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## Prostate cancer classification from ultrasound and MRI images using deep learning based Explainable Artificial Intelligence



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#### ABSTRACT

Prostate cancer is one of the most common forms of cancer in men in many countries. The survival rate can be significantly enhanced with early detection of the cancer so that appropriate intervention can be administered. In this work, a novel automated classification algorithm by fusing a number of deep learning approaches has been proposed to detect prostate cancer from ultrasound (US) and MRI images. In addition, the proposed method explains why a specific decision is made given the input US or MRI image. Several pre-trained deep learning models having customs-developed layers are added on the top of the respective pre-trained models and applied to the datasets. The best model generates a maximum accuracy of 97% on US images and 80% on MRI images of the test set. The model that produced the best classification performance was selected to use as feature extractor from the dataset to build a fusion model as a next step. To improve the models performance, especially on the MRI dataset, a fusion model is developed by combining the best performing pre-trained model as feature extractor with some other shallow machine learning algorithms (e.g., SVM, Adaboost, K-NN, and Random Forests). This fusion approach remarkably improves the performance of the system by achieving the accuracy from aforementioned 80% to 88% on the MRI dataset, Finally, the fusion model is examined by the explainable AI to find the fact why it detects a sample as Benign or Malignant Stage in prostate cancer. The proposed approach can be adopted in smart clinics or hospitals for efficient prostate cancer detection and explanation.

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#### 1. Introduction

Prostate cancer is one of the most common cancer among males around world. For instance, American Cancer Society estimated prostate cancer will be the second main reason of death from cancer of men in the United States in 2021 [1]. If the prostate cancer can be precisely detected at early stages, the survival rates can be significantly increased than the current rate and appropriate intervention can be administered.

At present, the standard of care process to diagnose prostate cancer is a combination of the US, prostate-specific antigen test, and magnetic resonance imaging (MRI) test [2]–[3]. Currently,

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TRansrectal UltraSound (TRUS) imaging is the first modality of choice to image the prostate and detect abnormalities including cancer. Often MRI and TRUS imaging were performed to fully detect the cancer but still it lacks high accuracy and often regions that may be cancers could be avoided or neglected. Hence, automatic detection using machine learning architecture can be exploited to deliver high accuracy of detecting the cancer. Machine learning (ML) methods have been applied on a large as well as small scale database with the help of probabilistic and statistical methods for various medical applications, especially in the imaging field. For instance, imaging feature processing and ML-based prediction or classification have shown quite good potential in aiding the radiologists for as accurate diagnosis as possible to decrease the diagnosis time as well as the cost. Moreover, it can aid the radiologist to consider regions of interest for predicting cancer which would have been neglected otherwise.

Many studies found the application of ML methods to classify the type of cancer through analyzing MRI image data. However,

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very little studies used the state-of-art deep learning technology (e.g., Convolutional Neural Network) to analyze US images for detection of pro-state cancer. While using ML for detecting/classifying cancer from MRI images, the most popular approach is to extract features from the input image and then apply ML models using the extracted features. Conventional feature analysis approaches are mostly based on extracting features from texture, contour, intensity, and various statistical features to apply with a ML classifier such as Decision Trees, Support Vector Machines (SVM), Adaboost, and deep learning to detect cancer [4– 6]. Deep ML approaches have already demonstrated applicable in many image processing and computer vision application areas such as object-detection, video surveillance, and infected/diseased regions in medical images [7-11]. Among other deep learning approaches, convolution neural network (CNN) is the most successful architecture which are capable of extracting robust features from the input images that considers features from low level to the high level. In typical CNN algorithm, after a hierarchy of layers representing convolution and pooling to reduce the size of the filtered outputs, a dense layer(where neurons are fully connected) at the final/last part of the convolutional neural layers are added to convert the convoluted/extracted features into the probabilities of certain classes to take the decision. Other type of layers in CNNs, such as batch normalization layer to normalize the input of a layer and dropout layer to ignore nodes, that are selected randomly, have contributed to improve the overall performance of deep learning-based approaches [12-14]. However, an optimal structure of the different layers as well as appropriate fine-tuning of the hyper-parameters are quite useful in this regard, which can be seen as one of the key challenges of deep learning to apply in different important research (e.g., medical image processing). In that study, the authors conducted 2-D classification of the target region with the help of Residual Network (ResNet) with addition of handcrafted features. In another study [15], the authors applied VGGNet based on 3-D CNN the images on ProstateX challenge dataset. They used 341 patient data for training and 140 patients for testing. Their algorithm resulted in 80% of accuracy on test set. In a recent study [16], the authors compared the classification performances of deep learning versus non-deep learning methods on different MRI-slices of 172 patients. They applied VGGNet consisting of five convolution layers where they achieved accuracy of 84% on their test dataset. Thus, in addition to the aforementioned models, there are other pre-trained deep learning models such as MobileNetV2, ResNet50V2, Resnet101V2, Resnet152V2, Xception, InceptionResNetV2, and InceptionV3 which could be applied for to detect prostate cancer from given imagesets [17-19]. The current work explores such models to detect prostate cancer from US and MRI images. Though the pre-trained models have been successful in different applications but they can also be utilized for generating a fusion with shallow machine in the form of transfer learning.

Artificial Intelligence(AI) has achieved a remarkable momentum in recent years [20–44]. To meet the expectations, the AI community is now facing the barrier of explainability problem (i.e., XAI) occurred during the recent success of AI. XAI is a vital feature for the practical applications of current AI models. Since XAI seems to continue its trend as one of the core future research focuses of AI community, it would be quite sensible to deeply examine the contributions already achieved in XAI so far and focus on the prospects towards what are to be achieved yet. Hence, AI researchers should target with the concept of trustworthy AI through exploring XAI for the large-scale implementations of AI techniques in organizations majorly concentrating on explainability, fairness, and accountability. The recently observed good success of ML models has been mostly possible with the help of efficient deep learning algorithms in huge parametric space,

which includes hundreds of layers and millions of parameters. Such status makes the deep learning models as complex blackbox models. Hence, black-box ML models are progressively being employed day by day to do significant predictions in crucial contexts, pushes the demand of transparency.

Feature significance explanation techniques for explainability show the inner functioning structure of a model by computing significance/importance scores for its variable parameters. The scores provide the sensitivity that a feature consists considering the output generated by the model. A comparison of the significance scores of the variables shows the importance of the variables to the model while producing the outputs. The typical goal of feature relevance explanation methods is to illustrate the functioning of an unclear model by ranking the influence, relevance, and importance the features have on the predictions of the model to be explained. One useful and popular contribution to is SHapley Additive exPlanations (SHAP) where the researchers presented a technique to calculate feature importance scores for each prediction made by the considered model with respect to desirable properties such as local accuracy, missingness and consistency. Most of the techniques that attempt to simplify model focus rule extraction techniques. Among these, the most popular ones uses local post-hoc explanation which follows the approach of "Local Interpretable Model-Agnostic Explanations" (LIME). LIME works by generating local linear models to predict an impervious ML model for explaining it. Hence, LIME can be categorize as those rule-based local explanations XAIs. Where, a new system is built based on the explanations by simplification on the trained model. Then, this simplified model is used to optimize its resemblance to its predecessor model functions with a parallel focus toward reducing the complexity while keeping a similar classification performance. LIME has been tried in many practical applications to explain AI decisions including medical imaging, due its faster capability of explaining over SHAP.

In this work, a number of pre-trained deep learning model is fused with other shallow ML approaches (i.e., Randoms Forests, Support Vector Machine, Gradient Boosting, and Nearest Neighbor) to achieve superior performance over the conventional approaches to detect prostate cancer from a publicly available medical dataset. Besides, a robust XAI approach (i.e. LIME) is applied to focus the interesting region in the classified images once the decision is made by the pre-trained and fusion-based robust method. The contributions of this work are summarized as follows:

- An automated computational tool by fusing a number of pre-trained models is developed to analyze and classify Prostate cancer using US Image as follows:
  - Several pre-trained models have been custom-modified to add one or more layers and the achieved model was applied to the datasets. The best model achieved an accuracy up-to 97% accuracy on test data.
  - The pre-trained models were also applied to MRI data and achieved an accuracy of 80% on test data.
  - A multi-modal fusion model combining the above pretrained models and few other ML classifiers was developed to enhance the classification accuracy for MRI dataset.
- The fusion model enhanced the classification performance from to 88% accuracy comparing with the best of performance of base pre-trained model, i.e., 80%.
- Explainable AI was used to identify why specific patients' data were classified as Benign or Malignant.

#### 2. Background

Machine learning algorithms apply linear or nonlinear transformations at a high level on small or large databases. Hence, they are applied in the vast fields of applications such as health care like cancer detection, disease prognosis and diagnosis, image analysis and object detection, continuous signal processing and speech recognition, feature extraction and image classification, and natural language processing. In the proposed methodologies we used a number of existing, pre-trained deep learning models and ML classifiers. For the sake of completeness, in this section a brief description of each of the existing methods, that have been used in our methodologies, is provided.

A Support Vector Machines (SVM) constructs one or more high-dimensional hyper-planes to solve classification and/or regression problems [45]. In SVM, a good separation boundary can be achieved by obtaining an optimized hyperplane that is located in the largest distance to the nearest training-data samples. Generally, the bigger the margin represents lower generalization error of the classifier and vice versa. SVMs can be generally seen as most used models for small datasets due to their good prediction and generalization performance.

Random Forest is a well known classifier that is built by inducing a number of decision tress through selecting the root of each of the tree randomly. Decision trees follows hierarchical structures for decision making which can be used to apply for classification problems [46]. Though decision trees are usually easily simulated models, their properties however can render them decomposable. The utilization of decision trees has been mostly linked to decision making contexts given that their complexity and understandability have been the vital consideration. Currently, tree ensembles can be arguably considered as the most accurate models in use these days. Individual decision tree for ML usually prone to overfitting. To resolve this issue, tree ensembles combine different trees to obtain an accumulated prediction. Thus while its efforts on gaining effectiveness against overfitting, the combination of models makes the interpretation of the overall ensemble complex.

In Gradient Boosting, performance of weak classifiers is enhanced through using a number of weak classifiers. The residual of one weak classifier is used as input to another weak classifier. Typically, decision tree is used as weak classifier to enhance the classification performance. A learning rate is used to monitor the gradient of learning of the chained weak classifiers as mentioned above. If the gradient is negative the approach appreciates it and hence the name is Gradient Boosting.

Nearest Neighbors (NN) classification algorithms handles the problems in a very simple way [47]. It predicts the class of a sample by voting the corresponding classes of its K nearest neighbors. The neighborhood is represented by the measure of distance between samples. For regression problems, the voting methods is replaced by the average of the target values associated with the K nearest neighbors. The interesting matter is, this approach of prediction resembles the experience-based human decision making where decision is made based on the results of past similar cases.

#### 2.1. Convolutional neural network

Convolutional Neural Network (CNN) consists of multiple layers and is usually based on the animal visual cortex. In CNNs, earlier layers are used for obtaining the features (e.g., edges and shapes) that can be used in the later layers to form high level features [26,48]. To handle the dimensionality limitations of the extracted features, pooling is done. Thus, convolution and pooling is repeated there to fed into a perfectly linked multilayer perceptron. The final layer or output layer recognizes the

features in the image by applying back-propagation algorithms. The deep layers of processing, convolutional, pooling, and a fully connected classification layer makes it happen in various successful applications, mostly in image processing and computer visions. CNN can produce better accuracy and represents better performance of the system because of its local connectivity and shared weights. One of the limitations of the feature map of convolutional layers is that they store precise position of features where a small movement in the position of the feature in the input image may result in a different feature map. Such problems are usually handled by down sampling where a low-resolution version of the input data is made while containing the important structural elements. That may lose the fine details of the input, but they may be sacrificed for greater purpose such as for better classification accuracy task. The down sampling is normally done by changing the stride of the convolution across the image. However, the more robust approach is to use a pooling layer for such cases. Pooling layers are usually layers added just after the convolutional layer in the network. There are two popular kind of pooling process: maximum and average. Prior to the pooling, Nonlinearity (e.g. ReLU) can be applied to the feature maps from convolutional layer. Thus, a typical CNN layers consist of input image, convolutional, nonlinearity, and pooling layers. Finally, a fine-tuning process is added to tune the hyper parameters of the network. Thus, a typical convolution layer can be represented as

$$Conv_k^{(i+1)}(m,n) = ReLU(p), \tag{1}$$

$$ReLU(p) = \sum_{(g=1)}^{z} \Omega(m, (n-g+\frac{z+1}{2}))W_k^i(g) + \alpha_k^i$$
 (2)

where  $Conv_k^{(i+1)}(m,n)$  represents the convolution of (m,n) coordinates for the layer (i+1) and kth convolution map.  $W_k^i$  represents the kth convolution matrix (or kernel) for the ith layer.  $\alpha_k^i$  represents the bias for layer i and kth convolution map.  $\Omega$  is the map that was used/generated in the previous layer. z represents size of the convolution matrix/kernel. ReLU here is the activation function that computes the summation of weights of the previous layer which is fed as input to the next layer.

The typical max pooling layer (i+1), kernel k, row x, and column y can be shown as

$$Pool_k^{i+1}(x, y) = \max_{1 < r < s} (Convolution_k^i(x, ((y-1)+s)))$$
 (3)

where *s* represents the length of the pooling window. All the layers of the convolutional neural network works in similar way except the last layer where a dense/fully connected layer is used. The fully connected layer uses the following equation:

$$FullConnect_{j}^{(l+1)} = ReLU(\sum_{i} X_{i}^{l} W_{ij}^{l} + \alpha_{j}^{l})$$
(4)

where  $W_{ij}^l$  matrix contains the weight values of the node i from the layer l to the node j from the layer (l+1).  $X_i^l$  is the content at the node i from layer l.

#### 2.2. Pre-trained deep learning models

The training of deep learning methods usually follows a greedy approach that works well with large datasets. Having such kind of large data was initially a major concern. However, with the emergence of big databases in different fields and the availability of hardware-accelerated fast devices like graphical processing unit (GPU), cluster computing, research in deep learning got exploded as evidenced by having a large number of deep learning models (e.g., VGGNet, ResNet, MobilNET, etc.) in last five years [17]. For the sake of completeness, few popular deep learning models are

introduced here because these models have been used in our proposed approach.

The VGG-16 model is a popular deep convolutional neural network that has 16-layers (convolution and fully connected). VGG-16 has been built on the ImageNet database (ImageNet is one of the popular large database of huge images). VGG-16 model was created by the Visual Geometry Group at the University of Oxford. There exist a variant of VGG-16 known as VGG-19. The concept of the VGG19 is same as the VGG16 excepts the network is 19 layers deep.

Residual Networks (ResNet) ensures that the performance of top layers is as good as the lower layers without vanishing gradient and optimization problem. There exists many variants of ResNet architecture where the same concept but different number of layers are used. The naming of each variant of the ResNet is done as follows. Each variant of ResNet uses the name ResNet and then following this name two or more digits are added. These numbers imply the architecture and number of layers that have been used to form the respective variant of the ResNet. Few examples of variant of ResNet are ResNet-18, ResNet-1202 etc. There is another variant of ResNet referred to as ResNet V2 which is an extension of ResNet V1. The extension is made through adding a second non-linearity as an identity mapping function.

Inception is a convolutional neural network that can achieve very good performance and has lower computational cost comparing with other variations of convolutional neural network architectures. The latest generation of Inception is Inceptionv3 which is another type of convolutional neural network with a depth of 48 layers for assisting in image analysis and object detection, and got its start as a module for Googlenet. The connection weights/size of the parameters of Inception V3 are smaller than that of both VGG and ResNet, which takes a memory space of 96 MB.

Another extention of Inception architecture is Xception where Inception modules were replaced with depthwise separable convolutional layers. In Xection, 36 depthwise separable (convolution) layers have been used on a linear stack. Each layers were connected through linear residual connections. There are a depthwise convolutional layers and pointwise convolutional layers in Xception model. Xception architecture has the similar parameters as Inception V3 but the better performance can be gained by efficiently adjusting the model parameters.

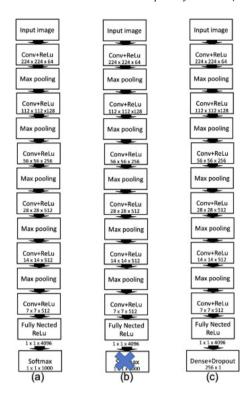
MobileNet has 17 MB of network size with 4.2 million which is small compared to other typical networks that have faster performance. They are mostly useful for mobile applications. MobileNetV2 is Light Weight Model for Image Classification that usually can outperform MobileNetV1.

#### 3. Methodology

Before describing the proposed method first an attempt was made to classify prostate cancer using conventional pre-trained deep learning CNN approaches. Hence, first we discuss how conventional approaches performed for the dataset used in this study. Then, we justify the need to design a new method through modifying and/or adapting existing method following the description of the developed method.

### 3.1. Prostate cancer classification using conventional deep learning approaches

The aim of this study is to develop an automated computational approach to efficiently classify prostate cancer by analyzing MRI and US images. In order to test the efficacy of already exist-



**Fig. 1.** (a) VGG16 model architecture; (b) the last layer of VGG16 was removed; (c) Added dense and dropout layers to classify binary data.

ing popular deep learning approaches, a list of pre-trained deep learning models (e.g., MobileNetV2, ResNet50V2, Resnet101V2, Resnet152V2, Xception, VGG16, VGG19, InceptionResNetV2, and InceptionV3) were applied to classify the data used in this study. To be able to classify the data into either benign or malignant each of the pre-trained models were modified as follows:

Usually, pre-trained models have been generated in such a way so that they can be used for any problems with many classes. Since, our problem is restricted to a binary class problem, the last layer of the pre-trained model was truncated and new layers were added as the last layer so that the model is suitable for binary classification problem. Fig. 1 shows how the original VGG16 architecture was modified to be applicable for binary class problem. The modified structure is then trained using back-propagation algorithm and the training dataset.

The list of pre-trained models as mentioned above was modified to be applicable for binary class problem and the performances were analyzed. The analysis suggests that conventional deep learning approach can provide very good classification accuracy for US images (the results are presented and discussed in Section 5. However, for MRI images the classification accuracies were not at satisfactory level. Hence, these models need to be further enhanced so that the performance for the MRI image analysis and classification can be enhanced. The next section describes how the pre-trained models have been adapted.

#### 3.2. Fusion of pre-trained deep learning approach with ML classifiers

The pre-trained models adapted in the previous section utilizes combination of dense and dropout layers in the last layer of the respective deep learning architecture. In our proposed approach, input data are fed in parallel to all the pre-trained models as listed in Section 3.1. Our proposed model selects the model that achieves the best classification accuracy for the training dataset because, the conjecture is that the extracted features by

the selected model would provide the best discriminative feature set. Once the best performing model is selected, the last layer of this model is removed so that this model can be used as a feature extractor in place of an automated classifier. The extracted features for each of the input image of training dataset are then fed into well known ML classifiers (e.g., Random Forest (RF), Support Vector Machine (SVM), Gradient Boosting (GB), and Nearest Neighbor (NN)) to train the respective classifiers. This fusion of deep learning feature extractor with ML classifier is thus used to classify new MRI image data to either benign or malignant. Fig. 2 shows the steps of the proposed fusion model to classify prostate cancer. As shown in the figure, the best performing model is selected out of the nine models and this model is then used as a feature extractor. Following example further clarifies how the model works.

**Example.** Let us consider a set of deep learning pre-trained model as  $\mathcal{DL} \in \{MobileNetV2, ResNet50V2, Resnet101V2, Resnet152V2, Xception, VGG16, VGG19, InceptionResNetV2, InceptionV3\}. For the training dataset D assume the model Xception achieves the best classification accuracy. The last layer of the D is removed and the model after removing the last layer is used as feature extractor for any input image. Consider the features extracted for an input image <math>d_i$  where  $D \in \{d_i\}$ , and  $(i = 1, 2, 3, \ldots)$  are F;  $F \in \{f_1, f_2, f_3, \ldots, f_j\}$ , (j is the total features extracted from the image). These features of the respective input image is thus fed into the list of ML classifiers like RF, SVM, GB, and NN. Each of the classifiers will classify the input image through using the extracted features to either benign or malignant.

#### 3.3. Explainable artificial intelligence

Explainable Artificial Intelligence (XAI) has been recently emerged to justify why a specific AI tool made a decision. For example, for a given US image our proposed model classifies the image as benign. XAI would justify why the proposed model classified the input image as benign. The application of XAI can be better understood in the following example:

**Example.** Consider a DL classifies an image as cat which is correctly classified. However, it will be great to know why the classifier classified the image as cat. The explanation could be that the animal has fur, whiskers and claws hence it has been classified as cat. These explanation certainly would help the user of the automated system to decide whether he/she will trust the decision made by the DL classifier. There are a number of XAI tools available to explain a decision made by a classifier. In this study we use the popular Local Interpretable Model-agnostic Explanations (LIME). In this section, we briefly describe LIME algorithm following a given study [31].

In LIME, first the ith input image  $d_i$  is locally characterized considering closest images in the training dataset/generated dataset to the  $d_i$ . Dataset can be generated/simulated through many ways,e.g., through sampling of non-zero elements of  $d_i$  and randomly selecting features from those non-zero elements following a probability distribution. Let us consider the simulated instances are represented as k and the proximity between k and  $d_i$  is  $\pi_{d_i}(k)$ . For our proposed model represented as g the complexity is assumed as g (following the same symbol as reported in [31]) while the underlying function that is supposed to achieve is referred to as g (g). The measure g (g) represents how g fits in g or alternatively how much unfaithful g is to approximate the desired function g in the locality as defined by g (g). The aim is to reduce the measure of unfaithfulness so that interpretability and local fidelity are ensured as represented in Eq. (5) [31].

$$\arg\min_{g\in G} \mathcal{L}(f,g,\pi_{d_i}) + \Omega(g) \tag{5}$$

here, G represent the potential interpretable models.

In LIME, Eq. (5) represents the explanation of decision  $f(d_i)$  made by the model g. Because, this explanation depends on simulated instances within close proximity of input data  $d_i$  one such model based on local surrogate requires sufficient data to be generated around the input. In LIME, data are generated by sampling the neighborhood instances to the input data and/or generating data by randomly sampling non-zero elements of the input data which is referred to as perturbation technique. Finally, the explanation of the decision  $f(d_i)$  is achieved by Eq. (5).

#### 4. Experimental setup and dataset

#### 4.1. Experimental setup

For each of the pre-trained models used in this study the last layer was replaced with a dense layer of size 256 following the description in Section 3.1. For example, for the VGG16 pre-trained model, the following code fragment (in Python) was used to replace the last (top) layer with a dense layer and the other learning parameters are also shown in the code (see Listing 1). The same learning parameters and algorithm were used for the other pre-trained models. All the experiments were executed on a PC with Core i7 11the generation intel processor, 16GB DDR RAM and the software/methods were developed in Pyhton Version3.7 with Tensorflow 2.x and scikit learn 0.242 version.

**Listing 1:** The code fragment to use pre-trained VGG16 for binary class prostate cancer classification

For the fusion model described in Section 3.2, the following parameters were used for each of the ML classifiers.

- RF: No. of trees: 50
- KNN: Value of K: 5, similarity measure: Euclidean Distance
- **SVM:** Kernel: RBF, C=[1 10 50 100 1000], Gamma=[0.1 0.5 1.5]
- GB: No. of trees: 50, classifier: Decision tree

#### 4.2. Dataset

Prostate MRI and US image data were obtained from the publicly available open source database at the Cancer Imaging Archive [49–51]. The US data were acquired with Hitachi Hi-Vision 5500 7.5 MHz or the Nobulus C41V 2–10 MHz end-fire probe. MR imaging was performed on a 3 T Trio, Verio or Skyra

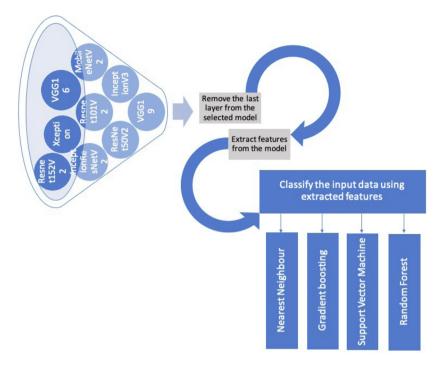


Fig. 2. Framework of the proposed model.

**Table 1** Classification accuracy of pre-trained models.

CNN Pre-trained model	Classification accuracy rounded (%)		
	US image data	MRI image data	
MobileNetV2	99.00	75.00	
ResNet50V2	99.00	81.00	
ResNet101V2	99.00	73.00	
ResNet152V2	99.00	82.00	
Xception	95.00	48.00	
VGG16	99.00	81.00	
VGG19	96.00	77.00	
InceptionRegNetV2	95.00	47.00	
InceptionV3	94.00	64.00	

scanner (Siemens, Erlangen, Germany). All the image data were in DICOM format. The open source database provided the information regarding the link between the MRI and US image for the given patient and simultaneously referred to the biopsy results where available. Our internal team of medical professional also viewed and analyzed the images with respect to the information provided in the database so that we use the appropriate data for our training and testing of the models.

In this datasets images were acquired from 1151 participants in a total of 2799 studies. A total of 61,1119 images were available in the open source database. In the current study we randomly selected 80% of the available data as training and the rest 20% data were used to test the efficacy of the trained model. While selecting the images randomly, we made sure so that images from each individual patient are not duplicated both in training and test data. Moreover, if a patient's image was selected as training data none of the images from the same patient was selected as test data so that the test data remained completely unseen to the models used in this study. MRI slice was randomly selected from a number of available slices of the same patient.

#### 5. Experimental results analysis and discussion

Table 1 presents the classification accuracies achieved by the various pre-trained models for classifying US and MR images. As shown in the table, pre-trained deep convolutional network achieved encouraging classification performance (99% accuracy) for US images. This experimental result empirically proves efficacy of deep learning technologies for analysis and automatically identification of malignant lesion in US images of the prostate. Note that, US is considered the first choice of modality to image the prostate and the most convenient way to diagnose prostate cancer. Based on echogenicity, capsule involvement and infiltration of surrounding structures, the radiologists provide diagnosis about the characteristics of prostate pathology, whether it is benign or malignant. The automatic identification of benign/malignant using deep convolutional neural network with such a high classification performance evidently can help radiologists/professionals in efficient diagnosis of prostate cancer patients. Even though conventional pre-trained deep convolutional neural network can achieve impressive performance to classify pro-state cancer using US data, as shown in Table 1, it could achieve up to 81% prostate cancer classification accuracy using MRI data. It is worth mentioning that, MRI till now is the best method of diagnosing any soft tissue pathology. It can play significant role to determine biopsy core and staging of pro-state cancer, which will help physicians to plan management of this very common cancer in men. Surprisingly, the classification performances of pre-trained deep learning technologies using MRI data could not achieve as good performance as that of using US image data. This could be attributed of using noisy or inaccurate MRI slice images where it is difficult to locate cancerous tissue. Note that, MRI process usually generates a number of slices/images and hence it is important to use the correct MRI image to be classified. In our experiment we selected the slice randomly from a number of slices for each patient. Hence, the selected slice might not contain cancerous tissue at significant level. This could attribute to poor

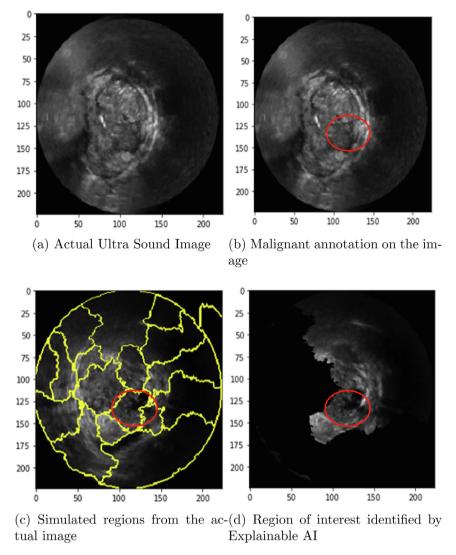


Fig. 3. Explanation for the decision of classifying as malignant using US Image.

**Table 2** Classification accuracy of VGG16 with different last layer classifier.

Pre-trained model	Last layer classifier	Accuracy (%)
VGG16	Nearest Neighbor	86.90
	Gradient boosting	87.10
	Support Vector Machine	87.15
	Random Forest	87.5

classification performance using the pre-trained deep learning technologies.

In order to enhance the prostate cancer classification using MRI data, a fusion of deep learning approach with ML classifiers is proposed in Section 3.2. Table 2 lists the classification accuracies of our fusion approaches. As reported in the table, the fusion of pre-trained convolutional neural network fused with Random Forest could achieve the highest classification accuracy of 87.5% among the four fusion models. This performance is 6.5% higher than that of the base pre-trained models shown in Table 1. Note, that the proposed fusion approach uses the best performing pre-trained model from Table 1 to fuse with ML classifier. From this enhancement of classification performance using MRI data we conjecture that, the proposed fusion approach can achieve

significantly enhanced performance of conventional pre-trained convolutional neural networks.

In medical domain physicians/professionals would prefer why a patient is diagnosed as malignant. To further justify the classifications achieved by using US images and MRI images, we applied XAI approach. Because, we are interested to explain the decision made by our automated computational approach for each individual patient, we applied the LIME approach to explain the classification outcome generated by the deep convolutional approach. Figs. 3 show the actual input US image and the region of interest for which the image was classified as malignant. Image in Fig. 3(a) is the actual US image that was fed as input to our automated deep learning bases computational system. Radiologists would look for hypoechoic lesion at peripheral zone with echogenic prostate to diagnose the patient as malignant. As seen in Fig. 3(b), the highlighted region (the region enclosed using red circle) is a hypoechoic lesion with mixed echogenicity prostate and hence this patient was diagnosed as malignant by professional radiologist. Fig. 3(c) shows resultant of simulated image generated from the input image following the procedure of LIME (see Section 3.3). This simulated image initially locates the regions that could be worth of investigation given the input image. Finally, LIME generates the image shown in Fig. 3(d) to

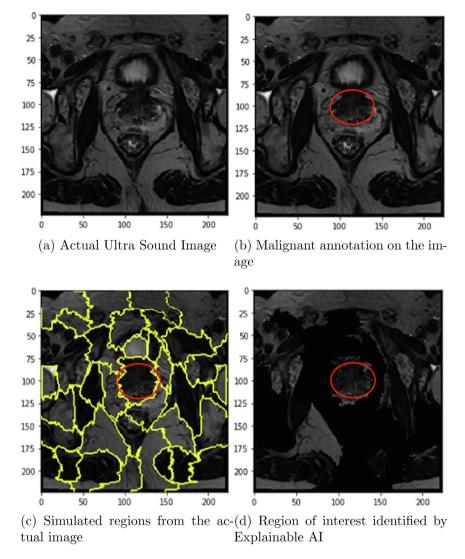


Fig. 4. Explanation for the decision of classifying as malignant using MRI Image.

explain why the automated computational approach classified the patient as malignant. As shown in this figure, the automated computational approach identified the correct region of interest that contains malignant lesion with uniform intact capsule (see the region within the red circle). Besides, the image does not show uniform intact capsule leading the diagnosis towards malignant lesion. The second image showing irregular capsule and hyperechoic prostate, diagnostic for malignant lesion, MRI is considered to be the best method of diagnosing any soft tissue pathology. Fig. 4 show the actual MRI slice and the explanation by LIME about why the respective image was classified as mmalignant. Figs. 4(b) and (d) represent the region of interest annotated by radiologist and the region of interest identified by LIME. It is encouraging that LIME could put emphasis to the region that shows hyperechoic prostate with vertebral involvement and thereby the respective patient was classified as malignant by our proposed approach. Moreover, the region of interest annotated by radiologist is also identified important by XAI approach.

The explainable AI helps us to understand the key features that led the algorithm to make the respective decision and classification. Image based XAI further helps visually the most important features of a given images that helps to make the final classification and decision.

#### 6. Conclusion

Prostate cancer is one of the most leading cancer in men in the United States. However, the prognosis of the disease is among the best of all cancer and it significantly improves if diagnosed early so appropriate treatment plan can be executed. Ultrasound is an non-ionizing, cost effective with high image resolution and first choice of imaging modality to image the prostate. MRI is also often used post US scan to further verify the disease and its extent. Automated intelligence process to detect cancer and classify between benign and malignant prostate tissue can significantly enhance the success of the treatment and it efficacy.

In this paper, we investigated a number of pre-trained deep learning models to obtain a robust prostate cancer detection system from US images from a publicly available dataset. The pre-trained models have been modified by adjusting the different layers and applied on the dataset where we have achieved a maximum of 97% accuracy on the test set. Furthermore, the robust model has been tried with MRI data from the same dataset as well and obtained an initial accuracy of 80%. Later, a fusion model has been applied on the dataset by combining the model and other shallow ML classifiers (e.g., SVM, Gradient boosting, and KNN), which achieved a remarkable improvement by yielding

the classification accuracy from 80% to 88%. Finally, a popular XAI algorithm LIME has been tried to identify the region of focus to the check the decision of the model as Benign or Malignant. In future, we aim to improve the proposed approach with more efficient features, ML models, and explanations of the models for better detection and explanation of prostate cancer images. The proposed fusion computational model performs very good classification for US and MRI images provided the input images include the prostate lesion. It is well known that MRI produces multiple slices/images and hence it is a challenge to select which MRI image to be fed as input to the fusion model. We conjecture if the best MRI slice can be selected the proposed approach would provide a better classification performance and the XAI would be able to explain the findings better.

The above results complement previous works on the application of deep learning for classification of disease from biomedical images. The current model significantly improved the classification accuracy of prostate cancer from MRI images and the pre-trained models showed high accuracy using ultrasound images. In conclusion, we have developed a novel fusion algorithm to improve classification accuracy using MR and US images for prostate cancer.

#### **CRediT authorship contribution statement**

Md. Rafiul Hassan: Conceptualization, Methodology, Investigation, Software. Md. Fakrul Islam: Software, Methodology, Writing – review & editing. Md. Zia Uddin: Data curation, Validation, Writing – review & editing. Goutam Ghoshal: Supervision, Writing – review & editing. Mohammad Mehedi Hassan: Writing – review & editing. Shamsul Huda: Writing – review & editing. Giancarlo Fortino: Writing – review & editing.

#### **Declaration of competing interest**

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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