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Review

Brain Tumor Causes Neurological Disorders in Brain

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Abstract

An automatic system for major normal and abnormal tissues detection and analysis from MRI brain has been proposed to facilitate accurate, fast and reliable computer-based diagnosis of brain diseases.

Introduction

Brain tumor, stroke, hemorrhage and multiple sclerosis (MS) disease are the life threatening diseases in both male and female. A brain tumor is the most common and widespread disease among these brain diseases. The worldwide cancer incidence of brain tumor is 3.4 per 100,000 people (men: 3.9 per 100,000, women: 3.0 per 100,000. A total of 256,213 affected worldwide (139,608 men and 116,605 women). The trend of new cases is rising and 189,582 sufferers worldwide. Every day about 700 people is diagnosed with a brain tumor [1]. 15 million people are affected by stroke and hemorrhage; of this 5 million die and another 5 million (2002 estimates) are permanently disabled. Today over 2,500,000 people around the world have MS [2].

Central nervous system (CNS) is the part of the human nervous network which integrates the coordination and processing of receiving neural information. CNS is contained by the brain and the spinal cord and constituted by two tissue components: GM, which is the main CNS element and consists of neuronal cell bodies; and white matter tissue WM, which is the second CNS component and it is mainly composed of myelinated axon tracts. WM and GM tissues occupy the most important part of the brain area. CSF is a bodily fluid present all over the brain evolving both CNS tissues. The central nervous system may be damaged by different affections caused by infections such as encephalitis, neurodegenerative diseases like Alzheimer or autoimmune and inflammatory diseases such as multiple sclerosis.

Early and accurate diagnosis of brain lesion is vital for determining specific treatment and prognosis. However, the diagnosis is a very challenging task and can only be performed by specialists in neuroradiology. There are at least two specialists required to examine and confirm of each medical report on imaging investigations. Any difficulty may necessitate invasive tests such as biopsy and surgery. Currently, the standard lesion pathological classification is based on histological examination of tissue samples through biopsy. Therefore, radiologists are continuously seeking for greater diagnosis accuracy by the modern medical imaging system. According to quantitative analysis of computer-aided diagnosis (CAD), it may aid radiologists in the interpretation of the medical images. Recent studies showed that CAD could help to improve the diagnostic accuracy of radiologists, lighten their increasing workload, reduce misinterpretation due to fatigue or overlooked and improved inter- and intra-reader variability [3]. Manual CAD task is mostly performed by drawing image regions slice-by-slice, limiting the human rater's view and generating suboptimal outlines with limited consistency across slices. Due to the limitations of manual methods, an automatic CAD framework is crucial for the study of medical phenomena, especially when it involves a large set of images. An automatic segmentation method is desirable because it reduces the workload of human experts and generates fully reproducible segmentations. A computer program also has the advantage of being able to process large amounts of information as typically presented within MR images in a more consistent manner compared to human raters. Automated identification of brain abnormalities in different medical images demands high accuracy since it deals with life. Also, computer assistance is highly sought in medical institutions because it could improve the results of humans in such a domain where the false negative and positive cases must be at a very low rate. It has been proven that

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double reading of medical images could lead to better abnormal region detection. But the cost incurred in double reading is very high; therefore good software to assist humans in medical institutions is of great interest nowadays.

An iterative implement of level set methodology has been proposed for the precise segmentation of normal and detection of abnormal tissues in MRI of the brain. Normal tissues such as WM, GM, and CSF with other parts of the human head such as skull, marrow, and muscles skin are segmented, and abnormal tissues such as hemorrhage, stroke, MS and tumor lesions can be detected if any by proposed methodology. The level set method is repeated based on the condition of sharp peak greater than three. The iterative segmented component generates a hierarchical structure for correct segmentation. In this paper automated normal and abnormal tissue detection and analysis from brain magnetic resonance imaging (MRI) is proposed.

Literature Review

MRI of brain image analysis is the task of identifying image components (pixels) into relevant anatomical components or describing the structural and intensity changes regarding the underlying functional process. The knowledge of the location, size, and shape of different anatomical structures is a fundamental step in understanding and analyzing medical images. Automated detection and analysis of normal and abnormal tissues in MR images with high accuracy and low error allow us to do more notable measurement than qualitative visual assessment.

MRI is the most frequently used neuroimaging technique for the evaluation and follow-up a review of patients with brain abnormalities for many reasons [4]. It does not use ionizing radiation like computed tomography (CT), single photon emission computed tomography (SPECT), and positron emission tomography (PET) studies. MRI has following list of benefits:

- MRI contrast resolution is higher than the other techniques, making it preferable for detecting small lesions and isodense lesions on unenhanced CT.
- It is more sensitive than CT to detect lesion enhancement. The ability of MRI devices to generate images in the sagittal, axial and coronal planes provides better localization of a lesion in the 3D space of the brain and allows structures involved by the abnormalities to be more clearly delineated.
- MR imaging eliminates the beam-hardening artifact produced by the skull base on CT, making it better for evaluating lesions in the posterior fossa and the inferior frontal and temporal lobes.
- The development of MR spectroscopy, MR diffusion imaging, and MR perfusion imaging now permits evaluation of tumor physiology with MR scanners.
- The acquisition of both functional and anatomical information about the tumor during the same scan may be the most important benefit of MR imaging [4] in 2001.
- It can noninvasively record brain signals (of humans and other animals) without risks of radiation inherent in other scanning methods, such as CT or PET scans.

The proposed techniques implemented based on brain MRI images consisting of normal and abnormal from a real human brain MRI dataset. The dataset used consists of axial, T2, T1, and PD MR Brain Images. These images were collected from the Harvard Medical School [5] website used for normal and abnormal brain images: (a) tumors, (b) strokes, (c) hemorrhage, and (d) MS. Standard simulations from brain web database [6] include parameter setting fixed to 3 modalities (T1, T2, and PD), five slice thicknesses (1, 3, 5, 7 or 9mm), and defining a volume (x, y, z). Tissue classes include GM, WM, and CSF but also muscle, fat or skin. The brain model used to generate the simulations can also be employed as ground truth. Another public domain dataset is used to conducting similar research. Easy Analytic Software, Inc. (EASI) MRI database for different brain abnormality MR images [7]. All mentioned dataset are used to evaluate the performance.

Proposed Method

Detecting correct type of brain tumor is a critical task for diagnosis and curing the tumor. Identifying the correct type of brain tumor can provide a fast and effective way to plan the diagnosis of the tumor. The proposed system provides a fast and efficient way to identify the correct type of tumor and classify it to the respective class label and it composed of multiple stages. In the first stage, MRI image is taken as input and is normalized. The second stage includes extraction of feature vectors from the image which results in reducing redundancy of data to serve as the input to the classifier. The classifier takes each tuple of feature extracted vector to produce classified output. Performance analysis shows proposed methodology performed very efficiently and accurately. Proposed work exhibits the application of Fuzzy Inference System (FIS) based classifier known as Adaptive Neuro-Fuzzy Inference System (ANFIS) to successfully classify the five major types of brain tumors.

Three phase level set is used as a basic segmentation by changing speed function, and introducing the concept of iteration because most of the existing method failed to find much accuracy on MR images. Iteration is used to divide the complex segmentation for easier and accurate segmentation. In the proposed approach, the intensity distribution is modeled in the image partitions using the Gaussian mixture to form a close approximation to the actual intensity distribution in the image. Anatomical constraints of brain structures especially in borders between tissues and inconsistent adjacent pixels are used to extract brain model characteristics.

It is stated that the T1 MR images have brighter pixels for white matter (WM), darker for gray matter (GM), and almost black for cerebrospinal fluid (CSF). The T1 images show abnormality with larger intensity value than normal tissue. Therefore, some lesions in the WM areas can look alike GM in T1 images due to the increase of water. Besides, the pixels with muscle tissue appear brighter than for fat. Almost the opposite intensity contrast will be expected in T2 images. The WM is less fluid-based. Thus the pixels with mostly this tissue class will appear white in T1 and dark in T2, which corresponds to high and low-intensity values, respectively. In the case of GM, it appears darker in T1 and brighter in the T2 images. Finally, the CSF shows a small peak but also a big lobe that almost overlaps all the classes. In proton density (PD) images white matter is brighter than gray matter, and gray matter is brighter than CSF. PD, T2, and T1 type of MRI with sarcoma brain abnormality is shown in **Figure 1.**

A brain tumor is a cluster of abnormal cells due to loss of normal aging and cell death. It may occur in any person at almost any age. It may even change from one treatment session to the next, but its effects may not be the same for each person. Brain tumors appear at any location, in different image intensities, can have a variety of shapes and sizes. Brain tumors can be malignant or benign. In this research work five major tumors glioma, meningioma, metastatic adenocarcinoma, metastatic bronchogenic carcinoma, and sarcoma types of tumors are used. Gliomas are a group of tumors that arise in the central nervous system. MR imaging is currently the method of choice for early detection of a brain tumor in the human brain. Low-grade gliomas and meningiomas are benign tumors. Glioblastoma multiforme is a malignant tumor and may arise anywhere in the brain. Metastatic adenocarcinoma and Metastatic bronchogenic carcinoma tumors are the most common type of brain tumors (30% of all) and are usually malignant one. Sarcoma arises in the nearer to surrounding structures of the brain. According to World Health Organization (WHO), there are 126 types of different brain tumors of which many of them arise from structures intimately associated with the brain such as tumors of the covering membranes to the posterior fossa. **Figure 2** shows the five major types of tumors in MRI images with arrows.

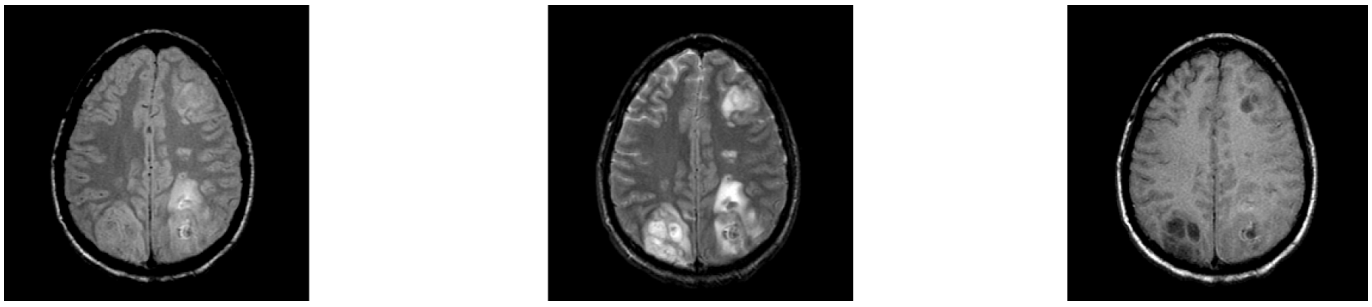

Figure 1: PD, T2, and T1 type of MRI with sarcoma type of brain tumor

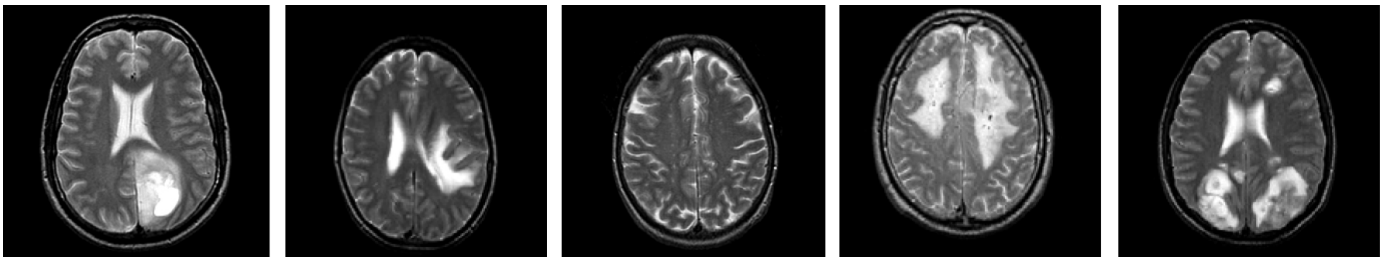

Figure 2: Five major brain tumors in MRI: a) Glioma, b) Meningioma, c) Metastatic adenocarcinoma, d) Metastatic bronchogenic carcinoma, and e) Sarcoma

Each of the generated feature vectors from the normalized grayscale image is calculated from 1st order histogram based features and features from Gray Level Co-occurrence Matrix. These values are based on the variation intensity values among the pixels in the selected slice. Each of the functions derives a single valued element in the feature extraction matrix for each of the 20 slices that are represented in **Table 1 and Table 2**.

Table 1: Feature vector from the normalized grayscale MR image

Image Sequence	Mean	Variance	Skewness	Kurtosis	Energy	Entropy
1	15.5399	446.433	0.000108	0.0000127	0.2816	3.6817
2	14.7607	427.681	0.000126	0.000151	0.2933	3.5751
3	15.5426	447.411	0.000108	0.000127	0.2810	3.6939
4	15.3294	434.847	0.000116	0.00014	0.2762	3.7014
5	15.9980	466.920	0.0001	0.000118	0.2718	3.8210
6	16.2995	455.317	0.000972	0.000117	0.2540	3.8918
7	16.8535	461.050	0.000906	0.00011	0.2365	3.9722
8	15.2010	463.274	0.000113	0.000132	0.2981	3.6796
9	13.6257	406.182	0.00015	0.000185	0.3333	3.2856
10	13.9531	413.331	0.000143	0.000175	0.3219	3.4029
11	13.1538	400.748	0.000161	0.000200	0.3529	3.2298
12	14.2234	417.177	0.000137	0.000165	0.3123	3.4526
13	13.6782	420.489	0.000142	0.000167	0.3506	3.2687
14	13.5103	417.582	0.000144	0.000169	0.3583	3.1849
15	13.2064	412.893	0.000151	0.000178	0.3698	3.1134
16	12.3658	388.257	0.000181	0.000226	0.3857	3.0153
17	12.9241	397.207	0.000167	0.00021	0.3573	3.2094
18	13.5875	407.496	0.000151	0.000185	0.3342	3.3352
19	14.2193	425.415	0.000137	0.000164	0.3174	3.4692
20	14.9834	443.361	0.000118	0.000138	0.3040	3.5664

Table 2: Feature vector from the normalized grayscale MR image (continuation of Table 8.1)

Image Sequence	Contrast	Correlation	Energy	Homogeneity	Inverse Difference	Absolute Value
1	0.3334	0.3878	0.4131	0.8726	56710.6	17910
2	0.3190	0.3833	0.4379	0.8774	57036.6	17210
3	0.3415	0.3862	0.4071	0.8697	56512.8	18328
4	0.3547	0.3508	0.4113	0.8659	56247.2	18914
5	0.3618	0.3884	0.3971	0.8663	56246	18994
6	0.3499	0.3785	0.3871	0.8652	56218.6	18910
7	0.3697	0.3640	0.3731	0.8592	55806.6	19812
8	0.3610	0.3920	0.4227	0.8712	56534.6	18504
9	0.2931	0.3803	0.4756	0.8861	57632.2	15936
10	0.2984	0.3755	0.4668	0.8831	57439.6	16314
11	0.2885	0.3749	0.4930	0.8896	57854	15516
12	0.3019	0.3595	0.4589	0.8800	57245.4	16676
13	0.2558	0.4260	0.4907	0.8970	58395.4	14258
14	0.2565	0.4179	0.4908	0.8972	58406	14248
15	0.2443	0.4349	0.5019	0.9011	58674.6	13668
16	0.2395	0.4074	0.5274	0.9029	58796.6	13412
17	0.2881	0.3883	0.4918	0.8902	57893.2	15446
18	0.2936	0.3933	0.4727	0.8867	57670.4	15878
19	0.3158	0.3685	0.4617	0.8804	57227	16858
20	0.3164	0.3804	0.4429	0.8786	57115.6	17050

Performance measurement is done by comparing the actual class labels and the predicted class labels for each of the individual classifiers. Let's now define the most basic terms of performance metrics. True Positives (TP) are cases in which predicted yes (they have the disease), and they do have the disease. True Negatives (TN) predicted no, and they don't have the disease. False Positives (FP) predicted yes, but they don't have the disease. False Negatives (FN) predicted no, but they do have the disease. Sensitivity measures the proportion of positives that are correctly identified as such. Specificity (also called the true negative rate) measures the proportion of negatives that are correctly identified as such. Recall in this context is also referred to as the true positive rate or sensitivity, and precision is also referred to as positive predictive value; other related measures used in classification include true negative rate and accuracy. The true negative rate is also called specificity. In the statistical analysis of classification, the F-score or F-measure is a measure of a test's accuracy. Performance measurement metrics value of 5 major tumor types as the different class has been shown in **Table 3.**

The performance of the classifiers is evaluated in terms of sensitivity, specificity, precision, accuracy and F-score. The classification performance of the proposed method is tested at a slice level. The average value of sensitivity is 0.90815166, the average value of specificity is 0.977151379, the average value of precision is 0.907038177, the average value of accuracy is 0.963461538, and the average value of F-score is 0.906558695 for an ANFIS. ANFIS uses both neural network and fuzzy logic which gives very good results. With such a low error rate and high accuracy value ANFIS proves its superiority even when the available training dataset is not too large.

Conclusion

Correctly identification and segmentation of primary normal brain tissues from MRI using iterative three phase level set segmentation that removes existing over segmentation and under-segmentation problem. This method maintaining hierarchical structure based on the sharp peak of the segmented region by level set provides good initializations, so the method has not any leakage and less sensitive to local minima and maxima than comparable methods. Any presence of abnormalities can be detected from that hierarchical structure. Major normal tissues such as WM, GM, and CSF with other parts of the human head such as skull, marrow, and muscles skin are segmented with greater accuracy compare to the existing method and abnormal tissues such as hemorrhage; edema and tumor can be detected.

Table 3: Classification rates of an ANN classifier for brain tumor

Metric	Class 1	Class 2	Class 3	Class 4	Class 5
True Positive (TP)	37	43	32	29	48
False Negative (FN)	4	4	5	2	4
False Positive (FP)	3	3	2	6	5
True Positive (TP)	164	158	169	171	151
Sensitivity (TP/(TP+FN)	0.902	0.914	0.864	0.935	0.923
Specificity (TN/(FP+TN)	0.982	0.981	0.988	0.966	0.967
Precision (TP/(TP+FP)	0.925	0.934	0.941	0.828	0.905
Accuracy (TP+TN)/(P+N)	0.966	0.966	0.966	0.961	0.956
F score (2TP/(2P+FP+FN))	0.913	0.924	0.901	0.878	0.914

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