A Dual Autoencoder and Singular Value Decomposition Based Feature Optimization for the Detection of Brain Tumor from MRI Images

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Keywords

MRI, Brain Tumor, Deep Learning, Computer Vision, Anomaly Prediction

Abstract

Introduction

The brain tumor is the growth of abnormal cells inside the brain. These cells can be grown into malignant or benign tumors. Segmentation of tumor from MRI images using image processing techniques started decades back. Image processing based brain tumor segmentation can be divided in to three categories conventional image processing methods, Machine Learning methods and Deep Learning methods. Conventional methods lacks the accuracy in segmentation due to complex spatial variation of tumor. Machine Learning methods stand as a good alternative to conventional methods. Methods like SVM, KNN, Fuzzy and a combination of either of these provide good accuracy with reasonable processing speed. The difficulty in processing the various feature extraction methods and maintain accuracy as per the medical standards still exist as a limitation for machine learning methods. In Deep Learning features are extracted automatically in various stages of the network and maintain accuracy as per the medical standards. Huge database requirement and high computational time is still poses a problem for deep learning.

Method

To overcome the limitations specified above we propose an unsupervised dual autoencoder with latent space optimization here. The model require only normal MRI images for its training thus reducing the huge tumor database requirement. With a set of normal class data, an autoencoder can reproduce the feature vector into an output layer. This trained autoencoder works well with normal data while it fails to reproduce an anomaly to the output layer. But a classical autoencoder suffer due to poor latent space optimization. The Latent space loss of classical autoencoder is reduced using an auxiliary encoder along with the feature optimization based on Singular value Decomposition (SVD). The patches used for training are not traditional square patches but we took both horizontal and vertical patches to keep both local and global appearance features on the training set. An Autoencoder is applied separately for learning both horizontal and vertical patches. While training a logistic sigmoid transfer function is used for both encoder and decoder parts. SGD optimizer is used for optimization with an initial learning rate of .001 and the maximum epochs used are 4000. The network is trained in MATLAB 2018a with a processor capacity of 3.7 GHz with NVIDIA GPU and 16 GB of RAM.

Results

The results are obtained using a patch size of 16x64, 64x16 for horizontal and vertical patches respectively. In Glioma images tumor is not grown from a point rather it spreads randomly. Region filling and connectivity operations are performed to get the final tumor segmentation. Overall the

method segments Meningioma better than Gliomas. Three evaluation metrics are considered to measure the performance of the proposed system such as Dice Similarity Coefficient (DSC), Positive Predictive Value (PPV), and Sensitivity.

Conclusion

An unsupervised method for the segmentation of brain tumor from MRI images is proposed here. The proposed dual autoencoder with SVD based feature optimization reduce the latent space loss in the classical autoencoder. The proposed method have advantages in computational efficiency, no need of huge database requirement and better accuracy than machine learning methods. The method is compared Machine Learning methods Like SVM, KNN and supervised deep learning methods like CNN and commentable results are obtained.

Key Words: MRI, Auto Encoder, SVD, Anomaly Prediction

I. Introduction

The brain tumor is a serious medical condition if not treated earlier will reduce the life span of the affected person. World Health Organization (WHO) classifies the tumor as benign and malignant. In malignant, the tumor has Type-I to Type-IV verities. Gliomas and Meningioma are malignant tumors that start as Type-I which affects the brain and spinal cord. The affected persons experience strong headaches, seizures, loss of balance, and weight loss. Treatments like surgery, radiation, and chemotherapy are suggested by the medical experts to either completely cure or partially ceases the growth of tumors. It is important to detect the tumor in an early stage to make use of the full effect of these treatments. The doctors perform the MRI scanning to examine the potential growth of the tumor inside the brain. These actions are performed by experts in radiography treatments. Manual inspection of cell growth often leads to judgment error and can be replaced by modern automatic analysis methods. Processing MRI images for detection and segmentation of tumor in the brain is an alternative method which can alleviate the error caused by manual inspection.

Automatic detection of tumor starts from simple thresholding [1], [2] and developed to various sophisticated methods like Deep Learning (DL). The methods are classified into three categories. At first, we have the segmentation through conventional image processing by several methods. Then Machine Learning (ML) with various feature extraction methods and finally the DL methods. The selection of a particular method is based on the problem selected. In medical diagnostics, the importance is given to accuracy in segmentation rather than the speed of operation. Here DL has a clear advantage over the other methods. The segmentation through conventional image processing is the simple image processing operations on the pixel values of the MRI like multilevel thresholding [3], [4]. Various methods for segmenting the required portion from an MRI is developed over the years. Some of these are Fuzzy Clustering [5], Watershed algorithm [6], Markov Random Field [7], and Genetic algorithm [8]. All the above method has advantages like the speed of operation which is useful if fast results are required. But they lack the performance when there are pixel intensity variations, diverse nature of the tumor, machine, and other noise effects.

To overcome the deficiencies specified above special features are extracted from the MRI belong to the tumor and other parts. These features are then used to train a classifier that can predict the tumor pixel

by pixel. The method is generally called Machine Learning. In our study, it is shown that some of the methods which segment the tumor accurately compared to the general image processing techniques. Some of the methods are Support Vector Machine (SVM) [9], [10], [11], [12] Random Forest (RF) [13], [14], [15] and Naïve Bayesian (NB) [16], K nearest neighbor (KNN) [17],[18],[19], Artificial Neural Networks (ANN) [20], [21], [22], [23] and hybrid methods [24], [25], [26] . All the methods above require special features separating a tumor pixel from a Non-tumor pixel. The accuracy of the methods depends on the feature value and the number of features extracted. Various methods are available for extracting low-level and high-level features from the MRI images. Since the classifiers need to be trained before classification a large number of data is required. The database can be collected from hospitals, or there is an open-source database for tumor detection challenges. One of such databases is BRATS. The database has different versions starting from 2012. Using the same database for different methods makes the comparison study effective. So, most of the methods discussed here use the latest BRATS database for training and testing.

Deep Learning does not require the features for training and testing. Features are extracted from the different layers in the training procedure. So, it makes the method user friendly but the complex nature of designing the deep layers emphasize the expertise required in the field. Segmentation of tumors using Convolutional Neural Network (CNN) [27] is popular among tumor detection methods. In [28] authors present a multichannel input CNN for feature extraction using CNN. Instead of giving the patches to the input layer, the authors find the superpixel segmentation of the image first because of saliency detection then each superpixel is applied to a different CNN architecture. Each CNN architecture generates hierarchical features and pooled to combine the final feature set. In [29], [30] the authors presented two experimental CNN architecture for multichannel input namely the Exception model and the Dense Net model. A high feature recognition rate is obtained as claimed by the authors. Like ML a huge database is required for training the network. The training process in CNN and Generative Adversarial Network (GAN) [31] is both complex and time-consuming. So, in this paper, we suggest a simple autoencoder based training. Instead of training on tumor pixels, autoencoder training is performed on normal pixels. The tumor is detected as an anomaly present in the brain. We hope this work will reduce the complexity and huge data requirement required for CNN and other supervised deep learning methods. To overcome this limitation, in [32], [33], the authors present an Autoencoder-based anomaly prediction. Different type of Variational Auto Encoder (VAE) is implemented and their performance is measured. The reconstruction is not the best due to the latent space loss and poor optimization.

To overcome the limitations specified above here we propose a Dual Autoencoder-based anomaly prediction for brain tumor detection. The main contribution of our work is as follows.

I. Instead of conventional square patches, we employ both horizontal and vertical patches for training an Autoencoder for normal brain image detection. This helps to keep more details inside the patch because of the heterogeneous nature of tumors in MRI images.
II. We employed separate Autoencoder for horizontal and vertical patches. An auxiliary encoder is also used to obtain useful latent space features. Singular Value Decomposition (SVD) based feature optimization is performed further.
III. The performance of the proposed method is analyzed and compared with existing Autoencoder-based anomaly predictors as well as deep learning and machine learning methods.

II. Experimental Procedure

Method

The architecture of the proposed method is presented in Fig.6. There are four stages in the overall approach. At first, we extract the horizontal and vertical patches from the training set. Two autoencoders are designed for training the patches separately. Latent space information from two primary encoders named as Z and Z' from an auxiliary encoder are combined for dimensionality reduction using Singular Value Decomposition (SVD). Finally, the optimized features are fed to a decoder for the reconstruction of normal MRI images.

Patch Extraction

Instead of traditional square patches we used horizontal and vertical patches. This will keep global and local appearance features in the patches. A dimension of 16x64 and 64x16 is kept for horizontal and vertical patches respectively. The mean intensity and variance of all the patches in the training set are extracted. All the patches are then normalized with zero mean and unit variance before fed into the autoencoder for training.

Autoencoder architecture

A classical autoencoder architecture is used here. The encoder network $Encode_{\theta}(X)$ with θ as the parameter project the training samples X to a lower-dimensional space called Z. Here the design consist of two autoencoders both for horizontal and vertical patches. The $Decode_{\Phi}(X)$ function then try to reconstruct the original samples from the latent space representation Z. Hence the network tries to recreate the normal brain samples from its lower dimensions by minimizing the loss function.

$$L_{autoenc} = (X^c - \hat{X}^c) \tag{1}$$

Where X^c is a horizontal or vertical patch and $\hat{X}^c$ is the patch reconstructed by the autoencoder. Here the autoencoder tries to reduce the $l1$ distance between the input patch and the reconstructed patch in both horizontal and vertical directions. The idea is to minimize the loss between input and output samples so that the network fails to identify the anomaly samples present in the brain MRI. Z is called the *latent space* or *manifold* representation of the input patches, which is either represented in the form of a 1-D vector or a higher-order vector in case of high-resolution MRI images for keeping the spatial context data for generating the high-quality data while reconstruction.

Auxiliary Encoder

An auxiliary encoder is adopted here for reducing the latent feature distance between the horizontal and vertical patches. While reconstructing the patches from both directions the decoders try to keep as much spatial information as possible. This creates a bottleneck while reconstructing the final image from patches. The auxiliary encoder reduces the difference in the latent space features of both horizontal and vertical encoders. One of the problems faced by classical autoencoder is the distribution distortion in the latent space. This also can be reduced using the latest features of auxiliary encoder Z' as a supporting feature for Z. Both the encoders in the first stage and auxiliary encoder has latent loss L_{en}s and L_{aux_enc} respectively.

Lower rank representation

SVD is a method used to represent a higher-order matrix to lower-order models. This is widely used as a discriminative model for outlier detection. The lower-dimensional data Z from the dual autoencoder

along with the auxiliary encoder Z' should be constrained. The variation image for each patch is localized so that it can be mapped to a lower-dimensional space. For each patch, there is a lower-dimensional latent representation$z_1, z_{2\ldots\ldots\ldots} z_n$. To construct a lower rank representation we optimize the following constraints.

$$min\ _{z_1,z_{2\ldots\ldots\ldots}z_n} \sum_{n=1}^{T} \|y_l - M_n Z_n\|_2^2\ ; st. rank(Z) = r \quad (2)$$

Where y_l, M_n represents the measurement sequence and measurement matrix respectively.

Image reconstruction

The lower-dimensional data-optimized using SVD is fed to the final decoder stage for the proper reconstruction of the images. If the input to an autoencoder is $x \in \mathbb{R}^{D_x}$, then the encoder maps the vector x into a vector $z \in \mathbb{R}^{D^{(1)}}$ as follows:

$$z^{(1)} = h^{(1)}(W^{(1)}x + b^{(1)}) \quad (3)$$

Where the superscript (1) indicates the first layer and $h^{(1)}: \mathbb{R}^{D^{(1)}} \rightarrow \mathbb{R}^{D^{(1)}}$ is the transfer function for the encoder, $W^{(1)} \in \mathbb{R}^{D^{(1)} \times D_x}$ is the weight matrix and $b^{(1)} \in \mathbb{R}^{D^{(1)}}$ is the bias vector.

The decoder maps the encoded data z into an approximation of x as follows:

$$\hat{x} = h^{(2)}(W^{(2)}z + b^{(2)}) \quad (4)$$

Where the superscript (2) represents the second layer. $h^{(2)}: \mathbb{R}^{D_x} \rightarrow \mathbb{R}^{D_x}$ is the transfer function for the decoder, $W^{(2)} \in \mathbb{R}^{D_x \times D^{(1)}}$ is the weight matrix and $b^{(2)} \in \mathbb{R}^{D_x}$ is the bias vector. The image reconstruction loss while minimizing the distance between the input vector and output vector during this process is as follows:

$$L_{rec} = \mathbb{E}_{x \sim P_x} \|x - \hat{x}\|_1 \quad (5)$$

So that the overall loss function is the sum of 2 encoders, 2 decoder loss along with auxiliary encoder, the low-rank loss, and the reconstruction loss. It is represented as follows:

$$L_{TOT} = L_{Enc1} + L_{Enc2} + L_{aux\_rec1} + L_{aux\_rec1} + L_{aux\_enc} + L_{SVD} + L_{rec} \quad (6)$$

The experimental procedure is describes as follows

A. Database

Four sets of data each consist of 760 images are considered for training and evaluation. A single image is having a size of 512x512. There are 3 namely T1 – Weighted, T2-Weighted, FLAIR images are available in an MRI dataset. Our dataset contains T1-weighted contrast enhanced images. The database has Low-Grade Gliomas (LGG), High-Grade Gliomas (HGG), meningioma, anaplastic astrocytoma, and glioblastoma multiform tumor images. Since our work mainly focuses on detecting gliomas and meningioma the images corresponding to this area selected from the database. Normal MRI images are collected from the HCP dataset. All the datasets were normalized to maintain the uniformity before going to patch extraction. All the images are then aligned and the skull is stripped before the training setup. The patches are extracted from normal images as well as non-tumor part of the tumor images.

B. Setup

Normal MRI images are employed in the training process. An autoencoder is set up for both horizontal and vertical patches separately. A total of 1, 94,560 of both horizontal and vertical patches are extracted. Patches are collected from normal images as well as tumor images having non-tumor parts. The patches are collected manually from non-tumor parts to avoid errors in the collection. Horizontal patches of size 16x64 and vertical 64x16 are applied to the corresponding autoencoder after being normalized. The hidden layer of both autoencoder is set to a size of 64, 128, and 256 for analysis. Sparsity Regularization and L2WeightRegularization are set to default values 1 and .001 respectively. A sparse mean square error loss function is employed for training and the maximum epoch is set to 4000. The learning rate was found to be decreasing for each iteration in the training process. Autoencoder is implemented using the Neural Network Toolbox of MATLAB.

C. Training and Optimization

The dataset consists of four set of 760 images of gliomas and meningioma were used for training and validation. While for training the network MRI with no tumors is selected. The patches are extracted from true images and also from the tumor images excluding the tumor parts. Around 1,94,560 horizontal and vertical patches are procured by this process and normalized as explained above before applied to the network architecture for training. A logistic sigmoid transfer function is used for both encoder and decoder parts respectively. SGD optimizer is used for optimization with an initial learning rate of .001 and the maximum epochs used are 4000. The network is trained in MATLAB 2018a with a processor capacity of 3.7 GHz with NVIDIA GPU and 16 GB of RAM. The obtained results along with a comparison with other networks are explained in the next section.

D. Evaluation

Three evaluation metrics are considered to measure the performance of the proposed system such as Dice Similarity Coefficient (DSC), Positive Predictive Value (PPV), and Sensitivity. The DSC is a measure of overlap between the ground truth and the automatic segmentation. It is given by

$$DSC = \frac{2TP}{FP + 2TP + FN}$$

Where TP, FP, FN are the True Positive, False Positive, and the False Negative detections respectively. PPV is measured from the TP and FP is defined as,

$$PPV = \frac{TP}{TP + FP}$$

Finally, Sensitivity measures the proportion of positives that are correctly identified, being defined as

$$Sensitivity = \frac{TP}{TP + FN}$$

III. Discussion

Brain MRI images are having a highly complex structure. Fig.1 shows the sample images from the HCP dataset. The top row shows the normal MRI images from the HCP dataset and the bottom row are MRI images with the tumor. The first two images in the second row are meningioma variety and the rest are glioma images. We use only normal images for training. To include more data diversity we used a non-tumor part of tumor images for training. During the inference, the final decoder makes a reconstruction error for tumor pixels which is identified as anomalous samples. Some post-processing is also necessary to remove skull portions which are identified as tumor pixels.

The latent space representation of single autoencoder and the reduced representation by SVD are shown in Fig. 2. 3D scatterplot is used to represent the latent features. Multiple loss functions are to be calculated from Dual encoder and auxiliary encoder data before giving the features to SVD for

dimensionality reduction. The obtained features were statistically more independent as compared to features from the encoder outputs. The final decoder then analyses the features for the reconstruction of the samples.

The idea behind the anomalous detection of tumors is that the autoencoder failed to reconstruct the tumor pixels. Using a simple distance classifier as a hypothesis we can segment the tumor pixels from non-tumor pixels. We tried both meningioma and gliomas tumor for testing the performance of the proposed method. Some examples of the performance of the proposed dual autoencoder are shown below in Fig.3 for reference. To avoid the detection of skull regions they are stripped out before given to the tumor segmentation. The distance images are further processed to get a clear view of the tumor. This is shown in Fig. 4. The results in Fig.4 are obtained using a patch size of 16x64, 64x16 for horizontal and vertical patches respectively. Even though we tried other patch sizes the best results are obtained for a size 16x64 for horizontal and 64x16 for vertical patch. In Fig.4 MRI from (a) - (f) are Meningioma images while images from (g)-(j) are Glioma images. The segmented results obtained for Meningioma are better compared to the results for Gliomas.

Some post-processing operations for removing the unwanted parts detected as tumor pixels in Meningioma while Gliomas require further post-processing like region filling. In Glioma images tumor is not grown from a point rather it spreads randomly. This created voids in tumor parts. Region filling and connectivity operations are performed to get the final tumor segmentation. The results obtained after post-processing is shown in Fig.5 from (a)-(d) along with the ground truth representation (e) - (h).

Three evaluation metrics are employed here to measure the performance of the proposed system namely DSC, PPV, Sensitivity. The proposed method uses another patch size of 16x32 but with lower performance compared to a patch of 16x64. Also, the model is tested for a conventional square patch of size 16x16. The obtained results are given in Table.1. The anomalous tumor prediction in [33] uses the Area Under the Curve (AUC) for the evaluation. The paper also compares the classical autoencoder, Vibrational autoencoder for their performance in anomalous tumor detection. The comparison of these with the proposed method is given in Table. 2.

IV. Conclusion

Dual autoencoder based architecture is proposed here for tumor detection and latent space optimization is done using SVD. Instead of conventional square patches, we employed horizontal and vertical patches. This keeps the complex spatial information in the patches. Performance analysis shows this provides better results than square patches. The reconstruction error of the final decoder from the optimized latent features is used to identify tumor pixels from normal pixels. The experimental analysis states that the proposed method can be compared to a deep learning method in terms of performance but with less design complexity. The huge dataset requirement, complex design, and rigorous training cost of deep learning-based models are bypassed using normal brain samples for training and testing. Treating tumor pixels as anomalous samples lead to the development of unsupervised tumor segmentation models. Overlapped skull and tumor regions still create performance degradation in the proposed system. In the future, this can be overcome by using a semi-supervised model where the tumor pixels are treated as forged on normal brain images. Due to its simplicity in design, we hope the proposed method using autoencoder will lead to more sophisticated anomaly prediction designs.

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VI. Figure Legends

Fig. 1: Normal MRI images (First row), Tumor Images (Second row*)*

Fig.2: Plot (a) shows the Latent space features collected from two encoders and one auxiliary encoder. Plot (b) is the lower-dimensional features obtained after the SVD method.

Fig. 3: Example of the proposed method of MRI images. Meningioma (First row), Glioma (Second row). The first image in each section is the tumor image, the second is the reconstructed image by the proposed method, and the third is the difference of tumor image from the reconstructed image.

Fig.4: The first row represents the tumor images, second row is the result obtained after processing the reconstructed image from the proposed method. The third row is the ground truth representation.

Fig.5: Images in the first row represent the results after post-processing, while second row shows the corresponding ground truth representation.

Fig6. Overview of the proposed method

Declaration

I have the pleasure of sending you the manuscript entitled "**A dual autoencoder and SVD based feature optimization for detection of brain tumor from MRI images** "authored by **Aswani. K** to be considered for publication as a research article in your prestigious journal **BMC Medical Imaging**. Paper is containing original research and has not been submitted / published earlier in any journal and is not being considered for publication elsewhere. All authors have seen and approved the manuscript and have contributed significantly for the paper.

Ethical Procedure

• The research meets all applicable standards with regard to the ethics of experimentation and research integrity, and the following is being certified/declared true.

• As a research scholar and along with co-authors of concerned field, the paper has been submitted with full responsibility, following due ethical procedure, and there is no duplicate publication, fraud, plagiarism, or concerns about animal or human experimentation.

A DISCLOSURE / CONFLICT OF INTEREST STATEMENT

• None of the authors of this paper has a financial or personal relationship with other people or organizations that could inappropriately influence or bias the content of the paper.

• It is to specifically state that "No Competing interests are at stake and there is No Conflict of Interest" with other people or organizations that could inappropriately influence or bias the content of the paper.

Authors Contributions

Aswani

Study conception and design: The concept of the work is developed. The work is based on the deep learning in medical image analysis

Acquisition of data: The data is acquired from a publically available data set (https://figshare.com/articles/brain_tumor_dataset/1512427)

Analysis and interpretation of data: The dataset contain 4 se of 760 images having Gliomas and Meningioma tumor. The images are in MATLAB format .mat and contain the ground truth mask for analysis. Each image is 512x512 in size and 16 bit resolution. The images are pre-processed before put in to training and testing.

Dr.D.Menaka

The drafting of the manuscript and critical revision is done

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Table.1: Study and comparison of the proposed method and various deep learning and machine learning methods.

Method	Patch size	Type	DSC	PPV	Sensitivity
Proposed	**16x64**	**Meningioma**	***0.84***	**0.88**	**0.90**
	16x32		*0.83*	0.85	0.87
	16x16		*0.81*	0.82	0.83
	16x64	**Glioma**	***0.82***	**0.84**	**0.86**
	16x32		*0.81*	0.825	0.85
	16x16		*0.78*	0.80	0.81
CNN [27]	16x16	Glioma	*0.84*	0.85	0.86
SVM [5]		Glioma	*0.80*	0.81	0.82
KNN,SVM [18]		Various	*0.81*	0.815	0.83
ANN [23]		Various	*0.83*	0.82	0.84

Table.2: Comparison of AUC for different autoencoder architectures

Method	AUC
Proposed	**0.995**
Adversarial [33]	0.994
AE	0.764
VAE	0.816
VAE-H	0.74
eeVAE	0.867
ADAE	0.892
EB	0.95

Figures

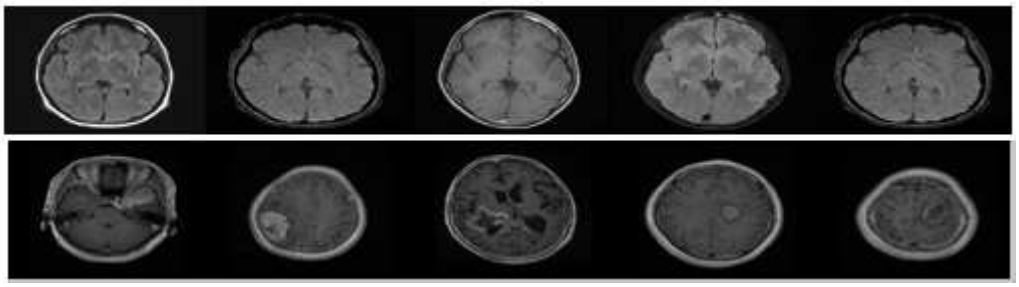

Figure 1

Normal MRI images (First row), Tumor Images (Second row)

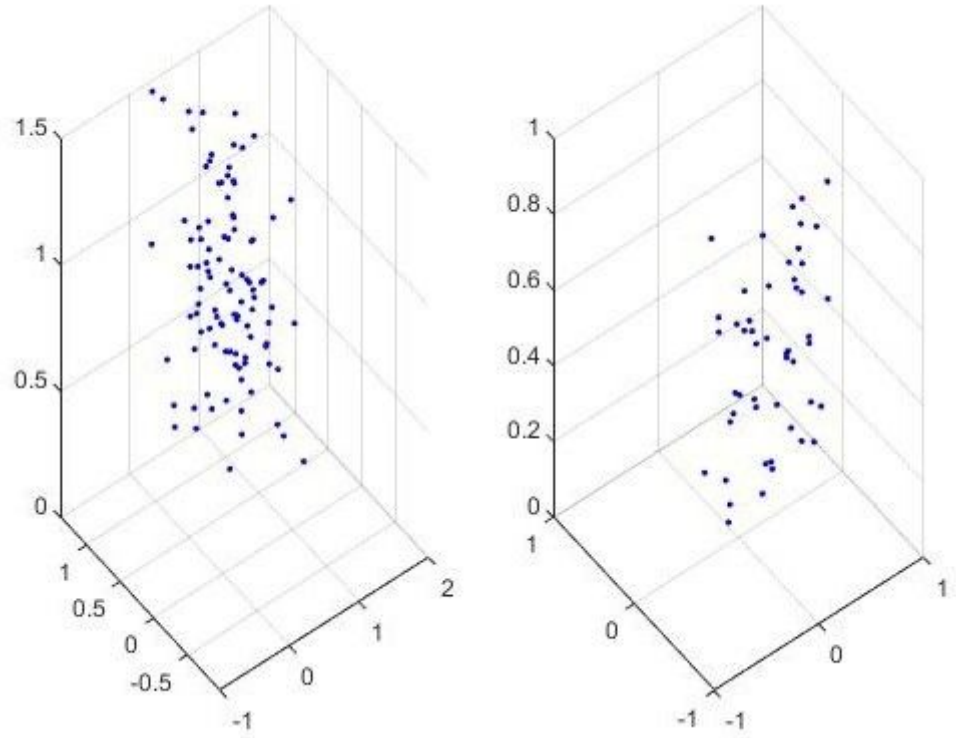

Figure 2

Plot (a) shows the Latent space features collected from two encoders and one auxiliary encoder. Plot (b) is the lower-dimensional features obtained after the SVD method.

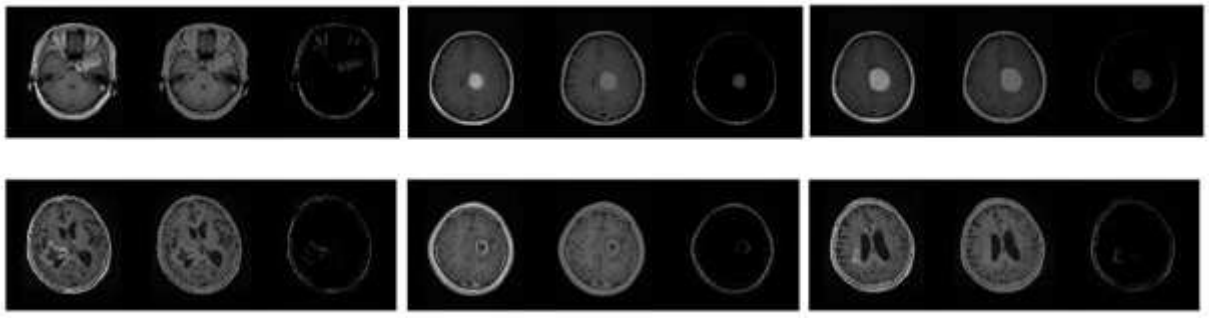

Figure 3

Example of the proposed method of MRI images. Meningioma (First row), Glioma (Second row). The first image in each section is the tumor image, the second is the reconstructed image by the proposed method, and the third is the difference of tumor image from the reconstructed image.

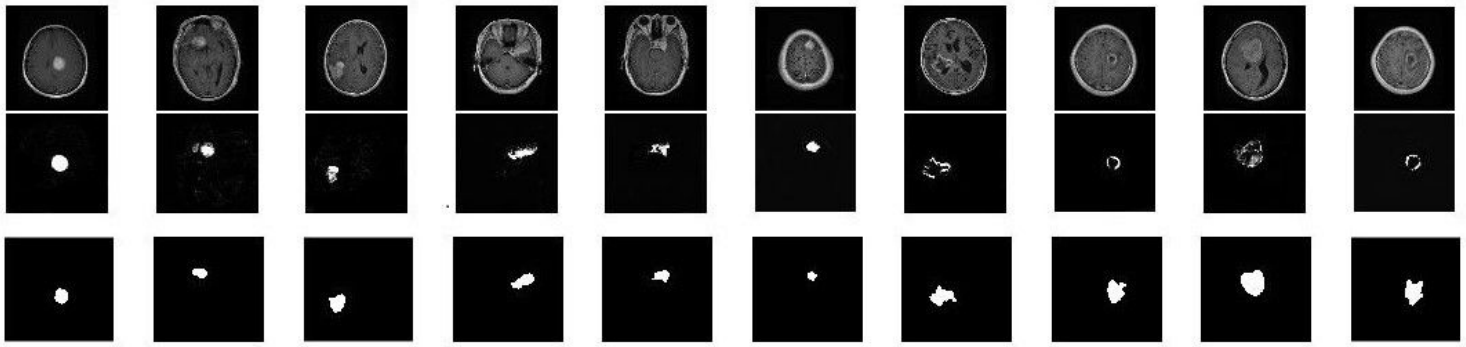

Figure 4

The first row represents the tumor images, second row is the result obtained after processing the reconstructed image from the proposed method. The third row is the ground truth representation.

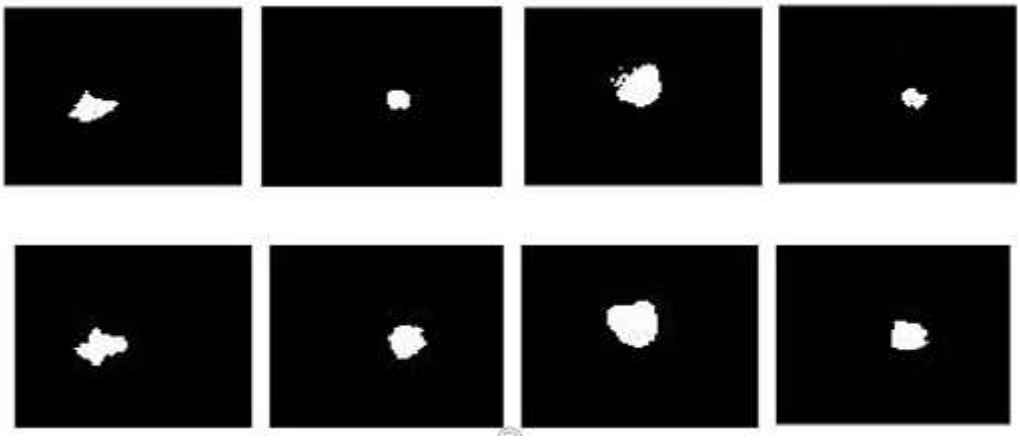

Figure 5

Images in the first row represent the results after post-processing, while second row shows the corresponding ground truth representation.

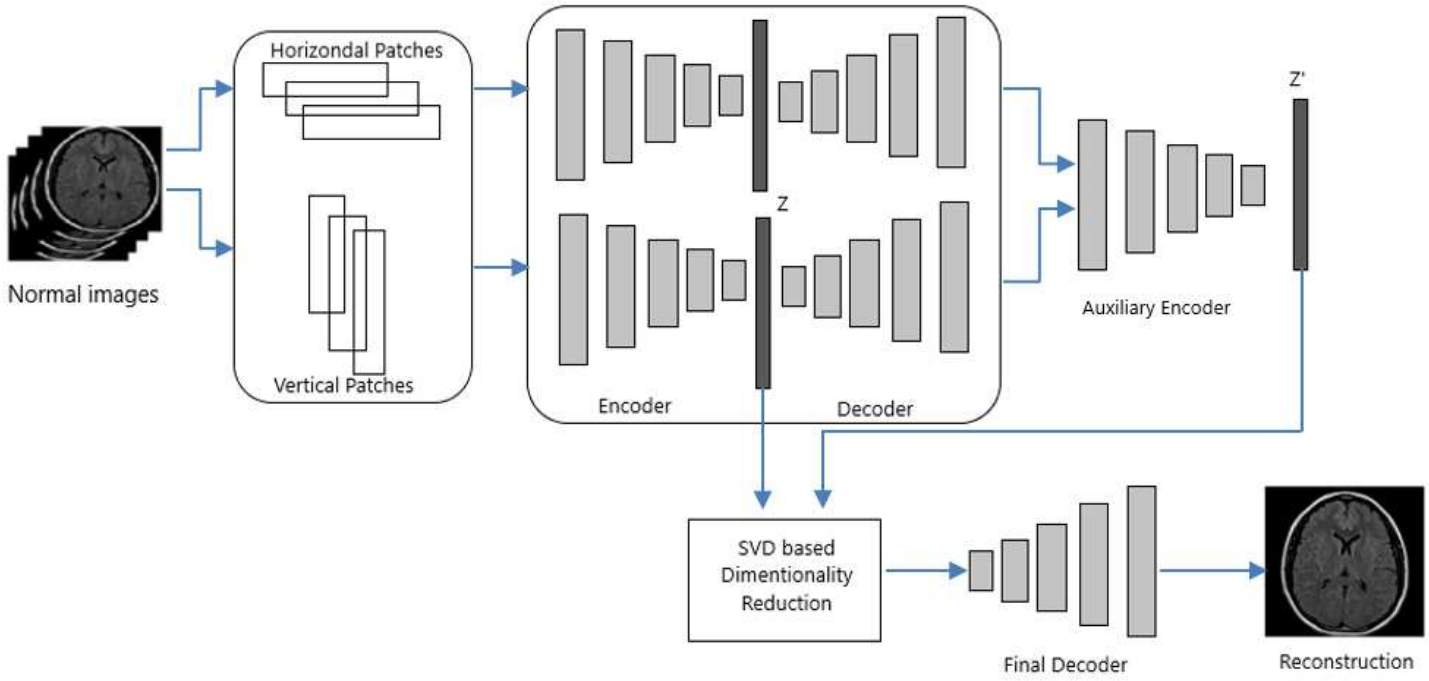

Figure 6

Overview of the proposed method