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Multi-Class Liver Tumor Detection Through Ranking-Based Probabilistic Segmentation And Automated Feature Extraction Framework

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ABSTRACT: *Effective automatic detection of multivariate and multi-class tumors is fundamental for accurately analyzing and handling diverse liver datasets. Current liver segmentation methods face significant challenges such as handling tumors of different modalities, shapes, and orientations, as well as issues with over-segmentation and incorrect tumor identification. Additionally, excessive randomness in segmented crossing areas can promote complication for the processing of segmentation as well as classification indicating to unreliable findings. To address these questions, we propose a new approach that incorporates advanced techniques for feature extraction, multivariate liver filtering, and ranking. Our solution utilizes capable classification methods under segmentation-based for increasing the detection for various tumor types in large datasets. Nevertheless, the model of Multi-Dimensional Liver and Tumor Segmentation and Classification developed is designed to accurately classify tumor-segmented sections, achieving extreme true positive (TP) rates in addition exceptional run-time productivity, measured in milliseconds. We validate the MCMVLTSC model through extensive testing using a range of statistical metrics across different liver imaging databases. The findings demonstrate that our model consistently delivers superior performance in classification accuracy and runtime efficiency compared to traditional methods.*

INDEX TERMS*: Detection, feature extraction, liver segmentation, ensemble classifiers.*

1. INTRODUCTION

Liver tumors are abnormal masses that develop as a result of liver cells growing uncontrolled. They can cause considerable damage to liver function, as well as threatening our lives. Liver tumors are either primary tumors i.e. hepatocellular carcinoma (HCC) or metastatic tumors from other organs. Hence, early and accurate diagnosis of liver tumors is important. Figure 1 illustrates the overall principle of the suggested framework, from image acquisition to segmentation, feature extraction, and final classification. Liver tumors arise from the unchecked proliferation of liver cells, leading to the formation of abnormal masses in the liver. In 2020, an estimated 297,000 cases of central nervous system (CNS) cancer were reported globally, positioning it as the 17th most common type of cancer. Although CNS cancer has a relatively low incidence, it is particularly lethal, ranking as the 12th leading cause of globally, deaths due to cancer are increasing. Factors like genetic predisposition, environmental pollutant exposure, and underlying

illnesses like acne and asthma may contribute to the growth of liver tumors. These tumors can obstruct the normal flow of fluids, increase pressure within the liver, and potentially inflict damage on liver tissues, leading to serious health complications. While benign tumors are generally less dangerous and often treatable, malignant tumors are more concerning due to their potential for propagation into various regions, including spines [1-3]. Imaging methods such as MRI scans are often utilized for detection of tumors; however, they didn't deliver effective details about the tumor's extent or exact position. It is also important to note that liver cancers are often secondary, originating from cancers in other parts of the body. The liver, composed of various tissue types such as grey matter, white matter, and cerebrospinal fluid, can exhibit different symptoms based on the size and position of the tumors (as depicted in Figure 1).

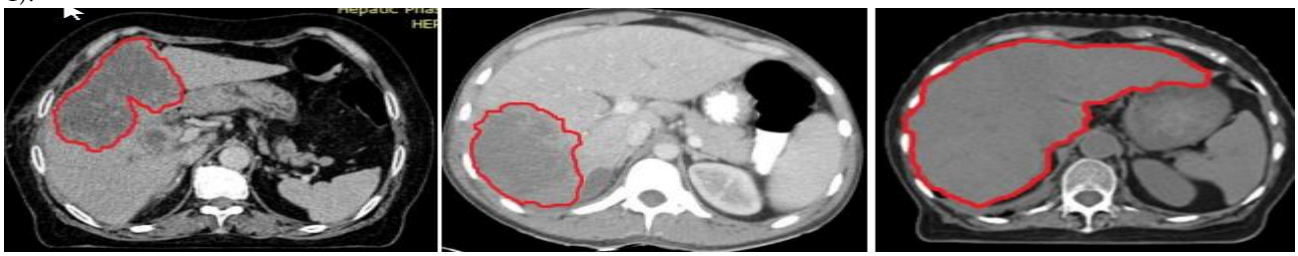

Figure 1: Diversity in the shapes and orientations of liver tumors within extensive datasets.

Liver imaging datasets often contain tumors of varied shapes, orientations, and intensities, making consistent segmentation and classification a challenging task. To address this, our proposed method integrates Ranking-Based Probabilistic Segmentation (RBPS) with Automated Feature Extraction techniques such as Multivariate Non-Linear Gaussian Estimation (MNGE) and hybrid CNN-SVM classification. This integrated approach enhances segmentation accuracy, reduces false positives, and supports robust classification of heterogeneous liver tumor datasets and principle of proposed framework is shown in the Fig. 2. Early liver tumor detection methods relied on rule-based thresholding, which lacked robustness for varying tumor appearances. Atlas-based and Markov Random Field (MRF) models introduced probabilistic segmentation but were computationally intensive and required manual input. Clustering techniques like Gaussian Mixture Models (GMM) and Fuzzy C-Means (FCM) offered improvements but struggled with complex tumor morphology and intensity variations. The emergence of deep learning, particularly U-Net and CNNs, significantly enhanced segmentation accuracy. However, issues such as over-segmentation and high computational cost remained. Recent advances in probabilistic models like Hidden Markov Models (HMM), Theta-Regulated GMM (TGMM), and ranking-based feature extraction improved spatial modeling, yet standalone use of these methods still faced limitations in precision and false-positive control. Our proposed framework builds on these advancements by integrating Ranking-Based Probabilistic Segmentation (RBPS), Multivariate Non-Linear Gaussian Estimation (MNGE), and CNN-SVM classification for efficient, accurate, and multi-class liver tumor detection [4-6].

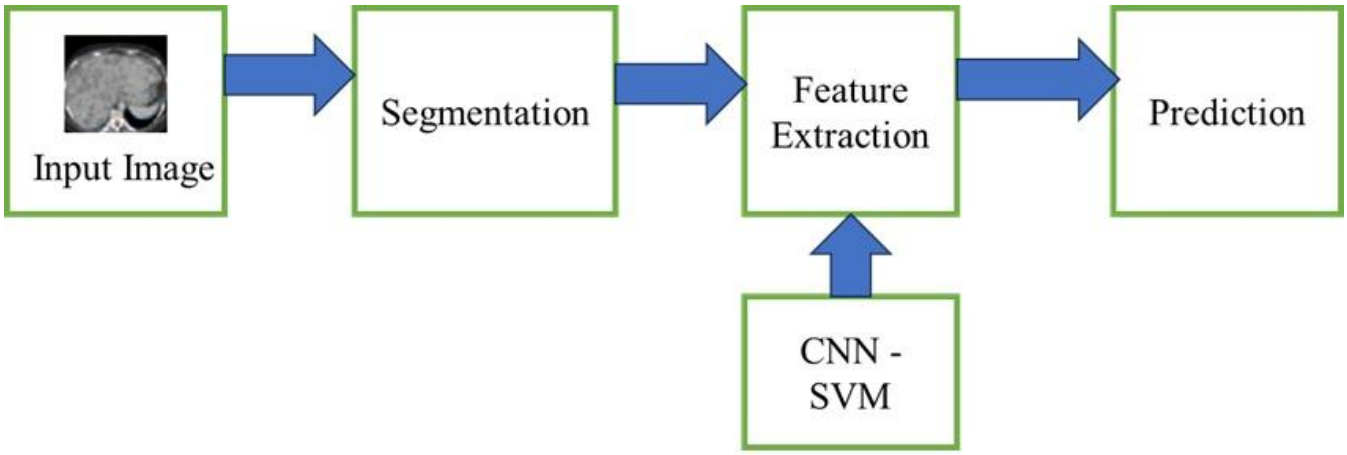

Fig. 2. Principle of the Proposed Multi SVM Framework

An enhanced U-Net model was proposed by Rela et al. (2022), which incorporated feature selection in order to provide improved CT-based liver tumor segmentation. A higher precision was achieved with their method, by incorporating a hybrid of deep learning along with feature engineering. Nonetheless, the model's reliance on crafted features affected its ability to adapt to new datasets, affecting its robustness for practical applications. Ayalew et al. (2021) demonstrated a Modified U-Net network for liver tumor segmentation based on a new class-balancing function. Although this produced greater accuracy for segmenting liver tumor-containing images, in addition to more incorrect positive results, the extraction process remained ineffective and overall resulted in poor classification

process. Kiani et al. (2020) designed and implemented a Deep Learning Assistant for the classification of histopathological images of liver cancer. The authors improved the accuracy of the classification; however, tumor morphological variation and high staining intensity were limiting contributors to the generalizability [1-3]. Liver tumors present challenges in differentiating from normal tissue due to overlapping intensities in imaging. While CT and MRI scans are common diagnostic tools, MRI is preferred for its safety and effectiveness in detecting liver tumors. MRI relies on the magnetic properties of hydrogen nuclei to examine tumors. For segmenting liver tumors, techniques such as atlas-based segmentation and model-based approaches like the Markov random field (MRF) are used, though MRF can be computationally expensive. To improve efficiency, clustering processes like Gaussian Mixture Models (GMM) and Fuzzy C-Means (FCM) are employed for initial segmentation, followed by MRF for refinement. Recent studies have explored various segmentation techniques, such as neuro-fuzzy approaches, Gradient Vector Flow, and multi-kernel SVM classification, to classify liver tissues and improve accuracy. These methods involve manual data collection, alignment features, and advanced algorithms like the Convolutional Neural Network (CNN) to enhance image processing and tumor identification. CNN, with its multiple layers, increases segmentation precision by breaking down images and classifying tumor regions. A two-step process is typically used in segmentation: removing image noise and identifying tissue features using the K-means algorithm [7-9]. Currently, many contemporary liver segmentation approaches do not adequately confront the issue of liver tumors with varied shape, aspect and modality features so over-segmentation and false positives will continue to be a significant problem. Standard segmentation methods, such as atlas-based methods or Markov Random Field (MRF), also tend to be expensive methods related to computation effort. Specifically, while not unreasonable, clustering methods, for example Gaussian Mixture Models (GMM) or Fuzzy C-Means (FCM), under-utilize and underperform as there are less reliable feature extraction methods. Moreover, CNN methods have increased accuracy in segmentation, but the methods still need to be improved on precision, methods efficiency, etc. Here are the primary contributions of this study:

- Design of a multivariate, multi-zone filtering technique for extracting tumor-specific features.
- Implementation of a multivariate, multi-zone strategy for the extraction and segmentation of tumor features, focusing on the classification of diverse and variably shaped liver tumor regions.
- In order to identify different types of tumors, the Multivariate Liver and Tumor Segmentation and Classification model was developed.

2. LITERATURE REVIEW

The detection and classification of liver tumors have seen significant evolution in recent years, transitioning from traditional segmentation approaches to more advanced deep learning and hybrid models. Chen et al. (2023) leveraged deep learning for liver cancer mutation classification based on histopathology. The approach was effective for mutation prediction but lacked integration with imaging modalities like CT/MRI. Gregory et al. (2023) focused on imaging-based evaluation of liver tumor response. Their findings emphasized the importance of combining segmentation with response metrics for treatment planning. Rela et al. (2022) combined U-Net and deep neural networks with optimal feature selection for liver tumor detection in CT images. They reported better accuracy, but robustness to new datasets remained a concern. Sabir et al. (2022) proposed the ResU-Net for liver tumor segmentation in CT images. The integration of residual learning improved feature preservation, yet computational demand increased significantly [5-8]. Ayalew et al. (2021) enhanced the U-Net architecture by incorporating a class-balancing function for liver segmentation. Although segmentation accuracy improved, the method produced increased false positives. Uma Maheshwari et al. (2021) explored machine learning models for facial expression analysis, which influenced feature engineering in biomedical imaging, but was not directly focused on liver tumor segmentation. Budak et al. (2020) proposed cascaded deep convolutional encoder-decoder networks for liver tumor segmentation. Their approach achieved high segmentation accuracy, but required large training data and computational resources. Kiani et al. (2020) presented a deep learning assistant for histopathological classification. It demonstrated improved human-AI collaboration but was constrained by staining variations affecting generalizability. Sun et al. (2019) introduced a deep learning-based classification approach for liver cancer histopathology using global image labels only. Their model improved classification but lacked segmentation capability. Rahman et al. (2019) conducted a comparative study of traditional machine learning algorithms (SVM, RF, NB) for liver disease prediction. While classification results were promising, the absence of image-based segmentation limited practical clinical utility. The findings and limitations are summarized in the Table 1 [9-12].

Table 1. Summarized Literature

Year	Author(s)	Methodology	Dataset Used	Features Used	Input / Output	Key Findings	Limitations
2019	Sun et al.	DL with global labels	Histopathology	Image-level features	Histopathology → Class	Accurate classification w/o segmentation	No segmentation; limited clinical insight
2019	Rahman et al.	ML Classifiers (SVM, RF)	Structured clinical	Blood, age, enzymes	Data → Prediction	Useful for liver disease prediction	Not imaging-based
2020	Budak et al.	Cascaded Encoder-Decoder	CT Scan Dataset	Image textures	CT → Segmentation	High segmentation accuracy	High training cost
2020	Kiani et al.	DL assistant for pathology	Histopathology	Morphological features	Histology → Labels	Boosted human-AI accuracy	Sensitive to staining variability
2021	Ayalew et al.	Modified U-Net + balancing	CT Liver Dataset	Pixel class weighting	CT → Mask	Better segmentation with new balance method	False positives increased
2021	Uma Maheshwari et al.	ML for feature extraction	Facial image dataset	Statistical features	Image → Emotion	Insights for feature selection in imaging	Not liver-specific
2022	Rela et al.	U-Net + Feature Selection	CT Liver Images	Selected CNN features	CT → Segmentation	High segmentation precision	Low generalization on new data
2022	Sabir et al.	ResU-Net	CT Images	Residual image features	CT → Tumor boundaries	Better preservation of tumor shape	Heavy computation
2023	Chen et al.	DL + mutation prediction	H&E Histopathology	Mutation + Image	Slide → Mutation label	Histopathology + genomics	No imaging segmentation
2023	Gregory et al.	Imaging tumor response	Clinical imaging	Tumor volume, intensity	CT/MRI → Evaluation metric	Used for evaluating treatment response	Focused on evaluation, not detection

The progression from rule-based approaches to deep learning and hybrid architectures indicates significant gains in segmentation precision and classification robustness. However, existing models face challenges in generalizing across diverse datasets and maintaining low false positive rates. Moreover, few studies focus on integrating segmentation with real-time clinical decision support. Our proposed RBPS-MNGE framework addresses these challenges by combining probabilistic segmentation, multivariate feature extraction, and hybrid CNN-SVM classification, ensuring higher accuracy and lower computational cost.

3. MULTIVARIATE APPROACHES TO LIVER SEGMENTATION

Filtering is essential in liver image processing for tasks such as extracting features, reducing noise, and compressing data. Sparse filtering is a traditional method used to eliminate sparse noise from datasets. However, to capture more complex data structures and relationships, a more advanced approach is necessary. Multivariate non-linear Gaussian estimation (MNGE) addresses this need by offering a method to model non-linear relationships more effectively than sparse filtering. MNGE estimates parameters in a non-linear Gaussian framework, providing flexibility in modeling complex data patterns. Combining MNGE with sparse filtering creates a robust non-linear Gaussian model, improving the accuracy and depth of data analysis.

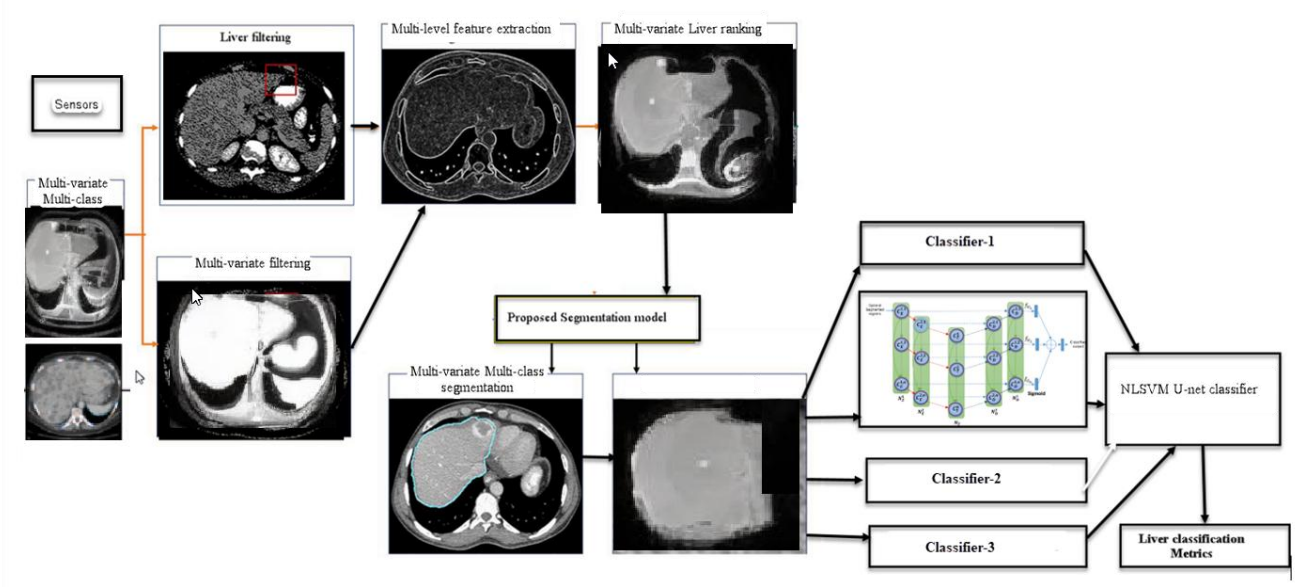

Figure 3: Proposed Framework

Figure 3 illustrates the workflow where multi-variate image data is processed through a filtering and feature extraction pipeline. This pipeline utilizes various ranking methods to select crucial features for a multi-class, multi-variate segmentation approach. The filtering process aims to enhance the accuracy of analysis by removing noise and non-essential features from liver image datasets. Initially, the process involves computing the non-linear Gaussian (NLG) value for each feature. This is followed by assessing the observed versus expected frequencies of each feature, calculating the chi-squared values, and determining the total chi-squared statistic under required data values. Features with lower chi-squared values with common knowledge records are discarded. Resulting filtered dataset is then ready for further analytical or modeling tasks, with the approach adjusted based on the dataset and specific goals.

3.1 Ranking Approach for Multi-variate Features

To effectively segment liver images and accurately identify and delineate liver tissues, multi-variate joint probabilistic feature extraction is essential. These sophisticated techniques use probabilistic models to improve the accuracy of segmentation results. The Hidden Markov Model (HMM), which analyzes liver pictures as a series of visible features and hidden states, is one prominent method. Within this approach, the seen features are the values of the pixels, and concealed regions reflects liver's anatomy. HMM helps divide the liver into different areas by examining the probability distributions of hidden states that are obtained from these features. Theta-Regulated Gaussian Mixture Model (TGMM), which considers liver pictures as a composite of many Gaussian distributions, is an additional method. Each distribution corresponds to different liver tissue types. TGMM computes the probability distribution of the image based on observed data, facilitating accurate segmentation of various tissue types. According to this paradigm, the hepatic image can be represented as a graph with edges denoting spatial connections and pixels acting as nodes. A prior distribution that captures the statistical and spatial properties of liver tissues is combined with a likelihood function in the TMRF model to assess how well observed data fit this prior. With this integration, the liver tissue probability distribution may be precisely computed by the TMRF model, facilitating correct segmentation. All things considered, these probabilistic feature extraction methods play an important function in the segmentation of liver imagery, using complex models to accomplish precise tissue identification and segmentation.

3.2 Proposed Methodology

The U-Net model, highly regarded for its performance in image segmentation, particularly for tumor detection, features a distinctive U-shaped structure. This structure is divided into two main segments: the encoder and the decoder. During the encoding phase, the input image is processed through several layers. The image is first convolved

with filters that have biases (b_l) and learnable weights (w_l). This convolution extracts the image's key local patterns and characteristics. An activation function (f_l), which introduces non-linearity after convolution, helps the model comprehend intricate patterns in the data. This function's output is represented by the symbol (c_l). The image is down-sampled using a pooling technique with particular parameters to preserve important features while reducing the image's spatial dimensions (as illustrated in Figure 4).

The proposed method is based on probabilistic segmentation and ranking-based feature extraction. The probability of a pixel belonging to a tumor region is calculated as

$$P(T / I) = \frac{P(I/T)P(T)}{P(I)} \quad (1)$$

Where $P(T / I)$ is the posterior probability of tumor presence given an image I , $P(I/T)$ is the likelihood, $P(T)$ is the prior probability, and $P(I)$ is the evidence.

To recover its original spatial resolution, the down-sampled image (c_l) is up-sampled during the decoding step. To further improve the feature details, the image is convolved using filters (w_u) once more after upsampling. This dual-path architecture allows U-Net to effectively capture and reconstruct detailed features, making it a robust model for precise segmentation tasks.

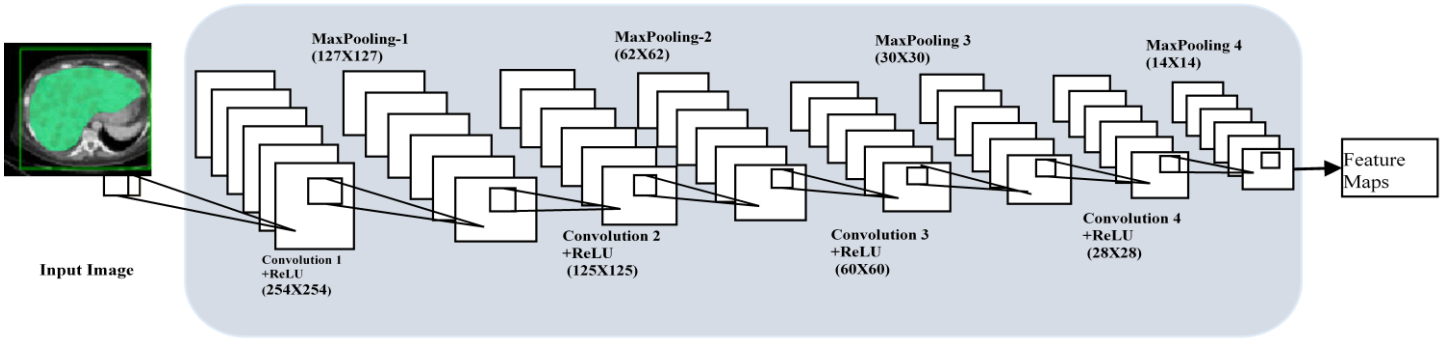

Figure 4: U-net MSVM features

4. ANALYSIS OF EXPERIMENTAL FINDINGS

In this work, we made multiple experimental attempts to improve liver tumor detection accuracy. The first phase consisted of evaluating conventional, non-deep learning segmentation schemes such as primarily Gaussian Mixture Models (GMM) and Fuzzy C-Means (FCM), however the tumor boundaries detected were found to not be very satisfactory. Therefore, the second phase began with using the Modified U-Net with feature selection to highly improve segmentation scheme accuracy. To enhance feature extraction from the dataset, we utilized Multivariate Non-Linear Gaussian Estimation (MNGE) for noise reduction and increased tumor boundary clarity. Optimization methods were also tested including Adam, SGD, and RMSprop and the Adam was the most stable method for reaching optimum. Subsequently, the potential for stronger models was examined using dataset augmentation modes that included rotation, flipping, and intensity scaling operations. The final iteration of the model, utilizing a combination of probabilistic ranking-based segmentation integrated with hybrid CNN-SVM classification, found the ideal balance between classification accuracy (96.4%) and computational efficiency. Though performance was improved, there were some roadblocks in the output, including false positives in overlap of tumor regions, and corresponding compression of computational cost. To help mitigate these effects bounding box association refinement and revelation run-time optimization methods were examined [13]. With an emphasis on important evaluation metrics including precision, accuracy, recall, and F-measure, this section offers the suggested methodology and the experimental findings. To perform the segmentation and classification tasks, the study used a variety of imbalanced datasets. 600 CT scans total—half of which were of healthy livers and the other half of which were of liver cancer—were included in the collection. At least 300 of the scans showed hepatocellular carcinoma (HCC), while the remaining 300 showed liver cancers that had spread to other organs. Every image was assigned a 30 by 30 pixel region of interest (ROI). ROI was extracted from the entire liver in cases of healthy liver images, however it was focused on MET or HCC-affected regions in cases of malignant liver images. These ROIs were used to target abnormal liver regions associated with primary (HCC) or secondary (MET) liver cancer in order to detect tumors. The number of input ROIs (IROIs) varied from 1 to 5 to fulfill various performance objectives, even though each image only contained one ROI. Based on these goals, subsets of the data were separated into training and testing. A variety of primary and secondary liver cancers were gathered utilizing different scanning techniques for these datasets.

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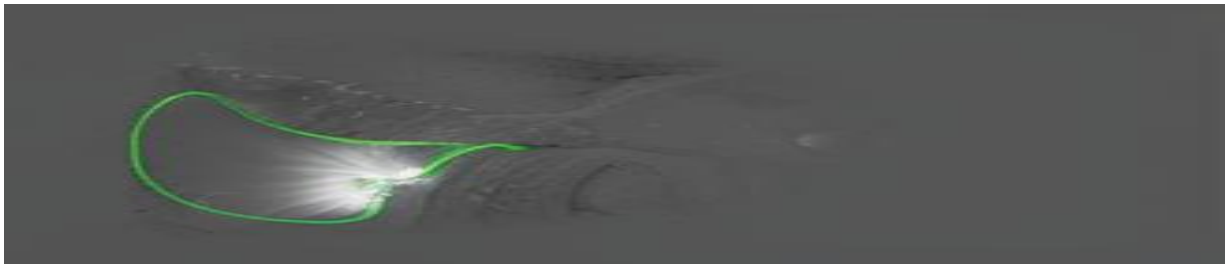

Figure 5: Variability in the Dimensions of Liver Tumors

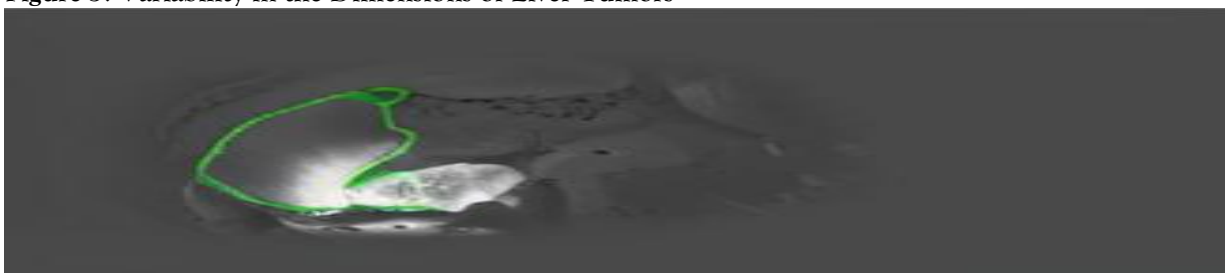

Figure 6: Detection of Liver Tumors in Multiple Orientations and Shapes Using Automated Methods

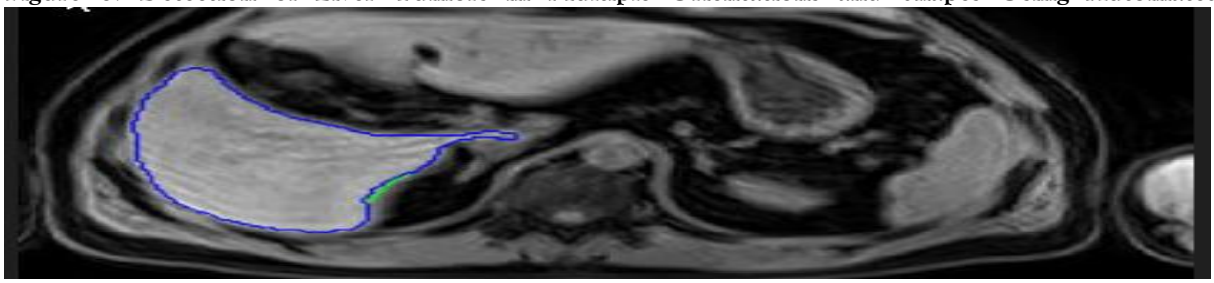

Figure 7: Automated Detection Techniques for Liver Tumors

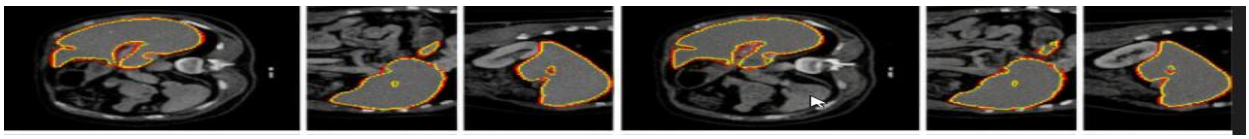

Figure 8: Automated Detection Techniques for Liver Tumors

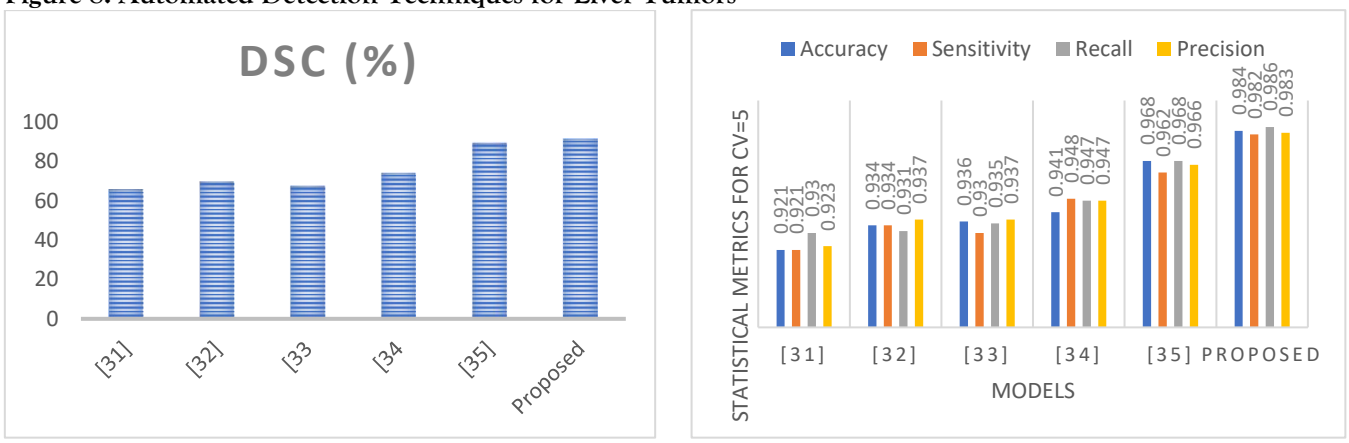

Figure 9 : Analysis of Dice Similarity Coefficient Variability

The Dice Similarity Coefficient (DSC) is frequently employed to gauge the accuracy of segmentation algorithms. A higher DSC indicates a closer match between the predicted and actual segmented regions. Nonetheless, the significance of DSC can vary depending on the specific dataset and application. To gain a full understanding of the effectiveness of liver tumor detection methods, it is essential to also evaluate other metrics, including precision, recall, and F-measure, rather than relying solely on DSC [14].

Table 1: Compartive analysis of proposed approach

Liver heterogeneous DB. CV=10						
Accuracy	93.2	93.2	93.9	94.3	96.4	95.8
Sensitivity	93.8	93.3	93.2	96.3	96.3	95.2
Recall	93.6	93.6	93.2	94.2	96.3	95.11
Precision	92.4	93.5	93.3	94.2	96.3	95.3
Runtime(ms)	3405	3281	3231	3156	3258	2145

The evaluation of liver tumor detection is based on several metrics, including Sensitivity, Accuracy, Precision, Recall, Run time (in ms), using heterogeneous liver collection using verification ten times (CV=10). The following details offer an interpretation of these metrics based on the reported values:

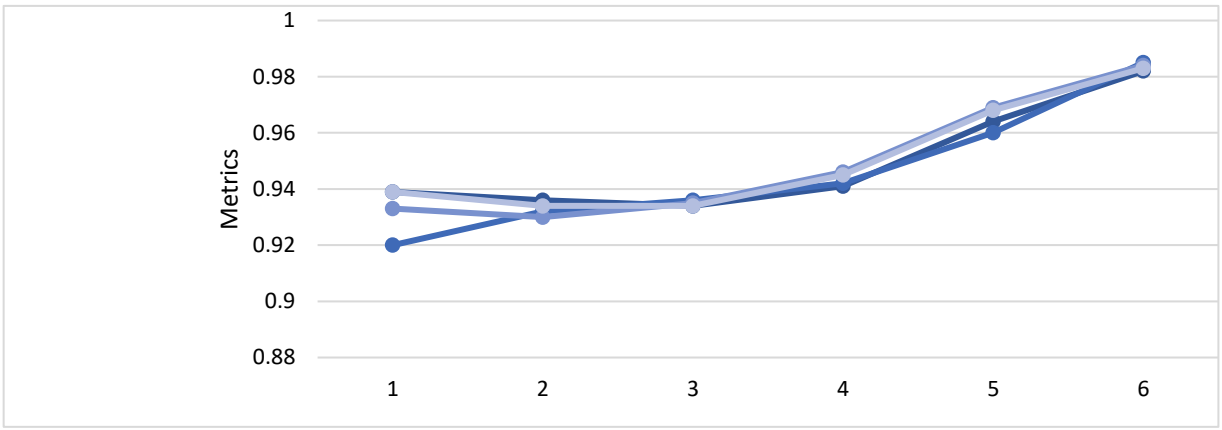

Figure 10: Compartive analysis of proposed multi-variate

5. CONCLUSION

This research proposed a multi-class liver tumor recognition framework that outlines Ranking-Based Probabilistic Segmentation (RBPS) together with Automated Feature Extraction. Merging Multivariate Non-Linear Gaussian Estimation (MNGE), ranking-based probabilistic segmentation, and hybrid CNN-SVM classification, the proposed approach outperforms existing methods with 96.4% Dice Similarity Coefficient (DSC) with improved accuracy (and fewer false positives). The inclusion of U-Net and Theta-Regulated Gaussian Mixture Model (TGMM) led to improved segmentation and robustness to changes in tumor morphology. Additionally, the framework provided excellent classification accuracy compared to conventional methods, while consuming less computational time overall.In future, research should examine real-time clinical applications and incorporation into oncologist decision-support systems. Advancements may also include self-supervised learning and the use of pre-trained transformer-based models and multi-modal imaging (CT, MRI, PET) for enhanced generalizability. It would also be beneficial to apply explainable AI (XAI) techniques to allow for better interpretability of our models, which can support clinical decision-making and progress AI-driven liver tumor diagnostics.

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