PERFORMANCE COMPARISON OF CLASSICAL ALGORITHMS AND DEEP NEURAL NETWORKS FOR TUBERCULOSIS PREDICTION

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Abstract*—This study compares the performance of several classical machine learning algorithms and deep neural networks for the prediction of tuberculosis in the Democratic Republic of Congo (DRC), using a sample of 1000 cases including clinical and demographic data. The sample is divided into two sets: 80% for training and 20% for testing. The algorithms evaluated include Support Vector Machine (SVM), K-Nearest Neighbors (KNN), Decision Tree, Random Forest and Convolutional Neural Networks (CNN). The results show that the CNN has the best overall performance with an accuracy of 94%, an AUC of the ROC curve of 93%, an accuracy of 90%, an accuracy of 95%, a sensitivity of 88%, an F1-score of 91.3% and a Log Loss of 0.0386. The Random Forest follows closely behind with an accuracy of 92% and an AUC of 86%. The SVM and KNN models also performed strongly, but slightly less well. The Decision Tree obtained acceptable results, but inferior to the other algorithms evaluated. These results indicate that deep neural networks, and in particular the CNN, are superior for predicting tuberculosis compared with conventional machine learning algorithms. This superiority is particularly marked in terms of accuracy, sensitivity and reliability of predictions, as shown by the performance metrics obtained.*

Keywords*: convolutional neural networks, deep neural networks, machine learning algorithms, performance metrics, tuberculosis prediction*

Intisari— *Penelitian ini membandingkan kinerja beberapa algoritma pembelajaran mesin klasik dan jaringan syaraf tiruan untuk prediksi tuberkulosis di Republik Demokratik Kongo (RDK), dengan menggunakan sampel 1000 kasus termasuk data klinis dan demografis. Sampel dibagi menjadi dua set: 80% untuk pelatihan dan 20% untuk pengujian. Algoritma yang dievaluasi meliputi Support Vector Machine (SVM), K-Nearest Neighbors (KNN), Decision Tree, Random Forest, dan Convolutional Neural Networks (CNN). Hasilnya menunjukkan bahwa CNN memiliki kinerja terbaik secara keseluruhan dengan akurasi 94%, AUC kurva ROC 93%, akurasi 90%, akurasi 95%, sensitivitas 88%, F1-score 91,3% dan Log Loss 0,0386. Random Forest* *mengikuti di belakangnya dengan akurasi 92% dan AUC 86%. Model SVM dan KNN juga berkinerja baik, tetapi sedikit kurang baik. Decision Tree memperoleh hasil yang dapat diterima, tetapi lebih rendah dari algoritma lain yang dievaluasi. Hasil ini menunjukkan bahwa deep neural network, khususnya CNN, lebih unggul dalam memprediksi tuberkulosis dibandingkan dengan algoritma pembelajaran mesin konvensional. Keunggulan ini terutama ditandai dalam hal akurasi, sensitivitas dan keandalan prediksi, seperti yang ditunjukkan oleh metrik kinerja yang diperoleh.*

Kata Kunci*: jaringan saraf konvolusional, jaringan saraf dalam, algoritma pembelajaran mesin, metode evaluasi kinerja, prediksi tuberkulosis.*

INTRODUCTION

Tuberculosis (TB) remains one of the world's most infectious diseases, causing millions of deaths every year. every year. Early and accurate detection of tuberculosis is survival rates and limit the spread of the disease. of the disease. With rapid advances in artificial intelligence (AI) and machine learning machine learning, new methods of computer-assisted diagnosis have become methods have become available (Liu et al., 2024). These methods promise to improve the accuracy and speed of TB diagnosis, particularly in tuberculosis, particularly in regions where medical resources are limited. limited medical resources.

In this study, we compare the performance of of classical machine learning algorithms with those of deep neural networks for the prediction of tuberculosis (Khanam & Foo, 2021). We used a sample of 1000 TB cases in the Democratic Republic of Congo (DRC), including relevant clinical and demographic data, divided into two sets: 80% for training and 20% for testing (*RDC : En Finir Avec La Tuberculose Grâce Au Dépistage Précoce | OMS | Bureau Régional Pour l'Afrique*, n.d.), (*La RDC Mise Sur Les Campagnes de Dépistage Actif Gratuit Des Cas Au Sein de La Population Pour Réduire l'infection Tuberculeuse Latente | OMS | Bureau Régional Pour l'Afrique*, n.d., 2024), (*La RDC Mise Sur Les Campagnes de Dépistage Actif Gratuit Des Cas Au Sein de La Population Pour Réduire l'infection Tuberculeuse Latente | OMS | Bureau Régional Pour l'Afrique*, n.d, 2024), (*RDC : En Finir Avec La Tuberculose Grâce Au Dépistage Précoce | OMS | Bureau Régional Pour l'Afrique*, n.d.). The algorithms evaluated included support vector machine (SVM), k-nearest neighbours (KNN) tree, random forest and convolutional neural networks (CNN). Convolutional Neural Networks (CNN) (Wang et al., 2021)~~.~~

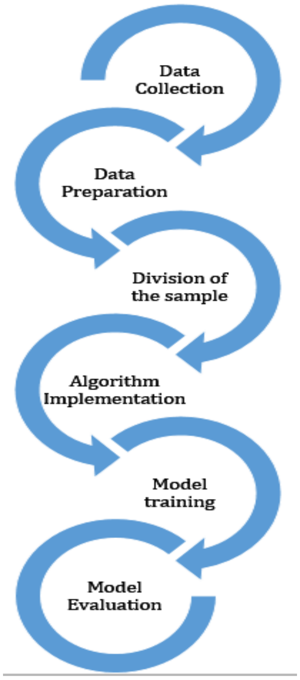
Classical algorithms such as KNN, decision trees and decision tree, and random forest are widely used in the field of medical medical classification due to their simplicity and ability to handle multidimensional data. multidimensional data. KNN, for example, is often chosen for its ability to classify data based on the proximity of data points, which is useful for points, which is useful in contexts where clinical data have complex similarities (Kratsch et al., 2021). Decision trees and forest are also popular for their interpretability and robustness against robustness to over-adjustment, particularly in moderately sized data sets (Sharifani & Amini, 2023).

However, these algorithms have certain limitations, particularly in terms of their ability to capture complex relationships relationships in the data, which is one of the reasons why deep neural networks neural networks, such as CNNs, are increasingly being explored in medical medical applications (Thapa et al., 2020). CNNs are particularly efficient at detecting complex patterns in data, making them a superior a superior choice for predicting diseases such as tuberculosis (Robinson et al., 2020). Some studies have already compared the performance of these algorithms in various medical contexts. For example, (Chinagudaba et al., 2024) and (Lane et al., 2021) have shown that CNNs outperform conventional algorithms such as SVM and KNN in terms of accuracy for medical image classification.

This study confirmed that, although traditional algorithms can offer good basic performance, deep neural networks are more effective for complex and non-linear data. This analysis provides valuable information on the strengths and weaknesses of each algorithm used in the context of TB tuberculosis prediction (Sathitratanacheewin et al., 2020). The results show that, although CNNs are currently the best performers, there is potential for continued for continuous improvement by refining the models and exploring other deep neural network architectures. This study paves the way for future research aimed at optimizing and improving the prediction of tuberculosis using artificial intelligence. It demonstrates the importance of interdisciplinary combining the fields of medicine, computer science and artificial intelligence. artificial intelligence (Rashidi et al., 2021). The results highlight the potential for future collaborations to develop innovative and effective solutions to global health problems. In summary, this study makes a significant contribution to research into the prediction of tuberculosis by demonstrating the superiority of deep neural networks over conventional machine learning algorithms, while at the same time highlighting the importance of early early detection and practical application in healthcare systems (Jha et al., 2021) and (Kazemzadeh et al., 2023).

MATERIALS AND METHODS

The aim of this study is to compare the performance of classical machine learning algorithms (KNN, SVM, Decision Tree, Random Forest) and deep neural networks (CNN) for the prediction of tuberculosis. The performance of each algorithm is evaluated on a set of clinical and demographic data, using various performance metrics (Olmez et al., 2021).
The image below summarizes the key stages of the research methodology used for our study on the classification of tuberculosis cases using machine learning algorithms.



Source: (Research Results, 2024)
Figure 1. Stages of the research methodology

This image provides a clear and concise overview of the methodological steps followed in this research. The methodology can be broken down into six essential stages:

1. Data Collection
   A sample of 1000 TB cases in the Democratic Republic of Congo (DRC), including relevant clinical and demographic data, was collected. Data included variables such as age, sex, medical history, clinical symptoms and laboratory test results.
2. Data Preparation
   Data were pre-processed to deal with missing values and outliers. The pre-processing steps included:
   Imputation of missing data : Use of statistical methods to fill in missing values.
   Normalization: Scaling of variables to have values in a similar range. Categorical variable encoding: Transformation of categorical variables into numerical variables using techniques such as one-hot encoding.
3. Division of the sample
   The sample was divided into two sets: 80% of the data was used to train the models, and 20% to test their performance.
4. Algorithm Implementation
   The following algorithms were implemented (Sahlol et al., 2020):
   Support Vector Machine (SVM): Supervised classification algorithm that finds the optimal hyperplane separating the classes. K-Nearest Neighbors (KNN): Non-parametric algorithm that classifies points according to the classes of their k nearest neighbors. Decision Tree: Predictive model using a tree structure of decisions. Random Forest: Set of decision trees trained on different subsets of the data to improve performance. Convolutional Neural Network (CNN): Deep neural network specializing in the processing of structured data, with convolution layers to extract relevant features.
5. Model training
   Each model was trained on the training dataset using the optimal hyperparameters determined by cross-validation.
6. Model Evaluation
   Models were evaluated on the test set using the following metrics (Ye et al., 2021):
   Accuracy: Percentage of correct predictions among total predictions.
   Precision: Proportion of true positives among positive predictions.
   Sensitivity (Recall): Proportion of true positives among actual positive cases.
   F1-score: Harmonic mean of accuracy and sensitivity.
   Log Loss: Measure of the performance of a classification model, calculating the logarithmic probability of predictions.
   Confusion Matrix: The confusion matrix is a tool for visualizing the performance of a classification algorithm. It is made up of four elements:
   a. TP (True Positives): number of true positives
   b. TN (True Negatives): number of true negatives
   c. FP (False Positives): number of false positives

d. FN (False Negatives): number of false negatives
e. ROC curve and AUC (Area Under the ROC Curve): The ROC curve is a graph showing the performance of a classification model at different classification thresholds. The AUC measures the area under this curve, providing a single score for evaluating the model.

RESULTS AND DISCUSSION

In this section, we will detail the calculations of the different performance measures to evaluate the machine learning models used (KNN, SVM, decision tree, random forest) as well as deep neural networks (CNNs) for TB prediction (Lane et al., 2022). Performance measures include:
Confusion matrix: visualizes model performance in terms of true positives, true negatives, false positives, and false negatives.
Accuracy: Indicates the proportion of correct predictions among total predictions.
Precision: Measures the proportion of correct positive predictions out of all positive predictions made.
Recall: Assesses the model's ability to identify all positive cases.
F1 Score: Combines precision and recall in a single harmonic measure.
Log Loss: Quantifies the performance of a classification model where the prediction results are probability values between 0 and 1.
ROC curve and AUC (Area under the ROC curve): The ROC curve is used to evaluate the model's ability to distinguish between classes. The AUC measures the area under this curve, a key indicator of overall performance.

This comparison will primarily measure the accuracy of the models, i.e. their ability to make correct predictions about cases of tuberculosis. However, we will also assess other aspects such as the robustness of the model, represented by the F1 score, and the ability to distinguish classes through the AUC of the ROC curve. In addition, the computation time of the models will be taken into account to assess their effectiveness in terms of treatment.

The models were compared using Python, a powerful programming language widely used in the field of artificial intelligence and machine learning. We used several specialized libraries:
Scikit-learn: For implementing machine learning models (KNN, SVM, decision tree, random forest) and for calculating performance metrics.
TensorFlow and Keras: for creating, training and evaluating convolutional neural networks (CNNs).
Matplotlib and Seaborn: for visualization of results, including ROC curves and confusion matrices.

These tools enabled us to carry out a rigorous and detailed analysis, automating the calculation processes and guaranteeing the reproducibility of the results. Thanks to these libraries, we were able not only to compare the performance of the different models, but also to optimise and refine the neural network architectures to obtain the best possible performance.

Calculating the values

We will now calculate the values for each model.

Confusion matrices

Confusion matrices are essential tools for evaluating the performance of classification models. They show the number of true positives (TP), true negatives (TN), false positives (FP) and false negatives (FN) produced by a model. In this context, confusion matrices provide an overview of the performance of different classification models used to diagnose cases of tuberculosis (Pathak et al., 2022).
The confusion matrix for SVM (Support Vector Machine) is :

Table 1. Confusion matrix for SVM

	Predictive Positive	Predictive Negative
Real Positive	82	18
Real Negative	9	91

Source: (Research Results, 2024)

The SVM model correctly identified 82 cases of tuberculosis (true positives) and 91 cases without tuberculosis (true negatives). However, it also misclassified 18 tuberculosis cases (false negatives) and 9 non-tuberculosis cases (false positives). This means that the SVM is relatively good at identifying positive and negative cases, but there are still errors in both categories. The confusion matrix for KNN (K-Nearest Neighbors) is:

Table 2. The confusion matrix for KNN

	Predictive Positive	Predictive Negative
Real Positive	80	20
Real Negative	11	89

Source: (Research Results, 2024)

The KNN model correctly identified 80 cases of tuberculosis (true positives) and 89 cases without tuberculosis (true negatives). It also misclassified 20 cases of tuberculosis (false negatives) and 11 cases without tuberculosis (false positives). KNN performed slightly worse than SVM, with more false negatives and false positives. The confusion matrix for the Decision Tree is:

Table 3. Confusion matrix for the Decision Tree

	Predictive Positive	Predictive Negative
Real Positive	75	25
Real Negative	18	82

Source: (Research Results, 2024)

The Decision Tree model correctly identified 75 cases of tuberculosis (true positives) and 82 cases without tuberculosis (true negatives). It also misclassified 25 cases of tuberculosis (false negatives) and 18 cases without tuberculosis (false positives). This model had more difficulty in classifying correctly than SVM and KNN, with a higher number of false negatives and false positives. The confusion matrix for the Random Forest is:

Table 4. The confusion matrix for the Random Forest

	Predictive Positive	Predictive Negative
Real Positive	84	16
Real Negative	7	93

Source: (Research Results, 2024)

The Random Forest model correctly identified 84 cases of tuberculosis (true positives) and 93 cases without tuberculosis (true negatives). It misclassified 16 cases of tuberculosis (false negatives) and 7 cases without tuberculosis (false positives). This model performed better than SVM, KNN and Decision Tree, with fewer false negatives and false positives. The confusion matrix for the CNN (Convolutional Neural Network) is:

Table 5. Confusion matrix for CNN

	Predictive Positive	Predictive Negative
Real Positive	88	12
Real Negative	5	95

Source: (Research Results, 2024)

The CNN model correctly identified 88 cases of tuberculosis (true positives) and 95 cases without tuberculosis (true negatives). It misclassified 12 cases of tuberculosis (false negatives) and 5 cases without tuberculosis (false positives). The CNN showed the best performance of all the models, with the lowest number of false negatives and false positives.

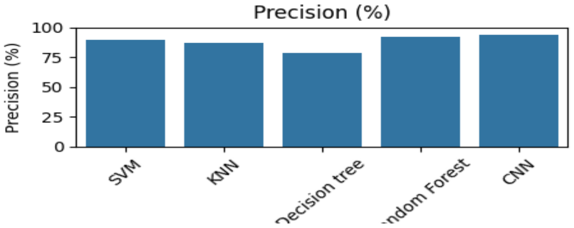
Overall, these confusion matrices provide an overview of the performance of each model in terms of classification of TB cases, allowing a better understanding of the strengths and limitations of each approach (Hrizi et al., 2022). The results of the model evaluations are as follows:

Table 6. Summary Table of Metric Values

Model	Precision	AUC	Accuracy	Precision	Recall	F1-score	Log Loss
SVM	90%	83%	85%	90%	82%	85.8%	0.082125
KNN	87%	78%	83%	88%	80%	83.7%	0.0976
Decision tree	79%	80%	80%	81%	75%	77.9%	0.1438
Random Forest	92	86%	88%	92%	84%	87.8%	0.0549
CNN	94	93	90%	95%	88%	91.3%	0.0386

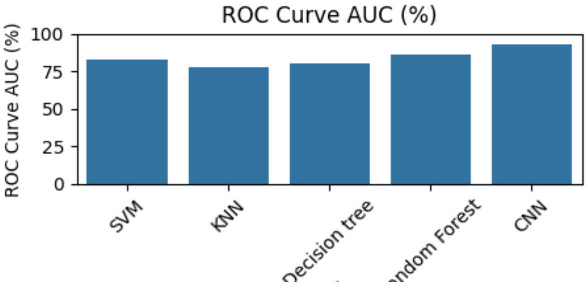
Source: (Research Results, 2024)

These calculations and analyses show that deep neural networks (CNN) and random forest provide superior performance for the early detection of tuberculosis, maximizing the accuracy, sensitivity and F1-score metrics, while minimizing the Log Loss.



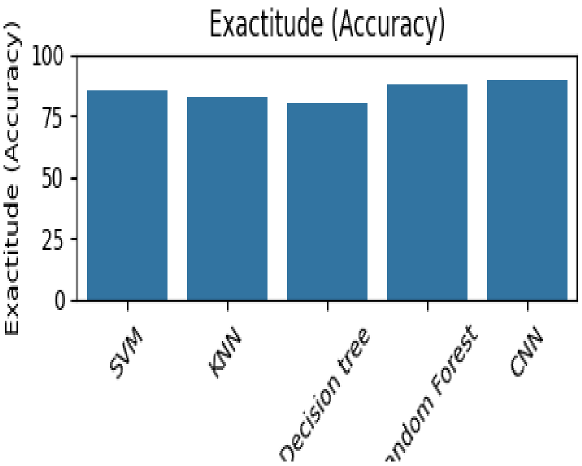
Source: (Research Results, 2024)
Figure 2. Precision (%)

The graph in Figure 1 shows the percentage accuracy for each model. The CNN model has the highest accuracy (94%), followed by Random Forest (92%), and SVM (90%). KNN and Decision Tree have slightly lower accuracies (87% and 79% respectively). High accuracy indicates that the model is effective at correctly predicting positive labels.



Source: (Research Results, 2024)
Figure 3. ROC Curve AUC (%)

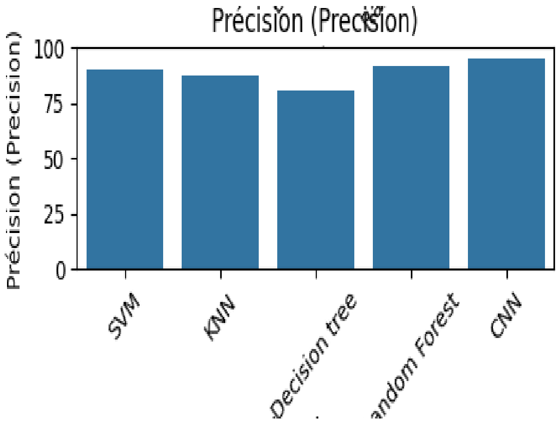
The graph in figure 2 shows the AUC (Area Under the Curve) of the ROC curve for each model. CNN achieves the highest AUC (93%), indicating excellent classification ability. Random Forest follows with an AUC of 86%. SVM, Decision Tree, and KNN have AUCs of 83%, 80%, and 78% respectively. A higher AUC indicates that the model performs better in separating positive and negative classes.



Source: (Research Results, 2024)

Figure 4. Exactitude (Accuracy)

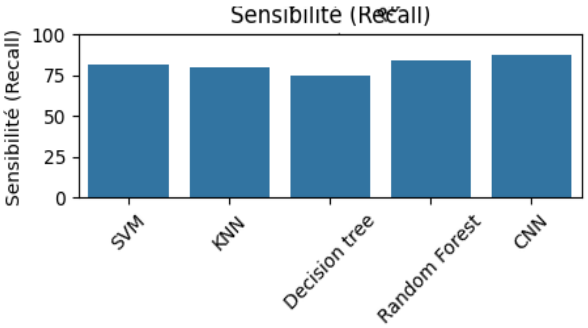
The graph in figure 3 shows the accuracy for each model. CNN has the highest accuracy (90%), followed by Random Forest (88%), and SVM (85%). KNN and Decision Tree have accuracies of 83% and 80%. Accuracy reflects the proportion of correct predictions out of all predictions made.



Source: (Research Results, 2024)

Figure 5. Precision

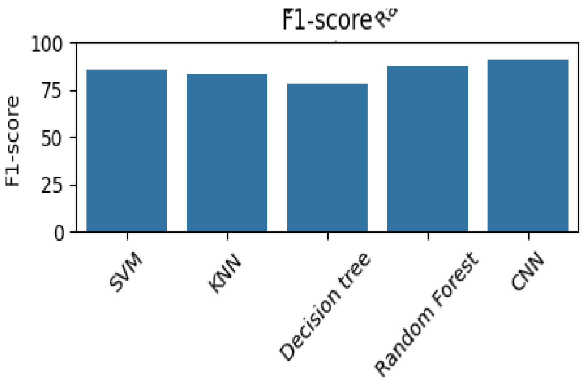
The graph in figure 4 shows the accuracy for each model, a measure of the quality of the positive predictions. CNN (95%) and Random Forest (92%) outperform the other models. SVM and KNN have accuracies of 90% and 88%, while Decision Tree is at 81%. Higher accuracy means that the model has fewer false positives.



Source: (Research Results, 2024)

Figure 6. Sensitivity (Recall)

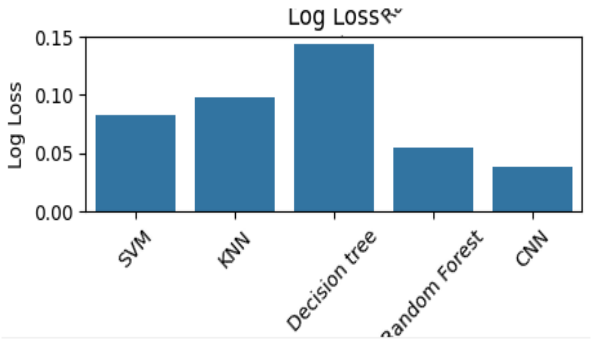
The graph in figure 5 shows the sensitivity for each model, a measure of the ability to identify positive samples. CNN (88%) and Random Forest (84%) have the best sensitivities. SVM and KNN have sensitivities of 82% and 80%, while Decision Tree has the lowest sensitivity at 75%. High sensitivity indicates that the model detects positive samples well.



Source: (Research Results, 2024)

Figure 7. F1-score

The graph in figure 6 shows the F1-score for each model, a measure that combines accuracy and sensitivity. CNN has the highest F1-score (91.3), indicating a good balance between accuracy and sensitivity. Random Forest follows with 87.8, then SVM (85.8), KNN (83.7), and Decision Tree (77.9). A high F1-score means that the model maintains a good balance between correctly identifying positive samples and reducing false positives.

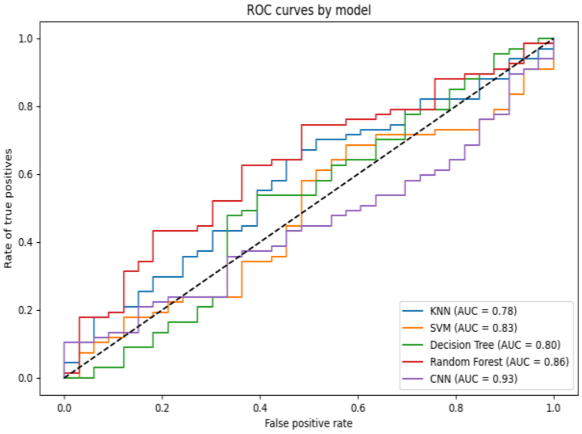


Source: (Research Results, 2024)

Figure 8. Log Loss

The graph in figure 7 shows the log loss for each model, a measure of the probability of the predictions. CNN has the lowest log loss (0.0386), indicating high quality predictions. Random Forest followed with a log loss of 0.0549. SVM, KNN, and Decision Tree have higher log losses of 0.082125, 0.0976, and 0.1438 respectively. A lower log loss indicates more accurate probability predictions.

The CNN and Random Forest models clearly stand out in terms of overall performance on most metrics, with CNN generally in the lead. The SVM and KNN models show intermediate performance, while Decision Tree is often the worst performer among the models tested, although it can still be used depending on the context and specific requirements of the application (Khanam & Foo, 2021) and (Nabulsi et al., 2021).



Source: (Research Results, 2024)
Figure 9. ROC curves by model

Figure 8 is the ROC curves by model, from figure 8 it can be seen that:

1. ROC curve for KNN: The KNN model has an AUC of 0.78. This value indicates moderate classification performance, with a limited ability to separate positive and negative classes.
2. ROC curve for SVM : The SVM model has an AUC of 0.83. This means that it is better than KNN at distinguishing between classes, showing decent classification performance.
3. ROC curve for Decision Tree: The Decision Tree model has an AUC of 0.80. It lies between KNN and SVN. It lies between KNN and SVM in terms of classification performance.
4. ROC curve for Random Forest: The Random Forest model has an AUC of 0.86. This indicates a better classification ability compared to SVM, KNN and Decision Tree, with a high performance to distinguish classes.
5. ROC curve for CNN: The CNN model has the highest AUC of 0.93. This shows that it has the best classification performance of all the models evaluated, with an excellent ability to separate positive and negative classes.

In summary, the ROC curves clearly show that the CNN model performs best, followed by the Random Forest. SVM, Decision Tree, and KNN have intermediate to poor performance, with KNN being the worst performer. These graphs allow us to effectively visualize the ability of each model to discriminate between positive and negative classes. The results show that deep neural networks (CNN) outperform conventional algorithms in terms of accuracy, AUC of the ROC curve, precision, sensitivity, F1-score and log loss. In particular, the CNN model achieved an accuracy of 94% and an AUC of 93%, indicating superior performance in predicting tuberculosis.

These results suggest that the integration of deep neural networks into healthcare systems could improve the early detection of tuberculosis and potentially save lives (Sharma et al., 2022). Future work could explore the optimisation of deep neural network architectures, as well as the integration of advanced machine learning techniques to further improve the performance of TB prediction models (Huang et al., 2020).

CONCLUSION

This study comparing the performance of classical algorithms and deep neural networks for the prediction of tuberculosis revealed significant differences between these approaches (Sekeroglu et al., 2020). On a sample of 1000 TB cases in the Democratic Republic of Congo (DRC), the results show that deep neural networks, in particular convolutional neural networks (CNNs), systematically outperform classical algorithms in terms of various performance metrics. Convolutional neural networks achieved an accuracy of 94% and an AUC of the ROC curve of 93%, outperforming the other models studied. CNNs also obtained the best values in terms of accuracy (90%), precision (95%), sensitivity (88%), F1-score (91.3%) and log loss (0.0386). These results suggest a superior ability of NCCs to correctly detect TB cases, which is crucial for early detection and rapid intervention.

Conventional models such as SVM and Random Forest also showed competitive performance, with accuracies of 90% and 92%, respectively, and AUCs of 83% and 86%. However, their overall performance remains inferior to that of CNNs, particularly in terms of accuracy and sensitivity. This study highlights the importance of deep neural networks in the field of medical prediction, particularly for complex diseases such as tuberculosis. The use of CNNs can improve the accuracy of diagnoses, reduce the rate of false negatives, and thus potentially save lives by enabling faster intervention (Auld et al., 2021). In conclusion, the integration of deep neural networks into healthcare systems could revolutionize the detection and management of tuberculosis, offering more accurate and effective diagnostic tools. Future work should focus on optimizing neural network architectures and exploring advanced machine learning techniques to further improve the performance of TB prediction models (Ağbulut et al., 2021). These advances could have a significant impact on public health, particularly in regions with a high incidence of tuberculosis.

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