BRAIN TUMOR DIVISION FOR MR BRAIN IMAGES UTILIZING ARTIFICIAL BEE COLONY WITH INTERVAL TYPE-II FUZZY STRATEGIES

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Annotation.

Exact prediction of brain tumors is imperative while getting to the discussion of medical image analysis, where accuracy in decision making is of central significance, and the issues are to be tended to forthwith. For over a decade, multitudinous medical imaging techniques utilizing machine learning and artificial intelligence have been declared. The current Research is planned to foster a calculation that fashions the functioning standards of Artificial Bee Colony (ABC) and Interval Type-II fuzzy logic system (IT2FLS) algorithm to outline the growth area, which has been incorporated by complex brain issues. The core of any restorative groupings to be achieved lies in the definitiveness of the oncologists, where the calculation introduced in this concentrate fundamentally use dynamic through mechanical mediation. The calculation proposed has flexibility in taking care of an extensive variety of picture successions accessible in the Whelps challenge datasets that have different degrees of obstructions, misfortunes and difficulties in distinguishing the deviant locales, and it gives better division results that have been subjectively approved and legitimized with measurements, like DOI, specificity and sensitivity. Expansion of the visual discernment for oncologists is the badge of this review, which thusly gives better knowledge and understanding in regards to the illness of the patient.

***Key words*:** Magnetic Resonance Imaging (MRI), Artificial Bee Colony (ABC), Interval Type-II fuzzy logic system (IT2FLS), Tumor segmentation

I. Introduction.

Gliomas are the brain tumors with the highest mortality rate and prevalence. These neoplasms can be graded into Low Grade Gliomas (LGG) and High Grade Gliomas (HGG), with the former being less aggressive and infiltrative than the latter. Even under treatment, patients do not survive on average more than 14 months after diagnosis. Current treatments include surgery, chemotherapy, radiotherapy, or a combination of them. MRI is especially useful to assess gliomas in clinical practice, since it is possible to acquire MRI sequences providing complementary information. The accurate segmentation of gliomas and its intratumoral structures is important not only for treatment planning, but also for follow-up evaluations. However, manual segmentation is time-consuming and subjected to inter- and intra-rater errors difficult to characterize. Thus, physicians usually use rough measures for evaluation. For these reasons, accurate semiautomatic or automatic methods are required. However, it is a challenging task, since the shape, structure, and location of these abnormalities are highly variable. Additionally, the tumor mass effect changes the arrangement of the surrounding normal tissues. Also, MRI images may present some problems, such as intensity inhomogeneity, or different intensity ranges among the same sequences and acquisition scanners. In brain tumor segmentation, I find several methods that explicitly

develop a parametric or non-parametric probabilistic model for the underlying data. These models usually include a likelihood function corresponding to the observations and a prior model. Being abnormalities, tumors can be segmented as outliers of normal tissue, subjected to shape and connectivity constrains. Other approaches rely on probabilistic atlases. In the case of brain tumors, the atlas must be estimated at segmentation time, because of the variable shape and location of the neoplasms.

Another class of methods learns a distribution directly from the data. Although a training stage can be a disadvantage, these methods can learn brain tumor patterns that do not follow a specific model. ABCs have been used to win several object recognition and biological image segmentation challenges. Since a ABC operates over patches using kernels, it has the advantages of taking context into account and being used with raw data. In the field of brain tumor segmentation, recent proposals also investigate the use of ABCs.

II. Literature survey.

Zikic et al. used a shallow ABC with two convolutional layers separated by max-pooling with stride 3, followed by one fully-connected (FC) layer and a softmax layer. Urban et al. evaluated the use of 3D filters, although the majority of authors opted for 2D filters. 3D filters can take advantage of the 3D nature of the images, but it increases the computational load. Some proposals evaluated two-pathway networks to allow one of the branches to receive bigger patches than the other, thus having a larger context view over the image. In addition to their two-pathway network, Havaei et al. built a cascade of two networks and performed a two-stage training, by training with balanced classes and then refining it with proportions near the originals. Lyksborg et al. use a binary ABC to identify the complete tumor. Then, a cellular automata smooths the segmentation, before a multiclass ABC discriminates the sub-regions of tumor. Rao et al. extracted patches in each plane of each voxel and trained a ABC in each MRI sequence; the outputs of the last FC layer with softmax of each ABC are concatenated and used to train a RF classifier. Dvoˇrak and Menze divided the ´ brain tumor regions segmentation tasks into binary sub-tasks and proposed structured predictions using a ABC as learning method. Patches of labels are clustered into a dictionary of label patches, and the ABC must predict the membership of the input to each of the clusters. In this paper, inspired by the groundbreaking work of Simonyan and Zisserman on deep ABCs, I investigate the potential of using deep architectures with small convolutional kernels for segmentation of gliomas in MRI images. Simonyan and Zisserman proposed the use of small 3×3 kernels to obtain deeper ABCs. With smaller kernels I can stack more convolutional layers, while having the same receptive field of bigger kernels. For instance, two 3×3 cascaded convolutional layers have the same effective receptive field of one 5×5 layer, but fewer weights.

In[1] Malignant gliomas are the most common and deadly brain tumors. Nevertheless, survival for patients with glioblastoma, the most aggressive gliomas, although individually variable, has improved from an average of 10 months to 14 months after diagnosis in the last 5 years due to improvements in the standard of care. Radiotherapy has been of key importance to the treatment of these lesions for decades, and the ability to focus the beam and tailor it to the irregular contours of brain tumors and minimize the dose to nearby critical structures with intensity-modulated or image-guided techniques has improved greatly. Temozolomide, an alkylation agent with simple oral administration and a favorable toxicity profile, is used in conjunction with and after radiotherapy. Newer surgical techniques, such as fluorescence-guided resection and neuro endoscopic approaches, have become important in the management of malignant gliomas. Furthermore, new discoveries are being made in basic and translational research, which are likely to improve this situation further in the next 10 years. These include agents that block 1 or more of the disordered tumor proliferation signaling pathways, and that overcome resistance to already existing treatments. Targeted therapies such as anti antigenic therapy with anti vascular endothelial growth factor antibodies (bevacizumab) are finding their way into clinical practice. Largescale research efforts are ongoing to provide a comprehensive understanding of all the genetic alterations and gene expression changes underlying gliomas formation. These have already refined the classification of glioblastoma into 4 distinct molecular

entities that may lead to different treatment regimens. The role of cancer stem-like cells is another area of active investigation. There is definite hope that by 2020, new cocktails of drugs will be available to target the key molecular pathways involved in gliomas and reduce their mortality and morbidity, a positive development for patients, their families, and medical professionals alike. In [2], have applied the method to three real datasets, representing different tumor shapes, locations, sizes, image intensity, and enhancement, as shown in Fig. 10. Tumor has a partially enhancing tumor that causes a large deformation of the normal structures. Tumor contains a large, partially enhancing tumor inside the brain stem. Tumor contains a low grade tumor which is not highlighted in the T1-enhanced channel. Two sets of segmentations are done manually by one human rater at different times. The first set of manual segmentations is considered to be the gold standard for validating the automatic segmentation method. We used the VALMET segmentation validation tool (Gerig et al., 2001) to generate five validation metrics. The volume overlap metric is the normalized voxel intersection count for the pair of segmentations, otherwise known as Jacquard's similarity coefficient (Jacquard, 1912). The other metrics are the maximum Hausdorff surface distance and the average surface distances (inside/negative, outside/positive, and absolute).

The overlap metrics are also high, with the exception of the Tumor segmentation. This is likely due to the small size of the tumor. The quantitative validation of the automatic segmentation method. The level of agreement based on surface distances is similar for all tumors. HoIver, the varying overlap values demonstrate that the overlap metric is sensitive to the size and complexity of the segmented objects. The level of agreement with the manual result for edema is lower than tumor. This is mainly due to the ambiguity in determining the edema boundary, especially the tumor-ede-ma boundary.

Magnetic resonance imaging (MRI) is the most important techniqu1e, in discovering the brain tumor. Brain tumor is an abnormal growth of cells in brain which affect the functioning of the brain. If I find the tumor in early stages, I can stop further growth of the tumor and proper treatment is undergone for the tumor. Brain is the main organ of the human central nervous system. A new combination technique based on the FCM (fuzzy cmean) and Support vector machine (SVM) for brain tumor classification is suggested. So, here I made an attempt for finding the tumor in brain MRI images. For preprocessing, used method like Gray scale contract, noise removal, thresholding etc. For clustering, I used the FCM clustering and the classification used the SVM classifier. Disadvantages are FCM gives result in expense of more number of iteration and Prediction efficiency is low.

III. Proposed methodology.

This system proposes a novel ABC-based method for segmentation of brain tumors in MRI images. I start by a pre-processing stage consisting of bias field correction, intensity and patch normalization. After that, during training, the number of training patches is artificially augmented by rotating the training patches, and using samples of HGG to augment the number of rare LGG classes. The ABC is built over convolutional layers with small 3×3 kernels to allow deeper architectures. The use of small kernels allows designing a deeper architecture, besides having a positive effect against over fitting, given the fewer number of weights in the network. In designing our method, I address the heterogeneity caused by multi-site multi-scanner acquisitions of MRI images using intensity normalization. I also investigated the use of intensity normalization as a pre-processing step, which though not common in ABC-based segmentation methods, proved together with data augmentation to be very effective for brain tumor segmentation in MRI images. The advantages of applying more non-linearities and being less prone to over fitting because small kernels have fewer weights than bigger kernels and Reduced the computation time and high accuracy.

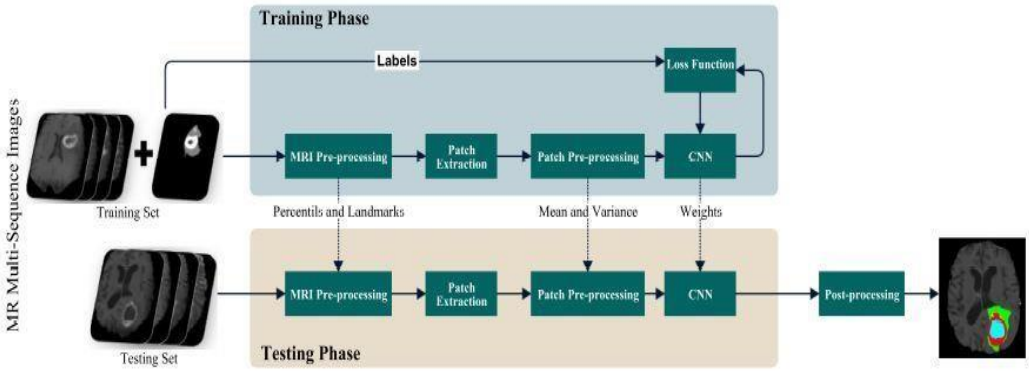

Fig.1. Block Diagram of Processed Methodology

Artificial Bee Colony (ABC)

ABC used to achieve some breakthrough results and win well-known contests. The application of Convolutional layers consists in convolving a signal or an image with kernels to obtain feature maps. So, a unit in a feature map is connected to the previous layer through the weights of the kernels. The weights of the kernels are adapted during the training phase by back propagation, in order to enhance certain characteristics of the input. Since the kernels are shared among all units of the same feature maps, Convolutional layers have fewer weights to train than dense FC layers, making ABC easier to train and less prone to over fitting. Moreover, since the same kernel is convolved over the entire image, the same feature is detected independently of the location translation invariance.

By using kernels, information of the neighborhood is taken into account, which is a useful source of context information. Usually, a nonlinear activation function is applied on the output of each neural unit. If I stack several Convolutional layers, the extracted features become more abstract with the increasing depth. The first layers enhance features such as edges, which are aggregated in the following layers as motifs, parts, or objects. The following concepts are important in the context of ABC:

V. Experimental results and discussion.

The efficiency of proposed ABC-IT2FLS techniques is evaluated using various datasets. The proposed algorithm was tested on the BRATS 2015, BRATS 2017 and BRATS 2018 data sets [3, 19 & 20]. Different sequences of skull-stripped MR brain images have been considered for validation. BRATS (2015) contains two subsets, tumor with high-grade gliomas (50 samples) and low-grade gliomas (50 samples), which have been considered. Similarly, for the BRATS (2017), high-grade (50 samples) and low-grade (50 samples) gliomas were considered for evaluation. In BRATS (2018), two subsets were used, one subset tumor with high-grade gliomas (50 samples) and another subset with low-grade gliomas (50 samples). The proposed algorithm was executed using the MATLAB tool on a system with an i5 processor (4 GHz) and 8 GB of RAM. Performance evaluation of the proposed ABC-IT2FLS algorithm with the related segmentation techniques was performed on different datasets.

The high-grade tumor segmentation of ABC-IT2FLS for the BRATS (2015) data set is visualized in Fig.2. The MRI slices of 50 different patients suffering from high-grade tumor were obtained from the BRATS (2015) data set. The segmentation results delivered by the proposed technique clearly show that the tumor present in multiple locations is identified effectually. The tumor and edema regions present in the input MR brain slices are segmented clearly by the proposed ABC-IT2FLS techniques. Finally, the segmentation results delivered by the proposed ABC-IT2FLS are compared with the ground truth images obtained from the BRATS (2015) data set to perform an effective validation. In particular, tumor with distinguished boundaries is presented using the proposed ABC-IT2FLS technique, and the same can be confirmed by observing Fig.3.

Table I

S. No	Parameters	Functioning of parameters
1	$R(x, y)$	Rosenbrock function
2	B_i	Initialization parameter for the objective function
3	α	Random number
4	B_n	New food/pixel resources
5	B_{ki}	Random chosen food source
6	$f_k(B_i)$	Fitness function
7	$Prob_m$	Onlooker bee probability
8	$f_k(B_m)$	The fitness function for the updated based on the previous and new positions
9	μ	Primary membership
10	$B_{n(low)}$	Low magnitude of pixel/food source
11	$B_{n(high)}$	High magnitude of pixel/food source
12	$\tilde{z}$	Fuzzy set
13	$hist(gr)$	Histogram
14	$\mu_U(gr)$	Membership value for upper limit
15	$\mu_L(gr)$	Membership value for lower limit
16	γ	Ultra- fuzziness determination
17	β	Pixel intensity modulated by weighted coefficient
18	C_i	Initial parameters of the lower bound

Parameters used in abc-it2fls

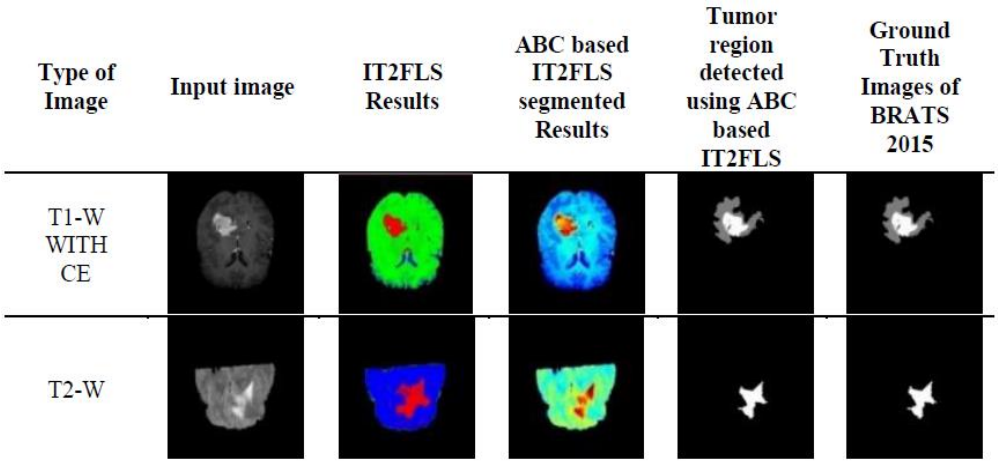

Fig. 2. Segmentation results (High-grade tumor) of ABC-IT2FLS for the BRATS (2015) data set

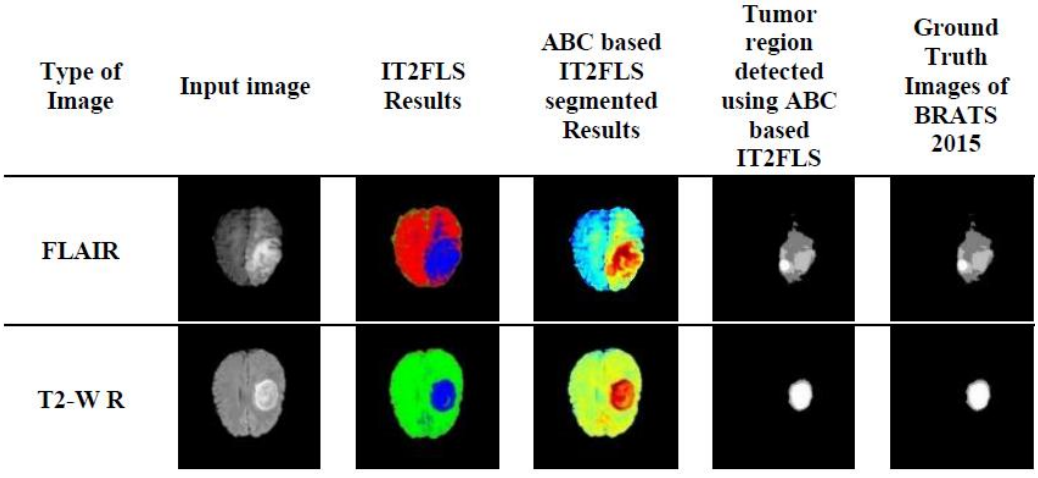

Fig. 3. Segmentation results (Low-grade tumor) of ABC-IT2FLS for the BRATS (2015) data set

The low-grade tumor segmentation results of ABC-IT2FLS for the BRATS (2015) data set are envisaged in Fig.3. The patients suffering from low-grade tumors (50 samples) are considered for efficiency testing. The ground truth image is compared with the segmentation results obtained

from ABC-IT2FLS for successful validation. Complex boundaries of tumor and edema regions in the MR brain slices are successfully segmented using the proposed ABC-IT2FLS.

Table II

Performance of the proposed abc-it2fls technique on the 2015 brats data set

Method	Dice Score (DOI)	Sensitivity	Similarity Index (SI)	Computational time in Seconds
ABC-IT2FLS	96±2.2	98±1.3	97±1.2	0.7±0.2
OMNET+CGA	88±1.2	89±1.2	88±1.4	1.1±0.2
OMNET	86±1.1	80±1.1	86±1.3	0.9±0.3
CCRFs Model	89±1.3	88±1.2	83±1.2	0.8±0.2
2PG-CNN	83±2.4	87±1.2	95±1.3	0.8±0.2
Hidden Markov Model (HMM)	91±1.4	93±1.3	68±1.3	0.9±0.4
Cuckoo-IT2FCM	56.6±1.1	93.2±1.2	91±1.3	7.6±1.1
BAT-IT2FCM	83±2.7	98±1.2	97.6±1.3	2.7±0.2
PSO-FCM	50.2±1.3	82±1.2	78±1.3	22±1.2
SOM	44.2±1.6	82±1.4	79±1.4	2.1±1.1

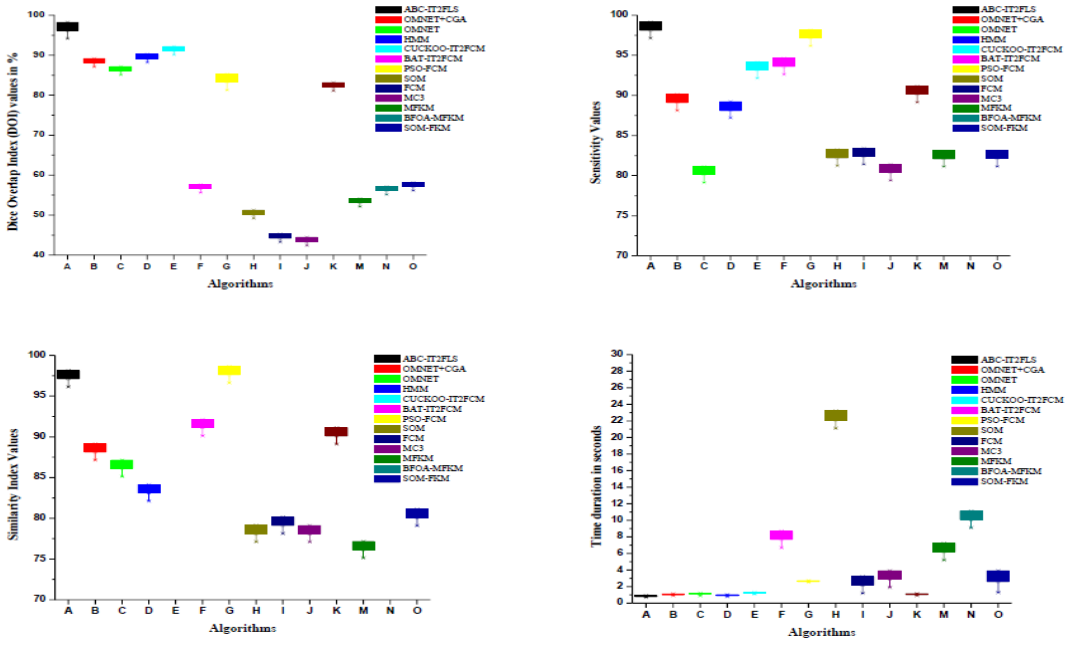

Fig.4. Performance comparison of ABC-IT2FLS on the BRATS 2015 data set

Furthermore, the BRATS 2018 Validation Set is used for checking the evaluation of the proposed ABC-IT2FLS technique. The results obtained through the proposed technique are compared with OMNET+CGA, CCRFs Model, 2PG-ABC, HMM, MC3, Cuckoo-IT2FCM, PSO-FCM, MFKM, BFOA-MFKM and SOM-FKM. The improved DOI value (97±2.3) obtained from the proposed techniques proves the more similar pixels are identified between the ground truth and demarcated image. The elapsed time (0.6±0.2 an average) required by the ABC-IT2FLS for performing high and low-grade segmentation in BRATS is much less compared to the related segmentation techniques. The sensitivity value deliberated through the ABC-IT2FLS is (99±0.4), which is much more impressive than the conventional technique. Adding IT2FLS with the ABC technique improves the performance and produces better segmentation results in the BRATS 2018 data set, as shown in Fig.5. The proposed technique is validated with the BRATS (2015, 2017 and

2018) data set. Different tumors with complex boundaries have been considered in different sequences. The suggested ABC-IT2FLS performs more accurately in delineating tumor and other regions in the MR brain images.

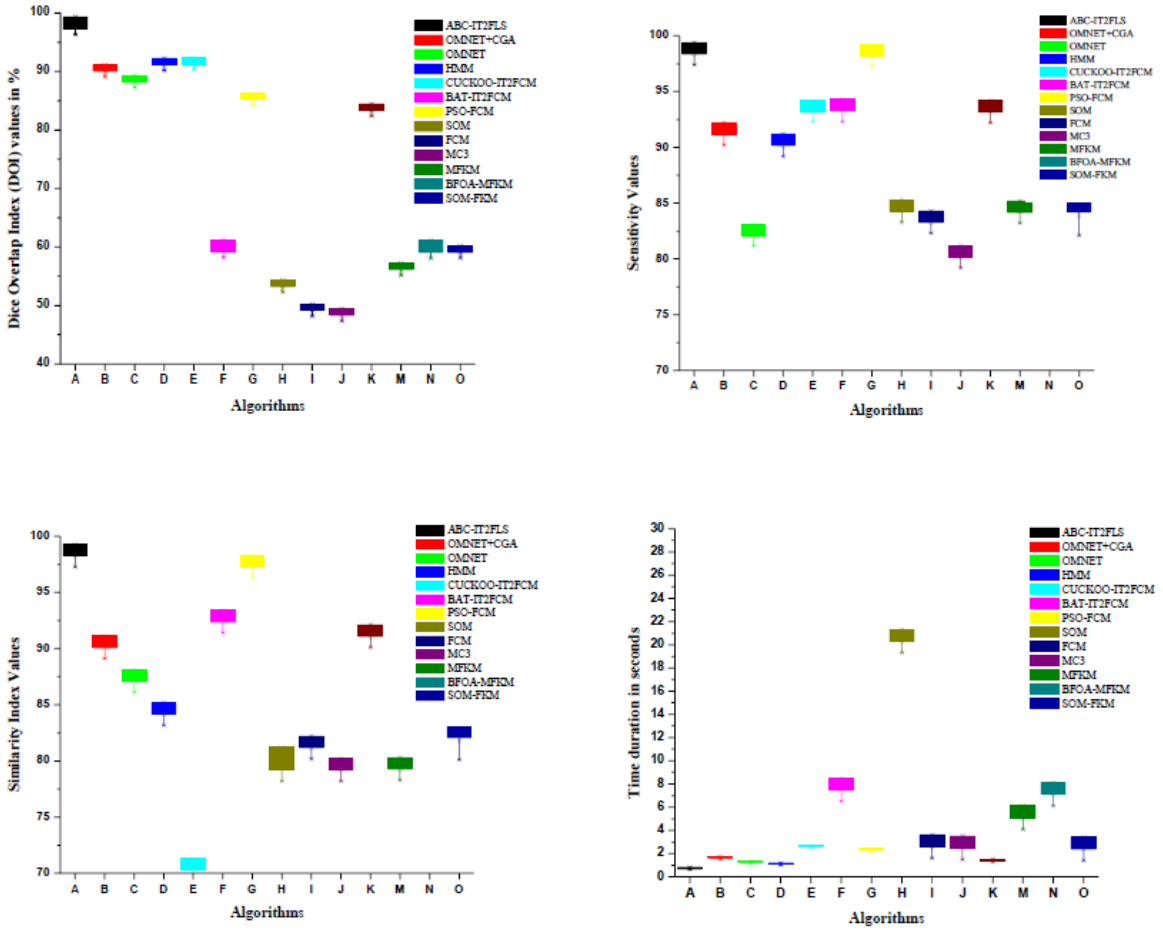

Fig.5. Performance comparison of ABC-IT2FLS on BRATS 2018 data set

VI. Conclusion.

I propose a novel ABC-based method for segmentation of brain tumors in MRI images. I start by a pre-processing stage consisting of bias field correction, intensity and patch normalization. After that, during training, the number of training patches is artificially augmented by rotating the training patches, and using samples of HGG to augment the number of rare LGG classes. The ABC is built over Convolutional layers with small 3 × 3 kernels to allow deeper architectures. In designing our method, I address the heterogeneity caused by multi-site multi-scanner acquisitions of MRI images using intensity normalization as proposed. I show that this is important in achieving a good segmentation. Brain tumors are highly variable in their spatial localization and structural composition, so I have investigated the use of data augmentation to cope with such variability. I studied augmenting our training data set by rotating the patches as well as by sampling from classes of HGG that were underrepresented in LGG. I found that data augmentation was also quite effective, although not thoroughly explored in Deep Learning methods for brain tumor segmentation. Also, I investigated the potential of deep architectures through small kernels by comparing our deep ABC with shallow architectures with larger filters. I found that shallow architectures presented a lower performance, even when using a larger number of feature maps. Finally, I verified that the activation function LReLU was more important than ReLU in effectively training our ABC. I evaluated the proposed method in BRATS 2013 and 2015 databases. Concerning 2013 database, I were ranked in the first position by the online evaluation platform. Also, it was obtained simultaneously the first position in DSC metric in the complete, core, and enhancing regions in the Challenge data set. Comparing with the best generative model,

I were able to reduce the computation time approximately by tenfold. Concerning the 2015 database, I obtained the second position among twelve contenders in the on-site challenge. I argue, therefore, that the components that were studied have potential to be incorporated in ABC based methods and that as a whole our method is a strong.

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