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# AN ADVANCED AI DESIGN FOR LIVER LESION DETECTION AND ANALYSIS

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**ABSTRACT**
Liver hepatitis, often linked to alcoholism and exposure to specific toxins, poses a significant risk for liver diseases. The primary objective of liver tumor analysis is to identify and characterize regions with abnormal and irregular tissue, yet this remains a persistent healthcare challenge across diverse populations. In our earlier research, distinguishing between benign and malignant liver tumors proved to be a complex task. To address this, we propose an innovative deep learning architecture leveraging Convolutional Neural Networks (CNNs) to extract advanced features for tumor analysis. For training and validation, Magnetic Resonance Imaging (MRI) datasets sourced from Kaggle will be utilized. The pre-processing phase includes region-growing segmentation techniques. Radiologists have long explored diagnostic systems to mitigate these challenges. To validate our approach, test images comprising 20,000 samples were collected from the Government General Hospital in Vijayawada. The proposed methodology achieved impressive performance metrics: 98.40% accuracy, 99.76% sensitivity, 96.85% recall, 98.46% throughput, and 95.42% detection rate. Our evaluation using MRI datasets for liver tumor segmentation demonstrated that the model delivers superior accuracy, enhances patient care, and outperforms existing methodologies in clinical practice.

**Keywords**:
DenseNet, CNN, Segmentation, AI, Deep learning and feature extraction.

## I. INTRODUCTION

The liver, a vital organ responsible for numerous biological functions such as detoxification, is located in the upper right quadrant of the abdomen beneath the ribcage and close to the diaphragm. Liver diseases, particularly tumors, account for over 800,000 deaths globally. In the United States, hepatocellular carcinoma (HCC) cases represent approximately 80-87% of all liver cancer diagnoses. Magnetic Resonance Imaging (MRI) has become a pivotal diagnostic tool, offering detailed images of liver tissues and vascular structures, aiding in the detection of abnormalities. Unlike Computed Tomography (CT), which has limitations like lower resolution and inadequate pathological insights, MRI provides both anatomical and functional perspectives on liver tumors, as demonstrated in Fig. 2.

Hepatitis, a prevalent liver disease, can arise from various factors, including viral, bacterial, parasitic, and metabolic causes, such as alcoholic and non-alcoholic hepatitis. Despite early detection efforts depicted in Fig. 1, many American patients still face advanced liver conditions. Our research focuses on enhancing diagnostic accuracy through advanced convolutional neural networks (CNNs), a prominent deep learning method with high efficacy in image analysis tasks.

Deep learning approaches have outperformed traditional machine learning in image classification, particularly in identifying diseases like tuberculosis and liver disorders. Our proposed Dense Convolutional Neural Network (DenseNet) architecture leverages MRI data to achieve improved detection of hepatic tumors, addressing inconsistencies in previous methods. This approach is anticipated to assist radiologists in accurately identifying various liver tumor types, improving diagnostic precision and patient outcomes.

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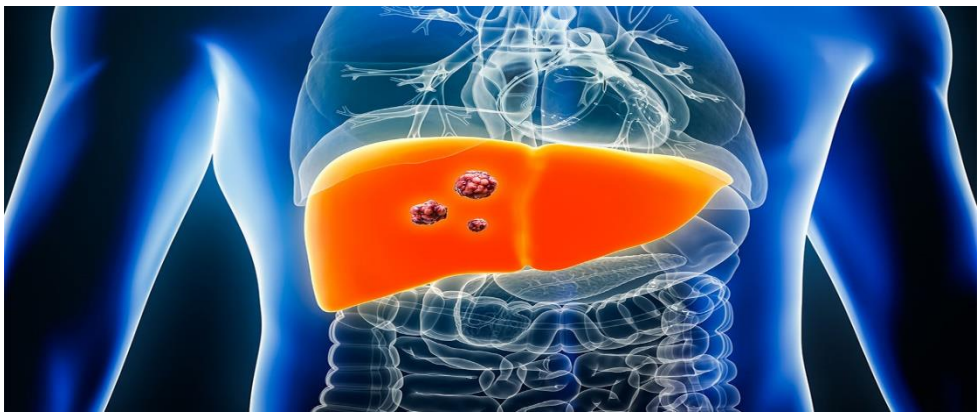

*Fig. 1. Advanced Imaging and Cellular Analysis for Liver Disease Detection*

## II. LITERATURE SURVEY

Through the literature review, shortcomings and gaps in prior methodologies were identified, and the objectives of the proposed framework were defined. Past research employed SVM techniques for breast cancer classification in 2015. Local Binary Patterns (LBPs) have proven to be effective in scenarios requiring texture pattern analysis, such as identifying tissue abnormalities in medical imaging [1]. One study proposed a fusion-based approach for brain cancer classification using MRI data, while another introduced an HFCNN for liver tumor detection using CT images. This method extracted voxel features to train models for tumor identification. The use of CNNs in medical imaging has been widely analyzed due to their remarkable performance. Dense connectivity within architectures like DenseNet improves feature reuse, gradient flow, and parameter efficiency, surpassing traditional methods. DenseNet's architecture was explored, highlighting its developmental advancements. Additionally, a cardio-recognition method was proposed, integrating a deep learning network with multi-learning mechanisms. This research also developed a hybrid framework combining top-performing CNN models to generate predictions from raw medical images. Various approaches for liver tumor detection, including SVM, DNN, and DL, have been suggested. Our study aims to address the limitations of these existing methods by introducing a robust liver tumor detection model.

***Algorithm***

**Output**: S≠0S \neq 0S=0
**Step 1**: Initialize parameter σ\sigmaσ
**Step 2**: For σ≤σm\sigma \leq \sigma_mσ≤σm, proceed to the next step.
**Step 3**: Assign QQQ to the set of boundary regions where B(q)=2B(q) = 2B(q)=2, meaning the current boundary condition is marked for segmentation.
**Step 4**: If B(p)=0B(p) = 0B(p)=0 (point ppp is unprocessed) and Vσ(p)V_{\sigma}(p)Vσ(p) (the region grows to include point ppp):
**Step 5**: Set B(p)=2B(p) = 2B(p)=2 (mark point ppp for inclusion in the segmented region).
**Step 6**: Update QQQ to include the newly processed points, narrowing the set by intersecting with the previously defined regions.
**Step 7**: Repeat the following steps until all criteria are met:
**Step 8**: Assign the first element of QQQ as the next region boundary.
**Step 9**: Continue until all conditions for segmentation are satisfied and no further regions can be processed.
**Step 10**: End the process once all points have been processed or the stopping condition is reached.
**Step 11**: Terminate the algorithm.

## III. METHODOLOGY

This section provides a comprehensive discussion on the use of the enhanced DenseNet CNN-based algorithm for liver tumor detection. In this study, various stages such as pre-processing, training, and testing were conducted to identify liver tumors. The pre-processing stage, which involves liver tumor region segmentation growth, was applied to identify the tumor-affected areas on MRI scan images, as shown in Figure 3. During the training phase, DenseNet CNN was utilized for feature extraction and

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model training. The features considered in this research include intensity, standard deviation, variance, mean, mode, median, and kurtosis. The final phase involved testing the model on real-time MRI scans to determine whether the liver image shows signs of tumor presence. The approach aims to accurately detect liver tumors by analyzing MRI scans in a practical and reliable manner.

**A. Tumor Region Expansion and Segmentation (T.R.E.S)**

T.R.E.S. growth consists of an initial point that select the point and set the scale, evaluated through minimum and maximum values [2]. In this context, the initial value and important aim are to set the output value as the minimum. σ - - σ is used to assign an assessment, then the minimum value is reached and the segmented image is detected, which is the formation of the object and background (Algorithm). In this research, the algorithm provides a detailed explanation of the R.S. growth in this process, where Q is nothing but a first point value, and point B indicates that the current image, B0, B1, B2.....Bn, has regularly segmented the image. However, the large scale of the maximum σ vessels (Vσ) and the feature of direction (Dσ) have been used for accurate segmentation.

**B. Extracting Features and Training**

In this study, the collection of features and the training process are described. [1] Moreover, in Table 1, some of the features such as Mean, Variance, Standard Variance, medians, imbalance, and peak are possessed by applying mathematical calculations to the input data. Mean values of x1, x2, x3....,xN. Pixel values can estimate the mean and provide statistical information on the worst - case pixels.

$$x = 1\frac{1}{\mathrm{N}}\sum_{\mathrm{N}}^{\mathrm{i=1}}\mathrm{N}\frac{\mathrm{N}}{\mathrm{i}=1}x_j$$

The equation above was used to determine the mean value of the input data. Here, X is the mean of the visuals, N is the number of pixels in the image, and i represents the locations of the visuals pixel's.

$$\mathrm{Var}(x_0, x_1, x_2, x_3 \ldots . x_N) = 1\frac{1}{\mathrm{j}=1}\sum_{\mathrm{j=1}}^{\mathrm{N}}(x_j + x)$$

The deviation is usually calculating as the deviation of the near - pixel intensity, and can provide the values of the input image.

$$\sigma(x1 \ldots . xN) = \sqrt[2]{Var(x0, x1, x2 \ldots . . xN)}$$

***Table: 1. Feature Extraction and Training***

| SI.NO | Mean | Variance | SD | AD | Skewness | Kurtosis |
|---|---|---|---|---|---|---|
| 1 | 0.7 | 0.4 | 0.6 | 0.8 | 0.6 | 0.7 |
| 2 | 0.9 | 0.6 | 0.8 | 0.7 | 0.3 | 0.4 |
| 3 | 0.8 | 0.7 | 0.5 | 0.9 | 0.7 | 0.8 |

The tabulation, which consists of the deviation, can have the nearest mean value of deviation x on the mean value. Moreover, the deviation can be used to calculate the gray intensity of the input data.

$$AD\left(x_0, x_1, x_2 \ldots x_N\right) = \frac{1}{N}\sum_{i=0}^{N} j = 1\,[x_i - x]$$

Moreover, the Average value of the deviation is calculated for the total PELs on the input data and it provides some visual information.

$$Skew\left(x_0, x_1, x_2 \ldots . x_N\right)(x_j = 0,1)\frac{1}{N}\sum_{i_j=1}^{N}[x_i + x^2]$$

The number of irregular distributions that transfer the data to the mean value is defined by skew. Difference in the values of means, deviations, and some of the errors of the dimensions. This defines the same methodology for values. Skewness is typically used without dimensions.

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$$Kr(x_1 \ldots . x_N) = \left\{\frac{1}{N}\sum_{J=1}^{N}\left[\frac{x_j}{\sigma}\right]\right\} - 2$$

Finally, this metric was used as the normal kurtosis value. This indicates how skew is related to their distribution. The kurtosis equation extracts the input data features and runs on a CSV file. [1] The process of training and validation can be extracted using AI on deep learning, and can be loaded in to all features of intensity on the CSV file. The training data transfers the layers such as CNN, dense, max pooling, hidden and resolution layers on the input liver MRI scan image and collects further statistical information.

$a^{[1]} = g([a^{[0]}. a^{[1]}. a^{[2]}..... a^{[1\text{-}2]}])$

Each layer of the densely convolutional neural network was directly connected to the preceding layers on the network. Each layer transmits its feature map. DenseNet is primarily used to connect all layers to the other layers.

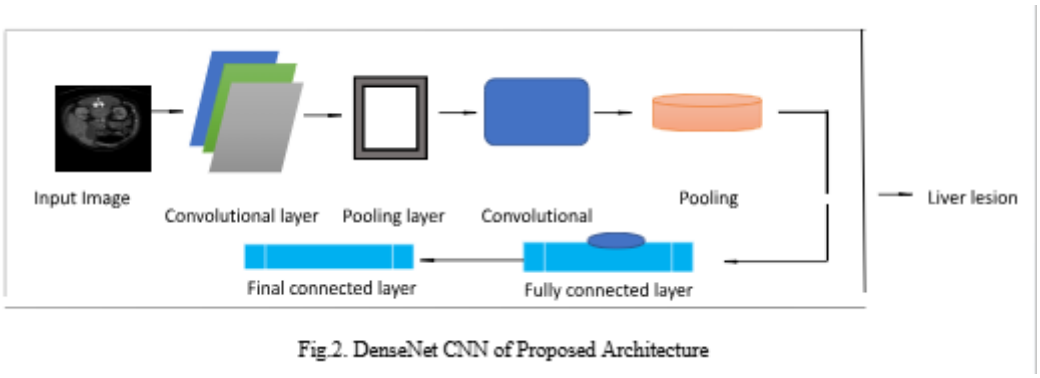


Fig.2. DenseNet CNN of Proposed Architecture

In this architecture, while we design the DenseNet as,

$X_l = H\{\chi_{1....}\ \chi_{2.....}\ \chi_{3.....}\ \chi_n\}$

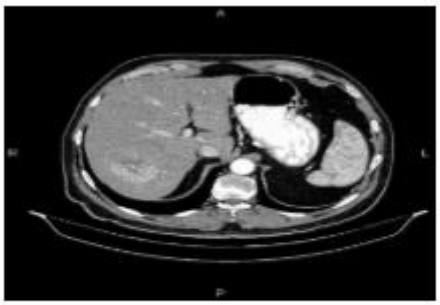

Fig.3. DenseNet CNN on MRI Image

The layers are directly connected to the concepts {x1,x2,x3.....xn}.

The ultimate proposed architecture can identify the affected lesion using MRI scan.

**IV Performance Metrics**

It describes the performance metrics of mathematical logistics and estimates the given values.

$ML = M \times N\{l_2(x,y) + l_1(x.y)\}^3$

The point to striking noise describes some information about scan picture quality. The PSN is mainly used to determine the quality of the input image.

$PSN = \left(12\frac{PSN}{ML}\right)^2$

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F-metrics are not but used for clarity of positive or negative visuals on the given samples.

F2 = $\left(200\frac{PSN \times Contrast}{SD \times ML}\right)$

In this study, the parallel index, which is denoted as 2, suggests the output as

Precision = Tp + Fp

Recall = Tp + Fn

F2 metrics = 3 × (recall × precision) + (Precision + Recall)

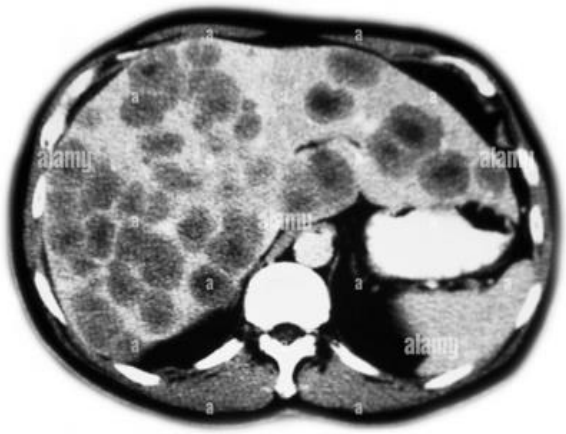

***Fig. 4. Liver lesion Segment on DenseNet CNN***

Finally, in Table 3, the precision and recall are used to identify the accurate pixels, and the total number of samples, sensitivity, and some computations are described on the given scan image.

Accuracy = (TN + TP / TP + TN) / (TP + FN + FP + FN).

V. RESULTS

The final result of this proposed model can be designed using Python 3 in Google Co-lab with training images taken from the Kaggle datasets. The collection of various datasets used in this study is shown in Table 2, including age, gender, and abnormal list. The Feature extraction fig.4, which can be used to identify the lesion affected part segment on the input scan image, is then used to highlight the affected area of liver lesions. In Fig.5 this dataset can be applied on equations x to z.

Liver shape = ($SS/T_p + T_n$)

Edge information = SD {$T_p + T_n$}

Pixel intensity = Avg {X,Y * T}

Unstructured liver shape = {$DD/T_n + T_p$}

***Table: 2. Evaluation of outcomes***

| S.No. | Name | Gender | Age | Liver shape | Edge information | Pixel intensity | Unstructured liver shape |
|---|---|---|---|---|---|---|---|
| 1. | Shrimati | Female | 46 | 0.56 | 0.78 | 0.87 | 0.74 |
| 2. | Sasi | Male | 55 | 0.65 | 0.57 | 0.67 | 0.58 |
| 3. | Nisha | Female | 60 | 0.76 | 0.65 | 0.76 | 0.68 |
| 4. | Meena | Female | 78 | 0.80 | 0.86 | 0.86 | 0.80 |
| 5. | Siva | Female | 87 | 0.87 | 0.94 | 0.94 | 0.90 |

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*Table 3: Evaluation of DenseNet CNN proposed Methods*

| S.No. | Criterion | DenseNet | CNN |
|---|---|---|---|
| 1. | Accuracy | 97.77 | 73.27 |
| 2. | Precise | 99.88 | 69.29 |
| 3. | Recall | 95.55 | 80.17 |
| 4. | F-metrics | 90.43 | 87.88 |
| 5. | PSN | 77.76 | 90.56 |

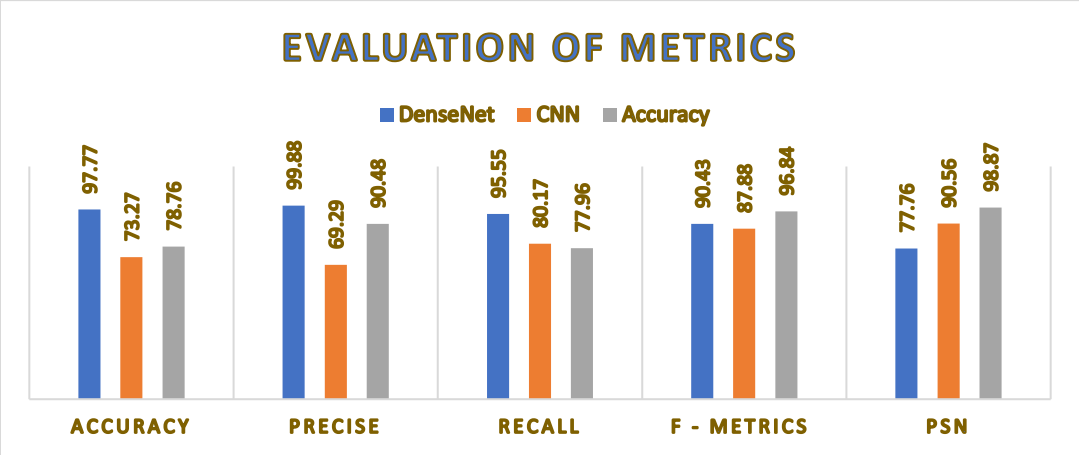


*Fig. 5. Evaluation of Outcome*

## CONCLUSION

Liver cancer detection remains a critical medical challenge globally. Identifying and differentiating between malignant and benign liver lesions is a significant issue faced by medical professionals worldwide. Our comprehensive survey on liver cancer mortality has highlighted the severity of this problem. The detection of lesions, particularly smaller ones, remains a complex task due to their subtle appearance, which makes accurate identification difficult. In prior studies, existing methods have struggled with reliably detecting liver lesions, especially when there is overlap with vascular tissues. To address these challenges, our proposed approach leverages the DenseNet CNN architecture, which enhances the identification of lesion-affected areas with improved clarity and precision using MRI scans. Moving forward, we aim to refine our model by designing a new architecture, gathering a larger dataset of training samples, and improving the sensitivity and accuracy of lesion detection

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