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Deep Learning Framework for Liver CT Image Segmentation and Risk Prediction

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Abstract Liver cancer is a life-threatening disease, with an estimated deaths of 2 million per year worldwide. Due to availability of abundant computational power recently the deep learning approaches have been explored in the medical fields. Earlier, some attempts were made using neural networks-based solutions for tumor identification in medical images. However, more computational effort is required for converting medical image format suitable for ANN processing. In this regard, in our paper, we suggested a deep learning framework which can directly process CT images for detecting the tumor growth and also estimating associated risk. For our experimentation, we have used LITS dataset for tumor detection and patients' specific details for risk prediction. Various ML techniques have been explored to identify most suitable one for complementing oncologists and medical professionals in the treatment process of this lethal disease.

Keywords Liver tumor · Random forests · CNN · ResNet · Segmentation

1 Introduction

In recent years, developing e-health systems has grown increasingly popular. Several recent studies have proposed machine learning-based tele-diagnosis and tele-monitoring systems for detection of tumors.

In a human frame the liver is the maximum important frame part, it has huge quantity of blood vessels and is hooked up with many critical organs, which include spleen, pancreas, gallbladder, etc. It is a prime organ most effectively determined

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in vertebrates which plays many important organic features which include detoxing of the organism, and the formulation of proteins and biochemicals is very important for digestion and growth. In human body, it's far positioned inside the proper higher quadrant of the abdomen, underneath the diaphragm. Automatic liver segmentation from abdomen scans is hard at the parts for precision of segmentation, automation, and lustiness. There are several methods for classifying and segmenting the liver. We categorize a segmentation approach in keeping with the photo-function it really works on, consequently highly summarizing the overall performance of every class and mainly locating a premier answer for a selected segmentation task. Generally speaking, it isn't always most effective subjective, however additionally wastes time if docs depend on revel to manually examine liver CT pictures and it becomes additionally difficult to decide the danger of any specific sickness manually which calls for greater skilled and green docs. So here, we additionally derive and validate a medical prediction version to estimate the danger of liver sickness prognosis, the use of deep getting to know strategies, and to transform the version to a simplified scoring device to be used in number one care of liver with most accuracy results.

Manual segmentation has been the usual approach for achieving the required outcomes, but it is a time-consuming process. There are a few abnormalities like confusing color ranges and ambiguous gray levels, uneven tumor forms, additional nearby organs, and various irregular tumor sizes that are ignored. Because of these factors, some automated, completely automated, and even semi-automated methods have been proposed. However, as machines continue to advance, addressing this issue has been made much easier by learning [1].

2 Literature Review

In 2013, Saika K from National Cancer Center published an article on cancer statistics in the world [2], and stated that stomach and liver cancers are typical of cancer incidence in Asia, while bladder cancer is typical of cancer incidence in the United States and Europe. In all of the nations analyzed, breast cancer and colorectal cancer rank highly. Incidence rates for breast cancer have been rising globally, with incidence rates in the United States and Europe being twice as high as those in Asian nations. In terms of overall cancer mortality, Asia has high mortality rates for stomach and liver cancers, which is also the case for incidence rates.

Hepatocellular carcinoma, the primary liver cancer that occurs most frequently, is still difficult to cure. The variability of primary liver cancer, regional preferences, and geographic variations in resect ability or transplant eligibility have led to the development of numerous staging systems. There are numerous therapeutic options available for this heterogeneous malignancy, and the management recommendations for liver cancer vary based on the specialty and region. Along with improved treatment strategies, new therapeutic procedures have evolved [3].

Depending on the pattern of elevation, the liver function tests can aid in organizing a differential diagnosis and identify a potential site of liver injury. Hepatocellular

disease is indicated by increase in ALT and AST that are not proportional to increase in alkaline phosphatase and bilirubin. A cholestatic pattern would be characterized by an increase in alkaline phosphatase and bilirubin that is out of proportion to ALT and AST. The ability of the liver to create albumin and vitamin K-dependent clotting factors can be used to grade the liver's actual performance as stated in article by Lala and Zubair [4].

Rather than clinical records, liver CT image will be efficient in terms of liver disease detection. According to Mharib [5], segmenting the liver using computed tomography (CT) data has become quite important in the field of medical image processing. Semi-automatic and fully automated procedures are the two main categories of liver segmentation methods. Under each of these two categories, a number of strategies, methods, and related difficulties and problems will be described and presented. The liver segmentation evaluation measurements and scoring are displayed, followed by a comparison of the available approaches. The advantages and disadvantages of each method will be clearly highlighted. Automatic Liver segmentation using CT scans can not be consider as a complete solution as there are several issues that are still unresolved and need to be addressed.

3 Proposed Framework and Methodology

In this section, we cover existing work, proposed work, datasets, ResNet architecture and layers, and methods for risk prediction.

3.1 Existing Work

- Liver sicknesses may be identified via diverse clinical imaging schemes along with computed tomography (CT), ultrasound (US), magnetic resonance imaging (MRI), laparoscopy, biopsy, etc. to segment the liver region.
- Various statistical techniques, threshold primarily based totally techniques, fuzzy primarily based totally techniques, clustering techniques, neural community fashions, and gadget mastering primarily based totally techniques had been followed with inside the beyond to predicting the liver situation primarily based totally at the given inputs.

3.1.1 Image Tests

Image tests give the better results comparatively to other types of diagnosis. Image tests like ultrasound, computed tomography (CT), and magnetic resonance imaging (MRI) will aid to accurately locate the liver and to analyze the spread of tumor to any other parts of body. All these cross-sectional images are combined to form a detailed

view, and after that we use different deep learning approaches for image analysis [6]. A CT scan can be used to measure the tumors' size easily.

3.1.2 Lab Tests

Lab tests are performed by clinical practitioner. He takes the blood sample from the patient body and generates the medical report containing various statistical values for different secreting enzymes in our body. Most basic cases can easily be treated based on clinical trial reports. A particular blood protein called alpha-fetoprotein is produced by malignancies and fetal tissue. This test might be used to forecast the risk of liver cancer (hepatocellular carcinoma). It additionally aids in assessing or suspecting the impact of malignancies and potential for specific liver tumors.

3.2 Proposed Work

For image segmentation, liver segregation requires precise knowledge of the liver surface (boundaries). Our goal is to segment the liver. The region growing approach is used to segment the interested region. The most effective and efficient strategy will be optimized and implemented here. This will help doctors make better automated liver diagnoses based on the images. Also the condition of the liver is analyzed based on the data of liver like Total Bilirubin, Alkaline Phosphates, Alanine Aminotransferase, Total Proteins, Albumin, and A/G Ratio and gives accurate results on the proposed model based on the technique we use. Here adaptive machine learning methodologies are applied to enhance the efficiency and effectiveness of various processes within our frame work.

3.3 Dataset

The liver is a common location for the development of primary and secondary tumors. Automatic segmentation of tumor lesions is extremely difficult and incredibly challenging due to their heterogeneous and dispersed nature. Due to this, it is difficult to create automated segmentation algorithms to separate contrasting liver lesions and enhance abdominal CT imaging. To segment the liver similarly to how neoplasm lesions are segmented, 130 CT images are required as shown in Figs. 1 and 2. LiTS—Liver Neoplasm Segmentation Challenge—provided this dataset (LiTS17).
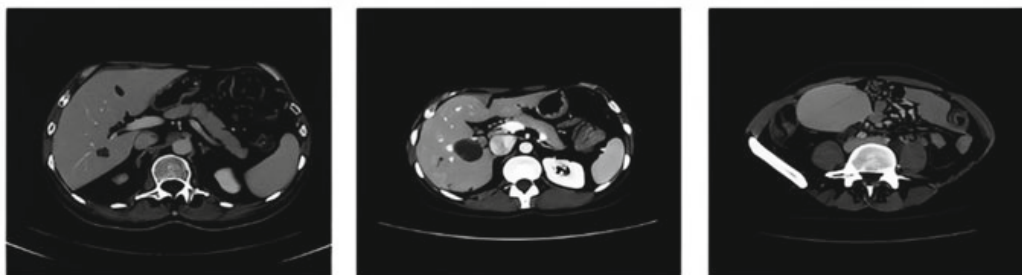
Fig. 1 Input CT images
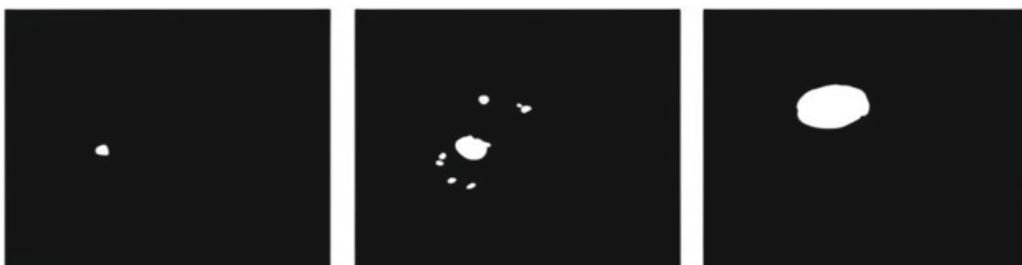
Fig. 2 Given ground truth

3.3.1 Dataset for Statistical Measurements

Dataset for statistical measurements is collected from Kaggle which contains the clinical reports of various patients. The dataset comprises 11 columns and size of 583 patient records. Each column specifies the statistically measured values of different enzymes some of which are mentioned below. Based on these values we classify and predict the risk of tumor whether a liver is healthy or not.

Columns

- Patients Age.
- Gender (M/F).
- Bilirubin.
- Alkaline Phosphatase.
- Aspartate Aminotransferase.
- Total Proteins.
- Albumin.
- Albumin and Globulin Ratio.

  Output column: contains either unhealthy liver or healthy liver

3.4   ResNet Architecture

- As first layer we apply 64 convolutions of size 7*7 kernel size and a padding of 3 with stride value equal to 2 which will result in output shape of 112*112 from 224*224.
- We apply batch normalization technique here to normalize the output.
- Now we apply max pooling which has strides 2 and padding 1 with kernel size 3*3 and this results in 56*56*64 output.
- Then we repeat the following three layers: a 1*1, 64 kernel, a 3*3, 64 kernel, and 1*1, 256 kernel for three times summing it to nine-layer architecture.
- The follow-up architecture contains 12 layers with 3 layers repeated for 4 times kernel[1] 1*1, 512, kernel[2] 1*1, 128, kernel[3] 3*3, 128.
- Next 3 layers with repetition of 6 times sequenced to build 18 layers. Three layers known as a kernel with a size of 1*1, 256 then two additional kernels with sizes of 3*3, 256 and 1*1, 1024.
- Two further kernels of 3*3, 512 and 1*1, 2048 were sequenced before the final addition of a 1*1, 512 kernel. With repetition for three times gives up to 9 layered block as described in Table 1.

Table 1 ResNet 50 architecture

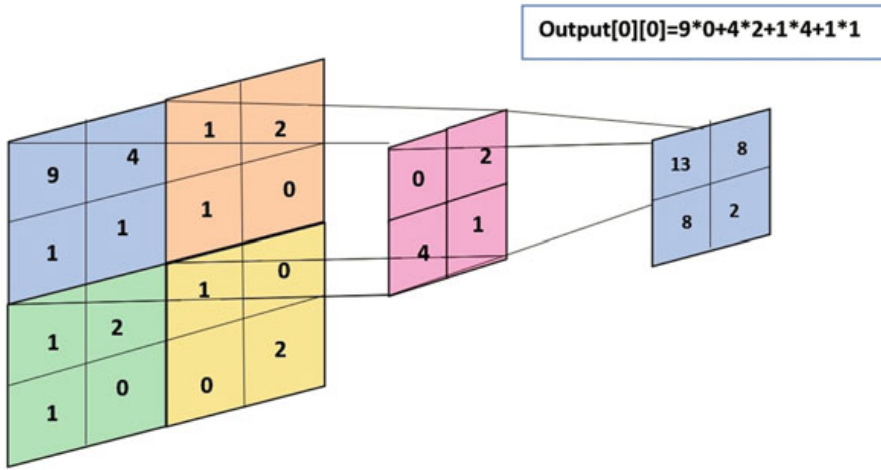| Layer name	Output size	50-Layer
Conv1	112×112	7×7, 64, stride 2
Conv2_x	56×56	3×3 max pool, stride 2
		$\begin{bmatrix} 1 \times 1,\, 64 \\ 3 \times 3,\, 64 \\ 1 \times 1,\, 256 \end{bmatrix} \times 3$
Conv3_x	28×28	$\begin{bmatrix} 1 \times 1,\, 128 \\ 3 \times 3,\, 128 \\ 1 \times 1,\, 512 \end{bmatrix} \times 4$
Conv4_x	14×14	$\begin{bmatrix} 1 \times 1,\, 256 \\ 3 \times 3,\, 256 \\ 1 \times 1,\, 1024 \end{bmatrix} \times 6$
Conv5_x	7×7	$\begin{bmatrix} 1 \times 1,\, 512 \\ 3 \times 3,\, 512 \\ 1 \times 1,\, 2048 \end{bmatrix} \times 3$
	1×1	Average pool, 1000 softmax

**Fig. 3** Convolution layer

3.4.1 Convolution Layer

The essential building block of the CNN is the convolution layer. It is responsible for the majority of the network's process load. A scalar product between two matrices is carried out by this layer as shown in Fig. 3, one of which is the set of learnable parameters known as a kernel, and the second, which is the receptive field's restricted area. The kernel has more depth but is lower in size than an image. Accordingly, if an image includes three (RGB) channels, the kernel height and width will be relatively minimal, but the depth will include all three channels or any combination of the three.

3.4.2 Pooling Layer

The pooling layer etymologizes an outline datum of the neighboring outputs in order to replace the output of the network at particular locations. This lessens the image's spatial dimension, which lessens the amount of computations and weights required. The pooling action is performed one by one on each slice of the picture. The average of the oblong neighborhood, L2 norm of the oblong neighborhood, and a weighted average supported the space from the central pixel are only a few of the unit pooling functions available. The most used strategy, however, is max pooling, which reports the max output from the neighborhood as shown in Fig. 4.

3.4.3 Fully Connected Layer

As in standard FCNN, neurons in this layer have complete property with all neurons in the preceding and following layers. This is why it is frequently computed using a matrix operation, such as matrix multiplication with a bias result. The FC layer aids in the mapping of the illustration between the input and output.
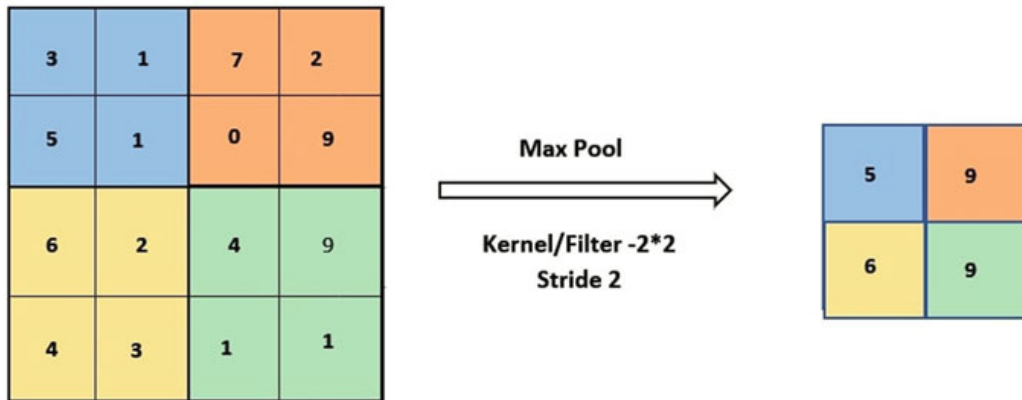
Fig. 4 Pooling layer

3.5 Approach for Risk Prediction

To find out the best results, we have tested three totally different information-driven strategies, from a widely known machine earning library scikit-learn (version zero.20): Random Forest, Logistic Regression, and Gaussian Naive mathematician.

3.5.1 Random Forests

A method called random forest or random decision forest works by building several Decision Trees throughout the training phase. The random forest selects the majority decision of the trees as the final choice. Simply said, a decision tree is a tree data structure that is used to choose a course of action. Each branch tree indicates a potential choice, event, or response. The most probable characteristic is used to divide the decisions.

3.5.2 Working of Random Forest

It generally works in two different phases including creation of random forest by combining several decision trees; secondly, make predictions based on generated tree. Working steps include selection of random data points from training dataset and then build decision trees based on different subsets of original dataset. After building N decision trees, it takes the average to improve the prediction accuracy of that dataset as shown in Fig. 5.
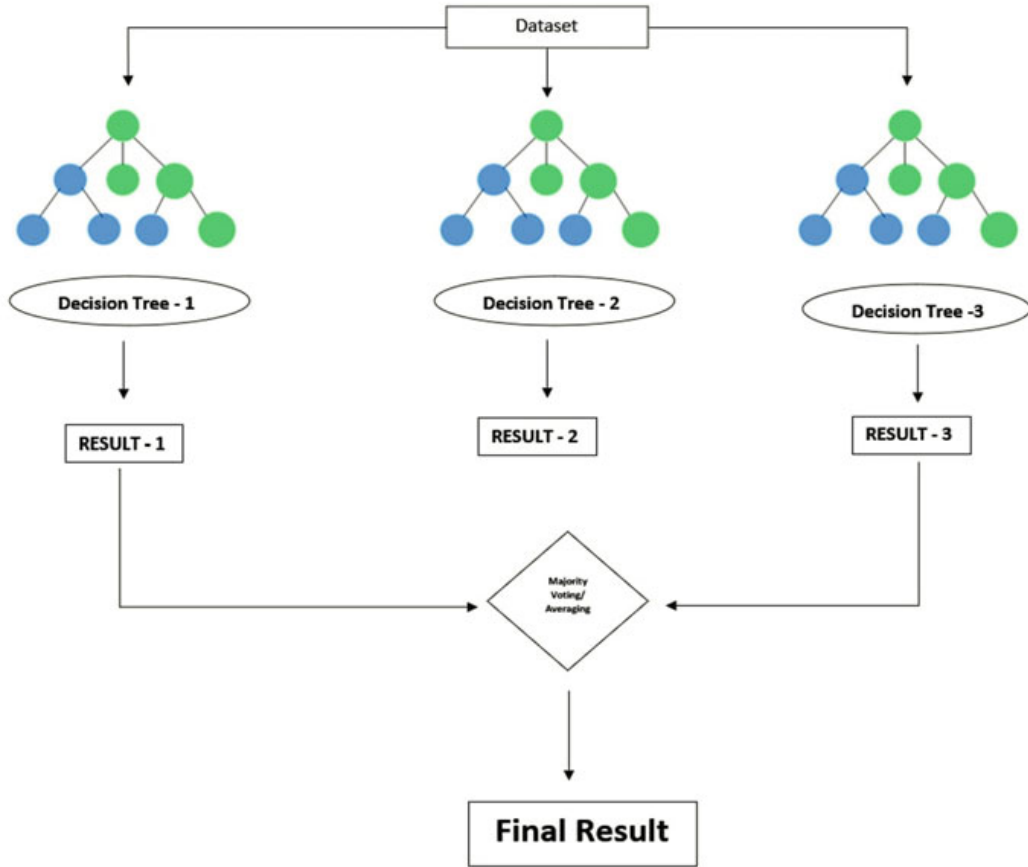
Fig. 5 Random forest workflow

4 Implementation

4.1 Liver CT Image Segmentation

We used the LiTS dataset for our experiments, which is made up of data and segmentations from several clinical locations worldwide. 130 CT scans were used for training and 70 CT scans were used for testing [7]. We used the transfer learning methodology to build the model for CT image segmentation as explained in "A Survey on Transfer Learning" [8]. ResNet 50 is the architecture with pretrained weights of ImageNet dataset which can be used for prediction, feature extraction, and activation functions which includes "ReLU" and optimizers are "Adam". The workflow for liver CT image segmentation is picturized in Fig. 6. We used the Indian Liver Patients dataset, which is a collection of 416 liver patient records and 167 non-liver patient records obtained from northeast of Andhra Pradesh, to analyze the status of the liver using clinical records [9]. Using this information, we built several classification models.
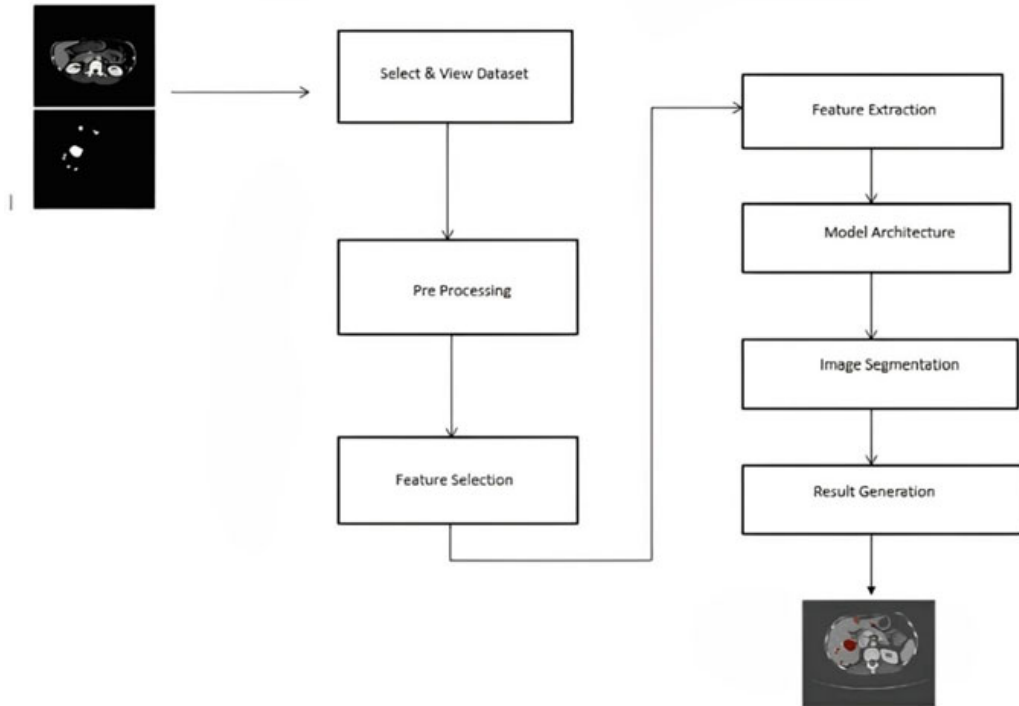
Fig. 6 Workflow of liver CT image segmentation

4.2 Liver Risk Prediction

We used the Indian Liver Patients dataset, which is a collection of 416 liver patient records and 167 non-liver patient records obtained from northeast of Andhra Pradesh, to analyze the status of the liver using clinical records [9]. Using this information, we built several classification models. The reason for using multiple algorithms is to make the most accurate prediction by considering the individual prediction of each algorithm. Every time, for each and every model, the chemical values are sent for prediction, and in result the five predictions are being concluded based on the higher frequency and the liver is classified as healthier or unhealthier as shown in Fig. 7.

5 Experimental Results

Our frame work resulted in the development of web application that can evaluate the patient's tumor status by using alpha-fetoprotein blood test result as input data (Fig. 8). This web tool used is unquestionably better than the conventional diagnostics for figuring out whether a patient has a tumor because it only requires the results of a blood test as shown in Fig. 9a, b. To get the most out of each module's
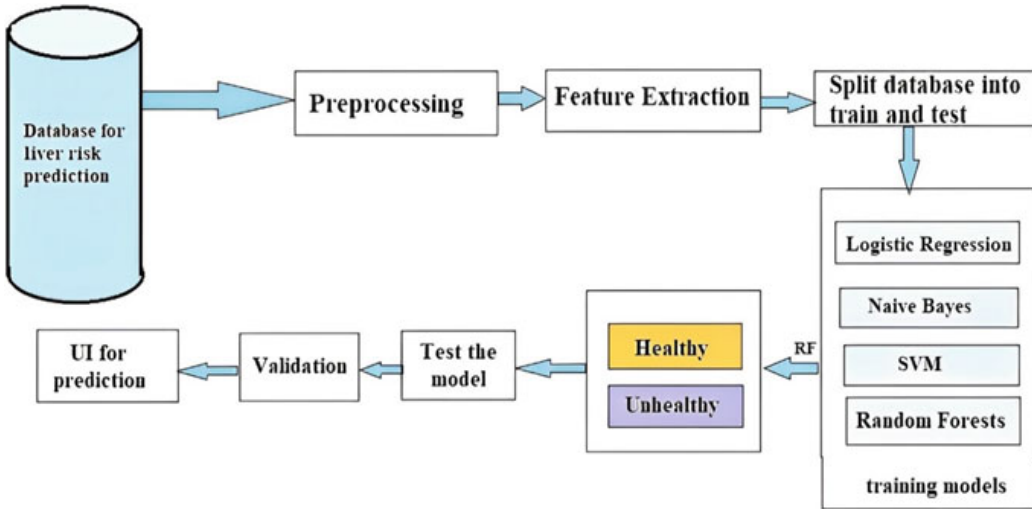
Fig. 7 Flowchart of liver risk prediction

functionalities, you'll have to import the module using an associated import statement. The import keyword is used with the module name to construct an associated import statement. This can be declared at the top of the code in a Python file, beneath any system lines or general comments.

As input we take liver CT image of a patient. In the given dataset, it contains the grayscale images and slices of each patient in the form of nii series and DICOM format along with liver images dataset contains the segmentation images which represents the ground truth (ground truth is a term utilized in statistics and machine learning to check with information assumed to be correct). As part of data preprocessing we link both masks and grayscale liver images. To get the Region Of Interest (i.e., liver part) with high accuracy, we generate slices. A network analysis of several parameters is carried out. This also suggests that there is plenty of room for more study into advanced corrosion, deep learning, and machine learning techniques. The results of the trials and analysis showed that the suggested method may be used to extract both healthy and moderately ill livers. Gundavarapu, M.R. et. al proposed genetic algorithm and NSGA-II for breast cancer analysis based on similar principles [10].
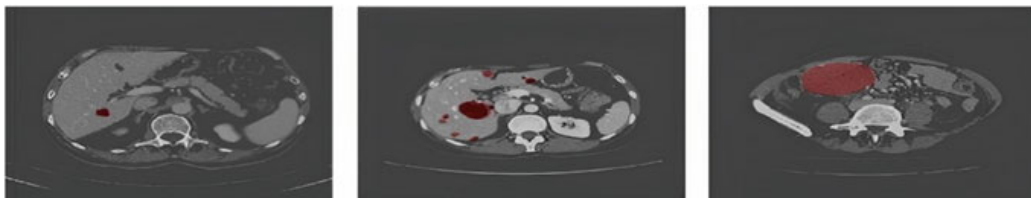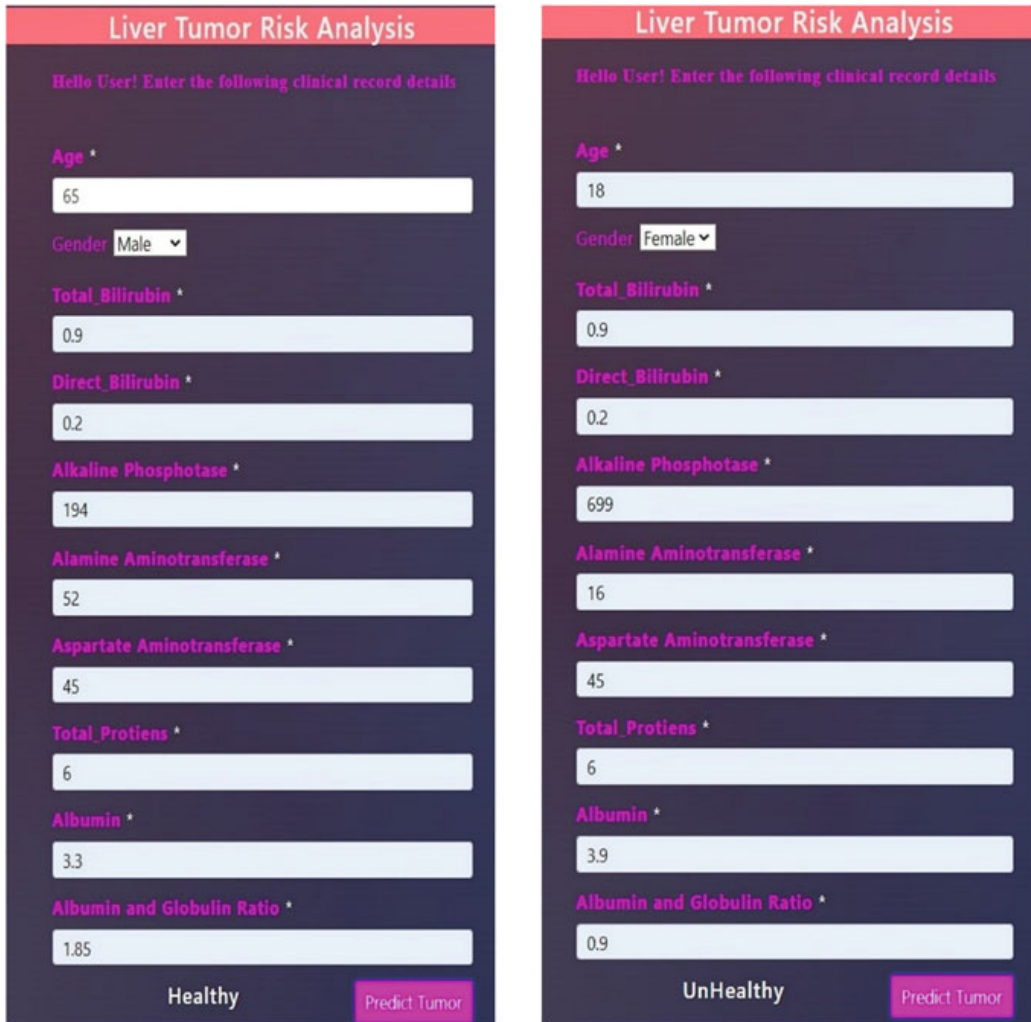

Fig. 8 Segmentation result

Fig. 9 **a** Healthy liver. **b** Unhealthy liver

6 Conclusion

The liver CT (computed tomography) picture was segmented using deep learning techniques as shown in Fig. 8. Manual, semi-automatic, or fully automated CT image segmentation techniques can all be used for liver segmentation. Future research will examine the use of new distinguishing agents as well as the combination of MRI-based biomarkers and liver volumetry. Machine learning is used to predict liver risk based on a set of input variables. The data ingestion phase was followed by data cleansing and processing, missing value analysis, and research. It closes with a data analysis, modeling, and evaluation. Mutual verification, calculation, precision, and recall are terms that are used to assess the correctness of machine learning methods. The suggested system considers relevant data, such as the patient's age, gender, total bilirubin, direct bilirubin, alkaline phosphates, alanine aminotransferase, aspartate aminotransferase, total proteins, albumin, and globulin ratio, and provides accuracy

of the proposed model based on the technique we use. The analysis clearly demonstrates the topic's potential. A network analysis of several parameters is also carried out. This also suggests that there is plenty of room for more study into advanced computer vision, deep learning, and machine learning techniques. From the experiments and analysis, it appears that the proposed approach could extract healthy livers as well as those mildly diseased liver segmentation has a wide range of clinical uses and is growing in popularity. To integrate volumetry into clinical practise more efficiently, clinicians can use semi-automatic or fully automated segmentation alternatives. This paper's uses are now limited, but with thorough research, amazing outcomes can be expected. There are some limits to this study, such as the size of the liver CT (computed tomography) pictures, the time it takes to segment and preprocess the image, and the high computational needs. However, there is room for improvement. Computation time could be significantly reduced with better algorithms. Furthermore, this paper could be expanded by developing a mobile application that allows clinicians to segment the liver in a fraction of the time.

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