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Incipient anomalous detection in a brain using the IBIGP algorithm

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ABSTRACT

The detection of an incipient anomalous growth of tissue in a brain is often a difficult task. Various algorithms for brain anomalous detection have been suggested abundantly in the existing literature. In the last decade, many detection methods have been suggested to improve and facilitate abnormal tissue detection. However, the most attractive techniques to many researchers are maybe those that are magnetic resonance imagery (MRI)-based algorithms. A technique known as the inverse of the belonging individual Gaussian probability (IBIGP) is applied to MRI in this work in order to mitigate incipient anomalous tissue detection in a brain. This study demonstrates that the IBIGP technique, applied to the MRI image, is extremely effective in early detecting an anomalous change in the brain MRI image. Although this technique is still in its infancy, it has a great potential to enhance brain anomalous early detection.

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1. INTRODUCTION

The brain behavior can be altered by brain anomalous change (i.e. tumor). The latter detection in a brain from magnetic resonance imagery (MRI) is a challenging and very difficult task. Several different methods have been suggested intensively in the literature for detection of anomalous tissue such as tumors from MR images.

Classical machine learning algorithms formed the baseline for the initial automated detection system and the support vector machines (SVM) demonstrated strong capability with recent support for correctly classifying brain tumors of 86.80% accuracy [1]. The k-Nearest neighbors algorithm, particularly capable in the form of a new density-based adaptive-distance (DAkNN) developed and tested, has provided great opportunity with good results achieved and an average-dice score of 0.9082 for tumor region - segmentation accuracy [2]. An improved kernelized rough-fuzzy c-means (KRFCM) approach has been developed for segmenting brain tissue using MRI data, which aims to reduce noise and enhance segmentation precision [3]. Random forest classifiers also provided for effective classifiers with ensemble techniques [1], followed by the decision tree approach with different decision tree regressor and describe an interpretable classification path, and naive bayes classifiers also provided for successful results using a probabilistic method for 99.32% accuracy detection of CA x-ray stroke lesion [4]. Multi-layer perceptrons (MLP)', have had a lower performance of accuracy when compared to other approaches [1]. Unsupervised ideas, which would include deep learning approaches have changed the new landscape for medical imaging methods. How? For example, convolutional neural networks (CNNs) have been recently claimed as gold standard with well-developed multiple architectural sophistication demonstrating accuracies above 99.87% for brain tumor detection [5].

ResNet architectures have been particularly ranked as ResNet-50 with identification of capability to capture elaborate spatial hierarchies from brain MRI scan images with 90.04% accuracy [6]. VGG networks, most notably VGG-16, are state-of-the-art for detailed feature extraction and are often utilized in combination with other architectures, as part of a hybrid approach [7]. The U-Net architectures have changed the field with their ability to present exact tumor boundaries from medical image segmentation [8]. Moreover, autoencoders and variations of autoencoders, such as Variational Autoencoders (VAE), have offered exciting new avenues for unsupervised anomaly detection by constructing normal brain patterns, and detecting anomalies from that normal reconstructed representation [9]. EfficientNet architectures have also shown intelligent original combining extensive feature selections, with numbers reaching 99.51% overall accuracy [10]. DenseNet and other novel and modern architectures have proven that it is possible to raise the ceiling on classification capabilities [8]. Furthermore, there have even been more modern advances, such as Transformer (i.e. Transformers with attention) based learning models, although their use in the context of medical imaging and brain MRIs has only just started to be fully realized [11]. Here generation models such as generative adversarial networks (GANs), have begun to be implemented in data augmentation for tumor reconstruction and/or generation of synthetic training data [11]. A hybrid strategy has been used that combines a modified CNN architecture for accurate tumor classification and a U-Net based model for robust tumor segmentation [12]. Another potential area is in modeling temporal MRI scan sequences, via long short-term memory (LSTM) networks, which can prove to be important in the context of tracking disease progression [11]. Despite the many efforts to yield different algorithms to enhance the data synthesis, there is still a limitation that is underlying the traditional approach [13], [14].

Most methods tend to be either a scoring method, or they rely on large amounts of labeled datasets to train on, which means they are especially vulnerable when detecting early presence of difficult to see anomalies which have not conditioned any of the typical signatures that the useful algorithms have been trained [13], [14]. The complexity and variability of brain tumors makes early-stage detection inherently difficult as abnormal and normal tissues may resemble each other in the early stages [5], [15]. The medical consequences of delayed diagnosis are extensive and quantifiable. For example, when brain tumors are detected and are less than 3cm in diameter, rate of complete surgical removal (gross resection) nearly doubles from 35% to 65-80% [16]. More importantly, five-year survival rates for malignancy can increase 40-60% with earlier detection [16]. There was indeed, a significant recent screening study that found 4.1% of asymptomatic patients who underwent an MRI and had an abnormality that warranted immediate medical attention. This highlights the point that silent pathology often precedes clinical symptoms [16].

The challenge is not only the accuracy of detection. The pool of data in MRI imaging is becoming larger, and the load on radiologists is becoming greater, it will not be practical to conduct manual inspections of MRI data moving forward [1], [14]. Individual human interpretation and standardization creates variation that automated systems may be able to address [15]. And of course, for the pediatric and young adult age group, where over 17,600 people under the age of 39 are diagnosed with a brain tumor every year in the US, the various nonspecific symptoms will lead to delays in making the correct diagnosis [17], [18]. As part of this backdrop of computational innovation and clinical need is the inverse of the belonging individual Gaussian probability (IBIGP) algorithm option that is potentially not the same as the machine learning or deep learning options that rely on scoring system or classification boundaries, but instead is based on pure probabilistic reasoning instead. In summary, it takes an MRI image(s) and converts it into a probability space, called IBIGP images, with the potential of highlighting subtle anomalies that Traditional scoring/performance algorithms may miss altogether. As we stand on the cusp of continuing computational advancement and increasing clinical need, moving toward more sensitive detection tools is no longer simply a technical goal, but a humanitarian object of necessity [11], [13], [14]. Algorithms like IBIGP have the possibility to work with existing algorithms to improve the diagnosis population and hope for an earlier intervention, better patient results, and have lives saved by earlier detection. The objective of the detection, in this paper, is to pursue any changes that may be occurring because of the probable incipient abnormal tissue in a human brain and since there is little real-world medical image data with small tumors in it, we introduced tumor-like features artificially into brain images. The detection method procedures, proposed in this article, are almost the same as the proposed techniques in the literature. However, the difference of the IBIGP/MRI method is that the IBIGP is able to make the slightest change in a brain tissue clearly visible, thereby assisting in the detection of the incipient abnormal tissue as you will see below.

2. METHOD

First, we start by segmenting each normal MRI image matrix line into small and regular stationary intervals and model each of them by an adequate Gaussian white noise (GWN) [19], for each interval, we will calculate the mean and variance parameters; these parameters will represent each segment, allowing us

to achieve compression and save only the parameters instead of the whole image, Once the optimal GWNs for the whole matrix are estimated, we replace their parameters which are the means and variances to compute the individual probability of each interval value of the abnormal MRI image. By inversing these probabilities, we obtain the IBIP image of the abnormal MRI image. The IBIGP technique operates through two principal phases: modeling and detection.

2.1. Modeling phase

- Step 1: Segment each MRI image matrix X line into small enough stationary segments as shown in Figure 1 and the (1):

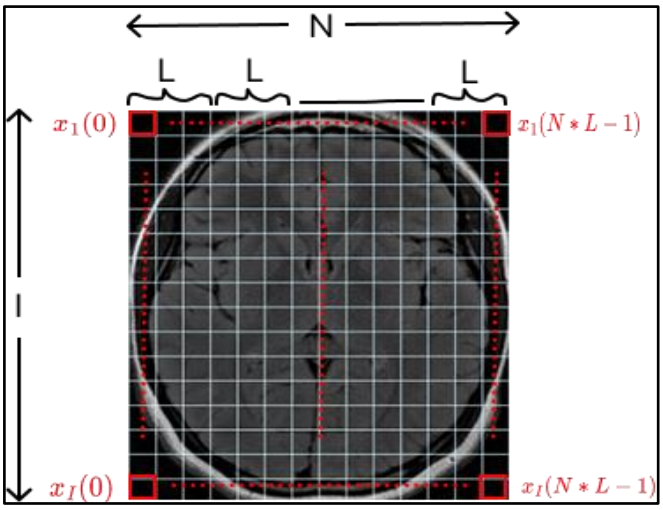


Figure 1. Segmentation of input normal brain image into L segments

$$X = \begin{bmatrix} \underbrace{x_1(0)x_1(1)\,x_1(L-1)}_{L\ samples} & \dots & \dots & \dots & x_1(N\cdot L-1) \\ x_2(0) & x_2(1)\dots & \dots & \dots & x_2(N\cdot L-1) \\ \vdots & \vdots & \vdots & \vdots & \vdots \\ x_I(0) & x_I(1)\dots & \dots & \dots & x_I(N\cdot L-1) \end{bmatrix} \quad (1)$$

- Step 2: Use (2) and (3) to estimate the parameters of each normal line interval in order to obtain an adequate mathematical model.

$$\hat{m}_{i,j} = \frac{1}{L}\sum_{n=(j-1)L}^{jL-1} x_i(n) \quad (2)$$

$$\hat{\sigma}^2_{i,j} = \frac{1}{L}\sum_{n=(j-1)L}^{jL-1}\left(x_i(n) - \hat{m}_{i,j}\right)^2 \quad (3)$$

where $\hat{m}_{i,j}$ and $\hat{\sigma}^2_{i,j}$ are the estimated average and variance of each interval j of each line i, $x_{i,j}(j-1)L, \dots, x_{i,j}(jL)$ are the values of the j^{th} $(j = 1,2, \dots, N)$ interval, L is the interval length and N is the number of segments in each line i.

- Step 3: The reconstruction of each normal GWN interval can be achieved using the built-in function "rand" (Scilab, Python, or MATLAB) to generate the GWN interval of L samples.
- Step 4: Gather these intervals in order to reconstruct the whole image model and check its quality by comparing the reconstructed image with its original. So, if the two images are reasonably the same, save these model parameters, else, reduce slowly the interval length and go back to step 2. Repeat the steps 2, 3, and 4 until achieving a mean square error (MSE) less than 0.01 corresponding to an acceptable reconstruction (Figure 2). Once the mathematical model is ready, compute the IBIGP of each segment of each normal image matrix line using the model parameters ($\hat{m}_{i,j}$, $\hat{\sigma}^2_{i,j}$) given by (2) and (3) above to obtain an IBIGP matrix (in 4).

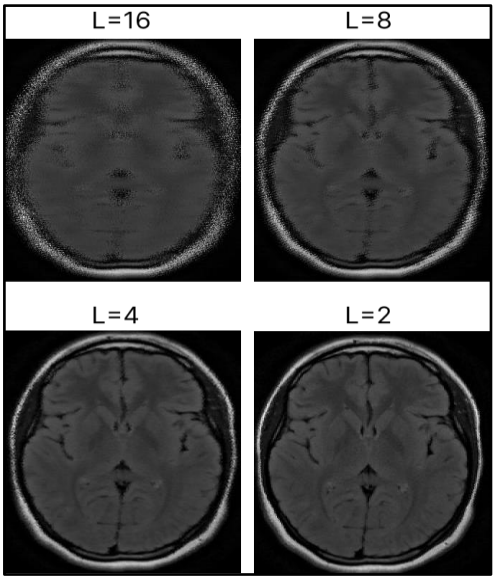


Figure 2. Modeling process of normal image with different segments length

2.2. Detection phase

Once an acceptable reconstruction is achieved, compute the inverse of the probability of each interval in the abnormal image using the normal interval GWN parameters ($\hat{m}_{i,j}$ and $\hat{\sigma}^2_{i,j}$) in (2) and (3) to obtain the following IBIGP matrix representation of the abnormal image.

$$\text{IBIP} = \begin{bmatrix} \frac{1}{\hat{p}_{11}} & \cdots & \frac{1}{\hat{p}_{1N}} \\ \vdots & \ddots & \vdots \\ \frac{1}{\hat{p}_{I1}} & \cdots & \frac{1}{\hat{p}_{IN}} \end{bmatrix} \tag{4}$$

It should be noted that the main idea of the IBIP algorithm is to consider any anomalous (change) in the brain MRI image as a rare event compared to the normal MRI image. Figure 3 illustrates this principle by comparing a standard Gaussian distribution with its inverse transformation. The Gaussian probability given by (5) below, to belong to the normal MRI, should be very small as indicated in Figure 3(a). So, by inversing the probabilities of the abnormal data, we obtain very big probability inverse values corresponding to rare events (anomalous) as illustrated in Figure 3(b). The basic idea of the IBIP algorithm is already described elsewhere [20], [21] and is reported in the following for more convenience. The individual gaussian probability of each sample n for each interval j in the i^{th} line is expressed as follows:

$$\hat{p}_{i,j}(n) = \frac{1}{\hat{\sigma}_{i,j}\sqrt{2\pi}} \exp\left[-\frac{\left(x_{i,j}(n)-\hat{m}_{i,j}\right)^2}{2\hat{\sigma}^2_{i,j}}\right] \tag{5}$$

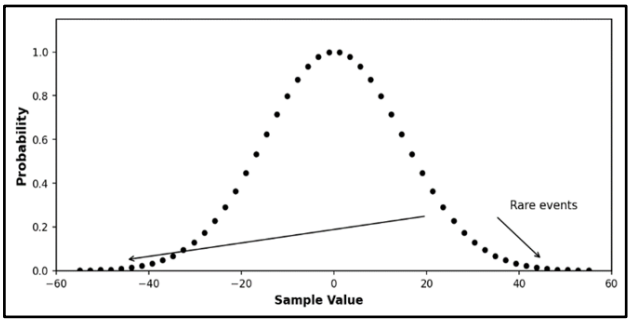
and its inverse is:

$$\frac{1}{\hat{p}_{i,j}(n)} = \hat{\sigma}_{i,j}\sqrt{2\pi} \exp\left[\frac{\left(x_{i,j}(n)-\hat{m}_{i,j}\right)^2}{2\hat{\sigma}^2_{i,j}}\right] \tag{6}$$

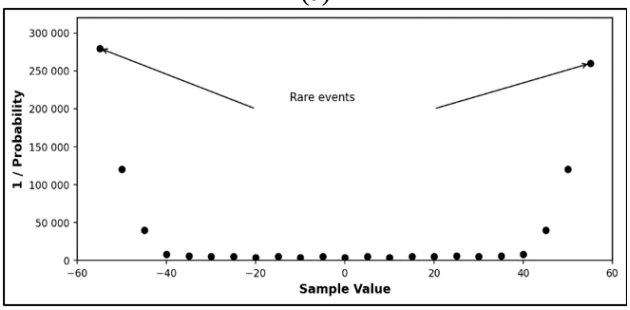
where $\hat{m}_{i,j}$ and $\hat{\sigma}^2_{i,j}$ are the estimated variance and average of each matrix line interval respectively. Since the Gaussian law is symmetrical with respect to the average, the rare events (pixels) corresponding to incipient abnormal tissues lie on both tails of the Gaussian law Figure 3(a). So, by inversing the probability of each pixel value of the image with early anomalous, the probability inverse (6) of these rare events will rise exponentially, whereas those belonging to the original image (normal) will remain equal to zero, as shown in Figure 3(b).

Figure 4 illustrates the complete flowchart of the IBIGP algorithm. The modeling phase (left panel) involves segmenting normal MRI images, estimating statistical parameters, and iteratively refining the

model. The detection phase (right panel) applies these parameters to abnormal images, computing inverse probabilities to highlight anomalies as bright spots in the output.



(a)



(b)

Figure 3. Illustration of the core IBIGP principle for enhancing rare event visibility (a) Gaussian law and (b) its corresponding modified inverse (IBIGP)

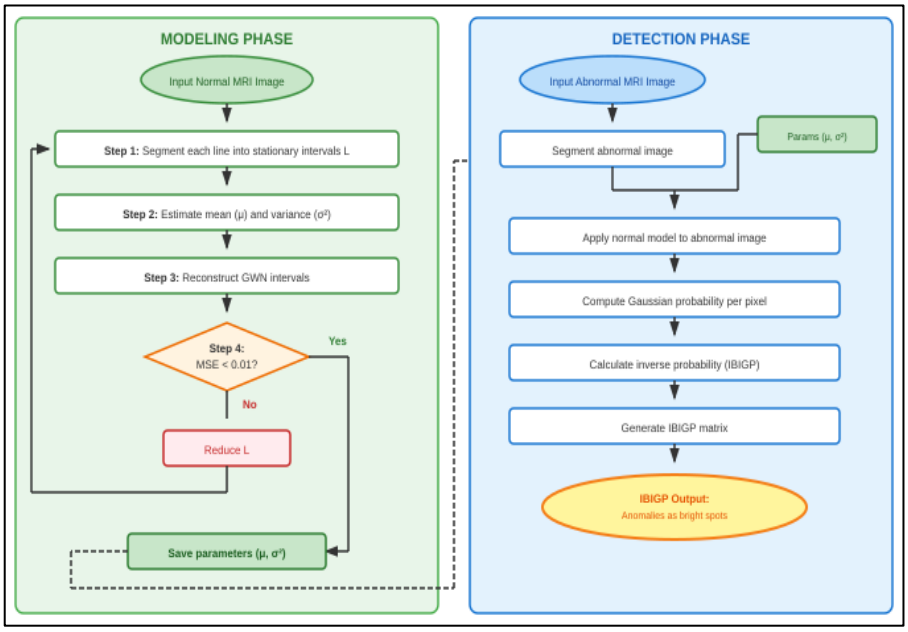
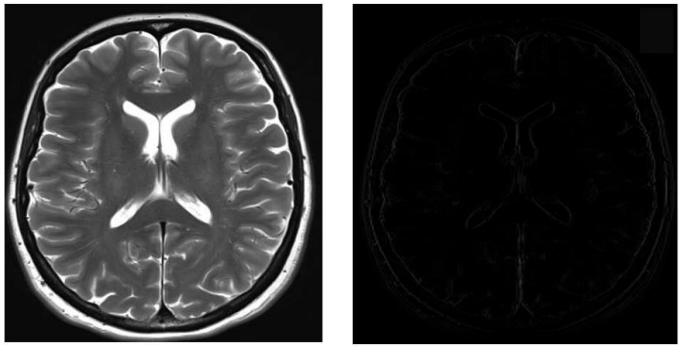


Figure 4. Flowchart of the IBIGP algorithm

3. RESULTS AND DISCUSSION

Figure 5 presents a baseline comparison between an original MRI scan and its IBIGP transformation for a healthy brain. Figure 5(a) indicates the reference brain MRI image at baseline prior to the visible development of tissue growth, whereas Figure 5(b) shows its corresponding IBIGP reference image.



(a) (b)

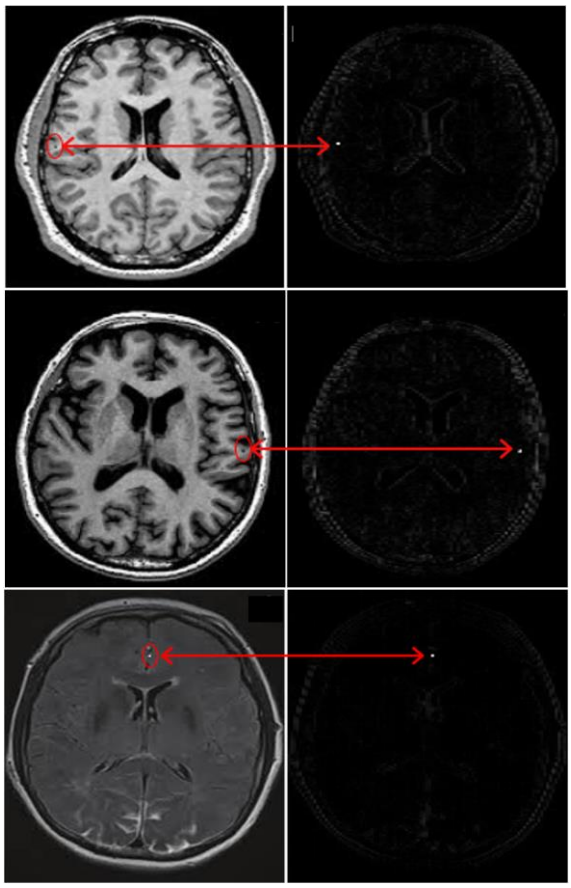
Figure 5. Baseline reference images for normal brain tissue (a) the MRI before any tissue growth and (b) its corresponding IBIGP image

Figure 6 illustrates the proposed IBIGP algorithm's effectiveness in increasing the visual detection of early changes in brain tissue. The original MRI is shown in Figure 6(a), and its corresponding IBIGP image is presented in Figure 6(b). The extracted Gaussian statistical features (the means and variances of stationary intervals along each of the rows in the matrix) were established or developed using the IBIGP algorithm. These statistical parameters represent the distribution for normal brain tissue and provide a reliable model of healthy behavior. When the model of normal brain tissue is applied to new images, it originates a means that allows us to consider how likely it is that each pixel value belongs to the "normal" distribution. The inverse probabilities computed using this model provide emphasis on regions of abnormality (highlighting) so that changes that are relatively small are made significantly more visible as shown in Figure 6(b). The original MRI image Figure 6(a) contains early stage tissue changes that have not gone unnoticed because there are changes that are visually indistinct and nearly impossible to perceive even by the naked eye with simple image processing functionalities. Again, these subtle spots can be overlooked entirely leading to the missed or delayed diagnosis. However, as shown in Figure 6(b), the model built with the IBIGP algorithm started to show a dramatic improvement in the highlights of the changes. The regions I have drawn arrows on, indicated the incipient paths physiological alterations related to brain pathology, where now significantly more visible. The improvement comes as a statistical suppression of "normal" regions, while enhancing the presence of deviations from the learned Gaussian model. The overall results strongly support that the IBIGP/MRI platform will provide value by routinely applying this comprehensive approach to real-world diagnostics, which will reveal changes in circulation and structure immediately, and with confidence so that any hidden abnormalities do not fester until more clinically problematic states establish. With a relatively low MSE (MSE < 0.01) associated with the model in reconstructing normal behavior each time it is used for each image, and high detection rates, it is evident that IBIGP is not simply an enhancement tool for visually depictive imaging, it is a statistical and evidence-based guide to decision making.

Compared to conventional supervised deep learning approaches, such as the fine-tuned EfficientNet architectures which have achieved high accuracy in brain tumor classification [22], the IBIGP algorithm demonstrates distinct advantages in the context of incipient anomaly detection. While supervised CNNs are robust when abundant labeled data is available, they often struggle to generalize to subtle or rare anomalies that deviate from the training distribution. To address the limitations of supervision, unsupervised generative models, specifically GANs and VAEs have been widely adopted for medical anomaly detection in brain MRI [23]. These methods, along with broader deep anomaly detection frameworks [24], typically identify abnormalities by learning the manifold of normal tissue and flagging deviations. However, they often require significant computational resources for training and inference. In parallel, classical statistical detectors like Local Outlier Factor (LOF) and Isolation Forests remain popular for their computational efficiency, but their performance can degrade on complex, high-dimensional imaging data, where subtle anomalies are embedded in rich texture patterns [25], While advanced deep learning segmentation models (e.g., U-Net variants) offer high precision, there is a growing need for efficient, low-resource alternatives for practical clinical deployment [12]. In this landscape, IBIGP occupies a unique niche: it operates on a probabilistic inversion principle that is computationally lighter than GAN-based methods while offering superior sensitivity to subtle, early-stage tissue changes compared to traditional statistical or supervised baselines.

Recognizing the continued importance of complementary statistical approaches, future research directions for this work include extending IBIGP to process three-dimensional MRI volumes, integrating it

with deep learning classifiers as an initial preprocessing step to enhance overall sensitivity to incipient changes, and validating the method using standardized benchmark datasets such as BraTS to enable comprehensive comparison with state-of-the-art anomaly detection methods



(a) (b)

Figure 6. Detection of incipient brain anomalies using the IBIGP algorithm across multiple patient cases (a) the MRI with incipient abnormal tissue growth and (b) its corresponding IBIGP image

4. CONCLUSION

We have applied the IBIGP technique to the brain MRI to enhance the detection of any incipient anomalous growth of a brain tissue. We have shown that the main strength of this technique is that it can exponentially magnify the MRI image spot intensity corresponding to the incipient change and reduce to zero those belonging to the original image before any change. It, thus, renders the incipient anomalous change much easier to detect. We have shown, in addition, one of the major advantages of the IBIGP/MRI technique is its ability to stock more data than the direct comparison between images. We believe, therefore, that the IBIGP/MRI technique has a great potential in enhancing the incipient abnormal tissue growth detection in human brain. is, therefore, a very promising technique for incipient anomalous change in a brain and can be considered as a crucial step towards a very important enhancement of incipient abnormal tissue growth detection in human brain.

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Benabdellah Yagoubi	✓	✓	✓		✓	✓		✓	✓	✓	✓	✓	✓	
Sidahmed Henni					✓		✓			✓	✓			

C : Conceptualization
M : Methodology
So : Software
Va : Validation
Fo : Formal analysis
I : Investigation
R : Resources
D : Data Curation
O : Writing - Original Draft
E : Writing - Review & Editing
Vi : Visualization
Su : Supervision
P : Project administration
Fu : Funding acquisition

CONFLICT OF INTEREST STATEMENT

Authors state no conflict of interest.

DATA AVAILABILITY

The data that support the findings of this study are available on request from the corresponding author, [M. N]. The data, which contain information that could compromise the privacy of research participants, are not publicly available due to certain restrictions.

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