International Journal of Scientific Research in Computer Science and Engineering
Vol.10, Issue.5, pp.27-36, October (2022)

Research Paper

E-ISSN: 2320-7639

Brain Tumor Detection using Cellular Automata based image Segmentation techniques

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Available online at: www.isroset.org | DOI: https://doi.org/10.26438/ijsrcse/v10i5.2736

Received: 10/Sept/2022, Accepted: 03/Oct/2022, Online: 31/Oct/2022

Abstract— A quick and effective diagnosis is critical to the treatment of any disease. In the case of cancer-related diseases, the success of the treatment is typically correlated to the time of accurate diagnosis of the disease. Thus, it is important to make a quick and accurate diagnosis. This work presents a cellular automata-based system capable of diagnosing tumors in medical data from various imaging techniques, including MRI and X-ray. This system is an Automated Cellular (CA) that uses the Moore neighborhood algorithm to detect the area of cancer cells in the image, by segmenting areas of abnormality from the background. We also present an analysis of different parameters of the Moore neighborhood algorithm for optimal detection of cancerous cells; the results of this analysis confirm the proposed method effectiveness on all data sets, with an accuracy of more than 93\% and 95\% precision.

Keywords— Cellular Automata; Tumor Detection; Magnetic Resonance Imaging; Segmentation

I. INTRODUCTION

Malignant tumors are among the most deadly diseases. Within the next two decades, it is expected that the cancer burden will double. In turn, this is expected to have a worldwide impact on both human and financial resources. However, these developments are tied to the global capability of timely detection and treatment of cancerous lesions [1]. The leading type of cancer that causes death in women is breast cancer. Its prevalence is increasing with time. Diagnosed as abnormal tissue in the breast, it may be classified as benign or malignant. Malignant tumors are deadly and must be excised from the body after a biopsy. Since there is no official cure for cancer, an early diagnosis is a key to the right course of action, be it treatment or ablation of the abnormal mass. Various imaging methods, such as X-ray and MRI, are frequently used to pinpoint the growth of the tumor..

Further analysis of these images is done using medical image processing techniques. Another type of cancer that is very common. A general classification of lung cancer cells is based on the cell size and is typically referred to as small- and non-small-cell lung disease [2], the assured survival rate in lung cancer is 15%; however, if the diagnosis is made at a very early stage, this survival rate can increase to 70% [3]. A major cause of lung cancer's high death rate is the delayed detection and subsequent treatment of the disease. In that regard, it is of paramount importance that a timely detection is made. Various imaging methods including MRIs and X-rays are used to diagnose different diseases. Their primary goal is to aid in the monitoring and detection of abnormalities using image processing, the raw data available from these imaging modalities can be transformed into meaningful information for clinical use [4]. To that end, Cellular Automata (CA) is one stream of information processing that is efficient, accurate, and used for detecting boundaries and edges and thus finds its application in multiple areas [5]. By leveraging CA, tumor detections can be made to assist timely diagnosis of potential cancer patients. In that regard, this study is very important as it serves as a tool to facilitate the clinicians.

CA can be represented in a regular and uniform pattern. This preserves heterogeneity, particularly concerning the dependency on the neighborhood and the structure of the overall lattice. CA comprises a cellular grid where each cell can take a particular state. The overall number of possible states is finite. A cell's state is periodically updated based on previous states of neighborhood cells [6]. A transition rule does this state change. One, two, or three dimensions can be CA models. One dimensional CAs consist of a linear set of cells. In 2D CA, the arrangement of cells is grid-like: rectangular or hexagonal. Importantly, the connections between the neighborhood cells are maintained by the grids [7]. 2D CAs are solved as digital image processing problems because cells are represented as digital images. In order to leverage cellular automata to design solutions, mathematical techniques such as lattice geometry, neighborhood size, and initial condition boundary problems, as well as cell states and their accompanying rules of transition, must be understood and carefully studied with reference to the problem at hand [8]. All adjacent cells are referred to as a cell adjacent to the reference (central) cell.

In this work, we show how to use the CA formalism to detect the presence or absence of abnormal cells in MRI images, for cancer diagnosis, tumor detection is absolutely critical and this study is a step in that direction to facilitate and automate the detection of tumors. The CA-based image -segmentation algorithm is deployed to isolate the tumor region from the normal background image. Due to the variate nature of the cell images, successful deployment of segmentation is difficult to achieve with reasonable accuracy. The kind of image segmentation approach one must take depends on the characteristics of the area of interest. Segmentation typically makes use of thresholding pixel values to differentiate pixels that are beyond a threshold value. Tuning the right threshold value greatly affects the kind of segmentation success one gets.

Cellular automata-based image segmentation rules can be modified depending on the image type to suit the application's needs. In cellular automata, operations based on neighborhood cell states are typical for processing images. In this work, we apply a 24-point neighborhood operation to isolate the abnormal cells from the background image.

the importance of this work in the application of cellular automata in tumor modeling lies in the ability to formalize tumor cells and monitor the dynamics of the tumor boundary level. where the study of tumors using cellular automata is similar to the study of tumor cell models in the laboratory. In addition to being a successful method for interpreting medical images, cellular automata are also computationally efficient, this method is useful for specialists in detecting the area of abnormal cells. and among the main contribution of this study is cellular automata based 24 point Moore neighborhood segmentation algorithm that leverages cellular automata to update the cell states as it traverses to subsequent cells, using updated states of the prior cells. It is also an application on brain tumor detection on MRI dataset.

The remainder of this work is structured as follows. we go over related work and explain the work concerned with CA-based techniques in section II. Section III proposes a methodology to segment cancerous areas from the background. In section IV, we evaluate the proposed methodology and discuss the results in light of our experiment. Conclusion and Discussion are made in section V.

II. BACKGROUND STUDY

This section expands on the basics of cellular automata, the cancer detection techniques used, and cellular automata based image segmentation.

A. Cellular automata basics

cellular-automata is a grid of cells and is considered as a computational model [6]. Each cell functions as finite automata having a particular state, and the state transitions happen with respect to a transition rule. CA exhibit uniform as well as dynamic and complex behavior. The complex behavior is determined by the various properties that constitute the CA transition rules. by observing cellular automata outputs collectively acquired in continuous actions, a pattern is generated. We denote a CA with a fairly simple expression.

$$CA = \{L, N, P, \delta, p_0\} \quad (1)$$

L: Is a reference to the normal cell..

P: represents a limited number of states.

p_0**:** The starting state, and $p_0 \in P$.

N : With regard to neighbourhood indices, N: is a finite set and $r \in L$ and $a \in N : r + a \in L$.

δ: is the process stage such that $P_m \rightarrow P$ [9].

Different CA structures have different applications depending on the problem under consideration. Typically, 1D, 2D, and 3D CAs are used. 1D CA may be represented as infinite cells in an array where two states are possible for each cell: 0 or 1. A 2D CA may have a rectangular or a hexagonal grid structure; however, for the representation of images, a rectangular grid is considered to assign each cell to an image pixel with the cell state as the pixel's intensity. The difference between 1D and 2D CA structures is evident in Fig. 1 and Fig. 2. As cells change their state, image transformations can be visualized. These image transformations can be implemented by performing operations based on the neighborhood in a CA. A reference cell's neighborhood is made up of the cells that are right next to it. The convention for one-dimensional CA entails that a reference cell has two neighbors along each of its sides. In two-dimensional CA, based on the algorithm, there are certain variations to categorize a cell as a neighbor. For example, the reference cell of a Von Neumann neighborhood CA has four neighbors, i.e., the horizontal and vertical cells surrounding the reference cell, moore neighborhood CA has eight adjacent cells in its neighborhood [9]. Fig. 2 is in fact Von Neumann CA, whereas Fig. 3 shows a 2D CA structure using the Moore neighborhood. The difference between Von Neumann and Moore algorithms in terms of neighborhood classification is shown in Fig. 2 and Fig. 3 where it can be seen that with respect to the reference (R) cell, the Moore neighborhood structure takes all adjacent cells into account.

Fig.1: 1D CA structure

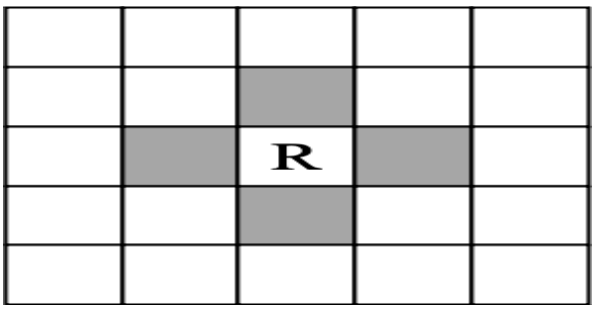


Fig.2: 2D CA Von Neumann structure

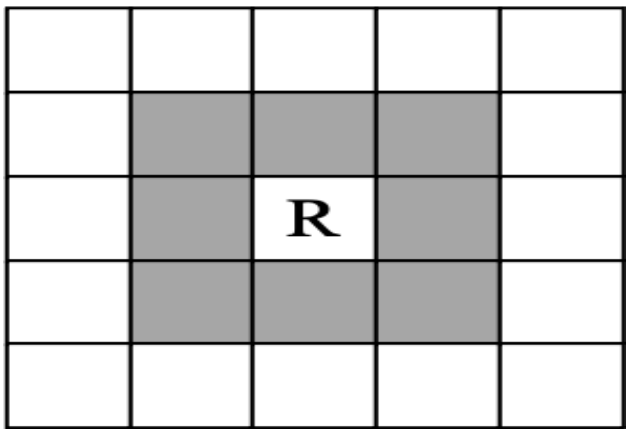


Fig.3: 2D CA Moore structure

B. Cancer Detection Techniques

The importance of early cancer diagnosis cannot be stressed enough. Due to the effectiveness of early cancer diagnosis, image processing and deep learning technologies help in rapid tumor detection. In this paper, we do research on tumor detection. Where we find one of the most prominent techniques in detecting tumors, x-ray imaging is imaging through which any signs of a tumor can be identified. Unfortunately, the radiographic image contains a lot of noise, and only the lighter pixels in the image can indicate a cancer cell. For the detection of breast cancer, R. Ramani et al. proposed a preprocessing mechanism for radiographs. [10], which has been successful in improving the quality of mammograms. It also reduces noise to help further detect abnormal cells, cancerous or otherwise. region splitting, growing, and the Watershed algorithm—helps identify regions with abnormal mass growth. The classic algorithm called the watershed algorithm [4] is a morphological technique for segmenting images related to specific regions. In this algorithm, the Watershed transformation considers images as topographic maps of each point standing out by its brightness. In order to perform watershed transformation [11], a computation is made for the distance transform over a binarized image before the gradient value marker-controlled method can be applied. Another approach for identifying breast tumors from a mammogram was proposed by A. Singh et al. [12]. First, the tumor region is extracted after smoothing and choosing a threshold. Then, the important outcomes image is created by making a box and enclosing the tumor region., brain tumor is yet another terrible illness. It is possible to detect it by analyzing the CT image of a brain. An automated approach for brain tumor diagnosis was presented by S.Sazzad et al. [13]. This approach started with an image enhancement technique to counteract the effects of variations in grayscale colors in the image. This was followed by filtering to get rid of the noise. Since grayscale images were used, OTSU-based segmentation was done. Using feature information from pathology experts, tumor regions were marked and identified. It is possible to detect lung cancer using different imaging techniques such as CT scans or X-rays of S.Tarawneh et al. [14] proposed an approach where the authors used the OTSU method for thresholding after cleaning the image. Segmentation allowed for certain features to be extracted, which was followed by binarization and masking. A clustering-based segmentation technique was presented by K. Senthil et al. [15]. Multiple filters were used for the enhancement of input images quality. The segmentation was then implemented using K-means, optimization techniques are then used. to distinguish the focus region and collect crucial tumor characteristics.

C. Image segmentation using cellular automata

One of the major concerns in medical imaging is robust and accurate detection of diseases that could include tumors or fractures. For an efficient detection of tumors in brain and other parts of the body, segmentation of image is typically employed to segregate an image into various parts and eventually extract a region of interest. The core objective of segmentation is to represent the abnormality in a simple way for analysis. Typically, segmentation detects edges or boundaries in the image [16]. Another important process in image processing is thresholding, as it directly affects the clarity of resulting image and contributes directly in determining the regions of interest. Utilizing cellular automata-based techniques for segmentation provides robustness and accurate detection of abnormal cells [17]. To that end, different methods have been applied in the past to detect edges in the image that facilitate isolating the tumor in the original image. These include leveraging CA to find edges on binary images [9] of hand X-rays, brain tumor images [17], as well as brain, lung, and breast images [18].

III. RELATED WORK

Malignant tumor is a mass of tissue in which cells grow abnormally. Therefore, brain tumors are one of the most critical areas to be studied. There are more than 150 types of brain tumors that differ from each other, and brain tumors are among the causes of death for many people; in 2021, more than 83,570 people in the United States were diagnosed with brain tumors, of which 59,040 were benign, and 24,530 were malignant [19]. Due to the importance of the topic, many methods have been suggested over the past four years to study brain tumors.

In paper [19], an automated system was used to detect brain tumors, which helps to detect the area of abnormalities, and this method also enables to improve the X-ray image quality. The outcomes, particularly those related to enhancing the X-ray image's quality, supported the suggested approach's effectiveness.

M. Diwakar et al [20], focused on Edge-Detection; this paper proposed Edge-Detection through the use of cellular automata. The result of this work was good in terms of accuracy, in addition to the use of a large database.
In the same context, Paper [21] presents a cellular-automata-based method to identify and segment the damaged area through MRI treatment, whereas, the proposed method concluded that in order to achieve better outcomes, the method should be included for the outer cells of the next level.

In paper [22], the effect of treatment on the development of vascular carcinoma was investigated using a random cellular model. The findings demonstrated that taking the medication consistently as prescribed by a doctor is more effective at halting the spread of cancer cells, as demonstrated by simulation results based on in vivo data.

In the same context, Paper [23], studied skin cancer such as melanoma, which is the most aggressive skin cancer. The study concluded that early detection has a significant role in the high rate of survival. This study relied on spatial domain analysis and feature extraction using statistical-techniques. The percentages of accuracy, sensitivity, and specificity reached 0.978, 0.944, 0.987, respectively; this makes the proposed method more effective.

In the paper [24], a new method for treating tumors based on CA was presented, where this method depends in the first stage on naturally growing of tumor, and then the treatment is done by reducing the settings of the model, where the results are that with the decrease in the parameters of the model, there is no change in contrast to the increase in the parameters, so the inactivity of the tumor was resolved and thus it was possible to eradicate it.

This paper [25] focuses on tumor detection using CNN techniques and CA, where CNN is considered one of the most prominent techniques in tumor detection and classification, and several applications have demonstrated the effectiveness of this method, and when it is combined with cellular automata, the simulation of cancer cells resembles the behavior of cells in reality, and this is due to the power of cellular automata in tumor simulation, as the study was also applied to the magnetic resonance imaging data set, and the results were generally satisfactory.

In paper [26] segmentation and detection was discussed utilizing fuzzy logic, and CA, where the proposed method was implemented on the BraTS data set, where the density of each pixel is relied on by feeding it to label each pixel, and the same process continues several times, where the accuracy rate in the stage before the improvement was 85.8%, while in the second stage, after analyzing the image, the accuracy reached 99.8%.

In paper[27] edge-detection was studied using Cellular-Automata, where the suggested technique shown success in terms of analyzing and clarity compared to other methods such as prewitt, sobel, and canny, which have some disadvantages.

In paper [28] a three-dimensional cellular-automated model was developed that works mainly on tumor modeling by relying on parameters, as this model simulates the growth of the tumor, and this model also enables the prediction of tumor motility over time, the work principal goal is to develop a novel model of the tumor, and the results of this method were acceptable.

The paper [29] focuses on tumor detection using electromagnetism and watersheds, where it focuses on the behavior of the tumor and the importance of detecting it at an early stage, several methods were discussed in this paper and among these methods, the suggested method yielded good results that demonstrate the effectiveness of the presented approach compared to other techniques.

The paper [30] aims to study tumor segmentation with high accuracy, and this paper also presented a set of works in order to compare and test the suggested method, and the results of partitioning confirmed the effectiveness of the proposed method.

In order to further clarify the relevant work, we have extracted the most important characteristics of the discussed works as shown in Table 1, where we define the objective of each study and the techniques used.

Table 1 shows the objective of each study and the techniques used in the relevant work

Ref	Year	Author	Objective	Techniques used
[19]	2022	R. Barik et al	Cancer Detection using Cellular Automata	-cellular automata - Edge detection
[20]	2022	M. Diwakar et al	Segmentation of brain tumors using cellular automata	-Cellular Automata - Edge-Detection
[21]	2022	K. Anil et al	Segmentation of brain tumors using outer totality cellular automata	-OTCA -Cellular automata
[22]	2019	P. Fateme et al	Targeting cancer and immune cells by using cellular automata	-Cellular automata
[23]	2022	L .B. Benjamín et al	Dermoscopic Image Melanoma Detection Using a Cellular Automata Classifier	-Pattern recognition -Cellular Automata Classifier
[24]	2018	S Shiva et al	Modeling the growth of an avascular tumor using stochastic cellular automata and immunotherapy	-Cellular automata -Immunotherapy

[25]	2019	R Kalantari et al	Brain Tumor Detection Using CNN and CA	-CNN - Cellular Automata
[26]	2022	K Roqaie et al	Segmentation of Brain Tumor Using Fuzzy Logic	-fuzzy Logic -Cellular Automata
[27]	2021	B Rupashri et al	Analysis and application to biomedical using cellular automata	-edge detection - cellular automata
[28]	2022	A. R. Kansa l et al	Brain Tumor Simulation Using 3D and CA	-cellular Automata
[29]	2018	A.C. Motagi et al	using watershed for brain tumor Detection	-watershed
[30]	2021	P . Jain et al	Detection of brain tumor	-morphological

The key components of the suggested literature are presented in Table 1. Among these features are the goals and techniques used, It also shows the great role of cellular automata in the study of tumors, in addition to the possibility of combining it with other techniques, which makes the study of the tumor more detailed. Moreover, cellular automata simulates the real reality of cancer cell development and transition from one state to another, and this highlights the effective role of cellular automata in the study of tumors compared to other techniques.

IV. MATERIALS AND METHODS

The suggested methodology for detecting tumors with CA is detailed together with the dataset and tools used

A. Dataset Used

The dataset used for this investigation contains MRI images of human brain segregated into two sets of images: those containing brain tumors and those without it. We have considered 40 images from each segregation for our work as beyond this number, the results do not vary significantly. Some samples in our dataset are presented in Fig.4.

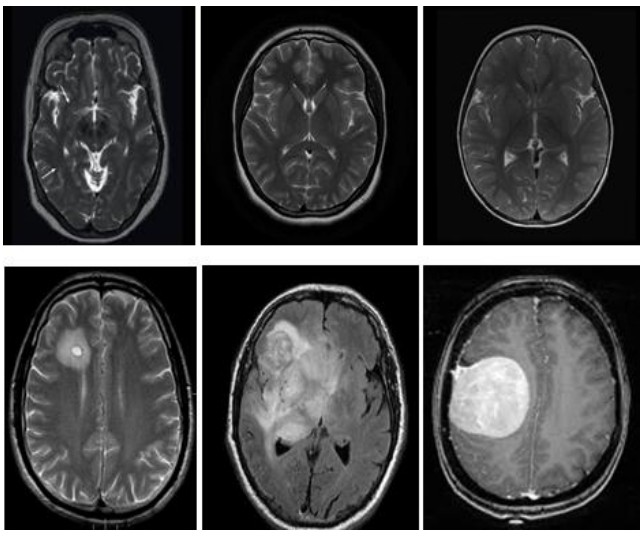


Fig.4: Some samples from the used dataset

B. Tools used

For all work, licensed software MATLAB has been used. Due to its ease of use and robustness in processing image data, MATLAB was the preferred software.

C. Proposed Methodology

In this work, we focused on detecting brain tumors. Figure 5 illustrates the methodology used.

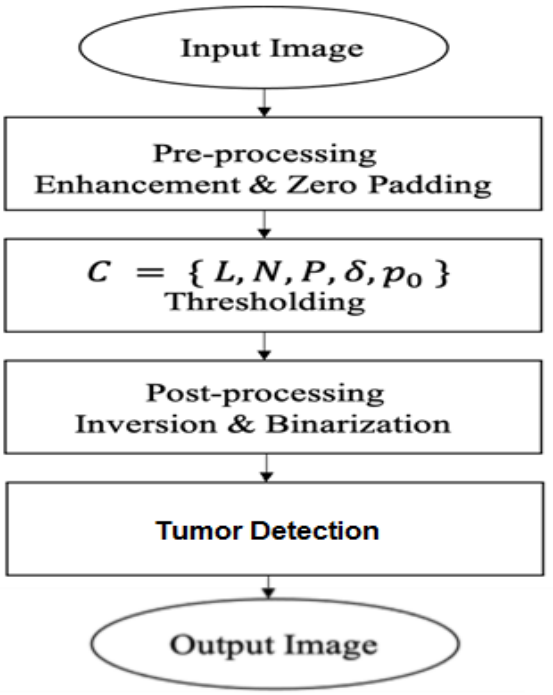


Fig.5: The diagram illustrates the suggested methodology

The main steps of the proposed methodology are as follows:

1. *Input image:* Firstly, the dataset Brain MRI is used as an input images.
2. *Preprocessing:* This step is to improve input image for further operations. Any noise in the image can affect the segmentation process; thus, *smoothing operations* are first done. This is achieved by using a Gaussian bilateral smoothing filter that preserves the edges when smoothing the image. Once this is done, the smoothened image is zero-padded to ensure that the reference cells at the boundary of the image have a suitable number of cells as their neighbors. Zero-padding ensures we have sufficient pixels as neighbors for the boundary reference cells. An illustration of cellular automata based 8 points Moore neighborhood algorithm at the boundary pixel location is shown in Fig. 6 where 'R' corresponds to the reference pixel, shown here at the boundary of the original image, and

'N' corresponds to a neighbor pixel. The black squares in the figure correspond to the zero-padded pixels in the image, and the white squares correspond to the original image. Thus, zero-padding ensures that the boundary pixels in the original image are not void of any neighbors.

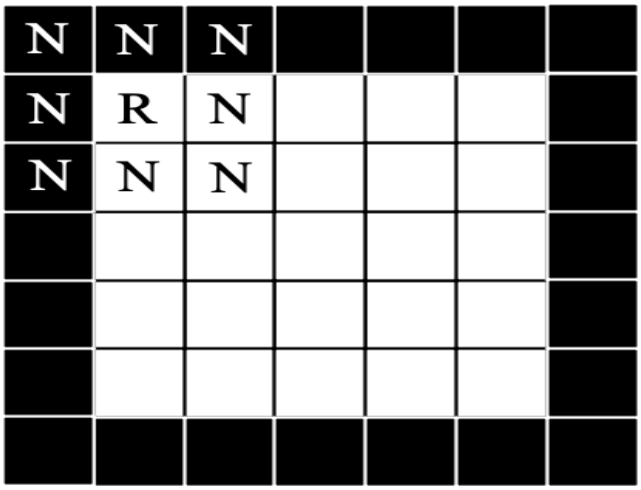


Fig.6: Illustration of zero-padding on 8 point neighbors

3. *Threshold and implementation of cellular automata*: After this pre-processing, we then perform cellular automata based Moore neighborhood segmentation technique that entails taking 24 adjacent points around the reference cells to compute their differences. A 24 point Moore neighborhood structure is shown in Fig. 7.

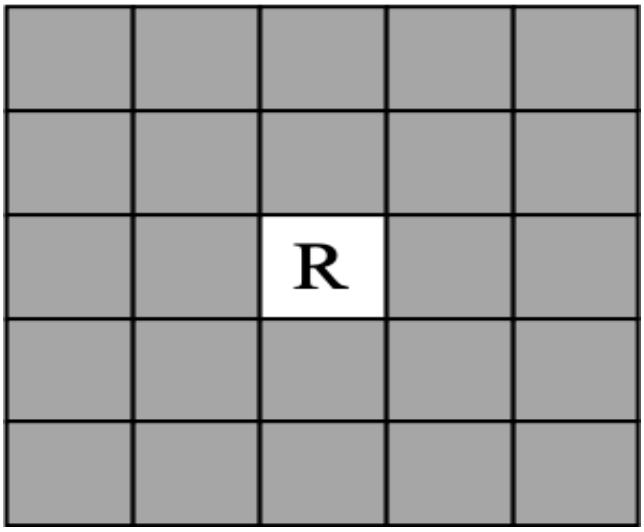


Fig.7: 2D CA 24 point Moore structure

The means to traverse from one cell to another, which in the case of an image is essentially a movement from one pixel to another, is done sequentially, row by row by keeping track of the indices of the image. We can refer to index locations for a particular reference cell as (i, j) refers to a row and column number, respectively. Any increments or decrements in these locations allow us to access the neighborhood cells, as shown in Fig. 8.

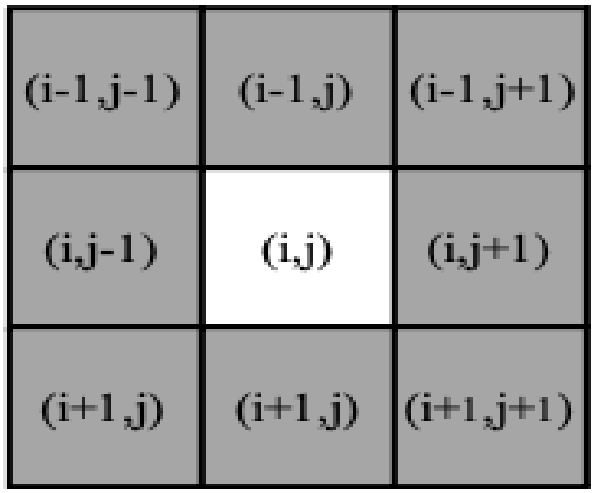


Fig.8: Reference cell and neighbor locations

With respect to Equation (1), our lattice of cells, L, is in fact the size of the image (512x512) since we are implementing CA on 2D images with N = 24 as there are 24 neighbors for each cell; P = 256 as we work on 8-bit images and P_0, the initial state is considered to be the input image's pixel value. The transition rule δ for this cellular automata implementation is such that if all differences of the reference cell from its neighbors are below a pre-set threshold value, we assign the reference cell a zero value. Otherwise, the reference cell value remains unchanged. This is done for all pixels in the image. This is the major step in implementing cellular automata based segmentation on 2D images: selecting neighbors according to Moore's algorithm to select cells adjacent to a given cell state $Y_{i,j}$ of the cell by:

$$\mathbf{M}_{(\mathbf{y_{0,0}})}{}^{\mathbf{N}} = \{(\boldsymbol{Y}_{(i,j)}) : |\boldsymbol{Y}_{(i,j)} - \mathbf{y_{0,0}}| \leq \mathbf{r}\}$$

For r=0, 1, 2, and 3, moore neighborhoods are Odd squares that make up the amount of cells in the Moore neighborhood of range r.$(2r+1))^2$.

state $Y_{(i,j)}{}^{t+1}$of the cell at time (t + 1) can also be specified by the native rule procedure f : $(Z_3{}^9) \rightarrow$ Z3 as follows:

$$\mathbf{Y_{(i,j)}}^{\mathbf{t+1}} = \mathbf{f}(\mathbf{Y_{(i,j)}}^{\mathbf{t}}, \mathbf{Y_{(i+1,j)}}^{\mathbf{t}}, \mathbf{Y_{(i+1,j-1)}}^{\mathbf{t}}, \mathbf{Y_{(i-1,j-1)}}^{\mathbf{t}}, \mathbf{Y_{(i-1,j)}}^{\mathbf{t}}, \boldsymbol{Y_{(i,j-1)}}^{\boldsymbol{t}}, \mathbf{Y_{(i-1,j+1)}}^{\mathbf{t}}, \mathbf{Y_{(i,j+1)}}^{\mathbf{t}}, \mathbf{Y_{(i+1,j+1)}}^{\mathbf{t}})$$

$$= \boldsymbol{b_0 Y_{(i,j)}}^{\boldsymbol{t}} + \boldsymbol{b_1 Y_{(i+1,j)}}^{\boldsymbol{t}} + \boldsymbol{b_2 Y_{(i+1,j-1)}}^{\boldsymbol{t}} + \boldsymbol{b_3 Y_{(i-1,j-1)}}^{\boldsymbol{t}} + \boldsymbol{b_4 Y_{(i-1,j)}}^{\boldsymbol{t}} + \boldsymbol{b_5 Y_{(i,j-1)}}^{\boldsymbol{t}} + \boldsymbol{b_6 Y_{(i-1,j+1)}}^{\boldsymbol{t}} + \boldsymbol{b_7 Y_{(i,j+1)}}^{\boldsymbol{t}} + \boldsymbol{b_8 Y_{(i+1,j+1)}}^{\boldsymbol{t}}$$

Where $\boldsymbol{b_0}, \boldsymbol{b_1} \ldots \in \mathbf{Z3}$ each cell's value for the following state, and then deciding threshold values based on the computed differences from each neighbor.

4. *Post-processing and detection*: The resultant image is then fed to the post-processing block where it is inverted and binarized for simpler viewing. The inversion of image subtracts the pixel value from 255

which is the maximum pixel value. The zero pixels become 255 and the 255 valued pixels become 0, hence the name inversion. Essentially, this is done for a better visualization as the image is now meant to show only the tumor mass in dark black pixels in image. We also perform binarization on this image, thus the image on contains 0s and 1s. This binary image is an even better visualization of the tumor. Thus, the result is the process of detecting the tumor using cellular automata.

5. *Output image:* It is the result of the model and performance, where we evaluate the results and performance parameters of the proposed methodology.

V. RESULTS AND DISCUSSION

In this section, we present a demonstration of proposed algorithm using cellular automata-based segmentation on a publicly available brain tumor MRI image dataset. The pseudo-code below shows the algorithm used in this paper

Procedure 1 CA based Segmentation

Require: *image, threshold*

```
procedure TUMOR DETECTION()
    Image enhancement via filtering
    Image padding with zeros
    Initialize threshold
    for each reference pixel do
        Neighborhood determination
        Difference computation
        Thresholding
        Update reference pixel value if needed
    end for
    Image inversion
    Image binarization
    Tumor Detection
end procedure
```

The proposed algorithm is shown to work on a brain tumor image to focus on the desired area i.e., The tumorous cells. The input image is shown in Fig. 9.a. Notice the tumor in the left center of the brain MRI image, which is the target area of segmentation and needs to be isolated for the physician. We apply a bilateral filter that performs Gaussian blurring while maintaining edges in the image. It smoothens the image as shown in Fig. 9.b.

This is followed by zero padding to ensure the cellular automata-based segmentation has neighbor pixels for the boundary pixels in the image. The zero-padded image looks the same as the smoothened image except that its size is now 516x516 since two pixels are added on each side of the image as padding because we consider two pixels in each direction of the reference pixel for neighbor determination. The zero-padded image is also shown below in Fig. 9.c The CA-based segmentation is done on this padded image to determine pixel values according to the CA transition rules discussed in Section III-C. When the CA rules are applied, they take into account a rectangular subset of pixels. The pixels on the border of the image do not have any neighbors. In order to provide neighbors to the bordering pixels, zero padding is done. The resulting image is shown in Fig. 9.d where it can be seen that tumor is successfully segmented. However, areas other than tumors are also evident in the image as unwanted artifacts. These additional areas show up because of the nature of the algorithm where it is focusing on determining the edges. Hence, the artifacts correspond to the edges of features in the brain image. A well-tuned threshold value can aid in the image to reducing these artifacts.

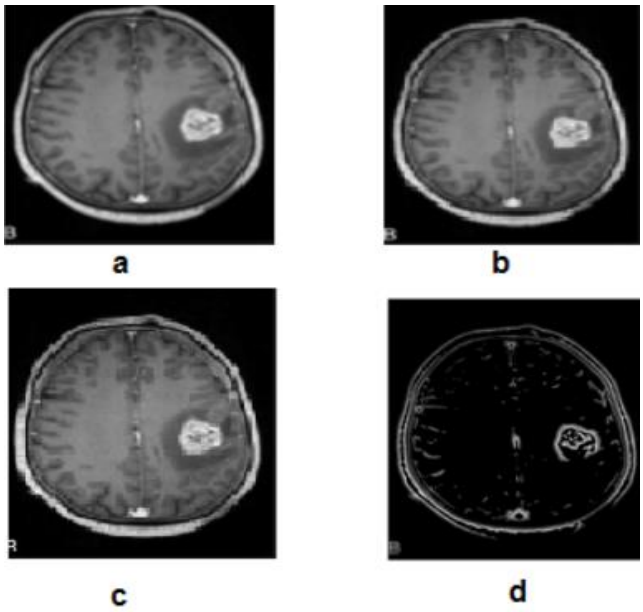


Fig.9: a: Brain input image, b: Smoothened image, c: Zero padded image, d: Image after CA based segmentation.

In order to make the tumor more visually apparent, we invert the image. This inverted image is shown in Fig. 10.

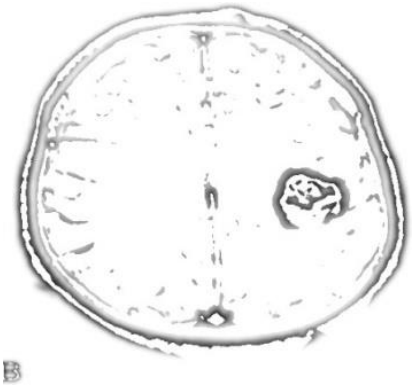


Fig.10: Inverted image

The inverted image is then binarized, which serves as an even better visual to exactly locate the tumor location in the image. This output binary image of the CA-based

approach is presented in Fig. 11, where it is visible through visual inspection that the algorithm has successfully detected the tumor in the original image Fig 12. e. It is noteworthy that thresholding values have a significant impact on the segmentation outcome. Thus, they need to be fine-tuned for successful results. In addition, the final image Fig 12. e, also gives a good result from MRI image with segmented tumor as shown in Fig12. f using CA in segmentation.

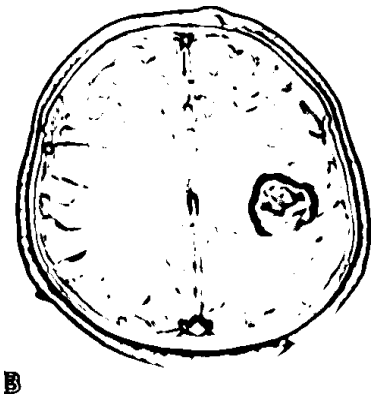
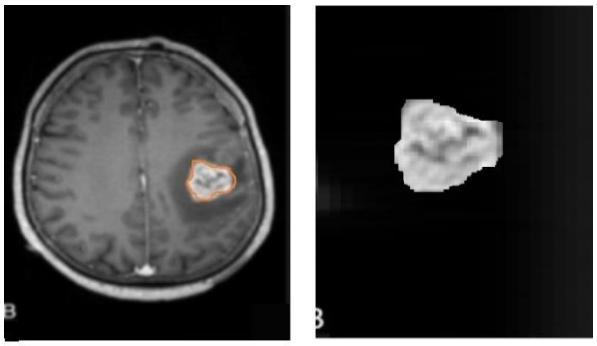


Fig. 11: Binarized image



e f

Fig.12: e: Tumor detection region, f: Segmented Tumor

A. Evaluation of results

We apply this CA-based segmentation technique on 40 tumors and 40 non-tumor images and visually confirm the presence or absence of the tumor detection, resulting in a confusion matrix shown in Fig. 13. From this confusion matrix, and by using four statistical indices, namely (FN : False_negative , TP : True_positive, FP : False_positive, TN True_negative).

We derive important evaluation measures like: F1-score, recall, accuracy, and precision. The results are assessed using several equations, including:

$$Precision = \frac{TP}{(TP + FP)} \quad 1$$

$$Recal = \frac{TP}{(FN + TP)} \quad 2$$

$$Accuracy = \frac{(TP + TN)}{(TP + FN + TN + FP)} \quad 3$$

$$F1 - score = \frac{2(precision * recall)}{precision + recall} \quad 4$$

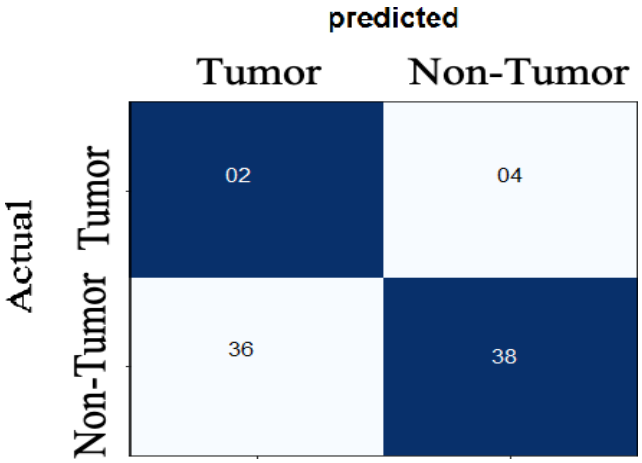


Fig.13: Confusion matrix

Therefore, the results of the performance measure evaluation are as shown in the chart below.

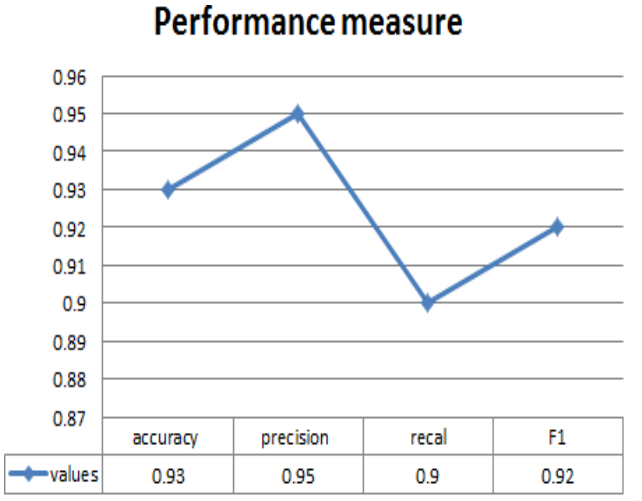


Fig.14: Performance measure

An accuracy of 93% confirms this proposed algorithm to be very respectable.

VI. CONCLUSION AND FUTURE WORK

Malignant tumors are considered one of the most deadly tumors, and many techniques have been discussed in this field, especially between 2018 and 2022. However, their results were limited, and we have discussed some of these techniques in the related works. Early tumor detection is important, as early diagnosis greatly increases the chances of survival. For this reason, an efficient and robust cytosolic-based methodology was presented in this study to detect tumors in the brain through the use of CA-based segmentation. The approved method is able to successfully

isolate tumor areas from the background with an accuracy of 93%. It is a good result compared to several other methods, and this method has many benefits, especially in terms of accuracy, clarity, and speed of implementation. However, there is still room for improvement, especially since the algorithm can also be extended to 3D, and better preprocessing steps can be put in place for image optimization before CA-based segmentation, which we will work on in the future. In addition, we will also focus on integrating CA with deep learning in order to detect other tumors, giving CA a very advanced role in medical image analysis.

ACKNOWLEDGMENTS

The authors would like to thank El houcine El fatimi, Department of computer Engineering, Ankara University, and Laila Boumlik, Department of computer Engineering, Laval University, for their important comments while doing this research.

DECLARATIONS

- **Funding:** There was no external funding for this study.
- **Conflict of interest:** No interest conflicts have been declared by the authors.
- **Informed Consent Statement:** Not applicable.

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