Knowledge Based Brain Tumor Segmentation
Graphical User Interface

Kotikalapudi Raviteja, Arun K Gupta, Maya D Bhat, Chandrajit Prasad

Abstract—This paper describes a knowledge based brain tumor segmentation system (KBBTS) using histogram interpretations for predicting brain tumor area from trans-axial Magnetic Resonance Imaging (MRI). A graphical user interface (GUI) was developed for the segmentation of brain tumor images. This system showed significant improvements over traditional threshold-based tumor segmentation methods. Although KBBTS is not designed to work in real time, it serves as potential research advancement for real time brain tumor segmentation using computer-aided systems with high performance.

Index Terms—Glioma, graphical user interface (GUI), histogram, knowledge based brain tumor segmentation (KBBTS), trans-axial magnetic resonance imaging (MRI)

I. INTRODUCTION

Glial neoplasms constitute more than 70% of primary malignant brain tumors, and result in more years of life lost compared to any other tumors [17]. Astrocytic tumors are the most frequent variety, making up more than three-quarters of all gliomas [15]. They are classified into four grades (I, II, III and IV), and the treatment and prognosis depends upon the tumor grade [16].

These are heterogeneous group of tumor vary from well circumscribed to highly infiltrative. Malignant tumor with its infiltrative nature makes it difficult to define on imaging however affect the image-pixel values particularly at the boundary and boundary-surrounding locations of the tumor. As a result, a quality knowledge based system becomes highly potential in supporting manual or automated tumor detection.

A classical approach where radiologists makes a subjective assessment and marks the tumor manually on MR images, is called manual tumor marking. Besides being a time-taking task for doctors, it does have an element of subjectivity hence it becomes important to challenge ourselves in advanced science and technology to develop a computer-based automated tool for continuing the same process with increased efficiency. Automated model which would use logic algorithms and knowledge base of radiologist and image processors could certainly prove to be a potential system for segmenting brain tumors.

With the aid of medical imaging and computer programming, automated tumor segmentation could immensely contribute to better diagnosis, accurate treatment and surgery planning in lesser time leading to increased life span of tumor survivors.

The primary aim of this paper was to design and develop a Graphical User Interface (GUI) for knowledge based automated tumor segmentation which would separate tumor from non-tumor areas through automated histogram curve interpretations.

The rest of the paper is divided into four sections. Section II reviews previous works in relevance to the aims of our research. Section III describes several algorithms forming the GUI and its experimentation on glioma data sets. Section IV presents the results for performance of our GUI in comparison with the ground truth, followed by experimental results, conclusion and future works.

II. REVIEW OF PREVIOUS WORKS

To the best of our knowledge, majority of efficient methods and comparative studies pertaining to brain segmentation were based on neural networks, fuzzy logic, region growing algorithms, segmentation by simple thresholding and knowledge based algorithms [3], [2]. The method proposed by MK Kowar and S Yadav, segments the tumor using histogram threshold technique [6]. In this method, presumption of thresholding completely depends on human visual interpretation which could significantly decrease the accuracy by gaining non-tumor pixels or loosing tumor pixels in the segmented image. User interface tools have also been proposed previously to segment low-grade gliomas and extra-axial tumors like meningiomas [5]. It assures high speed segmentation but the system might suffer low accuracy levels in case of high grade tumors. MC Clark et al., developed a model for tumor segmentation using knowledge based techniques [4]. The method showed significant results when compared with the ground-truth but was limited to three subjects. As a result, it is difficult to say if the method would be efficient over larger number of data sets. J Zhou et al., proposed a one-class support vector machine (SVM) for effective brain tumor segmentation [14]. But when J Zhang et al., compared it with two-class SVM, the later produced less false positives because of the separation information derived from tumor and non-tumor data [13]. Hence, the overall specificity of the model is reduced. WE Reddick et al., used artificial neural networks for automated segmentation and classification of magnetic resonance images [8]. The method was a hybrid neural network combining Kohonen self-organizing neural networks and multi-layer back-propagation neural networks. Gradient vector flow (GVF), Magneto-static active contour (MAC) and Fluid vector flow (FVF) has been implemented for segmentation of homogeneous tumors [10-12]. But these models fail to significantly differentiate tumors from similar background intensities. Such problems have been addressed

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by J Sachdeva et al., by developing a content-based active
contour model (CBAC) where intensity and as well as texture
inputs are taken from the active contour [9].
A variety of algorithms and their combinations to form
hybrid algorithms have been used in previous literature.
Having said that, these works have widely been
experimental, yet to be put in diagnostic use. Hence it gives
us further scope to research brain tumor segmentation using
automated models.

III. PROPOSED WORK
The proposed work is a series of steps involved in
segmenting brain tumor using KBBTS. Data acquisition,
pre-processing, tumor segmentation, morphological
operations and location-window filtering form the basic
logical components of the GUI. Fig 1 shows the block
diagram of the proposed work.

Fig 1: Block diagram of the proposed work divided into five
steps viz., acquisition, pre-processing, information analysis,
post-processing and statistical analysis.

A. Data
Data was acquired in the form of DICOM images. These
images were converted to NIfTI format using dcm2nii
gui software (available from www.mccauslandcenter.sc.edu).
The tumor slices of interest in NIfTI format were then saved as
.TIFF format images using MRI Cro (available from
www.mristudio.org).

B. Software application
MATLAB R2010a (developed by MathWorks) was used for
the design and development of the GUI. Image
processing, histogram analysis and statistical analysis were
also carried out by the same software.

C. Image pre-processing
Implementing skull-stripping and median filtering were
the two steps involving pre-processing of tumor images.

Skull-stripping
Non-cerebral bony tissues such as the skull were removed.
The process is often referred to as skull stripping. It was
successfully executed using the software, MRI Cro. A
certified radiologist carefully selected the slices-of-interest
(SOI) for further study. The SOIs were saved in TIFF format
which then consisted of pixel intensity values in x- and
y-directions, later to be used for 2-D tumor segmentation.

Median Filter
It is important to remove unwanted information, in this
case; the noise filled pixels. 2D-Median filter was used for
the reduction of salt and pepper noise from the image. It
reduces the noise and preserves edges at the same time. The
equation used for performing median filtering is given below:

\[
P(x,y) = \text{median} \{g(x, y)\}
\]

D. Histogram analysis
Histogram equalization, histogram smoothing and
identifying the lower and upper threshold formed the
histogram analysis.

Histogram Equalization
Image enhancement was performed by enhancing pixel
intensities using Contrast-Limited Adaptive Histogram
Equalization (CLAHE). Rather than the entire image,
CLAHE operates on small pixel groups in the image which
are known as tiles. The following command was used for
image enhancement:

Enhanced Image = adapthisteq (Image);

Local Regression Smoothing (LOESS)
Histogram smoothing was done by local regression
smoothing algorithm. Regression weights for each data point
were calculated using the following equation:

\[
w_i = \left[1 - \frac{d(x_i)}{d(x)}\right]^2
\]

where x is the assigned predictor value, which is associated
with response value (to be smoothed). The nearest neighbors
of x were xi (i = 1, 2, 3, … n). The distance between x and the
most distance predictor value is d(x). A weighted linear least
squares regression was performed. In case of loess, a second
degree polynomial function was used by the regression. This
allowed us to accurately select lower threshold (Tmin) and
upper threshold (Tmax).

Identifying Tmin and Tmax
The histogram of the image was represented by the
function, histogram (i), where i is an integer between 0 and
255. The finding of global thresholds is described in the
following steps:
1) The first step was to generate a histogram matrix;
histogram (m, 1) where m was the number of pixels. A
zero matrix; peaks (m, 1) was also created.
2) Local histogram peaks were calculated through the
following condition:
if histogram (i) > histogram (i+1) &&
    histogram (i) > histogram (i-1);
peaks (i) = histogram (i);
else peaks (i) = 0;
This step was repeated for a second time in order to further
filtering the peaks and retaining clinically significant peaks.
3) We compared the second maximum number of pixels;
histogram2max with the existing peaks to eliminate peaks
which were very small compared to histogram2max. The
following condition was used to eliminate non-significant
peaks:
        if   [peaks (i) / (histogram2max)]*100 < 10;
    peaks (i) = histogram (i);
else peaks (i) = 0;
We observed that the maximum number of pixels was
having an intensity value of zero, a majority of which was
background. Hence, second maximum value was conside red
for the condition.
4) Now, minimum and maximum values for each served
as the threshold value to segment the image into white
matter, gray matter, edema, tumor and necrosis. The
two thresholds for tumor segmentation were taken as
Tmin and Tmax.
E. Tumor segmentation
One of the key concepts used in the implementation of tumor
segmentation algorithm was the range of pixel intensities in
TIFF format images. The intensity range is specified as:
PixIntensityblack = 0 to PixIntensitywhite = 255
Hence, every pixel identified in the image would fall in a
range which is the subset of the intensity range. For each
range subset, there was a Tmin and Tmax which represented an
entire region of the brain. After determining the values for
Tmin and Tmax, following steps segmented the tumor:
1) Read Tmin and Tmax
2) Calculated image size = m × n; EnhancedImage [m, n]
3) Create SegmentedImage; a zero matrix for size = m × n
and the following condition was applied:
for i = 1:m
    for j = 1:n
        if EnhancedImage [i, j] > Tmin
            && EnhancedImage [i, j] < Tmax
            SegmentedImage [i, j] = 1;
        else SegmentedImage [i, j] = 0;
    end
end
This algorithm considered a single matrix element of tumor	slice and designated a pixel value of either 1 (white) or 0
(black) on satisfying the above mentioned condition. The
algorithm is an iterative process which runs till it reaches the
last element of the matrix.
F. Location-window filtering
A location window filter algorithm was developed in order
to remove non-tumor regions and speckles created after
segmentation. The algorithm makes use of location
co-ordinates and window size as the inputs.
The position of the pixel was considered as the location
information. Window was split into four quadrants namely
(X)Y), (-X)(-Y), (X)(-Y) and (-X)(Y). Hence, location
values for the windows were considered as (x,y) ∈ Q(x,y),
(x,y) ∈ Q(-x,y) and (x-y) ∈ Q(-x,y) respectively. The size of each window varies for a given value of x and y in
all the four directions.
G. Morphological operations
We implemented erosion and dilation as two features of
morphological operations on segmented images. Erosion
refers to decrease in size and dilation refers to increase in
size. As a result, erosion removes pixels from the boundary
of the image and dilation adds pixels to the boundary of the
image.
If A and B are sets in Z2, the equation for dilation of A by B
is given by:
A ⊕ B = (A ∩ B) ∪ A
This equation denotes the erosion of A by B is given by:
A ⊖ B = (A ∩ B) ∪ A
where A represents the image matrix on which
morphological operations were performed and B represents
the structuring element in morphological operations. z
denotes the displacements.
H. GUI for hand-labeling of tumor
A GUI was developed for the manual labeling of SOIs. All
the SOIs were hand-labeled by 2 certified radiologists. The
marking of tumor was done manually. Labeled images were
then used for further comparison with machine generated
images and statistical analysis was performed. A brief code
for the GUI has been supplied below:
global roilimage;
image = handles.image;
rolImage = roipoly (image);
axes (handles.axes2);
imshow (rolImage);
I. Statistical analysis
Sensitivity and Specificity are the two prime performance
parameters used in medical statistics. Sensitivity denotes the
value which is the number of patients who were correctly
identified with a disease [8], [1]. Specificity denotes the value
which is the number of patients who were correctly identified
as not having a disease [8], [1]. The equations for calculating
sensitivity and specificity are:
Sensitivity = TP/(TP + FN)
Specificity = TN/(TN + FP)
where True Positive (TP) indicates that patient suffered
diseases and result was positive; True Negative (TN)
dicates that patient did not suffer disease and result was
negative; False Positive (FP) indicates that patient did not
suffer disease and result was positive; False Negative (FN)
dicates that patient suffered disease and result was
negative.
Accuracy of a system can be referred to as the system’s
ability to produce the actual results. A system with higher
accuracy is reliable than a system with lower accuracy. In this
project, accuracy is defined by the following equation:
Accuracy = TP + TN/(TP + TN + FP + FN)
Positive Predictive Value (PPV) is defined as the
proportion of patients tested positive that actually have the
disease [8], [1]. It is referred to as the precision rate.

PPV = TP/(TP + FP)
Negative Predictive Value (NPV) is defined as the proportion of patients tested negative who actually do not have the disease [7], [1].

\[ \text{NPV} = \frac{TN}{(TN + FN)} \]

IV. EXPERIMENTAL RESULTS
This section presents all the results generated by the KBBTS.

Fig 1: The figures show the effect of skull-stripping on T1 post Gd image while using FFE sequence.

(a) Before                                      (b) After

Fig 2: The figures show the effect of image enhancement by adaptive histogram equalization

(a) Before                                      (b) After

Fig 3: GUI for hand-labeling of tumor

Fig 4: Knowledge Based Brain Tumor System: I displays the slice of interest, II is the viewer for Black-and-White image obtained after histogram analysis, III is the viewer for speckles/black spots left in the tumor, IV displays adding the threshold image and speckles, V displays the effect of location-window filtering, VI shows the image obtained after morphological operations, VII displays the hand-labeled tumor ROI used for comparison with the GUI output image and VIII is the operating panel for image browser, threshold selection, location-window filtering, morphological operation options, and performance parameters.

Fig 5: The figure shows the raw histogram of the image. The presence of consistent peaks throughout the histogram makes it difficult to identify tumor, white matter, grey matter and CSF.

Fig 6: Processed histogram for an efficient identification of tumor thresholds. The figure shows a detailed break-down of the histogram curve with each threshold range pertaining to a certain region of brain.

Fig 7: Location-Window filtering: The image represents four windows in four quadrants covering the entire tumor.
Fig 8: Effect of Location-Window filter: The implementation of the filter resulted in accepting the tumor pixels and rejecting pixels falling outside the windows.

Fig 9: Output image after morphological operations: It could be clearly observed from the image that most of the black speckles were consistently filled inside the tumor through low level morphological dilation. The area of the tumor could now be calculated by counting the number of white pixels (pixValue = 1).

Fig 10: Average number of True Positives and False Negatives generated by KBBTS.

Fig 11: Performance analysis when compared with tumor labeled by Radiologist 1.

Fig 12: Performance analysis when compared with tumor labeled by Radiologist 2.

V. CONCLUSIONS

In this paper we have presented a Knowledge Based Brain Tumor segmentation system. It was designed, tested and evaluated for efficient brain tumor segmentation. Two radiologists hand-labeled the tumor slices of interest and performance parameters were drawn by comparing these manually labeled slices with the ones generated by KBBTS. The images shown in the results showed that the system was successful in segmenting the tumor from healthy brain pixels. From Table 1, the mean values for sensitivity, specificity, accuracy, PPV and NPV were found to be 94.79%, 99.6%, and 99.39%, 91.64% and 99.76% respectively.

<table>
<thead>
<tr>
<th>Performance</th>
<th>Radiologist 1</th>
<th>Radiologist 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>True Positives</td>
<td>13251</td>
<td>13002</td>
</tr>
<tr>
<td>True Negatives</td>
<td>298575</td>
<td>298538</td>
</tr>
<tr>
<td>False Positives</td>
<td>1072</td>
<td>1321</td>
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<tr>
<td>False Negatives</td>
<td>702</td>
<td>739</td>
</tr>
<tr>
<td>Sensitivity</td>
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<td>94.62</td>
</tr>
<tr>
<td>Specificity</td>
<td>99.64</td>
<td>99.55</td>
</tr>
<tr>
<td>Accuracy</td>
<td>99.43</td>
<td>99.34</td>
</tr>
<tr>
<td>PPV</td>
<td>92.51</td>
<td>90.77</td>
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<tr>
<td>NPV</td>
<td>99.77</td>
<td>99.75</td>
</tr>
</tbody>
</table>

VI. FUTURE WORK

Prior knowledge for recognizing minima and maxima of curves was considered as the primary base for detecting lower and upper thresholds between which most of the tumor pixels were present. In this case, a completely automated GUI for recognizing tumor pixels from histogram should be developed. The system could successfully segment 2-D tumors from all the slices. This particular methodology should be implemented for 3-D tumor segmentation. We have tested the system for brain tumor images. KBBTS should also be tested for tumors occurring outside the brain.

REFERENCES

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