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A Review of Recent Efficient Deep Learning Methods for Liver Segmentation

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ABSTRACT

Introduction: The accurate and timely diagnosis of non-alcoholic fatty liver disease (NAFLD) and precise segmentation of tumors and liver are significant and critical for successful management of patients and improved medicinal outcomes. This review consolidates current developments in methodologies and algorithms used in medical imaging, particularly detection and segmentation of such intricate liver diseases. It explores the wide range of diagnostic techniques that extend from old school machine learning methodologies, such as classification tree-based methods of diagnosing NAFLD [1], to highly advanced deep learning models crafted specifically for analysis of ultrasound as well as computed tomography (CT) images. Specifically, we examine the application of deep learning models for ultrasound image classification in NAFLD and the development of advanced segmentation frameworks utilizing self-ONN-based decoders, U-Net architectures [6], and graph convolutional networks [8] for precise liver and tumor delineation. The availability of large-scale and carefully labeled medical image collections, such as the dataset created by Alshagathrh and colleagues [4], has been crucial for teaching and testing these advanced computer models. This has led to notable progress in how accurately we can diagnose liver conditions and precisely locate problems within the liver [5, 7]. This review brings together these advancements, highlighting how these computer-based methods have the potential to significantly improve the way we understand and manage liver diseases, ultimately leading to more efficient and dependable healthcare practices.

Objectives: The key objective is to bring together the advancements in recent efficient deep learning models, highlighting how these computer-based methods have the potential to significantly improve the way we understand and manage liver diseases, ultimately leading to more efficient and dependable healthcare practices.

Conclusions: In this review, the changing picture of liver disease segmentation and diagnosis, specifically the NAFLD, and tumor liver analysis via recent machine learning and deep learning strategies have been reviewed. Earlier contributions to this work were dependent upon rule-based statistical and classic procedures like trees in classification in the identification of factors that contribute to NAFLD [1]. With increasing computational power and sizes of medical image datasets, the paradigm has undoubtedly shifted towards encoder-decoder architecture and convolutional neural networks (CNNs), including UNet and its several variants [6][7][8].

Keywords: Liver disease, Medical imaging, Deep learning, Segmentation, Classification, Ultrasound, Artificial intelligence, Machine learning, Image analysis.

INTRODUCTION

Liver diseases, from non-alcoholic fatty liver disease (NAFLD) to complex ones like liver tumors, are now significant global health concerns. Artificial intelligence (AI) and deep learning techniques have transformed the medical imaging sector by enabling the detection and segmentation of livers and liver tumors automatically and with high accuracy. Historically, conventional diagnostic techniques, typically dependent on doctor's interpretation of medical images, were constrained by inter-observer variability and labor-intensive manual processing. As a result, the use of computational techniques, especially machine learning and deep learning, has become an exciting line of action for

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improving diagnostic accuracy and efficiency. Numerous studies have sought to examine and emphasize the capability of the application of computational methods in overcoming the challenges of NAFLD diagnosis. Birjandi et al. [1] investigated the application of classification tree techniques for the prediction and diagnosis of NAFLD and the identification of major associated factors that lead to disease development and progression.

Furthering this line of research, [3] implemented a combinational deep learning algorithm for NAFLD classification in ultrasound images, demonstrating the potential of deep learning to improve diagnostic precision. The creation of large, labeled ultrasound data sets, including those developed by Alshagathrh et al. [4], has provided a useful resource in allowing these sophisticated computational models to be trained and validated, thus enabling the translation of research into practice.

At the same time, considerable headway has been achieved in automatic liver tumor segmentation, a key step in surgery planning and monitoring patients' evolution along time. Akash H et al. [2] presented a comparison study of 10 U-Net architecture for liver and tumor segmentation, emphasizing the interdependence between architectural design to segmentation performance (accuracy). Song et al. [5] proposed new deep learning models that even further improve segmentation performance. In addition, Hettihewa et al. [7] investigated the application of U-Net models and multi-attention networks, respectively, towards effective liver segmentation from CT scans, explaining the potential of such deep learning architectures in representing complex anatomical shapes. Khoshkhabar et al. [8] used graph convolutional networks for self-supervised liver tumor segmentation, demonstrating the generalizability of such methods to highly complex medical image data. Following these developments, the potential of single-stage Self-ONN U-Net models with Swin Transformer encoders is a possible line of improvement in making simultaneous liver and tumor segmentation more efficient.

The aim of this review is to provide a comprehensive review of the current state-of-the-art in computation methods for diagnosing and segmenting liver diseases. By integrating the findings of these multidisciplinary research studies, our intention is to highlight the groundbreaking capabilities of these methods for improving clinic outcomes and leading medical imaging processing research. This review explores the advantages and limitations of different methods, offering inroads into future research and the integration of these technologies into clinical practice.

REVIEW OF RECENT WORK

[1] In the study, the Classification Tree (CT) model was utilized for prediction and diagnosis of Non-Alcoholic Fatty Liver Disease (NAFLD) and finding factors related to it. Out of 1,600 patients, the data was partitioned into test sets and training sets. Variables in the CT model were utilized by taking BMI, waist-hip ratio (WHR), triglycerides (TG), glucose, systolic blood pressure (SBP), and alanine aminotransferase (ALT) into account. These were found to be the predictors most important among the factors that were identified. The method applied the GUIDE method, in which predictor variables were divided according to chi-square tests of association and recursive partitioning and pruning for tree refinement. The resultant final model had accuracy of 80% on the training set and 75% on the testing set, having sensitivities of 74% and 73%, respectively, and specificities of 83% and 77%. Area under the ROC curve was 78% for training and 75% for test, which was a strong performance. The benefits of using the CT approach include its interpretability, potential to capture nonlinear interactions among variables, and feasibility in clinical practice without data distribution assumption. The drawbacks, on the other hand, involve possible overfitting, usage of correlated variables being restricted due to each split's selection bias, and reliance on thresholds specific to samples, which can constrain generalizability. Also, CTs would not be able to detect the cumulative effect of weaker predictors, as well as other statistical models like logistic regression. Despite such limitations, the study suggests that CT is a valid and practicable tool for the early diagnosis of NAFLD, especially in resource-limited settings.

[2] This paper offers an exhaustive comparison of ten U-Net-inspired architectures for liver segmentation from CT scans across three public datasets: LiTS, 3DIRCADb, and CHAOS. The key objective is to examine the performance of each model on various anatomical conditions and imaging scenarios using the same training procedures and evaluation protocol. The models that were tested are Vanilla U-Net, Attention U-Net, V-Net, U-Net 3+, R2U-Net, U2-Net, U-Net++, ResU-Net, Swin-UNet, and Trans-UNet. The preprocessing was the conversion of DICOM/NIfTI to JPG and HU clipping to [−200, +200] for improving the visibility of the liver. All the models were trained with Dice Loss and the NAdam optimizer for a maximum of 70 epochs, and early stopping was used. Results show that the

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Vanilla U-Net resulted in the maximum Dice Similarity Coefficient (DSC) of 0.9545 on the LiTS dataset and performed better compared to more complex models such as Trans-UNet (0.8632) and Swine-UNet (0.9352). The Attention U-Net performed well on CHAOS and 3DIRCADb, emphasizing the effectiveness of attention mechanisms for anatomical variation. Strengths of the study are the uniform benchmarking of various U-Net variants and multi-metric evaluation (DSC, IoU, VOE, RVD, accuracy, precision, recall). Weaknesses are uniform hyperparameter settings across models and absence of tumor segmentation even though LiTS includes tumor masks. The results highlight that simplicity in architecture, like in Vanilla U-Net, can lead to state-of-the-art outcomes when combined with strong preprocessing, particularly for CT scan liver segmentation.

[3] The article presents SALSA, a completely automated deep learning software for the detection and segmentation of liver tumors from CT scans, responding to an urgent need for consistent, reproducible, and scalable tumor quantification in cancer care. Trained on a heterogeneous set of 1,598 contrast-enhanced CT scans from 1,306 patients and 4,908 tumors, including primary and metastatic liver cancer, SALSA was tested over an in-domain test set as well as four external independent cohorts, including the LiTS dataset. The method utilizes a 3D U-Net cascade from the nnU-Net framework, exhibiting better performance than state-of-the-art transformer-based architectures and even radiologist inter-reader agreement. SALSA had a Dice Similarity Coefficient (DSC) of 0.760 on external validation by tumor and showed patient-wise detection accuracy of 99.65%, with lesion-wise accuracy of 81.72%. The approach placed strong focus on solid preprocessing (e.g., liver masking, cropping, Hounsfield Unit standardization) and utilized attentive architectural tuning coupled with ensemble modeling. The tool surpassed best-performing models within the LiTS challenge and was radiologist-validated with demonstrated balanced preferences for SALSA vs. manual segmentations. Important strengths are its applicability to various tumor types and acquisition protocols, its prognostic value (tumor burden highly correlated with survival, $p = 0.028$), and public accessibility. Weaknesses include inferior performance on tiny or hyperdense tumors and use of single-rater annotations for ground truth, which may impose bias. In summary, SALSA is a clinically translatable method of automatic liver tumor segmentation that provides reproducible, precise, and rapid quantification with the potential to simplify cancer staging, diagnosis, and treatment response assessment.

[4] The paper introduces an extensively curated and annotated ultrasound image dataset for Non-Alcoholic Fatty Liver Disease (NAFLD) and is derived from two large-scale Saudi hospitals, namely King Saud University Medical City (KSUMC) and National Guard Health Affairs (NGHA). For the methodology, 12,766 DICOM ultrasound scans were gathered, carefully filtered for their quality by practicing radiologists. Low-quality and incomplete images were excluded, yielding 10,352 high-resolution images. These were then transformed to PNG form in lossless compression and normalized to 768 × 1024 pixels utilizing padding technique to maintain image quality. Every image was associated with histologically verified liver biopsy information and tagged in terms of NAFLD Activity Score (NAS), including both stages of fibrosis (0–4) and grades of steatosis (0–3). The classification was also checked by agreement between three expert hematopathologists and achieved an inter-rater reliability of 92.2% with Cohen's kappa, where high annotation reliability was confirmed. Although the paper itself does not report traditional model training accuracy, the dataset itself offers future AI models with good diagnostic ability and reliability based on correct annotations and clinical validation. The major strengths of this dataset are its large size, patient diversity, full biopsy-linked labels, and high-quality preprocessing pipeline that maintains image integrity. It is designed for machine learning use in NAFLD detection, so it is a unique and valuable public dataset. In addition, format compatibility with standard tools such as Python and MATLAB makes it even more accessible. Despite that, the dataset too has limitations like demographic bias in middle-aged patients and variability of ultrasound equipment that can influence consistency. Further, subjectivity in interpreting ultrasound images and rejection of low-quality images can lower variability. Nevertheless, the dataset creates a solid ground for constructing AI-based diagnostic equipment for liver disease and is good for reproducible, clinically valuable research.

[5] This research suggests an improved deep learning model for automatic liver vessel segmentation from CT images to overcome the clinical problem of effectively delineating hepatic vasculature, usually hidden due to low contrast and intricate structures. The authors refined the 3D V-Net model by implementing several fundamental changes to improve performance. These consist of pyramidal convolution block integration to perform multi-scale spatial feature extraction, dilated convolutions to increase the receptive field without downsampling, and multi-resolution deep

supervision to enforce robust learning in all layers. In addition, the model uses the Tversky loss function, which is specifically designed to address class imbalance by modulating sensitivity to false negatives and false positives. The model was trained on two public data sets—LiTS17 and MICCAI Hepatic Vessel—via 10-fold cross-validation. It had a Dice Similarity Coefficient (DSC) of 72.53%, which was better than eleven other state-of-the-art approaches like 3D-UNet, nnUNet, and 3D-GCCN. With regard to evaluation time, the model was able to trade computational efficiency with segmentation quality, taking 5.97 seconds per inference, which is tolerable for clinical practice. The advantages of this approach include its ability to encode complex vessel patterns, partition minute structures accurately, and generalize effectively even in limited amounts of labeled data, because of dropout regularization and adaptive feature fusion. Also, modularity simplifies extension and integration into clinical practice. Despite the advantages, there are also disadvantages, including comparatively high computational requirement versus lightweight architectures, reliance on high-quality annotated data, and the risk of overfitting unless well-regularized. Additionally, the 3D segmentation strategy raises memory requirements, which could become a real-time limitation on lower-end platforms. Nonetheless, the proposed model is a solid and extensible solution to hepatic vessel segmentation with substantial repercussions in the diagnosis of liver tumors and surgical planning.

[6] In this research, the authors created and validated deep learning models to segment the liver and colorectal liver metastases (CRLM) automatically, with the goal of automating total tumor volume (TTV) evaluation in patients with initially unresectable CRLM. With 595 contrast-enhanced CT scans of 259 patients in the CAIRO5 trial, and an external validation set of 72 CT scans, the researchers trained two U-Net models, one for liver segmentation and one for tumor segmentation. Ground truth labels were generated via semi-automatic segmentation, refined by expert radiologists. Image preprocessing included HU clipping and histogram equalization to enhance contrast. The models achieved Dice similarity coefficients (DSC) of 0.96 for liver and 0.86 for tumor in the test set, and 0.82 DSC for tumors in the external validation. Intraclass correlation coefficient (ICC) for TTV estimation was as high as 0.97–0.98, demonstrating excellent concordance with manual segmentations. Advantages are the model's capacity to analyze heterogeneous multi-center CT data and facilitate high-throughput, reproducible TTV measurement—potentially better than RECIST 1.1 for assessing treatment response. Limitations involve decreased performance in external datasets, particularly for small tumors, and reliance on a single expert for ground truth annotations. Nonetheless, the study demonstrates the clinical promise of AI-driven segmentation tools for improving tumor response evaluation and supporting radiomics-based cancer analysis.

[7] We present MANet, a new Multi-Attention Network for accurate liver tumor segmentation from CT scans. Based on the U-Net framework, MANet improves segmentation by using deep residual learning as well as sophisticated attention mechanisms. The methodology embeds residual blocks in the encoder to resist vanishing gradients and leverages attention components on diverse levels: channel attention (for focusing 'what' features), spatial attention (to local 'where' features), skip connection attention gates (for filtering low-level features), and Convolutional Block Attention Modules (CBAMs) in the bridge. The framework was trained and tested using two publicly available datasets—LiTS17 and 3DIRCADb—within slice-based as well as volume-based experiments. MANet achieved a Dice Score of 81.45% (slice-wise) and 67.35% (volume-wise), comparing favorably against baseline models such as U-Net, Attention U-Net, and U-Net+CBAM, and performing more sensitivity (as high as 87.23%) and accuracy (99.47%). Generalizability between datasets was also shown by the model, preserving a 64% Dice score on 3DIRCADb. Benefits of MANet are that it can effectively identify tumors with fuzzy edges and varied sizes, higher sensitivity to small and complicated tumors, and fewer parameters than conventional models. The attention mechanisms enable fine-grained feature re-calibration, enhancing model concentration on the appropriate tumor areas. MANet also performed better than some state-of-the-art models with less computational resources. Limitations include longer inference time and greater computational complexity because of the multiple attention modules. Additionally, volume-based segmentation performance, although good, still falls short of slice-based performance—perhaps because of tumor heterogeneity and data heterogeneity. Also, the generalizability of the model to real-world, multicenter datasets with varying imaging protocols needs to be validated. In spite of these, MANet is a robust and efficient model for automated liver tumor segmentation.

[8] This paper presents a novel deep learning architecture for automated liver and tumor segmentation of CT images based on a mix of Simple Linear Iterative Clustering (SLIC) and Chebyshev-based Graph Convolutional Networks

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(GCNs). The novel SLIC-DGN model maps the CT image to a graph representation by dividing the image into superpixels as graph nodes with mean pixel intensity-based feature extraction. These properties are inlaid and processed by a four-layer Chebyshev GCN and then batch normalized, activated using ReLU, dropped out, and completed using a fully connected softmax classifier. The model is trained and validated with the LiTS17 dataset, using 987 images derived from 4158 preprocessed CT slices. Data augmentation and intensity normalization are implemented during preprocessing to improve robustness. The architecture is optimized with the Adam optimizer and validated using 10-fold cross-validation. The model scored a liver segmentation accuracy of 99.1% and tumor segmentation accuracy of 98.7%, and Dice coefficients of 91.1% for liver and 90% for tumors, and performed better compared to other models such as U-Net, Shortcut-CNN, and hybrid FCNNs. Its main strengths are high segmentation accuracy for both tumors and liver, noise robustness (being 90% accurate even at −4 dB SNR), and its light-weight nature that prevents heavy parameter tuning. Using graph structures allows it to model spatial relationships in a superior manner compared to regular CNNs. Yet, some of the disadvantages are that there is limited validation on just the LiTS17 dataset, which threatens generalizability, and using traditional data augmentation techniques over newer generative methods such as GANs. These notwithstanding, the presented model provides a new benchmark by merging the accuracy of GCNs with superpixel-based region encoding and thus is a potential radiology assistant for clinical liver tumor analysis.

[9] This research suggests a hybrid cascaded neural network that efficiently integrates both 2D and 3D convolutional neural networks to perform precise liver lesion segmentation with a specific emphasis on identifying small lesions frequently ignored by conventional models. The approach is a multi-step process with 2D CompNet architectures to segment the liver and large tumors from CT slices, and then a 3D CompNet to segment small lesions from volumetric data (32×32×32 cubes). The liver is localized first from CT images slice-by-slice using a 2D network, and large lesions are detected using another 2D model. For the small lesions, a distinct 3D model is used, taking advantage of spatial consistency between slices to decrease false positives. The model was trained and tested on the LiTS dataset, utilizing 58,638 liver slices and more than 11,000 volumes of small lesions. Without post-processing or pre-training, the model obtained a Dice score of 68.1% per case, which is second in published methods and first in non-pretrained methods. Its major strengths are that it can better find smaller liver lesions compared to conventional 2D networks, improved performance without using pre-trained weights, and efficiency in computation by using 3D processing only for small lesions. The hybrid architecture finds a balance between performance and resources. Furthermore, the model's capability to segment unannotated tumor-like areas promises its capacity to detect missed lesions. Yet, some limitations are added training complexity in dealing with both 2D and 3D networks and heuristic threshold dependency (such as 32×32 size) in differentiating lesion types. The model's segmentation accuracy is also limited by LiTS ground truth label imperfections, which might affect fairness of evaluation. Still, the architecture offers a stable, flexible, and scalable framework for liver lesion segmentation in automatic fashion.

[10] This work presents a combined framework of transfer learning and multi-task learning for improving segmentation and classification of liver lesions in CT scans. The framework makes use of a U-Net with SE-ResNet backbone that has been enhanced by Squeeze-and-Excitation (SE) blocks for more effective feature learning. Two key frameworks are explored: (1) a multi-task architecture (similar to Y-Net), where classification and segmentation outputs are learned separately, and (2) a joint pixel-wise classification model, where segmentation is achieved via pixel-wise classification and lesion type is determined by majority vote. The data collection consists of 332 CT slices from 140 patients with three liver lesion categories—cysts, hemangiomas, and metastases. To handle class imbalance and a small dataset size, the work employs transfer learning from ImageNet and the LiTS dataset whereby pre-trained models for liver segmentation are employed in cropping regions of interest. Results indicate that the joint learning model trained on LiTS data performs the best in terms of classification accuracy (86%), Dice coefficient for segmentation (71%), and segmentation recall (76%), far surpassing training-from-scratch and Y-Net variants. The benefits of this strategy are enhanced overall generalization, insensitivity to small amounts of data, and less overfitting using shared feature representation across tasks. Joint training achieves better performance for segmentation and classification as a result of shared context knowledge. Applying transfer learning enables faster convergence and enhanced accuracy with the use of domain-specific prior knowledge. But limitations are reliance on well-annotated external data such as LiTS for successful pre-training, and possible underperformance on lesion types poorly represented in the source data. Also, the pixel-wise classification approach can be challenged by very small or

overlapping lesions. Nevertheless, this framework presents a strong, data-efficient solution for liver lesion analysis, especially for clinical environments with limited labeled data.

[11] The Liver Tumor Segmentation (LiTS) Benchmark was created to give a unified platform for assessing and comparing automated liver and liver tumor segmentation algorithms from abdominal CT scans. The methodology of the benchmark included acquiring 201 contrast-enhanced CT volumes from seven medical institutions across the world, presenting a varied set of liver anatomy and tumor varieties, both primary and metastatic lesions. Manual segmentations were carried out by experienced radiologists and validated using a strict, blinded review process. Seventy-five algorithms competed in three grand events—ISBI 2017, MICCAI 2017, and MICCAI 2018—where the submissions were assessed on the basis of Dice score, Average Symmetric Surface Distance (ASD), and Relative Volume Difference (RVD). The highest-performing liver segmentation model had a Dice score of 0.963, and the highest tumor segmentation Dice scores were 0.674 (ISBI 2017), 0.702 (MICCAI 2017), and 0.739 (MICCAI 2018), showing improvement over the years.

Strengths of the LiTS benchmark are that it is diverse in image protocols, tumor cases, and equipment used for acquisition, thus highly representative of actual clinical data. It was instrumental in improving segmentation methods by stimulating development of resilient U-Net-based and hybrid 2D/3D models. The open dataset and Codalab benchmarking platform enabled reproducibility and comparative performance monitoring. Nevertheless, there are limitations: tumor segmentation performance is much lower than for liver segmentation, particularly for tiny or low-contrast lesions. The heterogeneity of the dataset—although a strength for generalization—also brings difficulties with algorithm training and testing. Further, the LiTS dataset has no annotations of tumor subtypes, which means it is limited in its usefulness for fine-grained classification applications. Notwithstanding these constraints, the LiTS benchmark is now a key resource for medical image segmentation research with ongoing innovation in liver tumor analysis.

[12] In this paper, RA-UNet is proposed as a new hybrid 3D deep learning framework that combines residual learning and attention mechanisms for accurate liver and tumor segmentation in CT scans. The framework is a three-step pipeline: (1) RA-UNet-I, a 2D residual attention U-Net, performs coarse liver localization and outputs a boundary box to decrease computational burden; (2) RA-UNet-II, a 3D U-Net that has been improved by residual blocks and attention modules, segments the liver from inside the boundary box; and (3) another RA-UNet-II does tumor segmentation in the segmented liver. Preprocessing involves HU windowing (–100 to 200), zero-mean normalization, and patch extraction. The model is trained on LiTS dataset and tested on LiTS and 3DIRCADb datasets. It produced Dice scores of 0.961 (liver) and 0.595 (tumor) on LiTS, and 0.977 (liver) and 0.830 (tumor) on 3DIRCADb and outperforms a number of state-of-the-art methods. RA-UNet has better segmentation accuracy, particularly in volumetric tumor detection, high generalizability across datasets, and potent combination of hierarchical features through residual and attention modules. It does not require post-processing steps such as CRFs; hence it is end-to-end trainable. Its modularity also facilitates adaptive learning of tumor size and shape, improving detection of small tumors. Yet drawbacks are the long training time resulting from 3D convolution operations and higher memory requirements, rendering it less optimal for systems with lower computational power. Tumor segmentation is still challenged in distinguishing low-contrast and irregular tumors despite improvements. In spite of such drawbacks, RA-UNet is a robust and versatile model with high clinical applicability for liver tumor diagnosis and treatment planning, which is a gold standard in fully automatic 3D medical image segmentation.

[13] This work introduces a sophisticated deep learning architecture called AIM-Unet, which combines the benefits of U-Net and Inception modules to attain accurate and fully automated liver and tumor segmentation from abdominal CT scans. The model extends the basic U-Net by integrating Inception modules into the skip connections, which facilitates multi-scale feature extraction and enhanced boundary localization. The architecture conducts image feature processes through four simultaneous convolutional branches with varying filter sizes and pooling operations to allow stronger and high-resolution edge feature learning. The training was conducted on three datasets: CHAOS, LiST, and a hospital-based dataset created by the authors, and image augmentation was employed to enhance training diversity. The model was trained from scratch on TensorFlow and optimized with the Adam optimizer and binary cross-entropy loss, with a real-time segmentation time of about 1.12 seconds per slice. The AIM-Unet model achieved Dice scores of 97.86% (CHAOS), 97.38% (custom dataset), and 95.77% (LiST) on liver segmentation and

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75.6% (LiST) and 65.5% (3DIRCADb) on tumor segmentation—better than several state-of-the-art models. Benefits of AIM-Unet are high segmentation accuracy on various datasets, insensitivity to irregular liver shapes and densities, and fast feature learning with inception-augmented skip paths. The model has no pre-trained weights and gives a nearly real-time answer, which can be deployed in clinical environments. In addition, the identification of faint liver boundaries and tumor segmentation from challenging CT images proves its applicability in aiding radiological diagnosis and radiotherapy treatment planning. Drawbacks include increased model complexity and GPU usage from the expanded architecture, which can lead to longer training time and deter deployment on low-resource devices. Moreover, liver segmentation is very accurate, yet it is relatively less accurate in capturing the tumor segmentation, particularly on smaller or less-prevailing datasets such as 3DIRCADb. Nevertheless, AIM-Unet offers a scalable solution with high accuracy for automated liver imaging analysis.

[14] This paper introduces H-DenseUNet, a new hybrid deep learning framework for unsupervised liver and tumor segmentation from CT volumes. The method merges a 2D DenseUNet for intra-slice feature extraction with a 3D DenseUNet to learn inter-slice spatial context, combined through a Hybrid Feature Fusion (HFF) layer in an end-to-end training pipeline. The 2D network leverages long-range skip connections and dense blocks akin to DenseNet to maintain high-resolution spatial information, and the 3D network refines the segmentation from contextual information available in neighboring slices. The combined strategy overcomes the drawbacks of isolated 2D or 3D networks—2D networks have limited volumetric context, and 3D networks are computationally intensive and memory-constrained. The model was trained on MICCAI 2017 LiTS dataset and evaluated on both LiTS and 3DIRCADb datasets. It recorded Dice scores of 96.1% (liver) and 72.2% (tumor) on LiTS, and 94.7% (liver) and 93.7% (tumor) on 3DIRCADb, which surpassed a number of state-of-the-art models, such as UNet and ResNet variants. The advantages of the H-DenseUNet are high segmentation performance on both tumors and liver, good memory efficiency, effective feature representation through dense connections, and enhanced generalizability. Transfer learning is supported by the architecture and it also cuts down the training time with respect to independent 3D models. In addition, it can handle both small and large tumors and generalize well across datasets. Limitations include increased training time as a result of dual-network optimization, high GPU memory requirements, and comparatively modest improvement in small tumor segmentation. Moreover, even with its robustness, the performance of the model can still be affected by differences in CT acquisition protocols. Nevertheless, H-DenseUNet establishes a new standard in fully automated liver and tumor segmentation, providing a scalable and clinically useful tool for medical image analysis**.**

[15] In this work, a new model is proposed, i.e., ECLMS (Edge Constraint and Location Mapping Segmentation), aiming to solve liver tumor segmentation in non enhanced MRI images that are generally of low contrast and with fuzzy borders. The methodology includes a dual-branch network and a localization network. The localization network first generates coarse tumor masks using a U-Net, followed by Xception to create accurate tumor location maps via class activation mapping (CAM). These maps guide the segmentation process. The dual-branch segmentation network has one branch focused on tumor region decoding and another focused-on edge information. The model utilizes squeeze-and-excitation (sSE) blocks, dense up-link connections, and a Bottleneck Multiscale Module (BMM) for enhanced attention towards important features as well as detection of multiscale tumor morphology. Training was on a private database of 215 patients (T2WI modality), enhanced to 2709 images. The model achieved Dice of 90.23%, precision of 92.25%, as well as accuracy of 92.39%, surpassing the performance of U-Net, U-Net++, BESNet, as well as RgGAN based on both detail segmentation and accuracy. Advantages of ECLMS include its improved performance on unenhanced images without using contrast agents, reduced risk and time for patients, and the detection of small and morphologically varied tumors with improved boundary sharpness. Detailed internal and edge segmentation is permitted through the use of dual-branch architecture, and location mapping eliminates background noise and misclassification. Additionally, the model demonstrates effective use of feature recalibration and context-aware processing. Yet, the drawbacks are higher model complexity (51.9M parameters), possibly expensive training time, and utilization of merely 2D image slices, which is insufficient for contextual continuity between slices. Additionally, dependence on concatenation for the integration of location maps might not fully exploit localization cues. Notwithstanding these, ECLMS has good potential for noninvasive and precise liver tumor diagnosis.

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[16] In this paper, the authors propose a deep learning method based on cascaded deep residual networks (ResNet) for precise liver and liver lesion segmentation from contrast-enhanced CT scans. The authors overcome the disadvantages of conventional fully convolutional networks (FCNs), especially VGGNet-based FCNs, by adding ResNet architectures capable of enabling deeper networks with skip connections. The model under proposal includes a backbone ResNet as an initial segmenter, preceded by a cascaded ResNet that fine-tunes predictions with learning from current input as well as past probability maps. The model is fed 2D axial slices from the LiTS dataset, multi-scale fusion utilized during testing for enhanced robustness across different resolutions. The HU window was clipped to [-160, 240] to be liver-relevant, and all volumes were normalized to [0, 1]. Data augmentation and ImageNet pre-trained weights fine-tuning were adopted for generalization. The most ideal setting—cascaded ResNet with multi-scale fusion—yielded Dice scores of 95.90% for liver segmentation and 50.01% for lesion segmentation, much higher than conventional FCNs and isolated ResNet models.

Benefits of such an approach are its capacity to train extremely deep networks without the presence of degradation due to residual connections. The cascaded architecture enables iterative boundary refinement of tumors and the multi-scale fusion strategy enhances scale invariance, necessary for datasets with different resolutions and lesion sizes. It is especially useful for segmenting lesions with ill-defined boundaries and small size, prevalent in liver pathology. Yet, drawbacks are high computational expense—training lasted around 7 days—and dependence on 2D slice processing, which can ignore spatial continuity between volumes. Moreover, though performance was enhanced, lesion Dice is still low, suggesting additional optimization is required. Nevertheless, this model is one of the best-performing solutions in the ISBI 2017 LiTS challenge, showing excellent clinical utility for liver lesion segmentation.

Table 1.1. A comparative overview of liver disease and tumor segmentation studies, highlighting their datasets, methods, performance, and limitations.

Paper No.	***Dataset***	***Methodology***	***Accuracy / Dice Score***	***Strengths***	***Limitations***
[1]	1600 clinical records	Classification Tree (GUIDE)	80% train, 75% test accuracy	Simple, interpretable, models clinical interactions well	Overfitting risk, biased splits, not ideal for weak predictors
[2]	LiTS, 3DIRCADb, CHAOS	Comparative study of 10 U-Net architecture	DSC up to 0.9545 (Vanilla U-Net)	Extensive benchmarking, consistent training, architectural diversity	Uniform hyperparameters, no tumor segmentation on LiTS
[3]	1598 CT scans, 4908 tumors, LiTS included	3D U-Net cascade with ensemble tuning	DSC 0.760 (external), precision 99.65%	High generalizability, radiologist-level agreement, survival correlation	Lower performance on small tumors, single-rater bias
[4]	10,352 annotated ultrasound images	Dataset preparation and validation	Not applicable	Large, annotated, biopsy-linked dataset; reproducible	Device heterogeneity, no model training accuracy reported
[5]	LiTS17, MICCAI Hepatic Vessel	Modified 3D V-Net	72.53% (vessel DSC)	Captures small vessels, modular and extensible	High memory usage, needs quality data, slower inference

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[6]	LiTS17,	SLIC + Chebyshev GCN	DSC 91.1% (liver), 90% (tumor)	High accuracy, noise robustness, lightweight	Limited dataset validation, no GAN augmentation
[7]	LiTS17, 3DIRCADb	MANet (multi-attention U-Net)	81.45% (slice), 67.35% (volume), 64% (3DIRCADb)	Handles fuzzy/complex tumors, high sensitivity	Higher inference time, generalizability varies
[8]	LiTS17	SLIC + Chebyshev GCN	91.1% (liver), 90% (tumor, DSC)	Noise robust, superpixel-aware, lightweight	Tested on one dataset, lacks GAN-based augmentation
[9]	LiTS	2D+3D Hybrid CompNet	68.1% (DSC, lesions)	Accurate small lesion detection, no pre-training needed	Threshold-based separation, complexity in training
[10]	LiTS, ImageNet	SE-ResNet U-Net + multi-task learning	86% (classification), 71% (segmentation DSC)	Transfer learning, robust with small datasets	Dependent on external data, weaker on small lesions
[11]	LiTS (201 scans)	Benchmark dataset & evaluation platform	Up to 96.3% (liver), 73.9% (tumor, DSC)	Diverse, reproducible, drove community progress	Low tumor DSC, no subtype labels, dataset heterogeneity
[12]	LiTS, 3DIRCADb	3-stage RA-UNet	96.1%/0.595 (LiTS), 0.977/0.830 (3DIRCADb)	Residual + attention fusion, strong generalization	High memory/training time, low-contrast tumor challenge
[13]	CHAOS, LiST, Custom	AIM-Unet (U-Net + Inception modules)	Up to 95.77% (liver), 75.6% (LiST), 65.5% (3DIRCADb)	Real-time, accurate, robust across datasets	Higher GPU load, tumor segmentation lower on rare data
[14]	LiTS, 3DIRCADb	H-DenseUNet (2D+3D + HFF)	96.1%/72.2% (LiTS), 94.7%/93.7% (3DIRCADb)	Dense features, generalizes well, supports transfer learning	High GPU demand, limited small tumor boost
[15]	Private MRI dataset (215 subjects)	ECLMS (dual-branch + CAM)	90.23% Dice, 92.39% accuracy	No contrast needed, edge-aware, non-invasive	2D only, high param count (51.9M), high training time
[16]	LiTS	Cascaded ResNet with multi-scale fusion	95.9% (liver), 50.01% (tumor, DSC)	Deep residual learning, iterative refinement	Long training (7 days), 2D-only, low lesion DSC

DISCUSSION

In this review, the changing picture of liver disease segmentation and diagnosis, specifically the NAFLD, and tumor liver analysis via recent machine learning and deep learning strategies have been reviewed. Earlier contributions to this work were dependent upon rule-based statistical and classic procedures like trees in classification in the identification of factors that contribute to NAFLD [1]. With increasing computational power and sizes of medical image datasets, the paradigm has undoubtedly shifted towards encoder-decoder architecture and convolutional neural networks (CNNs), including UNet and its several variants [6][7][8].

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Recent research has proposed innovations such as self-organized operational neural networks (Self-ONNs), graph convolutional networks [8], and attention-based multi-decoder architectures [7], all improving segmentation performance through architectural advances and improved spatial perception. In addition, the combination of residual and densely connected layers, as shown in H-DenseUNet and cascaded deep residual networks, has greatly enhanced lesion detection accuracy through multi-scale feature propagation [14][16].

A key facilitator of this advancement has been the presence of high-quality, annotated datasets like the LiTS benchmark [11], and domain-specific datasets like the Saudi ultrasound dataset for NAFLD [4]. These datasets not only enable comparative benchmarking but also compel generalization during model development. Despite this, challenges still exist owing to the inherent anatomical variability in the liver, imaging modalities (CT vs. ultrasound), low contrast between tumors and normal tissue, and the limited availability of labeled clinical data in some areas [5][10].

Even with segmentation precision of up to 97% in certain experiments [5][13], broad generalizability and practical clinician adoption continue to be problem areas. Solutions such as transfer learning [10], cascaded hybrid architectures [9], and CRF post-processing hold bright promise for advancing further. The journey towards realistic deployment, though, calls for advances in explanation, insusceptibility across institutions, as well as adaptation to clinical domains to support credibility across different real-world clinics.

In conclusion, the synergy of deep learning, medical imaging, and clinical collaboration has led to substantial improvements in liver disease analysis. Future research should prioritize the development of explainable AI models, integration of multimodal data, and expansion of publicly available datasets to bridge the gap between algorithmic success and clinical utility [15].

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