pixel value in the image and presents the relative frequency distributions of gray levels and describe how often one gray level will appear in a specified spatial relationship to another gray level within each image region. There are 14 features that may be extracted from Co-Occurrence matrix, but usually 4 or 5 features are more interested ones. In this paper 2 textural features were calculated from the Co-Occurrence Matrix.

In this work the co-occurrence features energy and entropy which can easily differentiate non-homogeneous region from homogeneous region are considered. Energy is called Angular Second Moment. It is a measure the homogeneousness of the image and can be calculated from the normalized COM. It is a suitable measure for detection of disorder in texture image. Higher values for this feature mean that less changes in the image amplitude or intensity result in a much sparser COM. The energy is formulated by the following equation:

$$J = \sum_{i=1} \sum_{j=1} (p(I,j))^2 \qquad (1)$$

Entropy gives a measure of complexity of the image. Complex textures tend to have higher entropy. Entropy is represented by the following equation:

$$S = -\sum_{i=1} \sum_{j=1} p(I,j) log\ (p(I,j)) \qquad (2)$$

The value of energy and entropy are high for homogeneous regions and low for non-homogeneous regions. The abnormal region in the ultrasound images appears to be homogeneous. So these parameters can identify a seed pixel from the abnormal regions.

### 3.2 Gray Level Run Length Features

Run length features are based on computation of continuous probability of the length and gray level of the primitive in the texture. After the selection of seed pixel from co-occurrence features, we can check whether the selected seed pixel belongs to abnormal region or not. This can be checked by calculating the Run length features. These features are calculated from the Run length matrix $P$ (i, j) which describes the number of times that the image contains a run of length j in a given direction consisting of points having gray level i.

The long run length emphasis is high for homogeneous region and low for non homogeneous region and the run length non uniformity is low for Homogeneous and high for non homogeneous. The run length features have been calculated around the points selected by co occurrence features. If all the run length features of selected point and its neighbourhood points are equal then the point is considered as a seed point.
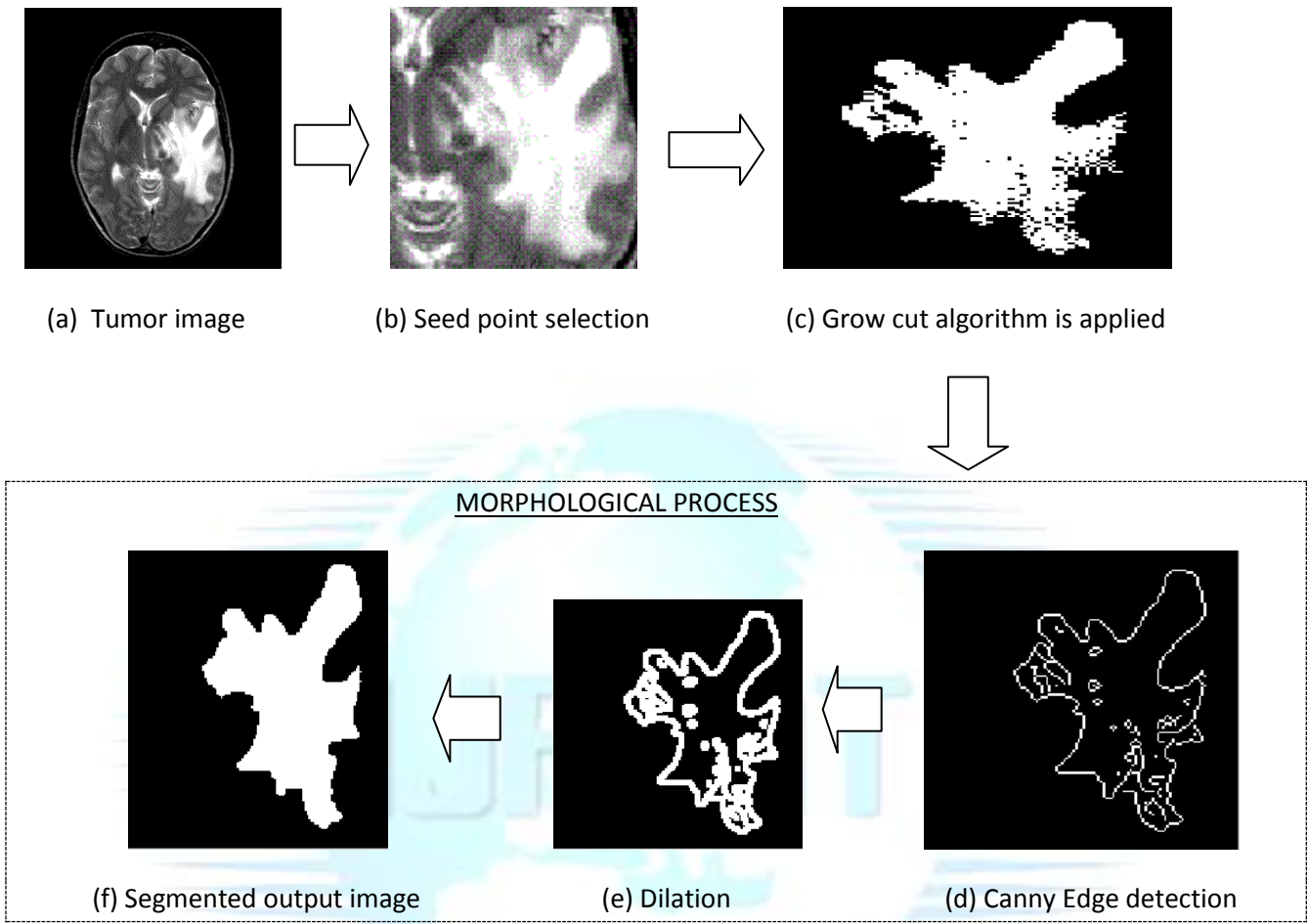
(a) Tumor image       (b) Seed point selection       (c) Grow cut algorithm is applied

MORPHOLOGICAL PROCESS

(f) Segmented output image       (e) Dilation       (d) Canny Edge detection

Fig. 2. Steps of the proposed tumor segmentation method

## 3.3 CA Algorithm Based On Seed Based Segmentation

The Grow cut is an interactive segmentation algorithm which uses CA as an image model. A cellular automata is basically a computer algorithm that is discrete in space and time and operates on a lattice of cells [6]. There are various attempts of using CA in image processing problems including: image enhancement (sharpening and smoothing) [7], image filtering, edge detection [6], and image segmentation (Grow-cut) [16]. The tumour region is grown by selecting seed point from abnormal region through texture features. Each individual cell is in a specific state and changes synchronously depending on the states of some neighbours as determined by a local update rule. They are parallel, local and homogeneous, since the state of any cell depends only on the states of the local neighbours at the previous time step and the update rules are same for every cell.

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There are various attempts of using CA in image processing problems including: image enhancement (sharpening and smoothing), image filtering, edge detection and image segmentation (Grow-cut). Grow-cut method uses a continuous state cellular automaton to interactively label images using user supplied seeds. The cells are corresponding to image pixels, and the feature vector is RGB or gray scale intensities.

Grow-cut algorithm is equivalent to the Belman–Ford algorithm, which calculates the shortest paths on a weighted graph. However, there, the motivation and emphasis was on fast hardware implementation of the CA algorithms, due both increasing availability of low-cost graphical hardware (GPUs), and CA algorithm's suitability to run on parallel processors. In this grow cut method, first we have find the maximum intensity variation which means that from this intensity to 0 we are sure that this is not the Rate of interest. Second we cut the histogram from MAX to 0. Then, we have to find the threshold from MAX to the highest intensity which separates the uncertainty area from the ROI. This is simply done using the well-known Otsu thresholding method. This is a parameter free thresholding technique which maximizes the inter-class variance. It is interesting to observe that the Otsu method is more accurate in cutting into two classes than a k-means for example, because the k-means just measures distances between data and classes centroids but Otsu also take care to get compact clusters using the inter-class variance. Region-based active contour models are widely used in image segmentation [10]. In general, these region-based models have several advantages over gradient-based techniques for segmentation, including greater robustness to noise.

## 3.4 Morphological Process

A shape (in blue) and its morphological dilation (in green) and erosion (in yellow) by a diamond-shape structuring element Mathematical morphology (MM) is a theory and technique for the analysis and processing of geometrical structures, based on set theory, lattice theory, topology, and random functions. MM is most commonly applied to digital images, but it can be employed as well on graphs, surface meshes, solids, and many other spatial structures.

Topological and geometrical continuous-space concepts such as size, shape, convexity, connectivity, and geodesic distance, can be characterized by MM on both continuous and discrete spaces. MM is also the foundation of morphological image processing, which consists of a set of operators that transform images according to the above characterizations.

The basic idea in binary morphology is to probe an image with a simple, pre-defined shape, drawing conclusions on how this shape fits or misses the shapes in the image. This simple "probe" is called structuring element, and is itself a binary image (i.e., a subset of the space or grid).

## 3.5 PNN Training and Classification

In this paper, the PNN has three layers: the Input Layer, Radial Basis Layer and the Competitive layer. Radial Basis Layer evaluates vector distances between input vector and row weight vectors in weight matrix. These distances are scaled by Radial Basis Function nonlinearly. Competitive Layer finds the shortest distance among them, and thus finds the training pattern closest to the input pattern based on their distance. In Radial base layer, vector distances

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between input vector p and the weight vector made of each row of weight matrix W are calculated. Here, the vector distance is defined as the dot product between two vectors.
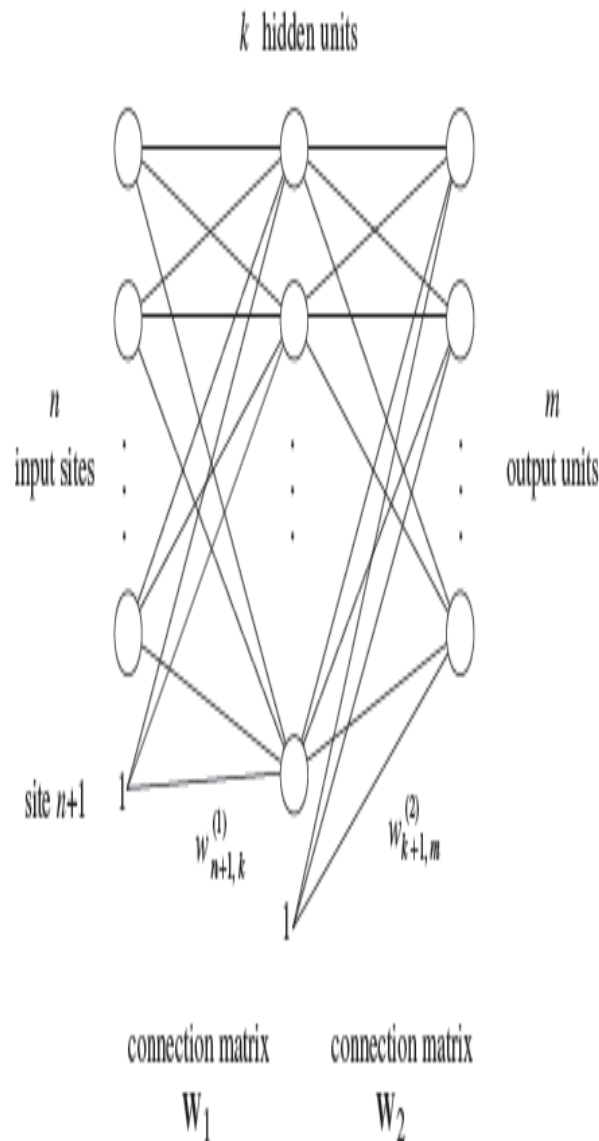


Fig. 3 Structure of neural network

Here, the vector distance is defined as the dot product between two vectors. Assume the dimension of W is $Q \times R$. The dot product between p and the $i^{th}$ row of W produces the $i^{th}$ element of the distance vector ‖W-p‖, whose dimension is $Q \times 1$. The minus symbol, "-", indicate that it is the distance between vectors. Then, the bias vector b is combined with ‖W- p‖ by an element-by-element multiplication. The result is denoted as n = ‖W- p‖ .*p. The transfer function inPNN has built into a distance criterion with respect to a center. This layer is defined as $radbas(n) = e^{-n^2}$ .Each element of n is substituted and it produces corresponding element of a, the output vector of Radial Basis Layer. The $i^{th}$ element of a can be represented as the $a_i = radbas(‖W_i - p‖.*p)$ where $W_i$ is the vector made of the $i^{th}$ row of W and p. A radial basis neuron with a weight vector close to the input vector p produces a value near 1 and then its output weights in the competitive layer will pass their values to the competitive function. It is also possible that several elements of a are close to 1 since the input pattern is close to several training patterns.

## 4. Conclusion

The paper developed a hybrid technique with normal and benign or malignant classes. Our medical decision making system is designed by Cellular automata for segmentation and neural network for classification. The proposed approach gives very promising results in classifying the healthy and pathological brain. The benefit of the system is to assist the physician to make the final decision. The proposed algorithm is efficient for classification of the human brain normal or abnormal (benign and malignant tumor) 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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