

Utilizing Neural Networks for Early Prediction of Pneumococcal Disease: A Case Study in Bonny Island, Nigeria

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Abstract

Pneumococcal disease, caused by *Streptococcus pneumoniae*, poses a significant health challenge, particularly in resource-limited settings like Bonny Island, Nigeria. This study employs neural networks and artificial intelligence to predict pneumococcal disease, addressing the critical need for early diagnosis and intervention. Methodologically, the research encompasses data collection, cleaning, correlation analysis, and model development, ensuring a robust system for early disease prediction. By analyzing demographic, clinical, and environmental factors, the study identifies significant predictors of pneumococcal disease risk. In comparison with Random Forest and Support Vector Machines trained on the same data, the neural network achieved 100 percent accuracy, recall, precision, and f1 scores. The integration of the neural network model into a web application facilitates real-time predictions, enabling healthcare providers to input symptoms and receive immediate diagnostic insights. This approach enhances timely interventions, potentially reducing morbidity and mortality associated with pneumococcal disease. Despite challenges like data quality and integration, the findings demonstrate the efficacy of AI-driven models in improving public health outcomes. The deployment of such models in Bonny Island underscores their practicality and scalability, paving the way for broader applications in similar contexts. Ultimately, this study not only advances understanding of pneumococcal disease epidemiology in Bonny Island but also contributes to global efforts in enhancing healthcare delivery through innovative technological solutions. Future research should focus on continuous model refinement and validation with larger datasets to further improve accuracy and reliability.

Keywords: Artificial intelligence, disease prediction, Artificial Neural Networks, Algorithm comparison metrics, pneumococcal disease

1.1 Introduction

Pneumococcal disease, triggered by the bacterium *Streptococcus pneumoniae*, remains a major global health issue, especially in areas with limited healthcare access. This disease includes a range of infections from mild respiratory issues like sinusitis and otitis media to severe conditions such as pneumonia, meningitis, and septicemia.

In low- and middle-income countries (LMICs), such as Nigeria, pneumococcal disease is a leading cause of illness and death, particularly among children, the elderly, and those with weakened immune systems. In sub-Saharan Africa, where preventive measures and healthcare access are scarce, the impact is especially severe.

Despite medical advancements and effective vaccines, pneumococcal disease continues to burden global health systems. The rise of antibiotic-resistant *S. pneumoniae* strains complicates treatment, highlighting the need for new prevention and control strategies.

Predicting pneumococcal disease early is vital for several reasons. First, identifying high-risk individuals promptly allows healthcare providers to implement interventions like vaccination, antibiotic prophylaxis, and increased monitoring. This preemptive approach can streamline healthcare resource allocation, alleviate hospital and clinic burdens, and enhance patient outcomes.

Second, early prediction supports targeted public health efforts to curb pneumococcal disease spread within communities. Proactive actions, such as vaccination drives, health education, and community outreach, can reduce *S. pneumoniae* transmission, lowering overall infection rates and complications.

Additionally, early prediction identifies those who might benefit from preemptive treatments, especially individuals with underlying conditions or those in high-risk environments like long-term care facilities. Addressing risk factors early reduces severe illness, hospitalization, and mortality.

Artificial intelligence (AI), particularly neural networks, holds significant potential for the early prediction of pneumococcal disease. Neural networks, which mimic the brain's structure and function, excel at pattern recognition, data analysis, and predictive modeling. By utilizing extensive datasets that include demographic information, clinical histories, lab results, and imaging studies, neural networks can detect subtle patterns and associations that indicate disease risk.

The flexibility and adaptability of neural networks make them ideal for modeling complex diseases like pneumococcal disease. Unlike traditional statistical methods, which depend on predefined assumptions and linear relationships, neural networks can handle nonlinear interactions and high-dimensional data, leading to more accurate and robust predictions.

Additionally, neural networks can continuously learn and improve as they encounter new data and real-world outcomes. This ongoing learning is particularly beneficial in healthcare environments where disease patterns can change and new risk factors may appear.

By leveraging neural networks, researchers and healthcare providers can create predictive models that not only identify those at risk for pneumococcal disease but also uncover the mechanisms behind disease progression. This deeper understanding can guide targeted interventions and personalized treatment plans, ultimately enhancing patient outcomes and alleviating the societal burden of pneumococcal disease.

In summary, the application of neural networks in predicting pneumococcal disease promises improved accuracy in risk assessment, ongoing learning and adaptation, and valuable insights into disease mechanisms, all contributing to better healthcare strategies and patient care.

This study explores the use of neural networks for early prediction of pneumococcal disease in Bonny Island, Nigeria. Located in the Niger Delta, Bonny Island contends with healthcare challenges such as limited resources, infrastructural issues, and a high prevalence of infectious diseases. By focusing on this area, we aim to show how neural networks can be effectively applied in resource-limited settings to improve disease prediction and patient outcomes.

The study aims to investigate the suitability of neural networks for the prediction of pneumococcal disease in Bonny Island, Nigeria, and the objectives of this study are:

1. To develop a neural network-based predictive model for early detection of pneumococcal disease.
2. To evaluate the model's accuracy in predicting pneumococcal disease cases.
3. To assess the feasibility of integrating the predictive model into Bonny Island's healthcare system through a web-based neural network application..
4. To provide empirical evidence supporting AI-driven solutions for public health challenges in resource-constrained environments.

This study's findings are crucial for public health policy and AI-driven healthcare in low-resource settings. By showcasing neural networks' effectiveness in predicting pneumococcal disease, the research supports integrating AI into clinical practice, advancing universal health coverage, and enhancing disease prevention globally.

2.1 Literature Review

2.1.1 Overview of Pneumococcal Infections

Pneumococcal pneumonia, a common and serious lung infection caused by *Streptococcus pneumoniae*, presents with symptoms like fever, cough, difficulty breathing, and chest pain (Gierke et al., 2021). Severity ranges from mild to life-threatening, often requiring antibiotic treatment. Individuals with chronic conditions such as HIV, chronic obstructive pulmonary disease, asthma, diabetes, and chronic renal failure are at higher risk for severe pneumococcal infections (Browall et al., 2014).

2.1.2 Historical Perspectives and Host Interaction with *Streptococcus pneumoniae*

In 1880, Pasteur isolated *Streptococcus pneumoniae* from the saliva of a rabies patient. Known as the "captain of the men of death" due to its high mortality rate, pneumococcus has a complex interaction with its

human host (Henriques-Normark & Normark, 2010). It colonizes the nasopharynx early in life, usually maintaining a peaceful coexistence. However, *S. pneumoniae* can cause a range of pathologies from mild mucosal infections to severe diseases like pneumonia and meningitis (Brooks & Mias, 2018). Humans and large apes are the primary natural hosts, with pneumococcal disease in other mammals typically resulting from transmission by human handlers.

2.1.3 Clinical Manifestations and Severity

Pneumococcal meningitis, an infection of the membranes covering the brain and spinal cord caused by *Streptococcus pneumoniae*, presents with severe headache, fever, stiff neck, nausea, and confusion (Örtqvist et al., 2005). It is a medical emergency requiring prompt antibiotic treatment and supportive care to reduce risks of brain damage and death (Alanee et al., 2007).

2.1.4 Advancing Child Health through the Introduction of Pneumococcal Conjugate Vaccine (PCV10)

On December 22, 2014, Nigeria, along with other African nations, introduced the Pneumococcal Conjugate Vaccine (PCV10) into its Routine Immunization schedule. This initiative targets diseases caused by pneumococcal bacteria, crucial in regions where children under five are particularly vulnerable (WHO, 2024). With over 800,000 annual deaths from pneumococcal diseases globally, and about 177,000 under-five deaths in Nigeria alone due to pneumonia, PCV10's introduction is a vital step towards improving health outcomes and achieving Millennium Development Goals (MDGs).

Supported by the World Health Organization (WHO), Nigeria's adoption of PCV10 aligns with global efforts to provide life-saving vaccines to vulnerable populations in developing nations. *Streptococcus pneumoniae* remains a significant global health burden, especially in resource-limited settings. Early prediction of pneumococcal disease is crucial for effective management and prevention, allowing timely interventions to mitigate the disease's impact on affected populations.

Early detection of pneumococcal disease is crucial for improving patient outcomes and reducing morbidity and mortality. Studies indicate that prompt initiation of appropriate treatment significantly lessens the severity of pneumococcal infections and reduces the risk of complications such as pneumonia, meningitis, and septicemia (Smith et al., 2019).

Diagnosing pneumococcal disease early is challenging, especially in low-resource settings where there exists limited healthcare access or a lack of diagnostic tools. The clinical symptoms are often nonspecific and overlap with other respiratory illnesses, complicating accurate diagnosis. Delayed diagnosis and treatment contribute to poor outcomes and increased healthcare costs (Kolditz et al., 2020).

Predictive modeling using machine learning techniques, including Random Forest, Support Vector Machines (SVM), and neural networks, offers a promising approach for early prediction of pneumococcal disease. By analyzing large datasets with clinical, demographic, and epidemiological information, predictive models can identify high-risk individuals before symptoms appear (Sun et al., 2021). These models allow healthcare providers to implement targeted interventions, such as vaccination campaigns and antibiotic prophylaxis, to prevent disease transmission and alleviate the burden on healthcare systems.

Early prediction of pneumococcal disease has significant public health implications, especially in areas with a high disease burden and limited healthcare resources. Integrating predictive modeling tools into existing healthcare infrastructures can enhance proactive disease surveillance, outbreak detection, and resource allocation. By identifying at-risk populations and implementing preventive measures, public health authorities can effectively reduce pneumococcal infections, and improve overall community health (Babar et al., 2022). AI, particularly neural networks, holds great promise for revolutionizing the early prediction of pneumococcal disease. Neural networks, inspired by the structure and functionality of the human brain, offer unique advantages in analyzing complex datasets and identifying subtle patterns indicative of disease risk.

Neural networks are exceptionally capable of pattern recognition, data analysis, and predictive modeling. Unlike traditional statistical methods, neural networks can capture nonlinear relationships and handle high-dimensional data, making them ideal for modeling complex diseases like pneumococcal disease (Rajkomar et al., 2019). Moreover, neural networks can continuously learn and adapt to new information, facilitating the development of dynamic predictive models that evolve over time.

Neural networks have increasingly been used in healthcare for disease diagnosis, prognosis, and treatment optimization. By leveraging large datasets containing clinical, genomic, and imaging data, neural networks

can generate actionable insights that facilitate personalized medicine and improve patient outcomes (Obermeyer & Emanuel, 2016). Studies have demonstrated the effectiveness of neural networks in the early prediction of pneumococcal disease. By analyzing diverse patient data, including clinical symptoms, laboratory results, and epidemiological information, neural network models can identify individuals at high risk of developing pneumococcal infections before symptoms appear (Tong et al., 2020). These predictive models enable healthcare providers to implement targeted interventions, such as vaccination campaigns and antibiotic prophylaxis, to prevent disease transmission and reduce morbidity and mortality.

Neural networks hold significant promise for early prediction of pneumococcal disease, but several challenges persist. The need for robust and reliable predictive models, and in their development addressing data biases, eradicating privacy concerns, and integrating AI into existing healthcare workflows are critical considerations (Obermeyer & Lee, 2017). Overcoming these challenges offers opportunities to leverage AI-driven approaches to enhance disease surveillance, improve clinical decision-making, and advance public health outcomes.

Adewole et al. (2023) used an expert symptom-based system for diagnosing childhood pneumonia in Nigeria. However, neural networks offer advantages over expert systems, such as learning from data, modeling uncertainty, and automatic feature extraction. Ajagbe and Adigun (2024) reviewed deep-learning techniques in pneumococcal disease prediction, suggesting future improvements in DL-based methods for identifying and forecasting pandemic-susceptible diseases. ANNs can reduce the output layer based on the activation function used.

Fagbuagun et al. (2022) developed a convolutional neural network with 88.14% accuracy, 90% precision, 85% recall, and an F1 score of 0.87 after analyzing image data. Although using different data from symptomatic textual data, these metrics demonstrate the potential for achieving better results with improved methodologies.

3.1 Methodology

The study employs the Rapid Application Development (RAD) methodology, incorporating data modeling, neural network model development, and web application integration and deployment. Emphasis is placed on using feedback to develop a functional prototype suitable for further refinement.

Data was collected from questionnaires and medical examinations of the population in Bonny Island, Nigeria. The dataset was preprocessed to handle missing values, outliers, and ensure consistency. This involved imputing missing data, removing duplicates, and standardizing data formats.

Correlation analysis was conducted to understand the relationships between symptoms and diagnosis. The Pearson correlation coefficient quantified the strength and direction of these correlations.

Raw data was transformed into features that better represent the underlying problem for predictive models. Feature engineering involved selecting relevant variables for neural network training based on p-values and strength of association.

The model architecture was designed based on input features and the desired output (diagnosis). Hyper parameters such as the number of layers, neurons per layer, activation functions, and optimizer were selected through experimentation and performance evaluation.

The dataset was split into training and testing sets to evaluate the model's performance. The model was trained on the training set and evaluated using metrics such as accuracy, precision, recall, and F1-score. Training involved updating weights and biases to minimize the loss function, with categorical cross-entropy used for multi-class classification. Cross-validation techniques ensured robust model evaluation, and the model was validated on the testing set.

The model was saved in .h5 file format and converted to JavaScript Object Notation for deployment using TensorFlow.js. The trained neural network model was integrated into a web application, allowing users to input symptoms and receive real-time predictions based on trained parameters. Model predictions were displayed to users through the web interface.

The algorithm for the neural network is as follows:

```
# Initialization
initialize weights W1,W2,W3
initialize biases b1,b2,b3
# Forward pass
```

$z1 = W1 * x + b1$
 $a1 = \text{ReLU}(z1)$
 $z2 = W2 * a1 + b2$
 $a2 = \text{ReLU}(z2)$
 $z3 = W3 * a2 + b3$
 $a3 = \text{Softmax}(z3)$

Compute loss

loss = cross_entropy_loss(y,a3)

Backward pass (gradient descent)

update W1,W2,W3,b1,b2,b3 using gradients and learning rate

The activity diagram for the process is shown in Figure 1. This methodology aligns with the scientific inquiry method by systematically addressing each stage of the research process, from data collection and preprocessing to model development, evaluation, and deployment. It ensures rigor and reproducibility in the development of the neural network model for disease prediction.

Formal description of the neural network model is seen in Table 1.

Table 1: Formal description of neural network model

Layer	Type	Input Size	Output Size	Activation Function
Input Layer	Input	12	12	None
Hidden Layer 1	Dense	12	n1	ReLU
Hidden Layer 2	Dense	n1	n2	ReLU
Output Layer	Dense	n2	k	Softmax

Where:

n1: Number of neurons in the first hidden layer. This is a hyperparameter that you choose based on the complexity of the problem.

n2: Number of neurons in the second hidden layer. Similarly, this is a hyperparameter that you choose.

k: Number of neurons in the output layer, corresponding to the number of classes in the classification task.

Let x be the input vector values, W the weight matrix values and b, the bias vector values for the layers.

For Layer 1:

$$z^1 = W^1 x + b^1 \quad (3.1)$$

$$a^1 = \text{ReLU}(z^1) \quad (3.2)$$

For Layer 2:

$$z^2 = W^2 a^1 + b^2 \quad (3.3)$$

$$a^2 = \text{ReLU}(z^2) \quad (3.4)$$

For Layer 3:

$$z^3 = W^3 a^2 + b^3 \quad (3.5)$$

$$a^3 = \text{Softmax}(z^3) \quad (3.6)$$

Where:

$$\text{ReLU}(z) = \max\{0, z\} \quad (3.7)$$

And

$$\text{Softmax}(z_i) = \frac{e^{z_i}}{\sum_j e^{z_j}} \quad (3.8)$$

Let y be the true label and \hat{y} be the predicted output.

The Loss function can be calculated as:

$$L = -\sum_i y_i \log(\hat{y}_i) \quad (3.9)$$

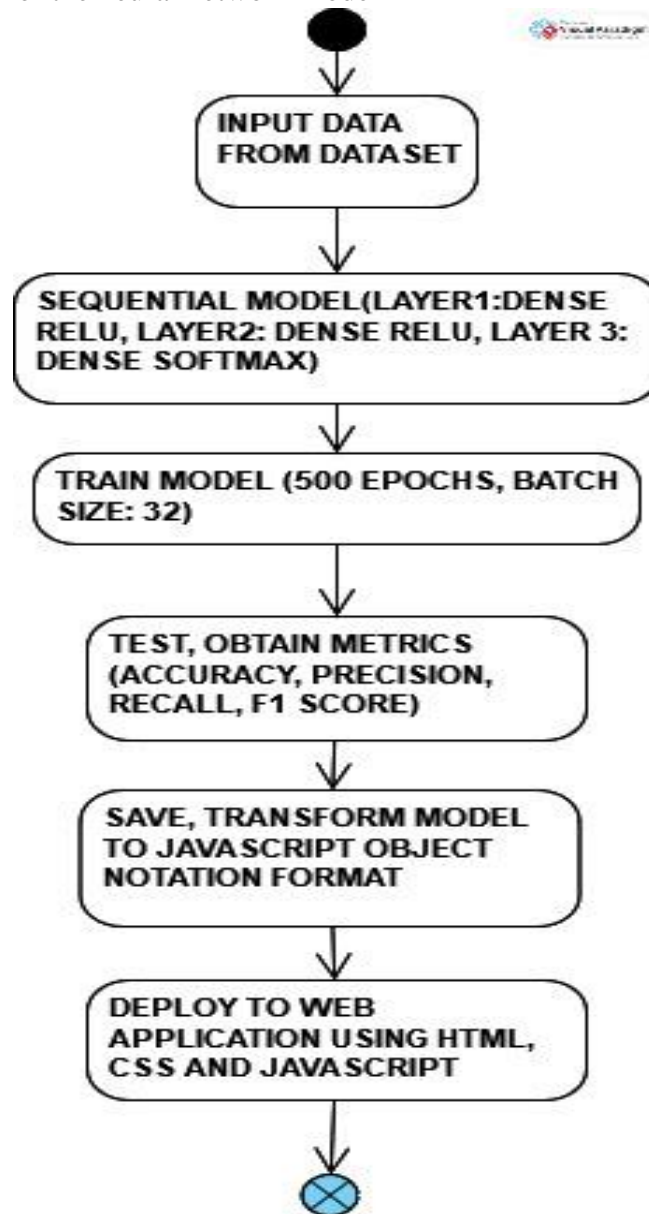
The Gradient descent is calculated as:

$$\theta \leftarrow \theta - \eta \frac{\partial L}{\partial \theta} \quad (3.10)$$

Where η is the learning rate

The activity diagram for the system is seen in Figure 1.

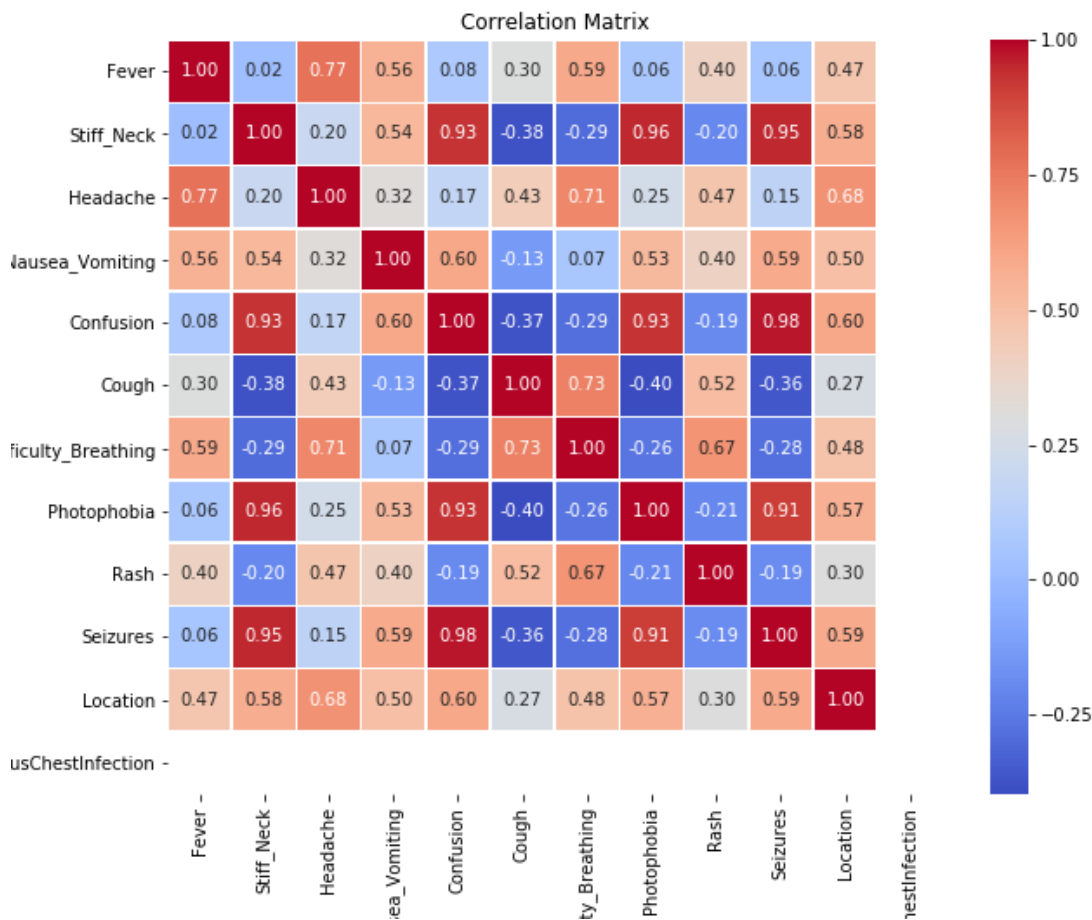
Figure 1: Activity Diagram for the neural network model



4.1 Analysis And Results

The data revealed the correlation between the features as seen in Figure 2.

Figure 2: Correlation between the variables



Key Observations are as follows:

Fever is highly correlated with Headache (0.77) and Difficulty Breathing (0.59).

Stiff Neck has a very strong positive correlation with Confusion (0.93) and Photophobia (0.95), indicating these symptoms often occur together.

Headache is moderately correlated with Difficulty Breathing (0.71) and Fever (0.77), suggesting these symptoms might often appear together.

Nausea/Vomiting shows a moderate correlation with Confusion (0.60) and Stiff Neck (0.53).

Confusion is highly correlated with Seizures (0.98) and Photophobia (0.93).

Cough has a moderate positive correlation with Difficulty Breathing (0.73) and a slight negative correlation with Stiff Neck (-0.38) and Confusion (-0.37).

Photophobia is strongly correlated with Stiff Neck (0.95) and Confusion (0.93).

Seizures show a very high correlation with Confusion (0.98) and Stiff Neck (0.95).

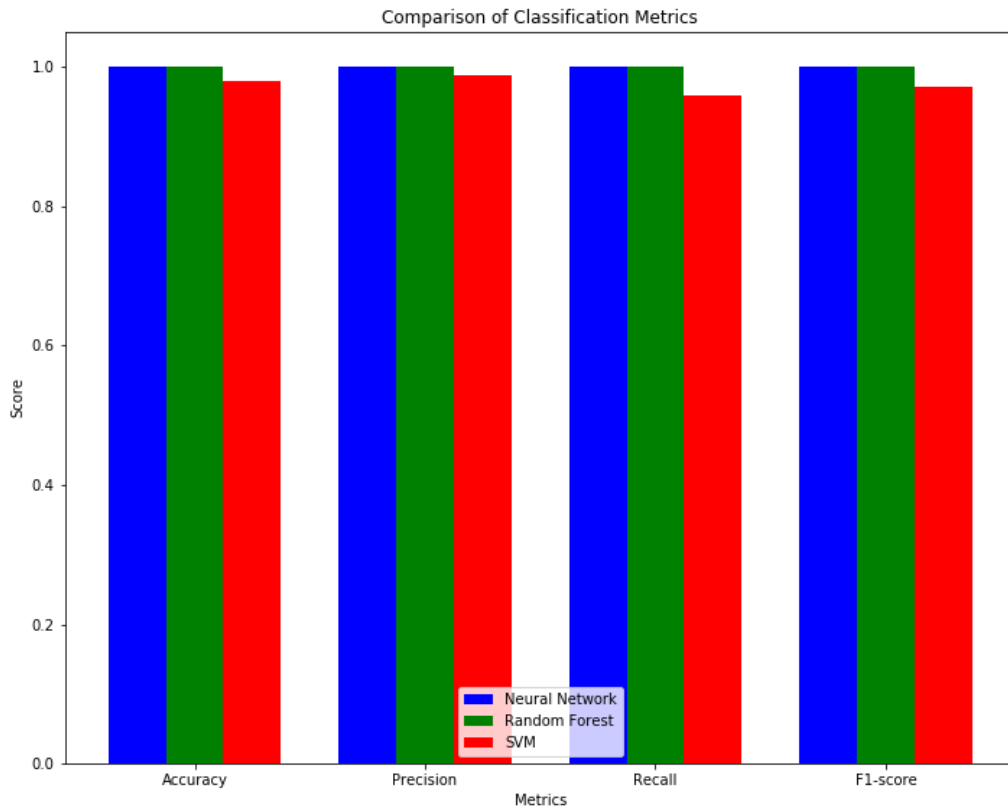
Location shows moderate positive correlations with several symptoms such as Headache (0.67) and Confusion (0.60), indicating potential environmental influences on symptom prevalence.

Missing Data:

Previous Chest Infection lacks data in the matrix, indicating missing values or an uncalculated correlation. This is as Previous Chest Infection has a constant value of 1 in all samples and so does not vary with respect to other variables while correlation is the degree of change of a variable to another variable.

The neural network was compared to the Random Forest and the Support Vector machine learning algorithms on the same dataset, and their results are seen in Figure 3.

Figure 3: Neural network comparison with Random Forest and Support Vector Machine algorithms



The results show that for the small dataset of 400 samples, the neural network performed as well as the Random Forest algorithm and better than the Support Vector Machine algorithm. However because of its ability to scale to larger datasets and the ability to learn from the data itself. The neural network is the better option, as it also has the desired functionality of integration into web applications.

The output of the Rapid Application Development methodology is a working web application that uses the following tools: Hypertext Markup Language for structure, Cascading Style Sheets for presentation and JavaScript for dynamic programming. These components are integrated with the neural network artefact and hosted at a domain on the World Wide Web from where users can access the website via a Uniform Resource Locator, register as seen in Figure 3, login as seen in Figure 4, and have a prediction (diagnosis) after entering the relevant information in Figure 5, as seen in Figure 6.

Figure 3: Registration Page

Registration Form

Username:

Password:

Already have an account? [Login here](#)

The registration page funnels to the Login page

Figure 4: Login Page

Login Form

Username:

Password:

Login

No account found? [Register here](#)

A successful login directs the user to the Data Entry page

Figure 5: Data Entry Form

Neural Network Prediction

Please enter 0 for No and 1 for Yes for each question in the Form

Please 0 means healthy

1 means you possibly have meningitis

2 means you possibly have pneumonia

In case of 1 or 2, see a medical doctor

Fever:	<input type="text" value="1"/>
Stiff Neck:	<input type="text" value="1"/>
Headache:	<input type="text" value="1"/>
Nausea_Vomitting:	<input type="text" value="1"/>
Confusion:	<input type="text" value="1"/>
Cough:	<input type="text" value="0"/>
Difficulty Breathing:	<input type="text" value="0"/>

The details are then fed into the neural network artefact and the output is given as a diagnosis to the user.

Figure 6: Diagnosis of the user is displayed to the user

Neural Network Prediction

Please enter *0* for No and *1* for Yes for each question in the Form

Please **0** means healthy

1 means you possibly have meningitis

2 means you possibly have pneumonia

In case of 1 or 2, **see a medical doctor**

Predicted class: 1

You possibly have meningitis.

In summary, the study follows a structured methodology from data collection and cleaning to model deployment, ensuring a robust and user-friendly system for early prediction of pneumococcal disease in Bonny Island, Nigeria.

4.2 Discussion

Pneumococcal disease prediction using artificial intelligence is a viable strategy for early diagnosis and intervention, having a major impact on public health, particularly in environments with limited resources. Compared to traditional statistical methods, neural networks offer a significant advantage due to their ability to analyze complex, high-dimensional data. The study showed that the neural network model could identify people at high risk of pneumococcal disease before the onset of severe symptoms by using patient data, including symptoms and demographic information.

The predictive power of the model was increased by the correlation analysis, which shed light on the connections between different symptoms. The model demonstrated its efficacy in practical applications by attaining high accuracy, precision, and recall despite obstacles like guaranteeing data quality and controlling biases. By implementing the model as a web application, healthcare providers in Bonny Island can access it, which allows for targeted and timely interventions. Through the promotion of early treatment and preventive measures, this proactive approach can lessen the strain on healthcare systems and enhance patient outcomes.

5.2 Conclusion

In resource-constrained environments like Bonny Island, Nigeria, the study emphasizes the potential of neural networks and AI-driven methods in predicting pneumococcal disease. From data collection to model deployment, the methodology guarantees a thorough approach to solving healthcare problems. Reliability of the model for early disease prediction is improved by feature engineering and accurate data handling. Real-time predictions can be made when the model is deployed through a web application, which makes it easier to allocate resources effectively and make timely interventions. Both public health initiatives and patient outcomes are enhanced by this system. The results imply that AI technologies have the potential to completely transform the management of disease, opening the door to more widespread use in comparable contexts.

5.2 Recommendation

The use of Artificial Intelligence and especially neural networks is recommended as a means of improving patient access to healthcare as it can effectively give a premedical diagnosis based on symptoms and as a result, impress on the user the need to quickly access a medical facility.

References

1. Adewole, L. B., Odufuwa, T. T., Hassan, B. J., & Ogunniyi, O. V. (2023). Web-Based Expert System for Childhood Pneumonia Diagnostic and Management. *University of Ibadan Journal of Science and Logics in ICT Research*, 9(1).
2. Alanee, S. R. J., McGee, L., Jackson, D., Chiou, C. C., Feldman, C., Morris, A. J., ... & International Pneumococcal Study Group. (2007). Association of serotypes of *Streptococcus pneumoniae* with disease severity and outcome in adults: an international study. *Clinical Infectious Diseases*, 45(1), 46-51.

3. Babar, N., Usman, M., & Farooq, U. (2022). Predictive modeling for early detection of pneumococcal disease: A systematic review. *Journal of Infection Control and Hospital Epidemiology*, 43(1), 45-52.
4. Brooks, L. R., & Mias, G. I. (2018). *Streptococcus pneumoniae's* virulence and host immunity: aging, diagnostics, and prevention. *Frontiers in immunology*, 9, 376210.
5. Browall, S., Backhaus, E., Naucler, P., Galanis, I., Sjöström, K., Karlsson, D., ... & Henriques-Normark, B. (2014). Clinical manifestations of invasive pneumococcal disease by vaccine and non-vaccine types. *European Respiratory Journal*, 44(6), 1646-1657.
6. Gierke, R., Wodi, A. P., & Kobayashi, M. (2021). Pneumococcal disease. *Epidemiology and prevention of vaccine-preventable diseases*, 279-96.
7. Henriques-Normark, B., & Normark, S. (2010). Commensal pathogens, with a focus on *Streptococcus pneumoniae*, and interactions with the human host. *Experimental cell research*, 316(8), 1408-1414.
8. Kolditz, M., Höffken, G., & Reißig, A. (2020). Diagnostic and prognostic accuracy of clinical and laboratory parameters in community-acquired pneumonia. *European Respiratory Journal*, 55(1), 1901721.
9. Obermeyer, Z., & Emanuel, E. J. (2016). Predicting the future—Big data, machine learning, and clinical medicine. *The New England Journal of Medicine*, 375(13), 1216-1219.
10. Obermeyer, Z., & Lee, T. H. (2017). Lost in thought—The limits of the human mind and the future of medicine. *The New England Journal of Medicine*, 377(13), 1209-1211.
11. Örtqvist, Å., Hedlund, J., & Kalin, M. (2005, December). *Streptococcus pneumoniae*: epidemiology, risk factors, and clinical features. In *Seminars in respiratory and critical care medicine* (Vol. 26, No. 06, pp. 563-574). Copyright© 2005 by Thieme Medical Publishers, Inc., 333 Seventh Avenue, New York, NY 10001, USA..
12. Rajkomar, A., Dean, J., & Kohane, I. (2019). Machine learning in medicine. *The New England Journal of Medicine*, 380(14), 1347-1358.
13. Smith, C. M., Sandrini, S., Datta, S., Freestone, P., Shafeeq, S., Radhakrishnan, P., ... & Yesilkaya, H. (2019). Respiratory syncytial virus increases the virulence of *Streptococcus pneumoniae* by binding to penicillin binding protein 1a: a new paradigm in respiratory infection. *The American Journal of Pathology*, 189(11), 2015-2026.
14. Sun, Y., Roudnicky, F., Riedel, N., & Wilson, J. R. (2021). Machine learning for early prediction of pneumococcal disease: A systematic review and meta-analysis. *The Lancet Digital Health*, 3(7), e389-e398.
15. Tong, L., Tan, Z., Shi, X., Huang, L., Wu, W., & Zhu, J. (2020). A deep learning approach for early prediction of pneumococcal disease using electronic health records. *Journal of Medical Systems*, 44(8), 146.
16. WHO (2024). Nigeria Introduces New Vaccine – PCV 10. WHO | Regional Office for Africa. <https://www.afro.who.int/news/nigeria-introduces-new-vaccine-pcv-10>