Scientific Research Publishing

Open Journal of Medical Imaging, 2017, 7, 17-27
http://www.scirp.org/journal/ojmi
ISSN Online: 2164-2796
ISSN Print: 2164-2788

Grading of Brain Tumors by Mining MRS Spectrums Using LabVIEW

—Metabolite Peak Height Scanning Method

Jayalaxmi S. Gonal[1], Vinayadatt V. Kohir[2]

[1]Department of Electronics and Communication Engineering, B.L.D.E.A.'s College of Engineering and Technology, Vijayapura, India
[2]Department of Electronics and Communication Engineering, PDA Engineering College, Gulbarga, India
Email: jayagonal@gmail.com, vvkohir@yahoo.com

How to cite this paper: Gonal, J.S. and Kohir, V.V. (2017) Grading of Brain Tumors by Mining MRS Spectrums Using LabVIEW. *Open Journal of Medical Imaging*, **7**, 17-27.
https://doi.org/10.4236/ojmi.2017.71003

Received: October 10, 2014
Accepted: December 10, 2014
Published: March 3, 2017

Abstract

In this paper, we attempt to resolve the problem of grading of brain tumors as grade 2, grade 3, grade 4, using information from magnetic resonance spectroscopy (MRS) image, to assist in clinical diagnosis. This paper proposes a novel approach to extract metabolite values represented in a graphical form in MR Spectroscopy image. Metabolites like N-acetyl aspartate (NAA), Choline (CHO) along with the metabolite ratios NAA/CHO and presence/absence of LACTATE peak play the most important role in deciding the tumor type. The proposed approach consists of several steps including preprocessing, metabolite peak height scanning and classification. Proposed system stores the metabolite values in dataset instead of storing MRS images; so reduces the image processing tasks and memory requirements. Further these metabolite values and ratios are fed to a BPN classifier. Experimental results demonstrate the effectiveness of the proposed approach in classifying the brain tumors.

Keywords

MR Spectrum, Metabolite Peak Height, Graph Scanning, Vision Assistant, LabVIEW, BPN Classifier

1. Introduction

Brain tumor is a deadly disease. It can be prevented if detected and treated at an early stage [1]. Brain tumors are of two main types: (i) Benign tumors; (ii) Malignant tumors. Benign tumors in the brain usually do not need to be treated and their growth is self-limited. They are incapable of spreading beyond the brain. They are homogeneous, and have well defined boundaries. Whereas, malignant brain tumors are cancerous brain tumors, grow rapidly, invade the surrounding

normal tissue, heterogeneous, not well defined, and grow in a disorganized manner. These tumors can spread outside of the brain. Malignant tumors of the brain are most harmful which may remain untreated and an aggressive approach is almost always warranted.

According to the World Health Organization, brain tumor can be classified into the following groups:

Grade I: Benign, slow growing, with well-defined borders (Pilocytic).

Grade II: Slow growing, rarely spreading with a well-defined border (Astrocytoma).

Grade III: Growing faster (Anaplastic Astrocytoma).

Grade IV: Malignant most invasive, spreading to nearby tissues and growing rapidly (Glioblastoma Multiforme) [2].

Magnetic Resonance Spectroscopy (MRS) Imaging provides detailed information about brain tumor *viz.*, tumor anatomy, cellular structure, making it an important tool for the diagnosis [3]. It is a noninvasive diagnostic test for measuring biochemical changes in the brain, especially the presence of tumors. While, conventional MR imaging measures signals emitted by hydrogen (proton) nuclei from small pixels which have been selected by spatial variations in frequency and phase. This spatial mapping enables the signal to be formed into images. However, when using frequency changes for spatial encoding, we lose our ability to discriminate much of the important information about chemical environment among the nuclei. Water, fat and other chemicals, typically amino acids, combine to produce a single net signal from each pixel. We have limited ability to distinguish relative contributions in MRI. Magnetic Resonance Spectroscopy (MRS) can extract information about the chemicals that reside on the frequency scale between water and fat in both a qualitative and quantitative manner. MRS uses the same principles as Magnetic Resonance Imaging (MRI) but rather than generating an image, a plot representing chemical composition of a region is generated. A RF pulse is applied to the sample. The signal from the sample is measured and Fourier transformed. MR spectroscopy uses position, signal intensity and line width along with spectral patterns to display chemical information. A "ppm scale" describes the "position" of the peaks or resonances on the x-axis. The parts per million or ppm refer to the unit of measure used to identify a peak location. The ppm is calculated by dividing the difference in frequency (in Hertz) of two peaks (with one peak being the reference) by the operating frequency of the MR scanner (in Hertz). The frequency of these metabolites is measured in units called parts per million (ppm) and plotted on a graph as peaks of varying height as shown in **Figure 1**.

MR spectroscopy analyzes molecules such as hydrogen ions or protons. Proton spectroscopy is more commonly used [3] [4]. There are several different metabolites, or products of metabolism, which can be measured to differentiate between tumor types: N-acetyl aspartate, Choline, Creatine, Amino acids, Lipid, Lactate, Alanine and Myoinositol. To get an accurate assessment of the tumor chemistry, the spectroscopic voxel should be placed over an enhancing region of

the tumor, avoiding areas of necrosis, hemorrhage, calcification, or cysts.

By measuring peak at each metabolite's ppm and comparing it to normal brain tissue, the neuroradiologist can determine the type of tissue present. Based on this knowledge they perform they perform the classification of tumors.

A sample MR Spectroscopy image for different grades of malignancy of brain tumors is shown in Figure 1. Each metabolite reflects specific cellular and biochemical processes. NAA is a neuronal marker and decreases with any disease that adversely affects neuronal integrity. Creatine provides a measure of energy stores. Choline is a measure of increased cellular turnover and is elevated in tumors and inflammatory processes. The observable MR metabolites provide powerful information [5].

In astrocytoma brain tumor, several studies have suggested an association between tumor grade and CHO levels, with the higher-grade tumors having

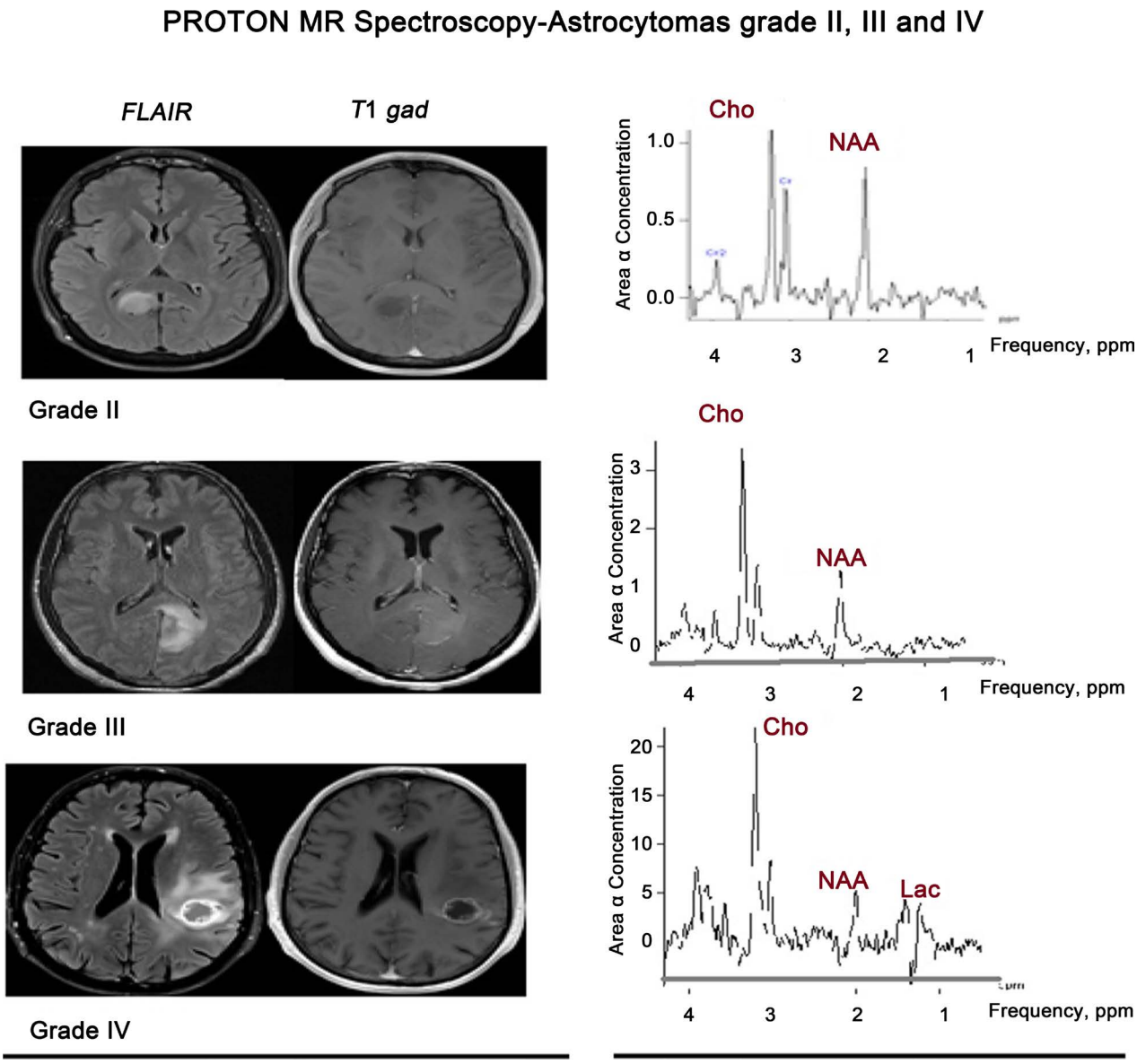


Figure 1. Sample of MR spectrum for grading of brain tumor.

greater CHO concentrations. The role of proton MRS in biopsy guidance is to recognize regions of high metabolic activity: regions of elevated CHO levels (and low NAA levels) indicative of tumor tissue; represent a good target for biopsy.MRS can be used to determine the degree of malignancy. As a general rule, as malignancy increases, NAA and Creatine decrease, and choline, lactate, and lipids increase. NAA decreases as tumor growth displaces or destroys neurons. Very malignant tumors have high metabolic activity and deplete the energy stores, resulting in reduced Creatine. Very hyper cellular tumors with rapid growth elevate the choline levels. Lipids are found in necrotic portions of tumors, and lactate appears when tumors outgrow their blood supply and start utilizing anaerobic glycolysis. To get an accurate assessment of the tumor chemistry, the spectroscopic voxel should be placed over an enhancing region of the tumor, avoiding areas of necrosis, hemorrhage, calcification, or cysts.

The common way to analyze clinical spectra is to look at metabolite ratios, namely NAA/CHO, and LACTATE peak. Degree of the abnormality is based on the values of metabolite ratios and lactate peak, as shown in the Table 1. By including a known reference solution when acquiring the MR spectral data, absolute concentrations of metabolites can be calculated. In proposed system metabolite values are extracted and computed NAA/CHO ratio and the presence or the absence of the lactate peak, which play important role in brain tumor detection. As the grade of the tumors increases, the NAA/CHO metabolite ratio decreases. The Lactate peak is present in grade 4 tumors.

A huge data is needed to be maintained in hospitals for brain tumor patients. This data is present in MRS image format. This dataset can be mined to get knowledge of metabolite values. In proposed system metabolite values are extracted from MRS images. Extracted values are stored in a dataset. Memory requirement for storing brain tumor dataset is much less than for MRS images. Generated dataset can be utilized for various clustering and classification techniques.

The paper is organized in following manner: critical survey of related work is carried in the Section 2. Proposed system is presented in the Section 3. Experimental results are discussed in the Section 4. The conclusion of the research work is presented in the Section 5.

2. Literature Survey

Numerous investigations have been recommended to increase the clinical utility of MR Spectrum based techniques for preoperative diagnosis of brain tumor [6] [7].

Hasan Aydin [8] evaluated MR Spectroscopy for brain tumor categorization. Brain tumors are classified into low-high grade glial neoplasms, menengiomas and metastasis. Brain tumors are categorized on the basis of CHO/NAA, CHO/CR and NAA/CR metabolite ratios.

P. Rajendran and M. Madheswaran [9] proposed association rule mining technique to classify the CT scan brain images. For this study three categories

have been taken namely normal, benign and malign. Low-level feature extracted from images and high-level knowledge from specialists is combined into system.

Ahmed Kharrat, Karim Gasmi, Mohamed Ben Messaoud [10], presented their work on A Hybrid Approach for Automatic Classification of Brain MRI Using Genetic Algorithm and SVM. This paper proposes a genetic algorithm and SVM based classification of brain tumor. It is concluded that, Gabor filters are poor due to their lack of orthogonality that results in redundant features at different scales or channels.

Andac Hamamci, Nadir Kucuk, Kutlay Karaman, Kayihan Engin, and Gozde Unal [11] presents fast and robust tool for segmentation of solid brain tumors. Tool assists clinicians and researchers in radio surgery planning with minimal user interaction.

Dina Aboul Dahab, Samy S. A. Ghoniemy and Gamal M. Selim [12] applied modified segmentation techniques on MRI scan images to detect brain tumor. Modified Probabilistic Neural Network based on Learning Vector Quantization with image and data analysis to classify brain tumor using MRI scans.

From the literature survey it is observed that most of the work on classification of brain tumors is based on features viz., intensity and texture. This is suitable for broad classification such as normal and abnormal. But they fail to grade the degree of abnormality. Grading of brain tumors can efficiently be done based on MR Spectroscopy images. But more memory is required to store the MR Spectroscopy images. Also processing of the graphical representation in these images is very tedious. Hence in the proposed work, we extract the metabolite values from the graphical representation and store the metabolite values in dataset instead of storing MR Spectrum images; this reduces the image processing tasks and memory requirements.

3. Proposed System

Proposed system takes MR Spectroscopy images as an input; extract values from MR Spectrum graph and perform grading of abnormality of the tumor. Further the dataset can be used in clustering or classification. Overall working of proposed Metabolite Peak Height-Graph Scanning is presented by: (i) Algorithm and (ii) Vision Assistant Code.

(i) Metabolite Peak Height-Graph Scanning algorithm

Input*: *MR Spectroscopy Image

Output*: *Height of the Peak and Value of the Metabolite

Step 1: Locate X-axis of input graph in MR Spectroscopy image.

Step 2: Locate Y-axis of input the graph using an "Advanced Straight Edge" tool in LabVIEW. It finds the left edge of the MR Spectrum graph by searching from left to right along a vertical axis.

Step 3: Find the Co-ordinate System Origin using a "Caliper" tool. It finds the intersection of the left and the bottom edges of the MRS graph.

Step 4: Locate the origin of the coordinate system, so that the system is invariant to shift and rotate of input MRS graph.

Step 5: Detect the edge by using 'search path' which is a line drawn across the X-axis at required ppm marking on the graph. Here "search path" is placed at 3 different markings:

At 2 ppm as NAA stored as Metabolite [0]

At 3.2 ppm as CHO stored as Metabolite [1]

At about 1.3 ppm as LACTATE stored as Metabolite [2]

Step 6: Measure the distance between edge point and X-axis using "Caliper" tool at the 3 markings.

Step 7: Take suitable scale "s" from user for each m in Metabolite[m].

Step 8: Result [m] = Temp x s.

Step 9: End.

Step 10: Store Result array.

The graph-scanning algorithm is about detecting the peak points from graph and noting the co-ordinate values. The distance between peak point and X-axis is measured using the Vision Assistant code shown in Figure 2. The calculated distance is multiplied with suitable user scale to get the metabolite value nearer to the original one. The standard set of metabolite values for normal and abnormal brain cases is shown in Table 1.

Extracted values are stored in excel sheet with the class of tumor as shown in Table 2.

(*ii*) Vision Assistant Code

A MR spectrum image is processed according to the Vision Assistant Code shown in Figure 2. The distance between peak edge point and X-axis is measured by carrying out various steps *viz.*, detecting X- & Y-axes, by locating the left and bottom edges of the graph. Then origin of the coordinate system is found at the intersection of the edges using the caliper tool in LabVIEW. The intersection of the edges and the right endpoint of the bottom edge, obtained from the previous steps, are used to compute the angle of the coordinate system.

The MR Spectrum image is fed as the input image to the system. Then it is processed as explained below.

Table 1. Grading using METABOLITE RATIOS.

Metabolite Ratios	Grade-1	Grade-2	Grade-3
NAA/Cho	<1.2	<0.6	<0.2
Lactate Peak	Absent	Absent	Present

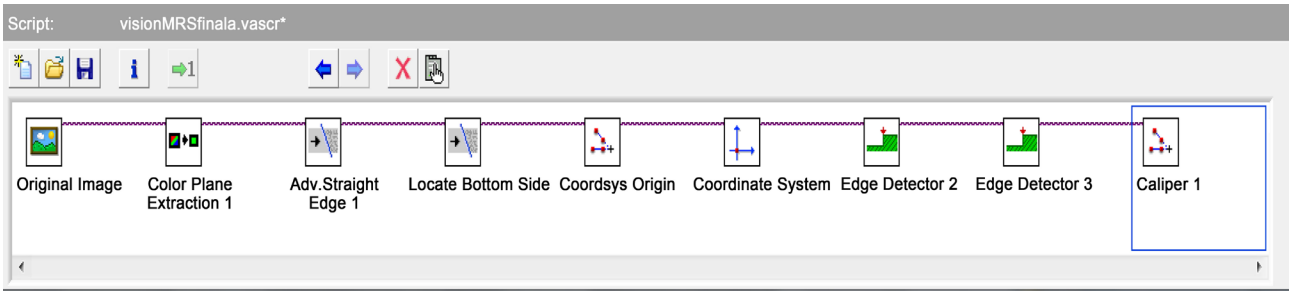


Figure 2. Finding height of the peaks from X-axis using vision assistant in LabVIEW.

Original Image: The MR Spectrum images are resized to 256 × 256 pixels. The input image is preprocessed for noise removal, converted to binary image, threshold and enhanced for highlighting the graphical representation in the image.

Color Plane Extraction: Extracts the luminance plane from the color image.

Locate Left Side: An Advanced Straight Edge step that finds the left edge of the MRS graph by searching from left to right along a vertical axis.

Coordinate system Origin: A Caliper step that finds the intersection of the left and bottom edges. The end points of the left and bottom edges, obtained from the previous steps, are used to compute the intersection of the edges.

Coordinate System: A Set Coordinate System step that defines a coordinate system based on the Caliper step. Because the MR Spectrum graph can shift and rotate from one image to another, the changes in the region of interest are accounted for using the Horizontal, Vertical, and Angular Motion mode. This mode adjusts the region of interest positions along the horizontal and vertical axes, and adjusts for rotational changes.

Edge Detection: The edge detection process looks for edges (sharp transitions in pixel values) along a search path. The search path is defined as the line that is drawn across the X-axis at required ppm marking and the graph. The line is drawn long enough so that it always cuts through the base even if the MR Spectroscopy graph peak moves from image to image. The Edge detection step is used four times by placing the search path at location on X-axis *i.e.*, at 2 ppm marking for NAA metabolite, at 3.2 ppm for CHO and at 1.3 ppm for Lactate metabolite.

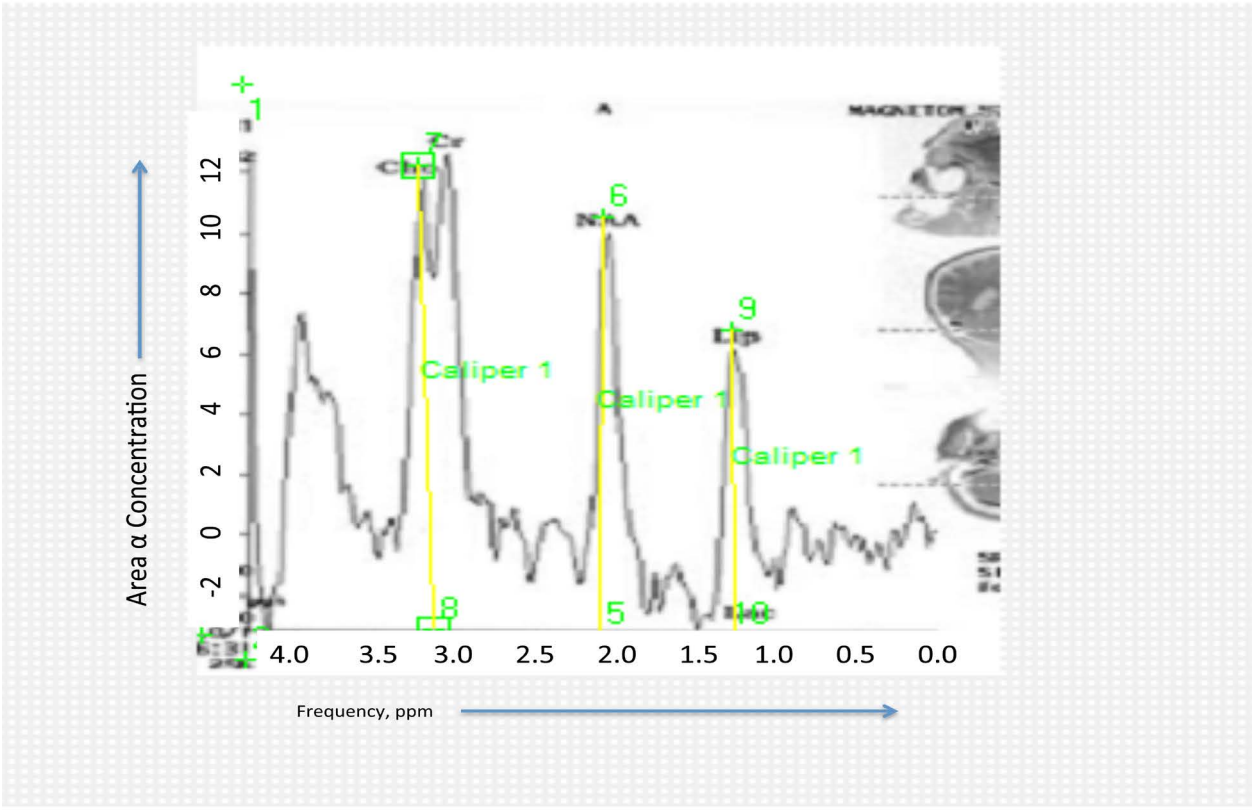
Caliper: Measures the distance between the points found on the search line. The caliper is used to measure the heights of the 4 peaks of interest.

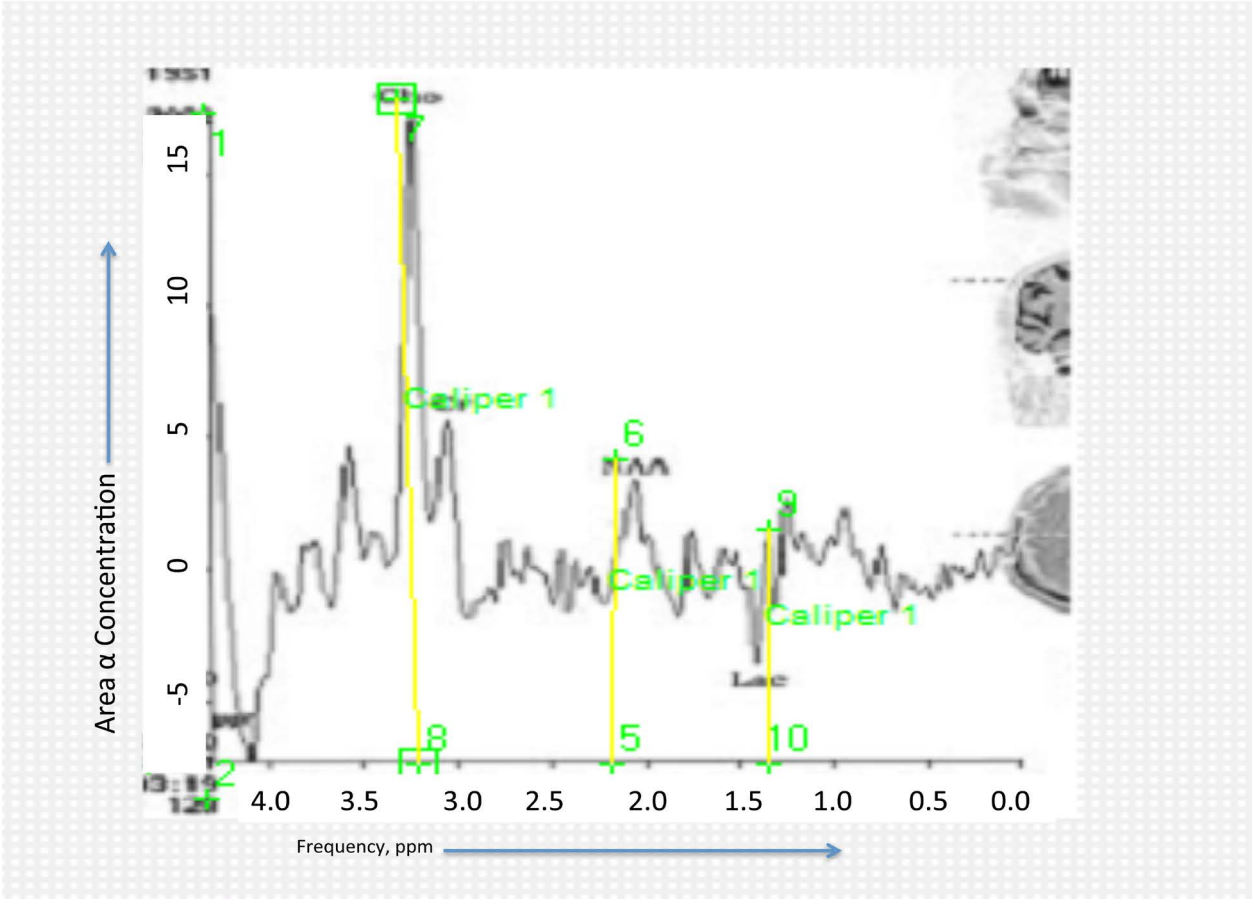
After finding the heights of the metabolite peaks from X-axis, the dataset of the values of the metabolites is generated. This dataset is further used for classification of brain tumors as normal or abnormal. The standard set of metabolite values for normal and abnormal brain cases is shown in Table 1.

The feature vectors are formed using extracted metabolite ratios for all MRS samples. BPN classifier is used to categorize the brain MRIs as comprising of grade 2, grade 3 and grade 4 tumors.

4. Experimental Results

The MR Spectrum images are collected from BLDEA's Hospital, Vijayapur. We have collected 28 MR spectroscopy images; ten cases of grade 2, ten samples of grade 3 and eight samples of grade 4 tumors. Figure 3 shows the result windows for different cases of MR Spectrum in 3 consecutive rows. In each case the heights of the peaks of metabolites: NAA, CHO and LACTATE are found using Vision Assistant tool of LabVIEW and the values of these heights are also available in excel sheets. These heights are further used for extracting the values of the metabolites using the Graph scanning algorithm. The metabolite values are fed to the BPN classifier. The output of the classifier is the class of brain tumor as grade 2, grade 3, and grade 4 brain tumors as tabulated in Table 2.


Area α Concentration
12
10
8
6
4
2
0
-2
Caliper 1
Caliper 1
Caliper 1
4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
Frequency, ppm


Area α Concentration
15
10
5
0
-5
Caliper 1
Caliper 1
Caliper 1
4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
Frequency, ppm

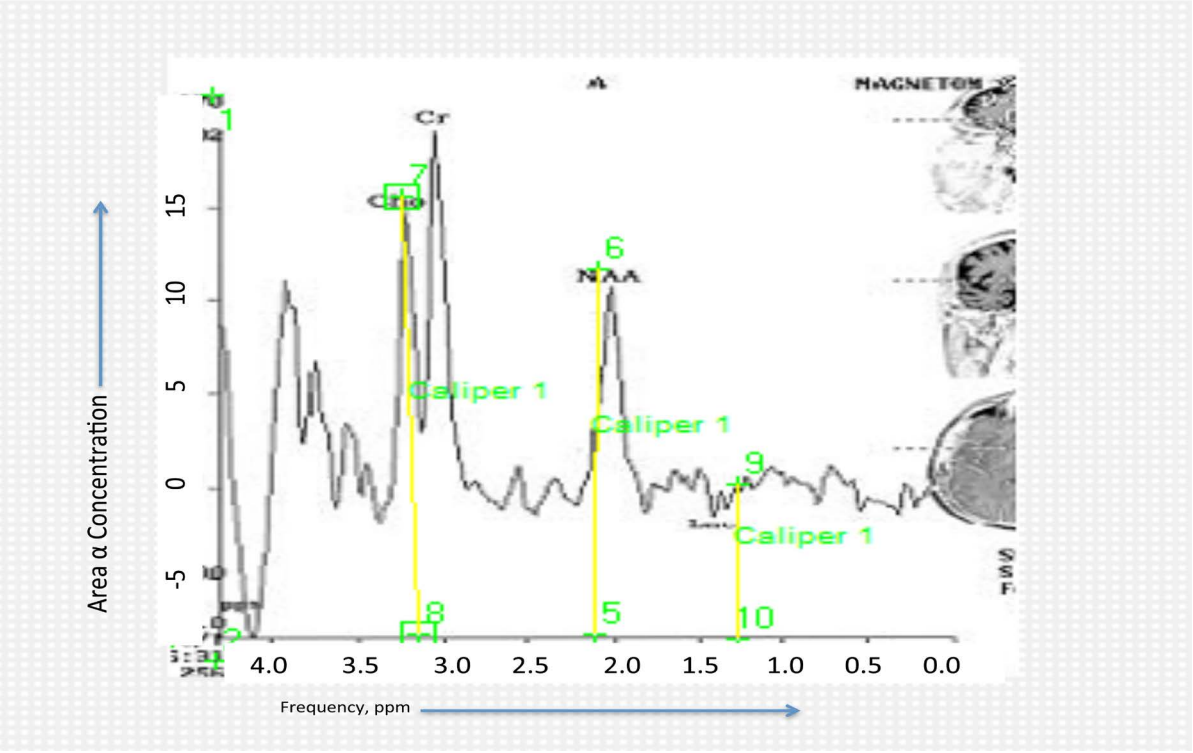


Figure 3. Finding height of the peaks from X-axis using vision assistant (shown in 3 consecutive rows for 3 cases of MR spectrums).

Table 2. Result of grading of tumors as grade 2, grade 3 and grade 4.

	A	B	C	D	E
1	NAA	CHO	LACTATE	NAA/CHO	GRDING
2	11.82	14.02	ABSENT	0.84	GRADE-2
3	6.32	15.37	ABSENT	0.42	GRADE-3
4	4.71	16.67	PRESENT	0.28	GRADE-4
5	10.67	14.98	ABSENT	0.71	GRADE-2
6	8.23	15.82	ABSENT	0.52	GRADE-3
7	3.42	18.67	PRESENT	0.18	GRADE-4

Table 3. Performance of using features from different MR modalities.

True positive (TP); False positive (FP) True negative (TN); False negative (FN)	MR spectrum image metabolite features (in %)	MR image GLCM texture features (in %)
Sensitivity = TP/TP + FN (%)	92.2	85.7
Specificity = TN/FP + TN (%)	90.1	78.6
Accuracy = TP + TN/TP + FN + TP + TN (%)	90.8	82.1

The grading of brain tumor performed using peak heights of metabolites in MR spectrums is more efficient than using the GLCM texture features derived from MRI images as indicated in Table 3.

5. Conclusions

MR spectroscopy data can direct the surgeon to the most metabolically active part of the tumor for biopsy to obtain accurate grading of the malignancy. NAA/CHO metabolite ratio and presence/absence of LACTATE metabolite play the most important role in grading of brain tumor. But the drawback of our proposed method is that it works only for the MR spectroscopy images obtained for the specified setting from the same MRI machine.

The grading of brain tumor performed using peak heights of metabolites in MR spectrums is more efficient than using the GLCM texture features derived from MRI images.

Acknowledgements

We are thankful to Radiology department, BLDEA's Medical College, Vijayapur, for providing the MR Spectroscopy images, for discussing information regarding brain tumor detection using metabolite values and for validating the results.

References

[1] JASCAP (2015) Brain Tumors. http://www.healthlibrary.com/book77_chapter947.htm

[2] Central Brain Tumor Registry of the United States (CBTRUS) (2013) FactSheet. http://www.cbtrus.org

[3] Magnetic Resonance, Functional (fMRI)—Brain (2013). www.radiologyinfo.org/en/pdf/fmribrain.pdf

[4] Meris (2014) Towards Better Health. http://mieuxprevenir.blogspot.in/2014/06/India

[5] Hesselink, J.R. (2013) Fundamentals of MR Spectroscopy. http://spinwarp.ucsd.edu/neuroweb/Text/mrs-TXT.htm

[6] Bulakbasi, N., Kocaoglu, M., Ors, F., Tayfun, C. and Ucoz, T. (2003) Combination of Single Voxel Proton MR Spectroscopy and Apparent Diffusion Coefficient Calculation in the Evaluation of common Brain Tumors. *American Journal of Neuroradiology*, **24**, 1989-1998.

[7] Burtscher, I.M. and Holtas, S. (2001) Proton Magnetic Resonance Spectroscopy in Brain Tumors: Clinical Applications. *Neuroradiology*, **43**, 345-352. https://doi.org/10.1007/s002340000427

[8] Aydin, H., Oktay, N.A., Spaholu, S., Altin, E. and Hekimoglu, B. (2010) The Efficacy and Value of Proton MR Spectroscopy IEvaluating the Brain Tumours. *The New Journal of Medicine*, **2010**, 37-42.

[9] Rajendran, P. and Madheswaran, M. (2009) An Improved Image Mining Technique for Brain Tumor Classification Using Efficient Classifier. *International Journal of Computer Science and Information Security*, **6**, 107-116.

[10] Kharrat, A., Gasmi, K., *et al.* (2010) A Hybrid Approach for Automatic Classification of Brain MRI Using Genetic Algorithm and Support Vector Machine. *Leonardo Journal of Sciences*, **9**, 71-82.

[11] Hamamci, A., Kucuk, N., Karaman, K., Engin, K. and Unal, G. (2012) Tumor-Cut: Segmentation of Brain Tumors on Contrast Enhanced MR Images for Radiosurgery Applications. *IEEE Transactions on Medical Imaging*, **31**, 790-804.

https://doi.org/10.1109/TMI.2011.2181857

[12] Dahab, D.A., Ghoniemy, S.S.A. and Selim, G.M. (2012) Automated Brain Tumor Detection and Identification Using Image Processing and Probabilistic Neural Network Techniques. *International Journal of Image Processing and Visual Communication*, **1**, 1-8.