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Machine Learning Approches for Brain Disease Diagnosis

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Abstract
Purpose Detection and segmentation of a brain tumor such as glioblastoma multi formed in magnetic resonance (MR) images are often challenging due to its intrinsically heterogeneous signal characteristics. A robust segmentation method for brain tumor MRI scans was developed and tested.
Methods Simple thresholds and statistical methods are unable to adequately segment the various elements of the GBM, such as local contrast enhancement, necrosis, and edema. Most voxel-based methods cannot achieve satisfactory results in larger data sets, and the methods based on generative or discriminative models have intrinsic limitations during application, such as small sample set learning and transfer. The promises of these two projects were to model the complex interaction of brain and behavior and to understand and diagnose brain diseases by collecting and analyzing large quanitites of data. Archiving, analyzing, and sharing the growing neuroimaging datasets posed major challenges. New computational methods and technologies have emerged in the domain of Big Data but have not been fully adapted for use in neuroimaging. In this work, we introduce the current challenges of neuroimaging in a big data context. We review our efforts toward creating a data management system to organize the large-scale fMRI datasets, and present our novel algorithms/methods
*Based on the output of the GREY LEVEL CO-OCCURRENCE MATRIX (GLCM) and spatial affinity models, conditional random fields theory was applied to segment the tumor in a maximum a posteriori fashion given the smoothness prior defined by our affinity model. Finally, labeling noise was removed using "structural knowledge" such as the symmetrical and continuous characteristics of the tumor in spatial domain. Finally, labeling noise was removed using "structural knowledge" such as the symmetrical and continuous characteristics of the tumor in spatial domain. The (**Bat Algorithm**) models were trained and tested on augmented images and validation is performed*
***Keywords: Bat algorithm**, GREY LEVEL CO-OCCURRENCE MATRIX (GLCM), segmentation of a brain tumor*

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I. INTRODUCTION

BRAIN AND TUMOR SEGMENTATION

Combining image segmentation based on statistical classification with a geometric prior has been shown to significantly increase robustness and reproducibility. Using a probabilistic geometric model of sought structures and image registration serves both initialization of probability density functions and definition of spatial constraints. A strong spatial prior, however, prevents segmentation of structures that are not part of the model. In practical applications, we encounter either the presentation of new objects that cannot be modeled with a spatial prior or regional intensity changes of existing structures not explained by the model. Our driving application is the segmentation of brain tissue and tumors from three-dimensional magnetic resonance imaging (MRI). Our goal is a high-quality segmentation of healthy tissue and a precise delineation of tumor boundaries. We present an extension to an existing expectation maximization (EM) segmentation algorithm that modifies a probabilistic brain atlas with an individual subject's information about tumor location obtained from subtraction of post- and pre-contrast MRI. The new method handles various types of pathology, space- occupying mass tumors and in ltrating changes like edema. Preliminary results once five cases presenting tumor types with very di erent characteristics demonstrate the potential of the new technique for clinical routine use for planning and monitoring in neurosurgery, radiation oncology, and radiology.

II. LITERATURE SURVEY

A SYSTEM FOR BRAIN TUMOR VOLUME ESTIMATION VIA MR IMAGING AND FUZZY CONNECTEDNESS.

In this work et.al[1]*Liu J, Udupa JK, Odhner D, Hackney D, Moonis G* has proposed This paper presents a method for the precise, accurate and efficient quantification of brain tumor (glioblastomas) via MRI that can be used routinely in the clinic. Tumor volume is considered useful in evaluating disease progression and

response to therapy, and in assessing the need for changes in treatment plans. We use multiple MRI protocols including FLAIR, T1, and T1 with Gd enhancement to gather information about different aspects of the tumor and its vicinity. These include enhancing tissue, no enhancing tumor, edema, and combinations of edema and tumor. We have adapted the fuzzy connectedness framework for tumor segmentation in this work and the method requires only limited user interaction in routine clinical use. The system has been tested for its precision, accuracy, and efficiency, utilizing 10 patient studies. Images acquired in most of the MRI protocols possess a bimodal histogram, wherein the first mode corresponds to the background while the second represents the foreground object that we are interested in-in our application, the patient's head.

A NONPARAMETRIC METHOD FOR AUTOMATIC CORRECTION OF INTENSITY NON UNIFORMITY IN MRI DATA

In this work et.al[2]*Sled JG, Zijdenbos AP, Evans AC* has proposed A novel approach to correcting for intensity non uniformity in magnetic resonance (MR) data is described that achieves high performance without requiring a model of the tissue classes present. The method has the advantage that it can be applied at an early stage in an automated data analysis, before a tissue model is available. This intensity non uniformity is usually attributed to poor radio frequency (RF) coil uniformity, gradient-driven eddy currents, and patient anatomy both inside and outside the field of view. Although these 10%–20% intensity variations have little impact on visual diagnosis, the performance of automatic segmentation techniques which assume homogeneity of intensity within each class can be significantly degraded. A robust, automatic, and inexpensive means of correcting for this artifact is essential for such automatic processing techniques to be accurate in labeling each voxel with a tissue type. Furthermore, correcting for intensity non uniformity may benefit quantitative measurements such as those used in tissue metabolite studies.

INTENSITY NON-UNIFORMITY CORRECTION IN MRI: EXISTING METHODS AND THEIR VALIDATION

In this work et.al[3]*Belaroussi B, Milles J, Carme S, Zhu YM, Benoit-Cattin H* has proposed In this paper, we propose an overview of existing methods. We first sort them according to their location in the acquisition/processing pipeline. Sorting is then refined based on the assumptions those methods rely on. Next, we present the validation protocols used to evaluate these different correction schemes both from a qualitative and a quantitative point of view. Finally, availability and usability of the presented methods is discussed. Magnetic resonance imaging (MRI) is a powerful noninvasive imaging technique for studying soft tissues anatomy and properties. It is characterized by an overall good quality of obtained datasets. Such data usually consist of either a collection of two-dimensional (2-D) MR images or a whole three-dimensional (3-D) isotropic volume. Efficient qualitative or user-driven quantitative analysis can be performed on MR data, but current needs are non-supervised, automated, quantitative analysis tools. In this paper, we have considered intensity non-uniformity correction as a global problem involving multiple communities with different objectives. We have proposed an overview of all existing methods available and we have suggested an original typology to sort them based on the way correction is performed and on the assumptions made.

III. EXISTING METHOD

In existing system the comprehensive survey of existing tumor enhancement and segmentation techniques. Each method is classified, analyzed, and compared against other approaches. To examine the accuracy of the tumor enhancement and segmentation techniques, the sensitivity and specificity of the approaches is presented and compared where applicable. Finally, this research provides taxonomy for the available approaches and highlights the best available enhancement and segmentation methods. it only categorized tumor segmentation techniques into mass detection using a single view and mass detection using multiple views. The mass detection using single view segmentation in turn is divided into four categories: model-based methods, region-based methods, contour-based methods, and clustering methods.

DRAWBACKS OF EXISTING SYSTEM:

- ✓ The techniques that were surveyed included: histogram based techniques, gradient based techniques, polynomial modeling based techniques, active contour based techniques, and classifiers based techniques.
- ✓ It only review the algorithms that have been proposed in the literature to enhance and segment tumor images that contain both masses and micro-calcification.
- ✓ There is no clear edge results.
- ✓ Dilate image sharpening to find tumor object is not possible.
- ✓ Less accuracy.

IV. PROPOSED SYSTEM

The proposed system Grey Level Co-Occurrence Matrix (**GLCM**) Homomorphic Function is chosen in order to distinguish the interior area from other organs in the MR image dataset. Then modified gradient magnitude region growing algorithm is applied, in which gradient magnitude is computed by Sobel operator and employed as the definition of homogeneity criterion. This implementation allowed stable boundary detection when the gradient suffers from intersection variations and gaps. By analyzing the gradient magnitude, the sufficient contrast present on the boundary region that increases the accuracy of segmentation.

To calculate the size of segmented tumor the relabeled method based on remaps the labels associated with object in a segmented image such that the label numbers are consecutive with no gaps between the label numbers used. Any object can be extracted from the relabeled output using a binary threshold. Here, BAT algorithm is adjusted to extract and relabeled the tumor and then find its size in pixels. The algorithm works well in two stages.

The first stage is to determine the input image labels and the number of pixels in each label. The second stage is to determine the output requested region to get total number of pixels accessed. Segmented areas are automatically calculated and to get desired tumor area per slice.

4.1 HARDWARE REQUIREMENTS:

SYSTEM : PENTIUM CORE 2 DUO
HARD DISK : 250 GB
RAM : 1 GB DDR 1
KEY BOARD : STANDARD 104 KEYS
MOUSE : OPTICAL MOUSE
MONITOR : 15 INCH VGA COLOR MONITOR

4.2 SOFTWARE REQUIREMENTS:

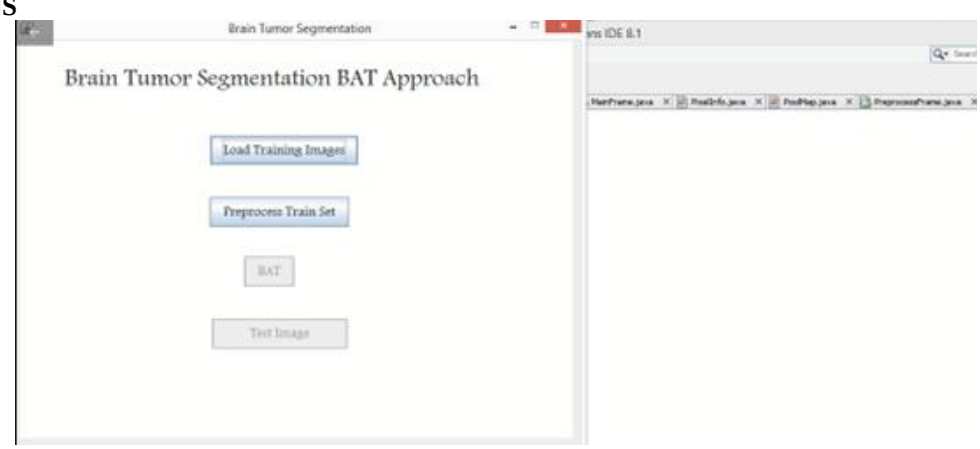
OPERATING SYSTEM : WINDOWS 7
FRONT END : JAVA

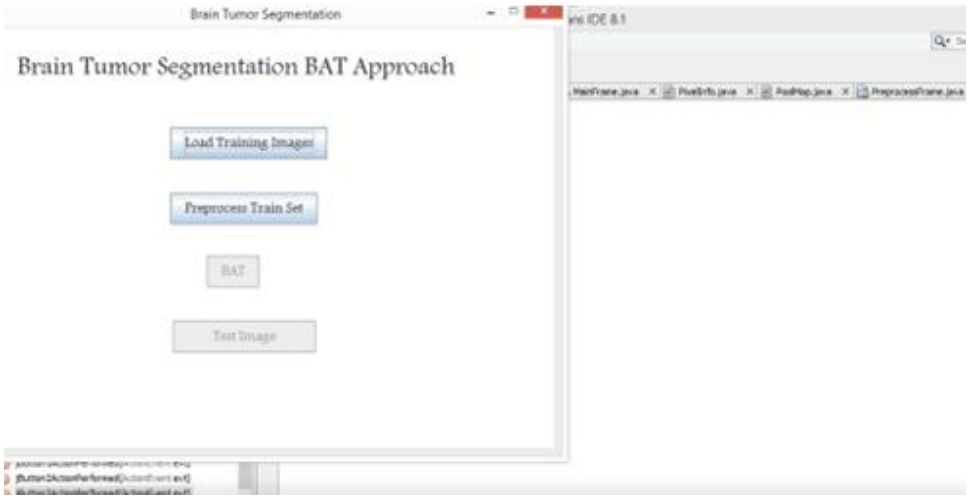
4.3 SOFTWARE FEATURES

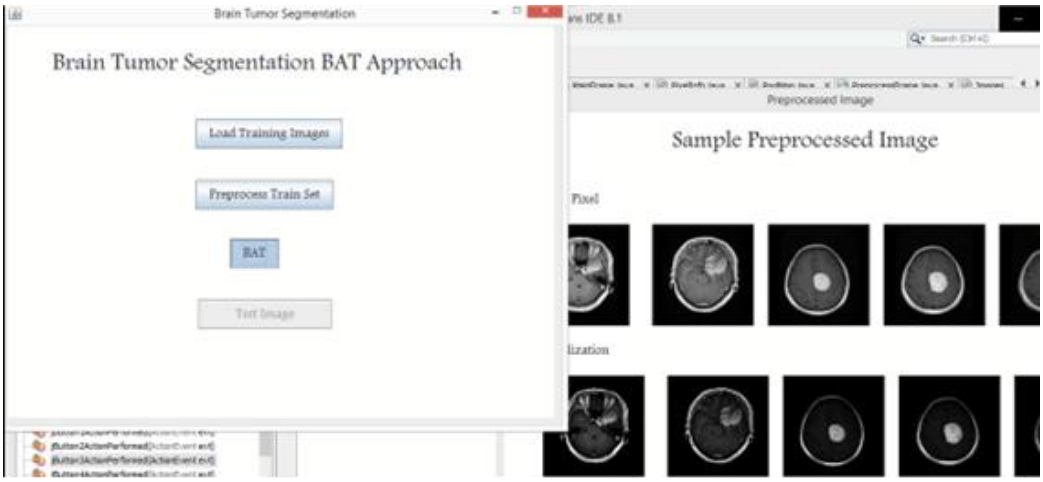
Image Processing Toolbox provides a comprehensive set of reference-standard algorithms and graphical tools for image processing, analysis, visualization, and algorithm development. You can perform image enhancement, image deblurring, feature detection, noise reduction, image segmentation, spatial transformations, and image registration. Many functions in the toolbox are multithreaded to take advantage of multicourse and multiprocessor computers.

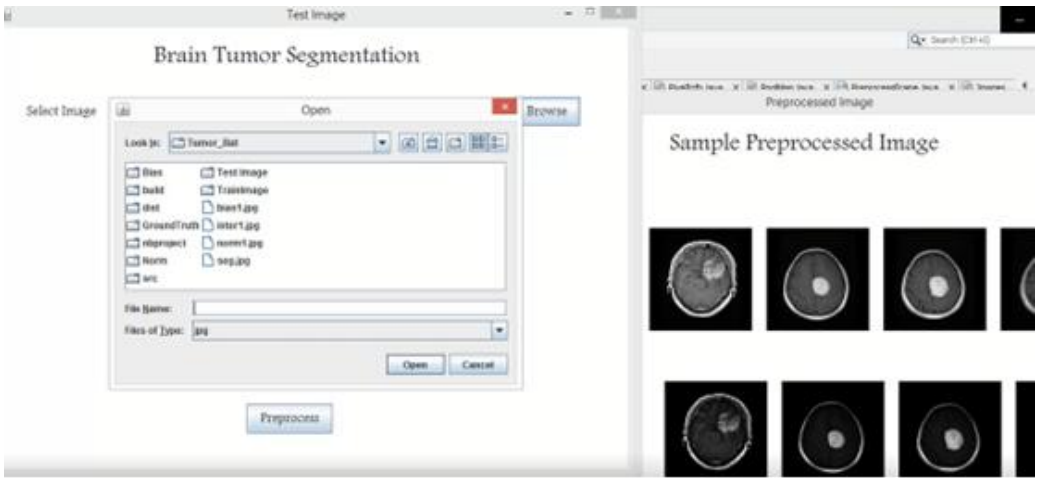
Image Processing Toolbox supports a diverse set of image types, including high dynamic range, gig pixel resolution, ICC-compliant color, and tomographic images. Graphical tools let you explore an image, examine a region of pixels, adjust the contrast, create contours or histograms, and manipulate regions of interest (ROIs). With the toolbox algorithms you can restore degraded images, detect and measure features, analyze shapes and textures, and adjust the color balance of images.

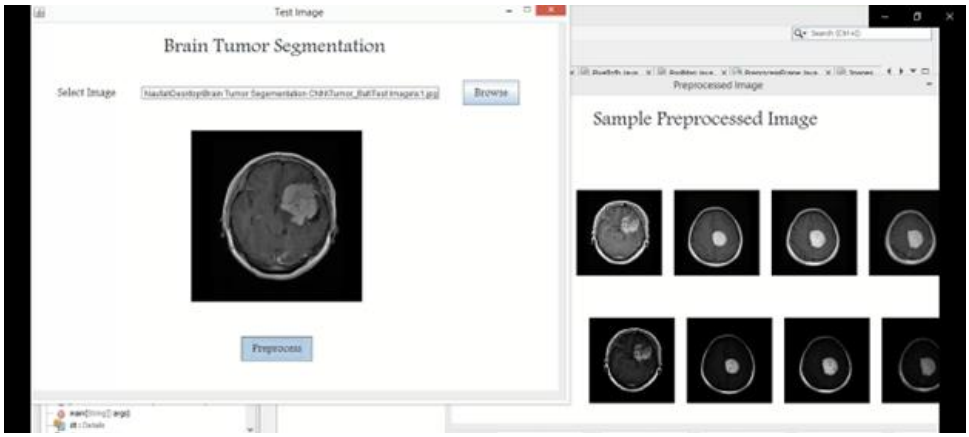
SCREENS

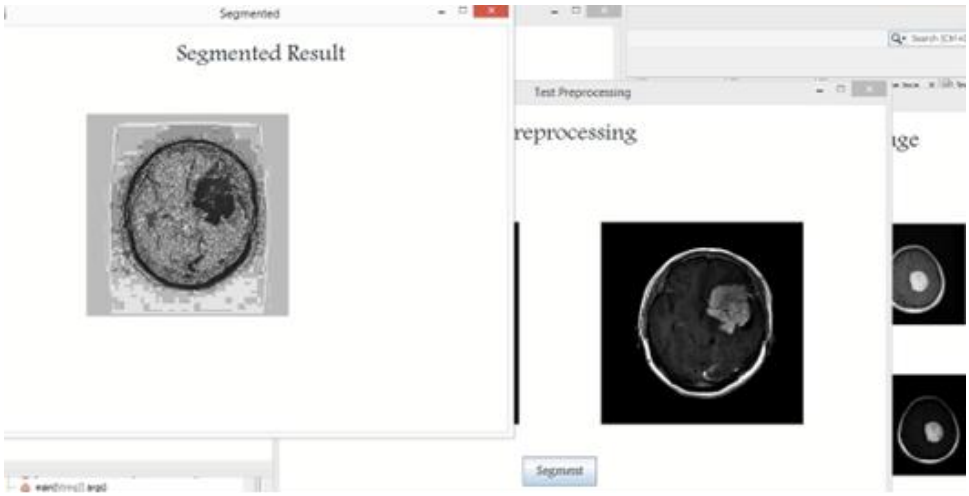



Brain Tumor Segmentation
Brain Tumor Segmentation BAT Approach
Load Training Images
Preprocess Train Set
BAT
Test Image


Brain Tumor Segmentation
Brain Tumor Segmentation BAT Approach
Load Training Images
Preprocess Train Set
BAT
Test Image
Preprocessed Image
Sample Preprocessed Image
Pixel


Test Image
Brain Tumor Segmentation
Select Image
Open
Browse
Preprocess
Preprocessed Image
Sample Preprocessed Image





MRI PREPROCESSING:

Preprocessing images commonly involves removing low frequency, background noise, normalizing the intensity of individual practical images, removing reflections and masking portion of images. Image processing is the technique of enhancing data images prior to computational processing. The following preprocessing steps involves realignment and unwarp slices within a volume, separately for every modality the overall flow diagram is shown in Fig.2

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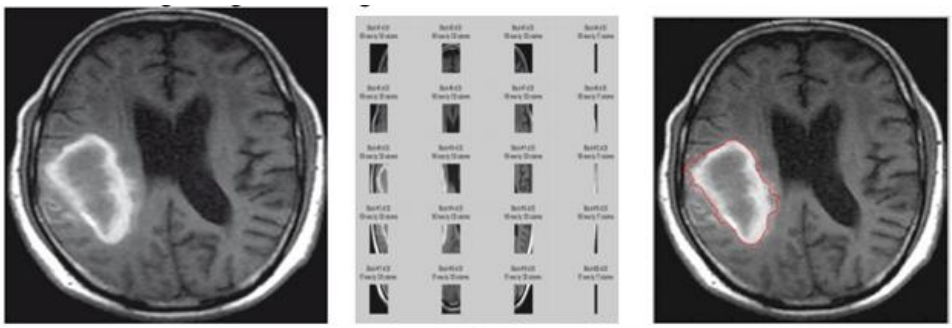

VI. FUTURE ENHANCEMENT

We use super pixel-based appearance models to reduce computational cost, improve spatial smoothness, and solve the data sampling problem for training GLCM classifiers on brain tumor segmentation. Also, we develop an affinity model that penalizes spatial discontinuity based on model-level constraints learned from the training data. Finally, our structural denoising based on the symmetry axis and continuity characteristics is shown to remove the false positive regions effectively. The training and validation were performed on high-resolution MR image dataset with augmentations and the result is compared with deep learning bat algorithm model Alexnet. The performance of all bat algorithm models is evaluated with the help of performance metrics recall, precision, F score specificity, and overall accuracy.

VII. CONCLUSION

Our paper brings together two recent trends in the brain tumor segmentation literature: model-aware similarity and affinity calculations with GREY LEVEL CO-OCCURRENCE MATRIX (GLCM) models with GREY LEVEL CO-OCCURRENCE MATRIX (GLCM)-based evidence terms. In doing so, we make three main contributions. We use super pixel-based appearance models to reduce computational cost, improve spatial smoothness, and solve the data sampling problem for training GREY LEVEL CO-OCCURRENCE MATRIX (GLCM) classifiers on brain tumor segmentation.

Also, we develop an affinity model that penalizes spatial discontinuity based on model-level constraints learned from the training data. Finally, our structural denoising based on the symmetry axis and continuity characteristics is shown to remove the false positive regions effectively.

Our full system has been thoroughly evaluated on a challenging 20-case GBM and the Bra TS challenge data set and shown to systematically perform on par with the state of the art. The combination of the two tracts of ideas yields better performance, on average, than either alone. In the future, we plan to explore alternative feature and classifier methods, such as classification forests to improve overall performance.

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