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**Article**

# A Neuro-Fuzzy-based Approach to Detect Liver Diseases

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**Abstract:** The liver is a crucial organ in the human body and performs vital functions essential for overall health, including metabolism, immunity, digestion, detoxification, and vitamin storage. Detecting liver diseases at an early stage poses challenges due to the liver's ability to function adequately despite partial damage. Early detection is crucial as liver diseases have significant clinical and socio-economic impacts, affecting other organ systems and requiring timely intervention to improve patient survival rates. Classical diagnostic methods for liver disorders may not always produce better results, thus necessitating more advanced and accurate diagnostic systems. Intelligent systems like predictive modeling and decision support systems, have shown promising results in recent years in disease detection and are aiding medical practitioners. In this research, a neuro fuzzy-based system integrating neural networks and fuzzy logic (FL) was implemented. Based on the risk factors present in the dataset that was used to benchmark the algorithm, this system offered a classification accuracy of 97% which is comparable with existing systems in the literature. This study creates a neuro-fuzzy system for early liver disease identification, solving diagnostic issues and offering healthcare improvements. The proposed system is validated by presenting the simulation results.

**Keywords:** Intelligent System, Liver Diseases, Machine Learning, Neurofuzzy

## 1. Introduction

### 1.1. Background and Motivation

As one of the body's most important organs, the liver oversees several critical functions. It purifies the blood by removing toxic compounds, produces bile for digestion, stores and delivers vitamins and minerals, and processes nutrients. These functions can be disrupted by disease of the liver. Chronic Liver Disease (CLD) is a worldwide pandemic affecting many people from a variety of different backgrounds, ranging in age and sex [1]. CLD is a multifaceted platform with potentially multiple triggers. In fact, Chronic liver disease is a catchall phrase encompassing a huge range of causes, from personal lifestyle choices to existing medical conditions responsible for liver disease. Nevertheless, let's not also lay aside liver disease and its linkages to its hereditary and metabolic roots. Similarly, liver diseases are metabolic genetic diseases caused by common genetic compatibility encapsulated in the L-Carnitine Deficiency of which is subsequently demonstrated as liver disease during the lifetime of a person, a metabolic or genetic disorder of an inherited cause. Furthermore, a risk factor for liver disease is smoking, obesity and poor dietary choices, and the root and severity of CLD may be caused and driven by inflammation and biochemical mismatches within the liver [2]. Chronic liver conditions stem from the following roots: toxins, alcohol, infections, autoimmune diseases, inherited genes defects, metabolic disorders and bad lifestyle decisions. Primary care liver function tests (LFTs) are insufficient to diagnose NAFLD and cirrhosis [3].

Improving non-invasive techniques for liver disease detection and treatment is crucial as liver disease fatalities grow [4]. Reference [5] suggested that a major cause of CLD is prolonged alcohol misuse, wherein the consistent and excessive intake of alcohol harms the liver cells, results in inflammation, scarring, and eventually leads to liver disease. Another significant contributor to liver diseases is exposure to toxins, which can come from various sources such as environmental pollutants, industrial chemicals, and certain medications. Ingestion of contaminated food and pharmaceuticals can also introduce harmful substances into the liver, further compromising its health. In the past decades, there has been growing public interest in the impact of environmental toxins on liver health primarily because of the widespread use of pesticides, the consumption of food contaminated with aflatoxin, and the presence of harmful cyanobacterial algae blooms in regions where liver disease is prevalent as reported in [1].

Infections also play a crucial role in liver disease as well. Viral hepatitis, including Hepatitis B, C, and D, is a leading

cause of chronic liver disease in different parts of the world [5] and these viral infections can result from exposure to infected blood or bodily fluids [6] unsafe medical procedures including contaminated blood transfusion and intravenous drug use [7], from mother to child or unprotected sexual contact [6]. Autoimmune diseases, where the immune system mistakenly attacks healthy liver cells, can also lead to chronic liver damage. It is highlighted in [8] that these groups of diseases, collectively referred to as Autoimmune Liver Disease (AILD) are grouped into Primary Biliary Cholangitis (PBC), Autoimmune Hepatitis (AIH), and Primary Sclerosing Cholangitis (PSC). Some other authors [9], [10] have further highlighted that both malnutrition and obesity can result in the progression of liver disease, including Non-Alcoholic Fatty Liver Disease (NAFLD), which, in turn, may lead to Non-Alcoholic Steatohepatitis and Cirrhosis in certain individuals. Liver disease is a major health concern worldwide, with significant morbidity and mortality. It is enunciated in [10] that liver diseases contribute to approximately 2 million deaths worldwide. Among these deaths, one million are attributed to complications arising from cirrhosis, while the other million result from viral hepatitis and hepatocellular carcinoma. Especially, Cirrhosis is the 11th leading cause of death globally, and liver cancer ranks as the 16th cause, collectively accounting for 3.5% of all deaths worldwide as reported in reference [10], World Health Organization, 2019 [11].

The global prevalence of viral hepatitis also remains high, which emphasizes the importance of raising awareness, prevention strategies, and access to treatment. In addition, drug-induced liver damage has emerged as a substantial contributor to severe hepatitis cases, further highlighting the need for proactive measures to mitigate such risks. By addressing the changeable risk factors associated with liver diseases, such as alcohol abuse, viral infections, obesity, and exposure to hepatotoxic substances, it is possible to reduce the incidence and burden of liver diseases.

The alarming statistics underscore the urgent need to prioritize public health interventions since most liver diseases are preventable, as in reference [9], and it is imperative to note that effective prevention and management efforts aiming at lowering the burden of liver disease depend on recognising and addressing these underlying causes. Reference [11] points out that promoting public health initiatives, including education, vaccination programs, early detection, and lifestyle modifications, can significantly improve liver health outcomes and enhance overall well-being and numerous studies have been conducted all around the world to look at ways to continuously screen for liver tumor cases. Professionals, including those in the medical field, are working hard to advance medical practices relating to liver diseases. Reference [12] enunciates that the best strategy is to stop liver cancer from occurring in the first place to lessen the severe harm it causes. Other authors in references [13], [14] believe that the spread of liver cancer cases can be stopped through immunisations and vaccinations. The research in [14] highlights that expanded programs for systemic immunization against hepatitis B virus have significantly reduced the number of new cases in many countries, including China. Conversely, [14] notes that as living standards improve, the prevalence of metabolic liver disease, including non-alcoholic fatty liver disease and alcoholic liver disease, is expected to increase, eventually leading to more cases of end-stage liver disease (liver failure, cirrhosis, and liver cancer). This provides a significant reason for an increased level of focus on the development of systems to effectively diagnose and treat liver diseases.

It is also noteworthy that since the liver operates normally even when it is partially destroyed, problems with it are difficult to identify in the early stages. The likelihood that a patient would survive liver disease is greatly increased by early diagnosis. Yet, as [3] enunciates, the detection of liver diseases at an early stage poses a challenge, as numerous patients exhibit minimal symptoms until the disease has progressed significantly, making intervention less effective. Also, early detection is crucial for effective treatment and management, yet current diagnostic methods can be time-consuming, costly, and invasive. When diagnosing liver illnesses, blood and enzyme levels are both examined and there is a lot of room for mistake in this diagnosis because of the several enzymes involved as well as the impact of patients consuming alcohol in different amounts. It has become a requirement that scientist's study and develop systems that can drastically reduce errors that occur during medical diagnosis and can guarantee an efficient method of liver disease diagnosis. Thus, this leads to the necessity of creating a neuro-fuzzy based system for early detection of liver diseases. The use of the NFS for early detection of liver diseases can change the paradigm of diagnosis and treatment of liver diseases. As indicated in, this system can allow for early, accurate, non-invasive, and inexpensive detection of liver diseases, based on the power of AI and FL, which can guarantee better patient outcomes and reduce healthcare costs. Therefore, the development of an NFS for liver disease diagnosis is fundamentally vital.

### 1.2. Literature Review

In addition to the study of disease prevention, the summary of machine learning approaches to the diagnosis of liver pathology is provided in the Reference [17]. The paper is completed with a presentation of the possibilities of early detection of the disease. The study of the potential of machine learning in this area is based on a review of the existing literature. The topic of the capabilities of machine learning remains relevant both in the context of preventing and recognizing liver pathologies, the depiction of which is provided in Reference [18]. As a continuation, in the Reference [19] an analysis of the possibility of early detection of liver disease due to the integration of smart technologies is presented. This investigation on intelligent prediction of liver disease should use a hybrid approach to better predict accuracy. The authors use the two combined explanations of how the specific restriction or K-Means method works and has improved accuracy in the hybrid approach.

The use of deep learning (DL) techniques for the classification of liver illness is the main focus of the study in

reference [20]. Their work shows that DL networks can enhance classification accuracy, yet there isn't a lot of information available about the dataset. A hybrid model for predicting liver illness is presented in reference [21], with an emphasis on the higher accuracy that comes from combining models. They combine Support Vector Machines (SVM), K-Nearest Neighbors (KNN), and Artificial Neural Networks (ANN) in their methodology, albeit they only touch on scalability in passing. The paper by [22] presents the application of Fuzzy C-Means (FCM) and Adaptive Neuro-Fuzzy Inference System (ANFIS) for intelligent diagnosis of liver disorders. The authors apply ANFIS and FCM to patient data, highlighting the improved diagnosis accuracy of the hybrid model; nevertheless, there is only a limited discussion of external validation. The research in [23] offers a unique FpcFHSS model for determining the risk of liver disorders. Their paper presents a mathematical approach utilizing FpcFHSS aggregations, exploring how the model handles periodicity and uncertainty. But there is still little talk about how applicable this is in the actual world. Using the Variable-Neighbor Weighted Fuzzy K-Nearest Neighbors (Variable-NWFKNN) approach, [24] provides a valuable contribution to the diagnosis of liver disorders. Their results point to better performance on unbalanced datasets, however, there is limited discussion on computational efficiency. The research in [25] investigates the accuracy prediction for liver illness in Indian patients using a variety of machine learning techniques. Their study, which applies SVM, Logistic Regression, KNN, and ANN, shows enhanced accuracy and reliability in predicting liver illness, albeit it only briefly addresses model interpretability. The research in [26] deals with machine learning methods for the identification and prognosis of liver disease. Their research shows improved accuracy when using a variety of machine learning methods, such as Random Forest, SVM, KNN, and Decision Trees. On the other hand, there is a limited conversation on external validation. It offers a thorough summary of machine-learning techniques for predicting liver disease [27]. Their work presents a thorough assessment and analysis of existing models, emphasizing the various and useful tools provided by ML models.

A logistic regression model is proposed by [28] for the early diagnosis of liver disease. They emphasize accuracy, precision, sensitivity, and kappa in their analysis, which makes use of confusion matrix, logistic regression, and secondary data from the UCI repository. Nevertheless, there isn't much talk about practical application or external validation. In order to predict liver illness, [29] compared three machine learning algorithms: logistic regression, kernel Neural Networks, and random forests. According to their results, Logistic Regression has the best accuracy, highlighting the necessity of investigating other possible algorithms in more detail. The research in [30] presents the best classification model for identifying liver illness to optimize prediction accuracy. By utilizing a variety of parameters, their study expands upon the earlier framework, attaining the objectives of precise disease identification and decision support. However, because of the short sample size, the study recognizes overfitting problems. [31] use a Mamdani fuzzy inference method to create a fuzzy expert system that detects liver fibrosis with a 95% accuracy rate. Although there is little discussion of the input variables, their multilayer fuzzy expert system, which is based on a fuzzy logic approach, has good classification accuracy. A fuzzy classifier for liver disease staging based on fuzzy inference is presented by [32]. With regard for cross-gender differences, their fuzzy classifier models in MATLAB Fuzzy Logic to assist in disease staging. The expert system diagnoses patients with 85% accuracy, however, because of sophisticated methods and limited sample size, overfitting is a worry. Together, the evaluated articles provide crucial information for the creation of a neuro-fuzzy system intended to identify liver disorders early on. Notably, a number of research highlight the effectiveness of machine learning algorithms in accurately predicting liver illnesses, including random forest, logistic regression, and KNN [28]. To improve prediction skills, these models make use of a variety of clinical factors, such as liver enzyme levels, bilirubin levels, and patient demographics.

When machine learning methods are compared, logistic regression stands out as having the highest accuracy for predicting liver illness [29]. Fuzzy logic and neural networks are also included in diagnostic models to improve their interpretability and flexibility, which leads to better decision-support systems [33]. A generative adversarial neural network was used in [33] for the prediction of Parkinson's disease, yielding a high accuracy of prediction based on the dataset used. It is carried out in [34] a performance comparison of Boosting techniques for classification of microarray data. The result obtained shows that XGBoost outperforms the other boosting techniques.

The assessment does point up several notable gaps in the available research, though. Although many computational approaches exhibit potential, issues with standardization, interpretability, and application in practical medical settings still exist. While several studies have attempted to solve these issues, the merging of fuzzy logic and neural networks comes with its own set of complications.

The main areas of weakness in the literature are the scant investigation of hybrid models that combine neural networks and fuzzy logic and the requirement for stronger validation on a wider range of datasets. The implementation of neuro-fuzzy systems in medical contexts presents some challenges, such as the complexities of managing missing or imprecise data. These issues call for additional research and development.

These identified limitations and the challenges of developing a complex neuro-fuzzy system for early liver disease detection serve as justification for the current investigation. This work intends to provide a novel approach that improves diagnosis accuracy and interpretability in real-world healthcare scenarios by combining the strengths of fuzzy logic and neural networks. A roadmap for progressing the field of liver disease detection is created by the synthesis of information from the examined publications, which serves as a strong basis for the proposed study.

### 1.3. Contribution

The significance of this study is in creating a method for automatically diagnosing liver diseases using risk factors. By utilizing a Neuro-fuzzy approach, the research adds to the field of medical diagnostics.

## 2. Materials and Methods

If an NFS is to become a method that can be practiced in the early diagnosis of liver disease, careful and complete planning and rigorous scientific execution are essential. This chapter details the procedure and what was necessary to do it, including the research methodology, scope, data collection instrument, data analysis methods, and ethical issues. By offering details into the steps implemented to execute the NFS and evaluate the NFS efficacy typical of the scientific rigor and reliability of the research, this section can help researchers better understand and appreciate the validity of the study. When the incorporation of neuro-fuzzy techniques in liver disease detection is being done, it becomes necessary for particular attention that the different essential aspects are not ignored, such as dataset selection, algorithmic structures, and validation methods. The author has elucidated the presented study design for a better understanding. Feature engineering was conducted using pre-trained models like mRMR, while ANFIS was used for classification. With a discourse predominantly targeting hepatobiliary science and having personal experience integrated, the article is expanded to include more content, and the original structure, and HTML elements are preserved.

### 2.1. Data Acquisition

This study involved gathering a small amount of information from patients at General Hospital Minna in Niger State during medical assessments. This included important medical data like liver function tests, patient histories, imaging findings, and clinical reports that were collected for analysis purposes. To ensure patient confidentiality, the data was anonymized. Initially, this data served as the raw data for testing the software. However, the software required a substantial amount of data to achieve accuracy, which posed a minor setback as the data obtained from the hospital was insufficient for the neuro-fuzzy software to perform optimally. To address this issue, additional data from Kaggle was incorporated alongside the existing raw data. The platform offers a diverse range of datasets contributed by researchers, organizations, and the data science community. For this work, the dataset specifically related to liver disease was chosen from Kaggle due to its direct relevance [35].

### 2.2. Dataset Description

The liver disease dataset was read from the file "indian_liver_patient_dataset.csv" using the pandas library's read_csv function, converting it to a panda data frame. Prior to creating the data frame, any whitespace within the data was eliminated to maintain uniform formatting. The dataset contained 5 rows representing instances and 11 columns representing variables, as indicated by its shape. The sample is shown in Fig. 1.

| | Age | Gender | Total_Bilirubin | Direct_Bilirubin | Alkaline_Phosphotase | Alamine_Aminotransferase | Aspartate_Aminotransferase | T |
|---|---|---|---|---|---|---|---|---|
| 0 | 65 | Female | 0.7 | 0.1 | 187 | 16 | 18 | |
| 1 | 62 | Male | 10.9 | 5.5 | 699 | 64 | 100 | |
| 2 | 62 | Male | 7.3 | 4.1 | 490 | 60 | 68 | |
| 3 | 58 | Male | 1.0 | 0.4 | 182 | 14 | 20 | |
| 4 | 72 | Male | 3.9 | 2.0 | 195 | 27 | 59 | |

**Figure 1.** First 5 rows of the data frame.

The dataset contains 11 columns, including Age, Total_Bilirubin, Direct_Bilirubin, Alkaline_Phosphotase, Alamine_Aminotransferase, Aspartate_Aminotransferase, Total_Protiens, Albumin, Albumin_and_Globulin_Ratio, and Liver_Problem. These are the attribute information of the dataset. The target column is Liver_Problem, which contains data values corresponding to the patient's possible liver problem status, where values of '1' represent a possible liver problem, and '2' represent non-liver problems.

The dataset's summary statistics were computed using the pandas info () function, offering valuable insights into its structure and features. The analysis provided the following key information about the dataset.

The columns encompass a mix of float64, int64, and object data types(strings). One column contains missing values, evident from the non-null counts. The Albumin_and_Globulin_Ratio has 1400 non-null values, while the expected number of rows of non-null values expected should be 1404, meaning there are 4 rows with missing data for the albumin column. This is shown in Fig. 2.

```
df.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 500 entries, 0 to 499
Data columns (total 11 columns):
 #   Column                      Non-Null Count  Dtype
---  ------                      --------------  -----
 0   Age                         500 non-null    int64
 1   Gender                      500 non-null    object
 2   Total_Bilirubin             500 non-null    float64
 3   Direct_Bilirubin            500 non-null    float64
 4   Alkaline_Phosphotase        500 non-null    int64
 5   Alamine_Aminotransferase    500 non-null    int64
 6   Aspartate_Aminotransferase  500 non-null    int64
 7   Total_Protiens              500 non-null    float64
 8   Albumin                     500 non-null    float64
 9   Albumin_and_Globulin_Ratio  496 non-null    float64
 10  Liver_Problem               500 non-null    int64
dtypes: float64(5), int64(5), object(1)
memory usage: 43.1+ KB
```

**Figure 2.** Summary statistics of the dataset.

### 2.3. Data Preprocessing, Splitting and Model Training

The obtained dataset underwent several pre-processing activities to ensure its appropriateness and quality for analysis. Various techniques were employed to address missing values, outliers, normalization, and inconsistencies within the data, ensuring its cleanliness and reliability. To assess the performance of the created models, a train-test split technique was utilized. The pre-processed dataset was divided into two distinct subsets: a training set and a test set. The data was divided into 70-30 train test ratio. That is the training set would be used to train our detection models, while the testing set would be used to evaluate the model's performance. The test and train split were performed to ensure a fair and unbiased evaluation of the model's future performance on unseen examples. Missing data were identified by calculating missing ratio for each row and then all columns with missing values were extracted using a list comprehension. The mean for each of the column was used to deal with the missing values in order to be robust to outliers. The missing values have been inputted by using the fillna() function to retain the key details that were necessary for the models performance. Categorical values were converted into numerical form in order to fit the data to the model while the numerical features were normalized with the Min-Max method in order to improve the model's performance. Cleaning and dealing it with missing values of the dataset has been performed. We are now ready to perform liver disease detection and evaluate the models for the performances.

## 3. Experimental Procedure

### 3.1. Data Augmentation and Algorithm Implementation

To tackle the issue of a small dataset, the raw dataset was augmented using the data augmentation. This can be achieved by performing slight transformations and deformations on images which has the effect of artificially increasing the number of images. This helps to make NFS more diverse and it learns complex patterns and potential feature points to represent liver diseases more effectively. As a result, the NFS will perform better than the above results, and the prediction accuracy will be higher. In the case of a small dataset, it uses the data augmentation approach which has a lot of potential for predicting the liver diseases earlier. The results of NFS after applying the data augmentation process are shown in Table IV. The ANFIS approach was employed to solve this problem because it is a hybrid intelligent system that integrates fuzzy logic with neural networks. In its core, an ANFIS is an ANN that implements a Takagi-Sugeno Fuzzy Inference System. A Takagi-Sugeno FIS is a FIS that uses the combination of FL and ANNs. The ANFIS is used in various medical related applications because it can effectively handle the complex patient data, is able to train itself and in the process adapt and learn the fuzzy rules based on input-output data pairs. This accuracy of ANFIS makes it suitable for any disease identification and for the diagnosis of the disease as well.

Let ΣΣ be the space of knowledge representations, and YY be the set of input-output harmonics. ANFIS dynamically evolves through the transformation in (1).

$$\Phi: \Sigma \times \Upsilon \rightarrow \Phi: \Sigma \times \Upsilon \rightarrow F \quad (1)$$

where $F$ encapsulates the intricate fusion of neural network dynamics and fuzzy logic orchestration. The algorithmic steps for the implementation of ANFIS is shown in Algorithm 1.

### 3.2. Feature Extraction

In order to create a predictive model for detecting unknown liver issues from test data, it is crucial to pinpoint valuable attributes within the dataset that will be utilized in training the model. Through the use of regression analysis and visual representations of data, pertinent features with significant importance and overlap were extracted. By utilizing Seaborn's FacetGrid and scatter plot, we visualized the relationship between Albumin_and_Globulin_Ratio and Total_Protiens for different gender and liver problem status combinations.

This visualization allowed us to gain insights into how these two features are distributed concerning liver problem status and gender. By visually exploring the data in this manner, it was identified that the following features are highly relevant: Total_Bilirubin, Alamine_Aminotransferase, Total_Protiens, Albumin, and Albumin_and_Globulin_Ratio. These extracted features serve as the primary input variables for the model, enabling it to learn from the relationships captured within the dataset. By focusing on these informative features, the model's performance is expected to be optimized, leading to more accurate and reliable predictions of liver problem status for unseen test records. As shown in Fig. 3, these features showed the highest level of correlation to existing liver problem cases from the dataset.

**Algorithm 1**

```
Start
Procedure ANFIS (input_data, output_data, num_epochs, learning_rate)
   Initialize membership function parameters randomly
   For each epoch from 1 to num_epochs do
      For each data point in input_data do
         ForwardPass(input_data)
         BackwardPass(output_data, learning_rate)
      End For
   End For
End Procedure

Procedure ForwardPass(input_data)
   Compute degree of membership for each input variable
   Compute firing strength for each rule
   Compute rule output
   Normalize firing strengths
   Aggregate rule outputs
   Compute final output
End Procedure

Procedure BackwardPass(output_data, learning_rate)
   Compute error between predicted output and actual output
   Update consequent parameters using gradient descent
   Update membership function parameters using gradient descent
End Procedure
Stop
```

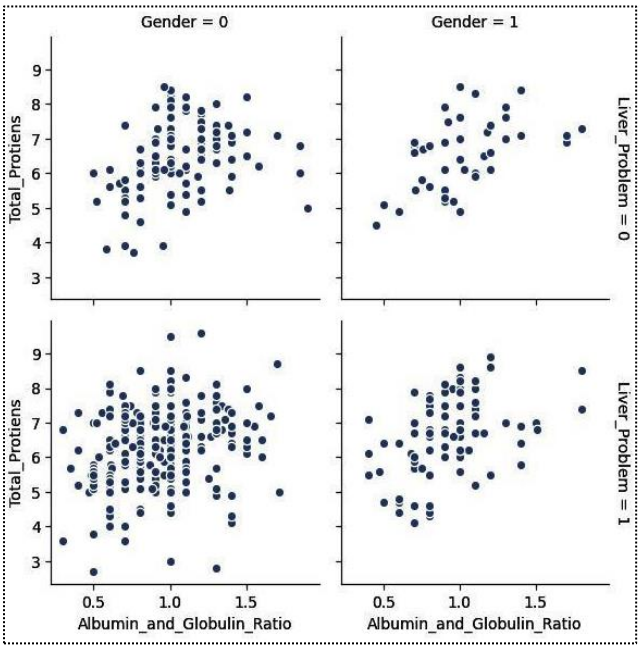



**Figure 3.** Correlation of selected feature sets and possible liver problem.

By examining the correlation values, we can identify the features that have the highest influence on the prediction of liver disease using neuro fuzzy techniques.

### 3.3. Train-Test Split for Model Training Implementation

To train the NF model for liver disease detection, we performed a train-test split on the pre-processed dataset. In order for a non-focal strategy to be developed (NFS) to be created for the early diagnosis of liver disease, a well-ruled and firmly-organized process of examination and scholarly science is required to reach the utmost precision in the graphic methods and technology. This section gives details about the implementation of scientific research methodology and the necessary materials required, such as the study, study population, data collection methodologies, data analysis techniques, and ethical considerations.

The dataset had been split into two sets - the one with (X, Y) and one where the testing set is (x, y). Using the train_test_split function, the model's performances were tested on the validation set with the train_test_split function used to divide the dataset into training and validation sets. The train_test_split function was applied with the parameter test_size=0.3, which denotes that 30% of the data is assigned for validation, and the remaining 70% is what is utilized for actual training. Also, 0.30, meaning 30% between the brackets was a parameter in the function representing the test_size value. The test_size, the parameters, and the X data, and y values are arguments; this statement has it.

### 3.4. Model Evaluation and Performance Metrics

The performance metrics used to evaluate the ability of the trained NF model to predict the IQ levels effectively and efficiently included the MAE:

#### *3.4.1. Mean Absolute Error*

This metric measures the average absolute difference between the evaluation of an NFS and its predictions. A smaller MAE value also means a higher level of accuracy and a higher scale of prediction errors. This metric assesses how the system performs.

$$MAE = n1\sum i = 1ne \mid log2(Yi) - log2(Y\hat{}i) \quad (2)$$

where:

- *Yi*: Actual value of the target variable for the *i*-th observation.
- *Y^i*: Predicted value of the target variable for the *i*-th observation.
- *n*: Total number of observations in the evaluation dataset.

#### *3.4.2. Loss*

Loss is the discrepancy between predicted and actual values used during model training. The objective is to minimize this loss through an appropriate loss function (e.g., MSE or MAE) to improve prediction accuracy on unseen data.

$$ULoss = \alpha \cdot MSE(Y, Y\hat{}) + (1 - \alpha)MAE(Y, Y\hat{}) \quad (3)$$

where:

- *Y*: Actual values of the target variable (vector).
- *Y^*: Predicted values of the target variable (vector).
- $\alpha$: Weighting factor for balancing Mean Squared Error (MSE) and Mean Absolute Error (MAE). It ranges between 0 and 1.

$$\text{Classification Accuracy} = \frac{\text{Total number of positive cases}}{\text{Total number of tested samples}} \times 100$$

Performance measures revealed the trade-off between misclassifying false positives and detecting genuine positives in the categorization of liver diseases by NF models.

## 4. Result and Discussion

### 4.1. Result of Classification

A "count" plot is a bar graph displaying the frequency of different categories in a dataset. It shows how many data points belong to each category, helping to visualise the pdf and compare them. The height of the bars represents the frequency for each category. The code first uses the Seaborn library to create a "count" plot, helping us to see how many patients in the dataset have liver problems. The "x" axis of the graph represents the two categories: "liver_problem," and the "y" axis represents the count of patients in each category. The code then calculates and prints the number of patients who were diagnosed with liver disease (LD) and the number of patients who were not diagnosed with LD. This makes comprehending the data more accessible and helps determine how many people in the dataset have liver issues. This is shown in Fig. 4.

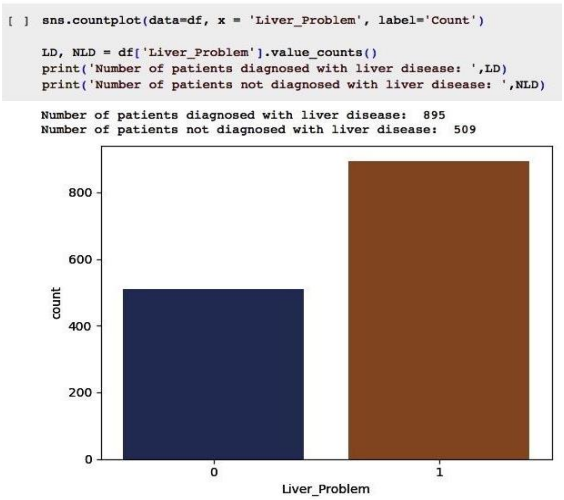



**Figure 4.** Classification result plot.

### 4.2. Result of Cross-Validation

The different folds were eventually used to shape the model with the nsplit = 5 parameter in cross-validation to find out how machine learning models are performing as well as to see its generalization capability on unseen data. The procedure goes through n cycling through the folds separately as the number of cycles match the number of the folds, so that the validation is done n times. The entire process is repeated for execution on each fold as the validation size is used only once for testing and the remaining k-1 folds are used as new training sets.

The model was trained using a tensor flow implementation of ANFIS, the five features discussed above Total_Bilirubin, Alamine_Aminotransferase, Total_Protiens, Albumin and Albumin_and_Globulin_Ratio, were the inputs used for the training of the model. The training parameters consist of 2 membership functions (gbellmf) which were applied for all inputs on training of the model as shown in Fig. 5.

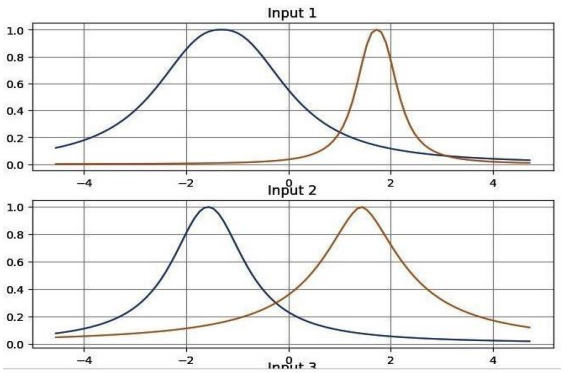



**Figure 5.** Sample model's membership function.

The model was then trained for 100 epochs using batch size of 1, stochastic gradient decent (SGD) optimizer and a mean absolute loss function. Early stopping was set in place to prevent the model from over training, as shown in Fig. 6.

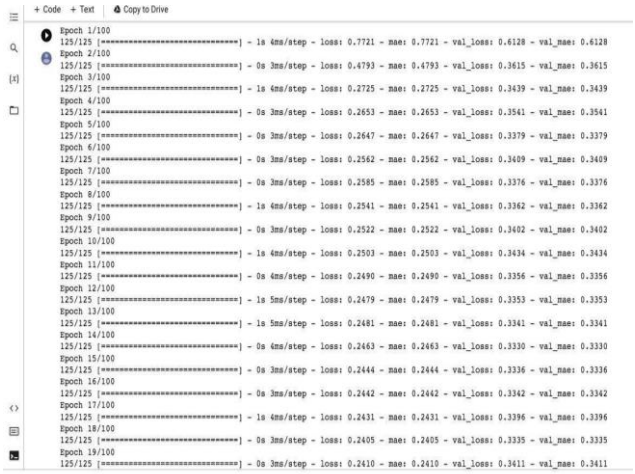



**Figure 6.** Epoch of the training process.

After the model had been successfully trained, evaluation was performed to verify the performance based on the earlier discussed metrics. The evaluation analysis from the first training set showed higher validation mean absolute error(val_mae) compared to the subsequent mean absolute error (MAE) as shown in Fig. 7. The MAE drops as the training epoch increases, indicating a better performance of the model.

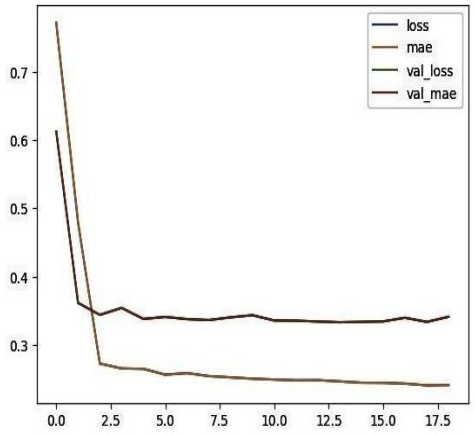



**Figure 7.** Performance result using the MAE.

With the result above, a lot more could be done in order to reduce the validation error as much as possible and improve upon the model prediction. Fig. 8 illustrates the mean absolute loss value during model evaluation, along with the accuracy achieved on the validation dataset.

The performance metrics and their values can vary depending on selected parameters, dataset characteristics, and other influencing factors.

The average classification accuracy result from the 5-fold cross validation shows that 412 samples were correctly classified as positive cases out of the 421 total test datasets. This result into approximately 97% accuracy. This result is comparable with similar work in the literature including [20], [22] and [24].

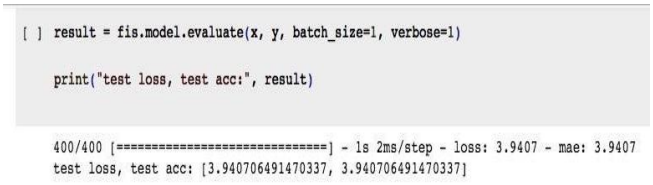



**Figure 8.** Result of the evaluation metrics in relation to MAE and loss.

## 5. Conclusion

This work developed a neurofuzzy based system for early detection of liver diseases. Benchmarked on a public dataset obtained from Kaggle, which was subjected to cleaning and preprocessing to ensure its reliability and appropriateness for analysis. Feature engineering techniques, including Regression statistics, was employed to select the most informative and relevant features for the prediction model. From this research, it can be concluded that the adopted algorithm shows positive potential in liver disease prediction. However, it is crucial to acknowledge that further investigation and analysis are necessary to comprehensively assess the models' ability to generalize and remain robust. The present study relied on a specific dataset and configuration, and outcomes may differ when applied to diverse datasets or scenarios. Consequently, continued research and exploration are imperative to validate and extend the applicability of these models in real-world scenarios. This validation process will help confirm the model's performance across different patient populations and data sources, ensuring its reliability in real-world clinical applications.

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