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Brain Tumor Retrieval in MRI Images with Integration of Optimal Features

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Abstract: This paper presents an approach to improve medical image retrieval, particularly for brain tumors, by addressing the gap between low-level visual and high-level perceived contents in MRI, X-ray, and CT scans. Traditional methods based on color, shape, or texture are less effective. The proposed solution uses machine learning to handle high-dimensional image features, reducing computational complexity and mitigating issues caused by artifacts or noise. It employs a genetic algorithm for feature reduction and a hybrid residual UNet (HResUNet) model for region-of-interest (ROI) segmentation and classification, with enhanced image preprocessing. The study examines various loss functions, finding that a hybrid loss function yields superior results, and the GA-HResUNet model outperforms the HResUNet. Comparative analysis with state-of-the-art models shows a 4% improvement in retrieval accuracy.

Keywords: medical images; brain MRI; machine learning; feature extraction and reduction; CBIR

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0 Introduction

In recent years, the utilization of digital images has become increasingly used in a variety of fields, including scientific experiments, the medical field, and many others. As a normal part of their operations, hospitals and other medical facilities produce a significant number of digital images everyday. Some examples of these images include X-rays, mammograms, and magnetic resonance imaging (MRI) scans. The work of interpreting medical images is difficult and calls for a significant amount of prior knowledge. Researchers have developed a variety of support systems, such as the Computer-Aided Diagnosis (CAD) system, and the Content-Based Image Retrieval (CBIR) system, to provide radiologists with assistance in the process of interpreting medical images[1]. Not only would CAD assist radiologists in making a diagnosis, but it would also act as a second opinion. But CBIR makes use of visual content to aid users in browsing, searching, and retrieving related medical images from databases according to the user's interests[2-3]. The research field has become much more active as a result of developments in image processing and medical informatics as well as advancements in the availability of multimedia elements in the medical field[4-5]. The color, texture, and shape of an object are all components of the source images in CBIR systems. During the process of indexing and retrieving information, they are retrieved for use later. Despite this, the vast majority of users are typically more interested in particular portions of the image instead of the entire image as a whole[6]. Therefore, the vast majority of the CBIR systems that are in use today are region-based, meaning that the features are taken only from the Regions of Interest (ROI). It has been discovered that the depiction of images on a regional basis is more similar to the way the human visual system works[7-10]. Imaging is used throughout the diagnostic process in today's healthcare, from diagnoses to patient management to surgical intervention and follow-up research. Because most imaging techniques have moved online, with the ever-increasing resolution, medical image processing has had to deal with the issues that come with high data quantities. Image processing and visualization methods

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must be changed as the amount of data grows. The shortage of data in medical image analysis is two-fold and much more acute: there seems to be a general shortage of publicly accessible datasets, and the high-quality dataset is even scarcer. Most of the datasets in the existing techniques had less than 100 patients[11]. Madhu et al.[11] presented a clustering and segmentation approach for medical image retrieval. K-mean clustering was used before feature extraction using Gray Level Co-Occurrence Matrix (GLCM). Then Euclidean distance was used to retrieve medical images. The major drawback of this approach was that it is limited to grayscale images only. Sivakumar and Ganeshkumar[12] proposed a Co-Active Adaptive Neuro-Fuzzy Inference System (CANFIS) approach for brain tumor segmentation and retrieval. In this approach, feature extraction was performed using GLCM then segmentation of similar regions was performed using CANFIS. This model was also limited to grayscale images. Swati et al.[13] presented brain tumor detection using the CBIR technique in which main feature extraction was on main focus. For efficient feature extraction, the Convolution neural network (CNN) model was used. The average precision rate was approx. 96%. The main drawback of this model was that it is limited to grayscale images only. Swati et al.[14] presented brain tumor detection using content-based image retrieval using ROI segmentation. The author presented a novel approach by introducing the concept of CBIR for ROI segmentation in medical images. For this harmony search optimization approach was used.

Polat and Güngen[15] presented the transfer learning model for brain tumor detection. But this model was unimodal. Nasiri et al.[16] proposed hybrid approach of SVM with genetic algorithm for detection. Nguyen et al.[17] also used genetic algorithm for feature selection. Jiang et al.[18] used cascaded UNet model for brain anomaly identification.

Wang et al.[19] used transformer network for brain tumor detection. Wang et al.[20] presented the 3D-Unet model. Rosas et al.[21] used the multi-scale Unet model for feature extraction. Zhou et al.[22] applied latent correlation for feature extraction. Menze et al.[23] presented the multi-modular approach for brain tumor identification.

Wickstrøm et al.[24] presented the significant limitations in deep learning-based image retrieval systems for CT liver scans, primarily their reliance on extensive labeled data and lack of transparency. To address these issues, they introduced a novel self-supervised learning framework that incorporates domain knowledge, improving performance and generalization. This approach is pioneering in its focus on explainability in the feature extraction process for CT liver images. A case study shows the framework's practical application, highlighting its potential in creating reliable and efficient image retrieval systems that effectively use unlabeled data. Nishimaki et al.[25] introduce the Loc-VAE, a specialized autoencoder for 3D brain MR images in CBIR systems, enhancing the interpretability and disease localization in neuroimaging, particularly for Alzheimer's diagnosis. Xu et al.[26] proposed the MDDCH hashing method for efficient retrieval of medical images, addressing challenges in cross-modal hashing and ensuring the uniqueness and discriminability of hash codes. Marin et al.[27] explored the use of a siamese network with ResNet-50 for Alzheimer's disease diagnosis, testing different MRI slice extraction methods and suggesting the integration of diverse data modalities to improve diagnostic accuracy. Each study contributes to the field of medical imaging by leveraging deep learning to enhance image retrieval, interpretation, and disease diagnosis accuracy.

1 Problem Identification

Imaging is crucial in modern healthcare, used in diagnostics, treatment planning, surgery, and follow-up studies. With most imaging techniques now digital and offering higher resolutions, the challenge lies in managing the resulting large volumes of data. Consequently, there is a need to adapt image processing and visualization algorithms to handle this increase in data efficiently. According to the given literature review high computational complexity and data imbalance issues, lower efficiency, more training losses, and did not used pre-processing application to reduce the complexity of existing models. According to these problem following research questions are derived for designing proposed methodology:

1) What are the complexities faced in diagnosing and retrieving infected regions from images using machine learning and image processing tools?

2) Does data pre-processing steps such as image denoising and feature reduction increase classification and retrieval performance significantly?

3) Neural networks overfit the samples because of class imbalance. How this issue is resolved in ROI retrieval from available medical images?

4) Can CBIR-based ROI segmentation apply to multi-modal images?

The key contributions of the paper are:

1) The paper is motivated to design and analyze combined weighted feature extraction and dimension reduction techniques using optimization techniques such as a genetic algorithm for content-based medical image retrieval.

2) The paper performed analysis to observe the impact of pre-processing steps and feature extraction and dimension reduction techniques on medical image retrieval.

3) Then a hybrid multi-modal architecture is proposed including feature reduction techniques with the ROI segmentation and improved performance efficiency for multi-modal medical images.

Therefore, Table 1 offers a comparative analysis of the proposed work's key features against existing research. It notes that while recent studies primarily focus on pre-trained models, the aspect of feature reduction has not been given significant attention.

Table 1 Research contributions using machine learning in medical imaging

Ref.	DS	LS	PP	MM	FR
[8]	MRI	Residual learning	No	No	No
[9]	CE-MRI	Scratch	No	No	No
[10]	BRATS 2012-18	Scratch	Yes	No	No
[11]	CE-MRI	Scratch	Yes	No	Yes
[12]	CE-MRI	Scratch	Yes	No	Yes
[13]	CE-MRI	Pre-trained	Yes	No	Yes
[14]	CE-MRI	CNN	Yes	No	Yes
[15]	TCGA-LGG	Pre-trained	No	No	No
[15]	CE-MRI	Pre-trained	No	No	No
Proposed	BRATS 2021, lungs infection, etc.	Hyperparameter-based fine-tune transfer residual learning	Yes	Yes	Yes

DS = Datasets, LS = Learning Strategy, PP = Pre-processing, MM = Multi-modal, FR = Feature Reduction

The rest of the paper is organized as: Section 2 presents the materials and methods used to design the proposed architecture. Then ablation study and result analysis are presented in Section 3. Further Section 4 presents the conclusion and future scope of the paper.

2 Materials and Methods

Medical image retrieval includes the ROI segmentation process as a key step toward enhancing disease retrieval, treatment planning, monitoring, and clinical trials. Disease retrieval includes the detection of diseases such as brain tumors[16-22]. But because of the following factors, segmenting abnormalities' positions accurately is a difficult problem.

Medical images can be acquired using a variety of protocols and typically have low contrast and inhomogeneous appearances, resulting in over-segmentation and under-segmentation.

In addition, some structures have a wide range of scales and shapes, making it challenging to build a prior shape model.

In this work, the tumorous region is retrieved out of MRI image of brain using advance features of machine learning. The research methodology outlined in Fig.1 consists of four primary steps: image pre-processing, GA-based feature extraction and dimension reduction (GA-FEDR), anomaly ROI segmentation (ROI Seg) using hybrid residual Unet (HResUNet), and similarity identification and disease retrieval (SIDR). The methodology integrated the advantage of genetic algorithm whose function is to extract out those pixels that are more relevant for tumorous candidate. Therefore, optimal features for region segmentation are extracted out by genetic algorithm. This will reduce the feature candidates for ROI segmentation processing which would ultimately reduces the computational complexity.

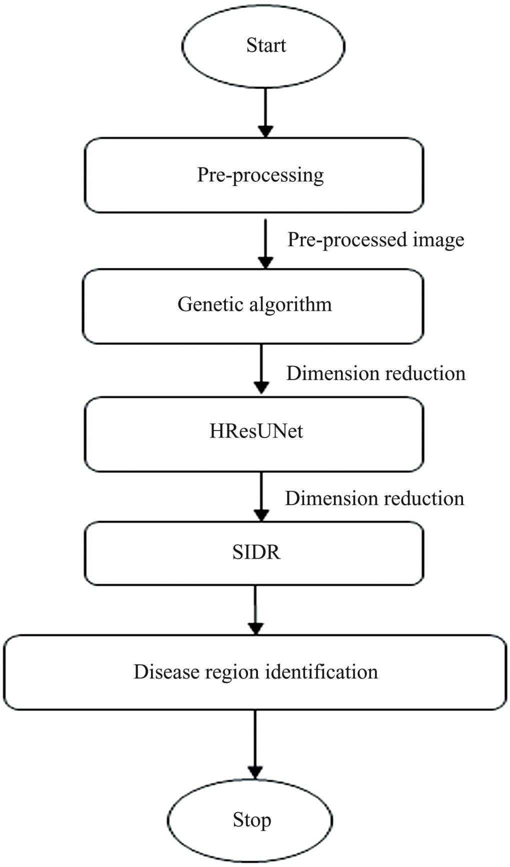


Fig.1 Flowchart of the proposed methodology

2.1 Medical Image Pre-Processing

Distinguishing healthy areas from anomalous regions in medical images is challenging. Therefore, pre-processing is essential before segmenting these abnormal areas. This process is outlined in Algorithm 1. Medical images often have a limited dynamic range, making it difficult to adequately expose all pixels. To address this, increasing the exposure in some under-exposed regions can enhance the visibility and clarity of the image. This is mathematically represented as in Eq. (1).

$$O_i = \sum_{i=1}^{M} X_i * q_i \tag{1}$$

where, exposure or enhancement is represented as q_i in image X_i with color channels M and result in improved exposure image. Algorithm 1: Medical Image Pre-processing:

Begin

1) I_i =Input images, O_i =Output images,

2) For $i = 1 : I_i$

3) Convert into intensity images, $I_i(x,y)$

4) Identify Min_I = minimum intensity,

Max_I = maximum intensity

5) Calculate weight matrix $\boldsymbol{q}$ based on

μ = enhancement degree controller determined according to deviation of Min_I and Max_I

6) $O_i(x,y) = \hat{\boldsymbol{I}}(x,y) * \boldsymbol{q}$

7) End for

8) Return O_i

End

2.2 GA-Based Feature Extraction and Dimension Reduction (GA-FEDR)

In this step, feature extraction and reduction are performed using a genetic algorithm. Which finds the best optimal result by applying fitness function over combined weighted features in the image such as color, shape, and color texture. In this methodology, genetic algorithm is used for feature extraction and dimension reduction technique because GAs are generally more suitable when dealing with large feature spaces or when the features are highly correlated. This is because GAs is capable of searching through a large number of potential feature subsets in a relatively short amount of time. Additionally, GAs can be used to optimize multiple objectives simultaneously, such as retrieval performance and feature dimensionality. This leads to more accurate retrieval of relevant medical images from a large database. Combining GAs with feature reduction and HResUNet for segmentation enhances segmentation accuracy, reduces computational costs, and improves interpretability of results. Feature reduction lowers training and inference costs, though choosing the optimal feature subset can be challenging. This hybrid approach makes segmentation maps easier to interpret, crucial in applications like medical imaging.

A genetic algorithm is made up of five basic steps[16-17]. The GA's basic flow is depicted in Fig. 2. Each step is described in detail below.

1) Initialization: A population is a group of individuals who start the procedure. Each individual is a potential solution to the issue. It has been discovered that employing a heuristic to start the whole population might result in highly identical solutions and minimal variability. Random solutions are the ones that lead the population to optimality, according to experiments.

2) Fitness evaluation: The fitness function indicates an individual's level of fitness. It assigns each individual a fitness score. The fitness score determines the likelihood of an individual being chosen for reproduction. Selection is a random occurrence that

selects a parent's chromosome from a population depending on each chromosome's fitness value[16]. The goal of the selection stage is to choose the fittest people and let them pass their genes along to future generations.

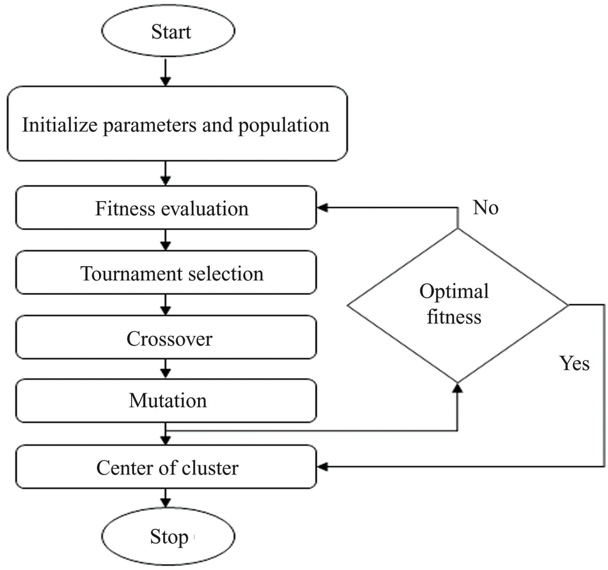


Fig.2 Flowchart of genetic algorithm

3) Crossover is the process of parents' chromosomes mixing to establish a new individual.

4) Mutation: Some of the genes in some new children can be susceptible to a mutation with a lower random frequency. Mutation happens to preserve population variety and avoid premature convergence.

In this step, the pre-processed image is converted in matrix of pixels. For grayscale images, this is a 2D matrix, and for color images, a 3D matrix (with color channels). Then its relevant features and properties are extracted such as color, textures, etc. These features are encoded as "string of genes" for input in genetic algorithm. Each gene represents the set of features selected randomly. This is termed as population and initialized with size 20. Then fitness function is applied to select the optimal features out of the genes. Crossover and mutation process is applied to number of iterations and optimal features are selected out of it. The mutation factor ranges from 0.1 to 1. Then the image with selected features is passed for ROI segmentation.

2.3 Anomaly ROI Segmentation (ROI-S)

This step is designed to segment anomalies or abnormalities in medical images. The output of genetic algorithm is fed into HResUNet for ROI identification. The HResUNet is a type of convolutional neural network, such as Residual UNet (ResUNet). The basic contracting and expanding architecture of UNet is represented in Fig. 3. In this step, the output images of genetic algorithm are converted in feature map and fed into residual blocks of HResUNet.

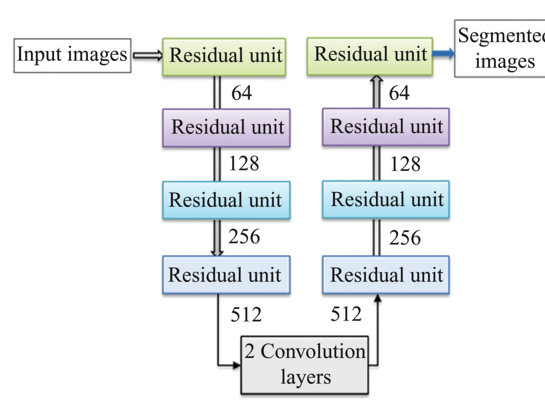


Fig.3 HResUNet architecture

The HResUNet is cascading of residual blocks in contracting and expanding part of the UNet. Each residual block composed of convolution layer with Batch Normalization (BN), Parametric Rectified Linear Unit (PReLU) activation function and Maxpooling with stride 1. The contracting and expanding portion of the UNet is joined with double convolution layer. The model is trained to retrieve the anomaly region in the tumorous images and segment out the matched regions. The model used the ADAM optimizer. The batch size is taken to be 64 for 100 epochs. The input image size is taken to be 240 * 240.

2.4 Similarity Identification and Disease Retrieval (SIDR)

For medical image retrieval, machine learning techniques have shown promising results. Traditionally, methods like cosine similarity and Euclidean distance were commonly used for medical image retrieval. However, these techniques are relatively simple and often fall short in addressing the complexities of high-dimensional medical images due to the semantic gap that exists between the complex visual features of these images. In contrast, the approach discussed here utilizes softmax probability-based similarity (p_{sim}) for image classification and retrieval, offering a more sophisticated method to handle the intricacies of medical imaging. The softmax probability is defined as follows:

$$p_{\text{sim}} = \frac{\exp(u_C)}{\sum_{i=1}^{C} \exp(u_I)} \tag{2}$$

where, u_C represents the class C feature vector. The hybrid loss function used with combination of Weighted Cross Entropy (WCE) and Generalized Dice loss (GDL).

$$\text{WCE} = -\frac{1}{B}\sum_{b=1}^{B}\sum_{i=1}^{C} w_i g_{tib} \log(s_{ib}) \tag{3}$$

$$\text{GDL} = 1 - 2\frac{\sum_{i=1}^{C} w_i \sum_{b=1}^{B} g_{tib}\, s_{ib}}{\sum_{i=1}^{C} w_i \sum_{b=1}^{B} (g_{tib} + s_{ib})} \tag{4}$$

where, class or label is represented with C, the batch size is represented as B with weight w_i and segmented pixel as s_{ib} with ground truth value of g_{tib}.

3 Results and Discussion

In this section, result analysis is performed on brain tumor MRI datasets[23]. The study conducts result analysis using the BraTS 2019 brain tumor MRI dataset. This dataset includes ground truth data for 259 high-grade glioma (HGG) and 76 low-grade glioma (LGG) patients, covering four MRI modalities. The data is organized into sequences of T1, T2, Flair, and T1Ce, with each volume consisting of 155 slices. Out of these, the top 210 volumes are selected for analysis. For training and testing purposes, approximately 750 multi-modal images from the dataset are used. The entire model is implemented using Python on Google Colab.

3.1 Performance Parameters

To improve the quality of medical images, a few parameters and quality metrics are used:

Peak Signal to Noise Ratio (PSNR): PSNR is a highly significant technique for improving image quality. The higher the PSNR score, the superior the method. The formula to evaluate the PSNR is given in Eq.(5), where MSE is the mean square error.

$$\text{PSNR} = 20\log_{10}\frac{\text{MAX}_{\text{f}}}{\sqrt{\text{MSE}}} \tag{5}$$

Structural Similarity Index (SSIM): Structural similarity has been one of the quality evaluation methodologies in digital image processing. SSIM is a program that finds and measures the similarity between images and videos. The SSIM formula is calculated using multiple windows for assessing x and y of the same size $N \times N$ as illustrated below:

$$\text{SSIM}(a,b) = \frac{(2\mu_a\mu_b + p_1)(2\sigma_{ab} + p_2)}{(\mu_a^2 + \mu_b^2 + p_1)(\sigma_a^2 + \sigma_b^2 + p_2)} \tag{6}$$

where, μ_a, μ_b = mean of a and b respectively, a and b are respective images before pre-processing and after pre-processing. σ_a^2, σ_b^2 = variance of a and b, σ_{ab} = co-variance of a and b , p_1 and p_2 are variables to stabilize the division with a weak denominator.

Dice coefficient: It represents the area of overlap between segmented images ground truth images.

Sensitivity/ Recall: It is used to determine the true positive rate and evaluated as:

$$\text{Sensitivity} = \frac{(\text{TruePositive})}{(\text{TruePositive} + \text{FalseNegative})} \tag{7}$$

Accuracy: The accuracy represents the correctly classified outcomes among all classification subjects.

$$\text{Accuracy} = (\text{TruePositive} + \text{TrueNegative}) / (\text{TruePositive} + \text{TrueNegative} + \text{FalsePositive} + \text{FalseNegative}) \tag{8}$$

Precision: It represents the positive predicted samples with respect to all samples and evaluated as:

$$\text{Precision} = \frac{(\text{TruePositive})}{(\text{TruePositive} + \text{FalsePositive})} \tag{9}$$

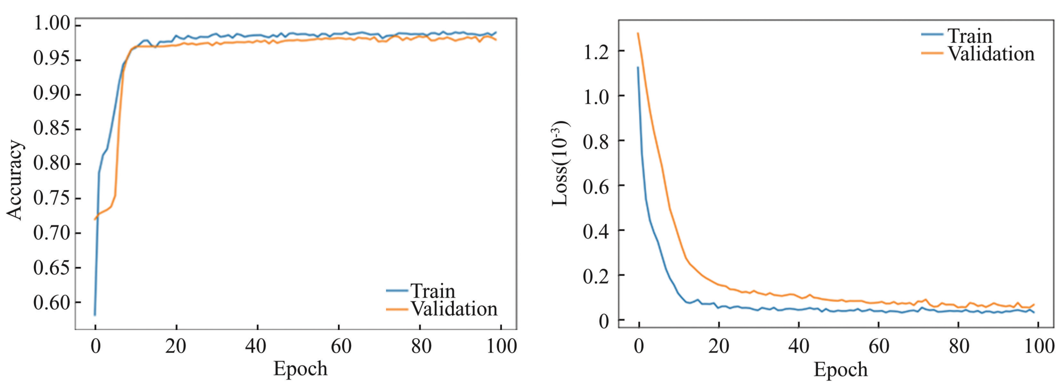
3.2 Result Analysis on Pre-Processing

In medical images, retrieval of anomaly regions is also affected by image quality and leads to wrong ROI segmentation. Consequently, there are often several local optima in a noisy search space. In addition to demonstrating effectiveness in breaking out of local optima, the segmentation process gains a great deal of flexibility thanks to machine learning. Compared to conventional segmentation techniques, machine learning image segmentation may provide more precise retrieval. With an increasing volume of medical data, high dimensions will increase the computational complexity. Feature extraction and dimension reduction are critical and challenging tasks in medical image retrieval, particularly for the segmentation and identification of regions of interest. Nowadays, many researchers use a genetic algorithm to address the feature extraction and reduction[1-2]. The genetic method allowed for more rapid convergence to the ideal outcome. Preliminary findings show that GA-based approaches outperform conventional methods in terms of quality[3-4]. The summary of the results for pre-processing brain MRIs indicates that the process achieves a high Peak Signal-to-Noise Ratio (PSNR) of approximately 56 and a Structural Similarity Index (SSIM) of about 99%. These values suggest that the combination of image enhancement and the genetic algorithm results in minimal information loss from the input images. This underscores the effectiveness of the pre-processing step in maintaining information integrity while also enhancing image retrieval efficiency.

3.3 Multi-Modal MRI Brain Tumor Retrieval Using HResUNet Model

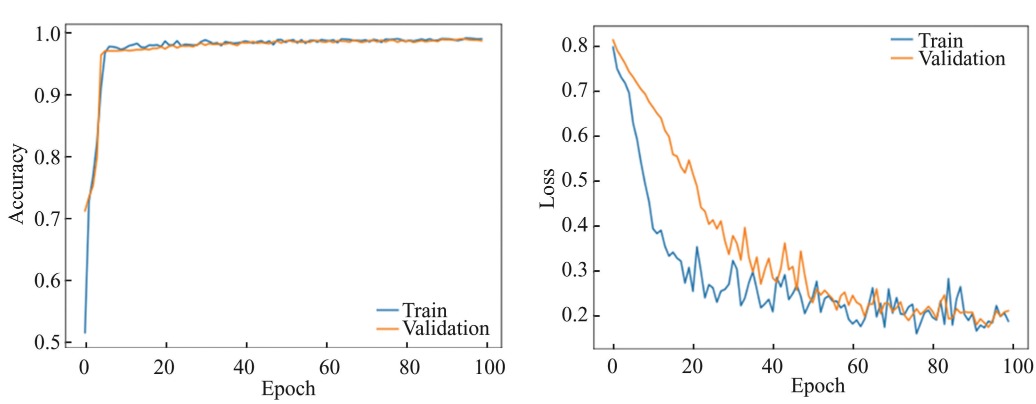
In this section, the result analysis focused on different loss functions: weighted cross-entropy loss (WCEL), dice loss (DL), and hybrid loss (HL). Fig.4(a) displays the training and validation accuracy for HResUNet in brain tumor segmentation using WCEL, with an average accuracy of about 96.1%. Fig. 4(b) shows the training and validation loss for the same segmentation using WCEL.

Fig. 5(a) presents the accuracy versus epoch graph for HResUNet using dice loss in brain tumor segmentation, averaging around 97.2% accuracy. Fig.5(b) illustrates the training and validation loss for brain tumor segmentation using HResUNet with dice loss.



(a) Training and validation accuracy (b) Training and validation loss

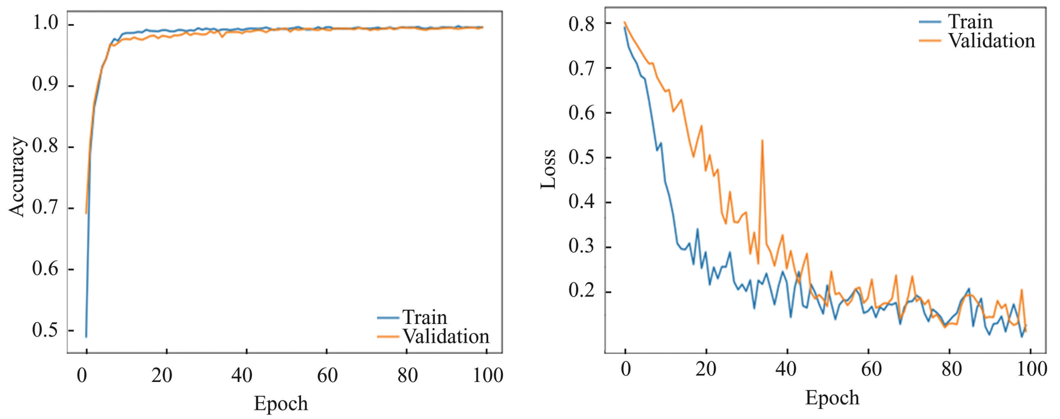
Fig.4 Multi-modal brain MRI using HResUNet with WCEL



(a) Training and validation accuracy (b) Training and validation loss

Fig.5 Multi-modal brain MRI using HResUNet with DL

Fig. 6(a) depicts the training and validation accuracy for HResUNet in brain tumor segmentation, achieving an average accuracy of approximately 97.7%. Fig. 6(b) shows the training and validation loss for brain tumor segmentation using HResUNet. These results demonstrate the effectiveness of HResUNet in brain tumor segmentation with different loss functions, highlighting high accuracy and informative loss trends over epochs.



(a) Training and validation accuracy (b) Training and validation loss

Fig.6 Multi-modal brain MRI using HResUNet with HL

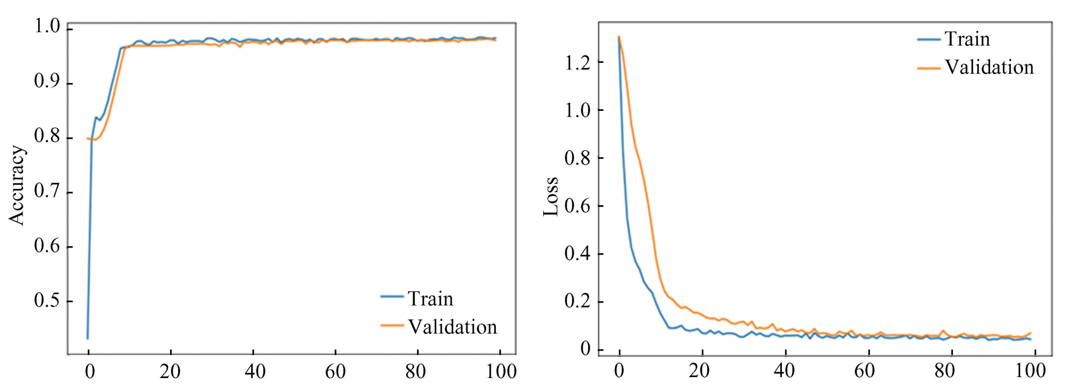
Table 2 shows the comparative analysis of brain tumor retrieval using ROI segmentation with HResUNet. Three loss function is studied in the proposed work. For HL accuracy is 96.7%. The dice coefficient is 64.1% and the sensitivity is 98.4%. For WCEL accuracy is 96.1%. The dice coefficient is 3.11% and the sensitivity is 95.0%. For DL accuracy is 97.2%. The dice coefficient is 65.4% and the sensitivity is 98.3%.

3.4 Multi-Modal MRI Brain Tumor Retrieval Using GA-HResUNet Model

Fig. 7(a) shows the accuracy versus epoch graph for Brain MRI using GA-HResUNet with WCEL. The average accuracy of the model using WCEL is 96% for the training and validation set. Fig.7(b) shows the loss versus epoch Graph for Multi-Modal Brain MRI using GA-HResUNet with WCEL. The average loss of the graph is 0.16.

Table 2 Brain tumor retrieval using HResUNet with different loss functions

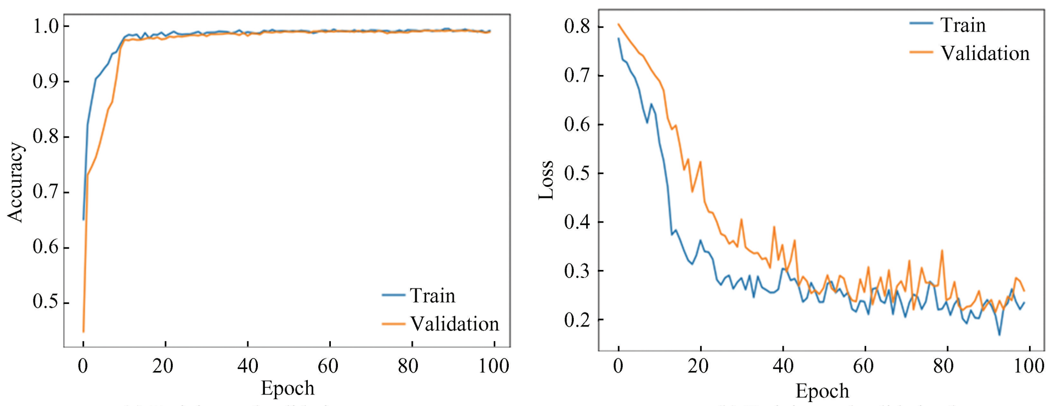
Metrics	Accuracy(%)	Dice Coefficient(%)	Sensitivity(%)
Hybrid Loss (HL)	96.7	64.1	98.4
Weighted Cross Entropy Loss (WCEL)	96.1	31.1	95.0
Dice Loss (DL)	97.2	65.4	98.3



(a) Training and validation accuracy (b) Training and validation loss

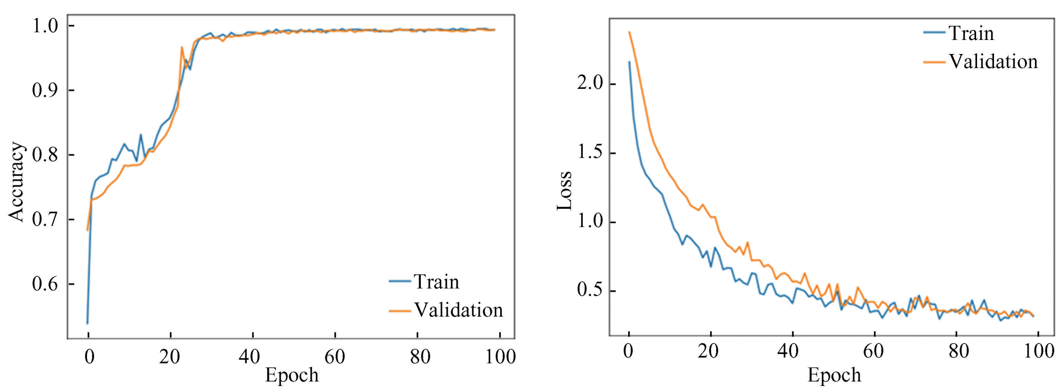
Fig. 7 Multi-modal brain MRI using GA-HresUNet with WCEL

Fig. 8(a) shows the accuracy versus epoch graph for Brain MRI using GA-HResUNet with DL. The average accuracy of the model using DL is 96.4 % for the training and validation set. Fig. 8(b) shows the loss versus epoch Graph for Multi-Modal Brain MRI using GA-HResUNet with DL. The average loss of the graph is 0.35. Fig. 9(a) shows the accuracy versus epoch Graph for Multi-Modal Brain MRI using GA-HResUNet with HL. The average accuracy of the graph is 98%. Fig.9(b) shows the loss vs epoch Graph for Multi-Modal Brain MRI using GA-HResUNet with HL. The average loss of the graph is 0.68.



(a) Training and validation accuracy (b) Training and validation loss

Fig. 8 Multi-modal brain MRI using GA-HresUNet with DL



(a) Training and validation accuracy (b) Training and validation loss

Fig.9 Multi-modal brain MRI using GA-HResUNet with HL

Table 3 shows the comparative analysis using GA-HResUNet for brain tumor retrieval using ROI segmentation with different loss functions considering accuracy, dice coefficient, and sensitivity. The accuracy, dice coefficient, and sensitivity for HL loss are 98%, 62.5%, and 98.7% respectively. The accuracy, dice coefficient, and sensitivity for WCEL loss are 96%, 40%, and 97% respectively. The accuracy, dice coefficient, and sensitivity for DL loss are 96.4%, 63.4 %, and 98.7% respectively.

Table 3 Brain tumor retrieval with GA-HResUNet on different loss functions

Metrices	Accuracy(%)	Dice Coefficient(%)	Sensitivity(%)
Hybrid Loss (HL)	98	62.5	98.7
Weighted Cross Entropy Loss (WCEL)	96	40	97
Dice Loss (DL)	96.4	63.4	98.7

3.5 Performance Comparison of HResUNet and GA-HResUNet

Fig.10 shows the comparison of IOU using GA-HResUNet and HResUNet with different loss functions for brain tumor retrieval using ROI segmentation. For whole tumor region (WT), tumor core region (TC) and enhancing tumor region (ET) IoU are the maxima for GA-HResUNet which is 82%, 78%, and 68 % respectively. Fig.11 shows the comparison of Dice Score using GA-HResUNet and HResUNet with different loss functions for brain tumor retrieval using ROI segmentation. For WT, TC, and ET dice scores are maximum for GA-HResUNet which is 90%, 87%, and 81% respectively.

Some of the examples of the ROI segmentation output is presented in Fig. 12. Among these regions, WT, TC and ET are further retrieved.

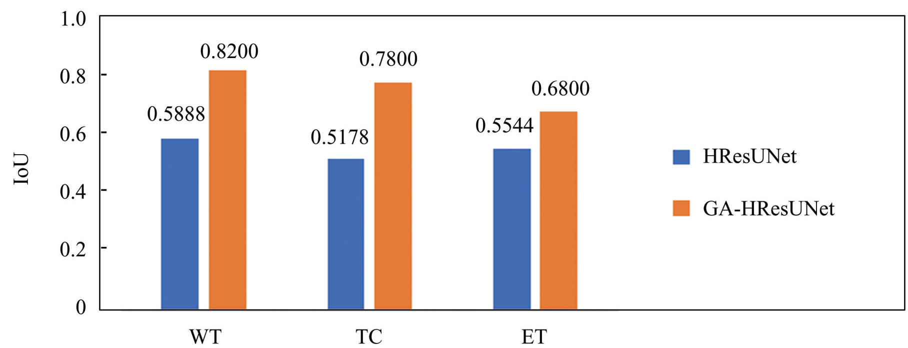


Fig.10 IoU comparative analysis with GA-HResUNet and HResUNet

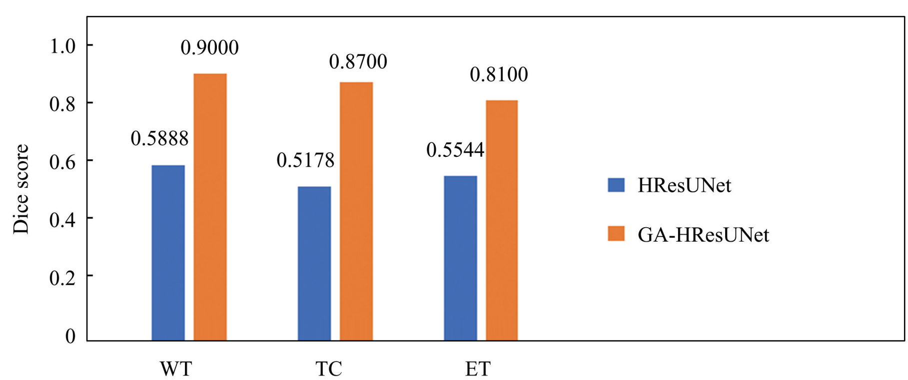


Fig.11 Dice score comparative analysis with GA-HResUNet and HresUNet

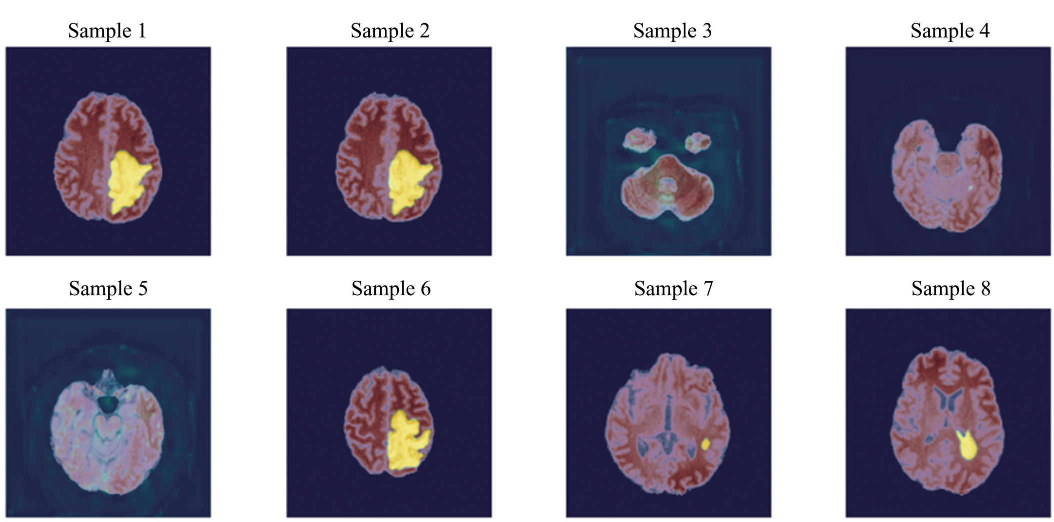


Fig.12 Examples of segmented regions

3.6 Comparative State-of-Art

Table 4 shows the comparison of various state-of-art for brain tumor retrieval using ROI segmentation considering WT, ET, and TC. For WT, the dice score for cascaded UNet[18] is 88.79%, and UNet[19] shows a dice coefficient of 85. 2%.

Modified UNet[20] shows a dice coefficient of 86.5%, Fusion Network[21] shows a dice coefficient of 87%, and Latent Correlation Net[22] has achieved a dice coefficient of 87%. DenseUNet+ model was proposed by Ref.[28] and achieved a whole tumor dice score of 88%. HMNet[29] achieved a dice score of 89% for WT. Whereas our proposed work has a maximum dice score, which is 90%. For ET, the dice score for cascaded UNet is 83.2%, UNet is 77.8%. Modified UNet, it is 77.5 %, Fusion Network shows a dice coefficient of 72% which has a minimum when compared to another one. The proposed method GA-ResUNet shows a maximum dice score, it is 90%. Similarly, for ET, GA-ResUNet achieved the highest dice coefficient of 88%. Whereas for TC, the dice score for cascaded UNet is highest i.e., 83.6%, and GA-ResUNet has a dice score of 81%. From the comparative analysis, it can be concluded that GA-HResUNet gives more deeper retrieval of tumorous pixel among all pixel candidates. This is due to hybrid nature of model. The model gives better result in identification of WT as well as ET regions as compared to TC.

Table 4 Dice score comparative state-of-art

Models	WT	ET	TC
Cascaded UNet[18]	0.8879	0.832	0.836
U-Net[19]	0.8520	0.778	0.798
Modified UNet[20]	0.8650	0.775	0.789
Fusion Network[21]	0.8700	0.720	0.710
Latent Correlation Net[22]	0.8700	0.710	0.720
DenseUNet+[28]	0.8800	0.860	0.860
HMNet[29]	0.8900	0.770	0.830
GA-HResUNet (Ours)	0.9000	0.880	0.810

Below in Table 5, retrieval performance of comparative state-of-art models are presented. The accuracy achieved by machine learning models such as k-NN[2], SVM[5], SEResNet[30], DResCN N-HSO[31] and GA-HResUNet (Ours) have achieved 94%, 90%, 94%, 83% and 98% respectively. Therefore, it is seen that GA-HResUNet (Ours) have achieved 4% improvement in terms of accuracy.

Table 5 Comparative state-of-art for medical image retrieval

Methods	Accuracy(%)
k-NN[2]	94
SVM[5]	90
SEResNet[30]	94
DResCN N-HSO[31]	83
GA-HResUNet (Ours)	98

In summary, the GA-HResUNet method for brain tumor retrieval shows significant improvements over existing models like Cascaded UNet and U-Net, particularly in accuracy and dice scores for tumor segmentation. This method aligns well with or exceeds the performance of previous studies. However, its complexity and the potential limitations of the datasets used might affect its general applicability and ease of use in varied clinical environments. Future research should aim to address these limitations and enhance the model's practicality and scope.

4 Discussion

The paper presents a methodology for brain tumor region retrieval using machine learning with optimized features. The following key observations are concluded:

1) Image preprocessing: Pre-processing are applied on brain MRIs that achieves high Peak Signal-to-Noise Ratio (PSNR) of approximately 56 and Structural Similarity Index (SSIM) of about 99%. This indicates minimal information loss and enhanced efficiency in image retrieval.

2) Optimal feature extraction: This step is integrated for extraction of optimal features relevant to the tumor using genetic algorithm that will reduce the computational complexity for ROI segmentation.

3) ROI segmentation: This step included the multi-modal residual Unet model and the analysis shows high accuracy of about 97% using different loss functions. GA-HResUNet (with optimal features) outperforms better as compared to HResUNet (without optimal features) in terms of IoU and dice score for different tumor regions.

These achievements indicate the effectiveness of the GA-HResUNet model in enhancing the accuracy and efficiency of brain tumor region retrieval.

5 Conclusions and Future Scope

With advancements of imaging technology in the medical field result in better clinical diagnosis and treatment planning for patient healthcare. Every day, a very large amount of medical data is produced that is used for robust clinical decision support. In recent studies, content-based image retrieval in medical imaging such as MRI, x-rays, or CT scans has received a lot of attention. Manual retrieval from large available medical data is quite a difficult, time-consuming, and challenging task for radiologists. To address, these issues automatic medical image retrieval using machine learning emerged as an efficient model. In this paper, we have focused on medical image retrieval for brain tumors using machine learning. To provide high-quality pre-processing output during the medical images, several image segmentation stages must be carried out. Problems in organ segmentation would result in inaccurate data, which would therefore cause errors in later disease retrieval and several other clinical applications. Therefore, precise and trustworthy methods are needed to increase the effectiveness of medical image analysis. In this work, a hybrid GA and machine learning-based ROI segmentation and classification model are presented for medical anomaly (such as tumor or infection) retrieval. The entire framework is divided into 3 major parts, i.e., pre-processing, feature selection and reduction, anomaly segmentation, and classification. The constructed model was trained to segment infected and non-infected regions retrieval from medical images. The performance of the model is presented in two different stages. In the first stage performance of the model was tested after pre-processing steps. In the second stage, the model is tested on brain tumor retrieval using ROI segmentation. Different parameters were evaluated on these datasets and it was observed that the model shows satisfactory results as compared to existing techniques. Therefore, in this research work, the following conclusions are observed:

1) Medical image retrieval performance is enhanced using pre-processing steps and combined weighted feature extraction using genetic algorithm optimization.

2) CBIR for ROI segmentation in medical images with integration of machine learning and feature extraction technique are more robust system for grayscale as well as multi-modal images.

3) Achieved average retrieval accuracy was approx. 98%.

In the future, the designed medical image retrieval will be implemented by using cyber-physical systems such as the Internet of Things (IoT) and Blockchain. The image is probably one of the most important medical tools because it offers a method for diagnosing patients' conditions, monitoring their responses to drug treatments, and managing their diseases while having the advantages of being a very quick, non-invasive procedure, having very few side effects, and having an excellent cost-effect relationship. Therefore, in the future recommendation system will be added with a retrieval system to support smart healthcare applications.

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