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Deep Feature Learning for Liver Tumor Diagnosis

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Abstract. Cancer is the second leading cause of mortality worldwide and represents a major public health concern due to its high disease burden and associated mortality rates. [1-3]. According to the World Health Organization, an estimated 9.6 million deaths were attributed to cancer in 2018, indicating that one in six deaths in developing countries is due to cancer. This number can be reduced if the disease is detected at its early stages. However, the most advanced diagnostic tool is still expensive to be adopted collectively. Frontal radiography is a commonly utilized diagnostic modality for liver cancer; however, its effectiveness is limited by the requirement for manual interpretation of each radiological image by trained radiologists.

Following extensive research on the automation of diagnostic procedures through the application of computational techniques to medical image analysis, the overall cost can be significantly reduced by enabling early-stage disease detection.

Recent improvements in deep learning have led to excellent image classification results regarding different cancer types. However, the application of deep learning in liver cancer diagnosis is still limited. Thus, this work focused on a deep learning applications.

We developed a framework that combined two networks, that are Variational feature learning and neural network, with inceptions to extract the features. The predicted mean μ in the last layer is used as an input to a softmax classifier to predict the image. The proposed framework achieved a state-of-art result with an accuracy of 98.36% for liver cancer classification.

Keywords: deep learning, NN4, image recognition

1 Introduction

Liver diseases contribute significantly to global mortality annually. Early-stage diagnosis remains particularly challenging due to the subtle and nonspecific nature of initial clinical manifestations. A major concern is that the disease often remains undetected until advanced stages, as the liver retains functional capacity despite partial damage during the early progression of the disease [4]. There is a possible to treat this dangerous disease only if it can be discovered in its early stage therefore so

many attempt are trying to focus on how to discover it using a deep learning and until now they are still trying to find out the best way to discover it earlier.

Early detection of liver disease is critical for improving patient survival outcomes. Although initial symptoms may be subtle, timely diagnosis can significantly enhance life expectancy. In this study, a deep neural network (DNN) is developed for early-stage liver disease detection. The proposed approach involves training the DNN using multiple clinical parameters, including age, bilirubin level, alkaline phosphatase, alanine aminotransferase, and aspartate aminotransferase, among others. The trained model classifies patients according to the presence or absence of liver disease. The deep neural network (DNN) used in this study is called NN4 deep learning. It is basically used for face recognition but we use it for two reasons, first the tumor can be visualized as a face and therefore we need to extract the most important features to help us to diagnosis the tumor, second NN4 with inceptions is a powerful tool used to extract the features of any images according to some experiments that have be conducted in our lap. We also created a Variational Feature Learning VFL loss function to be used to correct and updates the weights and therefore improve the model to predict the malignant or benign tumor in the liver. This process can increase the accuracy performance of the model significantly.

Therefore many researches work in this field, however, none of them reach accuracy higher than 90%. The reason behind that is the lack of medical images. Therefore, we have tried in this work to get a state-of art accuracy rate more than 90% with amount of dataset collected from Fudan hospital in Guangzhou-China, and some images taken from the cancerimagingarchive.org [5] website by combining two deep neural network with variational feature learning [6]. This framework will extract the representation of images to predict any unseen images with high accuracy. Fig 1 shows the apart of these two datasets.

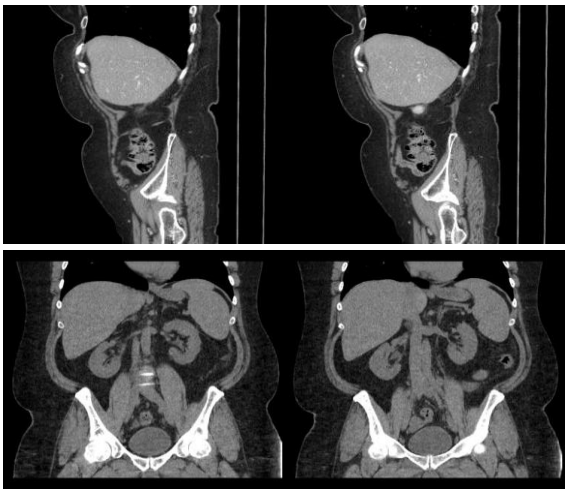


Fig. 1. Different Examples of images in the dataset used for training after merging the two datasets of cancer image archive dataset of liver and Guangzhou Fudan Hospital dataset.

The remainder of this paper is organized as follows: Section 2 reviews the most relevant related work. Section 3 describes the proposed methodology, including the dataset and the deep neural network architecture. Section 4 presents the evaluation and quantitative results, and Section 5 concludes the paper.

2 Related Works

Numerous studies have focused on medical image recognition, and the most relevant works are briefly discussed here.

Convolutional neural networks (CNNs) trained on the ImageNet dataset [7] have demonstrated the ability to learn a rich set of features that can serve as effective feature extractors across diverse image recognition tasks, often achieving competitive performance and surpassing traditional methods [8–10].

In the context of medical image analysis, one of the earliest applications of pretrained CNNs involved detecting pleural effusion and cardiomegaly in X-ray images [11]. In this study, an ImageNet-trained CNN was employed for classification and compared against models using features extracted via traditional algorithms, including local binary patterns [12, 13], Gist [14], PiCoDes [15], and combinations of established methods such as scale-invariant feature transform, Gist, and pyramid histogram of oriented gradients [14–17], optimized on a subset of ImageNet. In most evaluations, features derived from the pretrained CNN outperformed alternative approaches, with the highest performance achieved by combining CNN and PiCoDe features. This combination yielded area under the curve (AUC) values of 0.93 for right pleural effusion detection and 0.89 for cardiomegaly detection.

Another study [18] investigated the application of CNNs for colonic polyp classification, comparing pretrained CNNs, fine-tuned CNNs, networks trained from scratch, and traditional handcrafted features. The combination of pretrained CNNs with handcrafted features demonstrated superior performance.

In a separate approach, CNNs pretrained on ImageNet were used as feature extractors for detecting nodules in pulmonary computed tomography scans [19]. The extracted features were input to a support vector machine (SVM) to classify regions as containing nodules or not. These results were compared with a commercial computer-aided detection (CAD) system approved by the U.S. Food and Drug Administration on a private dataset of 1,000 images. While the commercial CAD system performed well, integrating it with the proposed CNN-based features increased the maximum sensitivity from 0.68 to 0.71.

Additionally, three approaches for applying pretrained CNNs to detect perifissural nodules were proposed and compared with handcrafted features [20]. This method achieved an AUC of 0.847, slightly lower than the handcrafted feature-based AUC of 0.868, yet comparable to the performance of trained specialists manually analyzing the images.

Some other methods used to detect the infected lung is proposed in [21]. The authors used a three pretrained networks to extract the features for tuberculosis detection: Simple CNN feature extraction bag of CNN features and ensembles that is, applying ensembles of classifiers trained using features extracted from multiple pretrained CNNs. In our study, we did not use any pretrained model and we used a more complicated networks that have not been used before in any medical researches.

Another study employed a convolutional neural network (CNN) to classify six hepatic tumor types using 494 lesions from multiphasic MRI scans [22]. Despite using a relatively simple CNN architecture, the system achieved a positive predictive value of 76.5% and a sensitivity of 82.9% in identifying the correct radiological features for each lesion. The authors reported a misclassification rate of 12% for the evaluated lesions.

A novel deep learning framework, termed Watershed Gaussian-based Deep Learning (WGDL), was proposed for accurate delineation of liver cancer lesions in computed tomography (CT) images [23]. The model was trained on a dataset of 225 images. Liver regions were first segmented using marker-controlled watershed segmentation, followed by lesion segmentation via a Gaussian mixture model (GMM). The authors reported a classification accuracy of 99.83%; however, the same dataset used for training was also employed for evaluation.

A recent study proposed MSAF-Net [24], a novel multi-space attention fusion network that systematically integrates five complementary feature spaces (R, B, Y, entropy, and LBP) with an SE-block–enhanced fusion mechanism and EfficientNet-Lite–based feature extraction. The authors reported that their framework achieves state-of-the-art performance by combining engineered feature spaces with deep learning, attaining a classification accuracy of 94.7%.

Another approach integrates two advanced deep learning models, V-Net and VGG16 [25]. In this method, V-Net was employed for tumor segmentation, while VGG16 was used for classification. The training dataset was augmented using various transformations and subsequently split into 70% for training and 30% for testing. The VGG16 model achieved a classification accuracy of 96.52%.

Diagnosing the liver tumor from the computed tomography (CT) images can be

considered as a challenging because of the complexities involved in such images during the evaluating of the liver. This challenge tackled by a study in [26]. In this study, the authors created an innovative deep learning model UNet70 for liver tumor classification where CT images are classified as either having a malignant tumor or a benign tumor. The authors claimed they obtained an accuracy performance of 94.58 % which considered as an excellent.

Another study proposed FasNet [27], a hybrid deep learning model combining ResNet-50 and VGG-16 architectures. FasNet leverages the robust feature extraction of ResNet-50 and the detailed spatial representation of VGG-16 to achieve enhanced liver tumor segmentation accuracy. Monte Carlo Dropout is employed to estimate uncertainty and improve model robustness, which is critical for high-stakes medical applications. The model was evaluated on the LiTS17 dataset, achieving state-of-the-art performance with a Dice coefficient of 0.8766 and a Jaccard index of 0.8487.

The most recent research in this field used the facial videos to predict the liver function [28]. The authors collected 120 a facial videos of 120 patients to be trained with internal validation and an additional 7 patients for external validation. They designed a network called a Region-Guided Dual-Branch Attention Network with cross-attention to integrate global and local facial features. The results were compared with conventional models and clinician assessments. They obtained an accuracy performance of 73.3% in internal validation and an accuracy performance of 73.6% in external validation. Although their research is really interesting but we our aim is to predict the early stage of the liver cancer tumor from the x-ray of the livers and the get an accuracy performance exceed the 90% accuracy.

In another study [29], a CT images used to classify the malignant and benign liver tumor by creating a new model to increase the efficiency of the liver tumor diagnosis. The dataset collected manually in this study and then an initially this dataset has been taken for pre-processing performed by histogram equalization and median filtering. An adaptive thresholding with level set segmentation used for segmenting the liver. A deep learning network called U-Net is implemented for segmenting and extracting the features of the tumor using a new Grey WolfClass Topper Optimization (GW-CTO) algorithm. The authors claimed that the learning percentage is 85%.

Another study [30] employed the explainable artificial intelligence (XAI) to identify lipidomic biomarkers for liver cancer and to develop a model that can early detect the liver cancer tumor. This study used 219 patients diagnosed with liver cancer and 219 healthy controls. The authors developed a machine learning models these are AdaBoost, Random Forest, Gradient Boosting. In this study, the untargeted lipdomics with explainable artificial intelligence (XAI) and machine learning can identify biomarkers for earlt detection of liver tumor.

The system for automatic liver tumor segmentation and detection (SALSA) was demonstrated in [31]. The SALSA is a fully automated tool for liver tumor detection and delineation which was developed on 1,598 CT scans and liver tumors. The authors claimed that they earned a superior accuracy in identifying the malignant cancer tumor that gives outperforming state-of-the-art models with a precision of 99.65%, and 81.72% at lesion level, in the external validation cohorts.

3 Method

3.1 Neural Network NN4

NN4 is a network used in training for face recognition and verification [32]. It can extract the most important features through inceptions blocks. The features extracted from this network will pass to Variational Feature Learning (VFL) to be learned again. Table 1 shows the structure of NN4 network.

3.2 Variational Feature Learning (VFL)

The VFL [6] model is a linear combination of features that takes a multidimensional input and returns one or more outputs. VFL employs Kullback–Leibler (KL) divergence loss function. Therefore, the mean μ and standard deviation σ of a

Gaussian distribution were predicted in this stage to calculate the loss function. This stage produces a high feature representation of the tumor. As far as we know, this is the first study that use VFL for medical image classification and the evaluation process showed that VFL achieved the best results.

3.3 Variational Feature Learning (VFL)

The proposed network incorporates Variational Feature Learning (VFL) [6] and the NN4 architecture [32] with inception modules for training on our dataset. Two fully connected (FC) layers are employed to predict the mean (μ) and standard deviation (σ) of a Gaussian distribution. The predicted mean (μ) is then passed to a third FC layer with a softmax classifier, as illustrated in Fig 2. The softmax classifier is defined in Equation 1, where v represents the output vector, t the target vector, and p the input to neuron j.

$$P(t, v) = \sum_{i=1}^{v} t_i log\left(\frac{e^{p_i}}{\sum_j^v e^{p_j}}\right) \quad (1)$$

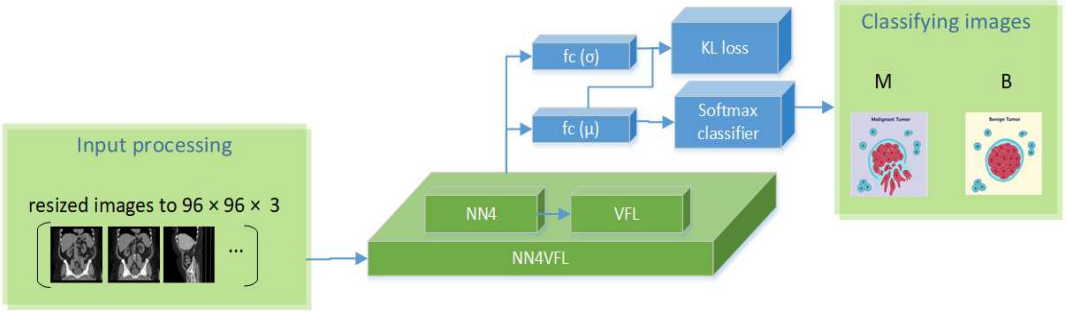


Fig. 2. Proposed network for Malignant/Benign Tumor classification.

Prior to network input, all images were resized to 96×96×3. These images were fed into the first convolutional layer, which consisted of 64 kernels of size 7×7 with a stride of 2. The second convolutional layer contained 64 kernels of size 1×1 with a stride of 2, while the third convolutional layer employed 192 kernels of size 3×3 with a stride of 2. Following these layers, an inception architecture was applied, comprising seven blocks labeled Inception 3a, 3b, 3c, 4a, 4e, 5a, and 5b [32]. Table 1 presents the NN4 model structure prior to its integration with the Variational Feature Learning (VFL) framework.

Table 1. The structure of NN4.

Type	Size in	Size out	Kernal	Feature map
ZeroPadding	96, 96, 3	102, 102, 3		
Conv1	102, 102, 3	48, 48, 64	7×7×3, 2	64
Norm	48, 48, 64	48, 48, 64		
ZeroPadding	48, 48, 64	50, 50, 64		
Max pool	50, 50, 64	24, 24, 64	7×7×3, 2	
Conv2	24, 24, 64	24, 24, 64	1×1×3, 2	64
Norm	24, 24, 64	24, 24, 64		
ZeroPadding	24, 24, 64	26, 26, 64		
Conv3	26, 26, 64	24, 24, 192	3×3×3, 2	192
Norm	24, 24, 192	24, 24, 192		
ZeroPadding	24, 24, 192	26, 26, 192		
Max pool	26, 26, 192	12, 12, 192	3×3×3, 2	

inception 3a	12, 12, 192	12, 12, 256		
inception 3b	12, 12, 256	12, 12, 320		
inception 3c	12, 12, 320	6, 6, 640		
inception 4a	6, 6, 640	6, 6, 640		
inception 4e	6, 6, 640	3, 3, 1024		
inception 5a	3, 3, 1024	3, 3, 736		
inception 5b	3, 3, 736	3, 3, 736		
Average pool	3, 3, 736	1, 1, 736	3×3×3, 1	
fc1(μ)	1×1×736	128		
fc2 (σ)	1×1×736	128		
fc3	128	2		

The final layer of the NN4 network is fed into the Variational Feature Learning (VFL) module, which begins with two fully connected (FC) layers to predict the mean (μ) and standard deviation (σ) for computing the Kullback–Leibler (KL) loss, as defined in Equation 2. Here, n represents the vector size of each image, set to 128. The KL loss is calculated for each training batch.

$$KL = \frac{-1}{2}\sum_{i=1}^{n}\left(1 + log(\sigma_i) - \mu_i^2 - \sigma_i\right) \quad (2)$$

The second loss function (KLD) differs slightly from the first and is computed as shown in Equation 3. It is calculated by taking the logarithm of the predicted mean (μ) divided by the standard deviation (σ), and then multiplying the result by μ. Here, n denotes the vector size of the intermediate layer, as in the first loss function.

$$kld = \sum_{i=1}^{n}\left(\mu\middle| i * log\left(\frac{\mu_i}{\sigma_i}\right) - 1\right) \quad (3)$$

4 Experiments

4.1 Database

All images used in the training in this work were examined in Fudan Hospital in Guangzhou, Guangdong, China. Some other pictures were obtained from the Cancer Image archive website for radiology studies [5] to increase the image number. These two datasets were classified manually into malignant and benign images with a total of 1083 images.

The collected dataset from the Cancer Image Archive website consists of 664 liver X-ray images from different directions. Of these images, 67 show the disease, and 597 do not present the disease. The whole images in this dataset have resolutions of 512 × 512 or 512 × 684 pixels.

The Guangzhou dataset collected in Fudan Hospital in Guangzhou, China, consists of 419 images. Of these images, 21 have the disease, and 398 do not have the disease. The radiographs' resolutions are either 512 × 512 or 512 × 684 pixels. Fig 1 shows a part of these two datasets.

4.2 Experimental Results

Due to the high-resolution input images, the classification accuracy was elevated. Prior to network input, all images were resized to 96×96×3. The network was trained for 70 epochs using a softmax classifier with the Adam optimizer [33] and an initial learning rate of 0.0001.

Table 2 summarizes the parameters used to evaluate the performance of our model. A micro-average calculation was applied with β=2, where β determines the relative

weighting of precision. Fig 3 presents a comparison of the evaluation metrics.

Table 2. Some evaluation parameters for measuring the performance.

Recall	Precision	F1 Measure
0.99	0.99	0.99

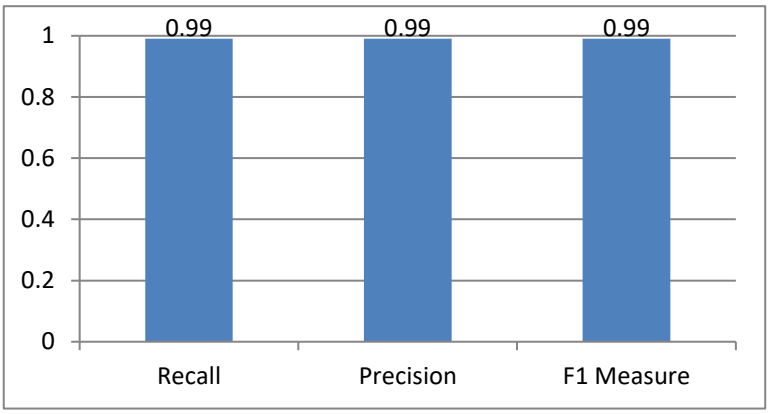


Fig. 3. Evaluation parameters for measuring the performance.

Table 3 shows that the accuracy average of the first class is 97.73%, whereas the accuracy average of the second class is 99%. Therefore, the whole mPA obtained is 98.36% which considered as a state of the art as compared to other previous studies. Table 4 shows a comparison of our study to the other previous studies. Fig 4 demonstrates a comparison chart for our method with previous studies.

Table 3. Classification accuracy for each class with overall accuracy.

Malignant%	Benign%	Overall accuracy%
97.73%	99%	98.36%

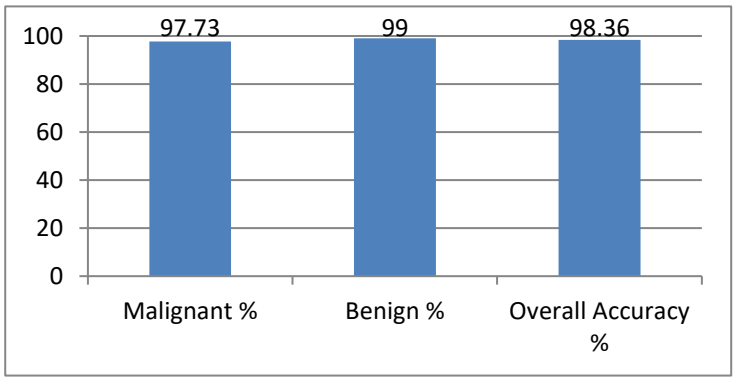


Fig. 4. Classification accuracy for each class with overall accuracy.

As compared to previous studies, we get the highest accuracy. Table 4 presents the comparison of previous studies compared to our study, while Fig 5 demonstrates a comparison chart for our method with previous studies.

Table 4. Accuracy of different liver disease diagnosis and methods.

Method	Accuracy classification
VGG-like CNN (500 epochs) [38]	65.31
fine-tuned AlexNet (100 epochs) [37]	77.55
modified GoogLeNet (60 epochs) [35]	81.03
Ensemble of Fine-Tuned [36]	82.48
RGB color PHOW [39]	84.01

hand-crafted feature collection [35]	84.46
transfer learned ResNet-152 [35]	85.38
classification of focal liver [34]	89.64
MSAF-Net [24]	94.7
UNet70 [26]	94.58
VGG16 [25]	96.52
Our network	98.36

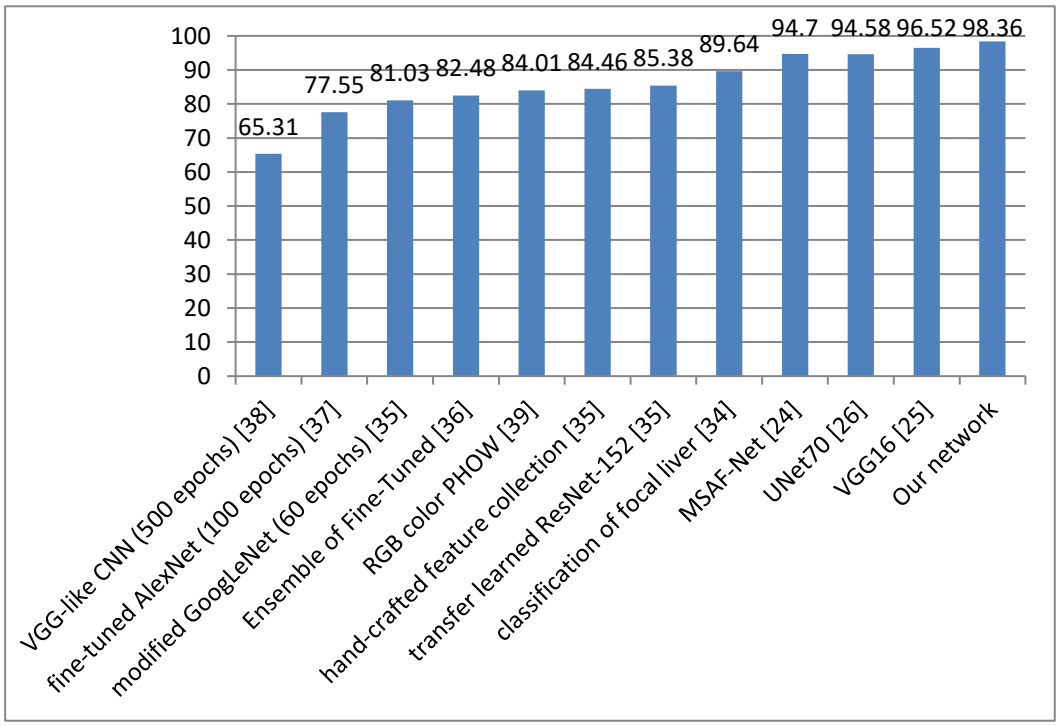


Fig. 5. Classification accuracy for each class with overall accuracy.

5 Conclusion

We have used a deep neural network with Variational Feature Learning (VFL) for training to diagnosis the liver tumor in human beings. We compare our method with other previous works related to liver tumor diagnosis and we found that the best results achieved by our method. The dataset was collected carefully for the training and a state-of-art result have been achieved while evaluating our models on real samples taken from hospital. A real-time system checker for liver tumor has been used in this study for diagnosis.

Although deep learning is essential for feature extraction, incorporating the VFL loss function during training enables the model to achieve state-of-the-art performance.

Carefully designed mathematical operations applied to features extracted by deep learning can further enhance the model's accuracy.

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Declarations

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2- Consent to participate declaration

Ethical approval and consent to participate:
The study was approved by the institutional review board of SAN YAT SEN University by Dr. Hamood Mohammed Abdulrahman Alkhasheb, and informed consent was obtained from all individual participants included in the study (or the requirement for written consent was waived by the institutional review board). All procedures performed in studies involving human participants were in accordance with the Helsinki declaration as revised in 2013 and its later amendments.

3- Data Availability

The datasets generated and analyzed during the current study are available in the DATASET XR LIVER
repository,
https://zenodo.org/records/20118983?token=eyJhbGciOiJIUzUxMiJ9.eyJpZCI6Ijc4ZDViMmVjLWEyYTYtNDk0MS05ZjcxLWI1MjJhMDg5NjM5YiIsImRhdGEiOnt9LCJyYW5kb20iOiI3ZmViYzNjNjE4NmIyOWRjZDMzNGE1ZTViYjZiMTg3NiJ9.AyylAtzFLX2gAuTR8XzWtbNfsmRdRSvowDO20ZCXO9r4ML8ofNrXdKrb7LnA41ZKrTbKWGfLkDjdDIg78Kv7Jw

4- Ethics Declaration

Ethics Approval and Consent to Participate:
This study was approved by the South China University of Technolgy. All procedures performed in this study involving human participants were in accordance with the ethical standards of the institutional and/or national research committee and with the

1964 Helsinki Declaration and its later amendments.

Informed Consent:
Informed consent was obtained from all individual participants included in the study.

Consent for Publication:
Consent for publication was obtained from participants where necessary.

5- Contributions of the authors:

Mohammed Al Alas wrote the manuscript text
Weiwei Lin review the the manuscript text
Mohammed Alghaili help in programming
Hamood Mohammed Abdulrahman Alkhasheb help in image classification of the dataset
Wang Jie help in classifying and collecting images

6- Competing Interest Declaration

The authors declare no competing interest.