Thermal Detection of Brain Tumors using Extreme Learning Machine

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Summary
Within the health care industry, detection of brain tumor is a challenging issue. The cells of tumorous tissues grow uncontrollably; nonetheless, several techniques are available to detect those cells. This paper advances an innovative method for detecting tumorous cells using their thermal behavior. It advances a design to develop a fully automatic structure for brain tumor detection in Magnetic Resonance Imaging with good segmentation accuracy.
Regular metabolic activities of human beings are reflected in body temperature, indicating their physical condition. Brain tumor cells produce more heat than normal cells, and hence, it is more apt to use the bio-heat equation to exploit the thermal activities of the brain. The current scrutiny is performed in three steps. First, segmentation is applied to extract a region of interest using the Fast Bounding Box algorithm. Second, Cattaneo bio-heat equation is used to generate bio-heat distribution model of the living tissues on the region of interest. The generated bio-heat distribution model is used to analyze thermal diffusivity in living tissues numerically. Third, Extreme Learning Machine is then applied to the bio-heat distribution model to determine the size and location of tumorous tissues with more accuracy and efficiency. The proposed framework is implemented using MATLAB on the Multimodal BRATS database.

Key words:
Magnetic Resonance Imaging, Cattaneo bio-heat equation, Fast Bounding Box Algorithm, Extreme Learning Machine, BRATS database.

1. Introduction

Brain tumors affect people belonging to all age groups. A tumor is an unwanted growth of abnormal cells. This abnormal growth of cells is categorized into two types. In other words, a brain tumor is of two types – benign and malignant. Benign tumor cells will grow faster when compared with malignant tumors.
Further, malignant tumors tend to expand into surrounding tissues rapidly. A deadly malady that results in high mortality rates, brain tumor requires an automated tool for early diagnosis using image-based techniques enabling the doctors to proceed into further treatment. Several analyses have been done on brain Magnetic resonance imaging (MRI) images for interpreting their relevant features for the diagnosis of malignant tissues of brain tumor. MRI provides high spatial resolution and soft tissue diagnosis. The main reason for the brain tumor is the unrestricted increase in the cells and their rapid growth. Such unnoticeable growth may cause brain damage or even death. The detection of a brain tumor depends upon the size and position of the tissue, as well as whether it is malignant or benign.
Brain tumors are generally categorized into meningiomas and gliomas tumor types. Presence of meningioma is clearly and easily distinguishable in the medical images. On the other hand, the features of gliomas are not easily distinguishable since they have the capacity of spreading and mixing with normal tissues. The present study focuses on the detection of meningioma tissues of brain tumor.
Techniques of imaging like X-Ray, CT scan, and MRI are widely employed by medical practitioners to identify the symptoms of brain tumor. Additionally, imaging techniques that are functional like SPECT scan, PET scan, and functional MRI are also made use of for malignancy detection, identification, analysis, and subsequent treatment.
Segmentation of region of interest from brain MRI containing tumorous tissues such as edema and dead cells and after that, the process of classification of such tissues play a vital role in the detection of the affected portion. With the advances in imaging techniques, doctors require sophisticated and automated quantitative image analysis tools that can guide them in the diagnosis of changes in the shape of malignant tissues of the brain. Fast Bounding Box (FBB) method is worn to fragment the ROI in bounding box algorithm. It considers the similarity and dissimilarity of gray level intensity histograms of symmetrical regions.
Human metabolism is directly connected with the body temperature. Cattaneo bio-heat equation generates a thermal diffusive model on living tissues. And this could accurately estimate the size and location of tumorous tissues.
Extreme Machine Learning (EML) is a widely used machine learning algorithm to classify living tissues into normal and meningiomas tissues. It employs Run-length Matrix for texture features based methods. Co-occurrence Matrix and Intensity, Euclidean distance, Gradient vector,

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and neighborhood statistics are used for classification. It is provided with a fast learning phase for large databases.
The remainder of this analysis is structured in the following manner: the next section undertakes a review of existing literature in the area of study. The literature review is trailed by an overview of the data and methods employed hereof. Experimental outcomes follow the overview. Conclusion forms the last part of the paper.

2. Review of Related Work

There exist numerous automated tools for tumor detection. Fuzzy based algorithm [1] classifies normal tissues against tumorous tissues with a precision of 95%. Self-Organizing Map [2] with a Neural Network based method that measures Tanimoto index (TI) in the brain tumor diagnosis has produced 80% accuracy. Another approach [3] based on active contours for segmentation of the tumor portion of the brain has been accurate with F-measure of 90%.
Skull stripping is an intra-cranial segmentation method which is used for finding the subdivision of brain tissue from the skull. Input magnetic resonance imaging also helps in distinguishing non-brain tissues within the cranium of the brain. It creates whole similarity mask and detects abnormality with good accuracy [4].
The tool using Extreme Learning Machine (ELM) [5] classifies the tumorous tissues accurately. Statistical value-based methods [6] are also available to detect the existence of tumor tissues in the brain. These methods use the intensity values to compute abnormality mean and compare these against the original values to identify the portion containing abnormality.
To evaluate the proposed work, the whole brain image dataset, BRATS 2012 that contains image sets of MRI brain images extracted from MRI head scans [7] are used. Feature extraction plays a vital step in the classification process. Texture-based features have to be extracted to know the granularity and iterative patterns of pixel distribution. This could be done by identifying the local description of the neighborhood with respect to the global, which can be formed as co-occurrence matrix of brain MRI tissues using gray level co-occurrence matrix (GLCM) process [8].
Another efficient system has been introduced with techniques such as PCA, KLD, entropy metrics, and boosting for feature-based techniques. To segment posterior-fossa tumor, features such as texture, intensity, and shape [9] are taken into account. This work has been verified with a set of 10 pediatric patients, constituting a total of 249 real MRI images.
An automated and localized framework [10] for brain tumor detection uses magnetic resonance imaging. Machine learning classification tools are introduced for increasing classification efficiency. There exists another method using a feedback mechanism [11] with a diverse density algorithm. This method produces good performance metric of content-based medical picture repossession. Another study uses soft computing technique [12] to retrieve brain image. This method used the shape features of 2-D Zernike moments. Outliers are removed using Fuzzy Expectation Maximization Algorithm. Still, researches are going on for finding the efficient and accurate method of detecting brain tumors.

3. Data and Methods

This section discussed the BRATS 2017 Database, Methodology, Preprocessing, Segmentation, Thermal Diffusion, Feature Extraction, and ELM Classifier.

3.1 Dataset – BRATS 2017 Database

BRATS 2017 has been employed widely in pre-surgery tomography scans. Here the focus is on segmenting heterogeneous neoplasm tissue that supports look, form, and microscopic anatomy. This information conjointly concentrates on predicting the total survival of the patient, through integrative analyses of radiomic choices and ML algorithms. The 2017 version of BRATS coaching database consists of 274 multi-modality tomography scans. Analysis can be done by resorting to the web analysis tool. The tool offers results along the lines for the three major neoplasm regions, namely whole, core, and active. Here, it has to be specially mentioned that reporting dice-scores as measures of performance is a general tendency. Finally, for every region of neoplasm, P1 stands for the metameric neoplasm space of projected methodology, whereas T1 represents actual neoplasm space within ground truth.

3.2 Methodology

The entire work in this paper is depicted in Figure 3.1. The study accepts brain MRI images as input. The input images are highly sensitive and hence need to be preprocessed. Preprocessing involves contrast enhancement using Histogram Equalization technique.
We value the performance of bounding box estimation for the input brain MRI. It is a commonplace first to describe the training and testing of BRATS 17 dataset and parameters set for training the tree. For training purposes, half set of MR images are deployed while the rest is used for validation and testing purposes. The datasets used for this analysis have well-defined locations, and it may be assumed that the patches have smart ground truth offset values.
We have to set the utmost depth, minimum variety of samples, and variance threshold to build a choice tree. To

get the most effective parameter of the tree cross-validation may well be used.

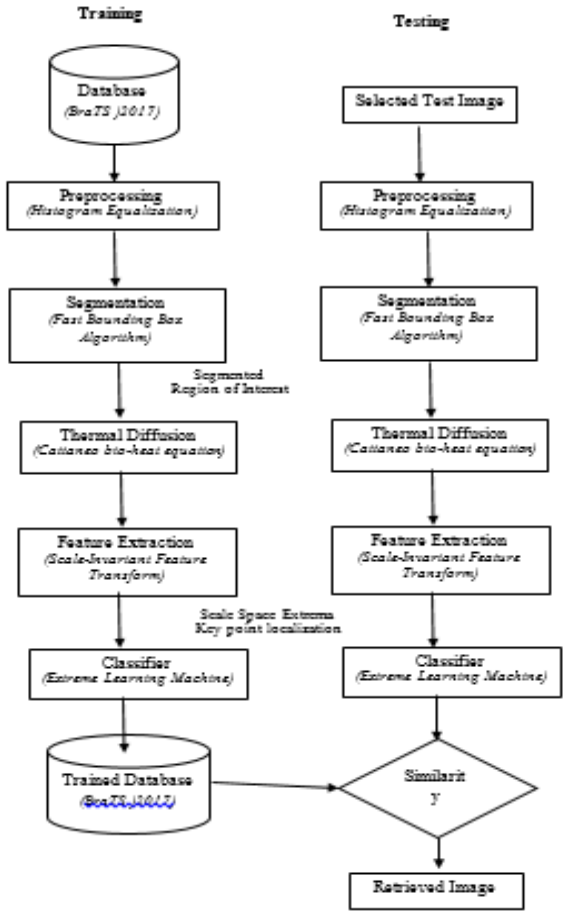

Fig. 3.1 Proposed Workflow of Brain tumor detection

Here, the parameters support our expertise is to test the hypothesis quickly. FBB algorithm is the segmentation algorithm implemented that helps us in selecting the region of interest. Cattaneo bio-heat equation is applied to generate bio-heat distribution model of the living tissues to obtain thermal diffusivity. As the next step, Scale-Invariant feature transformation is applied on ROI to extract the scale-space extrema, and key point localization is done to obtain the nearby accurate location. Finally, using the extracted features, ELM classifies the test image based on trained images using a similarity match.

3.3 Preprocessing

Histogram equalization method has been utilized to boost original image contrast. Initially, it converts the RGB image to grayscale and finds the probability of occurrence in the images of gray level and produces the output image with the same value for its size as the input. Histogram equalization usually works for the purpose much better than ancient alternative strategies. The density functions PDF and CDF can be acquired using the input image bar-graph. By applying these, the input image grey levels can be augmented to the new grey levels, to generate the processed image and bar graph for the resultant image. Juxtaposing input image bar graph with the processed image bar graph, we learn that the grey level intensities are stretched and depressed consistently. As a result, the bar graph of the output image shows a consistent distribution. Throughout the bar graph equalization approach, the mean brightness of the processed image is continually the middle grey level, notwithstanding the input mean.

P(rk) distribution value is shown below
$P(rk) = nk / n \; k = 0, \ldots, L-1$
Here, rk is the kth gray level value, and nk is the number of pixels in the image with gray level rk value. Finally, a mapping is done with cumulative distribution function,
$C(rk) = \sum P(ri)$ (i = 0 to k) as $Sk = (L - 1) * C(rk)$

3.4 Segmentation

MRI slices of the brain have left-right axis symmetry. The tumor perturbs this symmetry. Thus a segmentation over this symmetry gives the dissimilarity. The step by step tasks related to automated localization of a square box in MRI slice shows a tumor on the left aspect and right aspect of the brain on two T1C magnetic resonance imaging slices severally. Once machine-controlled world thresholding and subsequent post-processing, the OS border is detected. By calculating the angles between the main axis, OS border, and vertical axis are detected, and the angle of the OS is based. Then the OS is rotated at a particular angle, and hence the main axis turns vertical. A vertical line is drawn through the targeted mask. The positive peak and also the negative peak are superimposed and are displayed by dots. At intervals, the bounding boxes are placed on left and right sides to estimate the tumor. Finally, the tumor is concluded wherever the bounding box is displayed.
The FBB method is an unsupervised change detection method that identifies the most dissimilar region in between the left and the right halves of a brain in an axial view. MR slice is implemented using the following steps:
a. Apply binarisation on the input image so that narrow connections are removed.
b. Then morphological operations such as filling holes, and dilations are done.
c. The result is the boundary of the object that is it ensures the skull detection.
d. Compute centroid of the image.
e. A line is drawn in the center of the stripped skull and forms the two parts –the test image and the reference image.

f. The region of the reference image is at an axis-parallel rectangle, which shows the abnormality.

3.5 Thermal Diffusion

Cattaneo--Vernotte equation is used to analyze the thermal diffusion in living tissues by considering nonhomogeneous inner structure.

The Bio-heat Transfer Equation:

$$c[\tau \frac{\partial^2 T(x,t)}{\partial t^2} + \frac{\partial T(x,t)}{\partial t}] = [\lambda \frac{\partial^2 T(x,t)}{\partial x^2} + Q(x,t) + \tau \frac{\partial Q(x,t)}{\partial t}]$$

In the above equation c, λ denotes the volumetric values of the heat as well as the thermal conductivity of the input MRI tissues. Q (x, t) is the capability of inner heat sources owing to metabolism with blood perfusion, λ is the relaxation value, T is the temperature value of the tissue, x and t denote the spatial coordinates of the input MRI and time.

Then the Q(x, t) function is shown as per the below equation:

Q(x,t) = GBCB[TB – T(x,t)] + Qm

In the above equation, the GB denotes the blood perfusion rate of image, CB is the volumetric specific heat of the blood, TB is the artery temperature, and Qm is the metabolic heat source.

Then the Bio-heat Transfer Equation would be supplemented by the following boundary conditions: x = 0 : T(x,t) = Tb1(t)

x = L : T(x,t) = Tb2 and initial ones

t = 0 : T(x,t) = T0 ,

$$\frac{\partial T(x,t)}{\partial t} = 0$$

where, Tb1 (t), Tb2 are known boundary temperatures, and T0 is known initial temperature of biological tissue.

3.6 Feature Extraction

Shape features are extracted, and key point localization is performed using Scale-invariant feature transformation. Only the key points detected from the neoplasm region square measure accessorial to the coaching dataset are taken into account whereas the remainder of the square measure is discarded. Since SIFT feature vector is calculated from the neighborhood around a key point at totally different scales, the localized structure of neoplasm is exactly recorded by SIFT. Next step is to identify the best match for every key point in the image by distinguishing its nearest neighbor in the set of key points obtained. The closest neighbor is outlined as the key point with the minimum Euclidian distance for the invariant descriptor vector. Notice that a lot of key points won't have any correct match within the coaching set since they arise from background muddle or alternative brain structures.

Those key points supporting a predefined matching threshold are removed. An additional effective live is to compare the distance of the closest neighbor to that of the second-closest neighbor. This live provides additional stable results as we tend to add one additional constraint to the closest neighbor that it ought to have the closest neighbor considerably nearer than the closest incorrect match to realize reliable matching. The procedure potency of matching method is greatly improved by computing the inverse cosines of scalar product between key points extracted from the take a look at image and key points keep within the coaching dataset, then sorting them. Once matched key points square measure detected for the take a look at the image, it's necessary to get rid of the outliers before recognition as a result of a number of the matches could return from alternative elements of the image aside from tumors. Key point localization shows that features are invariant to transformation, and it also describes the surrounding region of the key point.

The Multiscale Difference of Gaussian (DoG) is obtained by,

D(x, y, σ) = L(x, y, kiσ) - L(x, y, kjσ)

Where L (x, y, kσ) is the convolution of the original image I(x, y).

Interpolation of nearby data for the accurate position is obtained by

$$D(x) = D + \frac{\partial D^T}{\partial x} x + \frac{1}{2x^t} \frac{\partial^2 D}{\partial x^2} x$$

Where D is the derivatives, x = (x,y, σ)

3.7 ELM Classifier

The Extreme learning machine (ELM) is a single-layer feed-forward neural-network (SLFNs) that selects a random number of concealed nodes and the output weights of SLFNs. The activation functions in the concealed layer are highly differentiable. During classification, ELM-LRF was employed to judge whether the tumorous growths were benign or malignant. Convolution and pooling were done within the input layer. The choice of input layer weights were arbitrary. The weights between the hidden layer and the output layer were calculated analytically by using the smallest amount technique. Watershed segmentation was indicative of tumors.

Consider a set of N distinct samples with (xi,yi) and xi ∈ Rd,yi ∈ Rd

Then a SLFN with M hidden neutrons is shown as below

$$\sum_{i-1}^{M} \beta_i f(w_i \quad x_i \quad + b_i)_{j \in [1,N]}$$

With f being the activation function wi the input weights to the ith neuron in the hidden layer, bi the hidden layer biases and the output weights.

The Hidden layer output matrix is given by, H is t.Hβ = Y

The algorithm proceeds as,

Given a training set (xi,yi) and xi ∈ Rd,yi ∈ Rd and an activation function f : R→R and M hidden nodes
1. Randomly assign input weights wi and biases bi, where i =1 …. M
2. Calculate the hidden layer output matrix H using f(wixi + bi)
3. Calculate output weights matrix $\beta = H^{\dagger} Y$

4. Experiment, Evaluation, and Results

This section gives details about the Preprocessing, Segmentation, and ELM Classifier.

4.1 Preprocessing

Histogram Equalization method enhances the visibility of the input image for further processing, and figure 4.1 shows the implementation. Histogram equalization is used for adjusting image intensities to enhance the image contrast. The image contrast is not necessary for a clear image. Histogram Equalization is essential to increase the image intensities for image processing.

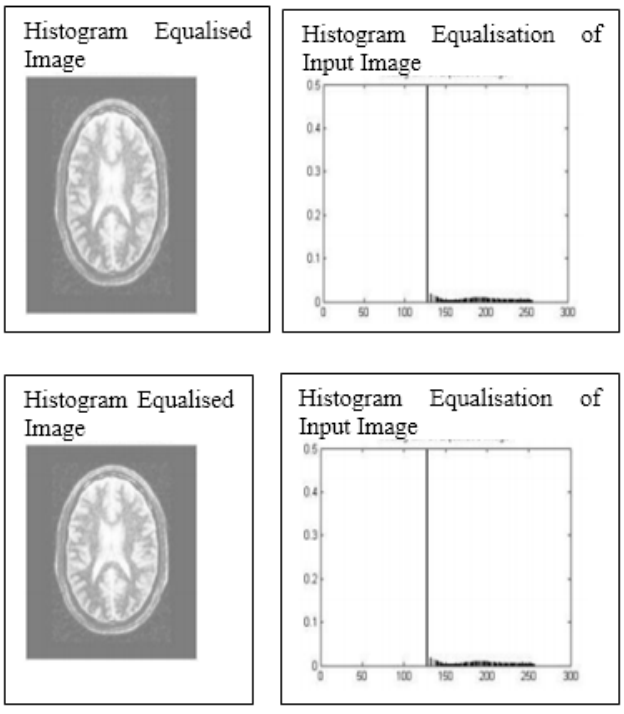

Fig. 4.1 Histogram Equalization method

So, before the image processing stage, i.e., at the preprocessing stage Histogram Equalization is essential for improving image contrast. Let's start histogram equalization by taking our input image. The histogram processing is done by the following process. First, we have to calculate the probability mass function of all the pixels in this image. The next step is cumulative distributive function calculation.
Here, two inputs MRIs are taken for Histogram Equalisation. From the output, we can observe that the MR image contrast has been enhanced and its histogram has also been equalized. As a result, the bar graph of the output image shows a consistent distribution. Throughout the bar graph equalization approach, the mean brightness of the processed image is continually the middle grey level notwithstanding the input mean. The significance note here is, during histogram equalization the overall shape of the histogram only changes. Whereas the histogram stretches the overall shape of histogram remains the same so that the images intensity contrast only changed not the image.

4.2 Segmentation

Regular metabolic activities of human beings are reflected in body temperature, indicating their physical condition. Brain tumor cells produce more heat than normal cells, and hence, it is more apt to use the bio-heat equation to exploit the thermal activities of the brain.

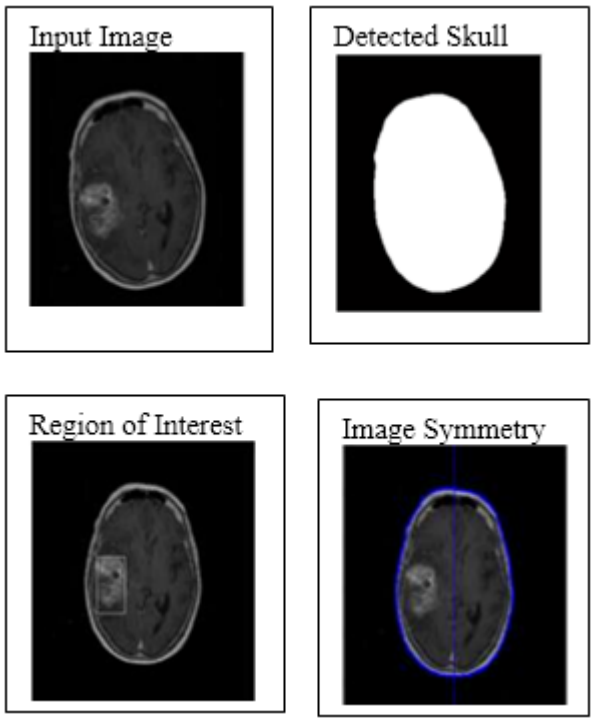

Fig. 4.2 Image segmentation extracts the abnormal portion from the input image

Figure 4.2 shows the image segmentation extracts the abnormal portion from the input image. Here, the input MRIs skull is detected at preprocessing stage. First, the

segmentation is applied to extract a region of interest using the FBB algorithm. Second, Cattaneo bio-heat equation is used to generate bio-heat distribution model of the living tissues on the region of interest. The generated bio-heat distribution model is used to analyze thermal diffusivity in living tissues numerically. The detected image symmetry is essential for classification.

4.3 ELM Classifier

Extreme Machine Learning (ELM) is a widely used machine learning algorithm to classify living tissues into normal and meningiomas tissues. It employs Run-length Matrix for texture features based methods. Co-occurrence Matrix and Intensity, Euclidean distance, Gradient vector, and neighborhood statistics are used for classification. It is provided with a fast learning phase for large databases. The input is chosen from the dataset, and the classifier will decide it is tumor cases or not. The advantage of our proposal is the learning speed of the extreme learning machine is faster, and training error is minimum when compared with other deep learning techniques. Figure 4.3 shows to classify the image.

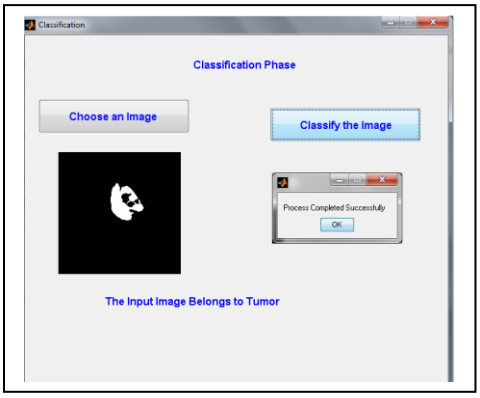

Fig. 4.3 Image Classification Phase

5. Conclusion

The current paper illustrates the generalization performance of the ELM algorithm for the benchmark dataset BRATS 2017 brain images. The 2017 version of BRATS database consists of 274 multi-modality tomography scans. Then from the dataset MR Images, the Dice Score, Sensitivity and Specificity for the three major neoplasm regions, namely whole, core, and active are calculated. Preprocessing involves contrast enhancement using Histogram Equalization technique. To get the most effective parameter of the tree cross-validation may well be used. Brain tumor MRI detection and segmentation system based on the machine learning algorithm is proposed. Histogram equalization method has been utilized to boost original image contrast.

Cattaneo Vernotte equation is used to analyze the thermal diffusion in healthy tissues by considering the nonhomogeneous structure. Shape features are extracted, and key point localization is performed using Scale-invariant feature transformation. Feature extraction on healthy tissue based on thermal diffusion is performed in this paper. The ELM classifier identifies the healthy tumor tissues of MRI images of BRATS dataset. We evaluate the performance of bounding box estimation for the input brain MRI. For training purposes, half set of MR images are deployed while the rest is used for validation and testing purposes.

FBB algorithm is the segmentation algorithm implemented that helps us in selecting the region of interest. Cattaneo bio-heat equation is applied to generate bio-heat distribution model of the healthy tissues to obtain thermal diffusivity. Scale-Invariant feature transformation is applied on ROI to extract the scale-space extrema in the next step. Finally, using the extracted features, ELM classifies the test image based on trained images using a similarity match. The ELM is a SLFNs that selects a random number of hidden nodes and the output weights of SLFNs. The activation functions in the hidden layer are highly differentiable. During classification, ELM-LRF was employed to judge whether the tumorous growths were benign or malignant.

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