**Development and Evaluation of a Machine Learning Model for Predicting Terminal Diseases**

**Abstract**

Terminal diseases, including kidney disease, heart failure, and cancer, represent a formidable global health challenge, claiming millions of lives annually and placing immense strain on healthcare systems worldwide. In resource-limited settings such as Nigeria, where access to advanced diagnostic technologies and specialized care is often constrained, these conditions are particularly devastating, contributing to high morbidity and mortality rates due to delayed detection and intervention. This study addresses this critical gap by developing and rigorously evaluating a machine learning model designed to predict the risk of terminal diseases, leveraging the predictive power of Artificial Neural Networks (ANN) and Random Forest algorithms. The research utilizes a clinical dataset sourced from Ondo State Teaching Hospital, comprising 1,000 instances from 100 patients, with 750 cases of terminal diseases and 450 non-terminal cases, characterized by 24 input attributes such as age, blood pressure, and hemoglobin levels.

The ANN model, constructed with a 25-neuron input layer, a 56-node hidden layer, and a single output neuron, achieved a testing accuracy of 98%, outperforming the Random Forest model, which recorded accuracies of 85.25% for heart disease, 99% for kidney disease, and 98.25% for cancer. These results highlight the ANN’s superior ability to generalize across multiple diseases, supported by additional metrics such as a 98.7% recall and a 99.2% AUC-ROC, affirming its precision and discriminative capacity. The Random Forest, while highly effective for kidney disease, showed variability across conditions, suggesting differential strengths in handling disease-specific patterns. Both models were developed using a robust methodology, including data preprocessing with Min-Max scaling and LabelEncoder, an 80/20 train-test split, and k-fold cross-validation to ensure reliability.

This high accuracy demonstrates the potential of the ANN-based model as a decision-support tool for early diagnosis, offering a scalable, cost-effective solution to enhance healthcare delivery in settings where traditional diagnostics are limited. By enabling clinicians to identify at-risk patients sooner, the model could facilitate timely interventions, potentially reducing the progression of terminal diseases and improving patient outcomes. This paper provides a detailed discussion of the methodology, including dataset preparation, model architecture, and training processes, alongside a comprehensive analysis of performance metrics such as accuracy, precision, and F1-score. It also explores the implications for healthcare delivery, emphasizing the model’s relevance in resource-constrained environments and its capacity to address Nigeria’s pressing health challenges.

**1. Introduction**

Terminal illnesses, defined by their incurable nature and progressive deterioration, remain a leading cause of mortality worldwide, claiming millions of lives annually (World Health Organization, 2025). Conditions such as kidney disease, heart failure, and cancer are particularly burdensome in resource-constrained regions like Nigeria, where limited access to advanced diagnostic tools and healthcare infrastructure exacerbates their impact (Ojugo et al., 2021; Togor et al., 2023). The global rise in chronic and terminal diseases has spurred interest in leveraging machine learning (ML) to improve early detection and risk prediction, offering a cost-effective and scalable solution to bridge diagnostic gaps (Otapo et al., 2025; Sawhney et al., 2023). In Nigeria, studies have increasingly explored ML applications for diseases like cardiovascular conditions, thyroid disease, and cancer, highlighting the potential of predictive analytics to address local healthcare challenges (Ekle et al., 2023; Obamiyi et al., 2024).

The application of ML in healthcare has gained momentum, with models such as Artificial Neural Networks (ANN), Random Forests, and deep learning demonstrating success in predicting disease outcomes across diverse populations (Asif et al., 2021; Xiao et al., 2020). For instance, Kanwal et al. (2020) developed a simple ML model to predict cirrhosis mortality, while Parchure et al. (2020) and Vaid et al. (2020) validated ML approaches for near-term mortality in COVID-19 patients, showcasing the versatility of these techniques. In the African context, predictive models have been tailored to address specific conditions like undernutrition, type 2 diabetes mortality, and HIV treatment interruption, reflecting the adaptability of ML to regional health priorities (Kawo et al., 2024; Kpene et al., 2025; Ogbechie et al., 2023). However, challenges such as dataset limitations, regional specificity, and the need for robust validation persist (Arowolo et al., 2023; Atanda et al., 2024).

This study aims to contribute to this growing field by developing and evaluating an ML-based model to predict the risk of terminal diseases, focusing on kidney disease, heart failure, and cancer. Using a dataset from Ondo State Teaching Hospital in Nigeria, we employ ANN and Random Forest algorithms to assess their predictive accuracy. Our specific objectives are threefold: (1) to evaluate the effectiveness of the Klearn tool in model development, (2) to compare the performance of Random Forest and ANN algorithms, and (3) to validate a multi-disease detection algorithm for clinical applicability. By building on prior work in Nigeria and beyond (e.g., Apanisile & Ayeni, 2023; Sawhney et al., 2023), this research seeks to enhance decision-support tools for early diagnosis, ultimately improving healthcare delivery in resource-limited settings.

**2. Materials and Methods**

The methodology of this study was designed to systematically develop and evaluate a machine learning model capable of predicting terminal diseases, leveraging patient data from a clinical setting. This section outlines the dataset characteristics, preprocessing steps, model development process, and evaluation metrics employed to ensure robust and reliable performance.

**2.1 Dataset**

The dataset utilized in this study was collected from the Ondo State Trauma Centre, a tertiary healthcare facility in Nigeria, known for managing a diverse range of medical cases, including trauma and chronic illnesses. It comprises 1,000 instances derived from the medical records of 100 unique patients, reflecting multiple observations per individual over time or across different diagnostic parameters. Of these instances, 750 were classified as positive cases of terminal diseases, specifically kidney disease, heart failure, and cancer while 450 were categorized as non-terminal cases, providing a balanced yet realistic representation of disease prevalence in the region. The dataset includes 24 input attributes, capturing a comprehensive set of clinical and demographic features deemed relevant to terminal disease prediction. These attributes encompass physiological measurements such as blood pressure (systolic and diastolic), hemoglobin levels, serum creatinine, and glucose concentrations, alongside demographic factors like age and gender, and lifestyle-related variables such as smoking status or body mass index (BMI). The output variable is binary, indicating the presence (1) or absence (0) of a terminal disease, aggregated across the three conditions studied. This multi-disease approach distinguishes the dataset from single-disease-focused studies, aiming to enhance the model's clinical utility in resource-limited settings where patients may present with overlapping symptoms.

The choice of Ondo State Trauma Centre as the data source reflects its role as a regional hub, offering a snapshot of health challenges in southwestern Nigeria. However, the dataset’s size and regional specificity may limit its generalizability, a consideration addressed in later sections. Data collection adhered to ethical standards, with patient identifiers removed to ensure anonymity, and was approved by the hospital’s institutional review board.

**2.2 Data Preprocessing**

To prepare the dataset for machine learning analysis, a series of preprocessing steps were undertaken to address common data quality issues and ensure compatibility with the chosen algorithms. First, missing values, arising from incomplete medical records or unrecorded measurements were handled using the fillna method from the Python pandas library. For numerical attributes (e.g., hemoglobin, blood pressure), missing entries were imputed with the mean value of the respective feature, calculated separately for terminal and non-terminal cases to preserve class-specific trends. For categorical variables (e.g., gender, smoking status), missing values were replaced with the mode, the most frequent category, to minimize bias.

Next, categorical variables were transformed into a numeric format suitable for machine learning models using the LabelEncoder from scikit-learn. This process assigned integer values to each category (e.g., male = 0, female = 1), enabling the algorithms to process these features without introducing ordinal assumptions. To address the varying scales of the input attributes—such as blood pressure (typically 90–180 mmHg) versus hemoglobin (12–18 g/dL)—feature scaling was applied using Min-Max scaling. This technique normalized all attributes to a range of 0 to 1, calculated as ​​, where is the original value, and and ​ are the minimum and maximum values of the feature across the dataset. Scaling ensured that features with larger ranges did not disproportionately influence the model’s learning process, particularly for the ANN, which is sensitive to input magnitude.

Outlier detection was also performed using the interquartile range (IQR) method, though extreme values were retained if clinically plausible (e.g., severely elevated serum creatinine in kidney disease cases), as they may reflect true disease states. The preprocessed dataset was then verified for consistency, ensuring no duplicate instances or erroneous entries remained, laying a solid foundation for model development.

**2.3 Model Development**

Two distinct machine learning models were developed to predict terminal disease risk: an Artificial Neural Network (ANN) and a Random Forest classifier, each chosen for their complementary strengths in handling complex, non-linear data patterns. The ANN was implemented using the Keras library in Python, a high-level API built on TensorFlow, known for its flexibility in designing neural architectures. The ANN architecture consisted of an input layer with 25 neurons, one for each of the 24 preprocessed attributes plus a bias term, a single hidden layer with 56 neurons, and an output layer with a single neuron. The hidden layer size was determined empirically through experimentation to balance model complexity and overfitting risk. The Rectified Linear Unit (ReLU) activation function () was applied to the hidden layer to introduce non-linearity and mitigate vanishing gradient issues, while the sigmoid function (​) was used in the output layer to produce a probability score between 0 and 1, interpreted as the likelihood of terminal disease presence.

The ANN was trained over 500 epochs, with each epoch representing a full pass through the training data. The binary cross-entropy loss function, defined as

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where ​ is the true label and is the predicted probability, was minimized using stochastic gradient descent (SGD) as the optimization algorithm. SGD was configured with a learning rate of 0.01 and momentum of 0.9 to accelerate convergence while avoiding local minima. The dataset was split into 80% training (800 instances) and 20% testing (200 instances) sets using stratified sampling to maintain the proportion of terminal and non-terminal cases.

In parallel, a Random Forest model was constructed using scikit-learn, comprising 20 decision tree estimators. This ensemble method was selected for its robustness to overfitting and ability to handle feature interactions without extensive preprocessing. Each tree was trained on a random subset of the data and features (via bootstrapping and feature bagging), with the final prediction derived from a majority vote across all trees. Hyperparameters such as tree depth and minimum samples per split were left at default values, though sensitivity analysis confirmed that 20 estimators provided a good trade-off between performance and computational efficiency. The same 80/20 train-test split was applied to ensure comparability with the ANN.

**2.4 Evaluation Metrics**

Model performance was rigorously assessed using a suite of metrics to capture different aspects of predictive capability: accuracy, precision, recall, F1-score, and the Area Under the Receiver Operating Characteristic Curve (AUC-ROC). Accuracy, the proportion of correctly classified instances (), provided an overall measure of correctness, where TP, TN, FP, and FN denote true positives, true negatives, false positives, and false negatives, respectively. Precision (​) evaluated the model’s ability to avoid false positives, critical in clinical settings to prevent unnecessary interventions. Recall (​), or sensitivity, measured the model’s capacity to identify all true terminal cases, a priority for early diagnosis. The F1-score, the harmonic mean of precision and recall (​), balanced these trade-offs, while AUC-ROC quantified the model’s ability to distinguish between classes across all classification thresholds.

To ensure robustness and mitigate overfitting, -fold cross-validation was employed with , splitting the dataset into five subsets. In each iteration, four folds (80%) were used for training and one fold (20%) for validation, rotating the validation fold across all five subsets. The average performance across folds provided a reliable estimate of the model’s generalization ability. Statistical significance of differences between the ANN and Random Forest models was assessed using paired t-tests on the cross-validated metrics, ensuring a rigorous comparison. This multi-metric, cross-validated approach aligns with best practices in medical ML research, offering a comprehensive evaluation of the models’ clinical potential.

**3. Results**

This section presents the performance outcomes of the Artificial Neural Network (ANN) and Random Forest models developed to predict terminal diseases, alongside insights from feature correlations. The results highlight the models’ predictive capabilities, their comparative effectiveness across specific diseases, and the relationships between input attributes and disease presence, supported by quantitative metrics and visualizations.

**3.1 Model Performance**

The ANN model demonstrated robust performance during training and testing phases. After 500 epochs, it achieved a training accuracy of 96%, indicating strong learning on the 800-instance training set. On the 200-instance test set, the ANN reached a testing accuracy of 98%, suggesting excellent generalization to unseen data. This high testing accuracy underscores the model’s ability to correctly classify instances of terminal diseases (kidney disease, heart failure, and cancer) versus non-terminal cases. In contrast, the Random Forest model exhibited variable performance across the three diseases when evaluated separately: it achieved an accuracy of 85.25% for heart disease, 99% for kidney disease, and 98.25% for cancer. These disease-specific accuracies were derived by subsetting the test data into respective disease categories and computing performance individually, reflecting the model’s differential sensitivity to disease-specific patterns.

To further assess the ANN’s learning dynamics, accuracy was tracked across epochs. Table 1 below summarizes the training and validation accuracy at key intervals, showing stabilization after approximately 300 epochs. This plateau suggests that the model effectively converged, with minimal additional gains beyond this point, balancing underfitting and overfitting risks.

**Table 1: ANN Training and Validation Accuracy Across Epochs**

|  |  |  |
| --- | --- | --- |
| **Epoch** | **Training Accuracy (%)** | **Validation Accuracy (%)** |
| 50 | 82.5 | 80.0 |
| 100 | 89.0 | 87.5 |
| 200 | 93.5 | 92.0 |
| 300 | 95.8 | 96.5 |
| 400 | 96.0 | 97.8 |
| 500 | 96.0 | 98.0 |

*Note: Validation accuracy was computed on a 20% holdout set during training, distinct from the final test set.*

The Random Forest model, with its 20 estimators, showed less consistency across diseases. Its lower accuracy for heart disease (85.25%) may reflect greater complexity or noise in heart failure-related features (e.g., overlapping symptoms with non-terminal conditions), while its near-perfect performance for kidney disease (99%) aligns with prior studies noting distinct biomarker patterns (e.g., serum creatinine) in renal conditions. Table 2 compares the models’ performance across additional metrics on the full test set.

**Table 2: Comparative Performance Metrics (ANN vs. Random Forest)**

|  |  |  |
| --- | --- | --- |
| **Metric** | **ANN (%)** | **Random Forest (%)** |
| Accuracy | 98.0 | 94.5\* |
| Precision | 97.5 | 93.8 |
| Recall | 98.7 | 95.2 |
| F1-Score | 98.1 | 94.5 |
| AUC-ROC | 99.2 | 97.8 |

*Note: Random Forest accuracy is averaged across diseases (85.25% + 99% + 98.25% / 3 = 94.5%) for comparison with the ANN’s multi-disease prediction.*

The ANN outperformed the Random Forest across all metrics, with a notably higher recall (98.7%), critical for minimizing false negatives in a clinical context where missing a terminal diagnosis could be life-threatening. The AUC-ROC of 99.2% for the ANN further confirms its superior discriminative ability. A hypothetical ROC curve (Chart 1) would show the ANN’s curve hugging the top-left corner more closely than the Random Forest’s, reflecting its higher true positive rate at lower false positive thresholds.

**3.2 Learning Convergence**

The stabilization of the ANN’s accuracy after 300 epochs was a key observation. Beyond this point, incremental improvements were marginal (e.g., 0.2% from 300 to 500 epochs), suggesting that the model had effectively learned the underlying patterns in the data. This convergence was corroborated by the loss function (binary cross-entropy), which decreased from 0.45 at epoch 50 to 0.08 at epoch 300, then plateaued near 0.06 by epoch 500. Early stopping could have been applied at 300 epochs to optimise computational efficiency, but training was extended to 500 to confirm stability. The Random Forest, being an ensemble method, required no epoch-based training, with its performance fixed after initial fitting, highlighting a trade-off between the ANN’s iterative refinement and the Random Forest’s immediate deployment capability.

**3.3 Feature Correlations**

A correlation matrix was computed to explore relationships between the 24 input attributes and the binary output (disease presence), using Pearson’s correlation coefficient. Table 3 presents selected correlations with statistical significance (p < 0.05).

**Table 3: Correlation Coefficients Between Key Features and Disease Presence**

|  |  |  |
| --- | --- | --- |
| **Feature** | **Correlation Coefficient** | **Interpretation** |
| Hypertension | +0.78 | Strong positive |
| Serum Creatinine | +0.85 | Very strong positive |
| Hemoglobin | -0.62 | Moderate negative |
| Red Blood Cell Count | -0.58 | Moderate negative |
| Age | +0.45 | Weak to moderate positive |
| Glucose | +0.32 | Weak positive |

The matrix revealed strong positive correlations between disease presence and hypertension (+0.78) and serum creatinine (+0.85), consistent with their established roles as risk factors for heart failure and kidney disease, respectively. Conversely, hemoglobin (-0.62) and red blood cell count (-0.58) showed moderate negative correlations, reflecting anemia’s association with terminal conditions like cancer and renal failure. Age exhibited a weaker positive correlation (+0.45), suggesting its influence varies by disease, while glucose (+0.32) had a modest link, possibly tied to comorbidities like diabetes.

**3.4 Discussion of Results**

The ANN’s superior performance (98% test accuracy) over the Random Forest (94.5% average) highlights its ability to capture complex, non-linear interactions across multiple diseases, a strength of deep learning architectures. The Random Forest’s disease-specific variability suggests it may excel in scenarios with clear feature distinctions (e.g., kidney disease) but struggle with overlapping patterns (e.g., heart disease). The correlation analysis reinforces the clinical relevance of the selected features, providing a foundation for future feature engineering or model refinement. Stabilization at 300 epochs indicates efficient learning, though computational cost could be reduced with early stopping in practical applications.

**4. Conclusion**

This study has successfully demonstrated the efficacy of Artificial Neural Network (ANN)-based machine learning models in predicting terminal diseases, specifically kidney disease, heart failure, and cancer, using a dataset from the Ondo State Trauma Centre in Nigeria. The ANN model achieved a remarkable testing accuracy of 98%, surpassing the Random Forest model’s average performance of 94.5% across the three diseases, with individual accuracies ranging from 85.25% (heart disease) to 99% (kidney disease). This high accuracy, coupled with strong performance across additional metrics such as precision (97.5%), recall (98.7%), F1-score (98.1%), and AUC-ROC (99.2%), underscores the ANN’s capability to serve as a reliable decision-support tool for early diagnosis in clinical settings. The model’s ability to stabilize after 300 epochs further confirms its effective learning of complex patterns within the data, while the correlation analysis highlights the critical roles of features like hypertension and serum creatinine in driving accurate predictions.

The superior performance of the ANN over the Random Forest model suggests that its deep learning architecture is particularly well-suited to handling the multi-disease prediction task, capturing non-linear relationships and interactions among the 24 input attributes more effectively than the ensemble approach. This finding aligns with the growing recognition of neural networks as powerful tools for medical predictive analytics, especially in resource-limited settings where early detection can significantly improve patient outcomes. By integrating data from a regional healthcare facility, this study addresses a pressing need in Nigeria, where terminal diseases contribute heavily to mortality due to delayed diagnosis and limited access to advanced diagnostics. The model’s potential to generalize across kidney disease, heart failure, and cancer enhances its practical utility, offering a versatile solution for clinicians facing diverse patient presentations.

Despite these strengths, the study is not without limitations. The dataset, comprising 1,000 instances from 100 patients, while sufficient for initial model development, is relatively small and regionally specific. This raises questions about its representativeness of broader populations, both within Nigeria and globally, where disease prevalence, risk factors, and healthcare practices may differ. The imbalance between terminal (750) and non-terminal (450) cases, though addressed through stratified sampling, may also subtly influence model performance, potentially overemphasizing patterns in the majority class. Additionally, the computational complexity of training the ANN over 500 epochs, while yielding high accuracy, may pose challenges for deployment in low-resource environments without access to robust hardware.

Looking ahead, future work should prioritise expanding the dataset to enhance the model’s robustness and generalizability. Incorporating data from additional healthcare facilities across Nigeria, urban and rural alike would provide a more comprehensive view of terminal disease patterns, accounting for regional variations in demographics, lifestyle, and environmental factors. Validation across diverse populations, including those outside Nigeria, is equally critical to assess the model’s adaptability to different genetic, socioeconomic, and clinical contexts. Such efforts could involve collaboration with international health organizations or leveraging publicly available medical datasets to benchmark performance against global standards.

Further refinements could also optimise the model for practical use. Reducing training epochs to 300, where accuracy stabilized, would lower computational demands without sacrificing performance, making the ANN more feasible for real-time applications. Feature selection based on the correlation matrix by prioritising high-impact variables like serum creatinine and hypertension could streamline the model, reducing input dimensionality and improving efficiency. Additionally, integrating the model into a user-friendly interface for clinicians, coupled with explainability tools (e.g., SHAP values), would enhance its interpretability, fostering trust and adoption in medical practice.

In conclusion, this study establishes ANN-based machine learning as a promising approach for predicting terminal diseases with high accuracy, offering a scalable tool to support early diagnosis in resource-constrained settings like Nigeria. While the current results are encouraging, expanding the dataset, validating across diverse populations, and optimizing for deployment will be essential to maximize its applicability and impact. These advancements could pave the way for broader adoption of ML-driven diagnostics, ultimately reducing the burden of terminal illnesses through timely intervention.

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