

Ministry of Higher Education and Scientific Research

Al-Andalus Private University for Medical Sciences

College of Biomedical Engineering

Prostate cancer diagnosis

Using MRI images

/Graduation project prepared to obtain a Bachelor's degree in Biomedical Engineering/

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A word of thanks

to
Qashine crying
M h Did not fulfil No, If don't care messenger

In the tents of my university studies, I only seek to seek it in my name

sugar words

To Dr. **F M** Hamad Daer

On the pain
In all the efforts he made in all elections

And the information you provide has contributed to enriching my study topics

Jamt Al
On its sides Gilfah

Why?

All the best, respect and kindness Your generous letter

Dedication

“

(And their last claim is that all praise is due to God, the Lord of the Worlds.

It has been a long and difficult road.

And to get the most out of the hardship was awe-inspiring and great

Oh God you strive and do good The parts

I graduated and I would not have done anything but God. Nina E

Praise be to God the beginning and at the end

Al-Isandiya and Al-Isandiyah is when you are weaker, but when you are stronger

Always with him... except for the first and last time... except for the one who is proud of his presence

Yinji is nothing but sacrifice Love, security and strength

And comfow to make someone happy who will never be forgotten

My love, my life

The most precious jewel...the candle let's come together, except for the hug

The one I resort to is the asylum seeker or the asylum seeker. I...I...I...I... We will prefer her claim.

T.N.
Yinji
I am here...unless I accept N... If I eat my eyes, I will put them If..the source of my happiness..I

The shoulder is the only one who can carry it. Life is sweet without its presence.

My dear, go E

Laugh in life.. except for those who love and care for them.. except for those who love and care for them..

My crime The only thing I can do without them is true love.

We Revive
The supporter two who held my hands all the way... were the ones who held me all the way.
N Life is life

brotherly (Alni, Isara) II

The family is complete with their presence, they add happiness, and they are support and brotherhood.

Brothers-in-law (Mohsen, Em. Mohamed)

The owner of the cheerful face and beautiful cheeks... I hope you don't miss her
Life...unless it blossoms
Lenn
Times... except for the fixed person
Revive...if you participate
Steps
Hi All of them...except my brother
Let's bring Life...slice of sugar
Hi

Nada E E

I stopped you Ffaji
We... except those who gather
the most beautiful coincidence
Yes
Life... except for the one we shared our joy and tears with... except for my companion Adrien... except for
the one I spent the most beautiful days of my life
The one who has beautiful situations is the support
who I lean on when I get weak Where do I go? If I am happy

Lifelong friend

Unless you are complete, I will be happy, and I will live the easiest except for a childless friend...
make the road easier with a kind word or a situation. Unless you are happy with me

We will not repeat
Life is life

Nora E E

E

If we are like brothers... if we depend on them... if we are like support
Vfaaa
Time

Lee Hamza
powerless

I spent the most beautiful days with them **Friends on this trip...**
but everything is easier without them **Attach the path**

Yamaam, Irhaf, Alaa

May you ease the bitterness of the days and share with them the most beautiful memories.

With their presence, I feel safe. Our conversations, our discussions, our laughter are engraved.

N
In memory

Engineer, Elaa, Atraq, Aarab, Elitha We

If it was a second, he embraced him and took refuge in him.

Khalin Fatima

E

E

E

E

E

E

IV

Dedication

The mountain that protect~~T~~here are no storms in life... except for the star that...

Adrenaline lit up...and the support I give ~~V~~the power to continue the journey

Make my dreams come true~~E~~

My dear father

The sun Let's get to know each other...and let ...

Hi...and the safe haven I resorted to, if it weren't for your claim I wouldn't have reached...

My beloved mother

unlessThe supporter, the supporter, the shoulder I lean on when life decides to be difficultN.E.E.

I sign the one who is absent

Childhood friends...soul brothers who share Yanafry will be sad ~~Y~~...I E

And the firmly established tree~~V~~phedrine, Edmtm~~V~~Blessings to the brothers

Amani, Ezine, Emjad

Except with whom I shared the most beautiful days and memories, and the most difficult and bitter days.

Abu Jordan, Azinba, Irbi', Irfiq...

E

E

E

V

Dedication

In the name of God, the Most Gracious, the Most Merciful

◦

(And say, "Work, for Allah will see what you have done, and [so will] His Messenger and the believers.")

Except he whom Allah has crowned with awe and dignity... Except he who ~~Giving~~ without giving

Waiting... for the one whose name I proudly carry

My dear father

Except ~~We~~ will do our best the UNVIS is my Gospel...the UNVIS is my Gospel HSR

Existence... unless its claim is secret H.E.

My dear mother

Exhausti~~for the generous~~on't Assenden Brothers and sisters

E E

Except for the reading I am not divided the hardship of the road is the most beautiful If

The world

Keninola ItzEthnic The lanterns, Edwin and Iduma are paying I'm going to knock

The best and the most beautiful

Zahraa E. E.

Except for those who know and obey Yenouaouahssen I I

A He is
And my They claim the Universal Lord We...

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Summary

The prostate is a male reproductive gland located in the lower abdomen and surrounding the urethra where it exits the bladder. The prostate produces seminal fluid in conjunction with the Cowper's gland, which nourishes sperm.

Prostate cancer (PCa) is one of the most common cancers in men, with 1.4 million men receiving a diagnosis and 300,000 dying from prostate cancer each year worldwide.

The importance of early detection systems for prostate cancer using dual-parameter magnetic resonance imaging (bpMRI) stems from the difficulty of detecting the disease in its early stages, as it does not cause any symptoms or factors in the early stages. It has been recommended by the European Association of Urology (EAU) guidelines for 2019 and the British National Institute for Health and Care Excellence (NICE) guidelines.

In this project, we aim to create a diagnostic system for prostate cancer cases using MRI images using a hybrid artificial intelligence system and processing descriptive data to facilitate the reading of images to assist the physician and support medical decisions.

A database of 404 cases was used and split into training and testing data for deep learning and regression learning systems, and the systems were built and processed using Matlab.

Six hybrid systems were built to diagnose prostate cancer cases. The accuracy of the systems was high (all systems had an accuracy above 80%). The best diagnostic system in terms of accuracy (Resnet+Boosted Trees) was chosen and implemented within a graphical interface for interaction with the physician.

Keywords: Automated diagnosis, prostate cancer, medical images, hybrid learning, dual-parameter magnetic resonance imaging, image processing

ABSTRACT

abdomen and surrounds the urethra where it exits the bladder. The prostate gland is a male reproductive gland located in the lower Prostate secretes semen in conjunction with the Cooper's gland, which nourishes the sperm.

With 1.4 million men receiving a diagnosis and 300,000 dying from Prostate cancer (Pca) is one of the most common cancers in men, prostate cancer each year worldwide

Binary parameter magnetic resonance imaging (bpMRI) comes from The importance of early detection systems for prostate cancer using The difficulty of detecting the disease in the early stages because it Does not cause any symptoms or factors in the early stages and is guidelines and the UK National Institute for Health and Care recommended by the 2019 European Association of Urology (EAU) Excellence (NICE) guidelines

In this project, we aim to create a diagnostic system for prostate intelligence system and perform metadata processing to facilitate cancer cases using resonator images using a hybrid artificial image reading for physician assistance and medical decision support.

A database of 404 cases was used and partitioned into training and test data for deep learning systems, regression learning systems, Systems building and processing using Matlab

(Resnet+Boosted Trees) was selected, and implemented it in an accurate graphical) and the best diagnostic system in terms of accuracy the accuracy of the systems was high (all systems were more than 80% Six hybrid systems were built to diagnose prostate cancer cases, and Interface to interact with the doctor

Keywords: *Automated diagnosis, prostate cancer, medical images, hybrid learning, biparametric MRI, image processing*

Chapter One

General framework of the project

1-1. Introduction

The prostate is a male reproductive gland located in the lower abdomen and surrounds the urethra where it exits the bladder.

It secretes seminal fluid in conjunction with the Cowper's gland, which nourishes the sperm.

Prostate cancer is the uncontrolled growth of cells in the prostate. Cancer begins when healthy cells in the prostate change shape.

The prostate grows out of control, forming a tumor. The tumor can be cancerous or benign. Prostate cancer is considered...

One of the most common types of cancer among men around the world, as in 2019 (Prostate cancer (PCa))

It was more than 45% of all men with a history of cancer in the United States have had Miller's disease (PCa).

(WHO) receives only (et al., 2019). 1.4 million men are diagnosed and 300,000 die from prostate cancer each year.

Worldwide, it is the leading cause of cancer death in men.

2-1. Importance of the project

One of the main challenges surrounding accurate diagnosis of it is a broad spectrum of clinical behavior. PCa can range from low-grade benign tumors that never progress to clinically significant disease to highly malignant PCa tumors with pests.

Aggression and invasion, i.e. Clinically significant PCa (csPCa) which can progress

Rapidly progressing to a malignant tumor leading to death. Johnson et al., 2014.

In clinical practice, prostate biopsies are used to assign Gleason score (.Gleason Score (GS)

Gleason ()(Epstein et al., 2017) Histologically, each lesion was graded as a measure of cancer aggressiveness (Gleason Grade Group (GGG)).

Non-targeted transrectal ultrasound is used (Non-targeted transrectal ultrasound

csPCa is generally overexpressed to guide biopsy extractions, but it remains highly susceptible to being missed (TRUS).

DiagnosisSlow-onset PCa (Verma et al., 2017).

3-1. Project objective

In this project, we aim to create a diagnostic system for prostate cancer cases using MRI images by building an intelligent system.

Hybrid artificial intelligence and metadata processing to facilitate image reading and determine the disease stage to assist the physician and support decision-making.

Medical.

4-1 Project Problem

The systems currently used to diagnose prostate cancer have not yet provided high diagnostic efficiency, hence:

The aim of this project was to improve the efficiency of the diagnostic and detection system by proposing new learning algorithms.

And increase the accuracy of classification.

5-1. Division of the thesis

The project will be implemented in two phases:

The first stage extends over a period of time that includes the first semester and includes:

- The theoretical part related to prostate cancer in terms of its concept, types, and diagnostic systems using digital images.

and others.

- Previous studies taken from recently published articles and research in the field of prostate cancer diagnosis starting from Digital images and the use of neural networks.

The second phase extends over the second semester and will include everything related to our project from a practical perspective: methods

The work, the smart algorithms that will be applied, etc., will also include the results that the project will produce.

Chapter Two

Reference studies

1-2. Introduction

To improve early diagnosis and treatment of prostate cancer, the goal was to accelerate the transfer of high-resolution MRI.

Quality from lab to patient to help improve early diagnosis of clinically significant prostate cancer and reduce biopsies
Unnecessary treatment of benign and subclinical diseases.

2-2 Challenepi-cai

Modern artificial intelligence algorithms paved the way for ()The Road to Artificial Intelligence (AI)
Powerful computer aided (.which rivals human performance in medical image analysis (Reference 7)CAD

Clinical trials are the gold standard for evaluating new drugs and interventions in a controlled and comparative manner, and are the equivalent of developing
AI algorithms are international competitions or "grand challenges." Grand challenges can address the lack of trust.
Scientific evidence and adequate verification between AI solutions, by providing the means to compare algorithms with each other.
Some in a bias-free manner, using shared training and test data. (Reference9)

Prior to this challenge, the only general criterion for detection/diagnosis wasWhich used, ProstateX is the csPCa challenge.
Test set consisting of140 mpMRI tests to evaluate and compare AI algorithms. However, the size
Small sample size, limited variability (all cases from the same center and MRI supplier), and evaluation format
Weak, limiting the ability to reliably draw final conclusions.

It is considered a completely new challenge, with more than 10,000 imaging scans (Prostate Imaging: Cancer AI) PI-CAI

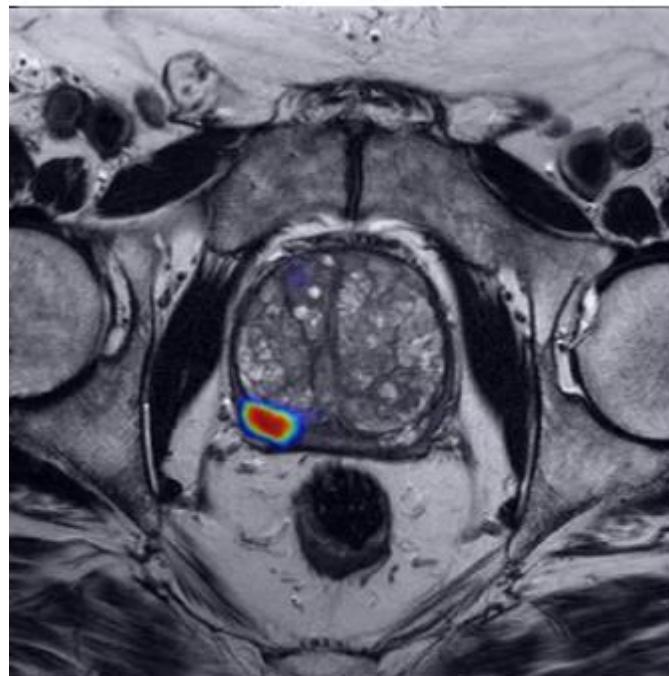
Prostate MRI scans were carefully curated to validate state-of-the-art AI algorithms and estimate performance.

Radiologists in detection and diagnosisKey aspects of the study design were created in conjunction with the CSPCA Council.

International multidisciplinary scientific consultant (16 AI experts for prostate, radiology and urology-

To unify existing guidelines and ensure meaningful prostate validation - AI towards clinical translation

(Reinke et al., 2021).



Shape (2—1) In an mpMRI scan of a patient's prostate, the area suspected of being cancerous (in red) is highlighted by

Artificial intelligence model (Turkbey et al., 2019).

It consists ofPrimarily from two PI-CAI sub-studies:

- Study of artificial intelligence (Annotated multi-center dataset of 1,500 AI tests :)

The MRI scans are publicly available to all participating teams and the research community as a whole. Teams can use the collection

This data is used to develop AI models and send their trained algorithms for evaluation.

At the end of this open development phase, all algorithms are ranked, based on their performance on a hidden test set.

Consisting of1,000 invisible scans. During the closed testing phase, regulators retrain the AI algorithms.

The top five ranked artificial intelligence using a larger dataset of 9,107 MRI scans

magnetic (including additional training checks from a special dataset). Finally, their performance is re-evaluated on

Hidden test set (with rigorous statistical analysis).

- Reader study (More than 50 world-class prostate radiologists conduct a Reader Study :)

Using a subset of 400 scans from the hidden test set. In each case, specialists

Radiologists complete their assessments in two rounds. This allows for comparisons between AI and current clinical practice (-PI

In general, the aim of this study is to estimate the performance of an average radiologist in detecting and diagnosing RADS v2.1.

csPCa in MRI.

Ultimately, it aims toIn exchange, AI Study aims to measure the latest AI algorithms developed at PI-CAI.

Prostate radiologists participating in the Reader Study - to evaluate the clinical feasibility of modern AI solutions

For prostate in detection and diagnosiscsPCA in MRI.

3-2. Previous studies on prostate cancer diagnosis using intelligent systems.

1-3-2.Comprehensive detection of prostate cancer in MRI images using 3D CNNs

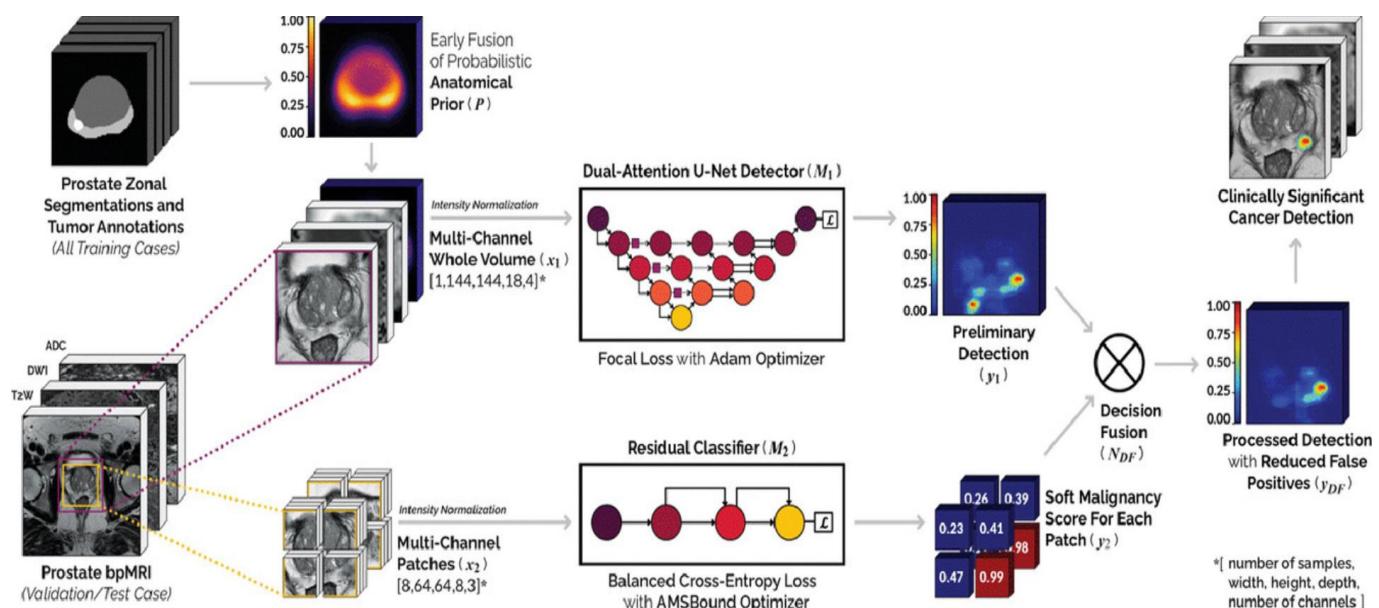
End-to-end prostate cancer detection in bpMRI via 3D CNNs

The researcher presented(CAD) and colleagues (2021) A three-dimensional model for computer-aided detection and diagnosis Seha

Stages of automated localization of clinically significant prostate cancer (In dual-parameter MRI (csPCa)
bpMRI.

Feature extraction mechanisms drive their detection network, targeting the structure and dimensions of highly discriminative features across Multi-precision. Its goal is to accurately identify pests.resulting from indolent cancer and a wide range of benign diseases csPCa which can affect the prostate gland. At the same time, the separate residual classifier is used to achieve positive reduction. False positive, without loss of high sensitivity or computational efficiency. In order to guide the generalization of the model with specific clinical knowledge In the field, a probabilistic anatomical prior is used to encode the spatial spread and logical differentiation ofUsing the .csPCa suite Large dataset consisting of1950 cases of prostate MRI combined with radiologically assessed anatomy, Researchers hypothesize that such models based onTo detect biopsy-confirmed malignancies in CNN

Independent group.



Shape (2-2) A comprehensive framework is proposed for calculating voxel-level detections of csPCa in bpMRI prostate validation/test samples.

For 486 tests, the 3D CAD system achieved 83.69%, 5.22%, 93.19%, and 2.96%.

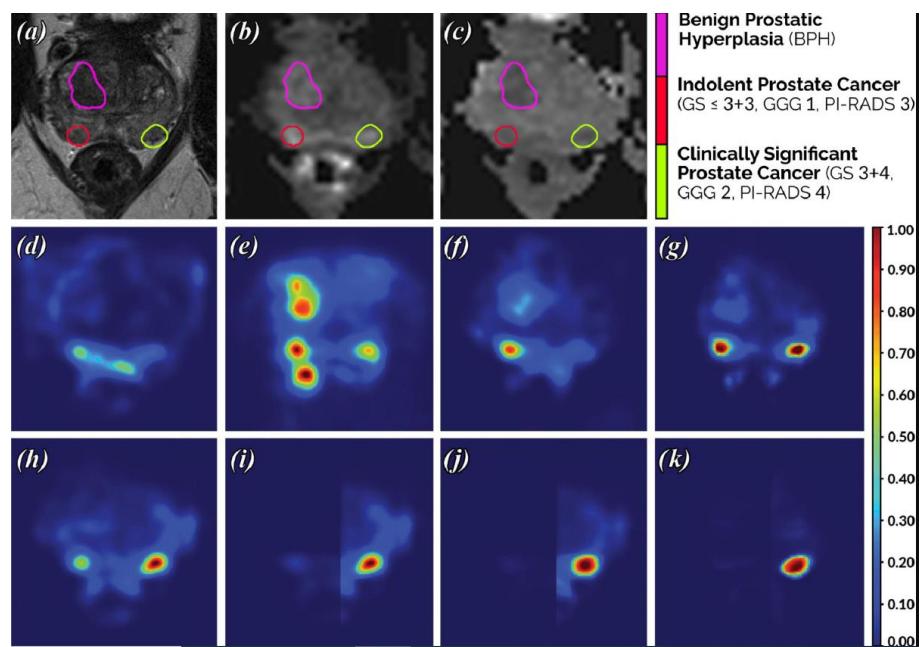
From the sensitivity of detection at 0.50 and 1.46 false positives per patient, respectively, significantly outperforming four state-of-the-art

Infrastructure (From the recent literature: Attention U-Net, nnU-Net, UNet++, U-SEResNet).

For 296 biopsy-confirmed external examinations, the combined CAD system shares moderate agreement with the expert consensus

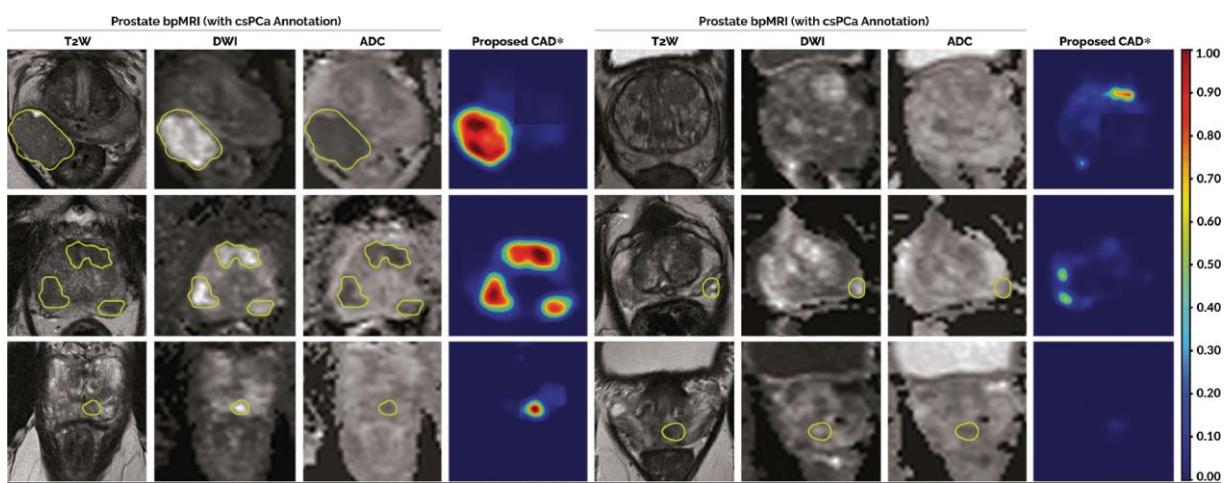
Rays 76.69%; kappa = 0.51, 0.04) and independent pathologists (81.08%; kappa = 0.56, 0.06); show

Strong generalization of diagnosis Histologically confirmed csPCa.



Shape (ADC scans the patient's condition in the external test set 2, followed by the detection map (a), DWI (b), T2W (c), 2—2

As predicted by each csPCa candidate system.



Shape (2-3) Six patient cases from the TS2 external test set and their corresponding csPCa detection maps, as predicted by the proposed CAD system.

Yellow lines indicate csPCa

2-3-2 Developing artificial intelligence for accurate diagnosis of prostate cancer using MRI

Magnetic

Magnetic resonance imaging developing artificial intelligence for precise diagnosis of prostate cancer using

Artificial intelligence (AI) advancements are essential for the successful deployment of community-wide prostate cancer diagnosis using MRI. AI systems must ensure the key benefits of avoiding biopsy while maintaining consistently high specificities across a range of disease prevalence rates. Given that all current AI/computer-assisted prostate cancer detection systems are still experimental, multiple development efforts are needed to realize the vision. Initial work should focus on developing systems as diagnostic support aids so that their results can be integrated into radiologists' workflows, including gland and target identification tasks for fusion biopsies.

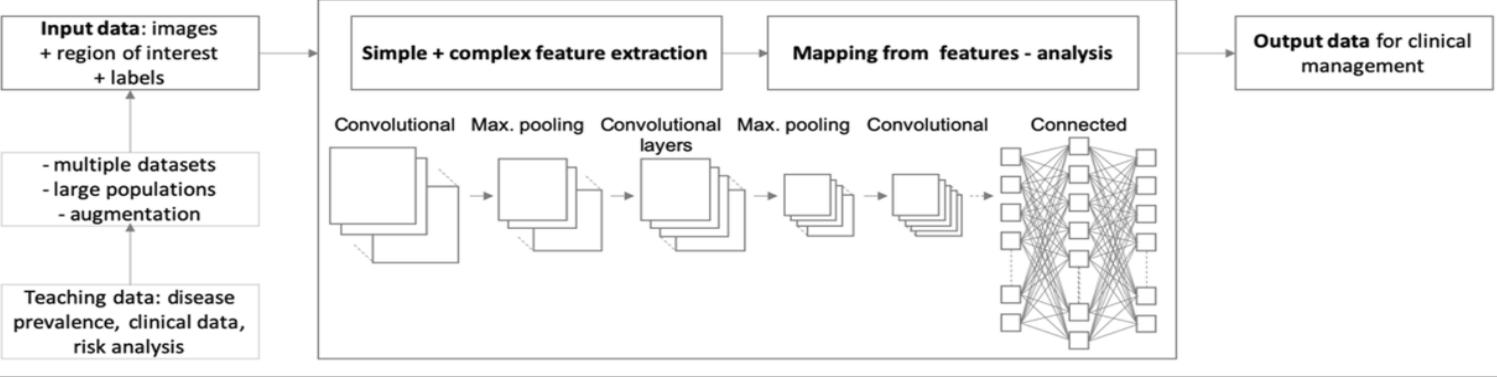
Robust, AI-based standard operating procedures will increase patient confidence, enabling wider adoption of MRI-guided approaches to prostate cancer diagnosis.

The MRI-guided pathway has been accepted by many national and international guidelines for the diagnosis of prostate cancer. The Prostate Imaging Reporting System and Multiparametric MRI Data (-) standard has also been adopted and reported in many principles (mpMRI) for the evaluation of multiparametric magnetic resonance imaging (RADS PI) Guidelines for the use of biopsies are being developed. As a result, there is an increasing global demand for diagnostic MRI and MRI-guided biopsies.

Radiology process



Deep learning process



(2-5) Comparative workflow of classical radiology and deep learning approaches for medical diagnosis

Comparative workflow of classical radiology and deep learning approaches for medical diagnosis: Workflow of the “classical” radiology process (top), and the deep learning process (bottom). Only a few quantitative features are used in radiological assessments, which are mostly based on visually assessed subjective features that include few quantitative measurements such as size or value or ADC unit Hounsfield or relaxation rates/time, while deep learning (and other AI-based techniques) do not rely on (HU) Artificial neural networks (ANNs) are not based on pre-defined features, but rather generate independent features (where complex features are combinations of simpler features) within ANNs to discriminate between desired target classes. All analysis methods ultimately aim to guide the clinical management of future patients with characteristics similar to the learning and validation datasets.

General considerations for AI developments in prostate MRI diagnosis

- Data Science Basics

Several issues need to be critically evaluated regarding the developments of AI and deep learning in prostate cancer diagnosis. It is important to verify whether there are clear technical, radiological, or clinical milestones for AI developments.

- Scientific accuracy

Scientific rigor is essential for clinical application, meaning that AI algorithms must be described to enable judgments about the validity of the application in context, supported by appropriate experimental setups and analyses.

Experience shows that object detection and classification require abundant, well-annotated data provided by experts to train and validate CAD and AI systems. High-quality datasets should include combinations of imaging, clinical, and histopathological data, and ideally, follow-up to document the ground truth of the presence/absence of significant cancer within the prostate gland.

- Large datasets: A single deep learning model that directly classifies images typically requires a large amount of data to train.

2-3-3 Classification of prostate cancer from ultrasound and MRI images

Using explainable AI based on deep learning

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

Prostate cancer is one of the most common forms of cancer in men. Early detection can significantly improve survival rates.

suggestAnd his colleagues in (2022) RaifiulA new automated classification algorithm by integrating several deep learning approaches To detect prostate cancer from ultrasound and MRI images. In addition, the proposed method explains why a particular decision was made given the input ultrasound or MRI image. Several pre-trained deep learning models with specially developed layers are added on top of the relevant pre-trained models and applied to the dataset. The best model generates a maximum accuracy of 97% on ultrasound images and 80% on MRI images for the test group. The model that produced the best classification performance was selected to be used as a feature extractor from the dataset to build a fusion model as a next step. To improve the performance of the models, especially on the MRI dataset, a hybrid model was developed by combining the best-performing model that was pre-trained as a feature extractor with some other machine learning algorithms (such asThis fusion approach improves the performance of Random Forests, K-NN, Adaboost, and SVM. The system is significantly improved by achieving accuracy from80% to 88% on MRI dataset.

Several studies have found the application of machine learning methods to classify cancer type by analyzing MRI data. However, very few studies have used modern deep learning techniques (e.g., convolutional neural networks) to analyze ultrasound and MRI images to detect cancer-promoting conditions. The most common approach is to extract features from the input image and then apply machine learning models using the extracted features.

Traditional feature analysis approaches mostly rely on extracting features from texture, contour, intensity and various statistical features to apply them with machine learning classifiers such as decision trees and support vector machines (Adaboost and Deep Learning (SVM) To detect cancer[4], [5], [6]. Deep machine learning approaches have already proven their applicability in many Application areas of image processing and computer vision such as object detection, video surveillance, and lesion/injury areas in medical images

Among other deep learning approaches, convolutional neural network (The most successful architecture capable of extracting powerful features (CNN) From the input images, it takes into account features from low to high level. In the algorithm CNN Typical,

4-2. Previous studies on hybrid systems

1-4-2 Early diagnosis of brain tumors from MRI images using hybrid techniques between deep learning and machine learning automated

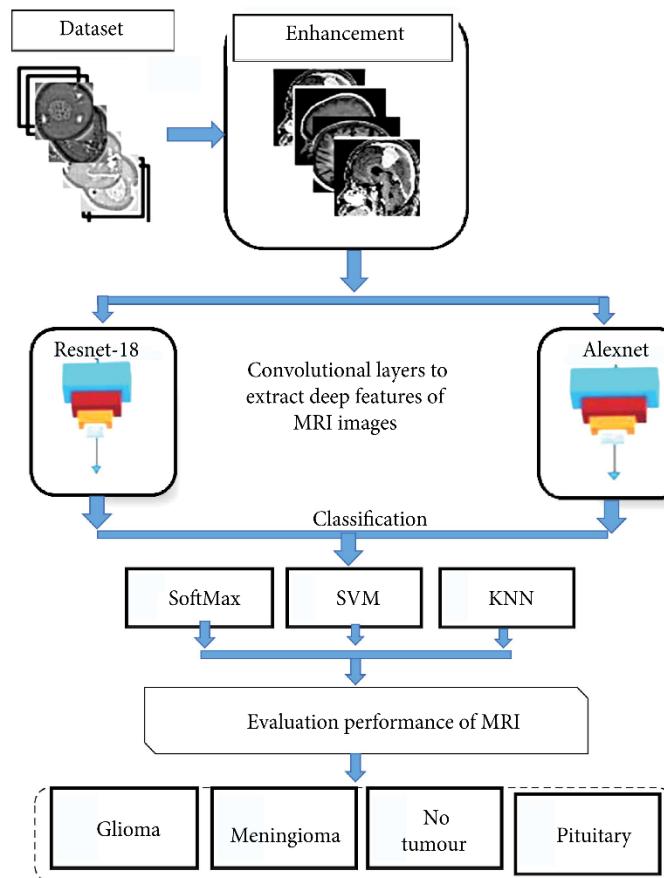
Early diagnosis of brain tumor MRI images using hybrid techniques between Deep learning and machine learning

The researcher didSenan et al. (2021) evaluated the performance of deep learning models using ResNet-18 and AlexNet. Early detection of brain tumors. To evaluate the performance of deep learning techniques (With machine learning techniques (ResNet-18 vector machine) and AlexNet Support)For early detection of brain tumors from ResNet-18+SVM and AlexNet+SVM, called (SVM), MRI images.

In this study, various experiments are conducted to diagnose brain tumors by combining deep learning with traditional machine learning techniques. For classification and diagnosis (SVM) with support vector machine algorithm ResNet-18 AlexNet Brain tumors. MRI images of brain tumors are enhanced using a median filter technique. Deep learning techniques are then applied to extract robust and important deep features through deep convolutional layers. The process of combining deep learning and machine learning techniques begins, where features are extracted using deep learning techniques, which are: These features are then classified using ResNet-18 and AlexNet-18.

All feature images are extracted through convolutional layers where two models are applied. ResNet-18 and AlexNet To extract the shape, color, and texture features of brain tumors.

All images are also diagnosed using deep learning techniques for two models, namely: The performance of each classifier is evaluated using accuracy metrics through SVM and using machine learning techniques through SoftMax, ResNet-18, and AlexNet. Sensitivity and privacy.



(2-6) General structure of combining deep and machine learning techniques

Result:

The features extracted from deep learning were classified using AlexNet + SVM: which includes two SVM experiments

and RestNet-18+SVM

In the first experience) The accuracy was 95.25% and specificity 98.50% and the model was able to (AlexNet + SVM Accurate diagnosis of glioma 93.9% accuracy for meningioma, 93.6% accuracy for benign cases, 94.9% accuracy for pituitary adenoma % accuracy 97.8

As for the second experiment)The model achieved 91.20% accuracy and 91.50% sensitivity (RestNet-18+SVM 100% privacy97 The model was able to diagnose glioma with 91.50% accuracy and meningioma with 86.10% accuracy. Healthy cases with % accuracy 92.40 and pituitary adenoma with 95.60% accuracy

Show hybrid modelOutperformed other models. Specifically, the model achieved AlexNet+SVM accuracy. Sensitivity and specificity95.1%, 95.25% and 98.50% respectively.

2-4-2 Classification of lung CT images using a hybrid 3D deep convolutional neural network architecture

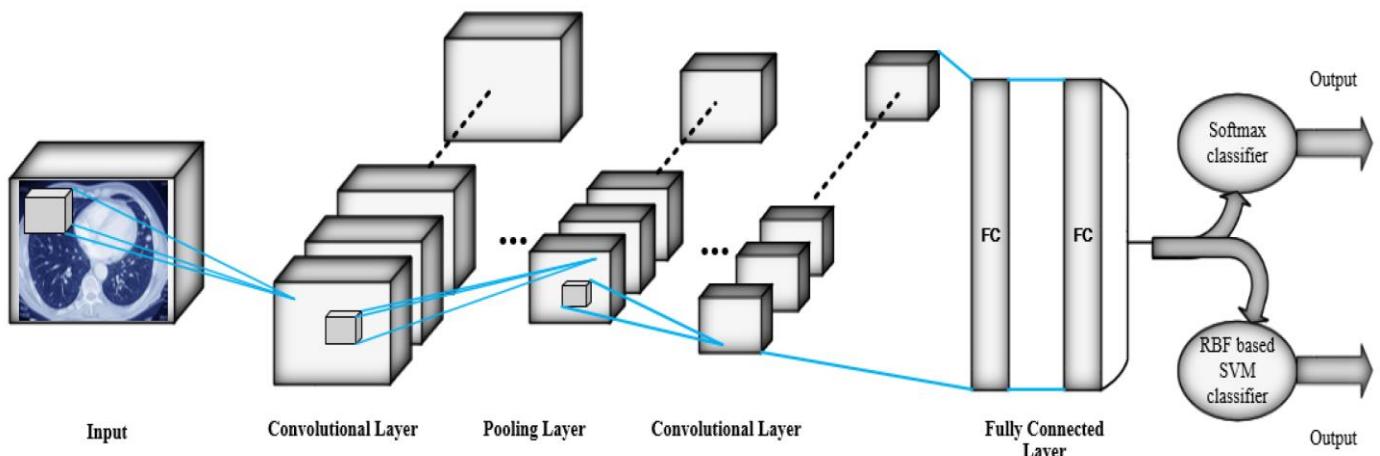
Classification of pulmonary CT images by using hybrid 3D-Deep learning neural network architecture

Using manual feature extraction methods on CT images is a complex process. Therefore, deep learning, as an effective field, can utilize automated feature extraction methods, which reduces the size and time required for the feature extraction process.

The researcher didAs two methods (CNN) and colleagues in (2019) proposed two models based on the convolutional neural network polat For deep learning to diagnose lung cancer on lung CT images. To verify the performance of the two proposed models (3D neural network withWith traditional basis function (3D-CNN) and hybrid 3D softmax neural network Radiation(D-GoogleNet and AlexNet D-3) and comparison with modified models of two well-known convolutional neural network architectures (RBF) - SVM.

The main structures of both network architectures contain:The proposed 3D CNN, which is used to extract features automatically, It has six convolutional layers, a maximum of four pooling layers, and two fully connected layers. The kernel size in all convolutional and pooling layers is considered. $3 \times 3 \times 3 \times 3$ and $2 \times 2 \times 2 \times 2$ in a row.

Activation function is appliedWith the lowest computational cost on the outputs of each convolutional layer and fully connected layers. In Relu The first convolutional layer is applied96 filters with filter size $3 \times 3 \times 3 \times 3$ on input images of size $227 \times 227 \times 227$. The reduced feature maps pass through the second and third convolutional layers. The second pooling layer is applied. Next, the fourth and fifth convolutional layers are applied to the reduced feature maps. The model continues with the remaining layers until it reaches two fully connected layers, where all neurons are connected to all neurons of the previous layer.



The shape(2-7) Architecture of the two proposed 3D CNNs

Experimental results showed that the performance of the two proposed models outperformed the two models D-GoogleNet and D-AlexNet3. Moreover, the hybrid 3D retina has achieved more satisfactory results with SVM (3D-CNN)

Where the accuracy was 91.81%, sensitivity 88.53%, and accuracy 91.91%, respectively.

(91.81%, 88.53% and 91.91% for accuracy, sensitivity and precision respectively) compared to the 3D network with softmax in lung cancer diagnosis which achieved the second highest accuracy rate of 90.23% while with D-Alexnet3 the accuracy rate was accuracy 85.79% and D-GoogleNet3 with an accuracy rate of (87.95%)

Experimental results show that both the straight-line and hybrid 3D models outperformed the other two models in lung cancer diagnosis. However, the proposed hybrid 3D mesh model achieved SVM-based RBF Important results: Accuracy rate 91.81% accuracy, 88.53% sensitivity, and 94.23% specificity compared to the 3D straight-line model. who used It has been proven that the softmax classifier is excellent at enhancing the performance of the SVM architecture.

3-4-2 Breast Cancer Diagnosis System Using Hybrid Support Vector and Automated Neural Network

artificial

Breast cancer diagnosis system using hybrid support vector machine-artificial neural network

Do all of the Using machine learning (CAD), Sheng and colleagues (2020) developed a computer-aided detection system. For classification purposes. Work has been done on 80 digital mammograms of normal breasts, 40 benign breasts, and 40 breasts Malicious. Malicious instances from a dataset MIAS miniature

This study consists of two phases: data training phase and system development phase. MATLAB R2019b for field application using CAD

In the data training phase, the images were first processed using a median filter to remove noise and enhanced using histogram equalization. Next, gray-level co-occurrence matrix features were extracted (For these images (GLCM) Before using it in the training phase of the pure model.

Then it was fragmented. 160 mammograms (80 normal mammograms, 40 benign mammograms and 40 malignant mammograms) were selected. Randomly selected from the micromammography system to determine the region of interest (ROI)

The classification was carried out in two stages through. The second is the artificial neural network model of SVM application. Identify neural network patterns available in MATLAB R2019b

The first stage was to classify whether the mammogram was normal or abnormal. The second stage was to determine whether the tumor was benign or malignant. Classification was performed. To run linear models SVMs by selecting each SVM Quadratic, cubic, fine Gaussian, mean Gaussian and coarse Gaussian In one short form. Then SVM was Choose the best model with the highest accuracy.

It was accurate Hybrid SVM-ANN achieves high accuracy of up to 99.4% in differentiating between normal and abnormal cases. Benign and malignant cases,

The network model was selected. To test new data due to its hybrid CAD accuracy to be imported into the SVM-ANN system. The high that reached 99.4% accuracy for classifying normal and abnormal cases and benign and malignant cases, respectively. The system starts System starts Developed with mammography selection, filtering, and CAD object removal functions. Large-area extraction, potential tumor region, segmentation, image contrast adjustment, feature extraction, and classification. This system can classify tumor images as normal or benign.

Chapter Three

theoretical study

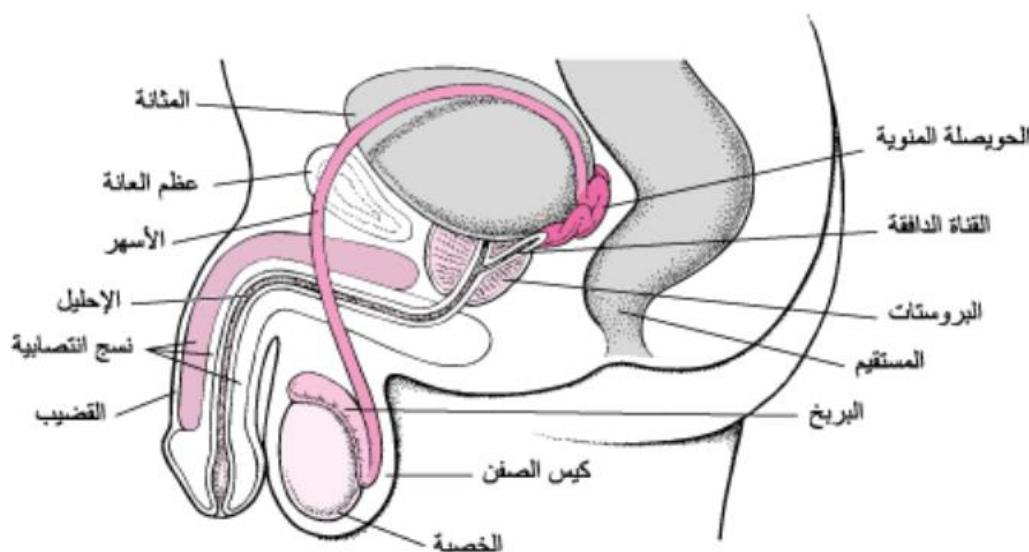
1-3. Definition of the prostate

The prostate is a gland located between the bladder and the penis in men, and the tube (urethra) passes through it. urethra which carries urine from the

The bladder and just outside the penis through the middle of the prostate, as shown in the figure (1-3).

The prostate produces a fluid that keeps sperm healthy, and it produces almost all of the fluid a man ejaculates during intercourse.

The prostate is about the size of a walnut in young men, but it becomes larger with age.



Shape (3—1) Male reproductive organs.

2-3 Prostate cancer

Prostate cancer is cancer that forms and develops within the prostate gland, which is shaped like a walnut.

Responsible for producing semen that nourishes and transports sperm cells.

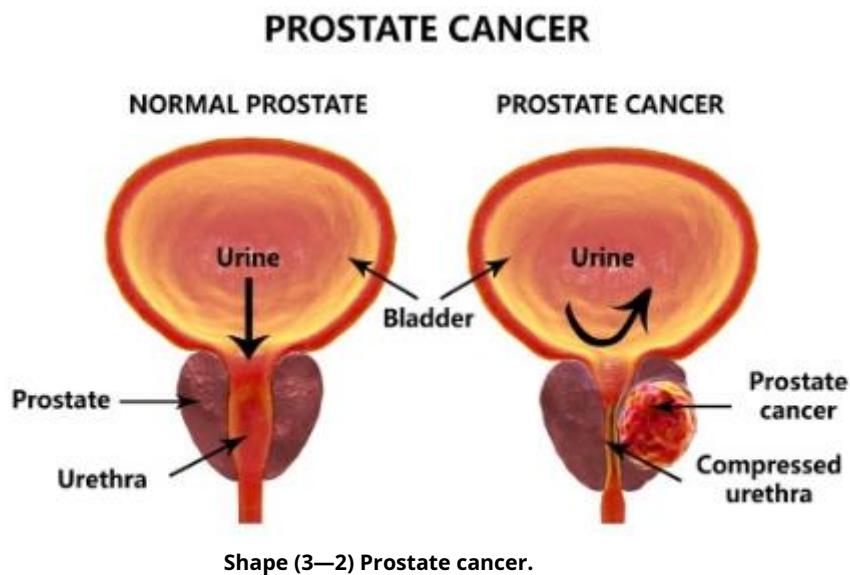
Prostate cancer is one of the most common cancers that occur in males. Obtaining a diagnosis result

Confirming prostate cancer can be a frightening and worrisome event, not only because it is a life-threatening disease but also because...

Also because prostate cancer treatment can lead to a variety of side effects, including problems

Such as sexual weakness, bladder control, pain during urination and frequent urination due to pressure on the urethra passing through

The prostate as shown in the figure ((Litwin & Tan, 2017) 2-3.



Diagnostic methods and treatment options available for prostate cancer have improved greatly in recent years, which

This is helped by the fact that prostate cancer usually remains confined to the prostate gland, so the damage is not severe.

Big and dangerous.

While some forms of prostate cancer grow moderately and require only minimal or no treatment,

Prostate treatment, on the other hand, there are other types of it that can be aggressive and spread quickly.

If prostate cancer is detected in the early stages of the disease when it is still confined to the prostate gland

The chances of getting treatment that will overcome prostate cancer are greater (Litwin & Tan 2017).

3-3. Symptoms of prostate cancer

In its early stages, prostate cancer is usually not accompanied by any distinguishable and noticeable side effects.

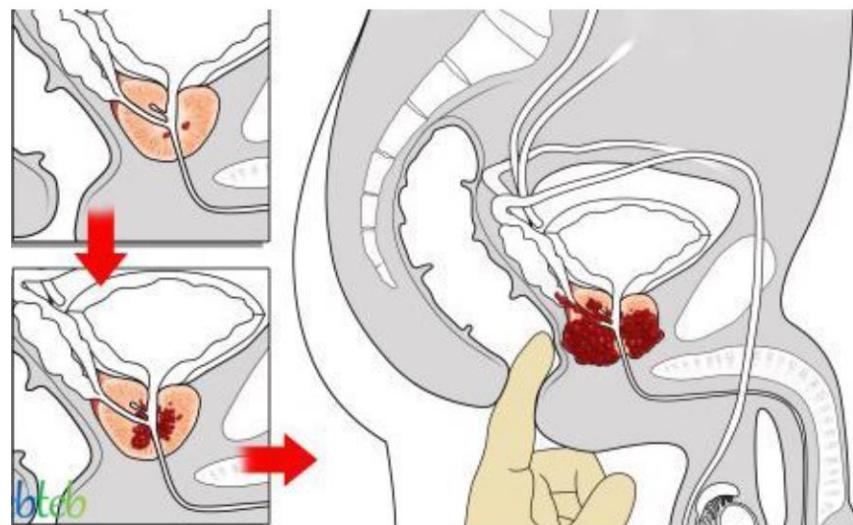
These are cases in which prostate cancer is not diagnosed until the cancer has spread outside the gland.

In most men, prostate cancer is first detected during a routine antigen screening test.

Prostate specific (Or during a digital rectal examination as shown in (PSA - Prostate - specific antigen)

Shape (3-3) When early symptoms or signs already appear, the nature of which is related to the degree of development of the cancerous tumor or the extent of its spread.

In other organs.



Shape (3—3) Diagnosis of prostate cancer.

The first symptoms of prostate cancer may include problems urinating due to the pressure it creates.

Cancerous tumor on the bladder or on the tube that carries urine from the bladder.

Urination problems can usually be a sign of many benign, non-malignant problems of the prostate gland, Such as: benign prostatic hyperplasia, or prostatitis, where less than 5% of prostate cancer cases are

Accompanied by urination problems as the first and primary sign.(Litwin & Tan, 2017)

Some symptoms of prostate cancer:

1. Signs of urination problems

- Signs that may indicate urination problems include the following:
- Difficulty urinating.

▪ Urinary incontinence that starts and then stops more than once during urination.

- Increased pressure in urine flow.

2. Signs of its spread in nearby areas

Prostate cancer or cancer in areas near the prostate gland can cause the following symptoms:

- Appearance of blood in the urine.
- Appearance of blood in semen.

3. Signs of spread to the lymph nodes

If prostate cancer has spread to the lymph nodes, it may lead to the following:

- Swelling in the legs.
- Feeling of discomfort in the pelvis.

4. Signs of its spread to the bones

If prostate cancer has spread to the bones, it can lead to the following symptoms:

- Constant bone pain.
- The appearance of bone fractures.
- Pressure on the spine.

4-3. Causes and risk factors of prostate cancer

Cancer is a group of abnormal cells that multiply faster than normal cells and refuse to die.

Cancer has the ability to invade and destroy healthy tissue, either by growing directly on top of

From the surrounding tissues and either after moving to other organs in the body through the bloodstream or through the lymph nodes.

Microscopic cancerous tumors that can only be seen with a microscope can develop as small clusters that continue to grow.

And develop into a denser and more rigid tissue.

The exact cause of prostate cancer formation and development is not yet known, and why certain types behave differently.

Certain cancers develop differently than others. Researchers believe that a combination of several different factors is responsible for

This development is key to understanding it and these factors include:

1. awareness Awareness of the risk factors for prostate cancer is an important element that can help one make informed decisions.

His decisions about whether he needs to be screened for early detection of prostate cancer.

2. the age When exceeding the age 50 years of age increases the risk of developing prostate cancer.

3. Family medical history If a sibling or father has prostate cancer, the risk of developing it increases.

And it is much higher than other men.

4. Nutrition Men who eat a high-fat diet and men who are overweight are more likely to develop cancer.

Prostate, one theory says that fat encourages the production of testosterone (Testosterone

It can encourage the production of cancer cells.

5. High levels of testosterone:

Since testosterone stimulates and accelerates the growth of the prostate gland, men who take a medication that contains this hormone

Men with high levels of it or a major component of it are more likely to develop prostate cancer than men with lower levels of it.

Testosterone.

Doctors also note with concern that testosterone therapy may stimulate the spread and metastasis of prostate cancer if it is present.

Indeed, long-term, continuous testosterone therapy may also lead to prostate enlargement (ref.

6).

5-3. Complications of prostate cancer

Complications from prostate cancer may be a direct result of the disease itself or a result of treatment.

Today, there are various treatments available that can address and treat these problems. The most common complications are:

Symptoms associated with prostate cancer include the following:

- Depression.
- Cancer spread and metastasis.
- Pain.
- Difficulty urinating.
- Poor sexual performance or complete impotence.

6-3. Diagnosis of prostate cancer

1-6-3 Diagnostic Protocol

- After taking the patient's family history, which includes (name, profession, place of residence, lifestyle habits (smoking, (alcohol), genetic diseases)

We start with the patient's history, which may be as follows: surgical history (surgeries on the pelvic and perineal area, hernia, etc.).
(Arbi, water cysts, hemorrhoids, anal fissures) or any other operation

- We inquire about the patient's medication history (the medications that the patient usually takes, such as blood pressure and diabetes medications, or treatment for...)
Hormonal replacement therapy for testosterone or growth hormone) GH

We start with the clinical history, i.e. the reason that prompted the patient to visit the doctor, which may include (dribbling of urine, pain after finishing...)
Frequent urination, pain in the perineum, frequent urination, sexual dysfunction)

Clinical examination steps:

- Upon examination, we may find a surgical scar in the perineum or abdomen, and its presence leads us to suspect that prostate enlargement is one of its complications.
- Anal examination: This is done by inserting the index finger into the anus and palpating the prostate from the anterior wall of the anal canal.
The presence of a palpable prostate enlargement may indicate the presence of prostate cancer, but it is not certain because it is possible
To be a benign enlargement, especially in elderly men (fifty years and older)

- Ask about the general symptoms of cancer (weight loss, fever, emaciation, general weakness). If the symptoms of cancer are accompanied by...
The presence of an enlarged prostate indicates a greater likelihood that the enlargement is malignant.

Laboratory diagnostics:

- ❖ The patient undergoes laboratory analysis of the following (count and formula):))And the most important(PSA, CRP, white blood cell test, CPC
- ❖ High white blood cells andCRP may be caused by inflammation caused by cancer.
- ❖ The increase in the tumor markerIt is the most important laboratory diagnosis in diagnosing prostate enlargement, as PSA
- ❖ Tumor marker or specific antigenIt is a glycoprotein produced by the prostate in normal conditions (PSA).

But its increase above the normal limit indicates an enlarged prostate gland.

If a blood test for prostate cancer shows that your level off it does not exceed (4 ng/ml), then the patient's PSA is most likely

He does not suffer from a tumor, and the rate of tumor detection during biopsy in this case (%)0.5)

If the Higher than (20 ng/ml), the probability of detecting cancer reaches (75%). Therefore, at this PSA level

Level of cancer markers, a biopsy is immediately scheduled to confirm or exclude the presence of cancer from tissue examination

The greatest diagnostic difficulty is the so-called "grey zone," which is a group of patients who have a low level of the Since it is very difficult to detect prostate cancer, (PSA) (above 4 ng/ml and below 15 ng/ml)

In the early stages, and also not everyone undergoes a biopsy (this procedure is painful and sometimes accompanied by complications),

Other methods are used to increase the accuracy of the analysis, including:

1- Ultrasound imaging with biopsy:

In ultrasound imaging, it is taken into account whether the wall is heterogeneous (due to lack of

The cancer cells have differentiated to the degree that they differentiate into normal prostate cells, and in the presence of prostate enlargement,

We may also see in ultrasound imaging cases of dilatation of the urethra and bladder before it progresses to the stage of

Prostatic urethra

Through the biopsy, we calculate the degree of cancer using the Gleason scale.

2- Magnetic resonance imaging:

A multiparameter MRI is performed. If a contrast-enhanced area is found (levels

Gray matter is different from the gray matter levels of the prostate gland. Cancer is suspected and the degree of cancer is calculated from

gaugePI-RADS v2

2-6-3 Types of examinations

Prostate cancer may not be accompanied by any symptoms at first. It is very possible that the first symptom that appears is:

It is a specific problem that is only detected by performing one of the various scanning tests, such as:

A. FRE - Finger Rectal Examination

Prostate-specific antigen (PSA) test.

C. Ultrasound imaging through the anus.

D. Biopsy of the prostate gland.

Multiparameter Magnetic Resonance Imaging of the Prostate (mpMRI)

7-3. Prostate cancer classification

When the biopsy results confirm the presence of a cancerous tumor, the next step is classification, which aims to determine the extent of the tumor's spread.

Cancer and its spread: Tissue samples are examined and a comparison is made between cancer cells and healthy prostate cells.

The greater the degree of difference between cancer cells and healthy cells, the higher the level of cancer lethality and the greater the likelihood of it spreading.

faster

Cancer cells usually differ from each other in terms of shape and size. Some of these cells may be very deadly, while others may not.

Some of them are completely deadly, and a pathologist can identify the two most deadly types of cancer cells.

And diagnose their severity and danger.

The most common staging for prostate cancer is by taking a biopsy and is determined according to a scale.

Gleason or scalePI-RADS v2 MRI images

1-7-3 Determining cancer by the Gleason score

The sum of the two numbers obtained determines the overall stage of the cancer in the particular person undergoing

For examination, this grading can range from 2-10 It is a very deadly cancer.

After determining the severity and degree of lethality of prostate cancer, the next step is called staging, which determines the extent to which it may have spread.

The cancer has spread and metastasized. Prostate cancer is usually graded into four levels depending on how far it has spread:

first class)(t1This grade indicates a very early stage of cancer, as it is still confined to a microscopic area that is not

The doctor can feel it by touch.

Second classAt this stage, the cancerous tumor can be felt, but it is still confined to the prostate gland only.

Third degreeAt this stage, the cancerous tumor has spread outside the prostate gland and into the vesicles.
sperm or to nearby tissues.

Fourth degreeAt this stage, the cancerous tumor has spread and metastasized to the lymph nodes, bones, lungs, or
Other organs in the body ((Litwin & Tan, 2017)).

2-7-3 Cancer detection using the PI-RADS v2 score

To meet the requirements for diagnosing prostate cancer, the American College of Radiology (,)American College of Radiology

European Society of Genitourinary Radiology (ESGUR)European Society of Urogenital Radiology (ESUR).

And the institutionAn international expert panel was convened to develop version 2 of the AdMeTech Prostate Imaging Reporting and Data System.

(Weinreb et al., 2016) (Prostate Imaging Reporting and Data System version 2 (PI-RADS v2))

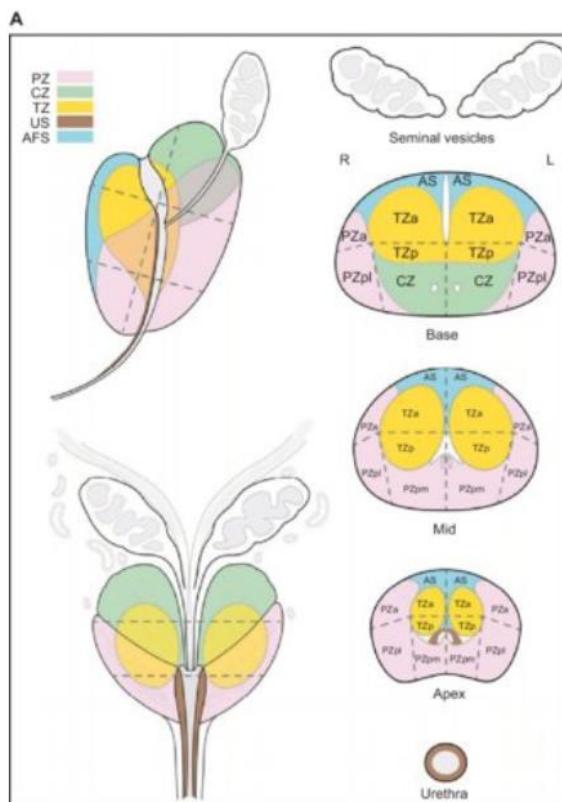
DesignedTo standardize image acquisition and interpretation techniques for prostate MRI, PIRADS v2

Critical for management, communications, and comparative research involving multiple institutions, and quality assurance of multi-disciplinary experiments.

Centers. It has beenWith rapid and widespread international acceptance among radiologists and urologists, PI-RADS v2 is used

Widely used in everyday practice and research (Ref.12) Figure (3-4) shows the divisions of the prostate in order to determine:

Cancer grade.



Transition zone			
T2W	DWI	DCE	Pirades
1	Any	Any	1
2	Any	Any	2
3	≤4	Any	3
4	5	Any	4
5	Any	Any	5

Peripheral zone			
DWI	T2W	DCE	PIRADS
1	Any	Any	1
2	Any	Any	2
3	Any	–	3
4	Any	+	4
5	Any	Any	5

Shape (Thirty-nine regions of the prostate (a) Notes: PIRADS v2 (4-3).

In fact, recent studies have documented the impact of(Turkbey et al., 2019) csPCa detection by PI-RADS v2.

To ensure that radiologists are properly trained to:Educational courses are offered by many, PI-RADS v2

From organizations.

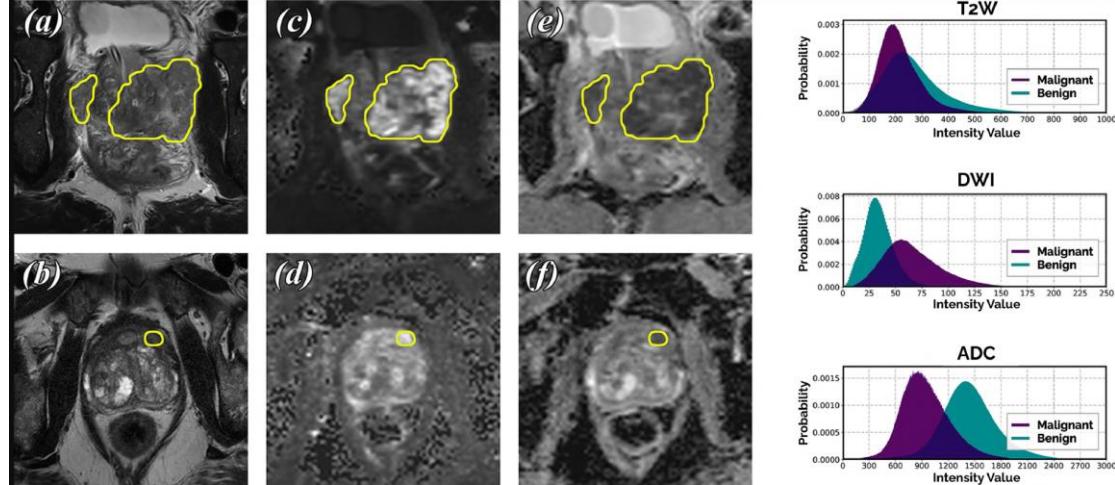
DevelopedThrough a consensus-based process using a combination of published data and PI-RADS v2 observations And expert opinions. And after3 years in development, released online (<https://www.acr.org/Quality> In late 2014 and published in early 2016 (Safety/Resources/PIRADS).

Later, many studies proved the validity of the value.But, as expected, some PI-RADS v2 also showed Inconsistencies and limitations. For example, inter-observer agreement was only good to moderate, and a number of evaluation criteria were identified. specific, which require clarification or modification. Furthermore, some technical issues related to obtaining data (Rosenkrantz et al., 2016) mpMRI may benefit from updating and improvement.

To address these issues, the Steering Committee recommended that:Again using a consensus-based process, with multiple PI-RADS Amendments toMaintaining the scoring framework for individual sequences and using these scores, PI-RADS v2 To derive a comprehensive evaluation category. Due to the limited scope of these updates, the updated version is calledPI-RADS v2.1 systemPI-RADS v2 is the standard guideline for reading and obtaining prostate MRI.

However, it follows a qualitative and semi-quantitative assessment that requires significant expertise to perform the appropriate MRI. At the time Same, it can appear.As multifocal lesions of varying shapes and sizes, they bear a strong resemblance to many csPCa cases.

Non-malignant, as shown in Figure ((Weinreb et al., 2016) 5-3.



Shape (3-5) The challenge of differentiating csPCa due to its morphological heterogeneity

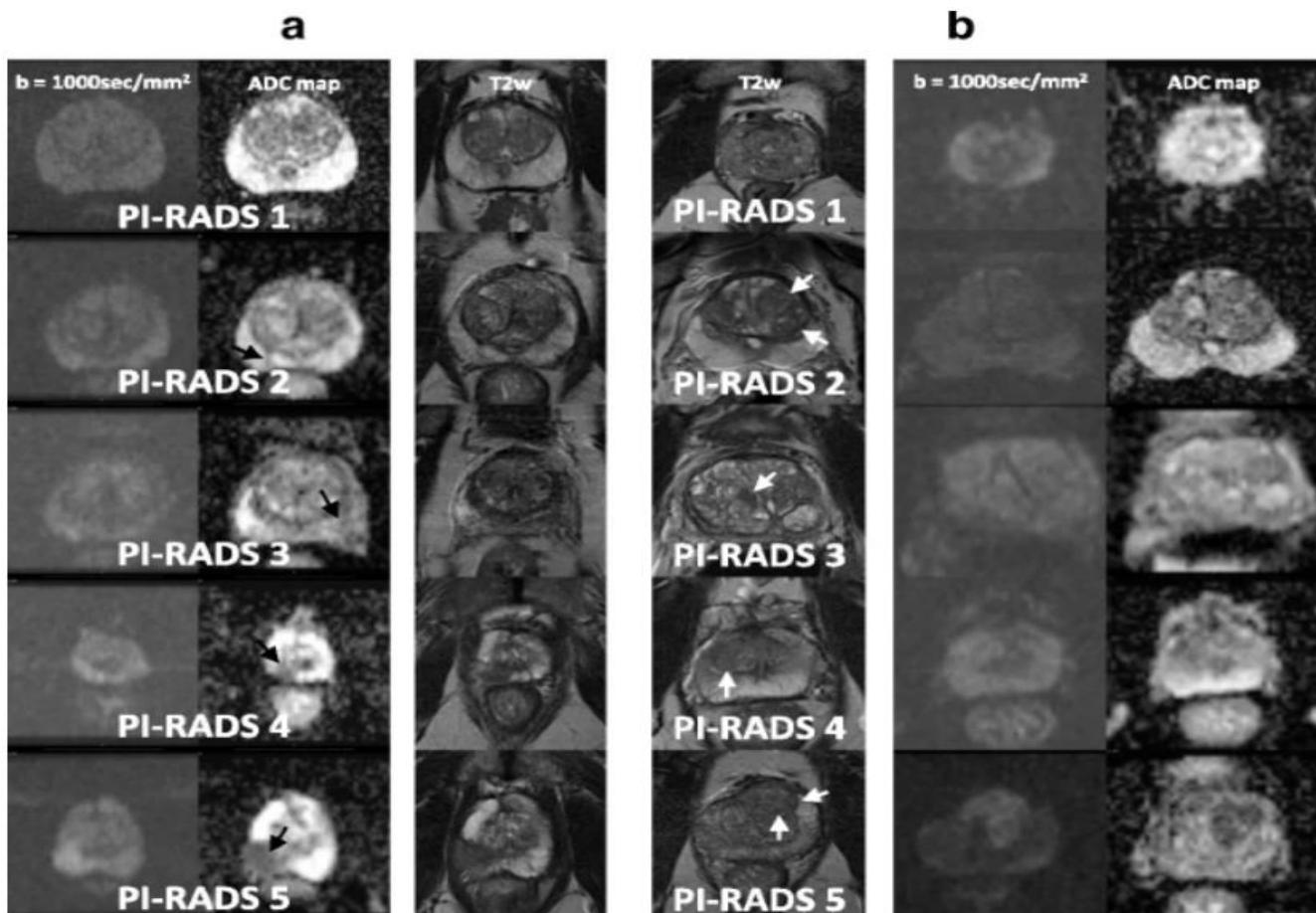
Evaluation categories

The probability of developing clinically significant cancer, defined as the presence of any of the six conditions, is predicted.

The following is in the form (6-3)

The risk of developing cancer is high when:

- 3 cases with Gleason score ≥ 7 (including 3+4 with prominent Gleason 4 component but not (prevailing))
- Size >0.5 ml
- Extension outside the prostateextraprostatic extension



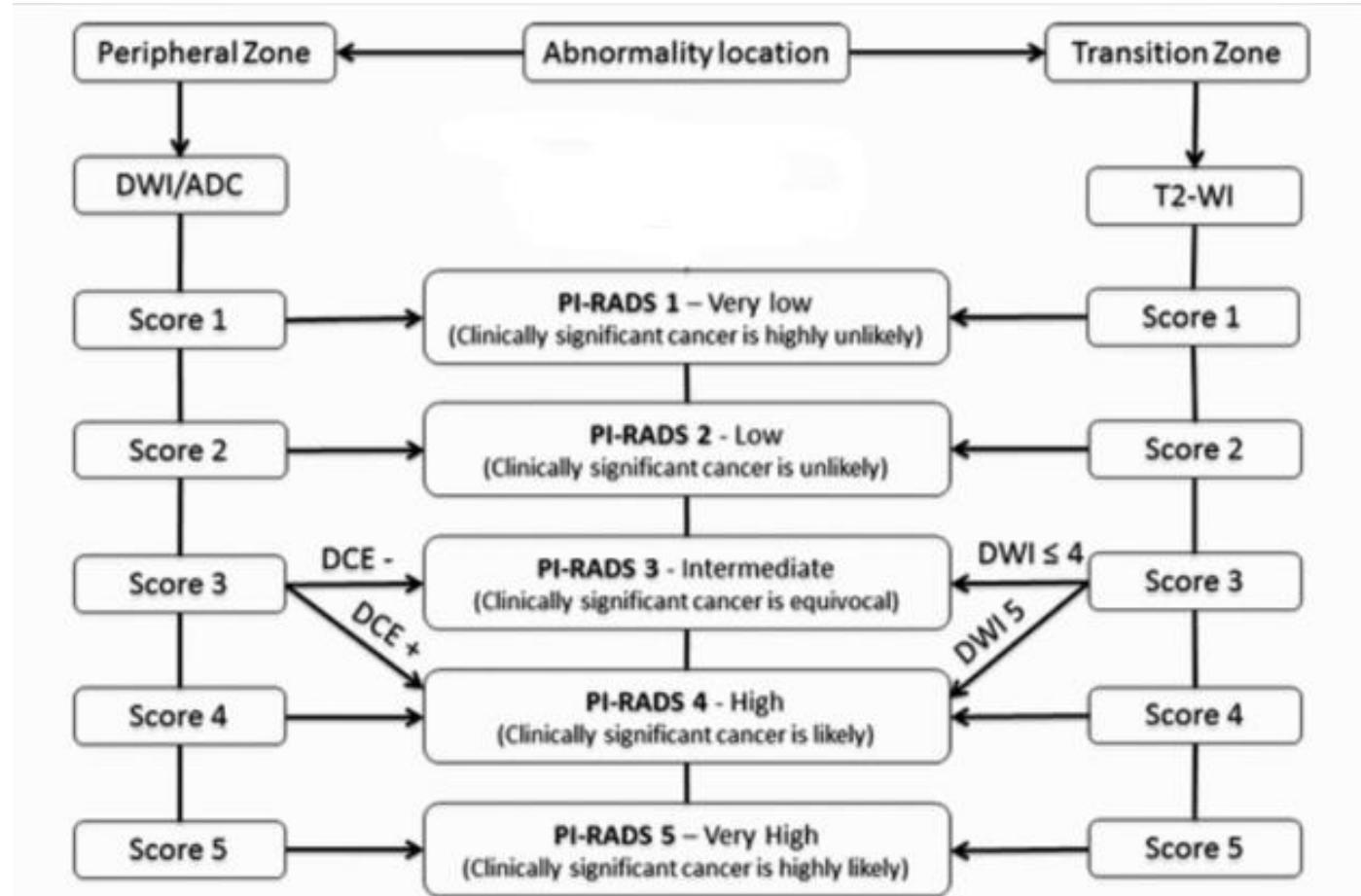
Shape (3-6) Assessment categories (Steiger et al., 2016) PI-RADS™ v2

A degree is assigned from 1 to 5 for each lesion indicates the possibility of clinically significant cancer as shown in Figure (3-7).

The grades are as follows:

- Very low (clinically significant cancer unlikely to be present): PI-RADS 1
- Low (clinically significant cancer unlikely to be present): PI-RADS 2
- Intermediate (presence of clinically significant cancer is uncertain): PI-RADS 3

- High (likely clinically significant cancer) :PI-RADS 4
- Very high (very likely clinically significant cancer): PI-RADS 5
- One of the test components is technically insufficient or was not performed: PI-RADS X



Shape (3-7) PI-RADS v2.1 Flowchart

Current guidelines for reading prostate MRI (i.e., Track semi-structured assessment (PI-RADS v2.1)

Quantitative, requiring considerable expertise for proper use. Furthermore, prostate cancer can present with a wide range of symptoms.

Clinical behavior and morphology are highly heterogeneous on MRI. As such, assessments are vulnerable.

Low consensus among readers (<50%), suboptimal interpretation, and overdiagnosis (Ref. 10).

Unlike the protocol bpMRI (dual-parameter MRI) does not include mpMRI.

Dynamic contrast-enhanced - reducing costs, eliminating any risk of adverse effects from the use of contrast agents,

And shortens examination times (Thus, although providing less diagnostic information than mpRI (Turkbey et al., 2019).

Then(Eklund et al., 2021) bpMRI is more appropriate within the scope of large-volume, population-based screening.

8-3. Prostate cancer treatment

There is more than one way to treat prostate cancer. For some men, a combination of several treatments is the best option.

For example: surgery with radiotherapy, or radiotherapy with hormonal therapy are the best solutions for their cases.

Choosing the best treatment method for each specific case depends on several factors, including the speed of growth of the cancerous tumor, and to what extent

The tumor has spread, the man's age, how long he is expected to live, and the potential pros and cons of each treatment.Litwin .)& Tan, 2017

The most common and widely used treatments for prostate cancer include:

1-8-3. External radiation treatments

In external beam radiation therapy, very powerful X-rays are used to destroy cancer cells. This type of radiation

It is very effective in destroying cancer cells, but it may also attack healthy tissue.

Complications and side effects of external beam radiation therapy include the following:

- Difficulty urinating.
- Loose stools and bloody stools, i.e. bleeding from the anus.
- Feeling of discomfort or distress during bowel movements, or feeling the need to have bowel movements constantly and continuously.
- Side effects during sexual activity.

2-8-3. Internal radiation treatments

The method of implanting the implant has become (In recent years, radiation therapy within the prostate gland has become an accepted treatment method (implant)).

It is commonly used to treat prostate cancer.

This implant, which is called a densification treatment,Brachytherapy is any radiation therapy that uses ionizing radiation.

The radiation source is placed at a short distance and close to the body or organ being treated, and gives a much higher radiation dose than

External radiation therapy over a longer period of time.

This treatment method is usually used to treat men whose cancerous tumor is small to medium.

Size, and those with low disease grade.

Complications and side effects of radioactive implantation include the following:

Difficulty urinating.

Side effects during sexual activity.

Anal symptoms.

3-8-3. Hormonal treatments

Hormone therapy aims to prevent the body from producing the male hormone testosterone, which can stimulate the production of cells.

Cancerous.

Side effects of hormone therapy include:

- Breast enlargement.
- Suppression of sexual desire.
- Sexual impotence.
- Waves of fever.
- Weight gain.
- Decreased muscle mass and bone mass.

Medications that contain hormones can cause nausea, diarrhea, fatigue, and liver damage.

4-8-3. Prostatectomy

The surgical removal of the prostate gland, called a prostatectomy, is often performed as a treatment for:

Cancerous tumor that is still confined within the prostate gland.) Litwin & Tan, 2017

During the procedure, the surgeon uses a number of special techniques to remove the prostate gland and the lymph nodes surrounding it.

This surgery can affect the muscles and nerve groups that control urination and sexual function.

Side effects of prostatectomy include impotence.

6-8-3. Other treatments

Treatments include:

- Chemical treatment.
- Cryotherapy.
- Gene therapy.

9-3 Magnetic Resonance Imaging (MRI)

1-9-3 The working principle of the MRI machine

MRI is consideredFrom the scanning devices, as the scanning process depends on the field (MRI) Strong magnetism with radio waves to create a detailed image of parts of the human body, such as internal joints. Cartilage, ligaments, muscles and tendons, which cannot be imaged by X-rays.Or X-ray devices Ultrasound.

The MRI machine produces a very strong magnetic field, which attracts the protons of the hydrogen element in the The chemical composition of the human body's water, which rotates in a spindle (axial) motion in a specific direction, in addition to the fact that it emits A stream of radio frequencies that causes variations in the value of the magnetic field, then the protons absorb that energy, which turns The direction of its rotation movement until the magnetic field is cut off, after which the direction of the protons' rotation returns to its normal position.

During this process of changing the direction of the protons' spin and returning to the original position, a radio wave is generated that is detected through A receptor is present in the MRI machine to be obtained as an image (Broadhouse, 2017)

2-9-3 Components of the MRI machine

An MRI machine consists of four main components: a main magnet consisting of superconducting coils, coils Radio frequencyGradient files, Radio frequency files, Computer systems, (RF

Main magnet: Early MRI magnetic systems used a magnetic sheet structure, where

The use of large quantities of magnetic plates makes the weight and size of the system relatively large and with the rapid development of technologies

Magnet The active sheet structure has been successfully developed for high field magnet system which greatly reduces the line range.

5 Gauss

Gradient coil: The gradient coil assembly is an important component in an MRI machine that produces magnetic fields.

A linear gradient is imposed over a uniform strong magnetic field. The uniform magnetic field is produced by a magnet.

Main, which is aligned with the direction of motion of the proton, the superimposed gradient magnetic field slightly changes the frequency or phase of the

The motion of the proton, thus encoding the spatial information of the imaged object into the frequency associated with a location in space, and in general it must

The magnetic field gradient produced by the step coils should be as linear as possible.

Radio frequency coils: coilIt is the main component of the MRI system, acting as a transmitter (RF).

As well as a future in forming the final images, there are different types of these files and the difference between them lies in their use.

For different parts of the human body, the field strengths are also different.Broadhouse, 2017

3-9-3 Physical foundations of magnetic resonance imaging

An MRI scanner is a giant magnet, and the strength of the magnets is measured in units called Tesla.(T

The magnetic field strength of most MRI scanners used in hospitals and research clinics is

Medical1.5 or 3 Tesla.

All hydrogen protons are located in random locations in the body and rotate on their axis, however this randomness changes

When we place the human body inside a very strong magnetic field, such as an MRI scanner

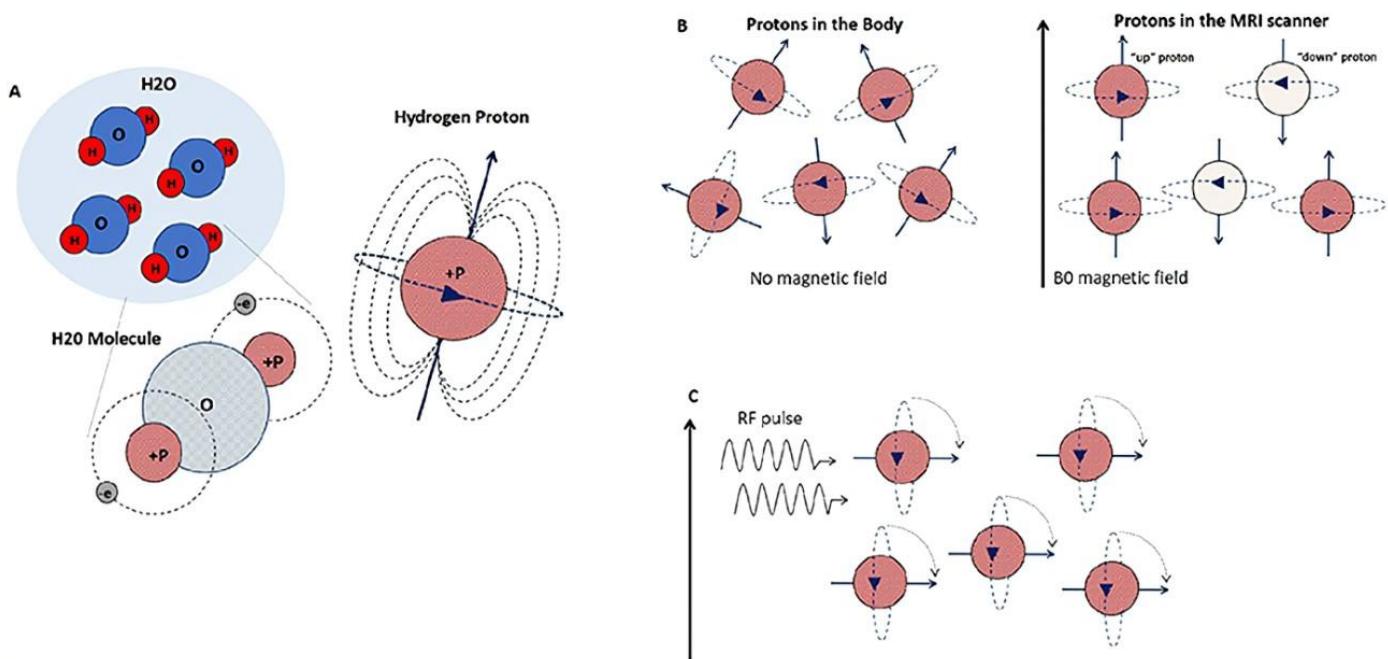
When randomly rotating hydrogen protons are placed inside an MRI scanner, their axes

Align it with the scanner's stronger magnetic field as shown in the figure (8-3), and is called the magnetic field.

For scanners in the fieldSome of the higher hydrogen protons line up (parallel to the magnetic field) and others line up, B0

Downwards (anti-parallel) while still rotating around its axis, due to the principle of quantum physics the number of protons pointing upwards will be

Slightly larger than the downward-pointing protons.



The shape(3-8) Hydrogen protons and how they move in a magnetic field

These small magnets almost cancel each other out, leaving only the magnetic field generated by a small percentage of the directed protons.

Up and this is the small area that can be measured using MRI.

The field does not affectNot only on the proton arrays but also on the speed of rotation of these protons (the frequency of motion B_0).

(orbital), and the frequency of the orbital motion depends on the strength of the magnetic field, and the stronger the magnetic field, the greater the speed.

Its rotation is very important for using MRI to measure the signal emitted by hydrogen molecules.

The difference between T_2 and T_1

thatTime to echo (TE) within the range (400-700 milliseconds) and repetition time (TR) need for T_1

Between (milliseconds 10-30)

whileThe T_2 is TE (+70 milliseconds) and the TR (+2000 milliseconds)

TheT when a high density signal from water is required such as imaging of the spine and joints, while $1T$ 2

When it is necessary to view the anatomy in multiple planes.Broadhouse, 2017

4-9-3 Dual-parameter MRI (bpMRI)

Dual-dimensional MRI (DMR) highlights: 2-bp MRI of the prostate combining morphology-weighted imaging

And the most likely widespread photography (As an alternative to DWI, apparent diffusion coefficient (ADC) and diffusion radius (DWI) imaging

Multimeter magnetic (To detect, locate, and guide targeted prostate biopsy in patients (mpMRI))

Those suspected of having prostate cancer (PCa)

Dual-parameter MRI overcomes some of the limitations of multiparameter MRI.

Such as the costs and time required to perform the study, the use of gadolinium-based contrast agents, and the lack of guidance (mpMRI).

For pest management class3 which cannot be determined for large individual prostate cancer.

Through experiments, it was found that the optimal and similar clinical results of dual-parameter MRI(bpMRI)

Compared to MRIWhat we consider DWI is primarily related to diffusion-weighted imaging (mpMRI).

Prevalent sequencing for tumor detectionSuspicious in both the transition zone and peripheral zone PCa

10-3 Software used:

1-10-3 MATLAB program:

MATLAB is considered one of the most important leading programs in engineering and mathematical applications and one of the most used programs by engineers.

Scientists around the world are producing the company. It is a high-performance language for technical computing. It integrates arithmetic, MathWorks,

Visualization and programming in a user-friendly environment where problems and solutions are expressed in familiar mathematical notation. Includes

Typical uses include:

Mathematics and computation, algorithm development, modeling, simulation and prototyping, data analysis and exploration, graphics

Scientific and engineering applications development, including GUI building.

MATLAB is an interactive system as shown in Figure (3-9) whose basic data element is an array that does not require Dimensions. This allows you to solve many technical computing problems, especially those involving matrix and vector constructions.

, in a fraction of the time it would take to write a program in a non-interactive numerical language like C or Fortran) Evolved, (Fortran

MATLAB has been developed over the years with input from many users.

In university settings, it is the primary teaching tool for introductory and advanced courses in mathematics, engineering, and science, and in

In industry, MATLAB is the preferred tool for high-throughput research, development, and analysis.

It is divided into two sections: MATLAB add-ons and Simulink add-ons. MATLAB add-ons are called boxes.

The equipmentThese boxes differ from each other (Toolbox)

If each box has a scientific specialty that it deals with, it contains programming instructions that lead to solving scientific problems in

The specialty for which the tool was created, such as the image processing tool, deals with the specialty of image analysis and writing algorithms.

To arrange the pixels.)5 website(

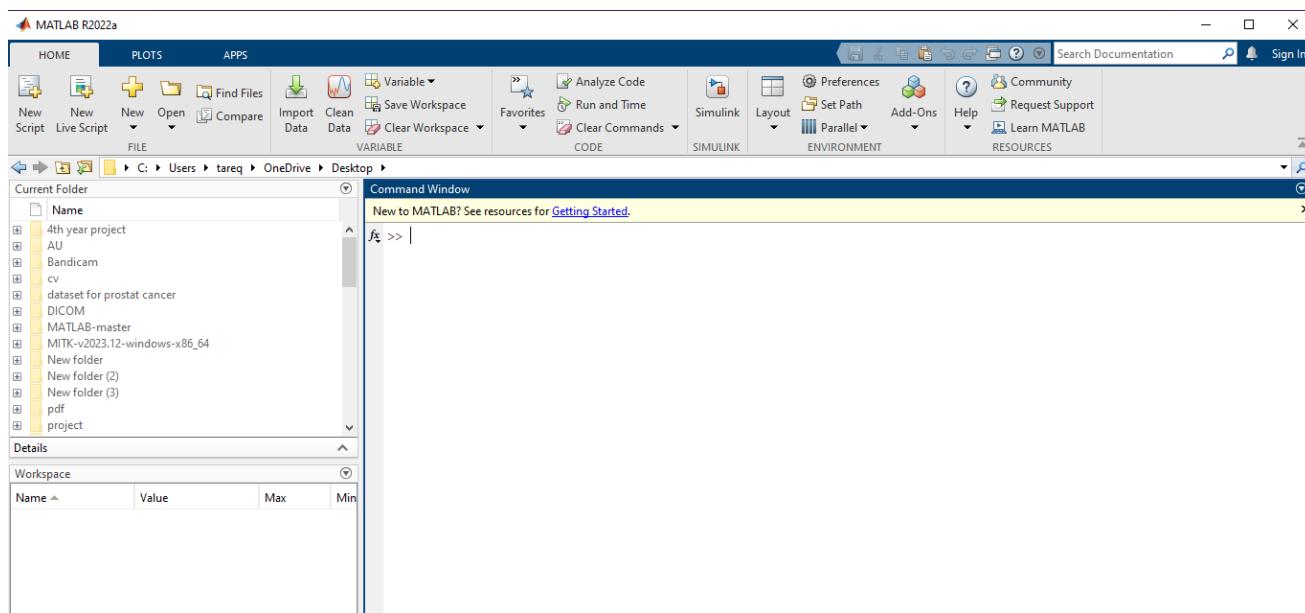


Figure (3-10) MATLAB interface

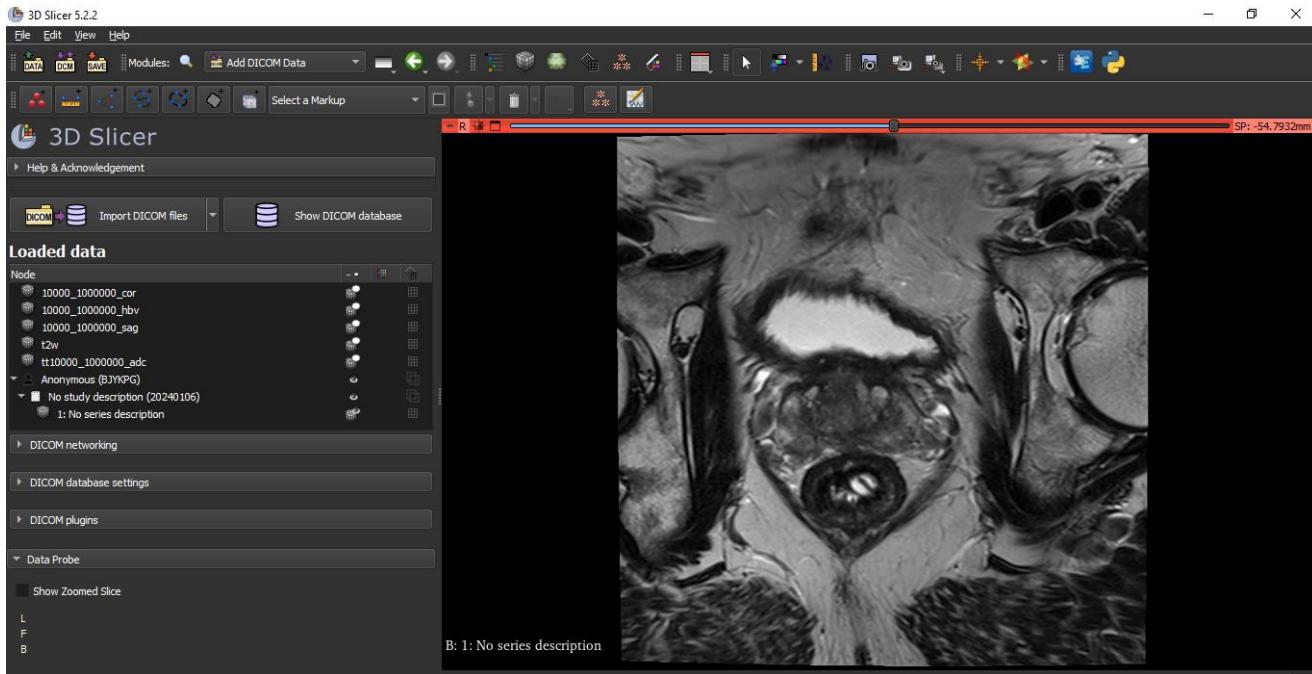
2-10-3 program:3D-slicer

It is a free, open source software and is a flexible, modular platform for image analysis and visualization as shown in 3D-slicer.

In the form (10-3).

ExpandedTo enable the development of both interactive processing tools and batch processing tools for a variety of 3D-slicers.

(From applications)(website 4



The shape(11-3) 3D-slicer interface

Advantages:3D-slicer

- ❖ Display levels in 3D
- ❖ Dealing with images Read/write a variety of other DICOM formats.
- ❖ Data integration and joint recording using software algorithms
- ❖ Automatic and manual image segmentation
- ❖ Analysis and visualization of diffusion imaging data
- ❖ Convert image formats to Dicom

3-10-3 Evorad workstation program:

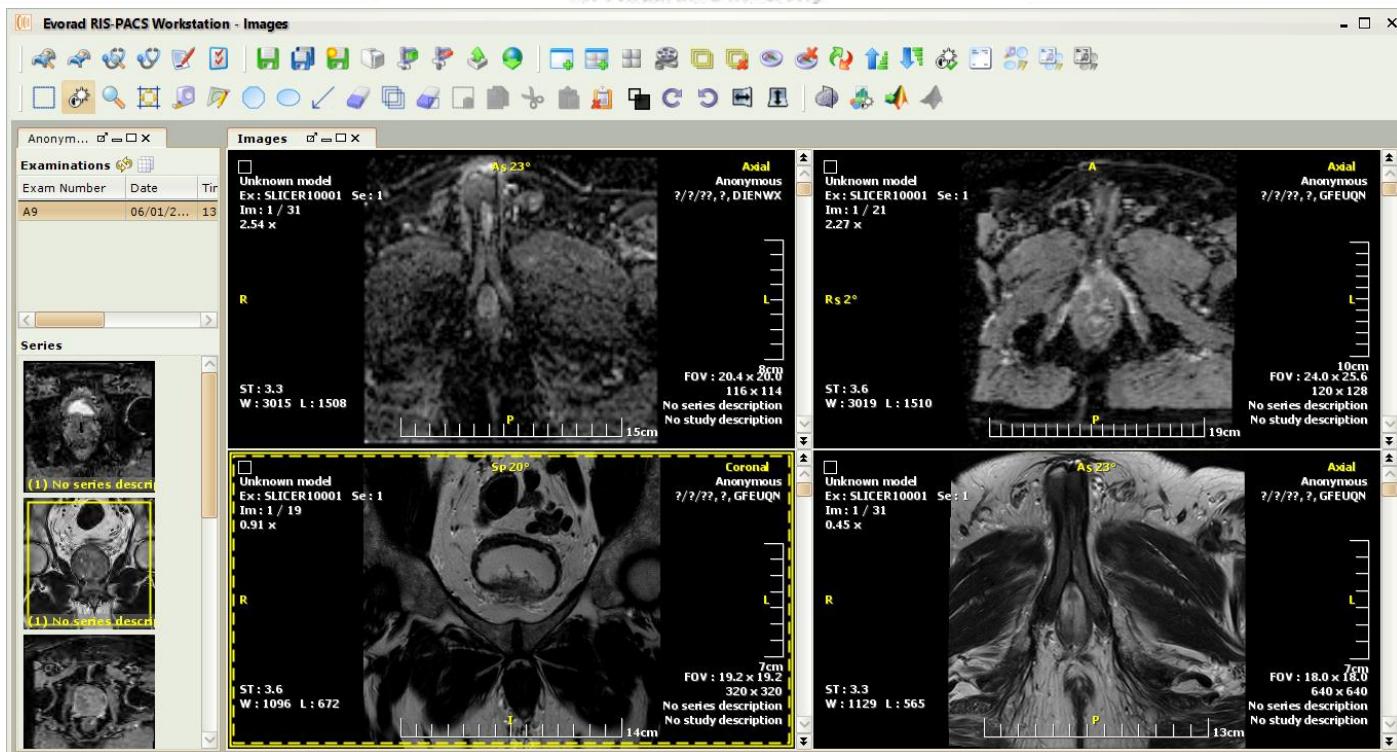
It is an easy-to-use workstation and processing platform, developed through several years of collaboration with radiologists.

Allows for advanced image processing capabilities including 3D reconstruction, volume rendering allowing for more

From a rebuilding process at the same time

It has a tabbed interface for an unlimited number of patients/tests open at the same time, along with many other features.

Such as the ability to convert audio to text for easy and quick reporting, as shown in the figure ((website 3)11-3



The shape(12-3) Evorad interface

11-3 Artificial Intelligence

3-1-11 Definition of Artificial Intelligence and its Applications

artificial intelligence and It is a scientific field that aims to automate activities that require human intelligence by building a set of software algorithms, this field has been used for the past two decades as a development tool in various fields such as prediction and care Health and security, and maps between the model's parallel inputs and outputs of available data using machine learning from By repeatedly presenting the model's inputs and outputs. (Ref. 20)

Artificial intelligence selects the appropriate model that achieves the desired results by matching it with the available budget.

And available training data. Artificial intelligence monitors the system and its performance, helping the organization build customer trust.

From treating and diagnosing cancer, to ensuring food safety for a growing population, to analyzing climate change.

As artificial intelligence provides key solutions to solve the challenges facing society.Kumar et al., 2023

2-11-3 The role of artificial intelligence in healthcare

Artificial intelligence can assist healthcare providers in a variety of patient care and health systems.

Smart. Artificial intelligence technologies ranging from machine learning to deep learning are spreading in healthcare to diagnose

Diseases, drug discovery, and patient risk assessment. Multiple medical data sources are needed to diagnose diseases.

Ideally using artificial intelligence techniques, such as ultrasound and MRI.

Mammography, genetic imaging, and computed tomography

Moreover, AI has primarily enhanced the clinic experience and accelerated the patient onboarding process.

To continue their rehabilitation at home.) Kumar.et al, 2023

Digital healthcare offers numerous opportunities to reduce human error, improve clinical outcomes, and track data over time.

Over time, AI approaches from machine learning to deep learning have a crucial role in many related fields.

In healthcare, including improving new clinical systems, patient information and records, and treating various diseases.

Artificial intelligence techniques are also more efficient in determining the diagnosis of different types of diseases.

Researchers have used several AI-based techniques such as machine learning and deep learning models to detect About diseases such as skin, liver, heart, Alzheimer's, cancer and other diseases that require early diagnosis.

As an example, techniques such as the Boltzmann machine are presented. Decision tree, SVM, Boltzmann support vector machine

(logistic regression) Artificial neural network, fuzzy logic, and logistic regression.

To diagnose diseases.Kumar et al., 2023

3-11-3 Machine Learning machine learning

It is a branch of artificial intelligence and one of the computer sciences, and the fact that this science focuses greatly on the use of data (training data) and algorithms. Simply put, machine learning is a method of enabling computers to perform specific tasks without explicit coding of each line in order to imitate the way humans learn and work on improving it gradually. Therefore, machine learning is a program that shows a cognitive ability that is very similar to the ability of humans. It aims to make computers think and solve various problems that they face in the way a normal human does, by taking advantage of statistical models and learning algorithms.

It consists of a series of nodes/neurons connected to each other. There are three different layers: the input layer, the hidden layer, and the output layer.

The input layer takes data into the network, where it is processed by nodes in the middle/hidden layer.

In the hidden layer are mathematical functions that can process the data coming from the input layer, and extract patterns with

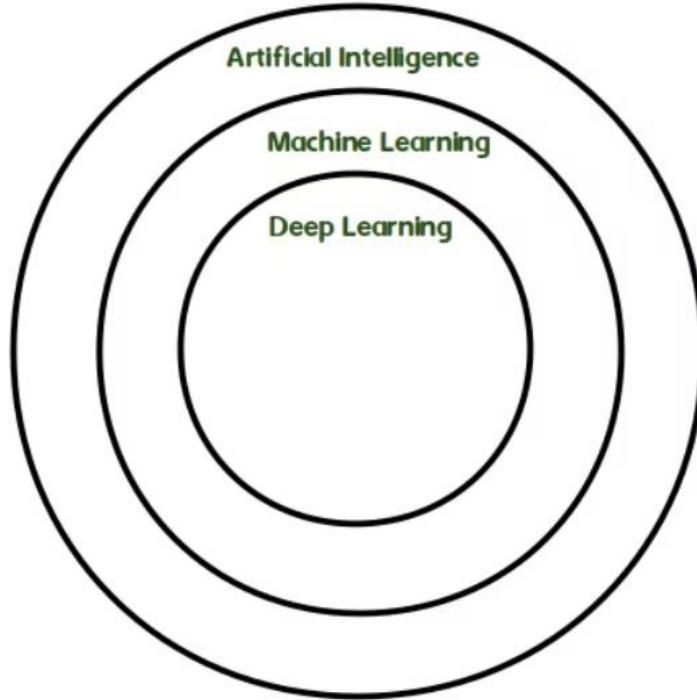
Relevance from input data. This is how a neural network "learns." Neural networks get their name from

The fact that it is inspired by the structure and function of the human brain.(website 1)

4-11-3 Deep LearningDeep learning

Deep learning is the term given to machine learning architectures that connect multiple layers of perceptrons together, such that there is not just one hidden layer, but many. The "deeper" a deep neural network is, the more complex patterns it can learn.

Deep layer networks composed of neurons are sometimes referred to as fully connected networks or fully connected layers, referring to the fact that a given neuron maintains connections to all of its surrounding neurons. Fully connected networks can be combined with other machine learning functions to create various deep learning architectures.) website 1



Shape (3-13) Illustration of deep learning

Differences between deep learning and machine learning:

First: Machine learning works on a limited amount of data, while deep learning works on a large amount.

Second: Machine learning divides the task into subtasks, analyzes them individually, and collects the results in the end, while deep learning does not divide the task.

Third: Machine learning takes less time to train than deep learning.

Fourth: Machine learning takes longer to test than deep learning.

There are a variety of deep learning architectures used by researchers and engineers, and each architecture has its own unique use cases. Some of the most important include:

Convolutional neural networks or CNNs, is a neural network architecture commonly used in creating vision. Computer systems. The architecture of convolutional neural networks enables them to interpret image data, converting it into numbers that a fully connected network can interpret. - The network contains CNN has four main components:

- ❖ Convolutional layers
- ❖ Reduction/Aggregation Layers
- ❖ Activation functions
- ❖ Fully connected layers

Convolutional layers are what take images as input into the network, parse the images, and obtain pixel values. Downsampling is where image values are transformed or reduced to simplify image representation and reduce the sensitivity of image filters to noise. Activation functions control how data flows from one layer to the next, and fully connected layers are what analyze the values that represent the image and recognize patterns in those values. website 1)

12-3 Hybrid Systems

As the research community advances in the field of artificial intelligence and deep learning, scientists increasingly feel the need to move toward hybrid AI. Hybrid AI is described as the ability to solve the fundamental problems facing deep learning today.

In artificial intelligence, symbolic artificial intelligence is a term given to a group of all methods in artificial intelligence research that are based on high-level (human-readable) symbolic representations of problems, reasoning, and inquiry.

Symbolic AI uses tools such as logic programming, production rules, semantic networks, and frameworks, and develops applications such as knowledge-based systems (especially expert systems).

Hybrid AI combines the best aspects of neural networks and symbolic AI. Combining massive datasets (visual, audio, text, emails, chat logs, etc.) allows neural networks to extract patterns. Rule-based AI systems can then process the extracted information using symbol processing algorithms.

When symbolic AI and neural networks are combined, symbolic AI and neural networks can form a good basis for developing hybrid AI systems. A hybrid AI model uses the neural network's ability to process and evaluate unstructured data while using symbolic AI techniques.
(website2)

Chapter Four

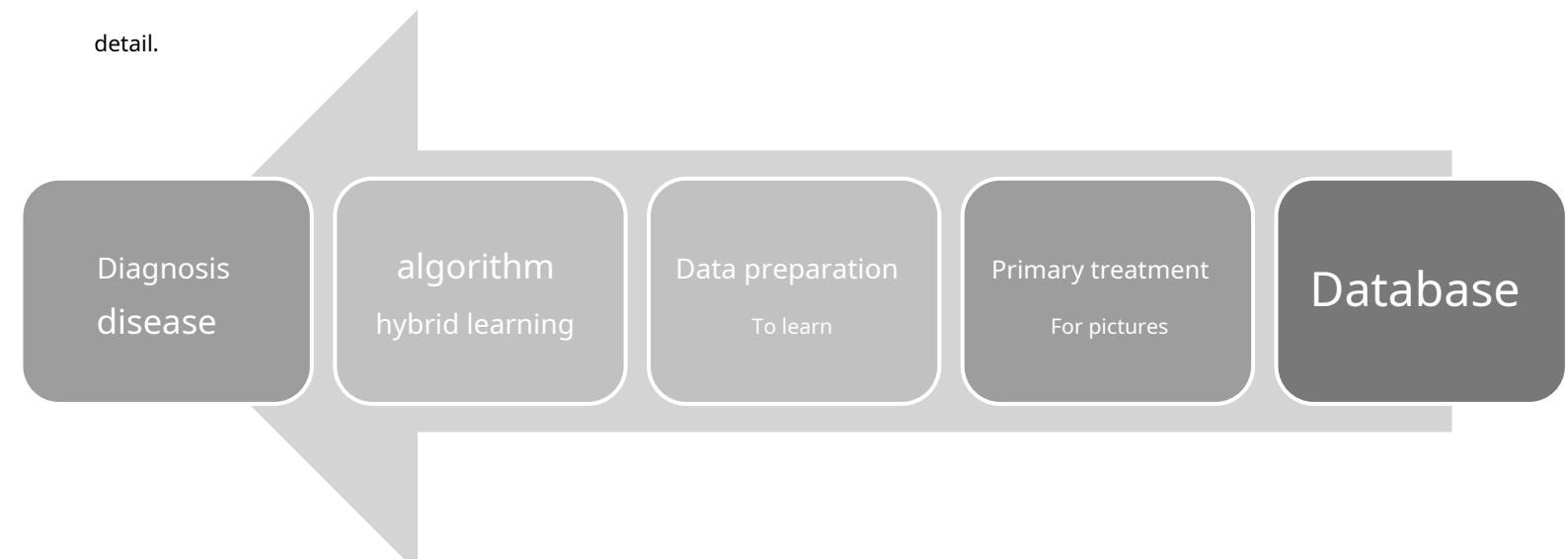
Practical section

1-4 Introduction

In this chapter, we will discuss the working method, including the algorithms for processing images before entering them into the system, and diagrams of the networks that were studied and trained on the special database. We will explain each step that was applied in the hybrid system.

2-4 Work plan:

As shown in Figure (4-1), the basic working diagram of the hybrid system contains the basic stages that will be explained in detail.



Shape (4—1) Work plan

1- Database: MRI images of the prostate gland in PDF formatIt is a special format used for medical images (MHA).

In the Retail and Registration Toolkit)

2- Preliminary processing: Converting images into DICOM format for input into MATLAB (a standard for communication and information management).

Medical imaging and related data) and selecting the appropriate slice and applying the cropping and merging algorithm

3- Data sorting: Sorting cases into benign or malignant tumors.

4- Hybrid learning algorithm: It consists of Decision trees /Deep learning + support vector machine

It will discuss the hybrid systems that have been trained and tested.

5- Disease diagnosis: It is the output of the hybrid learning algorithm in determining whether the patient is diagnosed with prostate cancer.

Or a benign tumor, and the graphical interface for diagnosing the disease will be built

3-4 Database

This is the database that was downloaded from the PI-CAI group from the Grand challenge website and the dataset contained:

1500 dual-parameter magnetic resonance imaging (BpMRI) cases and an Excel file containing case descriptions

Each case consists of the following:

1. T2 slice images: Transverse relaxation time, which is related to the interaction between the nuclei with each other, and it is the time

Necessary for the transverse magnetization component of the nuclei perpendicular to the direction of the applied magnetic field to vanish, and is used

theWhen a high intensity signal from water molecules is required, T2

2. Slide imagesDiffusion-weighted imaging (DWI)

A form of MRI that relies on measuring the random free motion of water molecules within tissue. In general terms, highly cellular tissues or those with cellular swelling exhibit lower diffusion coefficients. Diffusivity is particularly useful in characterizing tumors and cerebral ischemia.

3.Apparent diffusion coefficient (ADC): The apparent diffusion coefficient (ADC) is a measure of the diffusion magnitude of water molecules within tissue, typically calculated using MRI with diffusion-weighted imaging (DWI). It characterizes the water movement observed in the clinical setting, reflecting the limits at which pure diffusion *in vivo* cannot be easily separated from other sources of water movement.

4.Mask images: This is the mask for the prostate gland, where the gland is segmented directly from the images. It is a binary image that is multiplied by the original image to segment the prostate.

_ Diagnosing prostate cancer is complex and cannot rely on a single imaging parameter (such as T2, for example).

The global protocol for imaging the prostate gland is to image several parameters at the same time, which are:

By combining all the previous types of imaging, (T2+DWI+ADC+T1(Axial)+Dynamic contrast enhanced(DCE))

The disease can be accurately diagnosed using multiparameter magnetic resonance imaging (mp MRI), but it is very expensive.

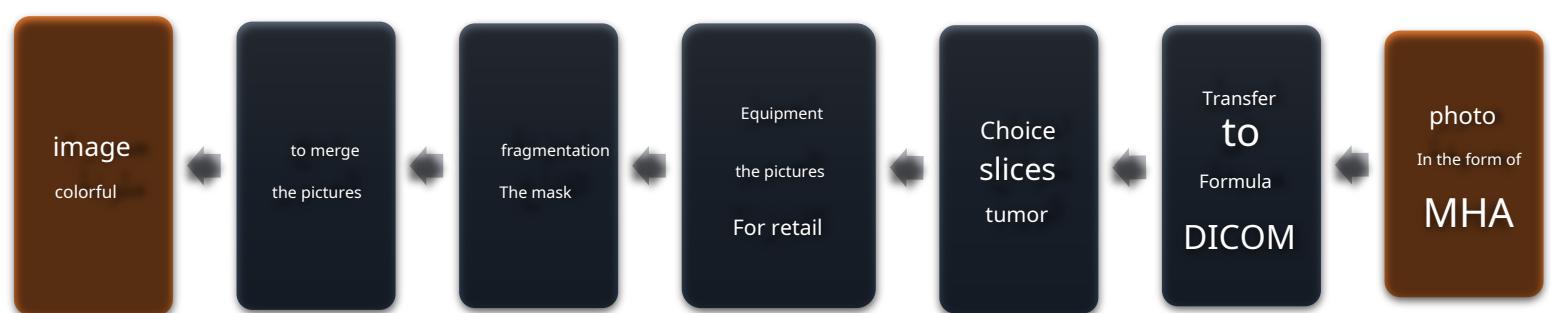
The use of DCE requires injection of a contrast material, meaning that the imaging process takes a long time.

The PI_CAI Challenge is a competition to find the best AI network model capable of diagnosing from fewer parameters.

Which is (T2+DWI+ADC), using dual-parameter MRI, which in turn will reduce

Cost and time required for the imaging process

4-4 Initial Image Processing



Shape (2-4) Preprocessing algorithm

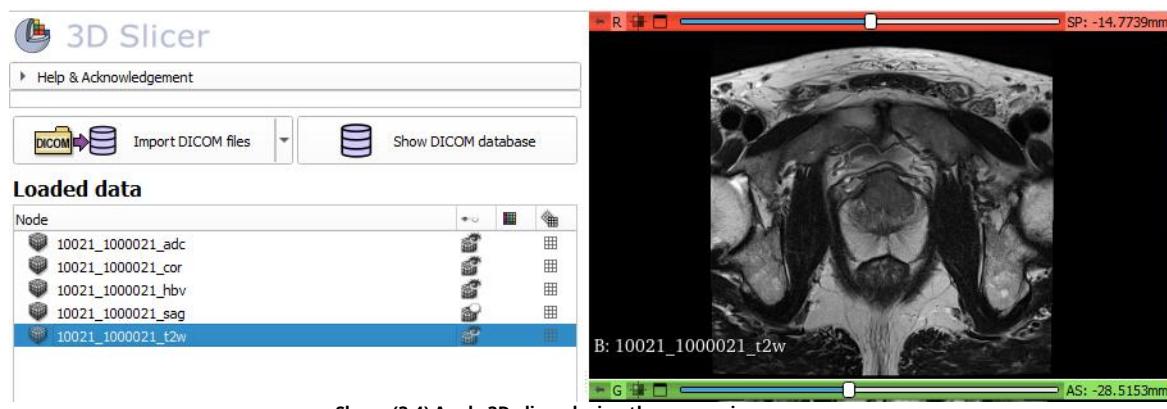
1-4-4 Convert from MHA format to DICOM format

MHA is a proprietary medical image format used in the segmentation and registration toolkit. This format cannot be entered

The format is processed on MATLAB, and then converted to DICOM format (a standard for communicating and managing imaging information).

Medical and related data) manually via 3D-slicer software (which is a flexible, modular platform for analyzing

Images and their conversion), as shown in the figure (3-4)



Shape (3-4) Apply 3D-slicer during the conversion process.

2-4-4 Selection of tumor slices from each case

Each case requires examination and analysis of the three types of imaging (T2 + DWI + ADC) to accurately determine the location of the tumor.

We previously studied the prostate gland and communicated with a radiologist to learn and understand how to select the correct images.

We relied on selecting images that contain the largest area of benign or malignant tumor.

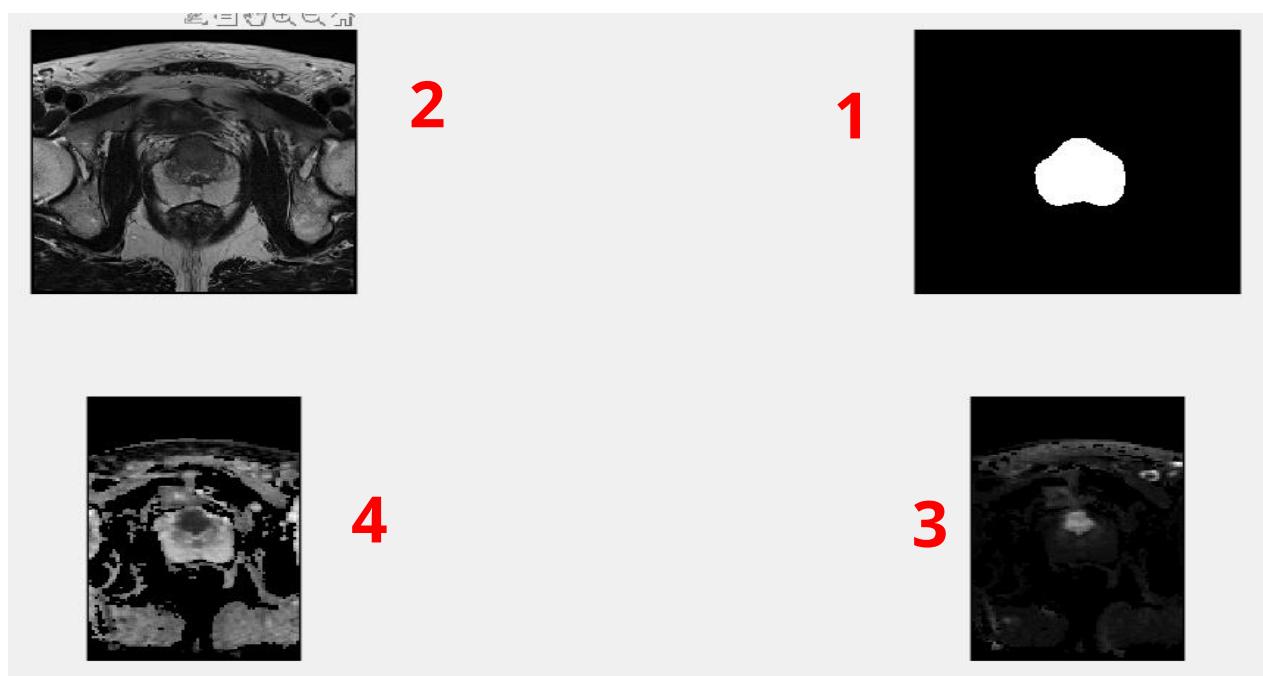
3-4-4 Preparing images for segmentation

First, we want all the images to be the same size so that they can be merged together. This is a basic condition for the multiplication process.

And integration.

Whereas T2 images are of size (1*640*640), DWI images are of size (1*120*128), and ADC images are of size (1*120*128).

(1*120*128) and mask images (640*640) are binary, as shown in Figure (4-4).



Shape (4-4) Pre-treatment images for case No. (21, which is cancerous). The first image is T2, the second image is the prostate mask, the image

ThirdDWI and ADC 4th image

So we apply the {imresize} instruction on the two images (DWI, ADC) to change the size to (640*640) as follows:

All images become the same size.

We crop the image to reduce the load on the neural network. To crop, we know that the gland

The prostate in the data does not necessarily have to be in the center of the image, so we need a special method to do that.

Cropped correctly to include the entire gland in the four new images.

So we apply the extract image properties instruction. 'Centroid', gdicom, table where { regionprops(

The gdicom is the binary mask image, and we extract the features of the center of the gland, which is a pixel in the middle.

The gland has two specified row and column values.

After determining the center of the gland, the largest size of the prostate gland was inquired about within the data and the coordinates of four points were determined.

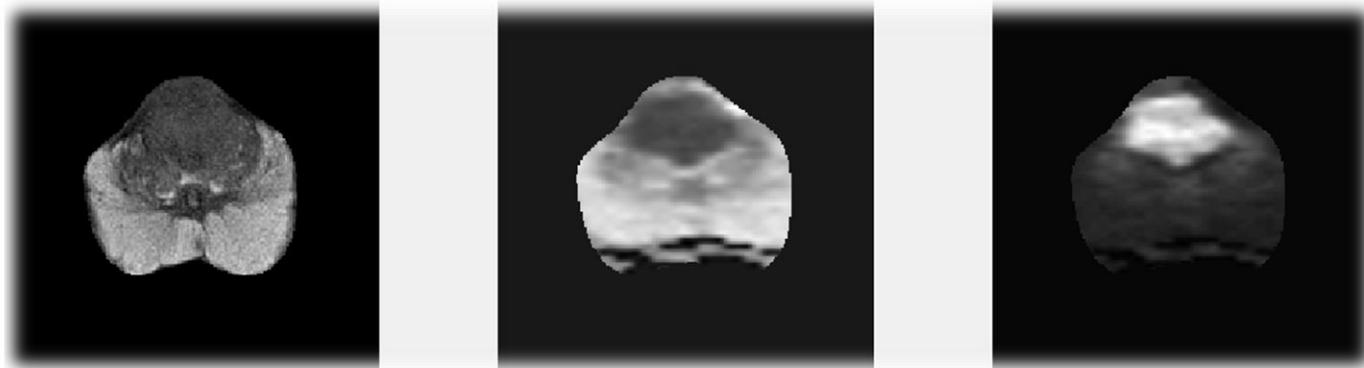
A square shape 93 pixels from the center which will be the corner points of the new image.

We apply the {imcrop} instruction to the four images, entering the previous coordinates to produce the cropped images in size.

(187*187).

4-4-4 Mask segmentation: After cropping the images) We apply the mask to each of (T2+DWI+ADC+MASK

T2, DWI, and ADC images are multiplied to produce images as shown in Figure (4-5).



Shape (4-4) Mask segmentation images from right to left: DWI image, ADC image, T2 image

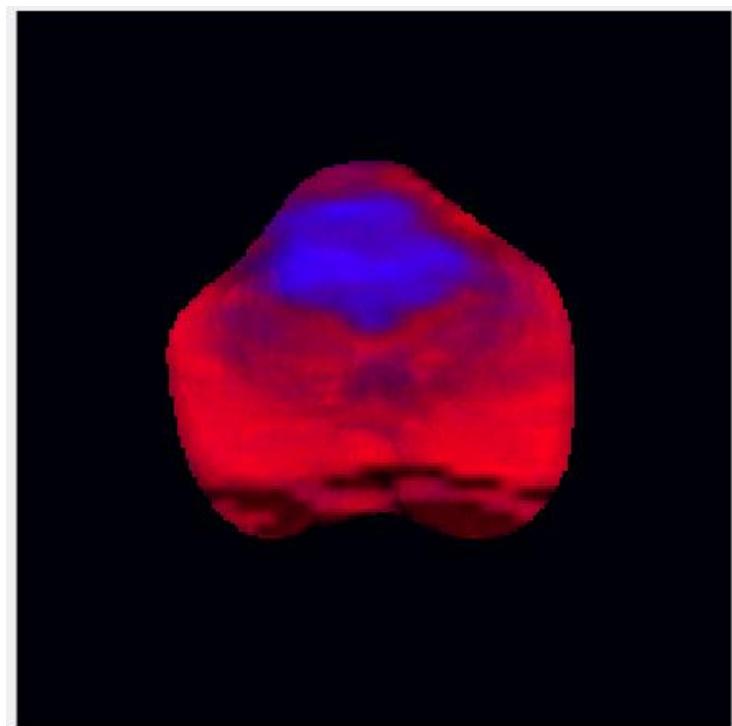
5-4-4 Merge images

In order to reduce the burden on the neural network, we need to combine the three images to form one colored image, by:

The `imfuse` instruction creates a composite RGB color image, where the gray areas in the composite image are shown. The places where

In which the two images are identical in intensity. The areas of different intensities show a color intensity corresponding to the image of different intensity. This results in

We have a new image with a size of (3*187*187) as shown in Figure (4-6).



Shape (6-4) Image of the application of merging the three images on a case of a cancerous tumor. The blue color shows the location of the cancerous tumor and the rest of the healthy areas share In red

The algorithm is applied to all images and converted to PNG format, then stored in a new file for sorting.(**algorithm**

Processing of raw data in Appendix A).

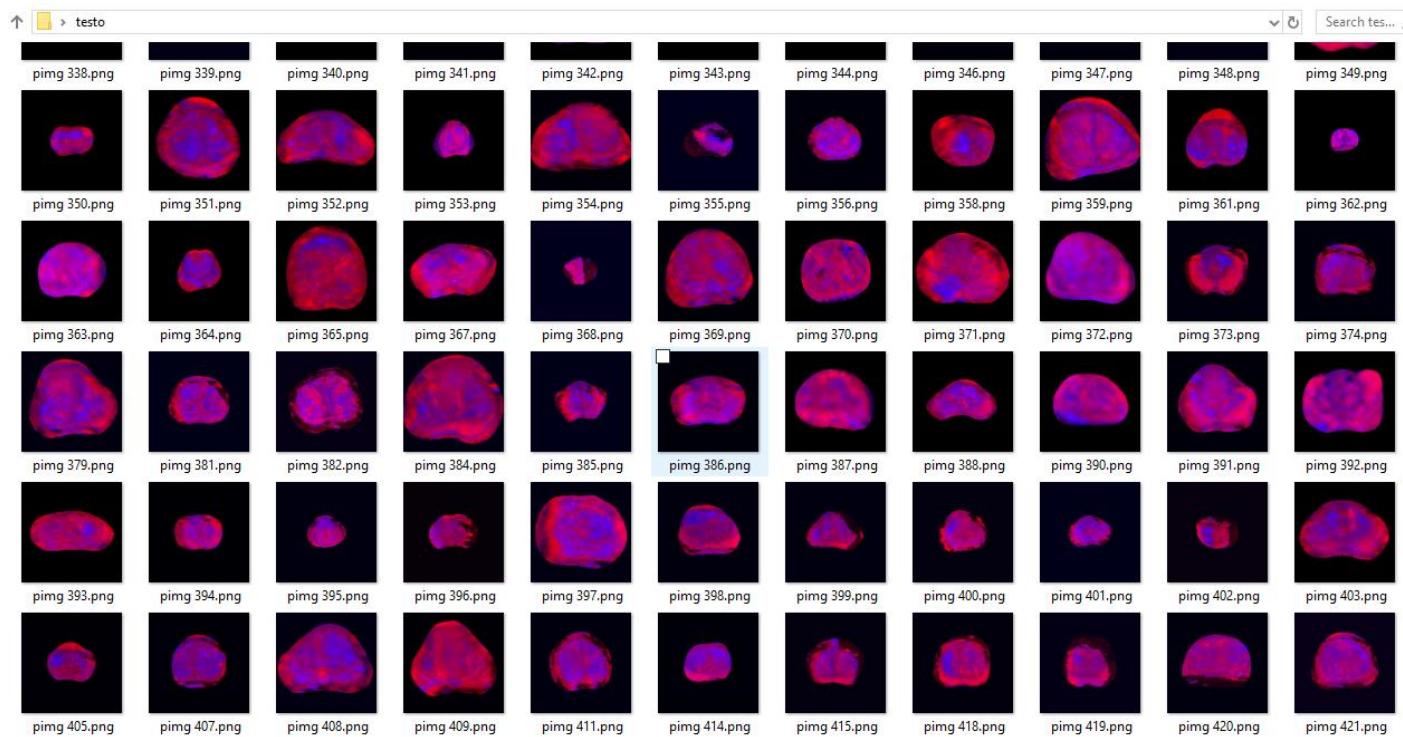
5-4 Preparing data for learning

Cases containing errors, high noise, or lacking the required information and not suitable for the detection process were deleted.

We selected 404 good cases to be input for the neural network, as shown in Figure (4-7), and the cases were sorted into benign tumors.

According to the data, 224 cases of malignant tumors, 180 cases of benign tumors (cancer tumors) and malignant cases (benign tumors).

Attached case descriptions.



Shape (7-4) Database after initial image processing and data preparation

Since the hybrid system is divided into two stages for training and testing, we divided the data as follows:

For the first stage, which is a deep learning network, 260 cases were used for training (140 benign tumors - 120 malignant tumors).

_ The second stage is a learning network by regression using one of the networks (SVM, bagged trees, boosted trees).

Use 304 (174 benign tumors - 130 malignant tumors) cases for training.

The test cases are 100 cases (50 benign tumors - 50 malignant tumors) and the test cases will be applied to the stage output.

The first (deep learning systems) and the second stage output for comparison (hybrid systems)

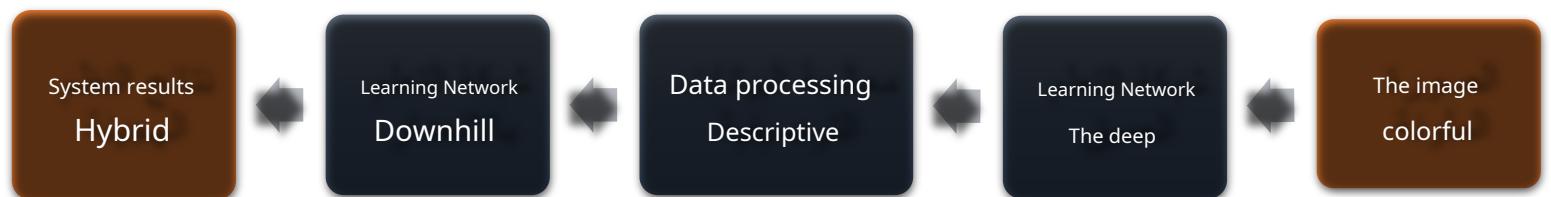
6-4 Hybrid System

For the first stage, we trained on several of the most important network templates, including:

Which are considered among the most successful classification systems (Resnet, Googlenet).

As for the second stage, we tried several learning systems (SVM, Boosted trees, Bagged trees).

1-6-4 Hybrid System Flowchart



The shape(8-4) Hybrid system workflow

2-6-4 Deep Learning Networks

1-2-6-4 Network (Res Network)

For visual recognition, Microsoft Research developed a deep learning model called ResNet, which was launched in 2015.

"Residual Networks" is short for ResNet.

The complete ResNet architecture consists of four parts:

1- Convolution layers: These layers play a fundamental role in feature extraction. Convolution includes:

Apply filters to the input images. These filters create

A two-dimensional array of values that represents the extracted feature,

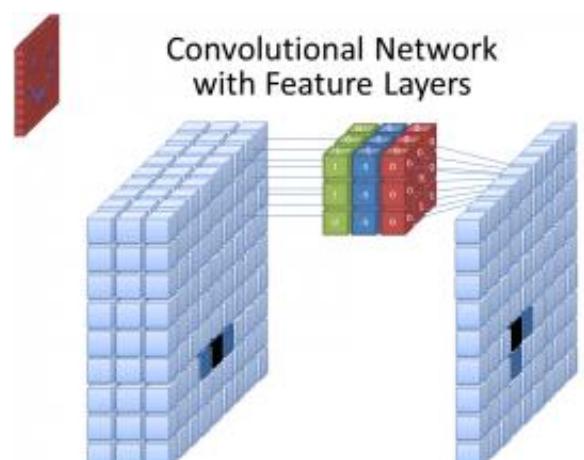
As shown in Figure (4-9), this allows the model to detect patterns.

and different edges and textures within the data.

Multiple filters are used, with different matrices performing the same function.

which created different filters to extract more representations.

"Deeper" complexity and the number of filters ranges from (32 to 2048)



The shape(9-4) The operation of the convolutional layer in extracting features

2- Convolutional blocks: These blocks consist of multiple convolutional layers, and they help in extracting high-level features from

Input data. Each convolutional block consists of:

- Convolutional layer(Convolution layers)
- Batch normalization(Batch Normalization)
- Activation function(ReLU)

Batch Normalization: Normalization is a data pre-processing tool used to transform numeric data.

to a common scale without distorting its shape, which helps speed up network training and prevent the network from reaching Over

It is the case when the network is able to classify the training data but is unable to classify any data (Fitting
(Outside training data))

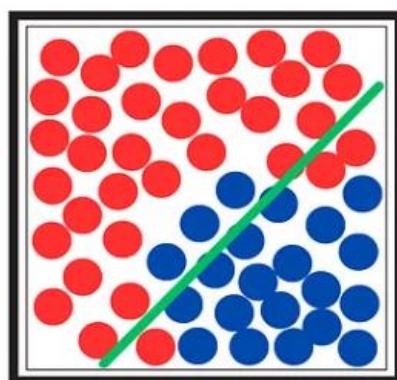
It is done by adding a new layer to the network after the convolutional layer. The new layer performs the unification and normalization operations on Outputs of the previous layer in successive batches.

Activation function: An activation function can be defined as a mathematical function that introduces nonlinearity into a neural network. This enables Models learn complex patterns and help them make accurate predictions, as shown in Figure (4-10).

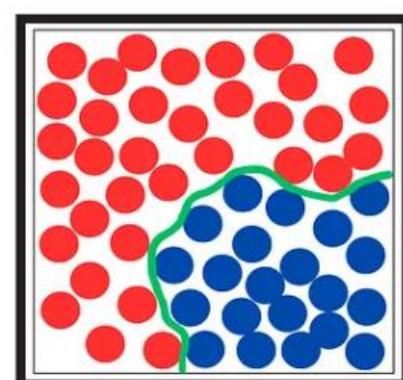
If the input is above a certain threshold, the neuron will activate, and if it is below it will remain inactive, through

By introducing nonlinear transformations into the network, activation functions help create more advanced and complex decision boundaries. This leads to:

To improve accuracy and predictive capabilities.



**Neural Network without
an Activation Function**

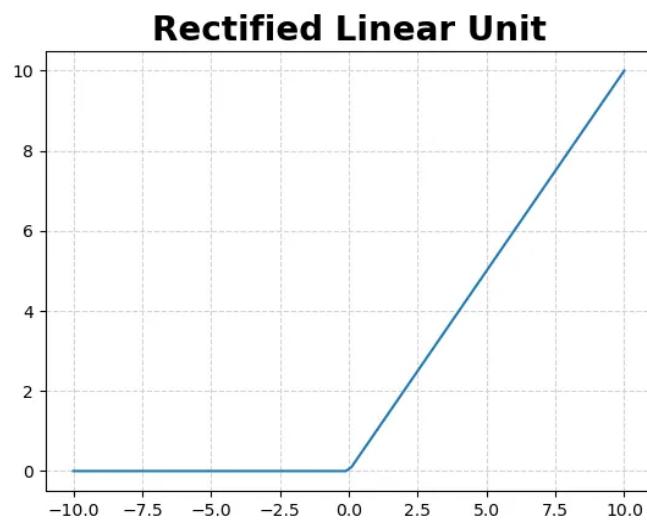


**Neural Network with
an Activation Function**

The shape(10-4) The effect of the activation function on the neural network

Activation Function (ReLU): Relu is the most common and widely used activation function. It allows the input value to pass through If it is positive, it returns zero if the value is negative, which reduces the problem of vanishing derivative gradient. When he approaches Derivative of the activation function from zero),

ReLU is primarily used in the hidden layers of neural networks because it brings convergence to the data. This means that Able to selectively activate only a subset of neurons and assign all other values to ReLU Zero. This leads to a more efficient representation of high-dimensional data, as Figure (4-11) shows the shape of the Relu activation function.



The shape(11-4) Relu activation function

3- Residual blocks: It is a simple block that works on recombining the input with the output, and it consists of one convolutional layer with a window size of (1*1) filtering to maintain the size of the filters followed by a normalization layer

The remaining blocks act as shortcuts or jump links that allow the model to skip one or more layers. This helps mitigate It eliminates the problem of vanishing gradient during training and helps in smooth flow of information.

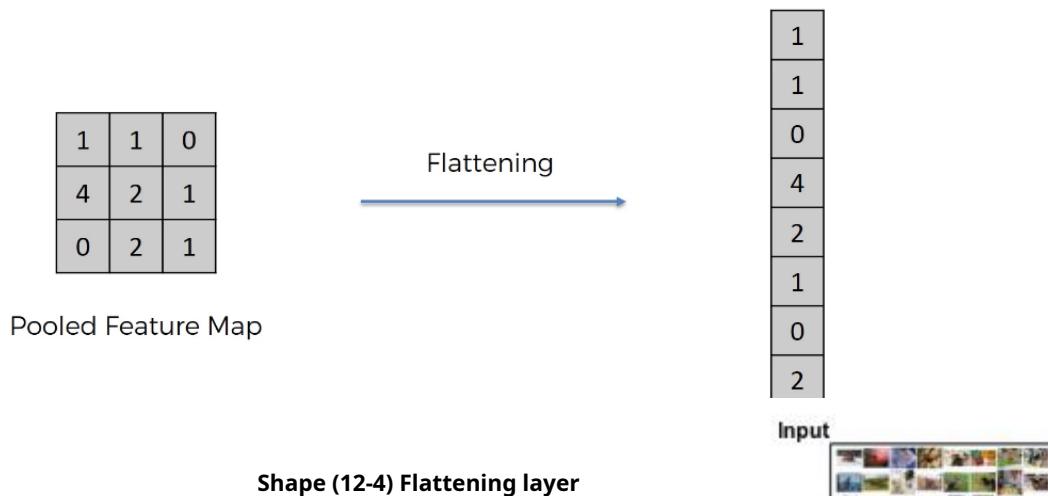
4- Flatten/fully connected layer: The flattening step is a simple step in building a network.

It involves taking the combined feature map created in the clustering step and converting it to a one-dimensional vector.

Here is a visual representation of what this process looks like in Figure (4-12), as these layers are responsible for making predictions.

Based on the extracted features. In the context of ResNet, fully connected layers map the learned features to classes.

Final outputs.



- Architecture and working principle of Res_Network

1- Income: First, images are stored with the instruction }It is {imageDatastore

An instruction that stores images with the classification of each case saved, then enters the data into

Convolutional layer with a window of (7*7) and a number of filters of 64 (the number of filters is

The number of neurons in this layer is represented by applying a padding of

(3*3) is an operation that adds three rows and three columns to the image.

(found in the parameters of the convolutional layer), as applying the convolutional layer

It leads to a reduction in the size of the image, thus losing information (pixels) in

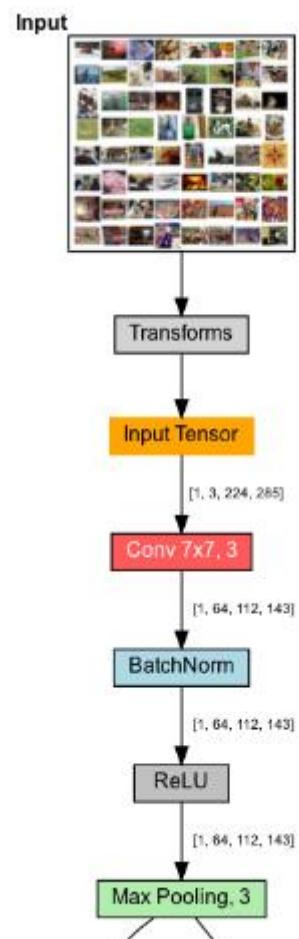
The edges of the image, that the first convolutional layer (64*94*94) came out

Then we perform the normalization process in one go, then apply the Relu activation function, followed by

Max pooling layer with size (3*3) The function of this layer is to apply a filter window

With a size of (3*3) and finding the highest value within the window and replacing it in a new matrix

Its size is (64*47*47), as shown in Figure (4-13).



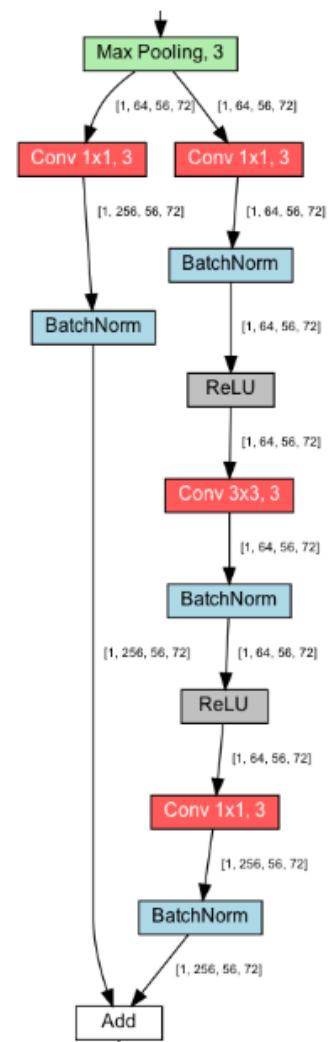
2- Duplicate template:

We now have 64 matrices of size (47*47) from the previous step, which will be entered into a template that will be repeated 16 times, as well as:

Figure (4-14) shows that the network is divided into two paths that we talked about previously:

The first path: It is the convolution blocks, which consists of three convolution blocks, where the first block has a window size of (1*1).

With 64 filters, the second block has a window size of (3*3) with 64 filters, and the third block has a window size of (1*1) with 256 filters, maintaining the image size (47*47) and the number of matrices becomes 256 in the output of the first path



The second path: These are the remaining blocks that we talked about previously, which characterize the Resnet network.

Where one convolutional layer is added with a window size of (1*1) and a number of filters of 256 to maintain

On a matrix size of (47*47) and a number of filters of 256

In order for two paths to be combined, the data in the two paths must be similar in size and number.

Matrices

This template is repeated 16 times in sequence to increase the training depth and extract complex features from

Benign and malignant tumors

**Shape (14-4) From the right path First,
and from the left the second path**

- Al Kharj:

Figure (4-15) shows the final path of the network, during the 16 iterations of the template.

The size of the matrices is reduced during deep feature extraction to (6*6) is 2048, meaning that there are 2048 features extracted with a size of (6*6)

In this path, the Average pooling layer is applied, which is a layer that selects

The average value of each matrix becomes the matrix size (1*1)

Then we input the fully connected layer (flattening layer) which we explained.

Prefixed and followed by the sigmoid function which inserts values within the range [0,1],

Specifying that any value higher than 0.5 is a benign tumor, and any value lower than 0.5 is a malignant tumor.

It is a malignant tumor.

Shape (15-4) Final output path of the network

(The output layer of the Google net network SoftMax has been removed and a sigmoid layer added to the output because the data is binary.

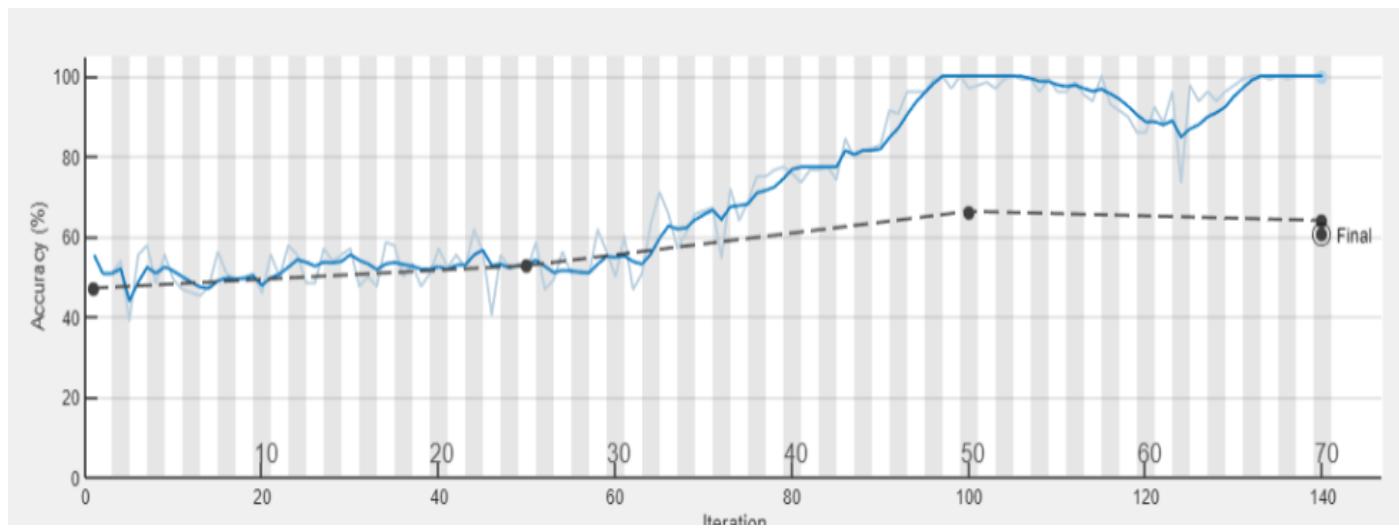
Either 0 or 1)

Resnet network training

As we mentioned previously, we trained on 260 cases with 140 repetitions, and in each repetition the weights were adjusted until reaching

To 100% training accuracy (which is testing the training cases in each iteration whether the expected value equals the actual value)

As in Figure (4-16), with the learning rate set at (0.001)



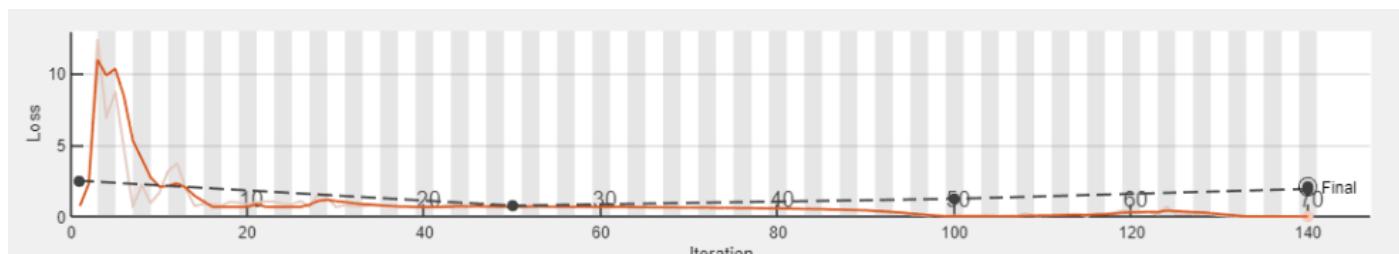
Shape (16-4) The training curve of the Resnet network, the blue color represents the training accuracy and the black color represents the test accuracy.

Note: The accuracy of the test in Figure (4-16) is low because only 20 cases were selected for testing during training, and the number of cases was modified.

Test data up to 100 as mentioned previously, and the test algorithm will be attached in the appendix.

Loss rate curve: It is a measure of the performance of a machine learning model, especially in the field of neural networks. The loss rate represents

The average error a model makes on a given task, such as image classification or data prediction, as shown in Figure (17-4)



Shape (17-4) Loss rate curve for Resnet network, the red color represents the loss rate in the training data and the black color represents the loss rate in the test data

2-2-6-4 Deep Learning Network (Google Network)

It is a deep convolutional neural network developed by researchers from the company Google

The structure was presented. ImageNet for Visual Recognition in 2014 at the GoogLeNet Competition

To solve computer vision tasks such as image classification and object detection (ILSVRC14)

- Architecture and working principle of the Google Net network

1-Income: The image with size (3*187*187) is fed into a convolutional layer.

With a window size of (7*7) and a number of filters of 64, followed by the Relu function, the output will be:

This layer is (64*94*94), and then it is followed by the Max pooling layer with a size of

The (3*3) window finds the highest value within the layer matrix and enters it into

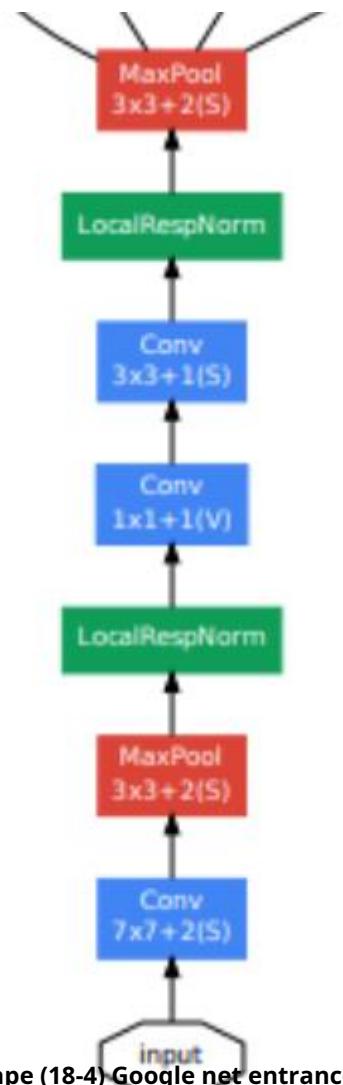
The new matrix becomes the output layer (64*47*47), then it is normalized.

Data.

The next layer is a convolutional layer with a window size of (1*1) and a number of filters of 64.

It is also followed by a convolutional layer with a window size of (1*1) and 192 filters, then normalization.

Finally, Max pooling with a window size of (3*3) to be the output of the input path (192*24*24), as shown in Figure (4-18).

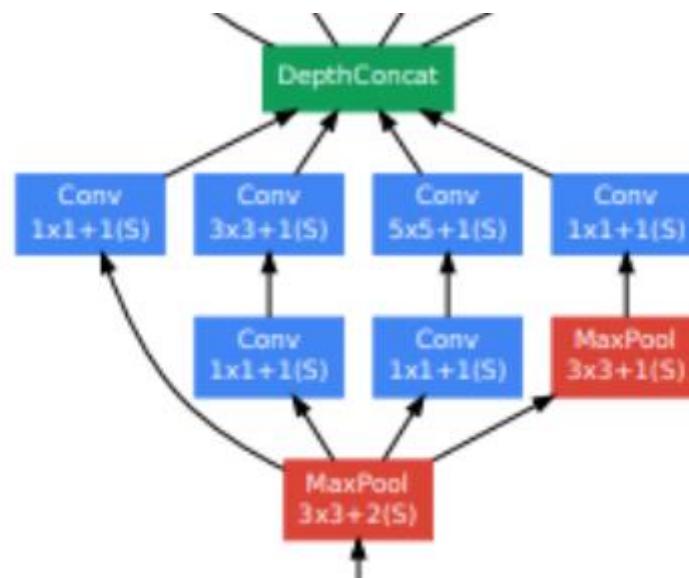


192 matrices, each matrix size (24*24)

2-Duplicate template: It is called a template because it is repeated 10 times in a row to increase the training depth and extract deeper features.

It is divided into four paths, and in each path convolution blocks are applied with specific parameters to maintain the size of the matrix.

Increase the number of filters, as shown in Figure (4-19), after applying the template repetition, the image size will be (6*6) and the number will be 1024 filters.



Shape (19-4) Duplicate template

3- Al Kharj:

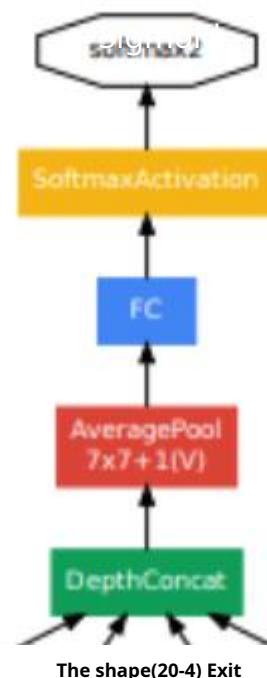
After the matrix size becomes (1024*6*6), it is inserted into the layer.

ooling La Liga Avarege p Find the mean value and substitute it into the new matrix.

, followed by a fully connected layer (Flatten) and then a Sigmoid layer for classification.

(The output layer in the Google net network is SoftMax, which has been removed and added

Sigmoid layer for output because data is binary (either 0 or 1)



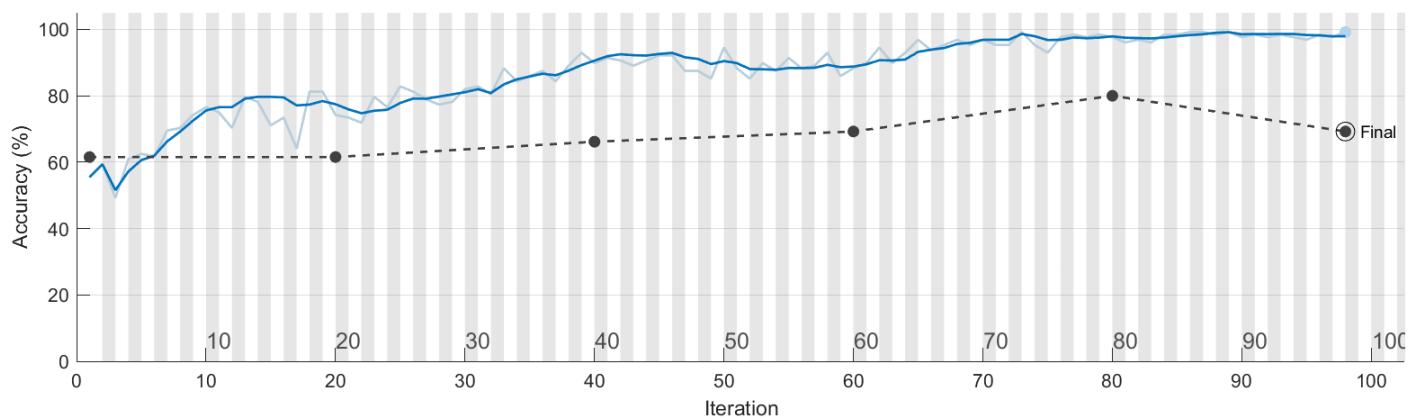
The shape(20-4) Exit

Google Network Training

260 cases were trained with 100 repetitions, and in each repetition the weights were adjusted until training accuracy was reached.

%100 (which is testing the training cases in each iteration to see if the expected value is equal to the actual value) as in the figure

(16-4), with the learning rate set at (0.001)

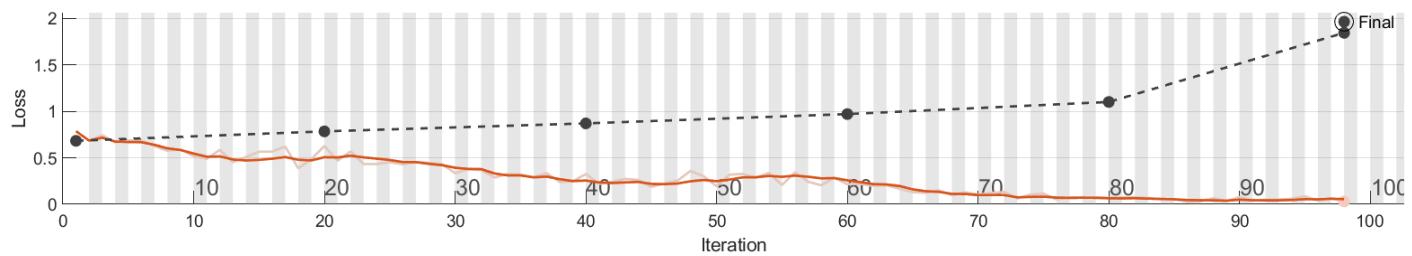


The shape(21-4) The training curve of the Googlenet network. The blue color represents the training accuracy and the black color represents the test accuracy.

Note: The accuracy of the test in Figure (4-21) is also low because only 20 cases were selected for testing during training, and

Modify the number of test data to 100 as mentioned previously, and the test algorithm will be attached in the appendix.

As for the loss rate curve, as shown in Figure (4-22):



Shape (22-4) Loss rate curve for Googlenet, the red color represents the loss rate in the training data and the black color represents the loss rate.

Loss of test data

3-2-6-4 Test results for the two networks

The two models were tested with 100 selected test cases, and the accuracy was calculated.

The sensitivity and specificity of each system, where a matrix of 100 lines and two columns was built

, and enter in the first column the values predicted by the system by calling

The system is within a for loop to calculate the output of all cases, while the second column contains the values.

The truth for cases (0 or 1), where (1) indicates the presence of a malignant tumor and (0) indicates the presence of a tumor.

Hamid, as shown in Figure (4-23).

The classification performance of the systems was measured using a confusion matrix.

Confusion matrix: The confusion matrix is a performance measurement technique.

For machine learning classification, it is a table that helps you know the performance of a model.

Classification on a set of test data until the true values are known.

This is done by calculating both TP (number of true positive cases) and TN (number of

True negative cases), FP (false positive cases), FN (number of

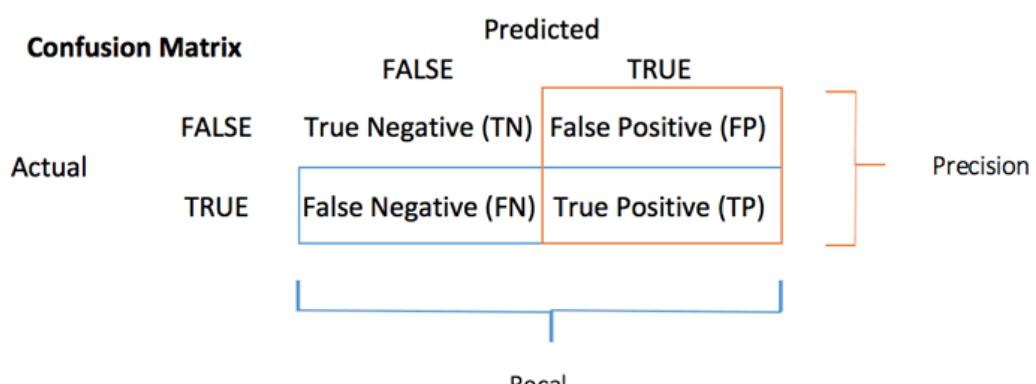
(false negative cases), provided that the malignant tumor has a predicted value higher than 0.5 and the benign tumor has a predicted value lower than 0. As shown

Figure (4-24)

matrix		
100x2 double		
	1	2
1	0.9994	1
2	0.9966	1
3	0.9769	1
4	0.9979	1
5	0.0060	1
6	1.0000	1
7	1.0000e-03	0
8	0	0
9	0	0
10	0.0066	0
11	0.0018	0
12	0.0059	0
13	0	0
14	0.0030	0
15	0.0080	0
..	0.0700	0

Shape (23-4) A matrix containing the predicted values.

It is provided by the system and the real values.



Shape (24-4) Confusion Matrix

Through the confusion matrix, each of the following is calculated:

- System accuracy Accuracy is the extent to which the system can handle all positive and negative situations in the system.

$$\text{Accuracy} = (\text{TP} + \text{TN}) / (\text{TP} + \text{TN} + \text{FP} + \text{FN})$$

- Allergy It measures the test's ability to detect all positive cases. Sensitivity is calculated:

Dividing the number of true positives by the total number of positive cases (which includes false positives).

$$\text{Sensitivity} = (\text{TP}) / (\text{TP} + \text{FN})$$

- Privacy Specificity measures how well our test classifies negative cases as negative.

Specificity is the number of true negatives divided by the total number of negatives (which includes false negatives).

$$\text{Specificity} = \text{TN} / (\text{TN} + \text{FP})$$

- The algorithm for calculating the confusion matrix, accuracy, sensitivity, and specificity is in the appendix C

The following table shows the accuracy, sensitivity, and specificity of the deep learning networks Resnet and Googlenet.

	Res Network	Google Network
Confusion Matrix	Tp=44, Tn=47 Fp=3 , Fn=6	Tp=32, Tn=35 Fp=15, Fn=18
Knöte system	91%	67%
senseThe system's fundamentals	88%	64%
SpecialThe regime's will	94%	70%

We note that the accuracy of the Resnet network is much higher than that of the Googlenet network in diagnosing malignant and benign tumors.

Resnet network algorithm in appendix B

3-6-4 Processing of metadata

At this stage, the data for the regression analysis systems will be prepared, where the results of the deep learning network and the variables have been collected.

Descriptive and analytical within a single matrix as shown in Figure (4-25), its columns in order:

1- Deep learning network output: The values are decimal in the range [0,1], where any value higher than 0.5 is a prediction for the system.

That the tumor is malignant and any value less than 0.5 predicts the presence of a benign tumor

2- Patient's age: Prostate cancer is related to the patient's age. The older the patient, the more likely he is to develop it.

He has more cancer

3- Tumor marker or specific antigen (PSA): It is a glycoprotein produced by the prostate in the case of...

Natural, but if it is higher than the normal level, it increases the possibility of developing cancer in the gland (explained).

Previously on the page22 (Diagnostic Protocol)

4- Prostate size: Prostate enlargement is related to the presence of a benign or malignant tumor.

It is a type of combination of prostate size and specific antigen to increase the accuracy of the analysis: PSAD-5

6- Actual output of cases: This column will be entered by the Regression learner application in Matlab as:

System output.

Matrix algorithm in appendixD

	1	2	3	4	5	6
1	0.9987	60	7.7000	55	0	0
2	2.9237e-07	64	8.7000	102	0.0900	0
3	5.8468e-04	58	4.2000	74	0.0600	0
4	5.3773e-06	72	13	71.5000	0	0
5	1.9007e-04	67	8	78	0.1000	0
6	0.9995	65	14.1000	51	0.2400	1
7	2.3633e-04	73	6.2000	27	0.1000	0
8	0.0061	68	3.8300	41	0.0900	0
9	0.9999	81	11.1000	56	0.2000	1
10	1.8480e-05	65	24	120	0	0
11	0.0136	67	6.1900	76	0.0800	0
12	0.2671	60	7.1000	34	0	0
13	0.2133	64	9.9000	70	0.2400	1
14	3.5093e-04	48	NaN	62	0.0700	0
15	0.0446	60	8.5000	71	0.1300	0

The shape(25-4) Regression Systems Input Matrix

4-6-4 Descent Learning Networks

Regression is a statistical measure that attempts to determine the strength of the relationship between one dependent variable and a series of other variables.

Regression learning networks are a type of supervised learning used to model the relationship between the dependent variable and one or more variables.

Independent, enabling prediction, decision-making and insights across various domains

1-4-6-4 Regression learner program

It is an application within MATLAB that trains regression models to predict data. This application explores data and identifies...

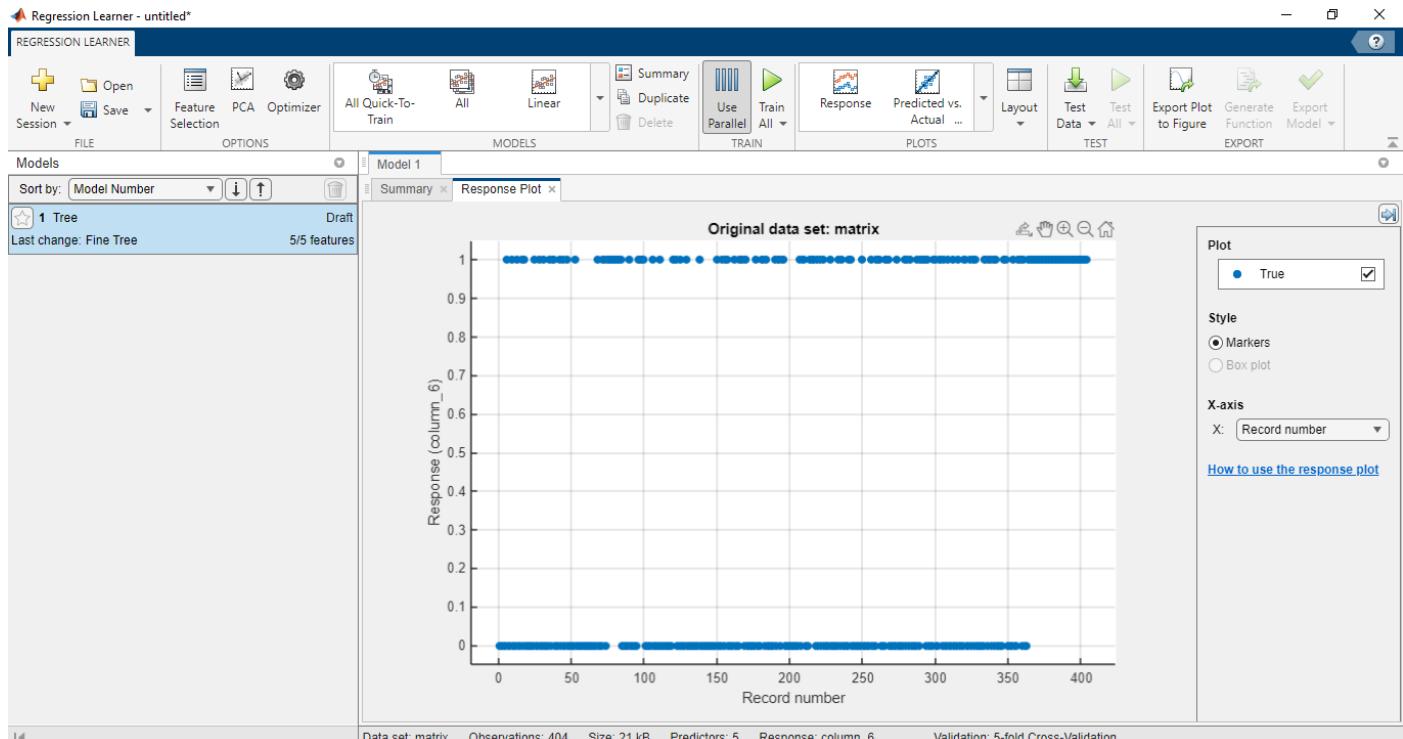
Features, model training, and evaluation of results. It enables automated training to find the best type of regression model, including:

(Including linear regression models) linear regression (and slope trees) Regression trees models

AI-Ghawsia and groups, (support vector machines) and support vector machines, (Gaussian process regression regression trees). (ensemble of regression trees)

Supervised machine learning is performed by providing a known set of observations of the input data (predictors).

And the known responses (case diagnosis), Figure (4-26) shows the application interface.



The shape(26-4) Regression learner application interface

_ By training on the previous input matrix of the two networks (Resnet, Googlenet) (i.e. by changing the values of the first column only)

According to the output of these two networks, we found three regression systems with low classification error rate (two tree-type systems

Decision and support vector machine system) achieved the highest accuracy in classification of inputs and we will explain the principle of their work

2-4-6-4 Decision trees

Decision trees, also known as classification and regression trees (CART) models, are machine learning-based methods.

Supervised. Simple classification trees and regression trees are easy to use and interpret, but they do not compete with the best

Machine learning methods. However, they form the basis for ensemble models such as bagged trees and forests.

Random forests and boosted trees, which, although less interpretable,

It is very accurate..



Shape (27-4) The principle of decision tree operation

These models branch out into non-overlapping terminal nodes (leaves), where each node is described by a set of rules that can be used.

To predict new responses, the expected value for each node is the mode (classification) or mean (regression).

According to Figure (4-27), the green dots represent the first classification, and the red dots represent the second classification.

Decision tree starting with a single node containing information about the coordinates of the red and green points

These models branch out into non-overlapping terminal nodes (leaves), where each node is described by a set of rules that can be used.

To predict new responses.

Through these branches (from top to bottom), in the ideal case the decision tree isolates one of the two classification data (points red) until it reaches a node that contains the entire data of the other classification (green points only), and thus the training is completed.

The system is trained until it arrives at the best split of the decision tree based on the predictor variable and the cutoff point that minimizes the function.

Cost, as the most common cost function for regression trees is the residual sum of squares (R-squared).

Decision trees repeat the splitting process for each child node until a stopping criterion is met, when continuing splitting no longer results in a successful outcome.

To greatly improve the model, when a new value is entered into the system, the classification is done by isolating this value according to the rules.

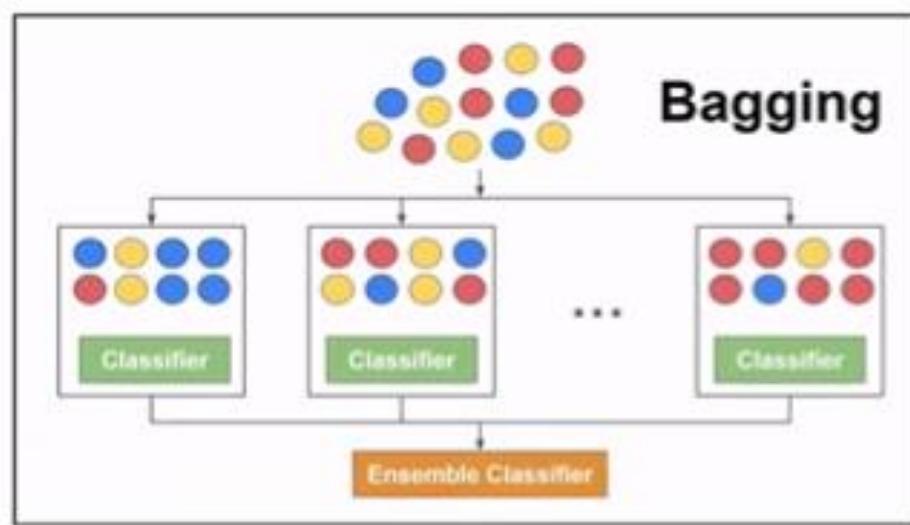
The topic.

- Bagging trees: It is a type of decision tree that depends on dividing the data equally.

With a technique called bootstrapping, each branch has a classifier at its end, and each branch is completely independent.

As for the rest of the branches, when training the system, no weights are assigned, and when testing, the system selects the most expected classification from among all.

Classifications, as shown in Figure (4-28),



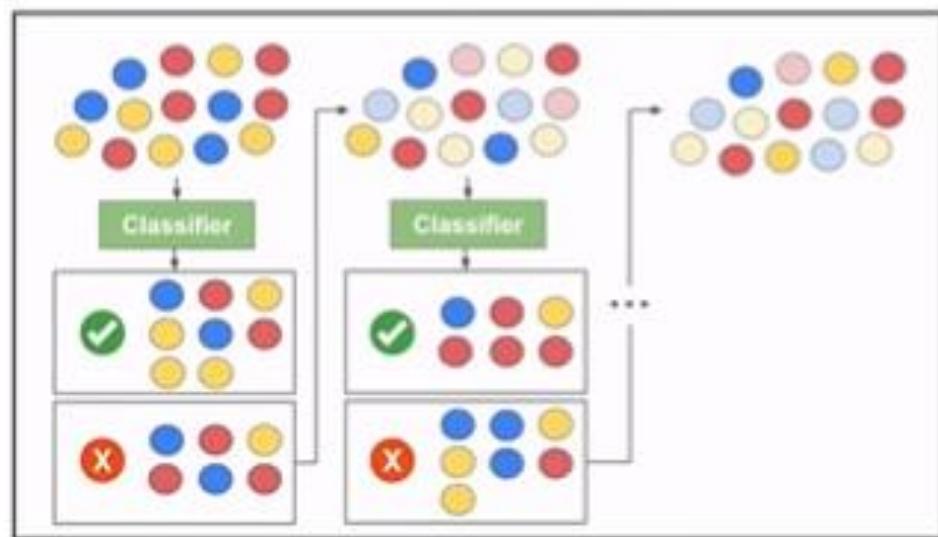
Shape (28-4) The working principle of the assembly trees

- Boosted trees system: It is a type of decision tree that initially classifies all data without

Division: When displaying the classification result for the first round, the system assigns weights to data that were not classified correctly.

Leaving the correctly classified data unweighted until the next cycle includes attention to the unclassified data.

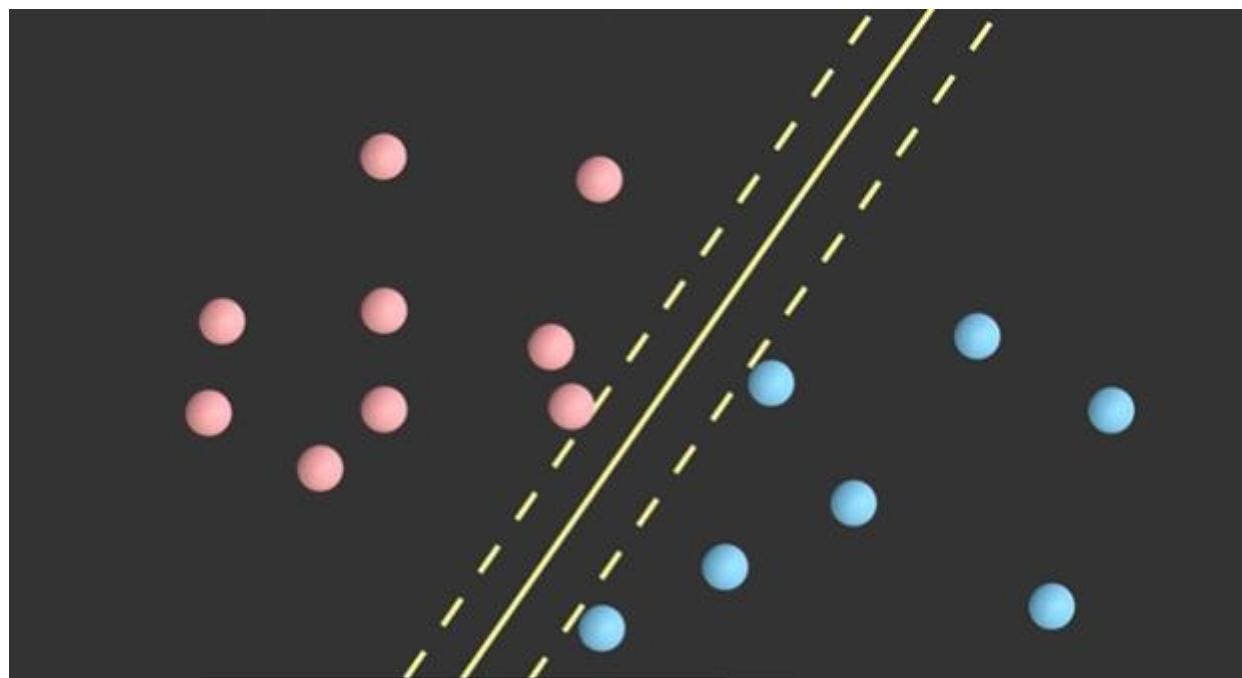
Correctly, and this process is repeated until the lowest error rate is reached, as shown in Figure (4-29).



Shape (29-4) The working principle of reinforced trees

3-4-6-4 Vector Support Machine: support vector machines

SVM is one of the simplest and most successful learning systems, as it represents data in a two- or three-dimensional state space. SVM finds the best separation line that can separate two classifications from each other. The points that are close to the separation line are called support vector points. Training is carried out until the best separation line is found for two or more classifications, as shown in Figure (4-30).



Shape (30-4) SVM working principle

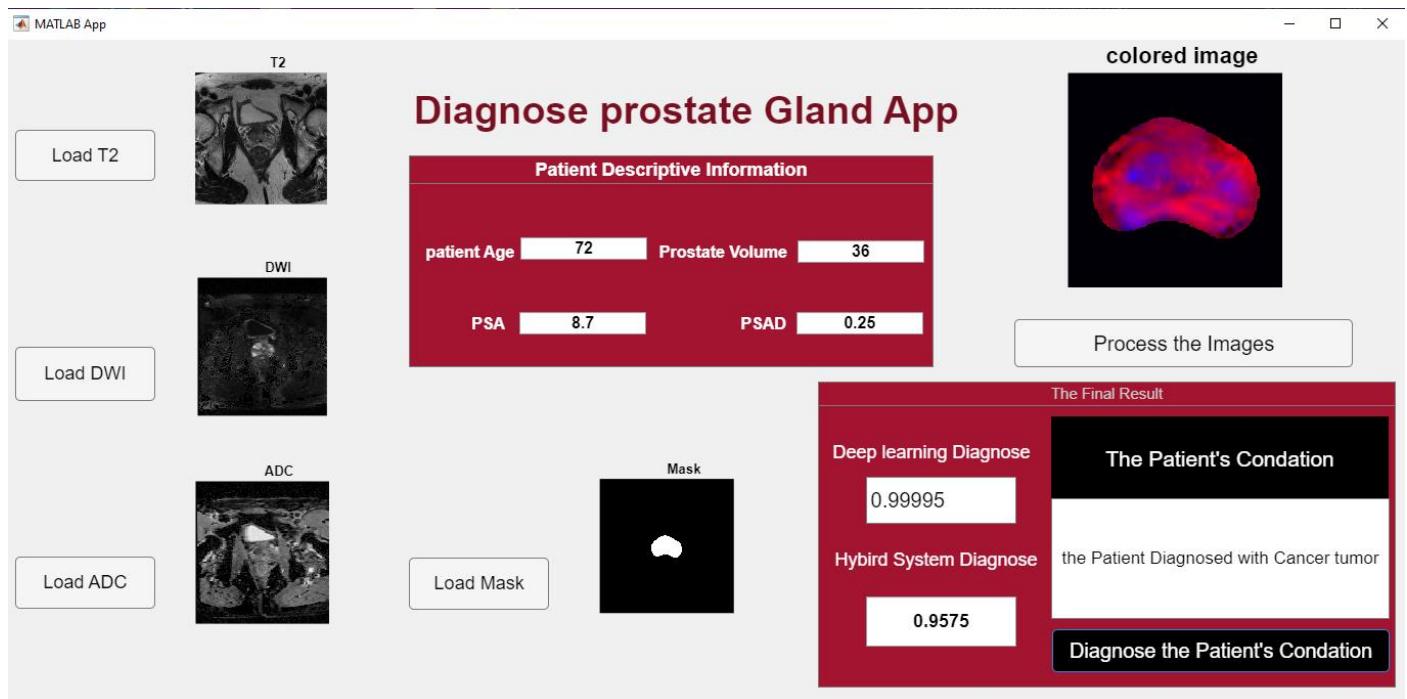
4-6-4 Hybrid System Results

The systems were tested with the same test data that the deep learning networks were previously tested with. The confusion matrix values were found and calculated.

Accuracy, sensitivity and specificity of each system. The following table shows the results of the hybrid systems.

	Res Network			Google Network		
	support machine the ctors SVM	Ashja R The reinforced trees Boosted	brave A assembly gnBaggi stree	support machine the ctors SVM	Ashja R The reinforced trees Boosted	A Sh ollecting eseBagging tr
accuracy	91%	%97	95%	80%	%87	85%
Allergy	89%	%96	96%	77%	%88	86%
Privacy	93%	%98	94%	83%	%86	84%

7-4 Disease diagnosis



Shape (31-4) Graphical interface

From the previous table, we find that the (Resnet+Boosted trees) system is the most successful system among the six systems, as it

Able to detect correct cases with 97% accuracy and able to diagnose cancerous tumors with 96% accuracy and diagnose tumors

Benign disease with 98% accuracy. Therefore, this hybrid system was chosen to diagnose the disease and apply it within a graphical interface so that it can

The doctor diagnoses the admitted cases. Figure (4-31) shows the graphical interface used.

Where the images of the case are uploaded (T2, DWI, ADC, Mask), then the data is processed and the color image is displayed.

Then the user enters the descriptive information in the (process the images) resulting from the (Colored Image) button.

Patient Descriptive Information section, which is the information mentioned above.

(The Final Result) and display the diagnosis of the disease in the (Patient Age, PSA, PSAD, Prostate Volume) section.

, by clicking the (Diagnose The Patient's Condition) button, so that the result appears in the white box as to whether the patient

Patient's condition (cancer or benign) and display specific diagnostic outputs from deep learning

(deep learning diagnose)

Hybrid System Diagnose, the code for building the graphical interface is in the appendix.**E**

8-4 Suggestions and Recommendations

In the future, we aim to:

By increasing the number of cases to 700 cases (Resnet, Googlenet), the efficiency of deep learning systems will be increased.

II. DWI improves the efficiency of regression learning systems by increasing the number of descriptive data by extracting descriptors specific to images.

Up to 25 descriptors are entered into the regression learning systems to train and improve the efficiency of the hybrid system.

Create a standalone application from MATLAB that can be downloaded to any computer, to help in making medical decisions. III

IV. Publish an article after applying the previous suggestions with the help of the supervising doctor, Dr. Muhammad Daer.

the reviewer

(2021). MRI-targeted or standard biopsy in prostate cancer screening. New England Journal of [1] Eklund, M., Jäderling, F., Discacciati, A., Bergman, M., Annerstedt, M., Aly, M., ... & Nordström, T.

Medicine, 385(10), 908-920.

Society of Urological Pathology (ISUP) consensus conference on Gleason grading of prostatic carcinoma: an update with discussion on practical issues to implement the 2014 International [2] Epstein, JI, Amin, MB, Reuter, VE, & Humphrey, PA (2017). Contemporary Gleason grading of carcinoma. The American journal of surgical pathology, 41(4), e1-e7

[3] Esteva, A., Kuprel, B., Novoa, R.A., Ko, J., Swetter, S.M., Blau, H.M., & Thrun, S. (2017).

Dermatologist-level classification of skin cancer with deep neural networks. nature, 542(7639), 115-118.

[4] Gupta, R. T., Spilseth, B., & Froemming, A. T. (2016). How and why a generation of radiologists must be trained to accurately interpret prostate mpMRI. Abdominal Radiology, 41, 803-804

[5] Johnson, L.M., Turkbey, B., Figg, W.D., & Choyke, P.L. (2014). Multiparametric MRI in prostate cancer management. Nature reviews clinical oncology, 11(6), 346-353.

[6] Litwin, M. S., & Tan, H. J. (2017). The diagnosis and treatment of prostate cancer: a review. Jama, 317(24), 2532-2542.

[7] McKinney, S.M., Sieniek, M., Godbole, V., Godwin, J., Antropova, N., Ashrafian, H., ... & Shetty, S. (2020). International evaluation of an AI system for breast cancer screening. Nature, 577(7788), 89-94.

R.L. (2019). Cancer treatment and survivorship statistics, 2019. CA: a cancer journal for [8] Miller, K. D., Nogueira, L., Mariotto, AB, Rowland, J. H., Yabroff, K. R., Alfano, C. M., ... & Siegel, Clinicians, 69(5), 363-385

L. (2021). Common limitations of image processing metrics: A picture story. arXiv preprint [9] Reinke, A., Tizabi, M.D., Sudre, C.H., Eisenmann, M., Rädsch, T., Baumgartner, M., ... & Maier-Hein, arXiv:2104.05642.

and Data System (PI-RADS), version 2: a critical look. American Journal of Roentgenology, 206(6), [10] Rosenkrantz, A. B., Oto, A., Turkbey, B., & Westphalen, A. C. (2016). Prostate Imaging Reporting .1179-1183

via 3D CNNs: effects of attention mechanisms, clinical priori and decoupled false positive [11] Saha, A., Hosseinzadeh, M., & Huisman, H. (2021). End-to-end prostate cancer detection in bpMRI .. Medical image analysis, 73, 102155.

Comparison of radiologists' and urologists' opinions regarding prostate MRI reporting: results from a [12] Spilseth, B., Ghai, S., Patel, NU, Taneja, SS, Margolis, DJ, & Rosenkrantz, AB (2018). A survey of specialty societies. American Journal of Roentgenology, 210(1), 101-107.

[13] Steiger, P., Thoeny, H. C. (2016). Prostate MRI based on PI-RADS version 2: how we review and report. report. Cancer Imaging 16, 9. <https://doi.org/10.1186/s40644-016-0068-2>

Weinreb, J. C. (2019). Prostate Imaging Reporting and Data System Version 2.1: 2019 Update of Prostate [14] Turkbey, B., Rosenkrantz, AB, Haider, MA, Padhani, AR, Villeirs, G., Macura, KJ, ... Imaging Reporting and Data System Version 2. European Urology. doi:10.1016/j.eururo.2019.02.033

Intelligence in radiology: 100 commercially available products and their scientific evidence. European [15] van Leeuwen, K. G., Schalekamp, S., Rutten, M. J., van Ginneken, B., & de Rooij, M. (2021). Artificial Radiology, 31, 3797-3804.

B. (2017). The current state of MR imaging-targeted biopsy techniques for detection of prostate [16] Verma, S., Choyke, P. L., Eberhardt, S. C., Oto, A., Tempany, C. M., Turkbey, B., & Rosenkrantz, A. cancer. Radiology, 285(2), 343-356.

S. (2016). PI-RADS prostate imaging-reporting and data system: 2015, version 2. European [17] Weinreb, J.C., Barentsz, J.O., Choyke, P.L., Cornud, F., Haider, M.A., Macura, K.J., ... & Verma, Urology, 69(1), 16-40.

S. (2016). PI-RADS prostate imaging-reporting and data system: 2015, version 2. European [18] Weinreb, J.C., Barentsz, J.O., Choyke, P.L., Cornud, F., Haider, M.A., Macura, K.J., ... & Verma, Urology, 69(1), 16-40.

Across 26 centers: experience of the society of abdominal radiology prostate cancer disease-focused Rosenkrantz, AB (2020). Variability of the positive predictive value of PI-RADS for prostate MRI [19] Westphalen, AC, McCulloch, CE, Anaokar, JM, Arora, S., Barashi, N.S., Barentsz, JO, ... & panel. Radiology, 296(1), 76-84

[20] Kumar, A.C., Koul, J.O., Singla, J.M., publications, 2023, . Artificial intelligence in disease diagnosis:a Department of Computer Engineering, Indus Institute of Technology1.systematic literature review and Engineering, Indus University, Ahmedabad, 382115 India

Website 1: <https://www.unite.ai/ar/deep learning>]21[

Websit 2: What is Hybrid AI? (analyticsindiamag.com)]22[

Website 3: Evorad (informer.com)]23[

Website 4: 3D Slicer image computing platform | 3D Slicer]24[

Website MATLAB - Knowledge 5 (marefa.org)]25[

ch and 2020,Multiparametric MRI: practical approa.*et al.*] Sawlani, V., Patel, M.D., Davies, N26[pictorial review of a useful tool in the evaluation of brain tumors and tumor-like

Insights Imaging.lessons

[27] Broadhouse, K. M. (2019). The Physics of MRI and How We Use It to Reveal the Mysteries of the Mind. *Front. Young Minds* 7, 23, 1-6. doi: 10.3389/frym.2019.00023.

Appendix (A) Crop and Merge Algorithm

```

';D:\the dataset\the selected slices\t2'; t2 ='D:\the
dataset\the selected slices\adc'adc =
';D:\the dataset\the selected slices\hbv'; hbv='D:\the
dataset\the selected slices\gland'gland=
(');'*.dcm'); t2f = dir(fullfile(t2,'*.dcm'));
adcf = dir(fullfile(adc,'*.dcm')); hbvf =
dir(fullfile(hbv,'*.dcm'))glandf =
dir(fullfile(gland,
j=0;k=0;i=0;
i = 1:1000for
,j,k);'p%d%dt2.dcm',j,k); tfilename = sprintf(
'p%d%dadc.dcm',j,k); afilename = sprintf(
'p%d%dhbv.dcm',j,k); hfilename = sprintf(
'p%d%dgland.dcm'gfilename = sprintf(
filepath = fullfile(hbv, hfilename);
) 'file'exist(filepath,if
gfilepath = fullfile(gland, gfilename);
hfilepath = fullfile(hbv, hfilename); afilepath =
fullfile(adc, afilename); tfilepath = fullfile(t2,
filename);
gdicom = dicomread(gfilepath);
hdicom = dicomread(hfilepath);
adicom = dicomread(afilename);
tdicom = dicomread(tfilepath);
[rw]=size(gdicom);
hb=imresize(hdicom,[rw]);
ad=imresize(adicom,[rw]);
;)')Centroid',gdicom,tablestats = regionprops(
center=stats.Centroid;
y=center(1);x=center(2);
xmin=x-93;xmax=x+93;ymin=y-93;ymax=y+93;
roi= [ymin,xmin,ymax-ymin,xmax-xmin];
cropg=imcrop(gdicom,roi);
cropt=imcrop(tdicom,roi);
cropa=imcrop(ad,roi);
croph=imcrop(hb,roi);
adcs=immultiply(cropg,cropa);
hbvs=immultiply(cropg,crop);
t2s=immultiply(cropg,cropt);
;)])0 2 1[,'ColorChannels','falsecolor"outpict = imfuse(t2s,adcs,
;)])2 0 1[,'ColorChannels','falsecolor"out=imfuse(outpict,hbvs,
imshow(out,[])
,j,k);'pimg %d%d.dcm'imgfilename = sprintf(
,imfilename);'C:\Users\tareq\OneDrive\Desktop\ooo'filepathimg = fullfile(
dicomwrite(tt,filepathimg);
k==9if
k=-1;j=j+1;
end
k=k+1;
else
k==9if
k=-1;j=j+1;
end
k=k+1;
end
end
end

```

Appendix B: ResNet Layer Construction Algorithm

```

lgraph = layerGraph();
tempLayers = [
    ) "input_1","Name"imageInputLayer([224 224 3],
) ]2 2[,"Stride",]3 3 3[,"Padding","conv1","Name"convolution2dLayer([7 7],64,
    ) 0.001,Epsilon,"bn_conv1","Name"batchNormalizationLayer(
        ) "activation_1_relu","Name"reluLayer(
;])]2 2[,"Stride",]1 1 1 1[,"Padding","max_pooling2d_1","Name"maxPooling2dLayer([3 3],
    lgraph = addLayers(lgraph,tempLayers);
    tempLayers = [
        ) 0,"BiasLearnRateFactor","res2a_branch1","Name"convolution2dLayer([1 1],256,
            ;])0.001,Epsilon,"bn2a_branch1","Name"batchNormalizationLayer(
                lgraph = addLayers(lgraph,tempLayers);
                tempLayers = [
                    ) 0,"BiasLearnRateFactor","res2a_branch2a","Name"convolution2dLayer([1 1],64,
                        ) 0.001,Epsilon,"bn2a_branch2a","Name"batchNormalizationLayer(
                            ) "activation_2_relu","Name"reluLayer(
                                convolution2dLayer([3
                                    ) "same","Padding",0,"BiasLearnRateFactor","res2a_branch2b","Name",64,]3
                                    ) 0.001,Epsilon,"bn2a_branch2b","Name"batchNormalizationLayer(
                                        ) "activation_3_relu","Name"reluLayer(
;)) 0,"BiasLearnRateFactor","res2a_branch2c","Name"convolution2dLayer([1 1],256,
            ;])0.001,Epsilon,"bn2a_branch2c","Name"batchNormalizationLayer(
                lgraph = addLayers(lgraph,tempLayers);
                tempLayers = [
                    ) "add_1","Name"additionLayer(2,
                ;])"activation_4_relu","Name"reluLayer(
                    lgraph = addLayers(lgraph,tempLayers);
                    tempLayers = [
                        ) 0,"BiasLearnRateFactor","res2b_branch2a","Name"convolution2dLayer([1 1],64,
                            ) 0.001,Epsilon,"bn2b_branch2a","Name"batchNormalizationLayer(
                                ) "activation_5_relu","Name"reluLayer(
                                    convolution2dLayer([3
                                        ) "same","Padding",0,"BiasLearnRateFactor","res2b_branch2b","Name",64,]3
                                            ) 0.001,Epsilon,"bn2b_branch2b","Name"batchNormalizationLayer(
                                                ) "activation_6_relu","Name"reluLayer(
;)) 0,"BiasLearnRateFactor","res2b_branch2c","Name"convolution2dLayer([1 1],256,
            ;])0.001,Epsilon,"bn2b_branch2c","Name"batchNormalizationLayer(
                lgraph = addLayers(lgraph,tempLayers);
                tempLayers = [
                    ) "add_2","Name"additionLayer(2,
                ;])"activation_7_relu","Name"reluLayer(
                    lgraph = addLayers(lgraph,tempLayers);
                    tempLayers = [
                        ) 0,"BiasLearnRateFactor","res2c_branch2a","Name"convolution2dLayer([1 1],64,
                            ) 0.001,Epsilon,"bn2c_branch2a","Name"batchNormalizationLayer(
                                ) "activation_8_relu","Name"reluLayer(
                                    convolution2dLayer([3
                                        ) "same","Padding",0,"BiasLearnRateFactor","res2c_branch2b","Name",64,]3
                                            ) 0.001,Epsilon,"bn2c_branch2b","Name"batchNormalizationLayer(
                                                ) "activation_9_relu","Name"reluLayer(
;)) 0,"BiasLearnRateFactor","res2c_branch2c","Name"convolution2dLayer([1 1],256,
            ;])0.001,Epsilon,"bn2c_branch2c","Name"batchNormalizationLayer(
                lgraph = addLayers(lgraph,tempLayers);
                tempLayers = [
                    ) "add_3","Name"additionLayer(2,
                ;])"activation_10_relu","Name"reluLayer(
                    lgraph = addLayers(lgraph,tempLayers);

```

```

tempLayers = [
2,["Stride",0,"BiasLearnRateFactor","res3a_branch2a","Name"]convolution2dLayer([1 1],128,
) ]2
) 0.001,Epsilon,"bn3a_branch2a","Name"]batchNormalizationLayer(
) "activation_11_relu","Name"]reluLayer(
convolution2dLayer([3
) "same","Padding",0,"BiasLearnRateFactor","res3a_branch2b","Name",128,]3
) 0.001,Epsilon,"bn3a_branch2b","Name"]batchNormalizationLayer(
) "activation_12_relu","Name"]reluLayer(
) 0,"BiasLearnRateFactor","res3a_branch2c","Name"]convolution2dLayer([1 1],512,
;])0.001,Epsilon,"bn3a_branch2c","Name"]batchNormalizationLayer(
Igraph = addLayers(Igraph,tempLayers);
tempLayers = [
) ]2 2,["Stride",0,"BiasLearnRateFactor","res3a_branch1","Name"]convolution2dLayer([1 1],512,
;])0.001,Epsilon,"bn3a_branch1","Name"]batchNormalizationLayer(
Igraph = addLayers(Igraph,tempLayers);
tempLayers = [
) "add_4","Name"]additionLayer(2,
;])"activation_13_relu","Name"]reluLayer(
Igraph = addLayers(Igraph,tempLayers);
tempLayers = [
) 0,"BiasLearnRateFactor","res3b_branch2a","Name"]convolution2dLayer([1 1],128,
) 0.001,Epsilon,"bn3b_branch2a","Name"]batchNormalizationLayer(
) "activation_14_relu","Name"]reluLayer(
convolution2dLayer([3
) "same","Padding",0,"BiasLearnRateFactor","res3b_branch2b","Name",128,]3
) 0.001,Epsilon,"bn3b_branch2b","Name"]batchNormalizationLayer(
) "activation_15_relu","Name"]reluLayer(
) 0,"BiasLearnRateFactor","res3b_branch2c","Name"]convolution2dLayer([1 1],512,
;])0.001,Epsilon,"bn3b_branch2c","Name"]batchNormalizationLayer(
Igraph = addLayers(Igraph,tempLayers);
tempLayers = [
) "add_5","Name"]additionLayer(2,
;])"activation_16_relu","Name"]reluLayer(
Igraph = addLayers(Igraph,tempLayers);
tempLayers = [
) 0,"BiasLearnRateFactor","res3c_branch2a","Name"]convolution2dLayer([1 1],128,
) 0.001,Epsilon,"bn3c_branch2a","Name"]batchNormalizationLayer(
) "activation_17_relu","Name"]reluLayer(
convolution2dLayer([3
) "same","Padding",0,"BiasLearnRateFactor","res3c_branch2b","Name",128,]3
) 0.001,Epsilon,"bn3c_branch2b","Name"]batchNormalizationLayer(
) "activation_18_relu","Name"]reluLayer(
) 0,"BiasLearnRateFactor","res3c_branch2c","Name"]convolution2dLayer([1 1],512,
;])0.001,Epsilon,"bn3c_branch2c","Name"]batchNormalizationLayer(
Igraph = addLayers(Igraph,tempLayers);
tempLayers = [
) "add_6","Name"]additionLayer(2,
;])"activation_19_relu","Name"]reluLayer(
Igraph = addLayers(Igraph,tempLayers);
tempLayers = [
) 0,"BiasLearnRateFactor","res3d_branch2a","Name"]convolution2dLayer([1 1],128,
) 0.001,Epsilon,"bn3d_branch2a","Name"]batchNormalizationLayer(
) "activation_20_relu","Name"]reluLayer(
convolution2dLayer([3
) "same","Padding",0,"BiasLearnRateFactor","res3d_branch2b","Name",128,]3
) 0.001,Epsilon,"bn3d_branch2b","Name"]batchNormalizationLayer(
) "activation_21_relu","Name"]reluLayer(
) 0,"BiasLearnRateFactor","res3d_branch2c","Name"]convolution2dLayer([1 1],512,
;])0.001,Epsilon,"bn3d_branch2c","Name"]batchNormalizationLayer(
Igraph = addLayers(Igraph,tempLayers);

```

```

tempLayers = [
    ) "add_7","Name"additionLayer(2,
;])"activation_22_relu","Name"reluLayer(
    lgraph = addLayers(lgraph,tempLayers);
    tempLayers = [
        2[,"Stride",0,"BiasLearnRateFactor","res4a_branch2a","Name"convolution2dLayer([1 1],256,
        ) ]2
            ) 0.001,Epsilon,"bn4a_branch2a","Name"batchNormalizationLayer(
                ) "activation_23_relu","Name"reluLayer(
                    convolution2dLayer([3
                ) "same","Padding",0,"BiasLearnRateFactor","res4a_branch2b","Name",256,]3
                    ) 0.001,Epsilon,"bn4a_branch2b","Name"batchNormalizationLayer(
                        ) "activation_24_relu","Name"reluLayer(
                ) 0,"BiasLearnRateFactor","res4a_branch2c","Name"convolution2dLayer([1 1],1024,
                    ;])0.001,Epsilon,"bn4a_branch2c","Name"batchNormalizationLayer(
                        lgraph = addLayers(lgraph,tempLayers);
                        tempLayers = [
                            2[,"Stride",0,"BiasLearnRateFactor","res4a_branch1","Name"convolution2dLayer([1 1],1024,
                                ) ]2
                                    ;])0.001,Epsilon,"bn4a_branch1","Name"batchNormalizationLayer(
                                        lgraph = addLayers(lgraph,tempLayers);
                                        tempLayers = [
                                            ) "add_8","Name"additionLayer(2,
;])"activation_25_relu","Name"reluLayer(
                                            lgraph = addLayers(lgraph,tempLayers);
                                            tempLayers = [
                                                0,"BiasLearnRateFactor","res4b_branch2a","Name"convolution2dLayer([1 1],256,
                                                    ) 0.001,Epsilon,"bn4b_branch2a","Name"batchNormalizationLayer(
                                                        ) "activation_26_relu","Name"reluLayer(
                                                            convolution2dLayer([3
                                                        ) "same","Padding",0,"BiasLearnRateFactor","res4b_branch2b","Name",256,]3
                                                            ) 0.001,Epsilon,"bn4b_branch2b","Name"batchNormalizationLayer(
                                                                ) "activation_27_relu","Name"reluLayer(
                ) 0,"BiasLearnRateFactor","res4b_branch2c","Name"convolution2dLayer([1 1],1024,
                    ;])0.001,Epsilon,"bn4b_branch2c","Name"batchNormalizationLayer(
                        lgraph = addLayers(lgraph,tempLayers);
                        tempLayers = [
                            ) "add_9","Name"additionLayer(2,
;])"activation_28_relu","Name"reluLayer(
                            lgraph = addLayers(lgraph,tempLayers);
                            tempLayers = [
                                0,"BiasLearnRateFactor","res4c_branch2a","Name"convolution2dLayer([1 1],256,
                                    ) 0.001,Epsilon,"bn4c_branch2a","Name"batchNormalizationLayer(
                                        ) "activation_29_relu","Name"reluLayer(
                                            convolution2dLayer([3
                                    ) "same","Padding",0,"BiasLearnRateFactor","res4c_branch2b","Name",256,]3
                                    ) 0.001,Epsilon,"bn4c_branch2b","Name"batchNormalizationLayer(
                                        ) "activation_30_relu","Name"reluLayer(
                ) 0,"BiasLearnRateFactor","res4c_branch2c","Name"convolution2dLayer([1 1],1024,
                    ;])0.001,Epsilon,"bn4c_branch2c","Name"batchNormalizationLayer(
                        lgraph = addLayers(lgraph,tempLayers);
                        tempLayers = [
                            ) "add_10","Name"additionLayer(2,
;])"activation_31_relu","Name"reluLayer(
                            lgraph = addLayers(lgraph,tempLayers);
                            tempLayers = [
                                0,"BiasLearnRateFactor","res4d_branch2a","Name"convolution2dLayer([1 1],256,
                                    ) 0.001,Epsilon,"bn4d_branch2a","Name"batchNormalizationLayer(
                                        ) "activation_32_relu","Name"reluLayer(
                                            convolution2dLayer([3
                                    ) "same","Padding",0,"BiasLearnRateFactor","res4d_branch2b","Name",256,]3

```

```

) 0.001,Epsilon,"bn4d_branch2b","Name"batchNormalizationLayer(
) "activation_33_relu","Name"reluLayer(
) 0,"BiasLearnRateFactor","res4d_branch2c","Name"convolution2dLayer([1 1],1024,
;])0.001,Epsilon,"bn4d_branch2c","Name"batchNormalizationLayer(
Igraph = addLayers(Igraph,tempLayers);
tempLayers = [
) "add_11","Name"additionLayer(2,
;])"activation_34_relu","Name"reluLayer(
Igraph = addLayers(Igraph,tempLayers);
tempLayers = [
) 0,"BiasLearnRateFactor","res4e_branch2a","Name"convolution2dLayer([1 1],256,
) 0.001,Epsilon,"bn4e_branch2a","Name"batchNormalizationLayer(
) "activation_35_relu","Name"reluLayer(
convolution2dLayer([3
) "same","Padding",0,"BiasLearnRateFactor","res4e_branch2b","Name",256,]3
) 0.001,Epsilon,"bn4e_branch2b","Name"batchNormalizationLayer(
) "activation_36_relu","Name"reluLayer(
) 0,"BiasLearnRateFactor","res4e_branch2c","Name"convolution2dLayer([1 1],1024,
;])0.001,Epsilon,"bn4e_branch2c","Name"batchNormalizationLayer(
Igraph = addLayers(Igraph,tempLayers);
tempLayers = [
) "add_12","Name"additionLayer(2,
;])"activation_37_relu","Name"reluLayer(
Igraph = addLayers(Igraph,tempLayers);
tempLayers = [
) 0,"BiasLearnRateFactor","res4f_branch2a","Name"convolution2dLayer([1 1],256,
) 0.001,Epsilon,"bn4f_branch2a","Name"batchNormalizationLayer(
) "activation_38_relu","Name"reluLayer(
convolution2dLayer([3
) "same","Padding",0,"BiasLearnRateFactor","res4f_branch2b","Name",256,]3
) 0.001,Epsilon,"bn4f_branch2b","Name"batchNormalizationLayer(
) "activation_39_relu","Name"reluLayer(
) 0,"BiasLearnRateFactor","res4f_branch2c","Name"convolution2dLayer([1 1],1024,
;])0.001,Epsilon,"bn4f_branch2c","Name"batchNormalizationLayer(
Igraph = addLayers(Igraph,tempLayers);
tempLayers = [
) "add_13","Name"additionLayer(2,
;])"activation_40_relu","Name"reluLayer(
Igraph = addLayers(Igraph,tempLayers);
tempLayers = [
2[,"Stride",0,"BiasLearnRateFactor","res5a_branch2a","Name"convolution2dLayer([1 1],512,
)]2
) 0.001,Epsilon,"bn5a_branch2a","Name"batchNormalizationLayer(
) "activation_41_relu","Name"reluLayer(
convolution2dLayer([3
) "same","Padding",0,"BiasLearnRateFactor","res5a_branch2b","Name",512,]3
) 0.001,Epsilon,"bn5a_branch2b","Name"batchNormalizationLayer(
) "activation_42_relu","Name"reluLayer(
) 0,"BiasLearnRateFactor","res5a_branch2c","Name"convolution2dLayer([1 1],2048,
;])0.001,Epsilon,"bn5a_branch2c","Name"batchNormalizationLayer(
Igraph = addLayers(Igraph,tempLayers);
tempLayers = [
2[,"Stride",0,"BiasLearnRateFactor","res5a_branch1","Name"convolution2dLayer([1 1],2048,
)]2
;])0.001,Epsilon,"bn5a_branch1","Name"batchNormalizationLayer(
Igraph = addLayers(Igraph,tempLayers);
tempLayers = [
) "add_14","Name"additionLayer(2,
;])"activation_43_relu","Name"reluLayer(
Igraph = addLayers(Igraph,tempLayers);
tempLayers = [

```

```

) 0,"BiasLearnRateFactor","res5b_branch2a","Name"convolution2dLayer([1 1],512,
    ) 0.001,Epsilon,"bn5b_branch2a","Name"batchNormalizationLayer(
        ) "activation_44_relu","Name"reluLayer(
            convolution2dLayer([3
) "same","Padding",0,"BiasLearnRateFactor","res5b_branch2b","Name",512,]3
    ) 0.001,Epsilon,"bn5b_branch2b","Name"batchNormalizationLayer(
        ) "activation_45_relu","Name"reluLayer(
) 0,"BiasLearnRateFactor","res5b_branch2c","Name"convolution2dLayer([1 1],2048,
;)0.001,Epsilon,"bn5b_branch2c","Name"batchNormalizationLayer(
    lgraph = addLayers(lgraph,tempLayers);
    tempLayers = [
        ) "add_15","Name"additionLayer(2,
;) "activation_46_relu","Name"reluLayer(
    lgraph = addLayers(lgraph,tempLayers);
    tempLayers = [
) 0,"BiasLearnRateFactor","res5c_branch2a","Name"convolution2dLayer([1 1],512,
    ) 0.001,Epsilon,"bn5c_branch2a","Name"batchNormalizationLayer(
        ) "activation_47_relu","Name"reluLayer(
            convolution2dLayer([3
) "same","Padding",0,"BiasLearnRateFactor","res5c_branch2b","Name",512,]3
    ) 0.001,Epsilon,"bn5c_branch2b","Name"batchNormalizationLayer(
        ) "activation_48_relu","Name"reluLayer(
) 0,"BiasLearnRateFactor","res5c_branch2c","Name"convolution2dLayer([1 1],2048,
;)0.001,Epsilon,"bn5c_branch2c","Name"batchNormalizationLayer(
    lgraph = addLayers(lgraph,tempLayers);

    tempLayers = [
        ) "add_16","Name"additionLayer(2,
        ) "activation_49_relu","Name"reluLayer(
        ) "avg_pool","Name"globalAveragePooling2dLayer(
) 0,"BiasLearnRateFactor","fc1000","Name"fullyConnectedLayer(1000,
    ) "fc1000","Name"sigmoidLayer(
;) "ClassificationLayer_fc1000","Name"classificationLayer(
    lgraph = addLayers(lgraph,tempLayers);
;)randomize[imdsTrain,imdsTest] = splitEachLabel(imgt,120,
falseVerbose0.001'InitialLearnRate'140'MaxEpochs','sgdm'options = trainingOptions(
    training -'Plots'
, 'validationdata'0.001LearnRateDropFactor,piecewise,LearnRateSchedule,plots,progress'
    valid);
%% Connect Layer Branches
% Connect all the branches of the network to create the network graph. ;)
    "res2a_branch1","max_pooling2d_1"); lgraph = connectLayers(lgraph,
    "res2a_branch2a","max_pooling2d_1"); lgraph = connectLayers(lgraph,
        );"add_1/in2","bn2a_branch1"); lgraph = connectLayers(lgraph,"add_1/
        in1","bn2a_branch2c"); lgraph = connectLayers(lgraph,"res2b_branch2a",
    "activation_4_relu");lgraph = connectLayers(lgraph,
        );"add_2/in2","activation_4_relu");lgraph = connectLayers(lgraph,
        );"add_2/in1","bn2b_branch2c"); lgraph = connectLayers(lgraph,
    "res2c_branch2a","activation_7_relu");lgraph = connectLayers(lgraph,
        );"add_3/in2","activation_7_relu");lgraph = connectLayers(lgraph,
        );"add_3/in1","bn2c_branch2c"); lgraph = connectLayers(lgraph,
    "res3a_branch2a","activation_10_relu");lgraph = connectLayers(lgraph,
        );"res3a_branch1","activation_10_relu");lgraph = connectLayers(lgraph,
        );"add_4/in2","bn3a_branch1"); lgraph = connectLayers(lgraph,"add_4/
        in1","bn3a_branch2c"); lgraph = connectLayers(lgraph,"res3b_branch2a",
    "activation_13_relu");lgraph = connectLayers(lgraph,
        );"add_5/in2","activation_13_relu");lgraph = connectLayers(lgraph,
        );"add_5/in1","bn3b_branch2c"); lgraph = connectLayers(lgraph,
    "res3c_branch2a","activation_16_relu");lgraph = connectLayers(lgraph,
        );"add_6/in2","activation_16_relu");lgraph = connectLayers(lgraph,
        );"add_6/in1","bn3c_branch2c");lgraph = connectLayers(lgraph,

```

```

;)"res3d_branch2a","activation_19_relu"lgraph = connectLayers(lgraph,
;)"add_7/in2","activation_19_relu"lgraph = connectLayers(lgraph,
;)"add_7/in1","bn3d_branch2c"); lgraph = connectLayers(lgraph,
"res4a_branch2a","activation_22_relu"lgraph = connectLayers(lgraph,
;)"res4a_branch1","activation_22_relu"lgraph = connectLayers(lgraph,
;)"add_8/in2","bn4a_branch1"); lgraph = connectLayers(lgraph,"add_8/
in1","bn4a_branch2c"); lgraph = connectLayers(lgraph,"res4b_branch2a",
"activation_25_relu"lgraph = connectLayers(lgraph,
;)"add_9/in2","activation_25_relu"lgraph = connectLayers(lgraph,
;)"add_9/in1","bn4b_branch2c"); lgraph = connectLayers(lgraph,
"res4c_branch2a","activation_28_relu"lgraph = connectLayers(lgraph,
;)"add_10/in2","activation_28_relu"lgraph = connectLayers(lgraph,
;)"add_10/in1","bn4c_branch2c"); lgraph = connectLayers(lgraph,
"res4d_branch2a","activation_31_relu"lgraph = connectLayers(lgraph,
;)"add_11/in2","activation_31_relu"lgraph = connectLayers(lgraph,
;)"add_11/in1","bn4d_branch2c"); lgraph = connectLayers(lgraph,
"res4e_branch2a","activation_34_relu"lgraph = connectLayers(lgraph,
;)"add_12/in2","activation_34_relu"lgraph = connectLayers(lgraph,
;)"add_12/in1","bn4e_branch2c"); lgraph = connectLayers(lgraph,
"res4f_branch2a","activation_37_relu"lgraph = connectLayers(lgraph,
;)"add_13/in2","activation_37_relu"lgraph = connectLayers(lgraph,
;)"add_13/in1","bn4f_branch2c"); lgraph = connectLayers(lgraph,
"res5a_branch2a","activation_40_relu"lgraph = connectLayers(lgraph,
;)"res5a_branch1","activation_40_relu"lgraph = connectLayers(lgraph,
;)"add_14/in2","bn5a_branch1"); lgraph = connectLayers(lgraph,"add_14/
in1","bn5a_branch2c"); lgraph = connectLayers(lgraph,"res5b_branch2a",
"activation_43_relu"lgraph = connectLayers(lgraph,
;)"add_15/in2","activation_43_relu"lgraph = connectLayers(lgraph,
;)"add_15/in1","bn5b_branch2c"); lgraph = connectLayers(lgraph,
"res5c_branch2a","activation_46_relu"lgraph = connectLayers(lgraph,
;)"add_16/in2","activation_46_relu"lgraph = connectLayers(lgraph,
;)"add_16/in1","bn5c_branch2c")lgraph = connectLayers(lgraph,
networkmodel_1=trainNetwork(imdsTrain,lgraph,options);
x = linspace(0, 140, 140);
plot(x,trainInfoStruct_1.tr )

```

Appendix (C) Systems Performance Calculation

```

TP=0; TN=0; FP=0; FN=0;
o = 1:100for
prcancer = matrix ( o , 1 )
truecancer = matrix ( o , 2 )
prcancer>0.5 && truecancer == 1if
    TP = TP + 1
prcancer<0.5 && truecancer == 0elseif
    TN = TN + 1
prcancer>0.5 && truecancer == 0elseif
    FP = FP + 1
prcancer < 0.5 && truecancer == 1elseif
    FN = FN + 1
end
end
Accuracy=(TP+TN)/(TP+TN+FP+FN)
Sensitivity = (TP)/(TP+FN)
Specificity=TN/(TN+FP)

```

Appendix D: Processing of Metadata

```

;"C:\Users\tareq\OneDrive\Desktop\testo"imgs=
;))*'.png'imgt = dir(fullfile(imgs,
;)'C:\Users\tareq\OneDrive\Desktop\marksheet 2.csv'datasheet = xlsread(
    data=num2str(datasheet(:,1));
    patient_age=datasheet(:,3);
    psa=datasheet(:,4);
caseofprostate=datasheet(:,11 )
prostate_volume=datasheet(:,6);
psad=datasheet(:,5)
caseisup=datasheet(:,10);
[m, n]=size(imgt);
matrix=zeros(m,7);
j=1;k=1;
i=1:2000for
t=imgt(j).name;
+t;"C:\Users\tareq\OneDrive\Desktop\testo\"tt=
    t1=imread(tt);
output=predict(trainedNetwork_1,t1);
outb=output(:,1);
outc=output(:,2);
o=t(6:8);
dd=datasheet(k,1);
dd=num2str(dd);
frst=dd(:,4);
scnd=dd(:,5);
hund=dd(:,3);
o== datanum datanum2=str2num(datanum )
datanum=[hund frst scnd];if
    matrix(j,2)=outc;
    matrix(j,3)=patient_age(k,1);
    matrix(j,4)=psa(k,1);
matrix(j,5)=prostate_volume(k,1);
    matrix(j,6)=psad(k,1);
matrix(j,7)=caseofprostate(k,1);
    j=j+1;
    k=k+1
else
    matrix(j,:)=0;
    k=k+1;
end
end

```

Appendix E: Graphical Interface Construction Algorithm

```

classdef prostate0diagnose < matlab.apps.AppBase
    % Properties that correspond to app components
        UIFigure matlab.ui.Figure
            properties (Access = public)
                PatientConditionEditField matlab.ui.control.EditField
                PatientConditionButton matlab.ui.control.Button
                PSAEditField matlab.ui.control.NumericEditField
                    PSAEditField matlab.ui.control.NumericEditField
                    PSAEditFieldLabel matlab.ui.control.Label
                    PSAEditFieldLabel matlab.ui.control.Label
                ProstateVolumeEditField matlab.ui.control.NumericEditField
                    patientAgeEditField matlab.ui.control.NumericEditField
                ProstateVolumeEditFieldLabel matlab.ui.control.Label
                    patientAgeEditFieldLabel matlab.ui.control.Label
                ProcesstheImagesButton matlab.ui.control.Button
                    LoadMaskButton matlab.ui.control.Button
                    LoadDWIButton matlab.ui.control.Button
                    LoadADCButton matlab.ui.control.Button
                    LoadT2Button matlab.ui.control.Button
                        UIAxes3_2 matlab.ui.control.UIAxes
                        UIAxes2_2 matlab.ui.control.UIAxes
                        UIAxes matlab.ui.control.UIAxes
                        UIAxes2 matlab.ui.control.UIAxes
                        UIAxes3 matlab.ui.control.UIAxes
                end
                properties (Access = public)
                    imgort2=0;
                    imgordwi=0;
                    imgoradc=0;
                    imgorgoland=0;
                    output=0
                end
                % Callbacks that handle component events
                    methods (Access = private)
                        %Button pushed function: LoadT2Button
                        function LoadT2ButtonPushed(app, event)
                            [fn1, pn1] = uigetfile({'*.dcm'},'select dicom file');
                            imshow(app.imgort2,
                                [],'parent',app.UIAxes2); app.imgort2=
                                dicomread(complete1); complete1 = strcat(pn1,fn1);
                        end
                        %Button pushed function: LoadDWIButton
                        function LoadDWIButtonPushed(app, event)
                            [fn2, pn2] = uigetfile({'*.dcm'},'select dicom file');
                            imshow(app.imgordwi,
                                [],'parent',app.UIAxes3); app.imgordwi=
                                dicomread(complete2); complete2 = strcat(pn2,fn2);
                        end
                        %Button pushed function: LoadADCButton
                        function LoadADCButtonPushed(app, event)
                            [fn3, pn3] = uigetfile({'*.dcm'},'select dicom file');
                            complete3 = strcat(pn3,fn3);
                        end

```

```

app.imguradc= dicomread(complete3);
imshow(app.imguradc,[],'parent',app.UIAxes3_2);
end

%Button pushed function: LoadMaskButton
function LoadMaskButtonPushed(app, event)
[fn4, pn4] = uigetfile({'*.dcm'},'select dicom file');
app.imgorgland= dicomread(complete4);
complete4 = strcat(pn4,fn4);
imshow(app.imgorgland,[],'parent',app.UIAxes2_2);
end

%Button pushed function: ProcesstheImagesButton
function ProcesstheImagesButtonPushed(app, event)
[ out,app.output]= fun(app.imgur2,app.imgordwi,app.imguradc,app.imgorgland);
imshow(out,[],'parent',app.UIAxes);
end

%Value changed function: patientAgeEditField
function patientAgeEditFieldValueChanged(app, event)
value = app.patientAgeEditField.Value;
end

%Value changed function: PSAEditField
function PSAEditFieldValueChanged(app, event)
value = app.PSAEditField.Value;
end

%Value changed function: ProstateVolumeEditField
function ProstateVolumeEditFieldValueChanged(app, event)
value= app.ProstateVolumeEditField.Value;
end

%Value changed function: PSADeEditField
function PSADeEditFieldValueChanged(app, event)
value = app.PSADeEditField.Value;
end

% Callback function
t=[app.output,valueage,valuepsa,valuepros,valuepsad]; function
PatientConditionTextAreaValueChanged(app, event)
app.feedbackTextArea.value=out2 out2 =
boostedtreesres2.predictFcn(t )
end

%Button pushed function: PatientConditionButton
function PatientConditionButtonPushed(app, event)
outt= app.output
valueage=app.patientAgeEditField.Value
valuepsa=app.PSADeEditField.Value;
valuepros=app.ProstateVolumeEditField.Value;
valuepsad=app.PSADeEditField.Value
%t=[outt,valueage,valuepsa,valuepros,valuepsad]
[v]=block2(app.output,valueage,valuepsa,valuepros,valuepsad )
app.PatientConditionButton.value=v
end

% Callback function
function predictDeeplearningButtonPushed(app, event)
out=app.ProcessstheImagesButton.Parent
end
end

methods (Access = private ) %
Component initialization

```

```
% Create UIFigure and components
function createComponents(app)

% Create UIFigure and hide until all components are created
app.UIFigure.Position = [100 100 1510 632];
app.UIFigure = uifigure('Visible', 'off');
app.UIFigure.Name = 'MATLAB App';
% Create UIAxes2
app.UIAxes2 = uiaxes(app.UIFigure);
app.UIAxes2.FontSize = 6;
title(app.UIAxes2, 'T2')
app.UIAxes2.Position = [148 420 342 201];
% Create UIAxes3
app.UIAxes3 = uiaxes(app.UIFigure);
app.UIAxes3.FontSize = 6;
title(app.UIAxes3, 'DWI')
app.UIAxes3.Position = [148 220 342 201];
% Create UIAxes3_2
app.UIAxes3_2 = uiaxes(app.UIFigure);
app.UIAxes3_2.FontSize = 6;
title(app.UIAxes3_2, 'ADC')
app.UIAxes3_2.Position = [148 9 342 212];
% Create UIAxes2_2
app.UIAxes2_2 = uiaxes(app.UIFigure);
app.UIAxes2_2.FontSize = 6;
title(app.UIAxes2_2, 'Mask')
app.UIAxes2_2.Position = [679 419 342 201];
% Create UIAxes
app.UIAxes.FontSize = 6; title(app.UIAxes,
'colored image') app.UIAxes =
uiaxes(app.UIFigure);
app.UIAxes.Position = [611 8 476 302];
% Create LoadT2Button
app.LoadT2Button = uibutton(app.UIFigure, 'push');
app.LoadT2Button.ButtonPushedFcn = createCallbackFcn(app, @LoadT2ButtonPushed, true);
app.LoadT2Button.Tag = 'imort2';
app.LoadT2Button.FontSize = 18;
app.LoadT2Button.Position = [12 495 137 50];
app.LoadT2Button.Text = 'Load T2';
% Create LoadDWIButton
app.LoadDWIButton = uibutton(app.UIFigure, 'push');
app.LoadDWIButton.ButtonPushedFcn = createCallbackFcn(app, @LoadDWIButtonPushed, true);
app.LoadDWIButton.FontSize = 18;
app.LoadDWIButton.Position = [12 280 137 53];
app.LoadDWIButton.Text = 'Load DWI';
% Create LoadADCButton
app.LoadADCButton = uibutton(app.UIFigure, 'push');
app.LoadADCButton.ButtonPushedFcn = createCallbackFcn(app, @LoadADCButtonPushed, true);
app.LoadADCButton.FontSize = 18;
app.LoadADCButton.Position = [12 77 137 51];
app.LoadADCButton.Text = 'Load ADC';
% Create LoadMaskButton
app.LoadMaskButton = uibutton(app.UIFigure, 'push');
app.LoadMaskButton.ButtonPushedFcn = createCallbackFcn(app, @LoadMaskButtonPushed, true);
app.LoadMaskButton.FontSize = 18;
app.LoadMaskButton.Position = [525 494 137 51];
app.LoadMaskButton.Text = 'Load Mask';
```

%Create ProcesstheImagesButton

```
app.ProcesstheImagesButton = uibutton(app.UIFigure, 'push');
app.ProcesstheImagesButton.ButtonPushedFcn = createCallbackFcn(app,
    app.ProcesstheImagesButton.FontSize = 20;
    @ProcesstheImagesButtonPushed, true);
app.ProcesstheImagesButton.Text = 'Process the Images';
app.ProcesstheImagesButton.Position = [731 331 238 49];
%Create patientAgeEditFieldLabel
app.patientAgeEditFieldLabel.HorizontalAlignment = 'right';
app.patientAgeEditFieldLabel = uilabel(app.UIFigure);
app.patientAgeEditFieldLabel.Position = [1143 508 92
22]; app.patientAgeEditFieldLabel.FontWeight = 'bold';
app.patientAgeEditFieldLabel.FontSize = 16;
app.patientAgeEditFieldLabel.Text = 'patient Age';
% Create patientAgeEditField
app.patientAgeEditField.ValueChangedFcn = createCallbackFcn(app,
app.patientAgeEditField = uieditfield(app.UIFigure, 'numeric');
    @patientAgeEditFieldValueChanged, true);
app.patientAgeEditField.HorizontalAlignment = 'center';
app.patientAgeEditField.Position = [1250 508
199 22]; app.patientAgeEditField.FontWeight = 'bold';
app.patientAgeEditField.FontSize = 16;
%Create ProstateVolumeEditFieldLabel
app.ProstateVolumeEditFieldLabel.HorizontalAlignment = 'right';
app.ProstateVolumeEditFieldLabel = uilabel(app.UIFigure);
app.ProstateVolumeEditFieldLabel.Position = [1104 412
131 22]; app.ProstateVolumeEditFieldLabel.FontWeight = 'bold';
app.ProstateVolumeEditFieldLabel.FontSize = 16;
app.ProstateVolumeEditFieldLabel.Text = 'Prostate Volume';
%Create ProstateVolumeEditField
app.ProstateVolumeEditField = uieditfield(app.UIFigure, 'numeric');
app.ProstateVolumeEditField.ValueChangedFcn = createCallbackFcn(app,
    @ProstateVolumeEditFieldValueChanged, true);
app.ProstateVolumeEditField.HorizontalAlignment = 'center';
app.ProstateVolumeEditField.Position = [1250 412
199 22]; app.ProstateVolumeEditField.FontWeight = 'bold';
app.ProstateVolumeEditField.FontSize = 16;
% Create PSADEditFieldLabel
app.PSADEditFieldLabel.HorizontalAlignment = 'right';
app.PSADEditFieldLabel = uilabel(app.UIFigure);
app.PSADEditFieldLabel.Position = [1185 358
50 22]; app.PSADEditFieldLabel.FontWeight = 'bold';
app.PSADEditFieldLabel.FontSize = 16;
app.PSADEditFieldLabel.Text = 'PSAD';
```

% Create PSADEditField

```
app.PSADEditField = uieditfield(app.UIFigure, 'numeric');
app.PSADEditField.ValueChangedFcn = createCallbackFcn(app, @PSADEditFieldValueChanged, true);
app.PSADEditField.HorizontalAlignment = 'center';
app.PSADEditField.Position = [1250 358
199 22]; app.PSADEditField.FontWeight = 'bold';
app.PSADEditField.FontSize = 16;
% Create PSAEditFieldLabel
; app.PSAEditFieldLabel = uilabel(app.UIFigure);'right'
app.PSAEditFieldLabel.HorizontalAlignment =
```

```

; app.PSAEditFieldLabel.FontSize = 16;bold
app.PSAEditFieldLabel.Position = [1197 459 38 22];
app.PSAEditFieldLabel.FontWeight =
;'PSA'app.PSAEditFieldLabel.Text =
% Create PSAEditField
;)'numeric'app.PSAEditField.ValueChangedFcn =
createCallbackFcn(app , app.PSAEditField = uieditfield(app.UIFigure,
@PSAEditFieldValueChanged, true);
:centerapp.PSAEditField.HorizontalAlignment =
; app.PSAEditField.FontSize = 16;bold
app.PSAEditField.Position = [1250 459 199 22];
app.PSAEditField.FontWeight =
%CreatePatientConditionEditField
;)'text'app.PatientConditionEditField = uieditfield(app.UIFigure,
app.PatientConditionEditField.Position = [1201 126 248 116];
%CreatePatientConditionButton
;)'push'app.PatientConditionButton = uibutton(app.UIFigure,
app.PatientConditionButton.ButtonPushedFcn = createCallbackFcn(app ,
@PatientConditionButtonPushed, true);
; app.PatientConditionButton.FontSize = 22;bold;
app.PatientConditionButton.FontWeight ='italic';
app.PatientConditionButton.Position = [1250 66 199 46];
app.PatientConditionButton.FontAngle =Patient Condition
app.PatientConditionButton.Text =
% Show the figure after all components are created
app.UIFigure.Visible = 'on';
end
end
% App creation and deletion
% Construct app methods
(Access = public )
% Create UIFigure and components
function app = prostate0diagnose
createComponents(app)
% Register the app with App Designer
registerApp(app, app.UIFigure )
if nargout == 0
clear app
end
end
% Code that executes before app deletion
function delete(app)
%Delete UIFigure when app is deleted
delete(app.UIFigure )
end
end
end

```

**Ministry of Higher education and research
Al-Andalus University for medical sciences
Faculty of Biomedical Engineering**

Diagnosis of prostate cancer using MRI

**/Graduation project prepared to obtain a bachelor's degree in
/medical engineering**

Prepared by:

Zeinab Makhlof

Basel Kaddor

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Supervised by

Dr. Mohammed Daer

YEAR

2023-2024

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