International Journal of Engineering

Improving the Accuracy of Brain Tumor Identification in Magnetic Resonanceaging using Super-pixel and Fast Primal Dual Algorithm

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PAPER INFO

A B S T R A C T

Brain tumors are one of the most common causes of death that have been widely investigated by scholars in research areas, including care and prevention. Despite various empirical studies on the brain tumor segmentatin, there is still a need for further investigation. This fact is more needed in the automatic methods of brain tumors detection. In the present study, a new method for improving brain tumor segmentation accuracy based on super-pixel and fast primal dual (PD) algorithms has been proposed. The proposed method detects brain tumor tissue in Flair-MRI imaging in BRATS2012 dataset. This method detects the primary borders of tumors using a super-pixel algorithm, and improves brain tumor borders using fast PD in Markov random field optimization. Then, post-processing processes are used to delete white brain areas. Finally, an active contour algorithm was employed to display tumor area. Different experiments were carried on the proposed method and qualitative and quantitative criteria such as dice similarity measure, accuracy and F-measure were used for evaluation. The obtained results showed the efficiency of the proposed method, such that in the accuracy and sensitivity of 86.59 and 88.57% and F1-Measure 86.37 were obtained, respectively.

NOMENCLATURE

BR	v		MRF	Marcov Random Field
E	Energy function		LGG	Low Graid Gliomas
x_p	Label belonged to object p		T_P	Is a tumor and tumor has been identified
$c_p(x_p)$	Potential function		F_N	Is a tumor and tumor has not been identified
$d(x_p . x_q)$	Distance measure		F_P	Is not a tumor and tumor has been identified
w_{pq}	Weight is considered for each binary cost function		T_N	Is not a tumor and tumor has not been identified

1. INTRODUCTION

Since timely diagnosis and proper therapy in cancers patients increase the improvement and lifetime of patients, image processing can be used as a decision-making tool by physicians for early cancer identification. In the 21st century, empirical studies on cancer have been changed into a common research effort. Based on the statistics, the international agency for research on cancer (2022) has estimated that there are 25 million people suffering from cancer [1-3]. Also, the American Cancer Society (2022) has reported that heart diseases have been officially replaced by cancer, such has been the main death factor. People's survival for each type of cancer is 63% on average [4-6]. Cancer is detected based on interfering methods such as surgery, radiotherapy and chemotherapy. As studies revealed, using new computer technologies, such as image processing mechanisms have been successful in the processes related to cancers identification and segmentation [7-9]. During the

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computations and processes related to tumor exact segmentation in brain tumor scanned images, it can be referred to some challenges, such as hardy in distinguishing tumor tissue and the tissue of cysts of the main tissue of the human brain, three-dimensional tumor tissue surrounded a wide part of the brain (but two-dimension images have been used in the processing system), and the lack of the probability of diagnosing the depth of tumor and diagnosing three-dimension area of tumor [10]. It seems that one of the challenges existing in tumor diagnosis is low accuracy since satisfactory results have been obtained by using the fast PD algorithm in similar or other studies [11]. Fast PD is a Markov random field optimizing algorithmthat attempts to solve an alternative problem instead of solving the main optimization problem. It occurs in an optimal repetitive process; therefore, good results are expected. Considering the title of the paper, the main purpose of the study is to integrate fast PD algorithms to identify cancer regions as well as increase the accuracy of tumor diagnosis in MRI images. Cobzas et al. [12] presented a fully automatic method based on superpixel algorithm. Kircher et al. [13] have presented tumor identification and localization based on statistical features and classification of support vector machine in images (FLAIR). Buchbender et al. [14] presented a new method to detect brain tumors in MR images by using convolutional neural network and Atsu thresholding. Roy and Bandyopadhyay [15] presented a new method in tumor segmentation using deep neural network technology coupled with imaging strategy using nanoparticles. Rehman et al. [16], provided an overview of MRI image segmentation methods in brain tumor diagnosis. Padlia and Sharma [17] presented a new method based on convolutional neural network. Vijh et al. [18] have used Generative Adversarial Networks with Transfer Learning. Akbari and Emadi [19] proposed imaging with nano-particles through neural networks molecular technology with FPCNN feedback pulses. Using previous imaging algorithms, they achieved a higher-level imaging which is very helpful for tumor diagnosis in images .Working on brain tumors in PET/MRI images, Harouni et al. [20] presented a fuzzy neural c-mean algorithm-based artificial neural network of PNFCM. Their purpose was segmenting tumor, white matter, gray matter and skull based on MRI features. Chattopadhyay and Maitra [21] used symmetrical analysis of brain images computed the ratio of tumors in right and left hemispheres and segmented growing region with labeling components connected to the diagnosis area. They attempted to distinguish brain from neck skin, bone and ventricle as well as distinguish brain regions from head skin and tumor tissue pathology from natural tissue in brain MRI images [22]. Bauer et al. [23] studied brain tumor extracted by MRI using mathematical image reconstruction. In this regard, they achieved a support

vector machine to compute tumors growing region in cancer growth trend. Sharma and Meghrajani [24] have used support vector machine for localizing cancer tumor growing region. Their study's unique feature was automatically combining divide the area of tumor and then, tumor contour based purification. The important feature of their work was using fuzzy patterns to diagnose and purify tumor area and its growth areas. Eberlin et al. [25] worked on brain tumor classifying in human. They classified various tissue groups in brain MRI images, including cerebrospinal fluid and white and gray matters. The outmost part of their study was organizer mapping and vector match. Sayed et al. [26] prposed combination of tissue segmentation and neural networks to diagnose brain tumor identificationis. They also achieved good results in TMRI identification brain tumor by changing gray surface of the image to a colored space image and image factor labeled by tumor clustering measure in order to identify the exact size of tumors and their area. Damodharan and Raghavan [27] investigated an algorithm comprised of the brain and segmentation of diagnosis measure of brain tumors. They computed tumor segmentation in 2D and 3D brain MRI images with different brightness level in tumor and non-tumor areas. Menze et al. [28] used learning and convolution algorithms to investigate imaging data analysis machine of MRI. They reported that it is possible to diagnose cancer tumors hidden in human brain mass in brain MRI images using deep learning and CNN-based prediction segmentation method. Kamnitsas et al. [29] investigated an algorithm comprised of the brain and segmentation of diagnosis measure of brain tumors. They computed tumor segmentation in 2D and 3D brain MRI images with different brightness level in tumor and non-tumor areas. Shenbagarajan et al. [30] studied deep learning and convolution algorithms to investigate imaging data analysis machine of MRI. They reported that it is possible to diagnose cancer tumors hidden in human brain mass in brain MRI images using deep learning and CNN-based prediction segmentation method. Chandra and Rao [31] proposed segmentation algorithm and area-based brain tumor segmentation method to classify cancer areas in brain to diagnose brain tumors. They used Livewire G-wire structural algorithm based on generalized multi-dimensional diagram formula. The feature of their method was exact segmentation of tumor areas even in noisy images. Havaei et al. [32] proposed a genetic algorithm-based method for brain tumor segmentation. In this study, they considered the number of genetic algorithm genes as a contain value. Then, the tumor susceptible areas identified by the algorithm were adjusted with learning training phase. After adjustment, the number of the algorithm genes changes and the previous stages were reiterated if tumor area was out of the identified area. Reiteration continues till reaching a favorable level of segmentation. The proposed method

has been tested on the images collected by Ishikawa [33] used a CNN- based method for brain tumor segmentation. In this study carried on MRI images with high and low grands, a new architecture of CNN has been employed for brain tumor identification and segmentation. In this architecture, the images are entered in parallel in 2 outputs to convolution filters. Under such conditions, the filters of on input have large size and the filters of the second input have small size. In the second stage, pooling operations is done on the images filtered by large filters to double the images of this input with the size of the second input images. In the next stage, the filtered images are integrated with a maximum rule to generate the single and final image and enter into fully connected neural network.

2. MARKOV RANDOM FIELD

One of the issues that is highly considered in machine vision and pattern identification and can be formalized is discrete labelling, and most problems can be stated in the form of discrete MRF. As a result, optimization problems in MRF are critical and have received considerable attention from researchers in recent years [34]. In other words, MRF optimization can be stated as follows: V objects exist in the problem space. In other words, these objects are the graph G's heads. The edges of this graph shown by indicate the relationship between these objects or graph heads. In this problem, a set of discrete labels also given. The main purpose is to consider a label for each objective or V graph heads. If x_p which is a label is given to object p (x_p a label belonged to object p), a cost based on potential function $c_\mathrm{p}(x_p)$ should be paid. In other words, when x_p label is selected on the object p, single cost should be paid based on the potential function of $c_\mathrm{p}(x_p)$. While if two related and dependent objects of p and q are given the labels of x_p، x_q, respectively. Another cost should be paid which is shown by binary cost function of d($x_p.x_q$). Notably, two single and binary cost functions of $c_\mathrm{p}(x_p)$، d($x_p.x_q$) are of the specified conditions of the problem and are considered as input. The main purpose is to select labels such that the leas cost is paid. According to the aforementioned, labelling should be performed such that the total of MRF potentials are minimized or MRF energy is minimized. That is, the purpose of problem solving is to minimize Equation (1):

$$E = \arg\min \sum_{p\in\cup} c_p(x_p) + \sum_{(p.q)\in\varSigma} w_{pq} d(x_p.x_q) \quad (1)$$

In Equation (1), a w_{pq} weight is considered for each binary cost function of $d(x_p.x_q)$. This weight is applied for scaling (high or low) the binary potential functions for each edge. With respect to the popularity of MRFs, it seems that MRF optimization problems is a vital issue. In

this regard, researchers have had many attempts for their optimization. This problem has not been so important up to now since all MRFs have been considered by convex energy functions. Now, if MRFs energy functions are not convex and their number of local minimums is high, their optimization is very hard. The main reason of MRF hard optimization is the convex characteristic of MRF related functions [35]. It should be noted that most of the functions considered in this study for optimization and minimization are also non-convex; therefore, it is hard to optimize them. Notably, the hardy and complexity of MRF optimization problem does not depend on single functions of $c_p(x_p)$. In other words, the main hardy in optimization is on binary functions of $d(x_p.x_q)$ such that each function of $d(x_p.x_q)$ is a sub-unit. MRFs can be optimized in multi-phrase time functions. For example, an overall optimizer is computed [36]. More simply, if each binary potential function of $d(x_p.x_q)$ is considered only a distance function (distance measure), optimization problem will be very hard. If a distance measure is considered for $d(x_p.x_q)$, NP optimization problem will be hard. If there is no primary assumption for $d(x_p.x_q)$ functions, there is no guarantee and only one local min can be given in output [18]. In MRF algorithm optimization, it is aimed to control MRF energies as much as possible and create an approximately optimal solution. As shown in Figure 1, vertical axis indicates the complexity of MRF problem and horizontal axis indicates binary function of MRF. Further, the complexity and hardness have been shown based on the considered function. Ideally, it is sought to select a global function for optimizing $d(x_p.x_q)$. That is, moving toward right side reaches to better choices on the horizontal axis and of course, its ability to propose an optimal solution is maintained. In other words, rapid responses are reached in the lowest possible point. Optimization problem and the algorithm presented should be big enough on the horizontal axis; that is, MRF in more general functions of $d(x_p.x_q)$ should be presented. In other words, the employed binary functions of $d(x_p.x_q)$ should be generalizable as much as possible while it should be placed in the lowest point in the vertical axis. The optimum state is to move under the dotted line as shown in Figure 1. The aim of this research is to make a binary cost function of $d(x_p.x_q)$ such that it is arbitrary, generalizable and is not in local minimums as much as possible and finally, overall minimums are appeared in output.

3.PROPOSED METHOD

The proposed method for tumor segmentation in FLAIR images without Tu-Deg-FPD is based on fast PD
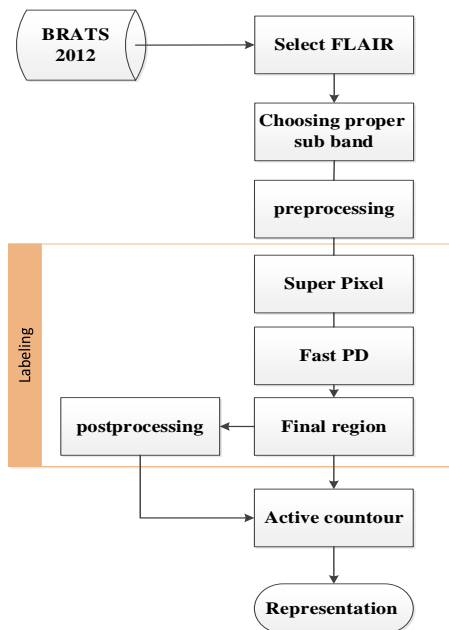
Figure 1. The block diagram of Tu-Seg-FPD

optimization for Markov random fields. After selecting the appropriate processing band with 3D Slicer 4.8.1 Software, the selected image is entered into the fast PD algorithm via appropriate pre-processors such as high-pass filters to optimize random fields. Figure 1 depicts the proposed method's block diagram. The database used in this research is BRATS2012. This database has 10 LGG (low graid glioma) patients. In LGG type brain tumor patients, the tumor is going through its hidden growth period and sometimes it can cause superficial paralysis in people. Also, there are 20 high graid gliuma HGG patients in this database, which usually results from the transformation of a LGG.

3. 1. Pre-processing   A Butterworth low-pass filter was used during pre-processing. High-frequency portions of the image, such as the edges and corners, are sharpened by this filter, making it easier to discriminate between the tumor and other parts of the brain.

3. 2. Fast PD Algorithm   The idea of discrete MRF can be defined as segmentation with the concept of labeling pixels. In Markov random fields, choosing labels with the lowest possible cost or with the smallest possible cost function is the main objective. According to the aforementioned, labeling should be carried out in a way that minimizes the total MRF potentials or the MRF energy.According to the aforementioned, labeling should be performed in a manner that minimizes the total MRF potentials or the MRF energy. Primal dual optimization is presented as a new fast PD method by to improve MRF. It is comparable to an expansion approach that ends with a set of graphs. In this method, MRF efficiency

is significantly increased. In the method, the generalized relations between the number of paths and gaps of primal-dual allocated by primal MRF its and dual are proved. Fast PD, in fact, is a combined optimization problem and has a high efficiency with respect to the importance of computational efficacy in machine vision applications (due to the nature of MRF in segmentation). In spite of the high efficacy, fast PD also minimize MRF energy considerably. In general, the main purpose of fast PD algorithm is to present a solution for MRF problem optimization. Figure 2 shows fast PD algorithm with its inputs.

To employ fast PD algorithm for segmentation, there is a need of regulating its parameters. These parameters have been identified based on the number of considered areas segmentation, label weight, the weight of edges among the labelled nodes and distance measure (metric measure is considered). Figure 3 shows the output of the algorithm.

After labelling Markov random fields by fast PD algorithm in a fully optimal manner, they should be changed into binary images in one stage to use active contour algorithm. In this stage, white areas of brain membrane are identified as tumor if the proposed pre-processing does not perform on the algorithm. This important fact highly appears in Low Grade Gliomas
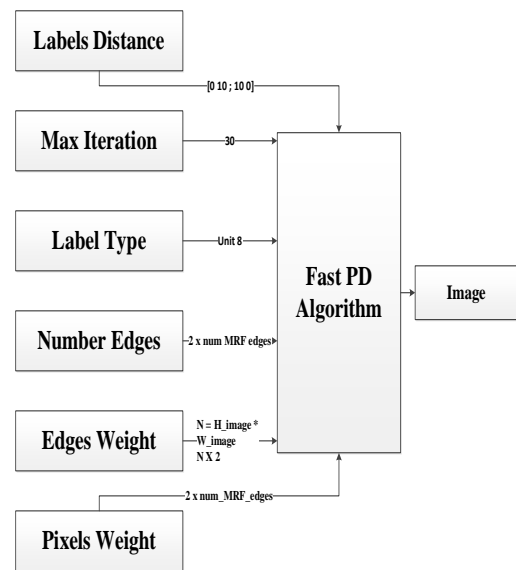

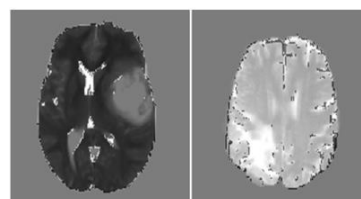**Figure 2.** Fast PD Algorithm

Figure 3. An Example of fast PD Algorithm outputs

(LGG) images. Low Grade Gliomas are brain tumors that originate from glial cells, which support and nourish neurons in the brain. Figure 4 shows an example of these outputs. Figure 5 shows most of areas existing in the image including brain tissue and skull. To complete pre-processing process through applying fast PD algorithm, pre-processing at one stage is performed through morphological functions. The employed pre-processing process is erosion and non-tumor areas are removed after using the method. Figure 5 shows the results obtained by pre-processing process.

4. RESULT ANALYSIS

The applied purpose of implementing the proposed Tu-Seg-FDP is to exactly identify the brain tumor tissue in Flair-MRI images. The proposed method is based on MRF random fields optimization through fast PD algorithm. To segment tumor area and depict it, active contour-based method has been used. In the following, the obtained results are discussed.

4. 1. Database   In this study, BRATS2012 database has been used [20]. In this study, only FIAIR images have been used to test the proposed algorithm. FIAIR images have been used due to high resolution of tumor area in white areas of the brain. These areas are identified as tumor areas by most of algorithms. FIAIR images in BRATS2012 database has a size of 240*240 and a spectrum of 155. In fact, these images are read by the software before using MATLAB Software in different formats.
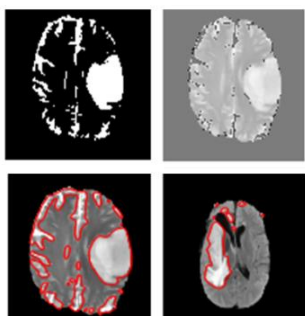

Figure 4. The output of tumor segmentation and identification without pre-processing with binary images after applying fast PD algorithm
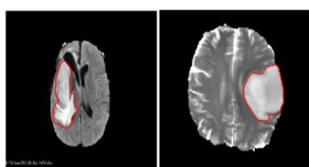

Figure 5. Segmentation output after pre-processing

4. 2. Analysis of Distance Measure   With respect to the aforementioned discussion, the best function in distance measures id metric and distance functions. However, regarding segmentation, the obtained results revealed that fixed distance has the best outcome. In other words, segmentation by fixed distance measure has better results. Figure 6 shows the results obtained by identifying tumor in different distance states. As shown in the figure, when the fixed distance and $d = 1000I_2$, there is no identification. According to the obtained results, the best state is $d = 10I_2$.

4. 3. Analysis of Kernel Dimension   Morphological operators were used to remove the white area of the brain membrane after segmentation in the fast PD algorithm in MRF. Operators are disappearing. The size and type of erosion operators window are critical. In terms of the importance of the tumor issue and the area that needs to be filled, the best type of window is a square window.

The white areas of the brain membrane are typically smaller in size than the tumor area, and this is true for LGG and HGG tumor images. Figure 7 depicts an HGG image with kernel sizes 7 and 11. As illustrated in Figure 8, the kernel size of 7*7 produced the best results.

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4. 4. Analysis of Energy in Active Contour   The main goal of active contour is to minimize and reduce energy of edge detection. The primary framework in this
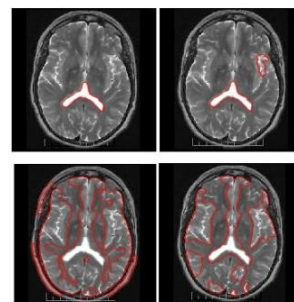

Figure 6. The results obtained by applying different distance functions in different distance states of a. $10I_2$, b. $100I_2$, c. $1000I_2$, d. $10000I_2$
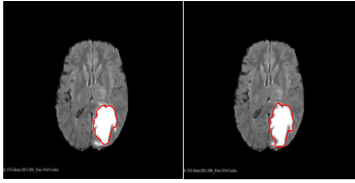
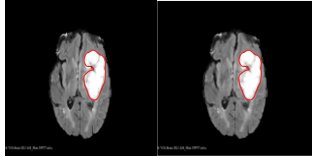**Figure 7.** The HGG images with two values of 0.15 and 0.20

Figure 8. The HGG image with the kernel size of 7*7

algorithm is a narrow line. This line is drawn around the considered area in the image using a specific function, namely the energy function. By reducing the energy amount in the function, the narrow line depicted on the image under processing approaches the edges of the considered areas in the image. The closer the narrow line gets to the area being processed, the less energy function there will be. This trend continues till the line is inserted on the considered area edges. This parameter can be intangibly perceived by hanging the weight of P function variable manually used for the energy such that tumor borders are displaced significantly. Notably, in HGG images with higher weighting values, better results have been obtained. While, in LGG images, the weight should be small as much as possible. After various experiments, the best P value for HGG and LGG have been reported 0.15 and 0.05, respectively. Figure 8 shows HGG images with two values of 0.15 and 0.20.

4. 5. Quantitative Analysis F1-measure measure has been employed to analyze and prove the proposed method. This measure is obtained by Equation (2) [37].

$$F1\_Measure = \frac{2*TN}{2*TP+FP+FN} \qquad (2)$$

In Equation (2), TP is a tumor and tumor has been identified. FN is a tumor and tumor has not been identified. FP is not a tumor and tumor has been identified. TN is not a tumor and tumor has not been identified.

4. 6. Accuracy and Sensitivity In accuracy test of algorithm, the proposed algorithm is analyzed by two measures of accuracy and sensitivity. The accuracy and sensitivity are computed by the parameters shown in Table 1. The accuracy and sensitivity index are formulated in Equations (3) and (4), respectively [38].

$$accuracy = \frac{TP+TN}{TP+FN+FP+TN} \ 100\% \qquad (3)$$

$$Sensitivity = recall = \frac{TP}{TP+FN} \times 100\% \qquad (4)$$

Tabel 1, shows the result of proposed method for brain tumor segmentaion. F1-measure, accuracy and sensitivity for 30 FLAIR image of BRATS2012 dataset were segmented. Also mean, standard deviation STD and confidence interval of measured value are represnted.

TABLE 1. The algorithm accuracy analysis

No.	Accuracy(%)	Sensitivity(%)	F1(%)
1	85.11	89.00	87.01
2	97.53	88.35	92.71
3	83.38	90.31	86.71
4	85.31	92.23	88.64
5	91.59	85.11	88.23
6	92.31	81.83	86.75
7	87.33	89.17	88.24
8	95.43	78.35	86.05
9	89.11	84.48	86.73
10	88.18	83.03	85.53
11	95..31	93.14	94.21
12	88.81	88.73	88.77
13	89.58	89.30	89.44
14	97.96	90.18	93.91
15	85.43	78.18	81.64
16	78.93	77.83	78.38
17	79.81	82.14	80.96
18	88.88	92.14	90.48
19	77.63	83.69	80.55
20	73.54	79.14	76.24
21	93.91	89.34	91.57
22	93.42	89.34	91.33
23	84.10	87.14	85.59
24	87.43	90.14	88.76
25	81.34	82.50	81.92
26	87.16	82.60	84.82
27	85.31	90.86	88.00
28	83.35	83.65	83.50
29	80.77	84.14	82.42
30	84.11	80.50	82.27
mean	86.59	88.57	86.37
STD	4.589	4.624	4.61
Confidence interval	[86.63 92.5]	[84.47 93.87]	[83.52 94.00]

The best accuracy value is 97.96 while the mean is 86.59. the STD and confidence interval for accurcay claim the results are acceptable. Also in F1-measure and Sensitivity mean values are 88.87 and 86.37, respectively. The same as accuracy STD and confidence interval of these criteria shows that the results are proper and also acceptable.

5. CONCLUSION

The purpose of the present study was to improve the accuracy of brain tumor segmentation in magnetic resonance imaging. The proposed method was based on markov random field and fast primal dual optimization algorithm. The FLAIR image in BRATS2012 MRI dataset were used for evaluating the segmentation results. In the proposed method first the imgae is clusterd using super pixel algorithm forr finding the ealy region and edges of tumor, then fast PD algorithms used for optimizing the Markov random fields to find the edge of tumor area in FLAIR images. In the proposed method post-processing stage add to final stage for improve tumor edge displayed in active contour algorithm. Various tests were carried on the proposed method. Qualitative evaluation shows the edge of tumor in proposed method are fined accurately. Also quantitative measures such as F1-measure, accuracy and sensitivity were used to evaluate and claim the Qualitative evaluation. Quantitative results fr 30 images of data set shows the superiority of proposed markov random field and fast primal dual optimization for segmetation.

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Persian Abstract

چکیده

تومورهای مغزی یکی از شایع ترین علل مرگ و میر هستند که به طور گسترده توسط محققان در زمینه های تحقیقاتی از جمله مراقبت و پیشگیری مورد بررسی قرار گرفته است. علیرغم مطالعات تجربی مختلف بر روی قطعه بندی تومور مغزی، هنوز نیاز به تحقیقات بیشتر وجود دارد. این واقعیت در روش های خودکار تشخیص تومورهای مغزی بیشتر مطرح است. در این مقاله، روش جدیدی برای بهبود دقت تقسیم‌بندی تومور مغزی بر اساس الگوریتم‌های سوپرپیکسل و پریمال دوگانه سریع (PD) ارائه شده است. روش پیشنهادی بافت تومور مغز را در تصویربرداری Flair-MRI در مجموعه داده BRATS2012 شبیه سازی شده است. این روش مرزهای اولیه تومورها را با استفاده از یک الگوریتم سوپرپیکسل شناسایی می‌کند و با استفاده از PD سریع در بهینه‌سازی میدان تصادفی مارکوف، مرزهای تومور مغزی را بهبود می‌بخشد. سپس از فرآیندهای پس پردازش برای حذف نواحی سفید مغز استفاده شده و در نهایت از یک الگوریتم کانتور فعال برای نمایش ناحیه تومور استفاده شده است. آزمایش‌های مختلفی بر روی روش پیشنهادی انجام شده است و از معیارهای کمی و کیفی مانند اندازه‌گیری شباهت تاس، دقت و اندازه‌گیری F1 برای ارزیابی استفاده شده است. نتایج بدست‌آمده نشان‌دهنده کارایی روش پیشنهادی بود، به‌طوری که در دقت و حساسیت به ترتیب ۸٦/٥۹ و ۸۸/٥۷ درصد و F1-Measure 37/86 بدست آمدند.