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Research Article

A hybrid statistical-fuzzy recommendation system for multi-disease prediction and patient risk assessment

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Abstract

A smart, information technology (IT)-based system has the potential to enhance the quality of life for patients with serious diseases by providing valuable health advice. This article presents the design and implementation of a hybrid statistical-fuzzy (Hybrid S-Fuzzy) model that offers disease prediction and personalized recommendations for patients with complex conditions, such as heart, liver, and kidney diseases (KDs). The primary objective of this study is to introduce a diagnostic method that accurately verifies a patient's condition and provides precise recommendations. Once the disease prediction is made, the Hybrid S-Fuzzy recommender engine generates medical advice by evaluating the severity of the patient's medical characteristics, the associated risks, and the probability of disease occurrence. The core goal of the Hybrid S-Fuzzy recommendation engine is to develop a personalized recommendation system (RS) using a medical database, which has been compiled and labeled in consultation with healthcare professionals. The performance of the system is assessed using accuracy as a key metric, and the health recommendations provided are based on data collected from online medical sources. The results indicate that the proposed recommendation method achieves an accuracy rate of 96.5%. The implemented model demonstrates high precision in disease prediction and recommendation generation, highlighting its potential contribution to e-health and clinical informatics.

Keywords

Hybrid statistical-fuzzy model, Multi-disease prediction, Personalized health recommendations, Clinical decision support system, Medical data analysis, E-health and clinical informatics.

1.Introduction

The internet has become a primary source for health-related information, with over one billion daily health queries on Google, accounting for 7% of total searches. While online resources can enhance health decision-making and disease self-management, they often lead to data overload, inaccuracies, and a lack of personalization. Additionally, varying health literacy levels make it difficult for users to interpret medical terminology and verify information sources [1].

A recommendation system (RS) utilizes advanced algorithms to deliver personalized suggestions based on user preferences, history, and behavior, thereby enhancing the user experience by filtering relevant content and optimizing the search process. In the healthcare domain, a healthcare recommendation system (HRS) tailors health-related information according to an individual's medical profile, using data from medical records, wearable devices, and user inputs to provide customized recommendations on diet, exercise, and medication, ultimately improving health management [2, 3].

A recent scoping review highlights gaps in HRS research, suggesting that future studies should assess HRS effectiveness across diverse patient populations and explore long-term health outcomes [4]. An RS

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consists of three key components: the user, the recommended item, and the recommendation methods. These components work in tandem to generate personalized recommendations based on user-specific preferences [5, 6]. *Table 1* summarizes these interactions.

Table 1 Mechanisms of the HRS [6]

HRS		**Details**
Health Domain		The medical situation or problem can range from common ailments like flu to serious ones like diabetes.
User	Target User	People who take health data references.
	User model	User-based features are utilized to model and make references.
Recommended item	Recommended data	The data, i.e., is being recommended through an HRS.
	Data source	The recommended items are sourced through data filters that refine the selection process.
Recommendation technology	Methods	Selection of recommended substances is required.
	System title and user interface (UI)	It clarifies the concept of HRS and its structure, including distinctions between web and mobile versions.
System assessment	Techniques and parameters utilized to evaluate for presentation and efficiency of HRS.	

Li et al. [7] proposed a machine learning (ML) model for heart disease (HD) diagnosis, utilizing various classification techniques such as k-nearest neighbors (KNN), naïve Bayes (NB), support vector machine (SVM), logistic regression (LR), artificial neural networks (ANN), and decision trees (DT). The study integrated feature selection (FS) methods and cross-validation techniques to evaluate model performance. Their findings showed that fast conditional mutual information model (FCMIM) with SVM provided a robust HD diagnosis system. Mustaqeem et al. [8] introduced a hybrid model for cardiac patients, offering disease predictions and medical recommendations by categorizing individuals into four groups. Their model, evaluated using precision and kappa statistics, achieved 94.6% accuracy with a statistical analysis-based HD recommender model (SAbHD_RM).

Olaniyi et al. [9] developed a three-step ANN-based approach for predicting HD in angina patients, attaining 88.89% accuracy. Liu et al. [10] introduced an HD classification model that combines relief and rough set methods, achieving an accuracy rate of 92.32%. Haq et al. [11] implemented a verification-based HD diagnosis technique, incorporating FS and classification algorithms such as the sequential backward selection algorithm (SBSFS) and KNN, resulting in high accuracy. Similarly, Mohan et al. [12] developed a hybrid ML-based HD prediction model, achieving 88.07% accuracy. Geweid and Abdallah [13] introduced an HD identification model based on SVM with duality optimization, improving classification performance.

Chinnasamy et al. [14] proposed a hybrid HRS using restricted Boltzmann machines (RBM) and convolutional neural networks (CNN) to analyze diverse healthcare data. Their system provides personalized recommendations, diagnoses, and treatment plans, while ensuring data privacy and security. Developed with TensorFlow and Python, it outperforms existing methods in accuracy and precision, offering a more effective solution for personalized healthcare.

A recent study by Shambour et al. [15] introduced a hybrid recommendation model combining content-based filtering and multi-criteria collaborative filtering to help patients find doctors that best match their preferences. This model incorporates multi-criteria decision-making, doctor reputation ratings, and comprehensive content details to enhance recommendation quality and address data scarcity issues. Experiments conducted on a real-world healthcare multi-criteria database demonstrated that this method outperforms traditional models in predictive accuracy and coverage, even when data is limited.

Data from University of California (UCI) highlights challenges in healthcare data science. Medical care relies on clinical data and technology to improve diagnoses, treatment plans, and outcomes. ML in healthcare must address causality, missing data, and outcome definitions. Causality helps determine variable relationships [16], but missing data can reduce accuracy. Observational data complicates causal modeling, and Simpson's paradox shows how additional information can change outcomes. Causal models are useful but require untestable assumptions [17]. Poorly designed healthcare systems can lead to fragmented care, communication breakdowns, and inefficiencies [18–20]. Health systems (HSs) face challenges in balancing public and private interests and require effective management and policy frameworks to address evolving patient needs and reforms [21].

This study has the following objectives:

- To explore and analyze a medical database gathered from the UCI ML Repository, containing heart, liver, and kidney disease (KD) patient data labeled by clinical experts.
- To evaluate and compare the effectiveness of the bee feature-based convolutional neural network (BFCNN) model in diagnosing multiple diseases.
- To propose a hybrid approach for evaluating disease severity levels and generating personalized recommendations.
- To calculate the efficiency of proposed model on different parameters and compare with existing techniques.

In this research, a hybrid statistical fuzzy (Hybrid S-Fuzzy) model was introduced for disease analysis and recommendation in patients with liver, heart, and KD. The study aims to develop a sophisticated RS specifically for individuals suffering from multiple disorders. The proposed model is supported by various classification and prediction methods, enabling it to accurately verify diseases and provide appropriate recommendations. The performance of the proposed system is evaluated using key metrics, including accuracy, sensitivity (SN), specificity (SP), and root mean square error (RMSE). Additionally, risk analysis (RA) is conducted to generate personalized recommendations, with clinical professionals providing expert guidance.

The study is structured as follows: Section 2 presents a literature review, focusing on existing recommendation and classification models. Section 3 details the methodology of the proposed RS in healthcare. Section 4 discusses the results obtained from the model, while provides an analysis of performance metrics, datasets, and key findings. Finally, Section 5 concludes the study and outlines the future scope of the proposed approach.

2.Literature review

Numerous investigators have contributed to classifying and recommending multiple diseases. They have explored ML, deep learning (DL), and artificial intelligence (AI) classifiers for the classification and recommendation of various diseases, including kidney, liver, and HDs. With the assistance of these fields, gathering healthcare data becomes more accessible. After gathering big data (BD) from the healthcare sector, we can easily classify and recommend human diseases such as heart, liver, and kidney issues. Raheja et al. [22] described chronic diseases as disorders that requires medical attention. Chronic illnesses such as HD, pneumonia, KD, and diabetes were major sources of loss and infirmity on the earth. It was considered a major challenge to sense these infections using systematic data analysis. ML models provided effective resolutions for perfect predictions and decision-making. ML methods experienced significant growth in healthcare. The implemented model attempted to prepare the analytical study of chronic diseases using ML.

These types of diseases were predicted by using LR, random forest (RF), KNN, DT, and CNN on chest X-rays. Sudharson and Kokil [23] implemented a computer-assisted diagnosis (CAD) technique designed for the detection of multi-class KD utilizing ultrasound imaging. The system was initially trained with two models: a ResNet-101 network and an SVM. The proposed model achieved better performance and accuracy than conventional methods. The recommended model originated as more effective than other classifiers such as KNN, DT, etc. Ramasamy et al. [24] introduced a classification model used for identifying several diseases. The neural network (NN) was applied as a novel approach to tackle practical classification challenges. Various classification techniques were applied to optimize the training process, enhancing performance, and accuracy, and reducing error. This invented method was designed for multi-disease detection, integrating the half of the threshold (HOT) method with Stassen’s matrix multiplication (SMM) technique. A hybrid method was used to train and validate the NN-based Stassen’s hot (SHOT) method. Bhatt et al., [25] suggested the k-modes clustering technique with Huang's beginning that can increase the classification accuracy rate. Techniques like

XGBoost (XGB), RF, DT, etc., were used. To improve the outcome, the metrics of the applied technique were hypertuned using GridSearch CV. A real-world dataset of 70,000 cases from Kaggle was used to analyze the suggested model. Data that was split 80:20 was used to train the models, and the following accuracy was achieved: XGBoost: 86.87% and 87.02% (with and without cross-validation), RF: 87.05% and 86.92% (with and without cross-validation), DT: 86.37% and 86.53% (with and without cross-validation), multilayer perceptron (MLP): 87.28% and 86.94% (with and without cross-validation). AUC values for the suggested techniques are as follows: 0.94 for DTs, 0.95 for XGBoost, 0.95 for RF, and 0.95 for MLP. The research work concluded that the accuracy of the MLP technique with cross-validation achieved 87.28% as compared with other techniques. Nayeem et al. [26] studied one of the leading causes of death. It was responsible for fatty signs in the arteries. Different categories of supervised ML methods have been applied in research to predict the existence of HD in the patient's body. Additionally, they proposed an effective method to improve the performance of other classifiers. The HD dataset was analyzed using the imputing mean value technique, information-gain FS, and models like KNN, NB, and RF. Maiwall et al., [27] described acute-on-chronic liver failure (LF) as a syndrome that is marked by a significant risk of premature death and rapid organ failure. The causes include significant systemic inflammation and bacterial infections. The only effective treatment is frequently an immediate liver transplant. In patients with acute-on-chronic LF, the kidneys are often impacted; 22.8–34% of them have been documented to have acute kidney injury (AKI).

The purpose of the paper is to objectively evaluate and analyze available evidence on acute (LF) AKI, reach a consensus, and offer suggestions for pathogenesis, early diagnosis, therapy, and prevention. In addition to focusing on domains of further research that will be crucial to herpetologists, liver transplant surgeons, and intensivists globally, it offers expert perspectives for advice. Dubey [28] described a DL methodology for multi-disease prediction in healthcare systems, utilizing ML algorithms to acquire medical datasets from multiple sources for diverse disease risk prediction studies. The proposed methodology uses DL algorithms to improve prediction models for diseases by integrating data from electronic health records (EHRs) and genetic databases. This approach enhances FS and outperforms traditional methods in medical dataset prediction, potentially improving early detection and prevention strategies, important to better patient results and concentrated healthcare costs. The proposed model was composed of the lion algorithm (LA) and butterfly optimisation algorithm (BOA), which enhances FS and outperforms traditional methods in predicting medical datasets. Cao et al., [29] found diagnostic indicators for patients with non-alcoholic fatty liver disease (LD) and chronic kidney disease (CKD). This study was conducted. Utilizing the microarray data from the gene expression omnibus (GEO) database, weighted gene co-expression network analysis was used to identify functional modules of non-alcoholic fatty LD, build gene expression networks, and assess differentially expressed genes (DEG). DEG from CKD and non-alcoholic fatty LD modular genes intersected to yield non-alcoholic fatty LD-related share genes. The outcomes of the functional enrichment analysis defined that the shared genes associated with non-alcoholic fatty LD were substantially enriched in an inflammatory response, immune-related pathways, and PCD. Four hub genes linked to non-alcoholic fatty LD were found to be diagnostic indicators" is repetitive. In the development of CKD, these genes might be significant targets of non-alcoholic fatty LD. For individuals with CKD who also have non-alcoholic fatty LD, the study may offer treatment targets and diagnostic indicators.

Md et al., [30] described an urgent need for effective diagnostic methods to identify LD at its early stages and prevent fatalities. Additionally, they highlighted the importance of raising awareness about LD risk factors and promoting healthy lifestyle choices to mitigate its prevalence. Ensemble learning (EL) algorithms, with superior performance, are increasingly popular for early detection, potentially saving lives. It utilized the Indian liver patient dataset (ILPD) to predict LD. The authors presented a unique architecture that makes use of EL and improved pre-processing. The data analysis techniques used by the model include robust scaling, multivariate imputation, log1p transformation, normalization, and six EL approaches. The model achieves high accuracy of 91.82% and 86.06%. Gupta et al., [31] described liver disorders that required timely medical care and data mining (DM) aids in early diagnosis. In India, 65% consume junk food, reducing metabolism and impacting liver health. Liver disorders pose a life-threatening risk due to their low survivability. Early detection and timely treatment are crucial, and there's a need for improved diagnostic methods and increased healthcare professional awareness to identify and provide appropriate care accurately. The authors employed medical DM techniques to predict LD by analyzing historical data and identifying underlying patterns. They utilized the SVM method for better prediction results. Poonia et al. [32] described KD, affecting over 750 million people globally, as the important cause of death due to renal failure. Risk issues comprise smoking, alcohol consumption, and high cholesterol (CHOL). The kidney collects and excretes waste and excess fluid, which is more prevalent in developing countries. There were acute and chronic types. Chronic kidney failure involves a slow deterioration of kidney function, often triggered by factors like an enlarged prostate, impaired urine flow, or kidney injury. It is prevalent in patients with diabetes, high blood pressure, or prolonged lead exposure. Renal failure affects just 11% of the world's population, and low-income individuals often die before receiving proper care because they cannot afford kidney transplantation. Early detection and treatment can prevent renal failure.

Shanmugarajeshwari and Ilayaraja [33] developed a DT classification algorithm that is increasingly used in ML to solve complex issues and techniques. This study uses ML and DL algorithms to predict and find out early KD patients by utilizing R Studio and Python software, identifying various phases of CKD. Islam et al., [34] described the utilization of ML and predictive modeling for early-stage prediction and treatment of CKD, aiming to prolong life. The study identifies 30% of 25 variables as the best subset for KD identification using twelve ML-based classifiers in a supervised learning (SL) environment. A survey of 12 ML classifiers found XGBoost to have the highest performance, suggesting that ML improvements could lead to new prediction solutions.

Ghosh et al. [35] utilized the UCI chronic kidney failure dataset in this work to examine ML methods for CKD risk assessment. The most accurate and reliable model is the hybrid model, which incorporates XGBoost, RF, LR, AdaBoost, and a unique technique. It achieves superior performance parameters like accuracy, etc. This methodology could revolutionize the diagnosis and treatment of CKD. Validation across various populations and datasets should be the main focus of future studies. Ashafuddula et al. [36] represented a completely computerised ML method for handling the complexity of healthcare CKD data. To improve performance, it applies FS and feature space reduction strategies. Issues with data imbalance are addressed by data balancing. Reliable categorization is achieved by using a classifier based on ensemble features. Clinical relevance is assessed using actual therapy data from Bangladeshi patients, and the method is validated on several datasets. When predicting previously unidentified treatment data for CKD, the model outperforms adaptive boosting, LR, and passive-aggressive ML classifiers by 96.48%. Its outstanding performance highlights its potential as a valuable CAD tool for medical professionals.

Various studies have made notable contributions to the classification and recommendation for multiple diseases using ML, DL, and AI techniques. These studies have demonstrated the potential of these technologies in improving disease diagnosis and treatment recommendations for chronic conditions such as heart, kidney, and LD. Despite these advancements, several challenges persist in these studies. One of the primary obstacles is the heterogeneity of healthcare data, which comes in various forms, such as structured clinical data, medical imaging, and unstructured patient records. Integrating and processing such diverse data types requires robust pre-processing techniques, including data normalization and FS, to ensure model accuracy and generalization. Another challenge is imbalanced datasets, where some diseases or patient groups are underrepresented, making it difficult to build reliable predictive models. For example, in HD prediction, models may be less effective for predicting rare conditions due to insufficient data.

Additionally, model interpretability remains a significant concern, as AI and DL models, particularly deep neural networks (DNN), are often viewed as "black boxes" with unclear decision-making procedures. This lack of slides can hinder trust and limit their widespread adoption in clinical environments. Data superiority problems like noisy inputs, missing values, and incomplete patient histories further complicate model development, making it difficult to achieve high accuracy across diverse patient populations. Finally, integrating data from different sources—such as EHRs, medical images, and genetic information—poses another challenge, as these datasets are often fragmented and may not seamlessly combine for comprehensive disease analysis. These challenges underscore the need for more advanced models and techniques that can effectively handle the complexities of healthcare data to enhance early analysis, treatment recommendations, and patient results. Our research tackles these issues by implementing SAbHD_RM and Hybrid S-Fuzzy recommendation methods, which combine fuzzy logic with advanced recommendation techniques to provide more accurate, reliable, and interpretable healthcare predictions while addressing data uncertainty, imbalance, and integration challenges.

3.Methods

This section discusses multi-disease classification and recommendation methods used in the HS). Multi-disease classification in healthcare involves using ML models to identify and diagnose multiple diseases in a patient based on clinical data, such as symptoms and test results. RS in healthcare then suggests personalized treatments or interventions tailored to the identified conditions, aiming to optimize patient outcomes and improve decision-making for healthcare providers. After that, it elaborated on the different methods, such as FCMIM-SVM [7], SAbHD_RM [8], BFCNN [37], and Hybrid S-Fuzzy recommendation methods. The FCMIM method is utilized for FS, while the SVM method is employed for HD classification. The SAbHD_RM model is implemented for recommendations, whereas the BFCNN method is applied for classification. Additionally, the Hybrid S-Fuzzy recommender model is used for the analysis of multiple diseases, including heart, liver, and kidney conditions.

This section details the research methodology, which is structured into three key modules:
(i) Data preparation,
(ii) Classification of multiple diseases using BFCNN and
(iii) RS using the Hybrid S-Fuzzy recommender method.

Figure 1 outlines the steps involved in the proposed classification and recommendation process. This research utilizes datasets collected from the UCI, ML Repository. Following data acquisition, the pre-processing module is applied to normalize the data, remove noise, eliminate duplicate entries, and clean outliers, ensuring high-quality input for the model.

Next, FE is performed using the kernel principal component analysis (KPCA) method, which helps derive reliable and valuable features. The extracted features are then optimized using a DL approach—the BFCNN, which integrates the artificial bee colony (ABC) algorithm with the CNN framework. The ABC technique is employed for FS based on a fitness function, ensuring that only the most relevant features are passed to the CNN model for multi-disease classification.

After classification using the BFCNN model, the Hybrid S-Fuzzy recommendation method is implemented. This model provides personalized recommendations based on probability scores, categorizing patients into different levels such as: need to visit a doctor, need for normal exercise, requirement for medical advice, need for proper treatment, and healthy status. Finally, performance evaluation is conducted using key metrics, including accuracy, SP, and SN. The following subsections provide a detailed explanation of each module.

3.1Data preparation

This step involves gathering and refining information at the initial stage to ensure the dataset is clean and well-structured. The data undergoes a high-quality processing phase, where irrelevant features are removed to improve clarity and model effectiveness.

A crucial aspect of preprocessing is data normalization, which ensures that all features within the healthcare dataset are scaled consistently. This process enhances the performance, accuracy, and efficiency of ML models by preventing discrepancies in feature ranges from affecting model predictions. By scaling features such as age, test results, and clinical measurements, the model can focus on important patterns without bias from differing value distributions.

Additionally, data separation is an essential step to ensure the model is evaluated on unseen data, enhancing its generalization capabilities. In the proposed Module I (Medical Database), after data labeling, the dataset is divided into two key subsets:

- Training Database: Used to train the model, allowing it to learn patterns and relationships for improved predictive accuracy.
- Testing Database: Represents real-world data, used to evaluate the trained model’s performance and measure its effectiveness in predicting outcomes.

The following subsections outline the detailed steps of the data preprocessing module.

3.1.1Data cleaning

Data cleaning involves detecting and rectifying errors, inconsistencies, and irrelevant information in the dataset. This step is essential to confirm that the data is correct and reliable for analysis. In healthcare datasets, data cleaning typically includes removing duplicate records, correcting erroneous data (such as unrealistic values for age or test results), and filtering out features that do not contribute to disease classification or prediction. Proper data cleaning helps eliminate noise and enhance the data quality, resulting in more reliable and efficient modeling.

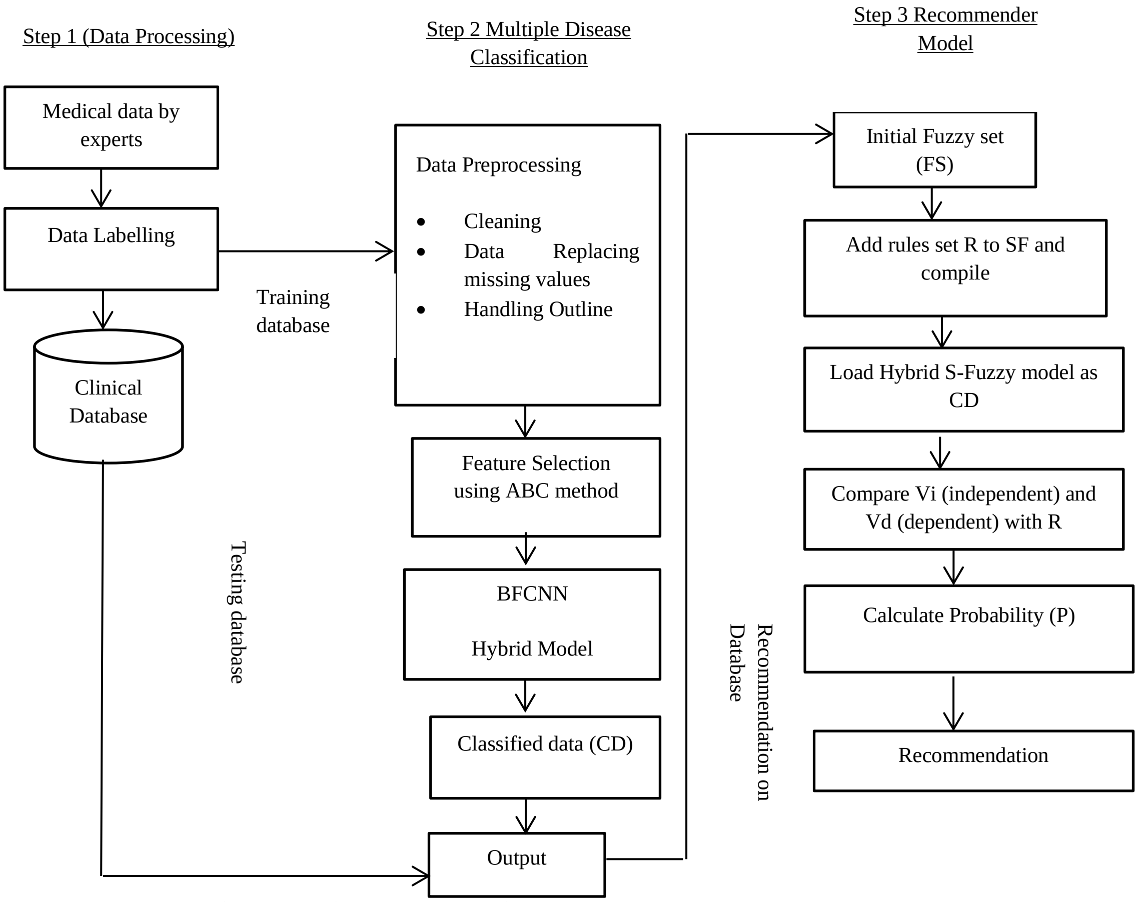

Figure 1 Enhanced fuzzy bee-featured CNN of severity and risk recommendation

3.1.2Replacing missing values

It is a vital part of the data pre-processing phase, particularly in healthcare datasets where incomplete records are common. Missing values can be imputed using various methods depending on the nature of the data. For numerical data, unwanted values may be filled with the mean, median, or mode of the column, whereas for categorical data, the mode is typically used as a replacement for missing entries. More advanced techniques, such as using ML algorithms. i.e., KNN or regression can estimate missing values using other data points. In some cases, rows with excessive missing values are deleted. This step ensures that dataset is complete and usable for model training.

3.1.3Handling outliers

Managing outliers is crucial to prevent extreme values from distorting the analysis or model predictions. In healthcare data, outliers might indicate rare diseases or errors in data collection. Identifying outliers can be done using statistical methods like Z-scores, box plots, or the interquartile range (IQR) method. Once detected, outliers can be addressed by capping values to a threshold, transforming them, or, in some cases, removing them entirely if they are deemed to be errors or irrelevant. Proper handling of outliers ensures that extreme values do not distort the model and also helps in making more accurate predictions by aligning with the typical data distribution.

3.1.4FS using the ABC method

FE is an essential step in ML or predictive modeling systems, especially in the domain of healthcare and disease prediction. It involves identifying and converting raw data into relevant features that the model can utilize for training, prediction, or analysis. The ABC algorithm can be used for FS by simulating the foraging behavior of honey bees. In this method, each candidate solution represents a subset of features encoded as a binary vector, where "1" indicates a selected feature and "0" indicates a deselected one. The ABC algorithm starts with an initial population of random solutions and assesses the fitness of each subset based on model performance (e.g., classification accuracy or cross-validation score). In the employed bees phase, bees explore their current solutions by making small modifications, and if a new solution improves fitness, it replaces the old one. During the onlooker bees' phase, bees choose solutions according to their fitness probabilities and explore them further, while scout bees create new solutions at random if stagnation is observed. The process continues iteratively, refining the feature subsets until an ending standard is met and the best solution (i.e., the most relevant feature subset) is chosen. ABC is advantageous for its ability to globally explore the search space and its simplicity.

3.2Multiple disease classification using BFCNN Model

The proposed method employs the BFCNN model, an enhanced version of the traditional CNN. The BFCNN model integrates swarm intelligence by mimicking the behavior of bee colonies to optimize FS and improve classification accuracy. In this bio-inspired approach, artificial bees (ABs) simulate the foraging behavior of real bees, enabling the system to explore optimal solutions for disease classification. This technique enhances model efficiency and robustness by dynamically selecting the most relevant features.

The proposed model was trained and tested using a clinical database containing patient records for various illnesses, including kidney and LDs. The dataset was compiled from multiple sources and labeled according to disease categories to ensure accurate classification.

To validate the model's performance, the dataset was divided into two subsets:

- 80% used for training, allowing the model to learn disease classification patterns.
- 20% reserved for testing, ensuring reliable performance assessment on unseen data.

The BFCNN is designed to perform binary classification (e.g., disease vs. no disease) and is particularly effective for diagnosing conditions from medical images or data where uncertainty is common, such as in early-stage diseases, rare conditions, or when diagnostic information is incomplete. By integrating fuzzy logic with CNNs, the proposed BFCNN aims to provide more reliable, interpretable, and accurate predictions, enhancing decision-making in clinical environments and improving personalized patient care. The method's ability to classify multiple diseases simultaneously can assist medical experts in conducting precise and early diagnoses, ultimately improving patient outcomes. *Figure 1* show the several phases involved in the classification phase II. Multiple disease feature vectors are planned and organized for various illness predictions using the preparation architecture concept. CNN is a study method that uses class labels to examine each patient's unique disease category and identify disease categories for patients. For a given layer array, a CNN model is developed, with the first stage being used to explain system engineering (SE) [38].

Table 2 describes CNN for image classification. It begins with an input layer for 28×28 grayscale images and passes through three convolutional layers, each increasing in the number of filters. A dropout layer (DOL) is comprised to prevent over-fitting, and the final layer leads to a classification outcome. The model uses a mini-batch size of 128 for efficient training and aims to predict entropy for classification tasks.

Table 2 Proposed BFCNN model parameter details

Name	**Dimensions**	**Category**	**Stride**	**Padding**	**O/P**
Input layer	28×28×1	Input	-	-	-
Con layer 1	8	Two-Dimensional (2D)	2	1	3×8
Con layer 2	16	2D	2	1	3×16
Con layer 3	32	2D	2	1	3×32
DOL	20%	Dropout	-	-	0.2
Fully connected layer (FCL)	1	Fully connected	-	-	1×1
Mini batch size	128	-	-	-	-
Output	Entropy and Prediction	Classification	-	-	-

Table 3 defines the optimization strategy for training a model using SGD. The training will be conducted over a set number of epochs, with a learning rate that starts at an initial value and gradually decreases during training. The learning rate reduction follows a scheduled approach, where it reduces by a specific factor after a predetermined number of epochs. Adjusting the learning rate in this way helps the model converge more effectively and avoid overshooting the optimal solution as training progresses.

Table 3 BFCNN model metric detail

Parameter	**Values**
Optimizer	Stochastic Gradient Descent (SGD)
Maximum epochs	30
Learning rate (LR)	0.0001
LR schedule	Piecewise
LR drop factor	0.1
LR drop period	20

3.2.1Convolutional layer (CL)

It is an important module of the CNN architecture [38] that performs FE that generally comprises a combination of non-linear (NL) and linear (L) operations that are convolutional processes and activation functions (AF). Convolution is a particular category of linear process utilized for FE, where a small array of statistics, well-known as the kernel, is useful through the input, which is an array of integers well-known as a tensor.

The plan is implemented on an input data array, also referred to as a filter or kernel, and a 2D array of weights (wts). A single value is the result of raising the clean with the input data array's unique time. A 2D array called feature_map, which shows the data filtering process, is produced when the clean is useful repeatedly over the input data array. A calculated formula is utilized to adjust the sizes of the feature maps, as shown in Equation 1.

$$\frac{(m_j + 2PDD - F)}{St} + 1 \qquad (1)$$

Here: m_j is the measurement of input data, $2PDD$ defines padding, F represents the measurement of the filter, and St denotes stride.

3.2.2Pooling layer (PL)

In NL down-sampling, when several NL functions are employed for pooling, max-pooling is a frequently utilized function. The objective of this layer is to minimize things in the network increasingly and, afterwards, manage the over-fitting issue. This layer processes the feature_maps individually to create a novel set of pooled feature_maps with consistent values. This process involves selecting an appropriate pooling method, such as a clean one, which is then useful to the feature_maps. The pooling size filter is small in comparison to the pixel feature map with a 4-pixel stride. In its place of learning, the pooling process is identified. A few pooling purposes are;

- **Average pooling (AP):** It calculates the mean rate of each patch on the feature_map.
- **Max-Pooling:** It determines the highest value for each patch of the feature_map.

3.2.3Fully-connected layer (FCL)

Finally, after multiple convolutions and max-pooling operations, the FCLs are introduced in the process. It evaluates the maxima level reasoning in the NN. *Figure 2* represents the flow diagram of the disease classification method.

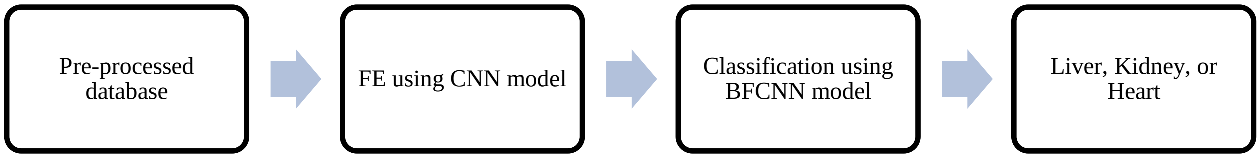

Figure 2 Flowchart for several disease classifications

The BFCNN method utilizes a multi-task learning approach to categorize several diseases instantaneously. The classification method using several disease classifications is a major improvement over current methods for health databases. It is precise, effective, and dependable, as is associated with the prior one. Algorithm 1 signifies the above-discussed steps of the research methodology.

Algorithm 1: Multiple disease classification using BFCNN

Initial data: Database (DB)

Results: Disease Type

```
Start
Read DB > = {DB}
{DB} train_db >= {DB} [0:g]
{DB} test_db >={DB} [g++:n]
```

```
BFCNN model = initial_BFCNN (BFCNN, size ([H,W]))  //= hidden; W = Weight.
Set metrics (PADD, St, F) // PADD = Padding; St = stride, and F filter.
Defined BFCNN comprising Conv_layer (BFCNN. F, St, PADD, sig(g))          // sig = Sigmoid Function
Feature_vector = [[n+2PADD – k]/St]+1]
Define PL (BFCNN, Sub-sampling_category, sub-sampling_rate || CLabels     // CLabels =Classified Labels
Set classifier (BFCNN)
For in j in 0 …Clabels do
 If(j==Clabels.size) then
   Classifier = (BFCNN, CLabels)
End if
End for
Disease Type = (classifier, {DB}, test_db).
Stop
```

3.3Recommendation using hybrid s-fuzzy model

A Hybrid S-Fuzzy model for RSs combines fuzzy logic with other techniques like collaborative filtering, content-based filtering, and ML to improve the accuracy and personalization of recommendations. Fuzzy logic is particularly useful for dealing with uncertainty in user preferences, like vague or incomplete ratings, by interpreting them more flexibly. By integrating fuzzy logic with other methods, the system can better understand and predict what users might like, even when the data is noisy or sparse. This hybrid approach allows the RS to give more relevant and tailored suggestions, making it more effective in providing personalized experiences.

The core function of the implemented Hybrid S-Fuzzy system is to generate personalized recommendations based on the severity of the disease and its associated risks. The primary objective is to deliver precise recommendations that help assess the risk level and its potential impact on patient health. The smart recommender system follows the prediction phase by analyzing patient data, identifying risk factors, determining disease severity, and estimating the probability of disease occurrence. The various phases of the proposed research method are detailed in Algorithm 2, which outlines the working mechanism of the Hybrid S-Fuzzy, RS in healthcare.

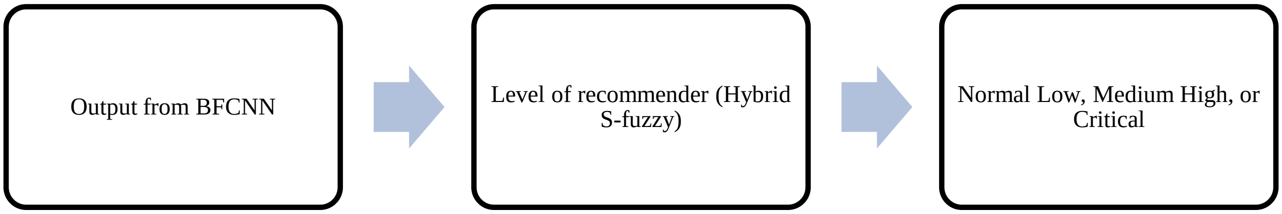

Figure 3 Flowchart: level of recommender

A Hybrid S-Fuzzy recommender is a two-stage system designed to assess the probability of a patient's health status and offer recommendations. It categorizes patients into different levels, ranging from normal to critical conditions. The Hybrid S-Fuzzy provides the output on all five levels on behalf of various parameter analyses exposed in *Figure 3*.

Figure 4 illustrates the flowchart of the proposed system. In the first stage of the hybrid RS, the upper and lower threshold values of key medical metrics are evaluated using training data. These thresholds are determined based on patients' historical health records, including blood sugar levels, blood pressure, and other clinical parameters.

The upper and lower bounds play a crucial role in the hybrid RS, as they help in assessing disease probability. The fuzzy logic component of the system utilizes these bounds to estimate the likelihood of disease occurrence and generate personalized recommendations accordingly.

Fuzzifier

The primary method of a fuzzifier is to modify the input data to a set of fuzzy values. It employs Gaussian (G) membership functions (MF), which are defined as follows:

$$\mu_B\,(b) = \exp\left[-\frac{1}{2}\left(\frac{b-m}{\sigma}\right)^2\right],\ n\ \in [n1, n2]\ \ (2)$$

Here, in Equation 2, n represents the mean and σ denotes the mean standard deviation (SD).

Statistical approaches create rule vector R during the processing of bonds, and with the help of standard notations of certain parameters, the fuzzy rules are defined at stage 2. These rules are a priority vector type of calculation that creates the probability matrix and generates a final compound probability (P) of disease with an impact on health. The value of probability was as much as high; the condition became serious and uncontrollable. Based on P conditions, Fuzzy generates the recommendation from normal to admission into the hospital for treatment.

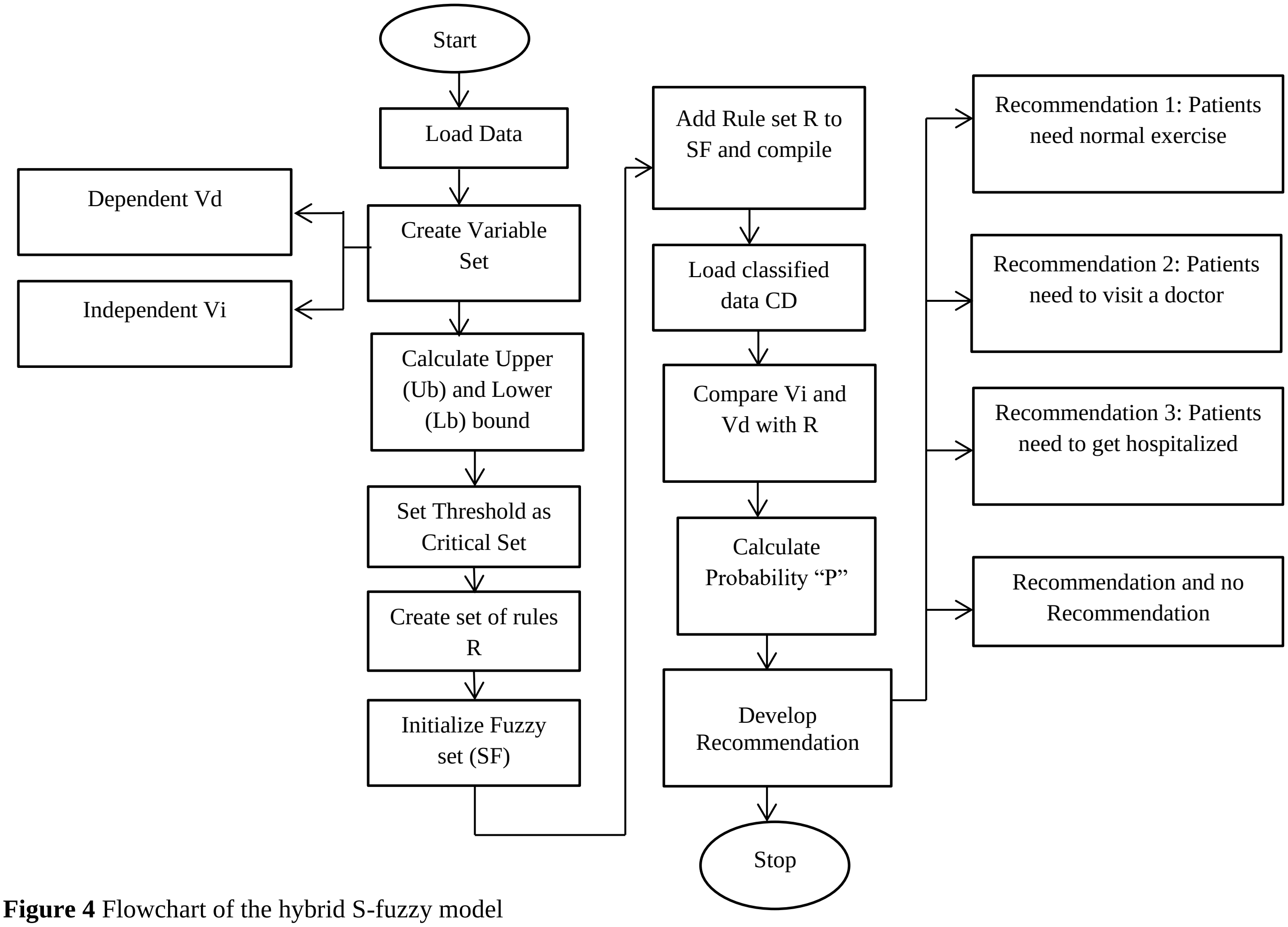

Figure 4 Flowchart of the hybrid S-fuzzy model

Rule control

The data input used by type-2 fuzzy system is represented as $[a_1 \in A_1, a_2 \in A_2, \ldots, a_p \in A_p]$, with the related fuzzy output sets denoted by $y \in Y$. The fuzzy rule for the system can be written as:

If a_1 is F_1 and a_2 is F_2 and … and a_p is F_p, then y is G.

Here, $F_k = [\mu(a_k), \mu(a_k)]$ represents the j^{th} antecedent of the ith rule, where $\mu(a_k)$ is the MF for input a_k. G indicates the consequence of rule i.

Inference engine

It is essential for calculating the firing level, a weight given to each activated rule. This level is determined by the input values and the backgrounds of the rules, and it is then used to determine the membership values of the resulting fuzzy sets.

The maximum and minimum firing levels for the resulting output fuzzy set, G_i, are computed as follows:

The firing level for the upper bound, f(a'), is given by Equation 3:

$$f(a`) = min\{\mu(a_1), \mu(a_2), \mu(a_3)\} \quad (3)$$

The firing level for the lower bound, f1(a'), is given by Equation 4:

$$f_1(a`) = min\{\mu(a_1), \mu(a_2), \mu(a_3)\} \quad (4)$$

Here in Equations 3 and 4, μ(a1), μ(a2), and μ(a3) are the membership values of the inputs a_1, a_2, and a_3 in their respective fuzzy sets.

Type reducer

In the Type-2 fuzzy logic inference system, the output set for each rule is called a Type-2 set. This set is then converted into a Type-1 fuzzy set [yr, ys] to improve computational performance using the center-of-sets type-reduction method.

In this process, y_r and y_s represent the two endpoints that define the reduced set. These values represent the centroids of the Type-2 subsequent set G for the ith rule. The evaluation for yr and ys is described in Equations 5 to 7 below.

$$[y_r, y_s] = \left[\frac{y_{r+1} \min \{ \frac{\sum_{i=1}^{M} f^i y^i}{\sum_{i=1} Reject1 f^i}, \sum Rejectw\, f^t \sum_{i=1}^{rejectt1^{ty}_{f^i}}}{2}, \frac{\overline{y} + max \left\{ \frac{\sum_{ir}^{rejectw} f^i \overline{\overline{y}}_s^t}{\sum_{i=1}^{Rejectt1} \overline{\overline{f^i}}}, \frac{\sum_{i=t}^{M} f^i \overline{\overline{y}}_s^t}{\sum_{i=t}^{Rejectt1} \overline{\overline{f^i}}} \right\}}{2} \right] \tag{5}$$

$$\underline{y_r} = min \left\{ \frac{\sum_{i=1}^{M} f^i y_i^i}{\sum_{i=r}^{M} f}, \frac{\sum_{i=1}^{M} f^{-i} y_i^i}{\sum_{i=r}^{M} f^i} \right\} - \left[| \frac{\sum_{i=1}^{M} (f^{-i} - \underline{f}^i}{\sum_{i=1}^{M} f^{-i} \sum_{i=1}^{M} \underline{f}^i} * | \frac{\sum_{i=1}^{M} \underline{f}^i (y_i^i - y_i^r) \sum_{i=1}^{M} f^{-i} (y_i^M - y_r^i}{\sum_{i=1}^{M} \underline{f}^i \left(v_i^i - v_i^r \right) + \sum_{i=1}^{M} f^{-i} (v_i^M - v_r^i)} \right] \tag{6}$$

$$\overline{y}_s(a) = max \left\{ \frac{\sum_{i=1}^{M} f^{-i} y_s^i}{\sum_{i=1}^{M} \overline{f^i}}, \frac{\sum_{i=1}^{M} \underline{f}^i y_s^i}{\sum_{i=1}^{M} \underline{f^i}} + \right\} + \left[| \frac{\sum_{i=1}^{M} (f^{-i} - \underline{f}^i)}{\sum_{i=1}^{M} f^{-i} \sum_{i=1}^{M} \underline{f^i}} * | \cdots \frac{\sum_{i=1}^{M} \underline{f}^i (y_s^i - y_s^r) \sum_{i=1}^{M} f^{-i} (y_s^M - y_s^i}{\sum_{i=1}^{M} f^{-i} \left(y_s^i - y_s^r \right) + \sum_{i=1}^{M} \underline{f}^i (y_s^M - y_s^i)} \right] \tag{7}$$

Defuzzifier

The de-fuzzification step is applied to every type-reduced set to produce a precise result from the Type-2 fuzzy logic inference system. The de-fuzzified value is determined as the average of the Type-1 set, evaluated by finding the midpoint between the two endpoints of the reduced se (Equation 8):

$$y(a) = \frac{y_r + y_s}{2} \tag{8}$$

Here, in Equation 8, y_r and y_s are the lower and upper limits of the reduced set, respectively.

3.3.1RA and recommendation

A critical aspect of this study is assessing how various factors or irregularities contribute to the likelihood of developing a specific disease. RA has been conducted for individual disease categories within the medical database. The risk assessment is evaluated using Equation 9:

$$RA = \frac{Prob\ (e)}{Prob(e')} \tag{9}$$

Here, Equation 9 represents the RA $Prob\ (e)$ and $Prob\ (e')$ signifies the likelihood of having a specific disease, both with and without an irregularity, correspondingly.

$$Prob\ (e) = \frac{Count_e}{Count_{tp}} \tag{10}$$

$$Prob\ (e') = \frac{Count_{e'}}{Count_{tp}} \tag{11}$$

Here, In Equation 10, $Count_e$ denotes the number of exposure events within the cluster or class $Count_{tp}$ and represents the total patient number within the cluster. Equation 11 signifies the count of non-exposure events in a cluster or class and indicates the total number of patients in that cluster.

Algorithm 2: Hybrid S-Fuzzy for health care system.

```
Input: Data as D, Classified output as CD
Output: Recommendation R, health probability P
Analyse the D with given relative variables set S={V1, V2, V3,………., Vn}
Analyse dependent and independent variables Vd and Vi
For [Vi, Vd] in S
    Calculate the upper Ub and lower Lb bound
    Set threshold th (clinical set)
    Load rule with R(i)=(th, Lb,Ub)
    Create set
End For
Initialize Fuzzy set SF
Add rules set R to SF and compile
Load classified data CD
Load Hybrid S-Fuzzy model as per CD
Generate probability P for CD
Compare Vi and Vd with R
Generate matrix of Cpi for Ri
Calculate P on Cpi
If P>0 and P<=0.5
    Recommendation 1: Patients need normal workout.
If P>0.5 and P<=1
    Recommendation 2:  Patients needs a visit to doctor.
If P>=1
    Recommendation 3: Patients need to get hospitalized.
If P<0
    Recommendation 4: No recommendation.
End of
Stop
```

3.4FCMIM-SVM

The FCMIM-SVM hybrid model integrates fuzzy c-means (FCM) clustering, mutual information (MIM) for FS, and SVM for classification [7]. FCM clusters data into fuzzy groups, handling uncertainty and overlapping data points. MIM selects the most informative features by maximizing MIM, ensuring only relevant features are used. SVM then classifies the data, achieving high accuracy in complex, high-dimensional datasets. This approach enhances classification performance, aids healthcare professionals in decision-making, and improves patient care by handling multifactorial conditions and incomplete data, leading to optimized treatment outcomes through a personalized RS.

3.5SAbHD_RM model

This hybrid system's core component is its recommendation model, which provides accurate and timely medical recommendations based on disease severity and risk level [8]. It analyzes clinical data to assess risk, severity, and disease progression, particularly for HD. The model is adaptive, updating recommendations as new data becomes available. A knowledge base, developed with cardiologist input, prioritizes key medical factors like age, history, and diagnostics. This system reduces workload, improves efficiency, and benefits patients in underserved areas. Ultimately, it enhances decision-making, lowers costs, and delivers personalized healthcare recommendations.

4.Results and discussion

The proposed Hybrid S-Fuzzy model was utilized to address the complex challenges inherent in the problem under investigation. The model combined the strengths of fuzzy logic and soft computing techniques, offering a more robust approach to handle uncertainty, imprecision, and non-linearity in the data. This section presents the simulation system used to evaluate the research analysis and recommendation models. Patients are identified based on a database containing heart, liver, and KD records. The proposed approach consists of multiple phases, including disease classification, prediction, and recommendation. The following sections outline the distinct methods employed in this research.

4.1Dataset used

The research focuses on the analysis of medical datasets related to various diseases, including heart, liver, and kidney conditions. These datasets, sourced from the UCI repository [39–41], are crucial for building predictive models and uncovering patterns in patient health data. Each disease category features a distinct set of attributes specific to the nature of the disease. For this analysis, a MATLAB-based desktop application was developed, utilizing a graphical user interface (GUI) to provide an intuitive platform for data interaction and model implementation. The application was created on a system with an Intel i5 processor, 8GB of RAM, and a Windows 11 operating system, ensuring efficient processing power for handling the datasets and executing ML tasks. This setup enabled seamless development and testing of the models within the MATLAB environment.

4.1.1HD dataset

The HD dataset [39] from the UCI ML Repository is commonly used for predicting the presence or absence of HD in patients. It includes 303 instances and 14 attributes, encompassing both categorical and continuous features. The attributes consist of factors such as age, sex, blood pressure (Bp), chol levels, maximum heart rate, and other elements linked to HD risk, along with a class label that specifies whether the patient has HD (1) or not (0). This dataset is commonly used for classification tasks in ML, and it provides valuable insights for predictive modeling in healthcare applications. It has been used in various studies to grow methods for early detection and risk assessment of cardiovascular diseases. *Table 4* displays the sample data from the HD.

Table 4 Dataset detail of HD

Variable	Role	Type	Demographic	Description	Units	Missing Values
Age	Feature	Integer	Age		years	no
Sex	Feature	Categorical	Sex			no
Cp	Feature	Categorical				no
Trestbps	Feature	Integer		resting blood pressure (at the time of hospital admission)	mm Hg	no
Chol	Feature	Integer		serum CHOL	mg/dl	no
Fbs	Feature	Categorical		fasting blood sugar > 120 mg/dl		no
Restecg	Feature	Categorical				no
Thalach	Feature	Integer		Maximum heart rate achieved		no

4.1.2LD dataset

The LD dataset [40] from the UCI repository contains data on patients with LD, including both categorical and continuous medical attributes. The dataset consists of 583 instances with 10 features such as age, gender, and various liver-related test results, including levels of bilirubin, alkaline phosphatase, alanine aminotransferase (ALT), and albumin. The target variable is binary, indicating whether the patient has LD (1) or not (2). This dataset is used for classification in ML, where the aim is to develop methods that can correctly predict the occurrence or nonappearance of LD based on the given medical data. It is particularly useful in healthcare research and predictive analytics for liver-related conditions, aiding in early diagnosis and better treatment planning. *Table 5* displays the sample data from the LD.

Table 5 Dataset detail of LD

Variable	Role	Type	Demographic	Description	Units	Missing Values
Age	Feature	Integer	Age	any patient whose age exceeded 89 is listed as being of age "90".	years	no
Gender	Feature	Binary	Gender	gender of the patient		no
total bilirubin (TB)	Feature	Continuous		Total Bilirubin		no
DB	Feature	Continuous		Direct Bilirubin		no
Alkphos	Feature	Integer		Alkaline Phosphatase		no
Sgpt	Feature	Integer		Alanine Aminotransferase		no
Sgot	Feature	Integer		Aspartate Aminotransferase		no
TP	Feature	Continuous		Total Proteins		no
Albumin	Feature	Continuous		Albumin		no

4.1.3KD dataset

The KD dataset [41] from the UCI repository contains data on patients with KD, providing significant insights for the development of predictive models in medical diagnostics. The dataset contains 400 instances with 24 features, such as age, blood pressure, etc., and other clinical measurements related to kidney function. The target variable is binary, with `1` representing the KD and `0` for the absence of KD. The dataset is primarily used for classification tasks to predict the likelihood of a patient having KD based on various health parameters. It is commonly used in ML studies for early detection, risk assessment, and improving healthcare outcomes related to kidney function. *Table 6* displays the sample data from the KD.

Table 6 Dataset detail of KD

Variable	Role	Type	Demographic	Description	Units	Missing Values
age	Feature	Integer	Age		year	yes
bp	Feature	Integer		blood pressure	mm/Hg	yes
sg	Feature	Categorical		specific gravity		yes
al	Feature	Categorical		albumin		yes
su	Feature	Categorical		sugar		yes
rbc	Feature	Binary		red blood cells		yes
pc	Feature	Binary		pus cell		yes
pcc	Feature	Binary		pus cell clumps		yes
ba	Feature	Binary		bacteria		yes
bgr	Feature	Integer		blood glucose random	mg/dl	yes

4.2Parameter values used for classification module

The BFCNN model is employed for classifying patients' disease categories. The training metrics, as outlined in *Table 7*, ensure the model's reliability in disease classification. Using a layered architecture, the system effectively categorizes patients based on medical conditions such as heart, liver, and KDs. By leveraging these trained metrics, the classification process accurately identifies affected individuals and evaluates their risk levels, aiding in early diagnosis and treatment planning.

Table 7 Classification model metrics

Metrics	**Values**
Type of Optimizer	Stochastic Gradient Descent (SGD)
Number of Iterations	100, 200, 500
Learning rate	0.001
Loss Function	Cross-entropy
Drop factor	0.5

4.3Metrics measured for recommendation module

The classification step involves assessing the risk level of a patient's disease. The statistical and type-II Fuzzy system ensures clinically relevant analysis by incorporating reliable health parameters derived from the patient's medical data. Baseline values for a healthy individual are obtained from medical specialists for conditions such as heart, liver, and KDs. These reference values are then used to quantify the patient's risk level. For health risk assessment, distinct metric thresholds are established to define healthy and diseased states. Medical experts extract key indicators at each stage to characterize disease severity and ensure accurate classification and diagnosis.

4.3.1Liver disease (LD)

The forecast task is to control whether a patient suffers from LD depending on the data related to various biochemical markers, adding albumin and other enzymes essential for metabolism. This database includes records of 584 patients, with 416 diagnosed with LD and 167 without the condition. In general, the liver facilitates the process of food absorption and concentration.

The factors selected to categorize LD's health state are:

(i) Serum-glutamic-pyruvic transaminase (SGPT).

(ii) Serum-glutamic-oxaloacetic transaminase (SGOT).

In human blood, the phases of both measurements are often very small. *Table 8* recovers the usual values mandatory for a fit liver. *Table 8* sets the values for ALT and AST when the test determines their minimum or maximum values. It indicates that the patient is abnormal and at risk.

Table 8 SGOT and SGPT normal levels in humans

Aspects for liver	**Values**
SGPT	7-56 units
SGOT	10-40 units

4.3.2Heart disease (HD)

All body functionality works with the help of the heart as the heart is vital organ in the human body. The human body's heart may be counted on to pump blood. Various factors influence its function in the human body. Bp and chol are the two primary characteristics. The patient's level of chol confirms the degree of cardiac disease. The Bp level is then used to determine the disease's probability rate. *Table 9* illustrates the different phases of chol and Bp that affect the body of a human being.

Table 9 Classification of HD based on Chol and Bp levels

Blood Pressure (Bp)		**Cholesterol (CHOL)**	
Range in (mm Hg)	**Disease risk**	**Range in Mg/dL**	**Disease Risk**
90-60: Low	High	100-129	Healthy
120-80: Normal	Healthy	130-159	Borderline
140-190: High	Very High	160-189	High
		190 above	Very High

4.3.3Kidney disease (KD)

The kidneys' primary functions include controlling the body's fluid balance and eliminating waste from the body. It diagnoses renal disease, and the work that has been done has considered (i) potassium (pot) and (ii) serum. These factors are crucial for maintaining kidney health. The Hybrid S-Fuzzy model is used to determine the kidney's health state and provides these values. The necessary data values to select an effective method are shown in *Table 10.*

Table 10 Identification of KD based on Pot and serum creatinine levels in the human body

Potassium (Pot)		**Serum creatinine**		
Range in (mmol/L)	**Disease risk**	**Male**	**Min**	**Max**
3.6-5.2	Normal	Male	60	120
5.3-5.5	High			
Above 6	High risk	Female	50	110

4.4Outcomes of hybrid s-fuzzy recommender model

The Hybrid S-Fuzzy model determines results based on predefined principles following classification. The model categorizes patients into different risk phases based on disease severity:

1. Low Risk: Indicates a minimal risk where the patient has a low probability of disease impact. The individual is classified as normal but susceptible to the illness.
2. Medium Risk: Suggests that the patient's test results fall within a moderate range, indicating a potential risk requiring further monitoring.
3. High Risk: Represents a significant disease risk, suggesting that the patient requires medical attention to manage the condition.
4. Normal: Indicates that the patient's health metrics align with standard values, signifying no immediate health concerns.
5. Critical: Patients categorized as critical require urgent medical intervention, as their condition poses a severe or life-threatening risk.

The research outcomes utilize the BFCNN approach to classify disease types for each patient. Accuracy serves as the primary metric for evaluating performance, as shown in *Table 11*. Equation 12 defines accuracy as the percentage of correctly classified cases, incorporating true positives (tp), true negatives (tn), false positives (fp), and false negatives (fn). However, accuracy alone is insufficient for imbalanced datasets, requiring additional metrics for a more comprehensive evaluation.

SP, as defined in Equation 13, measures the proportion of tn cases correctly identified, playing a crucial role in minimizing fp and preventing over-diagnosis. Similarly, SN, or recall, defined in Equation 14, evaluates the proportion of tp cases correctly detected, which is particularly important in medical applications where missing positive cases can have serious consequences.

RMSE, as defined in Equation 15, quantifies the average magnitude of prediction errors, comparing predicted values to actual observations. This metric provides insight into how well the model's predictions align with real-world data. Together, these metrics ensure a comprehensive assessment of the BFCNN model's classification capabilities, validating its effectiveness across diverse and critical healthcare applications.

Table 11 Performance parameters

Parameters	Mathematical formula's	
Accuracy (%)	$Accuracy = \frac{tp+tn}{tp+tn+fp+fn}$	(12)
SP	$Specificity = \frac{tn}{tn+fp}$	(13)
SN	$Sensitivity = \frac{tp}{tp+fn}$	(14)
RMSE	$RMSE = \frac{\sum_{i=1}^{n}(yi-yj)^2}{n}$	(15)

Here, in (15), yi refers to observed_values, and yj refers to predicted_values).

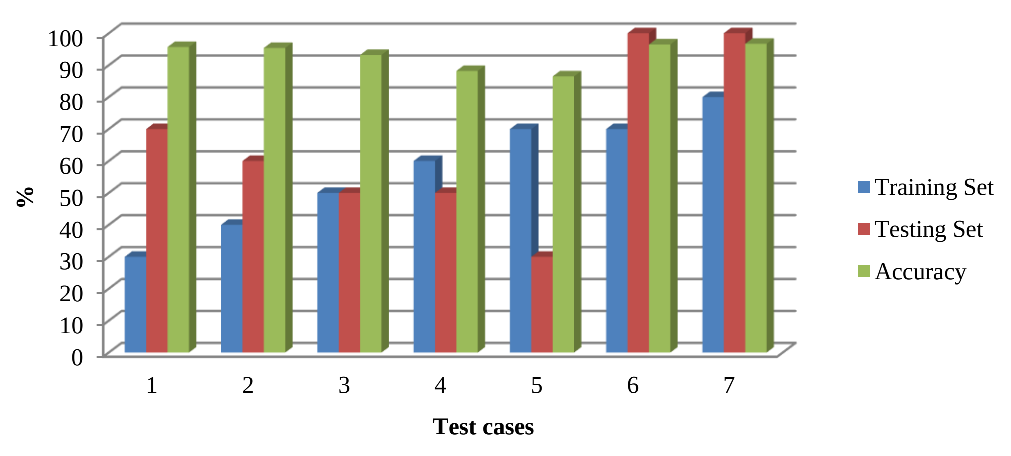

Figure 5 Accuracy (%) of classification model

Figure 5 illustrates the accuracy of the implemented method. The outcomes that were attained appeared capable of varying the extent of training and testing databases. The greatest accuracy at 8:2 is demonstrated in *Figure 6* when the maximum amount of data is used for training. This maintains an accuracy rate of 90% for all combinations of training and testing (86.5 and 96.7%).

4.5Recommendation outcome

To evaluate the classification efficiency, three models—fuzzy, statistical, and Hybrid-S Fuzzy—were tested and compared. Each model was assessed using key performance metrics, including accuracy, SN, and SP, to determine their effectiveness in classifying data and identifying positive and negative cases. The hybrid-fuzzy model outperformed the other two, demonstrating superior accuracy and robustness in handling complex classification tasks. This result highlights its higher reliability and efficiency compared to the standalone fuzzy and statistical approaches, making it a more effective choice for disease classification and medical diagnosis.

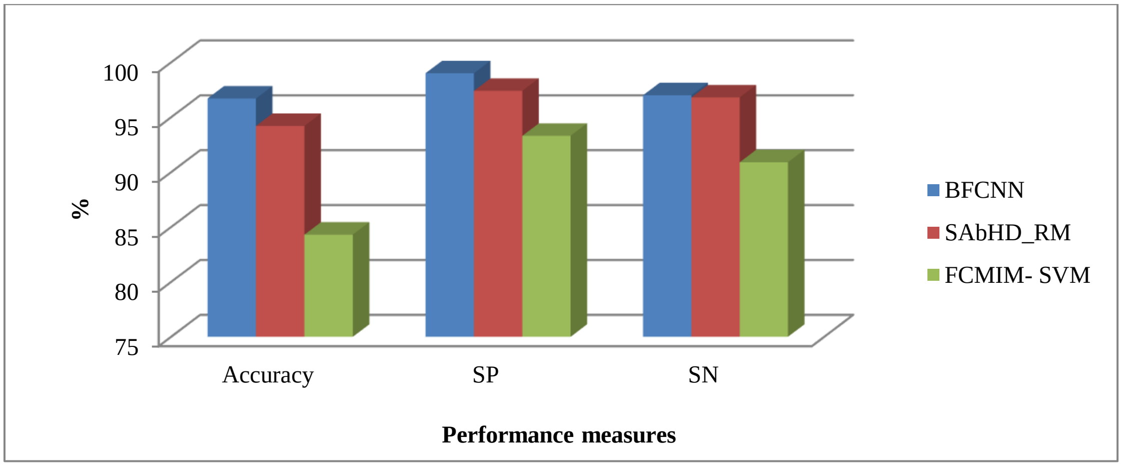

Figure 6 Visual comparative analysis – Recommendation (Fuzzy, Statistical, and Hybrid S-Fuzzy RS) Engines

The disease diagnosis risk is determined through the classification procedure using the BFCNN model. The categorized output is then processed by the Hybrid S-Fuzzy model, which evaluates and assigns risk levels. The system analyzes all patient cases, applying distinct verification checks to ensure accurate classification and risk assessment.

Based on the risk level, the Hybrid S-Fuzzy model predicts outcomes and provides recommendations:

1. Healthy (Outcome = 0): No disease detected; no recommendation required.
2. Low Risk (Outcome = 0.25): Suggests regular exercise as a preventive measure.
3. Medium Risk (Outcome = 0.5): A physician's consultation is recommended.
4. High Risk (Outcome = 1): Requires hospital admission for immediate medical attention.

Figure 6 presents a comparative analysis of recommender accuracy across Fuzzy, Statistical, and Hybrid S-Fuzzy models, demonstrating the superior performance of the proposed Hybrid S-Fuzzy system. *Table 12* outlines sample recommendations based on various disease categories.

Figure 7 illustrate the results of the predicted disease categories, as labeled by healthcare professionals. The performance metrics of the BFCNN, FCMIM, and SAbHD_RM models were evaluated, demonstrating that the implemented method achieved improved accuracy, SP, and SN.

Table 12 Sample for recommendations

Category of disease	Level	Recommendations
Heart	0.5	Need to visit a doctor
Heart	0.25	Need normal workout
Liver	0.5	Requirement of doctor’s advice.
Liver	1	Need proper treatment
Kidney	0	Need normal exercise
Normal	0	Healthy

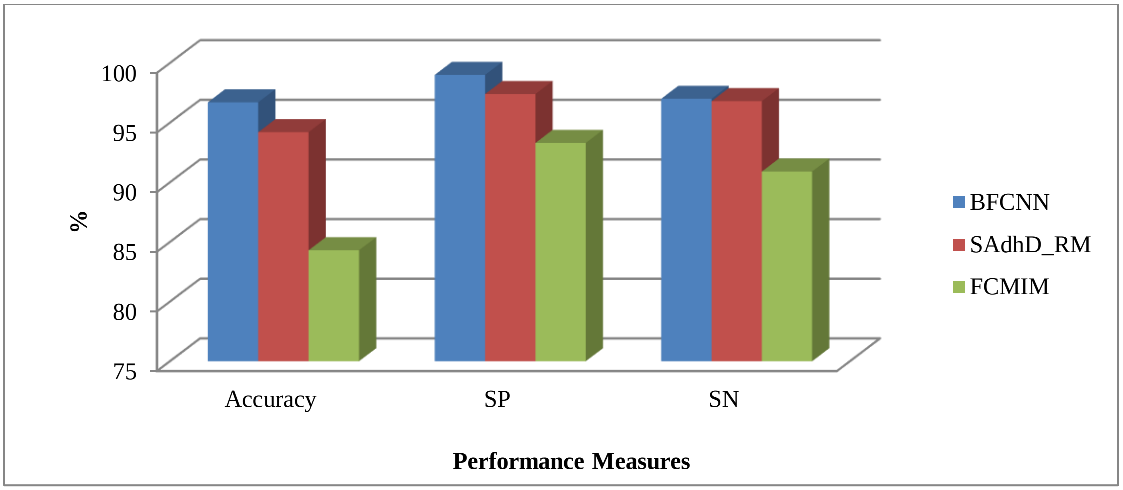

Figure 7 Comparative analyses of various methods (BFCNN, SAbHD_RM, FCMIM-SVM)

The findings emphasize the efficiency of the proposed models in disease classification and patient risk assessment. A comparative analysis was conducted among the Hybrid S-Fuzzy model, FCMIM, and SAbHD_RM, revealing that the Hybrid S-Fuzzy model outperformed the other two in classification accuracy and risk prediction. While FCMIM and SAbHD_RM achieved accuracy rates of 92.5% and 94.3%, respectively, the Hybrid S-Fuzzy model consistently outperformed them, achieving 96.7% accuracy when trained with 80% of the dataset, the highest accuracy recorded in this study. The superior performance of the Hybrid S-Fuzzy model is attributed to the integration of fuzzy logic and statistical techniques, which enable a more comprehensive disease classification and risk assessment approach. These results confirm that the Hybrid S-Fuzzy model is a superior solution for disease prediction and patient recommendation compared to traditional models.

Limitations

Despite its effectiveness, the proposed method has the following limitations:

- The model is computationally more complex than traditional methods, leading to longer processing times, particularly when handling large datasets.
- The integration of fuzzy logic and statistical methods makes the model's decision-making process challenging to interpret, which may limit clinical adoption.
- The model may require further optimization for different datasets and disease categories to ensure broader applicability across diverse patient populations.

Performance and comparative analysis

The proposed multi-disease classification and RS demonstrated promising results in detecting and categorizing chronic diseases, including heart, liver, and KDs, while also offering personalized treatment recommendations. The system integrates BFCNN for disease classification and the Hybrid S-Fuzzy model for treatment recommendations, achieving high predictive accuracy and actionable recommendations. Evaluation metrics, including SN and SP, validate the model’s superiority over conventional methods.

The BFCNN model outperformed traditional ML models such as RF and SVM, leveraging FS via the ABC algorithm, ensuring that only the most relevant features contribute to classification. Additionally, the Hybrid S-Fuzzy recommender effectively tailored treatment plans based on disease severity and risk levels, addressing existing gaps in clinical RSs.

A comparative study with existing approaches, including those by Raheja et al. [22], Sudharson and Kokil [23], and Karthick et al. [25], demonstrated that the proposed model not only improves disease classification accuracy but also enhances personalized care through superior recommendation capabilities. The system successfully mitigated data quality challenges through advanced pre-processing techniques, including data cleaning, handling missing values, and removing outliers.

Challenges and future enhancements

Despite the model's success, several challenges persist:

- Dependence on high-quality data for optimal performance.

- Complexity in interpretability due to the DL and fuzzy logic integration.
- Computational cost, making large-scale implementation challenging in resource-limited environments.
- Generalizability constraints, necessitating further fine-tuning across diverse healthcare datasets and systems.

To address these limitations, future research should focus on:

1. Enhancing interpretability through explainable AI (XAI) techniques, making the model's decision-making more transparent and understandable.
2. Improving adaptability by testing the system on diverse datasets and incorporating real-time clinical data.
3. Integrating the system into healthcare environments, leveraging edge computing to reduce computational overhead and enable real-time analysis.

A complete list of abbreviations is listed in *Appendix I*.

5.Conclusion

The research led to the development and implementation of a multi-level decision-making architecture for medical HRSs. The system utilizes the BFCNN model to classify patients into disease categories based on extracted medical features. This classification is complemented by a hybrid recommendation approach, offering personalized medical advice based on the severity of a patient's condition. For risk-level assessment, the Hybrid S-Fuzzy model provides a robust framework to analyze patient risk based on classification results. The study focuses on three major diseases—heart, liver, and KDs—and evaluates model performance using accuracy, SP, SN, and RMSE. The results indicate strong performance, with accuracy ranging from 86.5% to 96.7%, demonstrating stability across different training and testing datasets. Despite dataset variations, the system consistently maintained high classification accuracy, ensuring reliability across evaluation parameters. These findings confirm that the proposed models serve as an effective solution for disease classification, risk assessment, and personalized medical recommendations in clinical decision-making systems.

Acknowledgment

None.

Conflicts of interest

The authors have no conflicts of interest to declare.

Data availability

In this article, three datasets are used and analysed to the performance and publically accessible and can be found at http://archive.ics.uci.edu/ml/datasets/heart+disease, http://archive.ics.uci.edu/ml/datasets/chronic_kidney_disease, and https://archive.ics.uci.edu/ml/datasets/ILPD+(Indian+Liver+Patient+Dataset).

Author's contribution statement

Lakhvinder Singh: Analysis conception and implementation, draft research paper writing, complete article structure concept, conduct datasets, conduct the study, result analysis, and comparative result analysis. **Dalip:** Analysis conceptualization, dataset approval, and verification, supervision of conduct analysis, and validate and verify the result analysis, and comparison between existing methods.

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Appendix I

S. No.	Abbreviations	Descriptions
1	AB	Artificial Bee
2	ABC	Artificial Bee Colony
3	AFs	Activation Functions
4	AI	Artificial Intelligence
5	AKI	Acute Kidney Injury
6	ANN	Artificial Neural Network
7	AP	Average Pooling
8	BD	Big Data
9	BFCNN	Bee Feature-Based Convolutional Neural Network
10	BOA	Butterfly Optimisation Algorithm
11	CAD	Computer-Assisted Diagnosis
12	CHOL	Cholesterol
13	CKD	Chronic Kidney Disease
14	CNN	Convolutional Neural Network
15	DL	Deep Learning
16	DM	Data Mining
17	DNN	Deep Neural Network
18	DOL	Dropout Layer
19	DT	Decision Tree
20	DEG	Differentially Expressed Genes
21	EHRs	Electronic Health Records
22	EL	Ensemble Learning
23	FBS	Fasting Blood Sugar
24	FCL	Fully Connected Layer
25	FCMIM	Fast Conditional Mutual Information Model
26	fp	False Positive
27	fn	False Negative
28	FS	Feature Selection
29	GEO	Gene Expression Omnibus
30	GUI	Graphical User Interface
31	HD	Heart Disease
32	HOT	Half of The Threshold
33	HRS	Healthcare Recommendation System
34	HS	Health System
35	Hybrid S-Fuzzy	Hybrid Statistical Fuzzy
36	ILPD	Indian Liver Patient Dataset
37	IT	Information Technology
38	IQR	Interquartile Range
39	KD	Kidney Disease
40	KNN	K-Nearest Neighbor
41	KPCA	Kernel Principal Component Analysis
42	LA	Lion Algorithm
43	LD	Liver Disease
44	LF	Liver Failure
45	LR	Logistic Regression
46	MIM	Mutual Information
47	ML	Machine Learning
48	MF	Membership Function
49	NB	Naïve Bayes
50	NL	Non-Linear
51	NN	Neural Network
52	PC	Pus Cell
53	PCC	Pus Cell Clumps

54	Pot	Potassium
55	RA	Risk Analysis
56	RBC	Red Blood Cells
57	RBM	Restricted Boltzmann Machine
58	RF	Random Forest
59	RMSE	Root Mean Square Error
60	RS	Recommendation System
61	SAbHD_RM	Statistical Analysis-Based Hd Recommender Model
62	SBSFS	Sequential Backward Selection Algorithm
63	SE	System Engineering
64	SG	Specific Gravity
65	SGPT	Serum-Glutamic-Pyruvic Transaminase
66	SGOT	Serum-Glutamic-Oxaloacetic Transaminase
67	SHOT	Stassen’s Hot
68	SL	Supervised Learning
69	SMM	Stassen’s Matrix Multiplication
70	SN	Sensitivity
71	SP	Specificity
72	SVM	Support Vector Machine
73	TB	Total Bilirubin
74	tp	True Positive
75	tn	True Negative
76	UCI	University of California
77	UI	User Interface
78	wts	Weights