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## **PROJECT WORK**

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**2024**

# **THE APPLICATION OF IMAGE PROCESSING IN LIVER TUMOR DETECTION**

PROJECT SUBMITTED IN PARTIAL FULFILLMENT OF  
THE REQUIREMENTS FOR THE AWARD OF THE  
DEGREE OF **BACHELOR OF ENGINEERING**  
IN **COMPUTER SCIENCE AND ENGINEERING**  
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**Submitted by**  
**DHARANISH P**  
**(2017306)**  
**SIVAKUMAR S**  
**(2017317)**  
**DINESH J**  
**(2017501)**  
**SHIVARAM M**  
**(2017502)**

Under the Guidance of  
**Dr.T.RAJASENBAGAM M.E.,Ph.D.,**

**DEPARTMENT OF COMPUTER SCIENCE AND ENGINEERING**  
**GOVERNMENT COLLEGE OF TECHNOLOGY**  
(An Autonomous Institution Affiliated to Anna University)  
**COIMBATORE - 641 013**

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**PROJECT WORK**

**MARCH-2024**

This is to certify that this project work entitled  
**THE APPLICATION OF IMAGE PROCESSING  
IN LIVER TUMOR DETECTION**

is the Bonafide record of project work done by

**DHARANISH P (2017306)**

**SIVAKUMAR S (2017317)**

**DINESH J(2017501)**

**SHIVARAM M(2017502)**

of B.E. (COMPUTER SCIENCE AND ENGINEERING)

during the year 2023 – 2024

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Project Guide

**Dr.T.RAJASENBAGAM M.E.,Ph.D.,**

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Head of the Department

**Dr.J.C.MIRACLIN JOYCE PAMILA, M.E., Ph.D.**

Submitted for the Main Project(18SEE803) viva-voice examination held on

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Internal Examiner

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External Examiner

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# SYNOPSIS

Liver cancer is a significant global health concern, with early detection playing a pivotal role in patient prognosis and treatment outcomes. Conventional diagnostic methods often rely on medical imaging techniques such as CT scans, MRI, and ultrasound. However, accurately identifying liver tumors amidst complex anatomical structures remains a challenge. This project aims to address this challenge by harnessing the power of image processing techniques to enhance the detection and diagnosis of liver cancer.

The primary objective of this project is to develop a comprehensive image processing pipeline tailored specifically for the early detection of liver cancer using medical imaging data. By employing advanced algorithms for image segmentation, feature extraction, and classification, the project seeks to improve the accuracy and efficiency of tumor identification within liver images.

This project holds significant implications for improving the management of liver cancer by enabling earlier detection and intervention. By leveraging cutting-edge image processing techniques, the project aims to empower healthcare professionals with advanced diagnostic tools, ultimately enhancing patient care and outcomes in the fight against liver cancer.

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# **CHAPTER 1**

## **INTRODUCTION**

### **1.1 DESCRIPTION**

This project addresses a cancer detection approach based on digital image processing, specifically targeting liver cancer. It explains that tumors are abnormal tissue growths resulting from uncontrolled cell proliferation and can be benign or malignant. The paper focuses on hepatocellular carcinomas, the most common form of malignant liver cancer. It highlights the importance of early detection and analysis of tumors using imaging techniques like CT scans and MRI, with MRI being safer due to its avoidance of ionizing radiation. The process involves three major stages: image preprocessing, segmentation, and tumor area highlighting, with the use of techniques such as image resizing, contrast enhancement, and noise removal. The paper emphasizes the use of Artificial Neural Networks (ANNs) for automating tumor detection, which can streamline the analysis process and improve efficiency compared to manual methods. Overall, the research aims to improve liver cancer detection and analysis through advanced image processing techniques, potentially reducing mortality rates and improving patient care.

### **1.2 EXISTING SYSTEM**

#### **Computer-Aided Diagnosis (CAD) Systems**

CAD systems utilize image processing algorithms to assist radiologists in the detection and diagnosis of liver lesions. These systems often incorporate features such as image segmentation, texture analysis, and machine learning classifiers to identify suspicious regions indicative of liver cancer.



## **Automated Tumor Detection Algorithm**

Various automated algorithms have been developed for detecting liver tumors from medical imaging data. These algorithms typically involve image preprocessing steps to enhance image quality, followed by segmentation techniques to isolate tumor regions. Machine learning algorithms, including deep learning approaches such as convolutional neural networks (CNNs), are commonly used for tumor classification.

**Texture Analysis Methods:** Texture analysis techniques analyze the spatial arrangement of pixel intensities within medical images to characterize different tissue types, including liver tumors. These methods can help differentiate between benign and malignant lesions based on their textural patterns.

## **MRI and CT Image Analysis Software**

Commercial and research-grade software packages exist that specialize in the analysis of MRI and CT images for liver cancer detection. These software tools often provide a range of functionalities, including image visualization, segmentation, feature extraction, and quantitative analysis.

## **Open-Source Image Processing Libraries**

Open-source libraries such as ITK (Insight Segmentation and Registration Toolkit) and OpenCV (Open Source Computer Vision Library) provide a wide range of image processing algorithms and tools that can be utilized for liver cancer detection research and development.

## **Research Prototypes and Frameworks**

Academic research often produces prototypes and frameworks for liver cancer detection using image processing techniques. These systems may incorporate novel algorithms and methodologies aimed at improving the accuracy and efficiency of tumor detection and characterization.

## **Collaborative Platforms and Datasets**

Collaborative platforms and shared datasets facilitate research and development in the field of liver cancer detection. These platforms provide access to annotated medical imaging data, benchmarking challenges, and collaboration opportunities for researchers and developers working on image processing-based approaches.

Overall, the existing systems for the application of image processing in liver cancer detection encompass a range of methodologies, from CAD systems and automated algorithms to texture analysis methods and specialized software packages. Continuous research and development in this field aim to improve the early detection and accurate diagnosis of liver cancer, ultimately benefiting patient outcomes.

### **1.3. PROBLEM DEFINITION**

The problem at hand centers around the development of a robust predictive model utilizing image processing techniques for the detection and classification of liver tumors. Liver cancer presents a significant health challenge globally, with early detection being pivotal for effective treatment and patient outcomes. However, the current diagnostic process often relies heavily on manual interpretation of medical imaging data, which can be time-consuming, subject to inter-observer variability, and prone to errors. Therefore, there is a pressing need to implement automated methods that can streamline and enhance the accuracy of liver tumor prediction.

By harnessing the power of digital image processing algorithms, particularly those tailored for medical imaging analysis, such as CT scans or MRI images, this research aims to automate the process of tumor identification and characterization. This involves several key steps, including image preprocessing, segmentation, feature extraction, and classification. Image preprocessing techniques will be employed to enhance the quality of the input images, removing noise and artifacts that could distort the analysis results.

Subsequently, segmentation algorithms will be applied to isolate the liver region and delineate tumor boundaries accurately.

Feature extraction plays a crucial role in capturing the distinguishing characteristics of liver tumors from the segmented images. Features such as texture, shape, and intensity statistics will be extracted to provide discriminative information for tumor classification. Machine learning algorithms, including but not limited to artificial neural networks (ANNs), support vector machines (SVMs), or deep learning architectures, will then be trained on labeled datasets to classify tumors into different categories, such as benign or malignant, and potentially even subtypes of liver cancer. The ultimate goal of this research is to develop a predictive model that can accurately and efficiently detect liver tumors from medical imaging data. This model will not only aid radiologists and clinicians in making timely and informed diagnoses but also contribute to personalized treatment planning for patients. By automating the tumor prediction process, this approach has the potential to improve patient outcomes, reduce unnecessary interventions, and ultimately mitigate the burden of liver cancer on healthcare systems worldwide.

## **1.4 PROPOSED SOLUTION**

The aim of this study is to process and analyze MRI scan images in order to determine if they contain cancer cells or not, and if they do, which type of cancer cells they are. These images come from the Cancer Genome Atlas (TCGA) database, which is open to the public. To process the files, the experimentation procedure employs the MATLAB R2018 program. The segmentation and extraction process depicted in Fig 1 elucidates the overall methodology. The dataset for this study includes MRI scan images of liver cancer, as well as five images of adenoma, cyst, and hemangioma. Image preprocessing was performed because the images framed by the MRI scan have some noise and discrepancy. The picture is normalized in this step by

minimizing noise, changing contrast and scale, and eliminating blurriness all at once. The segmented image, which depicts the extracted liver with cancer cell, is now used to detect cancer cells. The function is extracted by cropping the region of interest, and the k-means algorithm is used to evaluate and judge if the given image is cancer cell or not. Table 1 shows the clusters formed as a result of the above-mentioned procedure. The number of pixels must be calculated for statistical analysis of the affected portion, which is done using MATLAB software.

**1. Data Source:** The MRI scan images used in the study are obtained from the Cancer Genome Atlas (TCGA) database, which is publicly available and contains a wealth of genomic and imaging data related to various types of cancers.

**2. Tool Utilized:** The MATLAB R2018 program is employed for processing the MRI scan images. MATLAB is a widely used programming environment for numerical computing and image processing tasks due to its extensive toolboxes and functions tailored for these purposes.

**3. Preprocessing:** Prior to analysis, the MRI images undergo preprocessing to enhance their quality and remove any noise or discrepancies. This step is crucial to ensure accurate segmentation and analysis. Preprocessing techniques typically include noise reduction, contrast enhancement, scaling, and sharpening to improve image clarity.

**4. Segmentation and Extraction:** The segmentation process involves delineating the region of interest (ROI) within the MRI images, which in this case is the liver area potentially containing cancer cells. Fig 1 likely illustrates the steps involved in segmenting the liver from the rest of the image. Once segmented, the extracted liver region is further processed to detect and analyze cancer cells.

**5. Cancer Cell Detection:** After segmentation, the focus shifts to detecting cancer cells within the extracted liver region. This involves applying image processing techniques and algorithms to identify abnormal cell structures indicative of cancer. In the described methodology, the k-means algorithm is employed for this purpose. K-means clustering is a popular unsupervised learning algorithm used for partitioning data into distinct clusters based on similarity.

**6. Cluster Analysis:** Table 1 likely presents the clusters formed as a result of applying the k-means algorithm to the segmented liver images. Each cluster represents a distinct group of pixels with similar characteristics, which may correspond to different types of cells or tissue structures within the liver, including cancerous regions.

**7. Statistical Analysis:** To quantify the extent of cancerous tissue in the segmented liver images, the number of pixels corresponding to affected areas is calculated. This statistical analysis is essential for assessing the severity and distribution of cancer within the liver and is performed using MATLAB software.

Overall, the methodology described outlines a comprehensive approach for processing and analyzing MRI scan images to detect and characterize cancer cells in liver cancer cases. By leveraging advanced image processing techniques and algorithms, researchers can gain valuable insights into the nature and extent of cancerous tissue, facilitating diagnosis and treatment planning.

## 1.5 ORGANIZATION OF THE PROJECT

**CHAPTER 2: LITERATURE REVIEW:** The already existing proposal and guidelines for the project are discussed in detail with description, merits, and demerits of the already existing system.

**CHAPTER 3: SYSTEM SPECIFICATION:** The system requirements such as the minimum Hardware and Software requirements are discussed.

**CHAPTER 4: PROJECT OVERVIEW AND DESIGN:** The basic architecture the proposed project is discussed with details of the Modules and the Stages involved.

**CHAPTER 5: IMPLEMENTATION AND EXPERIMENTAL RESULTS:** The project implementation with the source code of the Application and the experimental results are provided.

**CHAPTER 6: CONCLUSION AND FUTURE IMPROVEMENTS:** The conclusion of the proposed project and the features that can be scaled in the future are discussed.

**CHAPTER 7: REFERENCES :** All the references and the research papers used for the project are presented.

# CHAPTER 2

## LITERATURE REVIEW

### 2.1 Optimized Liver Tumor Detection and Segmentation Using Neural Network[2013]

**Cancer Overview :** The review starts by providing a general understanding of cancer, emphasizing the abnormal growth of cells leading to cancerous tumors. It highlights the significance of early detection in managing cancer effectively.

**Liver Cancer Incidence :** Liver cancer ranks among the most common cancers globally, with significant regional variations in incidence rates. It mentions that liver cancer is particularly prevalent in Eastern and South-Eastern Asia, Middle and Western Africa, while developed regions typically exhibit lower rates.

**Liver Anatomy and Physiology :** The literature briefly discusses the anatomy and physiology of the liver, emphasizing its importance as the largest gland and internal organ in the human body. It describes the liver's structure, blood supply, and its role in filtering nutrients and toxins from the bloodstream.

Optimized liver tumor detection and segmentation using neural networks offer several merits and demerits:

### **Merits:**

**1. High Accuracy:** Neural networks, particularly deep learning architectures, can achieve high accuracy in detecting and segmenting liver tumors from medical images. This is because neural networks can learn complex patterns and features from data.

**2. Automation:** Once trained, neural networks can automate the process of tumor detection and segmentation, saving time for medical professionals. This automation can lead to faster diagnosis and treatment planning.

### **Demerits:**

**1. Data Dependency:** Neural networks require a large amount of labeled data for training, particularly deep learning architectures. Acquiring such data can be challenging, especially for medical imaging datasets with limited sample sizes and stringent privacy regulations.

**2. Overfitting:** There's a risk of overfitting, where the neural network learns to memorize the training data instead of generalizing patterns. This can lead to poor performance on unseen data or variations in medical images.

## **2.2 Detection and Classification of Liver Cancer using CT images[2015]**

The literature review for this study encompasses several key aspects related to computed tomography (CT) imaging, liver cancer, tumor classification, and image enhancement techniques. Here's an overview:



Detection and classification of liver cancer using CT (computed tomography) images using various techniques including neural networks comes with its own set of merits and demerits:

### **Merits:**

**1. Early Detection:** CT imaging, coupled with advanced algorithms such as neural networks, can aid in the early detection of liver cancer. This early detection can potentially lead to better treatment outcomes and increased survival rates for patients.

**2. Accurate Localization:** Neural networks can accurately localize cancerous lesions within the liver from CT images, enabling precise diagnosis and treatment planning. This accuracy reduces the risk of misdiagnosis and ensures appropriate interventions.

### **Demerits:**

**1. Data Quality:** The performance of neural networks for liver cancer detection and classification heavily depends on the quality and diversity of the CT image datasets used for training. Poor-quality or biased datasets may lead to suboptimal results and generalization issues.

**2. Interpretability:** Similar to other neural network applications, the interpretability of the models used for liver cancer detection and classification from CT images can be limited. Understanding the rationale behind a model's decisions may be challenging, which can affect the trust of clinicians in the system.

## **2.3Diagnosis of Liver Tumor from CT Images using Digital Image Processing[2015]**

Liver cancer is a significant health concern globally, particularly in regions like Iraq where it ranks among the leading cancerous diseases. Current diagnostic methods, such as needle biopsy, are invasive and not always feasible for routine screening due to associated risks and patient discomfort [1]. As a result, medical imaging systems play a crucial role in assisting physicians in the detection and diagnosis of liver tumors.

Various imaging modalities, including computed tomography (CT), have been employed for liver tumor detection and characterization. CT imaging provides detailed cross-sectional images of the liver, aiding in the visualization of tumors and surrounding structures [2]. However, accurately segmenting liver boundaries and distinguishing tumors from surrounding tissues remains a challenge, particularly due to the presence of adjacent organs and internal tumors.

Diagnosis of liver tumors from CT images using digital image processing offers several merits and demerits:

### **Merits:**

**1. Non-invasive Procedure:** CT imaging is a non-invasive procedure, allowing for the diagnosis of liver tumors without the need for invasive techniques such as biopsies. This reduces patient discomfort and risk of complications.

**2. High Resolution:** CT images provide high-resolution anatomical details, allowing for accurate visualization and analysis of liver tumors and surrounding tissues.

**3. Fast Imaging:** CT scans are relatively quick to perform, providing rapid results for diagnosis and treatment planning.

**Demerits:**

**1. Radiation Exposure:** CT imaging involves exposure to ionizing radiation, which carries a risk of cumulative radiation dose over multiple scans, particularly for patients undergoing frequent imaging studies.

**2. Contrast Agents:** Contrast agents may be used in CT scans to enhance the visibility of liver tumors, but they can cause adverse reactions in some patients, including allergic reactions and kidney damage.

**3. Artifact Interference:** CT images may contain artifacts such as noise, beam hardening, and motion artifacts, which can degrade image quality and affect the accuracy of tumor detection and characterization.

# **CHAPTER 3**

## **SYSTEM SPECIFICATION**

### **3.1. SYSTEM REQUIREMENTS**

#### **Hardware requirements**

System	: Intel core i5 11 <sup>th</sup> Generation
Storage (ROM)	: 1 TB
RAM	: 16 GB

#### **Software requirements**

Operating System	: Windows 11
Programming Language	: HTML,CSS, Python
Tool	: Google Colab, VSCode,

### **3.2. SOFTWARE DESCRIPTION**

#### **3.2.1About Windows**

Windows 11, the latest iteration of Microsoft's operating system, introduces a refreshing and modernized user interface that seamlessly blends simplicity with advanced capabilities. Boasting a redesigned Start Menu, centered taskbar, and enhanced snap features, Windows 11 offers an intuitive and streamlined user experience. The new Widgets feature provides personalized at-a-glance information, while the Microsoft Store has undergone a significant revamp for a more curated and user-friendly app discovery. Under the hood, Windows 11 delivers improved performance, efficiency, and compatibility, catering to both productivity and entertainment needs. With

innovative features like Direct Storage for faster gaming load times and a renewed focus on productivity with virtual desktops and snap layouts.

### **3.2.2 CHARACTERISTICS OF WINDOWS**

1. Centered Start Menu and Taskbar
2. New taskbar icons.
3. Snap Layouts and Snap Groups for window management.
4. Redesigned Microsoft Store.
5. Direct integration with Microsoft Teams in the taskbar.
6. Revamped Microsoft Edge browser.
7. Support for Android apps through the Microsoft Store.
8. New gaming features, including DirectStorage and Auto HDR.
9. Redesigned system sounds and animations.
10. Minimum system requirements include TPM 2.0.

# CHAPTER 4

## METHODOLOGY

### 4.1. METHODOLOGY USED

Flow of events:

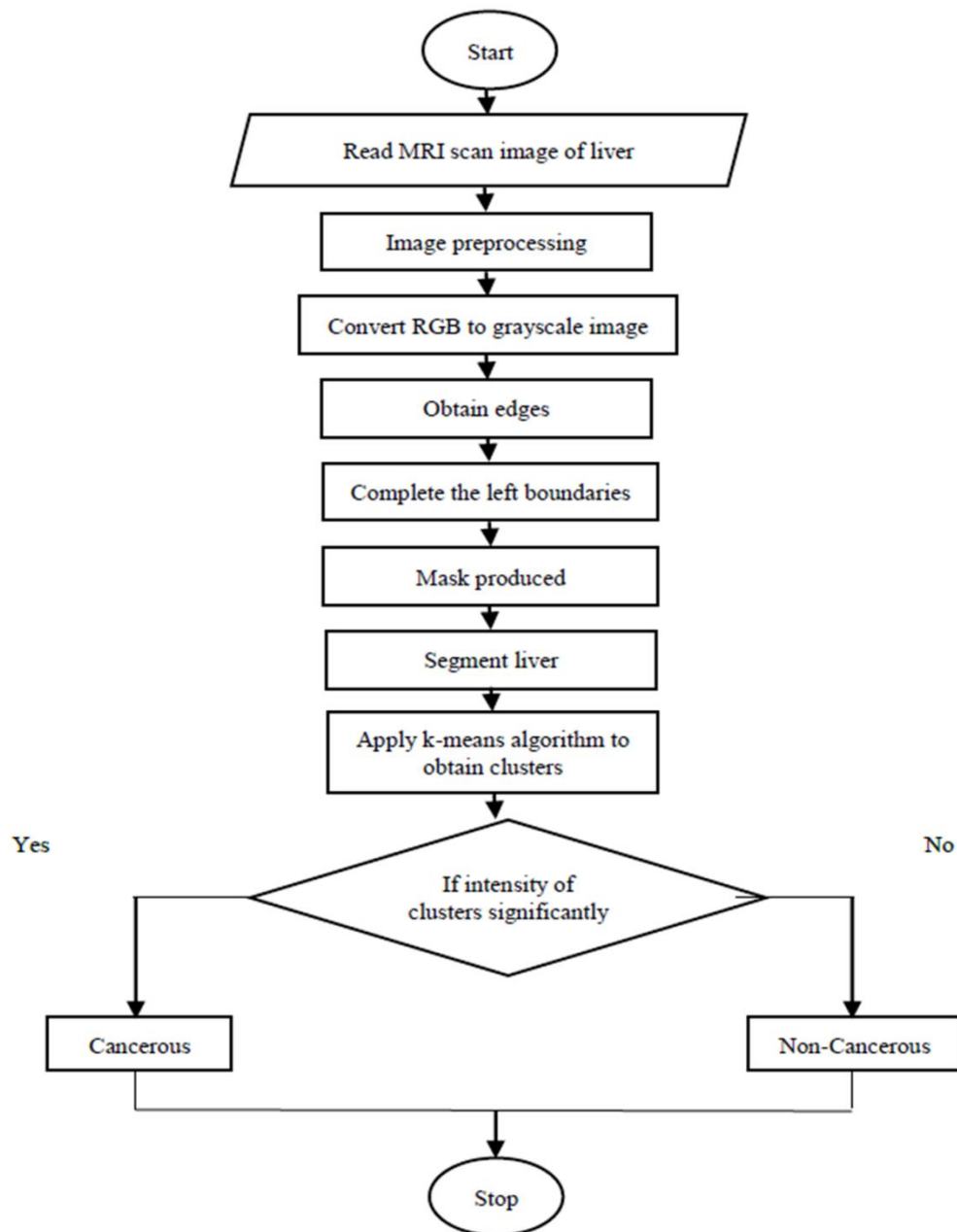


Figure 4.1 Flow chart of proposed Methodology

The flowchart starts with a box labeled "Start". The next box is labeled "Read MRI scan image of liver". This is followed by a box labeled "Image preprocessing". The image preprocessing step consists of three sub-steps:

- 1) Convert RGB to grayscale image
- 2) Obtain edges
- 3) Complete the left boundaries

After the image preprocessing is complete, a box labeled "Mask produced" is shown. Then, a box labeled "Segment liver" is shown. Here, the k-means algorithm is applied to obtain clusters to segment the liver.

The flowchart then branches into two paths, labeled "Yes" and "No". The "Yes" path leads to a box labeled "Cancerous", while the "No" path leads to a box labeled "Non-Cancerous". The final box in the flowchart is labeled "Stop".

Overall, the flowchart outlines a process for applying a lesion algorithm to a local center to analyze liver MRI scans to detect cancer

Artificial neural networks are used to automate cancer cell identification and further categorization in liver cancer, cyst, hemangioma, and adenoma. Artificial neural networks (ANNs), also known as neural networks (NNs), are computer structures that are loosely based on the biological neural networks that make up animal brains. The artificial neural network feedforward neural network was used in this study. It is made up of layers of neurons (nodes), such as input, hidden, and output layers. Nodes in neighboring layers have connections or edges connecting them. The input layer is made up of input nodes that provide information from the outside world to the network. This layer includes an MRI scan that is analyzed to

determine if it contains cancerous cells and, if so, further categorization. There are no direct relations between the hidden nodes and the outside world. They perform calculations and send data from the input nodes to the output nodes. While a feed forward network can only have one input layer and one output layer, a hidden layer is formed by a group of hidden nodes. A feed forward network may have zero or several hidden layers. Different masks are saved as hidden nodes in different hidden layers, and the expected edge is compared to all the masks stored in hidden layers, with the highest matching being chosen. The output nodes, collectively known as the “output layer”, are in charge of computing and distributing network information to the outside world. This layer automatically generates the segmented liver. Then, on a segmented liver, use the k-means clustering algorithm to predict the cancer-affected area. Tumor analysis and categorization were performed on the basis of statistical features into four categories: cyst, liver cancer, adenoma, and hemangioma.

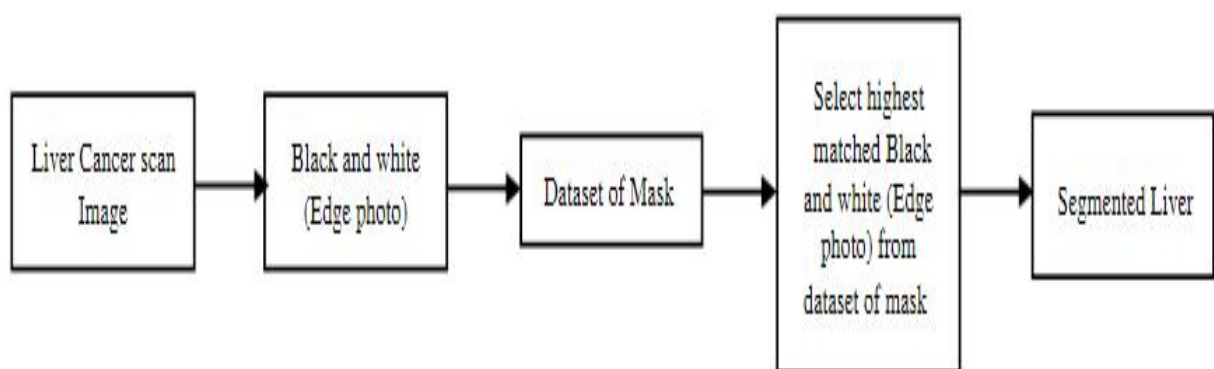


Figure 4.2 Automate Segmentation



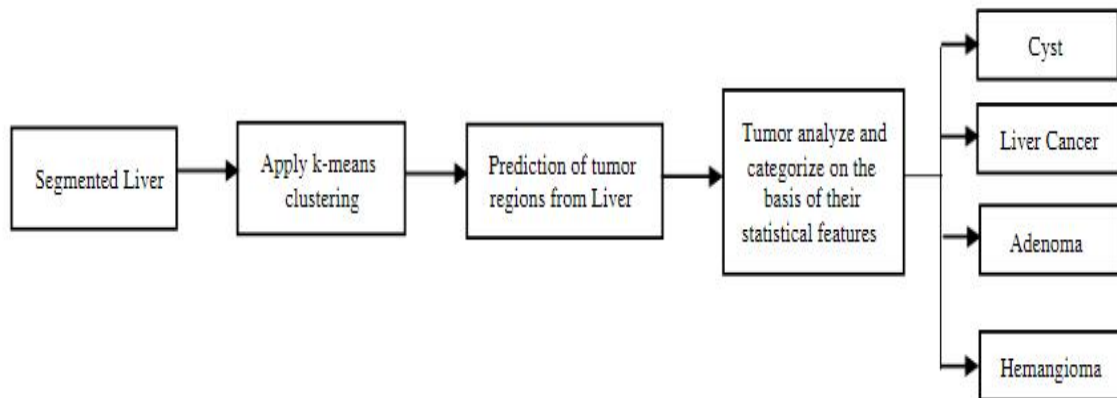


Figure 4.3 Tumour Categorization on the basis of Statistical Features

## 4.2. MODULE DESCRIPTION

### 1) Convert RGB to grayscale image

Converting an RGB image to grayscale means transforming a color image with red, green, and blue (RGB) channels into a single-channel image representing brightness or intensity. Our eyes perceive brightness differently for each color, so a simple conversion is needed.

Here's a breakdown of the conversion process:

**Assigning Weights:** Each color channel (red, green, blue) is assigned a weight based on its contribution to perceived brightness. A common formula uses 0.299 for red, 0.587 for green, and 0.114 for blue. These weights come from the NTSC standard, which approximates human perception of light intensity.

**Calculating Grayscale Value:** For each pixel in the RGB image, the red, green, and blue values are multiplied by their corresponding weights and

then summed up. This gives you a single grayscale value representing the overall brightness of that pixel in the original image.

**Replacing RGB with Grayscale:** The original RGB values for each pixel are replaced with this new grayscale value. This creates a new image with only one channel representing brightness variations, essentially removing color information.

Here's an analogy: Imagine a black and white photograph. It captures the light and shadow details (brightness) of the scene but lacks the color information present in a real-life scene. Converting an RGB image to grayscale achieves a similar effect in the digital world.

## **2) Obtain edges**

Obtaining edges in image processing refers to identifying the boundaries between different objects or regions in an image. These edges represent sudden changes in pixel intensity, often corresponding to where objects meet or where there's a significant shift in brightness or color.

Here's a deeper explanation of how edge detection works:

**Identifying Intensity Changes:** Edges are essentially locations in the image where the brightness or color values of neighboring pixels change drastically. Algorithms look for these significant differences between pixels.

**Filters and Kernels:** Image processing uses filters (small matrices called kernels) to analyze pixel neighborhoods. As the filter slides across the image, it compares the values of pixels within its area.

### 3)Complete the left boundaries

In the context of this liver MRI analysis flowchart, "complete the left boundaries" refers to a specific step within the image preprocessing stage. It's likely addressing a potential issue with the MRI scan itself, rather than a general image processing technique.

Here are two possible interpretations:

**Addressing Missing Data:** MRI scans can sometimes have artifacts or missing data, especially near the edges of the image. This might be due to factors like patient movement or limitations of the scanning technique. "Completing the left boundaries" could involve techniques to fill in these missing regions on the left side of the liver specifically.

Here are some possible methods for completing missing data:

**Mirroring:** The system might mirror the existing data on the right side of the liver to fill the gaps on the left. This assumes the left and right sides are symmetrical, which might not always be the case.

**Inpainting:** More sophisticated techniques like inpainting can analyze the surrounding image data and statistically infer what the missing information might be. This creates a more realistic reconstruction of the missing boundaries.

**Intensity Inhomogeneity Correction:** Liver MRIs can sometimes exhibit intensity inhomogeneity, where the signal strength (brightness) varies across the image. This can be caused by factors like the magnetic field of the

scanner not being perfectly uniform. "Completing the left boundaries" could be a step to address this specifically on the left side.

#### **4)Mask produced**

The mask produced in this study serves as a crucial step in the image processing pipeline for liver tumor detection. It is generated through liver segmentation preprocessing, using edge detection techniques followed by manual marking to ensure continuity. This mask plays a pivotal role in distinguishing relevant regions, enabling accurate analysis and classification of tumor areas.

#### **5)Segment Liver**

The segmentation process in the study focuses on isolating the liver region from the MRI scan images, a critical step in subsequent analysis to detect and classify potential cancer cells. Through segmentation, the liver area is delineated from surrounding tissues, allowing for targeted examination. This step is essential as it helps reduce the complexity of the image and provides a clear focus for further analysis. Various image processing techniques are likely employed during segmentation, such as thresholding, region growing, or edge detection, depending on the characteristics of the images and the specific requirements of the study. Once the liver region is successfully segmented, it becomes the primary area of interest for subsequent steps, including cancer cell detection and characterization. The accuracy and precision of liver segmentation directly impact the effectiveness of the overall analysis, making it a crucial aspect of the study's methodology.

## Liver Segmentation

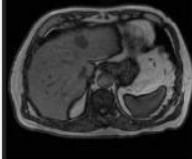

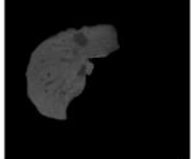
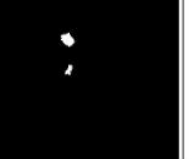

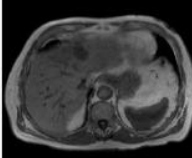

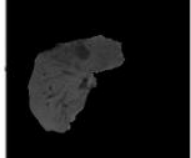


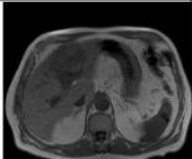

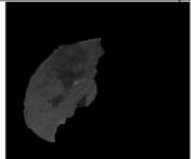


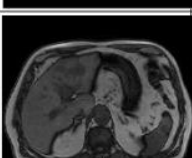

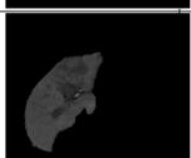


Sr.No	Original Image	Mask	Liver	k-means segmentation	Extracted feature
1					
2					
3					
4					

Figure 4.4 Liver Segmentation

### 6)Apply k-means algorithm to obtain clusters

The application of the K-means algorithm plays a pivotal role in the process of identifying and categorizing regions within the segmented liver images obtained from the MRI scans.

The K-means algorithm is a popular unsupervised clustering technique used extensively in image processing and pattern recognition tasks. Its primary objective is to partition a dataset into K clusters, where each data point belongs to the cluster with the nearest mean, serving as the prototype of the cluster.

In the context of liver tumor detection, the K-means algorithm is applied to the segmented liver images to group pixels with similar characteristics together,

effectively creating clusters representing different regions or structures within the liver. These clusters can then be analyzed to distinguish between tumor and non-tumor areas based on variations in pixel intensity, texture, or other relevant features.

By iteratively assigning pixels to clusters and updating the cluster centroids based on the mean values of the assigned pixels, the K-means algorithm converges to a stable solution where the clusters represent meaningful partitions of the image data. This process enables the identification of tumor regions as distinct clusters exhibiting characteristic features associated with cancerous tissue, such as abnormal texture, shape, or intensity.

Overall, the application of the K-means algorithm facilitates the automated segmentation and classification of liver tumor regions within the MRI images, providing valuable insights for medical diagnosis and treatment planning.

If the intensity of clusters significantly differs, it implies that there are distinct regions or structures within the segmented liver images with varying pixel intensities. In the context of liver tumor detection:

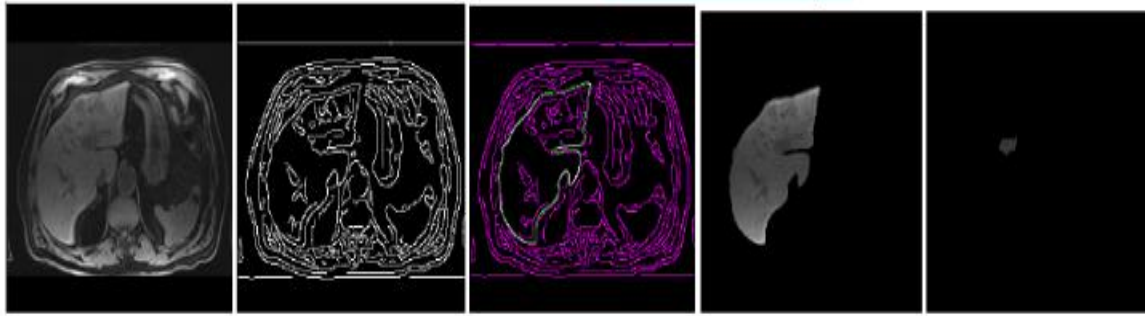
**1. Intensity Clusters(YES):** These clusters may correspond to areas of the liver that exhibit abnormal pixel intensities, potentially indicating the presence of tumor tissue. Higher intensity clusters could represent regions with elevated levels of contrast enhancement, irregular texture, or other characteristics associated with cancerous growth.

**2. Intensity Clusters(NO):** Conversely, lower intensity clusters may correspond to normal liver tissue or non-tumor areas. These clusters could represent regions with uniform pixel intensities, regular texture patterns, and similar characteristics commonly observed in healthy liver tissue.

## **CHAPTER 5**

### **IMPLEMENTATION AND RESULT**

- ✓ Cancer detection remains a challenging task due to its multidisciplinary nature and dependence on various parameters.
- ✓ A novel method for early cancer detection is proposed, which is precise, time-efficient, and simple to calculate.
- ✓ MRI scan dataset from the TCGA database is utilized after liver segmentation preprocessing.
- ✓ Masks for all images are generated using edge detection, followed by manual marking to ensure continuity.
- ✓ Kmeans clustering algorithm is employed for distinguishing cancerous from non-cancerous regions.
- ✓ Statistical analysis involves Skewness, Kurtosis, Energy, Entropy, Standard deviation, Eccentricity, and Circularity.
- ✓ Hemangioma shows highest values for Skewness, Entropy, and Standard deviation, with lowest Energy and Circularity.
- ✓ Liver cancer exhibits highest Energy and lowest Entropy, indicating mildness and less gray color.
- ✓ Adenoma has the smallest Skewness value, indicating irregular and non-homogeneous texture.
- ✓ Cyst demonstrates highest Circularity, while Hemangioma has lower Circularity.
- ✓ Liver cancer has highest Eccentricity, resembling a line segment, while Adenoma has lowest Eccentricity, resembling a circle.
- ✓ Artificial neural network algorithm is utilized for automatic tumor prediction in MRI scans.
- ✓ Real-time MRI scans are fed into the neural network for liver segmentation, followed by comparison with hidden layer masks.



5.1 Working of Proposed Model

## 5.1 REQUIREMENTS.TXT

The following packages were installed by using command  
**!pip install -r requirements.txt**

- Flask
- Tensorflow
- Tensorflow text
- Tensorflow hub
- Sklearn
- Matplotlib
- Numpy
- Pandas
- Spacy

## 5.2 IMPLEMENTATION

### 5.2 .1 MODEL.PY

```
import os
import numpy as np
import tensorflow as tf
from tensorflow.keras import layers, models
import nibabel as nib
```

```
def build_generator(latent_dim):
    model = models.Sequential()
    model.add(layers.Dense(128 * 7 * 7, input_dim=latent_dim))
    model.add(layers.LeakyReLU(alpha=0.2))
```



```

    model.add(layers.Reshape((7, 7, 128)))
    model.add(layers.Conv2DTranspose(128, (4,4), strides=(2,2),
padding='same'))
    model.add(layers.LeakyReLU(alpha=0.2))
    model.add(layers.Conv2DTranspose(128, (4,4), strides=(2,2),
padding='same'))
    model.add(layers.LeakyReLU(alpha=0.2))
    model.add(layers.Conv2D(1, (7,7), activation='tanh', padding='same'))
    return model

```

```

def build_discriminator(input_shape):
    model = models.Sequential()
    model.add(layers.Conv2D(64, (3,3), strides=(2,2), padding='same',
input_shape=input_shape))
    model.add(layers.LeakyReLU(alpha=0.2))
    model.add(layers.Dropout(0.4))
    model.add(layers.Conv2D(128, (3,3), strides=(2,2), padding='same'))
    model.add(layers.LeakyReLU(alpha=0.2))
    model.add(layers.Dropout(0.4))
    model.add(layers.Flatten())
    model.add(layers.Dense(1, activation='sigmoid'))
    return model

```

```

def build_gan(generator, discriminator):
    discriminator.trainable = False
    model = models.Sequential()
    model.add(generator)
    model.add(discriminator)
    model.compile(loss='binary_crossentropy', optimizer='adam')
    return model

```

```

def load_nifti_files(data_dir):
    nii_files = []
    for root, dirs, files in os.walk(data_dir):
        for file in files:
            if file.endswith(".nii"):
                nii_files.append(os.path.join(root, file))
    return nii_files

```

```
def read_nifti(filepath):
    ct_scan = nib.load(filepath)
    array = ct_scan.get_fdata()
    array = np.rot90(np.array(array))
    return array
```

```
data_dir = '../input/liver-tumor-segmentation'
real_images = [read_nifti(file) for file in load_nifti_files(data_dir)]
```

```
img_shape = real_images[0].shape
latent_dim = 100
```

```
discriminator = build_discriminator(img_shape)
discriminator.compile(loss='binary_crossentropy', optimizer='adam',
metrics=['accuracy'])
```

```
generator = build_generator(latent_dim)
```

```
gan = build_gan(generator, discriminator)
```

```
# Training loop
```

```
def train_gan(generator, discriminator, gan, real_images, latent_dim,
n_epochs=100, batch_size=128):
    for epoch in range(n_epochs):
        for i in range(0, len(real_images), batch_size):

            real_batch = real_images[i:i+batch_size]
            fake_images = generator.predict(tf.random.normal(shape=(batch_size,
latent_dim))))
            X_real, y_real = np.array(real_batch), np.ones((len(real_batch), 1))
            X_fake, y_fake = fake_images, np.zeros((batch_size, 1))
            d_loss_real = discriminator.train_on_batch(X_real, y_real)
            d_loss_fake = discriminator.train_on_batch(X_fake, y_fake)
            d_loss = 0.5 * np.add(d_loss_real, d_loss_fake)
```

```
noise = tf.random.normal(shape=(batch_size, latent_dim))
```

### 5.2.2 TRAIN.PY

```
file_list = []
for dirname, _, filenames in os.walk('liver-tumor-segmentation'):
    for filename in filenames:
        # print(os.path.join(dirname, filename))
        file_list.append((dirname,filename))

for dirname, _, filenames in os.walk('liver-tumor-segmentation-part-2'):
    for filename in filenames:
        file_list.append((dirname,filename))

df_files = pd.DataFrame(file_list, columns =['dirname', 'filename'])
df_files.sort_values(by=['filename'], ascending=True)
# Map CT scan and label

df_files["mask_dirname"] = "" ; df_files["mask_filename"] = ""

for i in range(131):
    ct = f"volume-{i}.nii"
    mask = f"segmentation-{i}.nii"

    df_files.loc[df_files['filename'] == ct, 'mask_filename'] = mask
    df_files.loc[df_files['filename'] == ct, 'mask_dirname'] = "liver-tumor-
segmentation/segmentations"

df_files_test= df_files[df_files.mask_filename==""]
# drop segment rows
df_files = df_files[df_files.mask_filename !=
"].sort_values(by=['filename']).reset_index(drop=True)
print(len(df_files))
df_files
#df_files_test
def read_nii(filepath):
    """
    Reads .nii file and returns pixel array
    """
    ct_scan = nib.load(filepath)
    array = ct_scan.get_fdata()
    array = np.rot90(np.array(array))
    return(array)
```

### 5.2.3 SERVER.PY

```
from flask import Flask, request, jsonify, send_file
from tensorflow.keras.models import load_model
import numpy as np
from PIL import Image
import os
from flask_cors import CORS

app = Flask(__name__)
CORS(app)

# Define the custom metric function
def dice_coefficient(y_true, y_pred):
    smooth = 1.0 # Smoothing factor to avoid division by zero
    intersection = tf.reduce_sum(y_true * y_pred)
    union = tf.reduce_sum(y_true) + tf.reduce_sum(y_pred)
    dice = (2.0 * intersection + smooth) / (union + smooth)
    return dice

# Register the custom object
custom_objects = {'dice_coefficient': dice_coefficient}

# Load the trained model
model = load_model('fcn_model.h5', custom_objects=custom_objects)

# Define input shape expected by the model
input_shape = (128, 128, 3) # Update this according to your model's input
shape

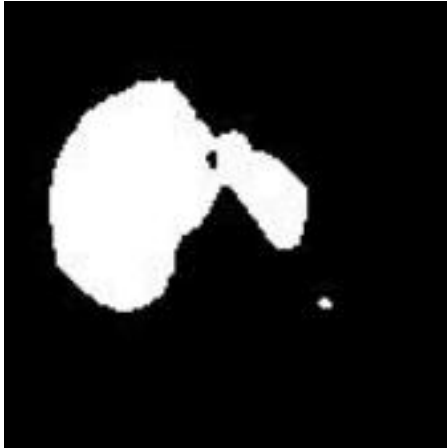
@app.route('/upload', methods=['POST'])
def upload():
    # Check if the request contains a file
    if 'file' not in request.files:
        return jsonify({'error': 'No file provided'}), 400

    # Get the file
    image_file = request.files['file']

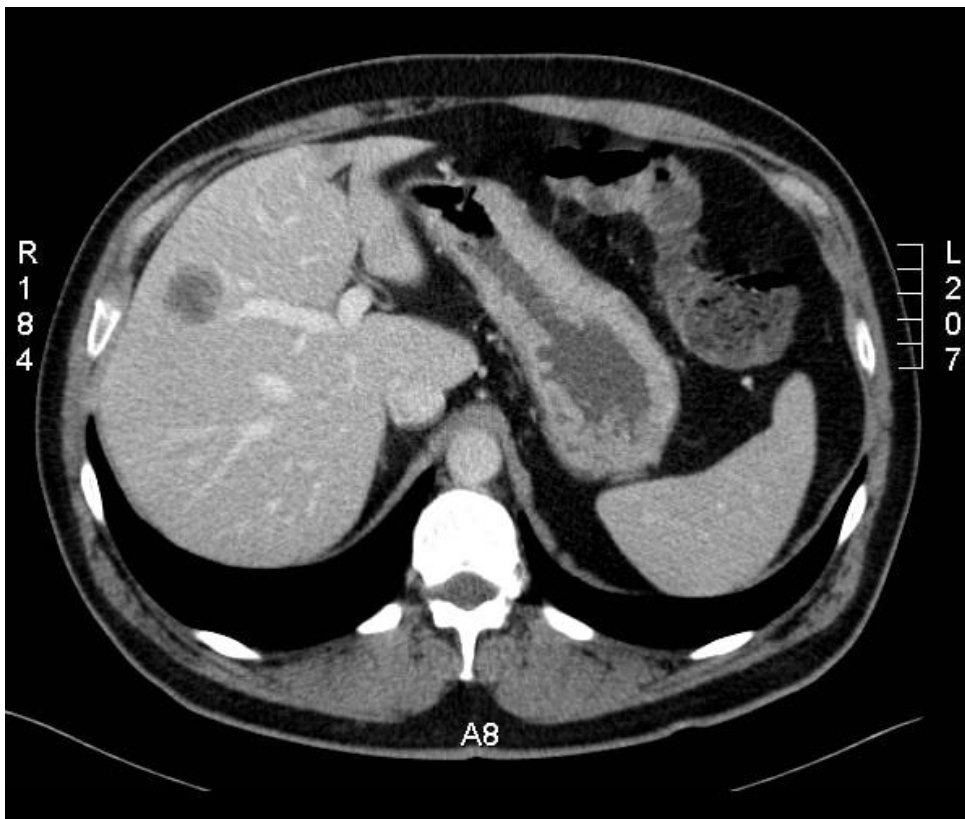
    # Save the file temporarily
    image_file_path = 'temp.jpg'
```

### 5.3 RESULTS

#### Predicted tumour mask



#### Test image



Tumour Present : Yes

Tumour Type : Type-2(Adenoma)

# **CHAPTER 6**

## **CONCLUSION**

Liver segmentation is a difficult task, and automating it is even more difficult, as it involves several steps such as preprocessing, segmentation, and classification. The analogous intensities of other organs such as the spleen, flesh, and muscles are all considered during preprocessing. The artificial neural network algorithm aids in the solution of this problem, automating it through the use of edge and manual marking to create a continuous edge system. The average accuracy rate of the whole liver segmentation using the artificial neural network algorithm is 0.9 percent. Furthermore, an automated method is being developed to identify tumors as benign or malignant, as well as a method to classify perpetual objects using features. It is self-evident that an automated method for classifying tumors as benign or malignant can be useful in object recognition, especially when dealing with medical imaging issues. In addition, a new classification for liver tumors is being considered, which includes more forms of benign liver lesions such as hemangioma, cyst, and adenoma.

# CHAPTER 7

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