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DEEP LEARNING AND MACHINE LEARNING USAGE IN CIRRHOSIS PREDICTION: A COMPARATIVE STUDY

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Abstract: The cirrhosis disease represents the final stage of hepatitis, characterized by the death of liver cells and irreversible liver damage. Although there are some methods used in the prediction of cirrhosis, especially those utilizing various artificial intelligence techniques, it is still difficult to accurately predict cirrhosis. The aim of this research is to detect cirrhosis by focusing on deep learning methods. In addition to analyzing the performance of deep learning methods for cirrhosis prediction, the study also compares the performance of traditional machine learning algorithms with deep learning techniques. Decision Tree (DT), k-Nearest Neighbors (kNN), Random Forest (RF) and Logistic Regression (LR) algorithms are used in order to achieve these goals. Considering the relatively lower performance of some of these algorithms, Deep Neural Networks performed the classification accurately. In the dataset used in the study, there were 362 patients with cirrhosis and 1023 without cirrhosis. Model performance showed that deep neural networks achieved high classification performance with metrics such as 95.96% accuracy. According to the results, deep learning methods showed strong performance, providing high accuracy and sensitivity for cirrhosis prediction alongside traditional machine learning methods.

Keywords: Cirrhosis, Deep neural networks, Hepatitis C virus, Machine learning, Classification, Performance evaluation

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1. Introduction

Hepatitis C virus (HCV) is a major health problem with 3-4 million new cases emerging worldwide each year. HCV infection is considered one of the main causes of liver diseases (Nandipati et al., 2020). Cirrhosis is a serious and progressive liver disease that represents the end stage of various chronic liver diseases associated with this virus, including hepatitis, alcoholic and non-alcoholic fatty liver disease (NAFLD) (Rinella, 2015; Goossens et al., 2016). The main features of cirrhosis, which is the final stage of the disease, are widespread hepatocellular damage, regenerative nodules that disrupt the architecture and function of the liver and excessive fibrosis. Over time, these damages disrupt basic liver processes such as protein synthesis from cells, detoxification and bile production, leading to devastating complications such as portal hypertension, hepatic encephalopathy and hepatocellular carcinoma (Schuppan and Afdhal, 2008; Tsochatzis et al., 2014). Early diagnosis and management of the disease are crucial because, without timely treatment, organ transplantation becomes the only option.

Treatment options for cirrhosis depend on the stage of the disease. In other words, considering the high morbidity and mortality associated with cirrhosis, determining the stage of the disease and diagnosing it as early as possible is critical for the patient's recovery (Chen and Morgan, 2006). While pharmacological treatments can slow progression in the early stages, liver transplantation is the only definitive treatment for end-stage cirrhosis (Chen and Morgan, 2006; Goossens et al., 2016; Limketkai et al., 2012). In the early stages, pharmacological interventions and lifestyle changes, as well as monitoring the evolution of the disease, can help slow disease progression. However, in advanced cirrhosis, where liver function is critically impaired, medical treatments lose their effectiveness. Patients often require invasive procedures such as liver biopsy to determine the stage of the disease and paracentesis to manage ascites (Tsochatzis et al., 2014). Although traditional methods used in the diagnosis and prognosis of cirrhosis include techniques such as liver biopsy, MR elastography, and serum biomarkers (Imbert-Bismut et al., 2001), these methods have various limitations in terms of accuracy, invasiveness, and cost (El Houby, 2018). For example, although liver biopsy is considered the gold standard in the evaluation of fibrosis, its invasiveness and proneness to sampling error raise questions about its use (Chen and Morgan, 2006).

Recent developments in regenerative medicine, including stem cell therapy, bio-artificial liver reactors, and extracorporeal liver support systems such as liver

dialysis, offer us potential alternatives. However, the use and effects of these methods are still being researched in order to be effective and fast (Chen and Morgan, 2006; Schuppan and Afdhal, 2008). Traditional machine learning (ML) techniques and pioneering artificial intelligence (AI) techniques like deep learning (DL) are particularly beneficial in this context for detecting cirrhosis and identifying prognosis (Hashem et al., 2018). By identifying intricate links in patients' clinical data and biochemical indicators, machine learning and deep learning techniques can evaluate substantial amounts of data based on prior patient records and improve the quality of prediction models (Reiser et al., 2019; Thirumarai Selvi et al., 2023; Sathya et al., 2023). Therefore, using artificial intelligence-driven models in the early stages of the disease may improve treatment techniques (Sweidan et al., 2016).

Machine learning techniques such as Decision Trees (DT), Support Vector Machines (SVM), k-Nearest Neighbor (kNN), Random Forest (RF), and Logistic Regression (LR) are often utilized, especially during the process analyzing Hepatitis data (Bayrak et al., 2019; El Houby, 2018; Hashem et al., 2018; Haydon et al., 1998; Nickbakhsh et al., 2018; Pournik et al., 2014; Reiser et al., 2019; Wei et al., 2018). But even though these techniques use clinical and biochemical data to detect cirrhosis, there are a number of limitations in the variables chosen for prediction and data visualization that could keep the accuracy of their predictions inadequate (Rouhani and Haghighi, 2009). Furthermore, it is challenging to produce reliable and accurate predictions due to the small number of patients in the data set (Arslan et al., 2024). However, by modeling the relational structure in larger and more complex as well as data utilizing both data from various sources, including laboratory test, patient history, medical diagnostic data simultaneously, deep learning (DL) can generate superior results when compared to other methods (Konerman et al., 2015; Reiser et al., 2019; Koca et al. 2022; Meewan et al., 2024). DL techniques have been shown to outperform traditional machine learning techniques in terms of classification accuracy (Sweidan et al., 2016; Wei et al., 2018; Zhai et al., 2024; Leng et al., 2022).

For this purpose, we compared the effectiveness of the DN-based modeling techniques in the study such as MLP and comparing the results ML-based classifiers, including DT, kNN, RF, NN, and LR. We used a large sample with 1,385 patients (362 cirrhotic patients and 1,023 controls) (Waked et al., 1995). Common evaluation metrics like accuracy, precision, F-measure, and Kappa were also used to assess the classification results. In addition to performance metrics, we conducted statistical significance testing, model interpretability analysis using SHAP and LIME, and evaluated computational complexity. The purpose of this research is to promote the use of AI-driven models in clinical hepatology to enhance early diagnosis, reduce reliance on invasive techniques, and improve patient outcomes.

2. Materials and Methods

The dataset used in this research was collected from Hepatitis C Virus (HCV) patients in Egypt (Waked et al., 1995). These patients were followed for approximately 18 months during and after their treatment. The patients' cirrhosis stages were attained by applying discretization to the information in accordance with professional counseling (Hashem et al., 2018). Table 1 provides information about the variables.

Table 1. The reference values and data types of features used in dataset for Egyptian Patients

Feature Names	Feature Explanation	Feature Values
Age	Age	Years (32-61)
Gender	Gender	Male, Female
BMI	Body Mass Index	22-35
Fever	Fever	Absent, Present
Nausea/Vomiting	Nausea/Vomiting	Absent, Present
Headache	Headache	Absent, Present
Diarrhea	Diarrhea	Absent, Present
Fatigue & GBA	Fatigue & generalized bone ache	Absent, Present
Jaundice	Jaundice	Absent, Present
Epigastric pain	Epigastric pain	Absent, Present
WBC	White blood cell	Absent, Present
RBC	red blood cells	2991-12101
HGB	Hemoglobin	3816422-5018451
Plat	Platelets	2-20
AST 1	aspartate transaminase ratio	93013-226464
ALT 1	alanine transaminase ratio	0-128
RNA	Base RNA Base	0-128
RNA EOT	RNA end-of-treatment	0-1201086
RNA EF	RNA Elongation Factor	0-808450
BHG	Baseline histological Grading	0-808450
BHS	Baseline histological staging	2-16
Cirrhosis	Presence of cirrhosis	Cirrhosis, Not Cirrhosis

MATLAB R2020b was used for all data-preprocessing tasks. Data was analyzed using Python 3.9.1. To predict cirrhosis, several algorithms were employed, including Deep Neural Networks (DNN), Decision Trees (DT), k-Nearest Neighbors (kNN), Random Forest (RF), Multilayer Perceptron (MLP), and Logistic Regression (LR). These algorithms were chosen because they successfully classified health data and could work with a variety of data structures. Decision Trees (DT) are a structure that divides the dataset into smaller groups by dividing them into branches according to certain rules. It facilitates the decision-making process by dividing large datasets into manageable pieces. In addition, it clearly shows which situations are more decisive by visualizing the effects of variables (Song and Lu, 2015). k-Nearest Neighbor (kNN) is a learning algorithm that classifies examples according to their nearest neighbors. This method performs classification by analyzing the data according to a specific set of examples. Thus, it is

determined which class a new data point belongs to according to its nearest neighbors. The computation may be longer in large - scale datasets because of the increase in possible outcomes, even though it performs well in small datasets (Rouhani and Haghighi, 2009).

Random Forest (RF) is an ensemble learning technique that combines multiple decision trees to improve predictive performance. The RF algorithm's essential idea is to build several decision trees, aggregate the output from each tree, and then select the best prediction (Hashem et al., 2018). The Random Forest algorithm's ability to improve prediction performance as the number of trees grows is one of its key benefits. Besides, RF minimize over-learning, and gives more reliable findings (Hashem et al., 2018).

Logistic Regression (LR), which is generally used for classification purposes for binary dependent variables, is a classical statistical classification technique that examines the relationship between independent variables and the dependent variable. It aims to determine the model that most effectively explains the relationship between the analyzed independent variables and the binary dependent variable. However, it is difficult to produce meaningful results in data sets that contain complex and non-linear relationships (Bertsimas and King, 2017; Hosmer Jr et al., 2013).

Multilayer Perceptron (MLP) is a type of artificial neural network that contains one or more hidden layers and solves classification problems by making sense of complex relationship patterns between inputs and outputs (Clevert et al., 2016; Filiz et al., 2021; Reiser et al., 2019). This type of artificial neural network comprises an input layer, several hidden layers, and an output layer. The input and output layers provide preprocessed data, inputs, errors and model validation values (Filiz et al., 2017; Haydon et al., 1998; Reiser et al., 2019).

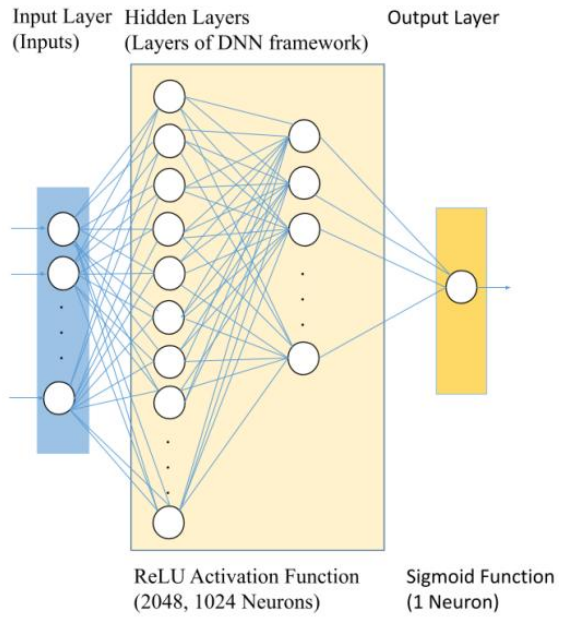

Figure 1. Structure of deep neural network.

Deep Neural Networks (DNN), an advanced extension of MLP, utilizes multiple hidden layers and increased neuron counts to capture more complex nonlinear relationships within the data. With these features, it shows high classification and prediction success in bioengineering and medical fields where complex relationships between data and big data are intense, such as medical image analysis and disease prediction (Clevert et al., 2016; Wei et al., 2018; Zhai et al., 2024). Figure 1 illustrates the data processing procedure of the deep neural networks.

The analysis results were obtained by using activation functions such as ReLU, Uniform and Sigmoid in the hidden layers of the model for 30 epochs and the sigmoid function in the output layer (Wei et al., 2018).

The formulas of the performance evaluation metrics used to evaluate the results are given in equations 1-5:

$$\text{Accuracy} = \frac{TP + TN}{TP + FP + TN + FN} \quad (1)$$

$$\text{Precision} = \frac{TP}{TP + FP} \quad (2)$$

$$\text{Sensitivity} = \frac{TP}{TP+FN} \quad (3)$$

$$\text{Specificity} = \frac{TN}{FP + TN} \quad (4)$$

$$\text{F Measure} = \frac{2*\text{Precision}*\text{Sensitivity}}{\text{Precision}+\text{Sensitivity}} \quad (5)$$

Accepted evaluation criteria such as accuracy, specificity, precision, sensitivity and F-measure were used to evaluate the performance of the algorithms. As it is known, accuracy represents the proportion of correctly classified samples, while precision shows the proportion of true positive predictions that are correctly classified among all positive predictions. Sensitivity, on the other hand, indicates the percentage of true positive samples that are correctly predicted, while the F-measure is derived as the harmonic mean of the sensitivity and precision figures. As it is known, the confusion matrix is used in these calculations. There are basically four elements in this matrix and the true values and predicted values are presented together. TP in the matrix cells represents true positive predictions, TN represents true negative predictions, FP represents falsely positively defined samples and FN represents falsely negatively predicted samples (Arslan et al., 2024; Karaboga et al., 2021).

Data preprocessing involved median imputation and the use of a StandardScaler fitted solely on training folds to prevent data leakage. Class imbalance was addressed using the ADASYN (Adaptive Synthetic Sampling) algorithm (He et al., 2008). ADASYN estimates the classification difficulty in the local neighborhood of the minority class and distributes the synthetic sample generation proportionally to this difficulty, thus increasing the minority sample density in difficult to learn regions near the decision boundaries (He et al., 2008). The method was applied only to the training data

and separately for each cross-validation layer, thus preventing data leakage. Thresholds were chosen per fold by maximizing Youden J statistic (Table 3).

In addition to Accuracy, Precision, Sensitivity, Specificity, and F1-Score, we also report AUROC (Area under the ROC curve) and AUPRC (Average precision) metrics. Deep-model hyperparameters (network depth, layer width, dropout rate, L2 regularization, and learning rate) were optimized using KerasTuner Random Search with Early Stopping based on validation AUC (Bergstra and Bengi, 2012).

3. Results

In this study, we compared the performances of different machine learning (DT, kNN, MLP, RF and LR) and DNN algorithms for the prediction of cirrhosis disease. Analysis process is given in Figure 2. Table 2 contains the comparison results for the accuracy, precision, sensitivity, specificity and F-measure criteria.

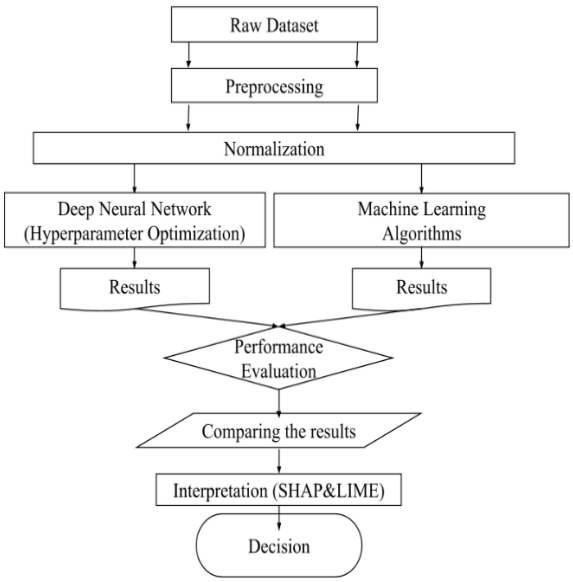

Figure 2. Data analysis process.

In Table 2, the results show that Deep Neural Network (DNN) achieved high classification accuracy rate (95.96%). The DNN model was successful model in correctly identifying cirrhosis patients with 94.19% sensitivity and 90.69% precision values. In addition, the specificity rate of 96.57% shows that it also provides strong performance in distinguishing individuals who do not have the disease. Compared to traditional machine learning algorithms, the DNN achieved good performance across all evaluation metrics, albeit with a higher computational cost and longer training time. Random Forest (RF) and kNN algorithms from machine learning algorithms showed strong performance with 97.69% and 97.47% accuracy rates, respectively. DT and LR showed average performance with 79.35% and 55.05% accuracy rates, respectively.

When examined in terms of F-measure, DNN reached the value (92.41%), proving its classification success once again. Among the machine learning methods, Random Forest (95.45%) and kNN (95.09%) had the high F-measure values. The DNN model achieved the highest sensitivity (along with DT), indicating superior capability in identifying cirrhosis cases at early stages.

For each model and outer fold, ROC (Figure 3) and Precision–Recall curves (Figure 4) with AUROC/AUPRC (Table 4) are provided respectively, demonstrating the discrimination ability of the models.

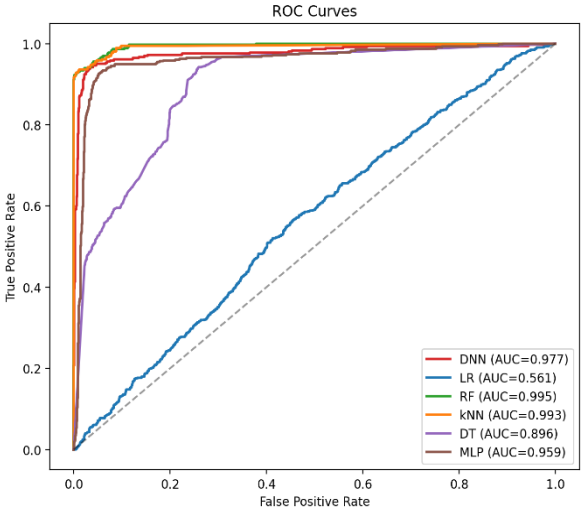

Figure 3. ROC-AUC curves of the evaluated models for cirrhosis prediction.

Fold-specific Youden J statistic thresholds resolved specificity≈0 artifacts under a fixed 0.5 cutoff. Across 10 outer folds, DNN achieved high median AUROC/AUPRC than baselines; paired Wilcoxon tests with Holm–Bonferroni correction showed statistical significance for AUROC.

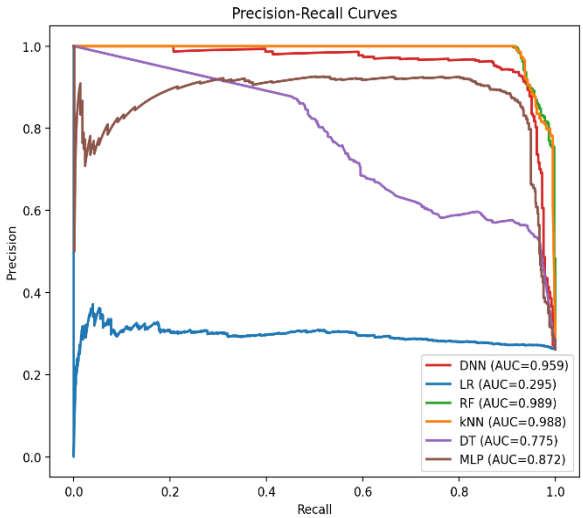

Figure 4. Precision–Recall curves of the evaluated models for cirrhosis prediction.

Table 2. Comparison of machine learning and deep learning models for cirrhosis prediction

Model	Accuracy	Precision	Sensitivity	Specificity	F-Measure
Deep Neural Network	0.95957	0.90691	0.94199	0.96579	0.92412
Decision Tree	0.79350	0.56271	0.94199	0.74096	0.70455
kNN	0.97473	0.96581	0.93646	0.98827	0.95091
Random Forest	0.97690	0.98246	0.92818	0.99413	0.95455
MultiLayer Perceptron	0.94224	0.86247	0.92680	0.94770	0.89348
Logistic Regression	0.55054	0.30545	0.56492	0.54545	0.39651

Table 3. Thresholds of algorithms

Model	Threshold
Deep Neural Network	0.55770
Decision Tree	0.10802
kNN	0.74802
Random Forest	0.43960
MultiLayer Perceptron	0.50434
Logistic Regression	0.49984

Table 4. ROC-AUC and PR-AUC of algorithms

Model	Roc-Auc	Pr-Auc
Deep Neural Network	0.97716	0.95935
Decision Tree	0.89629	0.77480
kNN	0.99275	0.98751
Random Forest	0.99490	0.98878
MultiLayer Perceptron	0.95890	0.87177
Logistic Regression	0.56122	0.29478

As a result, the DNN model was determined to be a successful method for cirrhosis prediction. These findings show that deep learning models can provide high accuracy and reliability in health data alongside traditional machine learning methods.

4. Discussion and Conclusion

This study aims to contribute to the use of artificial intelligence-based methods in cirrhosis diagnosis. In the rapid digitalization process in the health field with digital devices entering every area of our lives, the widespread use of these machine learning and deep learning models can accelerate disease diagnosis processes and strengthen clinical decision support systems.

In this study, the performances of traditional machine learning methods and deep learning algorithms for cirrhosis prediction were compared. The results show that DNN performs an accuracy rate of 95.96%. The DNN model achieved high classification accuracy success in correctly classifying patients with high sensitivity (94.19%) and precision (90.69%) values. The results demonstrated that the DNN, achieved good performance in cirrhosis prediction alongside traditional machine learning models, highlighting their potential to capture complex, nonlinear relationships within clinical data. These findings support the fact that deep learning models have higher prediction accuracy when working with large and complex health data (Clevert et al., 2016; Meewan et al., 2024; Pournik et al., 2014; Wei et al., 2018; Zhai et al., 2024).

Among machine learning methods, Random Forest and kNN have shown strong results in certain criteria while DNN showed the highest sensitivity and overall performance comparable to these models. Especially the low specificity. Decision Tree and Logistic Regression models indicate that it is difficult to correctly identify individuals who do not have the disease (Hashem et al., 2018). The success of machine learning-based methods is directly related to the size of the dataset and the relationships between variables (Rouhani and Haghighi, 2009).

Although nested CV reduces optimism, external validation on an independent cohort is a key next step. We discuss sensitivity–specificity trade-offs and threshold selection for screening vs. rule-in settings. SHAP & LIME analyses revealed stable top predictors across folds (Spearman and Top–K Jaccard), supporting clinical plausibility.

The high sensitivity observed in the DNN model indicates a stronger ability to correctly identify patients with cirrhosis, which is clinically valuable for early-stage detection. However, the slightly lower specificity implies a higher false-positive rate, which could lead to unnecessary diagnostic procedures. This trade-off should be considered when integrating AI systems into clinical workflows.

Compared with previous studies, this research comprehensively evaluates how machine learning algorithms perform in cirrhosis prediction. Nasr et. Al. (2017) and Hashem et al. (2018) have shown that artificial neural network-based models provide strong results in diagnosing liver diseases. The findings of this study show that DNN provides higher accuracy and reliability compared to existing prediction models. In addition, as stated by Bertsimas and King (2017), although logistic regression is strong in linear relationships, it has lower performance in complex clinical data.

From a clinical standpoint, the integration of deep learning-based decision support systems can assist hepatologists in identifying high-risk patients earlier, potentially reducing the need for invasive diagnostic procedures such as liver biopsy. Nevertheless, any clinical deployment should be accompanied by human oversight, interpretability tools, and rigorous validation in diverse clinical settings.

This study demonstrates that deep learning models offer an effective alternative to traditional methods in cirrhosis prediction. Future studies can focus on further improving the performance of the model by applying different deep learning architectures. In addition, the generalizability of the model can be tested with data obtained from different patient groups, and diagnostic accuracy can be further improved by combining ML and DL methods with hybrid approaches.

The origin of the dataset and potential sources of bias were addressed under the study's limitations. In particular, training the model on data from a single center was noted as a constraint for generalizability to diverse populations. Since the dataset originated from a single medical center in Egypt, external validation using multi-center or cross-national datasets is essential to assess generalizability. Future studies should also consider transfer learning or domain adaptation techniques to improve robustness across populations. These limitations were also highlighted in the discussion on clinical applicability, emphasizing the need for future validation studies on independent cohorts.

Another limitation of this study includes the relatively small sample size, potential bias in feature selection, and the lack of prospective clinical validation. Future work will focus on expanding the dataset, employing hybrid architectures such as CNN–LSTM and Transformer-based models, and integrating explainable AI approaches to enhance clinical reliability.

Author Contributions

The percentages of the authors' contributions are presented below. All authors reviewed and approved the final version of the manuscript.

	M.B.G.	H.A.K.
C	50	50
D	50	50
S	50	50
DCP	50	50
DAI	50	50
L	50	50
W	50	50
CR	50	50
SR	50	50
PM	50	50
FA	50	50

C=Concept, D= design, S= supervision, DCP= data collection and/or processing, DAI= data analysis and/or interpretation, L= literature search, W= writing, CR= critical review, SR= submission and revision, PM= project management, FA= funding acquisition.

Conflict of Interest

The authors declared that there is no conflict of interest.

Ethical Consideration

Ethics committee approval was not required for this study because of there was no study on animals or humans.

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