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An Enhanced Approach to Liver Disease Classification: Implementing Convolutional Neural Network with Attention Layer Gated Recurrent Unit

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ABSTRACT

The classification of liver diseases is of paramount importance in healthcare, assisting both in decision-making and diagnosis. Current methodologies for liver disease classification are often undermined by overfitting issues, inefficient feature learning, and problems arising from imbalanced data. This paper proposes an innovative model that integrates a Convolutional Neural Network (CNN) with an Attention Layer Gated Recurrent Unit (AGRU) to augment the efficiency of liver disease classification. The performance of the CNN-AGRU model was evaluated using a liver tumor dataset. The CNN model was employed to extract pertinent features from the input image dataset, which were subsequently applied to the AGRU. The AGRU technique, incorporating energy vector normalization, was designed to enhance unique feature learning and mitigate issues related to overfitting and imbalanced data. Furthermore, the network identified a context vector related to the spatio-temporal information in the input data, thereby bolstering the learning performance of classification. The proposed CNN-AGRU model demonstrated a commendable accuracy rate of 98.2%, outperforming the existing Google-Net model, which achieved an accuracy rate of 96.7%. This paper thus presents a promising advancement in the field of liver disease classification, offering potential improvements in both diagnostic accuracy and efficiency.

1. INTRODUCTION

Colorectal cancer, along with other conditions in the liver region, are typically caused by malignant polyps that form in the colon. Based on statistical data, colon cancer is the most prevalent type in the United States. Fortunately, the proliferation of early detection programs for these tumors and their precursor polyps is helping to mitigate the prevalence of colorectal cancer. It's broadly recognized that adenomatous polyps - benign lesions with dysplastic epithelium and varied malignancy potential - account for over 95% of colorectal malignancies. The progression from adenoma to carcinoma is well understood. Generally, this is a slow process, taking many years to manifest following an incremental accumulation of genetic alterations.

Malignant polyps penetrate the muscularis mucosa but remain confined to the submucosa (pT1). Adenomatous polyps may exhibit high-grade dysplasia and other non-invasive histological features. Such polyps constitute up to 12% of polypectomy series, a figure that is on the rise due to increasingly effective screening programs using colonoscopy. These programs not only prevent colorectal cancer but also treat some advanced polyps. Between 80% and 90% of adenomas are smaller than 1cm, enabling standard snare polypectomy to be executed more easily, especially for pedunculated polyps. Larger lesions are treated with endoscopic mucosal resection (EMR) and endoscopic submucosal dissection (ESD) at specialized centers, allowing for total rather than piecemeal excision. Full removal enables a more comprehensive histological examination, thus serving as the initial step in malignant polyp management. However, in clinical practice, scenarios often differ. A patient typically presents for examination after a resected polyp, initially thought to be benign during endoscopy, is subsequently found to have invasive adenocarcinoma upon pathological evaluation. This situation may be further complicated if the polypectomy site wasn't marked during the initial endoscopy, hindering endoscopic re-evaluation and making colon segment identification unreliable if definitive resection is required. The consulting physician will need to stratify risk by considering potential residual or recurrent disease, lymph node metastases, and operative risk. Current data indicates that this remains a contentious topic requiring a multidisciplinary approach. The prognostic features of malignant polyps will most significantly alter this risk profile. Effective management strategies will also be explored [1].

Colon cancer is the second leading cause of death worldwide and the third most common cancer. Expert physicians are necessary for early diagnosis of this malignancy [2]. Gastrointestinal diseases, such as Crohn's disease, cancer, polyps, bleeding, and ulcers, are prevalent. Researchers in the Computer Vision domain employ various computer-based techniques for early-stage liver cancer diagnosis, but the handcrafted features used in the process sometimes lead to misclassification. Feature extraction and lesion segmentation receive significant attention in image processing and Computer Vision across various applications, including agriculture, medical imaging, and surveillance [3]. Early

stages of small liver lesions often go undetected and can lead to fatal conditions. Hence, it's crucial to implement computer-based methods to aid doctors in effectively diagnosing and treating patients [4, 5]. Quantitative features, consisting of both visible non-texture features and invisible texture features, are extracted from input data and applied to the classification model. Statistical methods or machine learning techniques are utilized to build a robust classifier for the classification of gastrointestinal diseases [6].

Existing research has leveraged various feature extraction methods such as Log filter bank, texture features, Scale Invariant Feature Transform (SIFT), discriminative joint features, and color features [7, 8]. Feature reduction techniques employed include Principal Component Analysis (PCA) and Linear Discriminant Analysis (LDA), while classifiers such as K-Nearest Neighbor (KNN), Naïve Bayes, Support Vector Machine, and Artificial Neural Networks (ANN) have been applied for robust classification [9]. Backpropagation algorithms have been utilized to extract clinical features, and deep learning techniques have enabled models to handle a large number of training images. This capability allows machines to diagnose newly acquired clinical images based on a database of clinical features. Convolutional Neural Networks (CNN) are deep learning systems that accurately emulate the structure and function of brain neurons on computers [10, 11].

The CNN-AGRU model is proposed for liver disease classification to enhance efficiency. The input images undergo preprocessing for image augmentation and enhancement. The AGRU model performs the classification process, while the CNN model extracts features from the input images. The performance of the CNN-AGRU model in liver disease classification is evaluated and compared with existing machine learning and deep learning techniques.

Machine learning models, due to their lack of feature learning and difficulty with data imbalance, perform less effectively when classifying liver diseases. The proposed model was compared with the Decision Tree (DT), Random Forest (RF), Support Vector Machine (SVM), and K-Nearest Neighbors Algorithm (KNN) methods using machine learning techniques. Due to overfitting issues, SVM, KNN, and Decision Tree present unstable performance compared to Random Forest. Performance indicators compared include accuracy, sensitivity, and specificity. The accuracy rate for CNN-AGRU is 98.2%, while the rates for the DT, RF, SVM, and KNN models are 74.3%, 82.1%, 85.1%, and 86.2%, respectively. Similarly, CNN-AGRU's sensitivity value is 98.5%, while the DT, RF, SVM, and KNN models' respective sensitivity values are 76.2%, 83.2%, 86.7%, and 85.3%. Moreover, CNN-AGRU has a specificity value of 99.2%, whereas the DT, RF, SVM, and KNN models achieved specificities of 77.1%, 85.7%, 87.9%, and 86.8%, respectively.

The overfitting problem of the CNN model in the deep learning framework lowers classification performance. RNN models perform poorly in classification due to the loss of critical knowledge acquired early in the training process. The LSTM model's network updates also lose crucial data for classification due to the vanishing gradient problem. Meanwhile, the GRU approach has an overfitting issue in classification and discards new irrelevant features to improve learning. The CNN-AGRU model provides energy vector normalization to extract distinct features from the input data. The attention layer of the GRU better identifies pertinent features by learning the context vector of the spatio-temporal model. The accuracy of the CNN-AGRU model is 98.2%, whereas that of the RNN, LSTM, GRU, and CNN is 88.2%, 91.8%, 92.3%, and 95.1%, respectively.

Unlike conventional methods, the CNN-AGRU model discards recently learned irrelevant information, while the standard GRU model selectively identifies relevant features. The use of collaborative feature learning enhances the performance of the CNN-AGRU model when learning features with GoogleNet, ResNet-50, AlexNet, and TAS-RF. The CNN-AGRU model learns a context vector, which is responsible for selecting pertinent features for spatiotemporal input classification. A distinguishing feature of the CNN-AGRU model is its usage of energy vector normalization, which aids in learning distinctive features and addressing imbalances in data. CNN-based models using AlexNet, ResNet-50, and GoogleNet are limited by an overfitting issue. The LSTM-CNN model's performance is hindered due to increased overfitting, and the enhanced RCNN model is less efficient at feature learning. The CNN-AGRU model has an accuracy of 98.2%, while the accuracy of the GoogleNet, ResNet-50, AlexNet, and TAS-RF models is 96.7%, 95%, 97%, and 86.2%, respectively.

Convolutional Neural Network-Attention Layer Gated Recurrent Unit (CNN-AGRU) for Liver Disease Classification offers several advantages, including:

High Accuracy: The model has demonstrated excellent accuracy in classifying liver disease cases, assisting healthcare professionals in formulating more precise diagnoses and treatment plans.

Efficient Feature Extraction: The use of a Convolutional Neural Network (CNN) enhances the extraction of significant features from liver images, thereby improving disease classification accuracy.

Robustness: The method exhibits resilience against variations in liver image brightness and contrast, leading to more consistent and reliable diagnoses.

Attention Mechanism: The attention mechanism helps the model focus on the most relevant parts of the image, boosting the classification accuracy.

Attention Layer Gated Recurrent Unit (GRU): The use of a GRU helps the model capture temporal dependencies in image data, aiding in pattern recognition and accurate predictions [12].

Automated Diagnosis: The model can automatically diagnose liver diseases, reducing the workload of medical professionals and improving patient outcomes by facilitating early detection of disorders.

Non-invasive: As this method relies on routine medical imaging for diagnosis, it is non-invasive, avoiding the need for additional invasive tests or procedures.

The structure of this paper is as follows: Section 2 presents recent deep learning techniques for classifying liver diseases, while Section 3 describes the CNN-AGRU model. Section 4 provides details on the implementation of the CNN-AGRU model, and Section 5 presents the results of liver disease classification using the model. Finally, the conclusion of this research study is presented in Section 6.

2. RELATED WORKS

Liver cancer, characterized by the abnormal proliferation of tissues in the stomach and colon region, can be detected early, making endoscopy a vital tool in its early detection. This

section reviews recent research on the diagnosis of liver cancer using machine learning techniques.

Hmoud Al-Adhaileh et al. [13] put forth three deep learning methods—Alex-Net, ResNet-50, and GoogleNet—for disease diagnosis. Image enhancement and noise elimination techniques were applied prior to these deep learning methods. The Kvasir dataset, containing 5000 images across five classes of lower gastrointestinal diseases, was used to evaluate the proposed model. Transfer learning was leveraged to fine-tune the pre-trained CNN model for classification. The Softmax activation function was employed to categorize images into five classes of gastrointestinal disorders. The Alex-Net model showed superior performance in diagnosing gastrointestinal disorders compared to ResNet-50 and GoogleNet. However, deep learning techniques encountered the issue of overfitting, which reduced efficiency.

Gupta et al. [14] identified the Tumor Aggression Score (TAS) as a prognostic factor in machine learning for predicting colon cancer. The performance of various machine learning techniques was assessed using five-fold cross-validation. The constructed model achieved higher efficiency by determining the Tumor Aggression Score in TNM staging. The Random Forest model, in conjunction with the Tumor Aggression Score, achieved an F-measure value of 0.89. Random Forest outperformed other machine learning models in classification, achieving approximately 84% accuracy and an AUC of 0.82. However, the Random Forest model was unstable and prone to overfitting when handling diverse features.

Chen et al. [15] employed an enhanced Faster RCNN model with online complicated example mining for cancer detection. The performance of this enhanced model was evaluated using 1520 gastrointestinal CT images from 421 patients. The enhanced Faster RCNN model was compared to its predecessor and the Inception-v2 model in terms of detection time, Mean Average Precision, and F1 measure. The Faster RCNN model proved superior for cancer classification. The enhanced model scored an F1-measure of 95.71%, a map of 92.15%, and a detection time of 5.3 seconds per CT image. However, the Faster RCNN model suffered from overfitting.

Öztürk and Özkaya [16] integrated LSTM layers into each pooling layer of the CNN model for gastrointestinal cancer classification. The model was tested with various methods such as Google-Net, ResNet, and Alex-Net. Three sample datasets were used to evaluate the effectiveness of the developed model for cancer classification. The CNN-LSTM model outperformed other approaches in classifying gastrointestinal cancer, but overfitting occurred in the feature extraction and classification steps.

Singh and Singh [17] developed a method that combines ant lion optimization, feature weighting, and preprocessing to effectively classify gastrointestinal lesions. The high-dimensional gastrointestinal dataset, featuring shape, color, and texture properties from colonoscopy videos, was utilized to evaluate the model. Preprocessing was performed to address dominant, outlier, and zero-valued features. Feature weighting was employed to assign importance to features, enhancing classification performance. The enhanced ant lion optimization was used for simultaneous feature weight and SVM parameter searching. The developed technique, integrating texture and color data, demonstrated superior categorization performance. However, the enhanced ant lion optimization approach exhibited weak convergence of the search process and was easily caught in local optima.

2.1 Summarization

In this discussion, we delve into recent research on diagnosing liver cancer using machine learning and deep learning methodologies.

Various classes of data are harnessed in image processing tasks within the medical sector, according to existing literature on database compilation. These tasks involve identifying malignant or non-cancerous regions, assigning a particular class or category to the tumor, distinguishing between organ and non-organ parts of the image, and using a minimal number of images as input, taken via a vaguely defined type of non-invasive technology. In many of these methods, there's a lack of correlation maintained between the specific details of the organs and the type of cancer. The current work addresses this issue of image abundance and also elucidates how to interpret the stages of liver tumors and classify diseases based on their severity.

An exhaustive review of medical image processing literature suggests that feature extraction techniques are more suitable for diagnosing malignant liver conditions. In this current study, multiple features are extracted from a vast database, and classifiers are employed to enhance the accuracy of tumor detection. Enhanced images serve as the input for feature extraction, and a fitting algorithm distinctly differentiates between the intensity levels of normal and abnormal tumor images. The detection process yields a satisfactory classifier rate.

Thoroughly examining the literature on medical image processing reveals how different liver cancer conditions can be appropriately categorized. The current work improves the efficiency of tumor classification by leveraging multi-classifiers, a large database, and the extraction of numerous features. All classifiers maintain a steady classifier rate in detecting the disease. The classification of the substantial database yields a unique classifier rate, which helps to categorize the different types of liver cancer. This classification system for liver cancer enables a deeper understanding of a specific tumor class and aids in interpreting the tumor's stage.

Most techniques currently described in the literature depend on a handful of images that require enhancement for the development and testing of computer-aided diagnostic methods due to a lack of precise organ and disease details. Thus, it's not justified to assess detection and classification methods based on such databases.

Although a few researchers have combined different databases to categorize various tumor types, the database should also encompass clinically obtained images that radiologists deal with daily.

Therefore, the present work considers a composite database that includes various clinically identified liver cancer tumor classes.

This approach ensures the maintenance of an appropriate category of cancerous liver images in relation to the type of tumors, the field of view, the number of patients, machine settings, among other factors.

Furthermore, several methods for classifying a range of liver cancers will be tested on this substantial composite database to verify their generalizability. In order to combine images and provide relevant information, a large database was employed in experiments dealing with the detection, classification, and interpretation of tumors and tumor stages.

2.2 Limitations of existing system

Limited accuracy: While the system can classify liver disease accurately based on specific parameters, it may only sometimes provide the correct diagnosis. Other factors the system may need help to account for may result in incorrect classifications.

Data quality: The system's accuracy dramatically depends on the quality and quantity of data used to train it. The system's performance may deteriorate if the data used to train it is inadequate, biased, or of poor quality.

Limited scope: The system may be designed to classify only certain types of liver illnesses and may be incapable of diagnosing less prevalent or unusual conditions.

Need for expert validation: Before being utilized to make medical choices, the system's outputs may need to be confirmed by a medical expert. This takes more time and resources away from the diagnostic process.

Ethical considerations: Using AI systems for medical diagnosis raises ethical concerns about privacy, data protection, and the possibility of AI replacing human judgment in medical decision-making. Before deploying any AI-based diagnostic system, it is critical to address these challenges thoroughly.

2.3 Problem identification of existing system

Liver disease is a significant public health concern affecting millions globally. Accurate diagnosis and appropriate treatment can improve patient outcomes dramatically, yet diagnosis can be difficult and time-consuming for doctors. The classifications of liver diseases attempt to give a quick and precise diagnosis, which can help improve patient outcomes and lower healthcare costs. However, there are several challenges to liver disease classification, including a lack of standardized diagnostic criteria, complex and heterogeneous disease manifestations, and a scarcity of expert clinicians. Furthermore, because liver disease can be caused by various factors, such as viral infections, alcohol abuse, obesity, and genetic factors, classification is difficult.

As a result, the challenge of liver disease classification necessitates developing precise, efficient, and dependable diagnostic procedures that can assist physicians in diagnosing liver illness more effectively and efficiently, resulting in better patient outcomes and lower healthcare costs.

3. PROPOSED METHOD

The performance of the suggested model was assessed using the liver tumour dataset. The pre-processing for categorization used image augmentation and enhancement techniques. The feature extraction was done using Convolutional Neural Network (CNN) from the pre-processed image. The extracted features were applied to the AGRU method for the classification of Liver disease. Figure 1 shows the proposed CNN-AGRU model in Liver disease classification.

3.1 Pre-processing

Images of the Liver were pre-processed before applying to CNN models to resize and enhance the images. Color constancy was scaled in the image, and the image size was changed to 244×244 pixels for ResNet-50 and GoogleNet and 227×227 pixels for the AlexNet model. The three RGB channels mean it was calculated for Liver images, and an average filter was used to enhance the images. The average filter measures each pixel's average value with its neighbors and replaces it, and this process is carried out for the whole image.

CNN model is highly based on data volume, and training data in a more extensive set generates a model for promising results. The data augmentation method improves the classification accuracy for the CNN model, and data augmentation was applied due to the lack of medical images. The data augmentation also balances the dataset for some images between classes. The rotation, shifting, zooming, and flipping operations were used in augmented training data in this research.

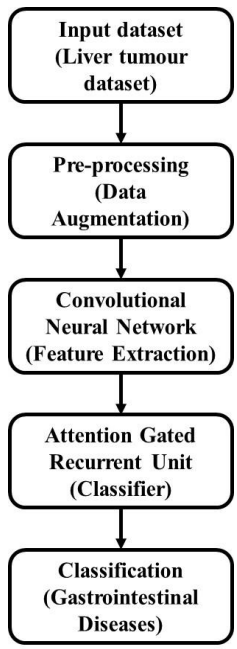

Figure 1. The CNN-AGRU model in liver diseases classification

3.2 Convolutional Neural Network

Convolutional Neural Network (CNN) is based on Deep Learning (DL) and Neural Networks (NN) [17, 18], which is suitable for handling 2D images. CNN model consists of Fully Pooling Layers (PL), Convolutional Layer (CL), and Connected Layers (FCL). Because CNNs acquire features through training and dramatically shorten the time for feature design or choosing the most distinctive features, they perform better than other machine learning techniques like Decision Tree, SVM, and Naive Bayes.

Convolution is an essential process in CNN, and the convolution layer is an important layer in CNN that performs a 2D convolution process on input and passes in kernels. Each Convolution Layer kernel's weights are randomly initialized, and the network training loss function is updated at each iteration. Final Kernels learn some types of patterns in input images.

CNN model consists of non-linear activation function, stack, and Convolution. Consider X as an input matrix and Convolution Layer has an output O and a set of kernels F_j exists $\forall_j \in [1, \cdots, J]$, then convolution output is defined in Eq. (1).

$$C(j) = X \otimes F_j, \forall_j \in [1, \dots, J] \quad (1)$$

The dot product of inputs and filter is defined using convolution operation $\otimes$.

In Eq. (2) a new 3D activation map is applied using $C(j)$ the activation map.

$$D = S(C(1), \dots, C(J)) \quad (2)$$

where, J stands for the total number of filters and S stands for the pile operation's channel direction.

Eq. (3) provides the 3D activation map D final output activation map and Non-Linear Activation Function (NLAF).

$$O = NLAF(D) \quad (3)$$

The output, filters, and input are three important matrixes with sizes S, as given in Eq. (4).

$$S(x) = \begin{cases} V_1 \times Q_1 \times H_1 & x = X \\ V_K \times Q_K \times H_K & x = F_j, \forall_j \in [1, \dots, J] \\ V_0 \times Q_0 \times H_0 & x = 0 \end{cases} \quad (4)$$

where, activation map of channels, height size, and width are denoted using three variables (V, H, Q), respectively. The output, filter and input are denoted using subscripts I, K, and O. It has two equalities: H_K indicate filter channel which is equal to the input channel H_I ($H_I = H_K$), the second number of filters J is equal to the output channel H_O that is H_O=J.

Eq. (5) and Eq. (6) measure values of (V_O, Q_O, H_O), A the stride, and padding denotes B.

$$V_0 = 1 + f_{fl}[(2 \times B + V_1 - V_K)/A] \quad (5)$$

$$Q_0 = 1 + f_{fl}[(2 \times B + Q_1 - Q_K)/A] \quad (6)$$

where, the term "floor function" is used as f_{fl}.

Eq. (7) selects rectified linear unit (ReLU) and NLAF is denoted as σ.

$$\sigma_{ReLU}(d_{ij}) = ReLU(d_{ij}) = \max(0, d_{ij}) \quad (7)$$

where, activation map D elements denote $d_{ij} \in D$. Sigmoid (SM) function and traditional Hyperbolic Tangent (HT) have considerable performance, and ReLU is a popular Non-Linear Activation Function (NLAF), as in Eq. (8) and Eq. (9).

$$\sigma_{HT}(d_{ij}) = \tanh(d_{ij}) = (e^{d_{ij}} - e^{-d_{ij}})/(e^{d_{ij}} + e^{-d_{ij}}) \quad (8)$$

$$\sigma_{SM}(d_{ij}) = \left(1 + e^{-d_{ij}}\right)^{-1} \quad (9)$$

ReLU is one-sided that is more plausible biologically than σ_{HT}. The CNN model is shown in Figure 2.

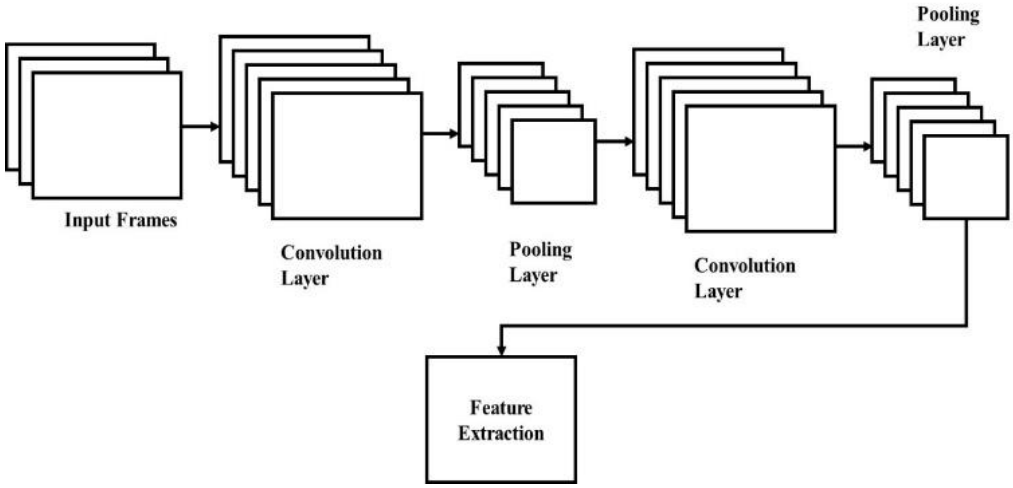

Figure 2. The CNN model

3.3 Attention Gated Recurrent Unit

Generally, the RNN suffer from vanishing and exploding gradient problem in the classification. RNN has a limitation of exploding gradient, and the term 'long-term' of gradient grows exponentially faster than short term. GRU [19] and LSTM [20] are RNN types, and unlike CNN, the RNN model backward connection affects the model accuracy, and the LSTM model is developed to tackle this problem. The LSTM model is designed for temporal features handled in long-range dependency, and cell blocks are present in LSTM internal structure. The hidden and cell states are transferred from one block to another, and that memory block is used to remember through gates.

A complex non-linear function is handled in sequence-to-sequence architecture, and encoder-decoder GRU networks with attention models jointly promote features. Specific spatial-temporal inputs are linked with a context vector at each time step t. Most relevant input features are adopted in the attention mechanism, as in Eq. (10).

$$e_{jt} = \tanh(W_a s_{t-1} + U_a h_{jt}) \quad (10)$$

where, weight matrices are denoted as U_a and W_a. The normalized weight of the energy vector is given in Eq. (11):

$$\alpha_{jt} = \left(\frac{\exp(e_{jt})}{\sum_{l=1}^{T} \exp(e_{lt})}\right) \quad (11)$$

where, input sequence of local region and target symbol denotes the alignment of attention probability in $\sum_{j=1}^{T} \alpha_{jt} = 1$, and α_{jt}. Attention probabilities of the encoded hidden state are measured based on weighted sum at each step at time step t of

the context vector.

Output prediction of different encoded input variables used to represent the vector. GRU model of sequence to sequence with attention to measure input sequence elements at required attention.

LSTM has three gates such as input, output, and forget. GRU model has two gates an update and a reset gate. The update gate checks earlier cell memory to keep it active, and the Next cell combines with the preceding cell memory, which is carried out by the reset gate. LSTM input and forget gate are merged to the update gate, and the reset gate of the hidden state is directly applied. The GRU cell of general equations is given in Eq. (12)-Eq. (15). GRU of multi-layer considers faster training based on a smaller number of parameters.

$$z_t = \Theta(W_z.[h_{t-1}, x_t] + b_z) \tag{12}$$

$$r_t = \Theta(W_r.[h_{t-1}, x_t] + b_r) \tag{13}$$

$$\widehat{h_t} = \tanh(W_h.[r_t.h_{t-1}, x_t] + b_h) \tag{14}$$

$$h_t = ((1 - z_t).h_{t-1} + z_t.\hat{h}_t) \tag{15}$$

The sequence representation of CNN is measured using multi-layered GRU for its effective sequence learning. Spatial feature extraction of CNN layers is measured from refined input data, and multi-layer GRU is fed into the model. Two CNN layers of the ReLU activation function are applied and followed by a kernel filter with the size of 2 in 1×16 and 1×8, which were applied for the first and second layers, respectively. GRU layers are applied with spatial extracted features. Two GRU layers used temporal characteristics, and a dense layer carried out the prediction. The GRU model is shown in Figure 3.

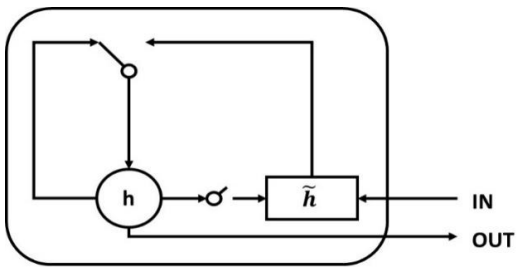

Figure 3. GRU model

3.4 Managerial implications

The proposed method can assist doctors and medical workers in more precisely and rapidly diagnosing liver illnesses, leading to better patient treatment outcomes. Deep learning techniques can also assist in uncovering trends in medical data that are not visible to the naked eye, resulting in more successful treatment strategies.

Using automated classification systems can reduce medical personnel workloads, allowing them to focus on other areas of patient care. This can result in improved patient outcomes and increased job satisfaction among healthcare professionals.

Automated classification systems can also minimize manual diagnosis and treatment expenses, which are significant in healthcare organizations. Deep learning techniques can assist in identifying potential health risks early on, avoiding the need for more expensive and intrusive procedures later on.

As with any program that handles patient data, it is critical to safeguard the system's security and patient privacy. Healthcare organizations must establish adequate security measures to ensure that patient data is not compromised or misused.

The proposed strategy is a foundation for future automated medical diagnosis and therapy studies. Building on this work, healthcare organizations and researchers can create more advanced deep-learning models for different medical applications, leading to better patient outcomes and healthcare delivery.

4. SIMULATION SETUP

The implementation details of the dataset and parameter settings of the proposed method are discussed in this section.

Dataset: The liver tumour segmentation dataset [21] is used to evaluate the CNN-AGRU model. This dataset consists of 130 CT images of the liver.

Parameter Settings: The Adam method is used as an optimizer in the CNN-AGRU method; the batch size is 128, epochs are 10, and the learning rate is 0.001.

Metrics: Accuracy, Sensitivity, and Specificity were evaluated from CNN-AGRU and compared with standard and existing methods. The formulas are given in Eq. (16)-Eq. (18).

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \times 100 \tag{16}$$

$$Sensitivity = \frac{TP}{TP + FN} \times 100 \tag{17}$$

$$Specificity = \frac{TN}{TN + FP} \times 100 \tag{18}$$

System Requirement: The CNN-AGRU approach for classifying liver diseases was implemented on an Intel i7 processor, a 6GB GPU, 16GB of RAM, and a Windows 10 operating system.

5. RESULTS

The CNN-AGRU model is proposed for Liver disease classification to increase efficiency. The pre-processing of image enhancement and augmentation were carried out in input images. The CNN model extracts the features from the input images, and the AGRU model performs classification.

The CNN-AGRU model is tested on Liver disease classification and compared with machine learning models, as given in Figure 4 and Table 1. Machine learning models perform less in Liver disease classification due to a lack of feature learning and an imbalanced data problem. The Decision Tree and Random Forest provide unstable performance due to the overfitting problem. The KNN model has outlier restrictions, but the SVM model struggles with data imbalance. The CNN-AGRU model offers a standard feature learning method that improves the feature learning efficiency in the GRU model. The context vector learning in the attention layer of GRU helps to learn the context vector of a spatio-temporal model.

The CNN-AGRU model is evaluated in Liver disease classification and compared with the deep learning model, as given in Figure 5 and Table 2. The CNN model's overfitting limitation degrades the performance of classification RNN

models do less well in classification because they lose the essential information learned early in the training process. The vanishing gradient problem in the LSTM model causes network updates to lose important information for categorization. GRU method washouts the new irrelevant features to improve the learning and has an overfitting problem in classification. The CNN-AGRU model provides energy vector normalization to learn the unique features from the input data. The attention layer in GRU learns a context vector related to the spatio-temporal model to select the relevant features and improves efficiency. The CNN-AGRU model has 98.2% accuracy, and GRU has 92.3% accuracy.

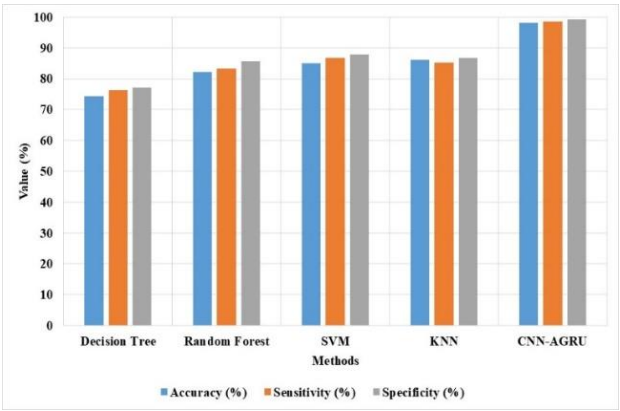

Figure 4. CNN-AGRU and standard classifiers in liver disease classification

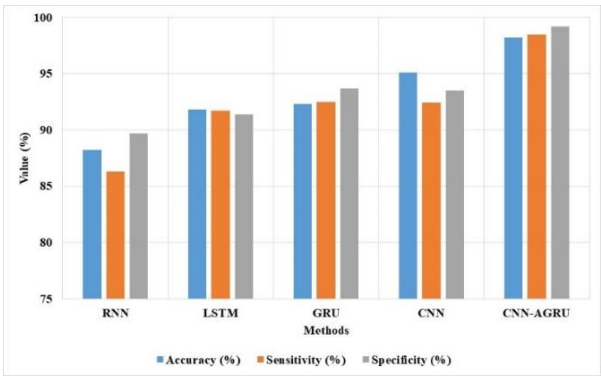

Figure 5. CNN-AGRU and deep learning models in liver disease classification

Table 1. CNN-AGRU model and standard classifier comparison

Methods	Accuracy (%)	Sensitivity (%)	Specificity (%)
Decision Tree	74.3	76.2	77.1
Random Forest	82.1	83.2	85.7
SVM	85.1	86.7	87.9
KNN	86.2	85.3	86.8
CNN-AGRU	98.2	98.5	99.2

Table 2. CNN-AGRU model and deep learning model comparison

Methods	Accuracy (%)	Sensitivity (%)	Specificity (%)
RNN	88.2	86.3	89.7
LSTM	91.8	91.7	91.4
GRU	92.3	92.5	93.7
CNN	95.1	92.4	93.5
CNN-AGRU	98.2	98.5	99.2

5.1 Comparative analysis

The existing methods in related works were compared with the CNN-AGRU model to show its efficiency.

The CNN-AGRU model is compared with existing Liver disease classification methods, as shown in Figure 6 and Table 3. Unlike the average GRU model, which chooses the pertinent features, the CNN-AGRU model discards newly learned irrelevant information. The CNN-AGRU model learns features collaboratively, which enhances the model's feature learning performance. When classifying spatiotemporal input, the CNN-AGRU model learns a context vector that chooses the pertinent features. The CNN-AGRU model has energy vector normalization that helps to learn unique features and solves imbalanced data problems. The CNN-based models of GoogleNet, ResNet-50, and AlexNet have the limitation of overfitting issues. The LSTM-CNN model increases the overfitting in the model and degrades the performance. The improved RCNN model has lower efficiency in feature learning. The CNN-AGRU model has an accuracy of 98.2%, and the Google-Net model has 96.7% accuracy.

Table 3. CNN-AGRU model and existing method comparison

Methods	Accuracy (%)	Sensitivity (%)	Specificity (%)
CNN-AGRU	98.2	98.5	99.2
GoogleNet [11]	96.7	96.6	99
ResNet-50 [11]	95	94.8	98.8
AlexNet [11]	97	96.8	99.2
TAS-RF [12]	86.2	89.4	90.5

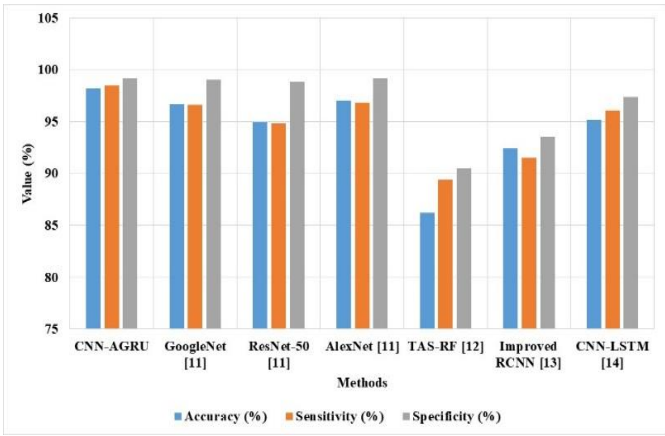

Figure 6. CNN-AGRU and existing methods in Liver disease classification

6. CONCLUSION

The most popular medical imaging technologies are quickly developing computer-aided diagnosis. Furthermore, the research in this area is still in its early stages due to a lack of infrastructure and environmental factors. There are a lot of people that are afflicted with various illnesses. Diseases must be accurately diagnosed before receiving the appropriate treatment. For the identification of liver disorders, computerized diagnostics do not need the assistance of medical radiologists. As a result, there is a good likelihood that medical professionals will have trouble identifying conditions. The difficulties include creating an effective learning

machine-based method for accurately and quickly classifying diseases and identifying disorders.

It is recommended that the CNN-AGRU model be employed to improve the categorization of liver diseases. While the CNN model extracts the relevant details from the input images, the AGRU model performs the classification. The CNN-AGRU model's performance in diagnosing liver disorders was evaluated using the liver cancer dataset. The current CNN-based model has an overfitting issue, whereas the LSTM and GRU models have vanishing gradient issues. The AGRU model employs an attention layer to learn the distinctive features based on energy vector normalization to address the overfitting imbalance issue. The CNN-AGRU model picks up on certain features and the context vector associated with spatiotemporal data. The CNN-AGRU model is evaluated for the categorization of liver diseases and contrasted with existing techniques, machine learning, and deep learning. Due to a lack of feature learning and difficulty with data imbalance, machine learning models perform less well when classifying liver diseases. The Decision Tree (DT), Random Forest (RF), Support Vector Machine (SVM), and K-Nearest Neighbours Algorithm (KNN) methods were evaluated with the suggested model using machine learning techniques. Due to the overfitting issue, SVM, KNN, and Decision Tree offer unstable performance compared to Random Forest. Accuracy, sensitivity, and specificity are performance indicators that are compared. The accuracy rate for CNN-AGRU is 98.2%, whereas the rates for the DT, RF, SVM, and KNN models are 74.3%, 82.1%, 85.1%, and 86.2%, respectively.

6.1 Future directions

Future directions for research into the suggested detection and classification processes are as follows:

- The success of reducing the detected information or its propagation is only partially satisfying since, before the rapid spread of diseases, asymptomatic phenomena, and patient carelessness, they may enter a critical stage with significant alterations. Therefore, a mechanism for detecting liver disease earlier should be created.
- Due to its complexity, the proposed mechanism's implementation must be handled correctly in real-world circumstances. Therefore, a more limited mechanism should be created in the future to address practical problems.
- A deep learning technique, such as a convolutional network, should be created to identify and categorize the various stages of liver disease.

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