# Automatic Detection of Brain Abnormalities and Tumor Segmentation in MRI Sequences

Soniya Goyal
Computer Science and Engineering Department
Indian Institute of Technology, Delhi
New Delhi, India
soniya-cs@student.iitd.ac.in

Sudhanshu Shekhar
Computer Science and Engineering Department
Indian Institute of Technology, Delhi
New Delhi, India
sudhanshu-cs@student.iitd.ac.in

***Abstract*- This paper presents an automated and clinically-tested method for detection of brain abnormalities and tumor-edema segmentation using the MRI sequences. Since currently available detection methods involve large amount of training data and rely on standard models, templates and atlases, they are applicable only to a limited domain of brain abnormalities. On the other hand our proposed method can detect injuries from a wide variety of brain images as it follows a Radiologist's approach to the brain diagnosis using multiple MRI sequences instead of any prior models or training phases. Our procedure consists of the following steps: a) Pre-processing of the MRI sequences, T2, T1 and T1 post contrast for size standardization, contrast equalization and division into active cells b) Identification of the T2 MRI sequence as normal or abnormal by exploiting the vertical symmetry of the brain c) Determination of the region of abnormality using its hyper-intense nature. d) Separation of tumor from edema using the T1 and its post-contrast (enhanced) sequences and e) Estimation of the volume of tumor found and generation of an anatomical differential of the possible disorders. This approach has been tested on more than a hundred real dataset both normal and abnormal representing tumors of different shapes, locations and sizes and results being checked by radiologists thus defining an efficient and robust technique for automated detection and segmentation of brain tumors.**

***Keywords- Automated brain tumor detection; Tumor-edema segmentation; robust estimation; Brain symmetry; Intensity outliers; Brain anatomical classification; T2, T1 MR images***

## I. INTRODUCTION

Diagnosis of Neuro Disorders has always been a challenging area for Medical Science because of the high complexity in the anatomical structure of brain, large variations in size, location and form of the brain tumors and the factors like patient's age, his pathological history and symptoms which demand highly specialized skills of the radiologists and the complete clinical examination of the patient. The situation gets critical because of the ever increasing count of the patients suffering from Neuro disorders from year to year throughout the world. It is even worse in developing nations like India where the Radiology group is too small and so is exposed to nearly 3-4 times the number of patients as compared to radiologists of other therefore is exposed to a large number of patients leading to a huge manual workload which is both time consuming and error prone.

This makes the automatic brain disorder detection not only desirable but also extremely essential. Over the decade, many methods have been proposed to make tumor segmentation automatic based on 2D and 3D image analysis algorithms like neural networks[1-2], support vector machine (*SVM*)[3], atlas based method[4], and outlier detection[5-6]. But unfortunately, in order to obtain satisfactory results by the above methods, either a complex prior model or a large amount of training data is required, thus restricting the range of application by the domain of training phase. Considering the above shortcomings, this paper gives an intuitive method which integrates the Radiologist perception with the Image processing techniques for the diagnosis of brain abnormalities. Unlike others, this approach uses multiple MRI sequences and the vertical symmetry of the brain which can be implemented in real-time and is robust to change in parameters, therefore is applicable to a much wider range of MRI data.

The rest of this paper is organized as follows. In section 2, we give an overview of the related work done in the brain abnormality detection or Tumor-Edema separation and our contributions. In section 3, the technical details of our work are provided and discussed. Section 4 gives experimental results. Finally, conclusion and future work are given in section 5.

## II. RELATED WORKS AND OUR CONTRIBUTION

### A. Related Works

Computer aided detection of brain tumors is one of the most difficult issues in field of abnormal tissue segmentations because of many challenges. The brain injuries are of varied shapes and can also deform other normal and healthy tissue structures. Intensity distribution of normal tissues is very complicated and there exist some overlaps between different types of tissues. All the brain disorder segmentation methods use the central-dogma of the difference of the abnormal brain MRI from its normal counterpart. Over the last decade various approaches have

been proposed for the same. Some regarded the segmentation task a tissue recognition problem, which meant using a well-trained model that can determine whether a pixel/voxel belongs to a normal or abnormal tissue based on neural network approach. However, use of training data restricts the efficiency of the method to the domain of the training data and is time consuming as well as couldn't be applied to real-time problems. Another approach is based on building a stochastic model for the normal brain tissues and using it as a template for registration with the abnormal MRI image. However, it has been always challenging to build a complete prior model in order to cover enough tissue information. Detailed comparison of the previous related works and this paper with their positives and limitations has been done in *Table 1*

TABLE I

| Author | Approach | Dataset and MRI Sequences used | Positives | Limitations |
|---|---|---|---|---|
| Marcel Prastawa et al | Outlier detection followed by geometric and spatial constraints | - 3 real datasets<br>- T1 and T2 sequences<br>- Use of registered probabilistic brain atlas | - Use of dual-channel MRI sequences<br>- Use of blobby nature of tumor and contiguous nature of edema with tumor | - Use of intensity as a method of classification of brain matter for outlier detection can leave out half-enhanced cases or may include false positive cases<br>- Use of the reference(template) image limits the efficiency of the results to the accuracy of the template/atlas and so makes it non-real time in nature<br>- Use of T2 channel for separation of tumor and edema is restricted to specific cases having distinct non-overlapping tumor-edema intensities only |
| J. Zhou et al | Image segmentation using one-class support vector machine (SVM) | - 24 MRI images | - Use of no *a priori* information<br>- Does not rely on any template image | - No structured use of the MRI sequences<br>- Requires training<br>- Lot of human interference to set up SVM parameters |
| Amir Ehsan Lashkar | Neural Network-based method using Zernike and Geometric moments | - 160 cases for Training Phase<br>- 40 cases for Testing Phase | - Use of large data set<br>- Handling of false positive and negative cases separately<br>- Calculation of performance parameters – specificity, accuracy | - Use of no specific MRI sequence<br>- Use of training limits the accuracy of the method to the domain of the training phase which makes it local and non-robust<br>- Time consuming and can't be implemented in real-time |
| Yu Sun et al | Symmetry Integration in several steps associated with segmentation, clustering and classification. | - MRI sequences of 2 patients, with 16 slices for each | - Use of no prior model or template<br>- No training required<br>- Comparison of results with ground-truth | - Use of no specific MRI sequence and so unstructured in nature<br>- Use of mere Symmetry based approach for classifying normal and abnormal tissues can lead to false results in case of asymmetrical age-related calcifications and artifacts in brain which are non-tumor in nature<br>- Use of small and unstructured dataset restricts the generality and clinical applicability |
| This Paper | Local Symmetry along with intensity thresholding which is then checked by corresponding T1 and T1 post contrast sequences | - 120 cases (65 normal + 55 abnormal)<br>- 3 sequences, T1, T2 and T1 post contrast each having 20 slices | - No use of atlas or registration or any training or testing methods<br>- Structured approach because of use of multiple MR sequences<br>- Can be applied in real time<br>- Clinically reliable as a detailed report is provided<br>- Very large database ensure robustness and precision | - Cases involving tumors of the very small, less detailed and overlapping regions of brain like pineal etc requires more efficient technique for segmentation |

### B. Our Contribution

While the related works in [1-6] either used training or registration or a global symmetry-integrated approach for brain tumor segmentation, our method approaches this problem in a very structured manner with the use of 3 MRI sequences, T2, T1 and T1 post contrast. By this approach, we overcome the limitations of other methods and make the following contributions:

a) Pre-processing of all the image sequences is done to overcome the issue of variation of brain size and brightness from person to person and from one MRI centre to another respectively.

b) Division of the entire image into vertically symmetric 32 active cells is done to reduce averaging and promotes enhancing of smaller local asymmetries rather than adopting a global symmetric approach as used earlier.

c) Fusion of symmetry integrated subtraction and intensity thresholding on the T2 sequence for abnormality detection makes it more precise than just considering symmetry which would include cases of age-related asymmetries like calcification other than just tumors.

d) The first time use of T1 post contrast for tumor-edema segmentation and then T1 for further verification makes the approach more systematic and accurate.

e) This approach then gives the approximate volume and the anatomical location of the tumor by mapping the tumor pixels with the biological location in the brain and the classification of the possible disorders thus giving a detailed report to the radiologist.

So this paper presents one of the first methods which make tumor segmentation fully automatic right from abnormality detection to tumor-edema separation and even co-relating it to the actual location making it very handy for the radiologists.

## III. TECHNICAL APPROACH

### A. Input Data Set

T2, T1 and T1 post-contrast (enhanced) MR Sequences each having 20 images, have been used in this approach.

### B. Pre-processing

1) *Size Standardization:* The variations in the brain size and shape of persons need to be taken into account before any general technique is applied. To handle this issue, each MRI image is first cropped by detecting the brain boundary and then resized to 512x512. (Fig1. B)

2) *Contrast Equalization:* Another issue is that there may be variations in the MR images taken from different centers due to change in contrast level. To account this, all the images are normalized by iteratively increasing or decreasing the average global intensity of the image by a small amount $\varepsilon$, till we get to a predefined contrast level

3) *Division into Active Cells:* An 8x8 grid is placed on the image creating cells of size 64x64. The cells which do not contain any portion of brain or are partly filled are removed from consideration. This leads to 32 active cells as shown in Fig1.C. These active cells are then numbered symmetrically about the vertical axis of the brain. This has been done to promote local enhancement of asymmetric regions thus including even smaller regions of abnormality than a global approach which actually averaged out that region and thus couldn't be identified.

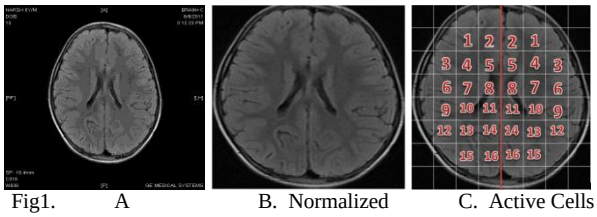



Fig1. A Original Image B. Normalized Image C. Active Cells Division

### C. Abnormality Detection

Before identifying tumor and edema, it is necessary to first detect regions in the T2 sequence which have properties deviating from a normal, healthy brain. Since tumors in the lower part of the brain like cerebellum and temporal lobes, are smaller in size and conflict with other bony structures which are not part of brain, so the analysis was done separately for a) *Infratentorial* b) *Supratentorial* regions of the brain.

1) *Subtraction – Vertical Symmetry Property:* As mentioned earlier, a T2 MR image would have a hyper intense region at the location of Edema and Tumor. Using this, the histogram of each cell is obtained and subtracted with the corresponding cell of the other half. Then the abnormal region in each cell is highlighted if its value is greater than a particular threshold value $\zeta$ which has been obtained by a similar method on the normal images of 65 different cases. Fig2. A and B shows the two histograms of the active cells of an abnormal image and its corresponding normal counterpart. This gives the area of asymmetry in the image considered.

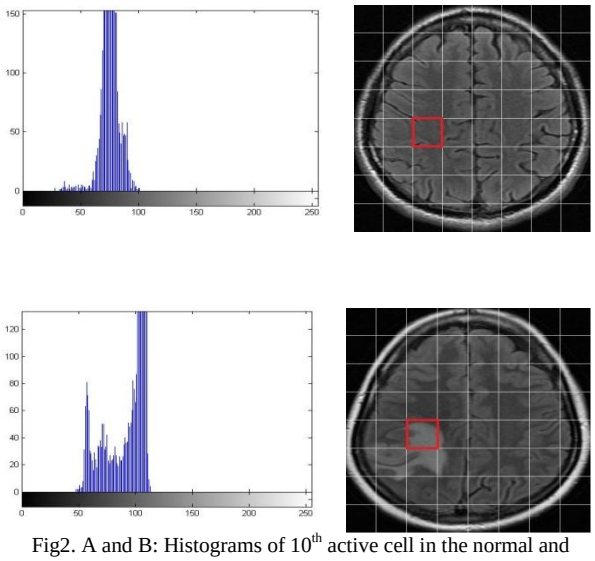


Fig2. A and B: Histograms of 10th active cell in the normal and abnormal images

*2) Intensity Thresholding:* Due to possible variation in the two halves even in the normal brain, Vertical Symmetry alone is not reliable. So, now the abnormal regions are again identified based on intensity thresholding. The threshold $\mu_i$ for each active cell $i$ is chosen using the robust estimate of the intensity of white matter, gray matter and CSF in the brain using a large dataset (Fig3. C).

*3) Fusion and Asymmetric Region Growing:* The results of *3.3.1* and *3.3.2* are then combined to get the set of common active cells of abnormal regions. For each active cell $a_i$ in the set, we consider its 8-neighbourhood, $N_8$ and expand the region of asymmetry using the threshold $\mu_i$ .This results in more refined and accurate area of abnormality as shown in Fig4.A which is used for tumor segmentation.

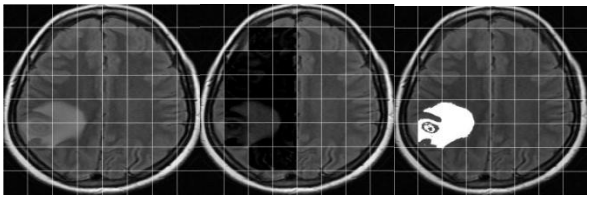


Fig3. A. Abnormal Image B. Subtraction of after pre-processing C. Intensity Thresholding right half from left

*D. Tumor-Edema Separation*

Similar pre-processing techniques as above are applied to T1 and its enhanced sequence (Fig4.B).

1) *Intensity Outliers in T1 post contrast:* Using the fact that only tumor gets enhanced in T1 post contrast sequence while edema don't, we process the same set of active cells given by the previous step in the T1 post contrast sequence. Again robust estimate of the white matter, gray matter and CSF in a normal T1 post contrast image is used to obtain thresholds for identification of intensity outliers in each of the active cells of this previously found abnormality set (Fig4.C)

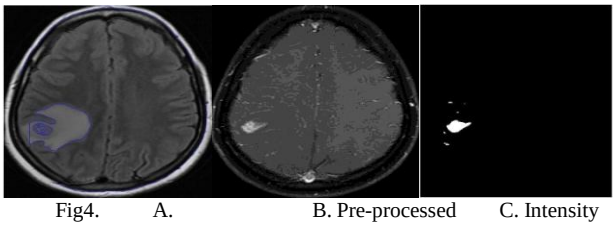


Fig4. A. Abnormal Region T2 B. Pre-processed T1 Post-contrast C. Intensity Outliers

*2) Applying Geometric and Spatial Constraints:* Along with tumor, blood vessels also generally get enhanced by the contrast agent and thus get identified in the outlier detection. These false positives are removed in multiple steps: a) the blobby nature of tumor is exploited to remove the small blood vessels using connected component algorithm and b) the fact that if any intensity outlier is tumor then it must be continued in consecutive slices rather than just once. These refine the tumor region further (Fig5.A).

*3) Verification from T1 Sequence:* It may happen that the region found in T1 post contrast is not a tumor but some other abnormalities like artifacts. So it is necessary to check the corresponding region in T1 (Fig5.B), where the tumor should not be enhanced. This finally confirms the presence of tumor inside the brain.

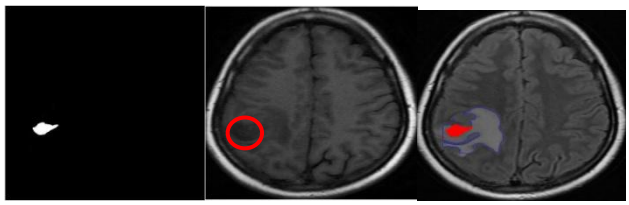


Fig5. A Tumor after applying Constraints B T1 image verifying presence of Tumor C Tumor in red and Edema in blue

*E. Volume Calculation and Differential Classification*

After the tumor regions are obtained in various slices, we generate a detailed report about the state of the patient.

*1) Volume Calculation:* Calculation of the volume of the found tumor is done using the standards of MR Imaging

(Slice Separation: 5mm; Slice Thickness: 1.5mm). A frustum model is used for the tumor between two consecutive slices with

area $A_i$ = number of pixels with tumor, converted into actual size by using the relation 1 pixel*1pixel = $(512/22)^2$ $mm^2$ in the image slice *i*

height *h* = slice thickness + slice separation

then the Volume V of the tumor is given by the summation of volumes of two consecutive slices, i.e.,

$$V = \Sigma ( h/3*(A_1 + A_2 + (A_1*A_2)^{1/2}) \quad (1)$$

where $A_1$ and $A_2$ denote the areas of the two consecutive slices having tumor.

*2) Differential Classification:* The tumor pixels found are then mapped to their anatomical locations in the brain. Based on this location and the age of patient, the differential classification of possible disorders is obtained [7].

## IV. RESULTS

*A. Dataset:* The experimental data set consists of 120 real cases, both normal (65) and abnormal (55) each having 20 slices of T1, T2 and T1 post contrast sequences.

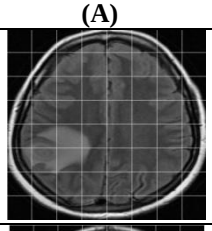
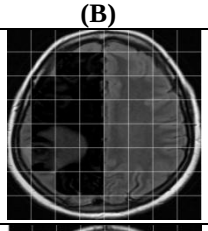
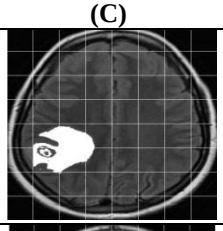
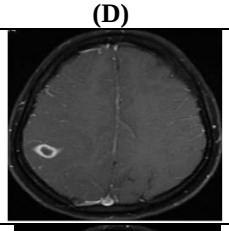
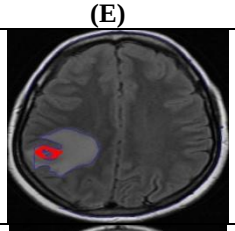
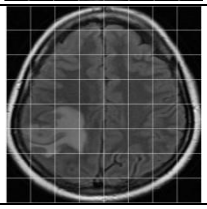
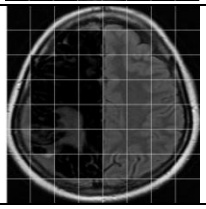
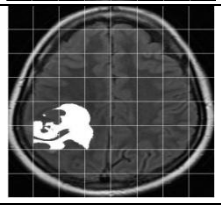
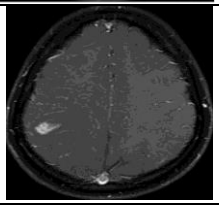
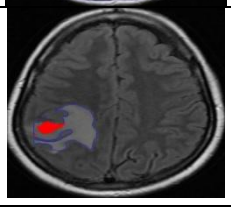
*B. Experimental Results:* Our method has successfully differentiated between a normal and abnormal case and located the region of asymmetry. It has also efficiently separated tumor from edema in the abnormal cases along with precise calculation of the volume and location of the tumor (Fig5C).

*Table II* shows 3 sample cases out of the 120 cases of our study. *Patient 1* has a tumor located in the lower right supratentorial region as suggested by his report from the Radiologist. Image A shows the original T2 image followed by the pre-processed image and then the abnormality location. Then using the T1 post contrast image (Image D), the method separates tumor from edema distinguishing them by different colours in figure E.

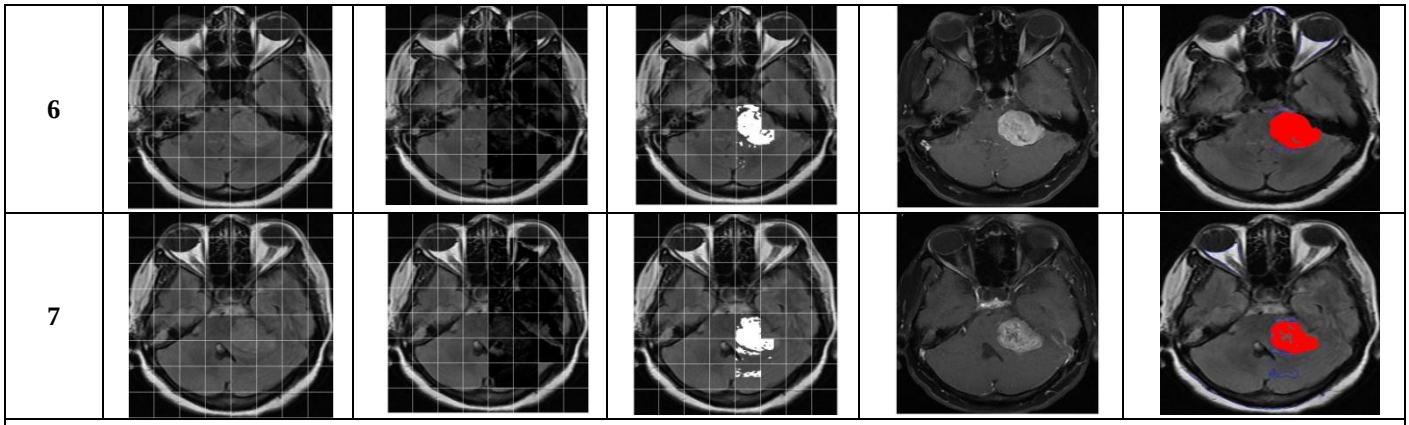
The challenging case was to locate tumors of the lower part of the brain which included cerebellum in which the MRI Image not only contained a smaller brain region but also other body parts surrounding it like eyes etc which conflicted while locating the intensity outliers of the abnormal regions. *Patient 2* is one such case. Figure E shows the successful detection of tumor by our method in this case also. *Patient 3* is one of the cases where false negatives are likely to come. It does have an abnormality in the T2 sequence but does not get enhanced in the post contrast sequence, thereby indicating the presence of a non-tumor abnormality. This has been successfully found by our structured method as when it tries to confirm the abnormality located in T2 by the T1 post contrast sequence, the unavailability of any enhancement in that particular region makes it a doubtful case and demands radiologist's review for its further analysis.

TABLE II

*PATIENT 1*

| Slice No. | Original T2 image (Pre-processed) (A) | Subtraction using Symmetry (B) | Intensity Thresholding (C) | Original T1 Post Contrast image (Pre-processed) (D) | Final Output (T2 image) (E) |
|---|---|---|---|---|---|
| **14** |  |  |  |  |  |
| **15** |  |  |  |  |  |

*PATIENT 2*

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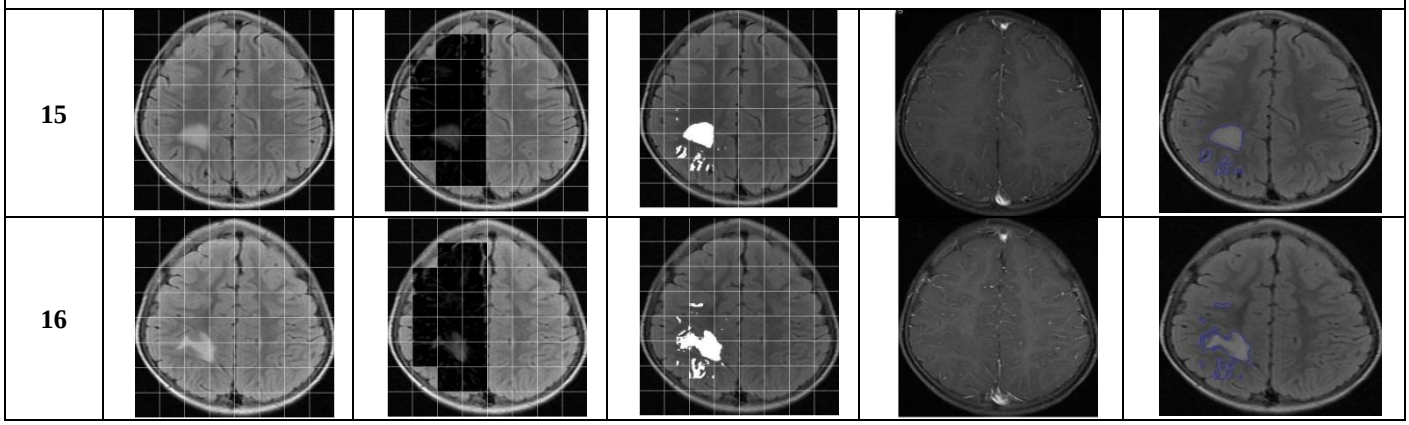


So in order to account for such false negative cases, the final result is given in three different ways: a) Normal b) Abnormal with tumor location and classification c) Needs Radiologist's Review to make it more clinically reliable.

## V. CONCLUSION AND FUTURE WORK

This paper provides an automated, clinically-tested approach for abnormality detection and tumor-edema segmentation. The method uses multiple sequences, thus making it more structured and overcoming the limitations of the earlier methods. It is also clinically more relevant as it gives a detailed report based on the tumor detected to the radiologist.

Our future work would be focused on identifying the tumors of the very small, less detailed and overlapping regions of brain like pineal, pituitary etc. and also decrease the number of false negative cases by the use of better segmentation algorithms and higher MR sequences.

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