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Revolutionizing Neonatal Care: A High-Precision Hybrid ANN-RF Model for Pneumonia Prediction

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Abstract

Neonatal pneumonia is a major health challenge, significantly contributing to morbidity and mortality among newborns. Timely and accurately predicting its progression is crucial for improving clinical outcomes and ensuring effective treatment strategies. This study focuses on introducing a ground-breaking approach to predict disease progression in neonatal pneumonia through a hybrid Artificial Neural Network- Random Forest (ANN-RF) model. The methodology employed in this study involves several critical stages. Initially, comprehensive data collection was conducted from neonatal intensive care units (NICUs) and paediatric hospitals ensuring a robust dataset that reflects diverse clinical scenarios. Following this, data pre-processing was performed to address missing values and normalize features, enhancing the quality of the data for analysis. Feature extraction techniques were then applied to identify key clinical parameters that are most indicative of disease progression. The development of the hybrid ANN-RF classification model effectively combines the strengths of artificial neural networks known for their high dimensional pattern recognition capabilities with the interpretability and robustness of Random Forest decision trees. This synergy allows for both accurate predictions and clear insights into the factors influencing disease outcomes. Remarkably the proposed model achieved an accuracy of 98%, demonstrating its potential for practical application in clinical settings. Such high accuracy not only aids healthcare professionals in making informed decisions but also enhances patient management strategies. Ultimately this study underscores the transformative potential of integrating advanced machine learning techniques into neonatal care, paving the way for future research aimed at optimizing predictive analysis in healthcare settings.

Keywords: *Artificial Neural Network, Disease Progression Prediction, Hybrid Model, Healthcare Analytics, Machine Learning, Neonatal Pneumonia, Random Forest.*

Introduction

Neonatal pneumonia is the result of a serious respiratory infection that affects the young, usually within the first 28 days of life. The in-hospital mortality rate for critically ill newborns admitted to neonatal intensive care units (NICUs) has remained stubbornly high, ranging from 6.4% to 10.9% over the past decade, even as medical advancements in perinatal resuscitation and neonatal care have progressed. This persistent challenge underscores the ongoing need for further research and improvements in neonatal care practices to enhance survival rates and improve outcomes of vulnerable newborns [1, 2, 3, 4]. It

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is an important cause of morbidity and mortality carrying a substantial proportion of the neonatal death toll particularly in developing countries [5]. The mortality rate in NICUs is influenced by a complex interplay of factors, such as pre-existing chronic health issues, infections linked to medical devices, underdeveloped immune systems and prolonged reliance on mechanical ventilation [6, 7, 8]. Worldwide, 15% of all neonatal deaths are a result of neonatal pneumonia, according to the World Health Organization - a health concern with significant implications for infant health. Prompt detection and appropriate management are essential to get a better prognosis for those infants [9, 10].

Neonatal pneumonia has different prevalence rates according to geographic area, healthcare infrastructure, and socioeconomic conditions. High-income countries have lower incidences, but incidence rates are drastically higher in low- and middle-income countries where poor access to healthcare services and suboptimal maternal and neonatal care are common. It has been reported that about 3 million neonatal pneumonia cases occur globally, the lion's share in South Asia and sub-Saharan Africa. Better surveillance and reporting of cases are necessary to map the total landscape of this disorder [11]. Its condition can be classified based on the timing and mode of acquisition: congenital (acquired in utero), intrapartum (acquired during delivery), or postnatal (acquired after birth). Congenital pneumonia is usually a result of transplacental infection or aspiration of infected amniotic fluid. Intrapartum pneumonia is the result of the inhalation of pathogens in the birth canal from above during parturition [12, 13]. Pneumonia in the postnatal period can be community or healthcare-associated and can also be acquired in the external environment. If left unnoticed, it may cause life-threatening respiratory complications in newborns due to great implications on the respiratory function of neonates [14].

Neonatal pneumonia has a variety of causes, including bacterial, viral and fungal pathogens. Bacterial pathogens are a common cause of meningitis in the newborn and typically include Group B *Streptococcus*, *Escherichia coli*, and Klebsiella species (transmitted from the mother during delivery). Viral agents including respiratory syncytial virus (RSV), cytomejson virus (CMV) and herpes simplex virus (HSV) may be vertical transmission or postnatally from acutely infected individuals. Fungal infections, mainly due to Candida species, are less frequent but may occur in immunocompromised infants. Premature birth, prolonged rupture of membranes, chorioamnionitis, birth asphyxia and congenital anomalies are important risk factors for neonatal pneumonia. It also carries a great risk of meconium aspiration associated with right upper-lobe infection being introduced and an explosion into the lungs during delivery [15, 16].

Finding out whether a newborn has pneumonia is not easy because the symptoms are not specific to pneumonia. Symptoms such as tachypnea, chest retractions, grunting, poor feeding, lethargy and fever are usually present. Cyanosis (bluish discolouration of the skin) and apneic episodes (pauses in breathing) may also be seen in some cases. Diagnostic tools include the clinical examination, chest radiography, and laboratory tests (e.g., blood cultures and complete blood counts). Measurements of pulse oximetry and blood gases are also vital in grading hypoxemia and respiratory distress. Neonatal pneumonia.

Treatment of neonatal pneumonia includes antibiotics, supportive care and in some cases, mechanical ventilation. Until culture results reveal the causative pathogenic organism, broad-spectrum antibiotics are usually empirically prescribed. Common antibiotics include Ampicillin, gentamicin, and cefotaxime. This may include oxygen through the tube, intravenous fluid to keep you hydrated and oral nutritional help. For the more severe

cases, mechanical ventilation was used to aid with their respiratory function. Urgent and aggressive treatment is necessary to prevent complications, including sepsis, meningitis and chronic lung disease [17].

The prevention of neonatal pneumonia is a combined strategy: maternal vaccination, good environmental practices and especially timely and adequate pre- AND postnatal care. Not all vaccines are created equal, but such diseases as Streptococcus pneumoniae and Hemophilus influenzae type b (Hib), ones for which we have excellent vaccines, can reduce the incidence of pneumonia greatly. Furthermore, by advocating breastfeeding and adequate nutrition, we can amplify immune responses among neonates. Neonatal pneumonia has reached epidemic levels and is related to significantly increased infant mortality and morbidity. Better awareness, early diagnosis, appropriate treatment and comprehensive prevention strategies can lead to substantial progress in combating this disease on a global scale. This study presents a comprehensive methodology for predicting disease progression in neonatal pneumonia using a hybrid Artificial Neural Network-Random Forest (ANN-RF) model. Healthcare providers, policymakers and research stakeholders must collaborate to achieve maximum progress in neonatal health and the well-being of newborns across the globe.

Related Works

Ventilator-associated pneumonia (VAP) stands as the second most common healthcare-associated infection among neonatal intensive care units (NICUs). This review aims to describe the currently available preventive procedures for VAP in neonates and update our knowledge about its prevalence. The incidence rate of ventilator-associated pneumonia (VAP) ranges from 16.1 to 89 episodes per 1000 ventilator days in underdeveloped countries versus 1.4 to 7 cases per 1000 ventilator days in industrialized countries [18]. The newly emerging programs for this nosocomial infection about the same patient illness, all of which lead to higher morbidity and mortality rates and increased length of hospital stay, creating a considerable financial burden on families for healthcare costs. The heterogeneous pathogenesis of VAP has spawned numerous recommendations intended for preventing its occurrence in the sickest NICU patients. For prevention, measures may be broadly divided into those that aim to reduce infections in general and those that specifically address VAP. Some of these treatments are very simple and easy to implement, such as hand hygiene practices and feeding schedules. Bundles are one group of initiates that seems to hold a lot of promise as it incorporates a lot of the preventative measures for VAP. Preventative strategies still need to be investigated.

Bacterial, viral and fungal pneumonia, an inflammatory lung disease, tends to be widespread in children due to the complexity of their immature immune response as their respiratory system is different from that of adults and also may rapidly change to severe critical Pneumonia during illness. Paired with the fact that those under five have weaker immune systems, this is all the more reason for paediatric pneumonia to be identified promptly. Radiographic abnormalities, variable clinical findings, and interpretation assessment make chest X-ray a less favourable tool for diagnostics, especially in paediatric situations. Deep learning and, more specifically, transfer learning holds promise to improve pneumonia diagnosis by leveraging large, labelled datasets. A bottleneck for creating efficient models is the number of annotated training data for paediatric chest X-rays [19]. They use self-supervised learning to address this problem, with the Masked Autoencoder (MAE) in mind. To overcome this data scarcity problem and to achieve higher accuracy in paediatric pneumonia diagnosis, they planned to train the MAE model using adult chest X-ray images and

then fine-tune the pre-trained model with a chest X-ray image set of children with pneumonia. An approach was proposed to perform competitively, with an AUC value of 0.996 and a precision equivalent of 95.69% in discriminating between healthy and infected groups [20]. Twenty-one of the newborns and 13 of the nurses supplied respiratory fluids. Using a TaqMan low-density array for 27 pathogens, sixteen of the twenty samples from newborns and four from nursing personnel were positive for HRSV. Four of the 16 newborns transferred to the hospital were housed in regular wards and 7 others in the intensive care unit. There were four cases of asymptomatic infection among the nursing staff. In addition, the second hypervariable region of 6 infants and 2 nursing staff were obtained to investigate the genetic characteristics of HRSV responsible for this epidemic. Phylogenetic analysis revealed that the 8 sequences (SY strains) were of the HRSV BA9 genotype. The results spit in the face of this hoopla and indicate that aggressive hygiene and disease control measures are necessary to prevent the spread of germs and keep dangerous respiratory illness epidemics under control.

It was aimed to explore the clinical management priority and plausibility of a novel multichannel sensor measured signals for the discrimination of newborn pneumonia (neoP) and treatment resistance evaluation. A new wideband multichannel piezoelectric sensor was constructed using 180 infants with pneumonia. A piezoelectric sensor was utilized for pathogen detection in the samples from newborns, and the conventional Kirby-Bauer (K-B) disc diffusion method was used for antibiotic resistance. There was no significant difference in the sensitivity and specificity between the K-B technique and the multichannel piezoelectric sensor (99.58% vs 99.32%, $P > 0.05$). The detection time of the K-B technique (17.25 h) was significantly higher than that of the multichannel piezoelectric sensor (7.43 h) ($P < 0.05$). By pathogen detection, the most common pathogens included *Klebsiella pneumoniae* (25.1%) with 13.4% due to *Staphylococcus aureus* and 12.33% associated with Haemophilus influenzae. There was a *Staphylococcus aureus* up to > 50% resistant rate shown against erythromycin, ciprofloxacin, gentamicin, and rifampicin, however, some strains might have 100% resistance toward vancomycin and rifampicin. The piezoelectric sensor arrays based on novel multichannel could detect pathogens within less time than other methods, with high sensitivity and specificity for newborn pneumonia. The majority was represented by bacteria with a Gram-negative characteristic, followed by bacteria Gram-positive and fungus. *Haemophilus influenzae*, *Klebsiella pneumoniae* and *Staphylococcus aureus* were the most common. Moreover, the bacteria that caused pneumonia in newborn babies showed high resistance to many antibacterial drugs such as chloramphenicol, meropenem, amikacin sulfate, chloropicrin and rifampicin.

Methodology

Data Collection

The first step is to collect detailed data based on which predictive model of disease progression in neonatal pneumonia can be developed. The purpose is to collect a comprehensive set of data on neonatal pneumonia cases. These data are pulled from neonatal intensive care units (NICUs) and pediatric hospitals, ensuring relevance and timeliness. Data must be both anonymized and gathered in a manner that protects patient confidentiality in compliance with ethical guidelines. The data to be collected should include patient demographics (age in days, gender), clinical parameters (birth weight, respiratory rate, and oxygen saturation levels), diagnostic results (blood culture results), treatment details (the antibiotics used, and for how long) as well as outcomes (recovered/ not recovered).

Creating a model that can generalize well across different populations and conditions requires collecting a diverse and comprehensive set of data. This phase may also include data ingestion from other source systems to have enough size of the dataset for training an ML model. Finally, it is also important to provide and publish the metadata of your collections processes so that the data itself carries meaning wherever and whenever it is used.

Data Preprocessing

After that, we preprocessed the data, which means cleaning and preparing your data before doing any analysis on it. This was a very important step as it ensured that the data was of high quality and useful for training machine learning models.

Data Cleaning

There were a few missing values in certain cells, which were either filled through the appropriate value or the whole record could also be dropped if it has many missing values. This step also involved cleaning data entry mistakes to maintain uniform units and formats throughout the data set. The data needed to be clean so that the model was not given certain variations just because there were errors in the data table.

Normalization

The second important part of preprocessing was normalization, which is especially useful for continuous variables like birth weight and respiratory rate. Scaling these variables to a standard scale allows all the features in the numerical column to contribute equally to the model during every weight update, without any feature having a large base effect on it. This was an intermediate step so that the equilibrium and comparability of different features could be held constant.

Categorical Encoding

Categorical encoding had to be performed so the random forests could process variables such as gender, blood culture result or antibiotic used. Based on the categorical nature, it was performed with techniques like one-hot encoding or label encoding. This was a necessary conversion to allow the model to make proper sense and use the categorical data.

Data Splitting

Data was split in a 70-15-15 ratio for Train, Validation & Test. The training set was used to teach the model, the validation set was to tune hyperparameters and prevent overfitting, and the test set was used to evaluate how well the model performed on data that had never been seen. This split served to evaluate the reliability and applicability of the model's performance. Breaking the data down into these different sets meant that we could test how well the model performed on data it had never seen before. Figure 1 shows the Architecture of the Proposed Model.

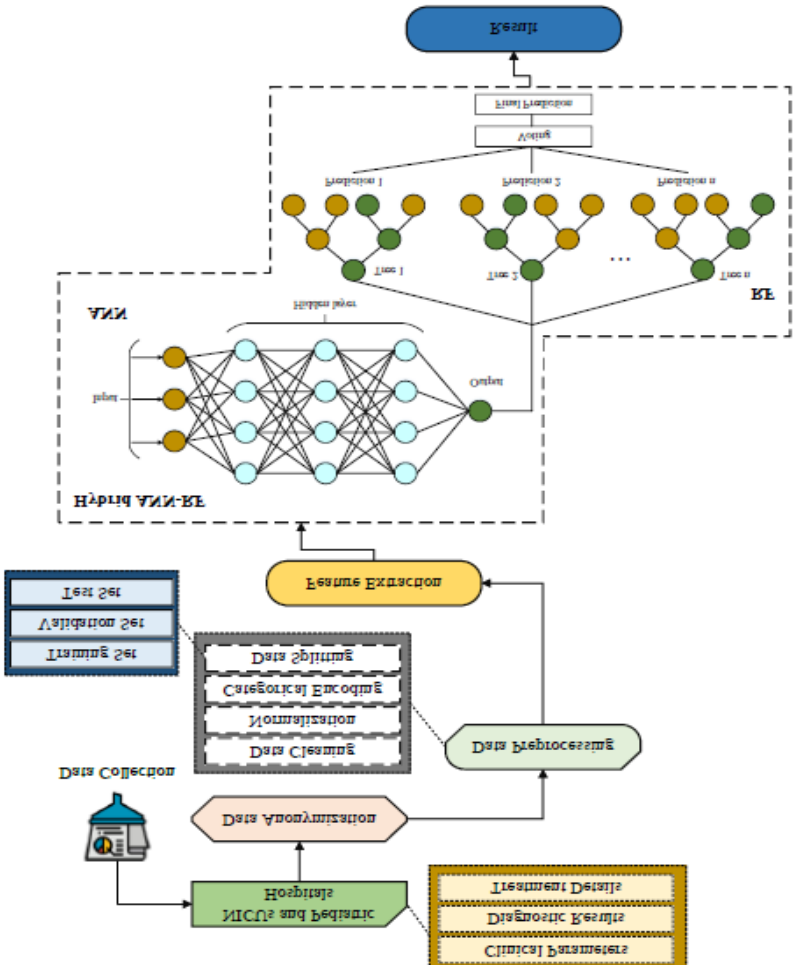

Figure 1. The Architecture of the Proposed Model

Feature Extraction

Identifying and Selecting Relevant Features

Feature extraction was also a process of identifying and selecting the most important features from the dataset to be an input for the model. This was very important as it defined the features that were useful and relevant to the model. We selected some of the key features that had a high importance in deciding the disease progression, namely birth weight, respiratory rate, peripheral oxygen saturation, blood culture result and antibiotics used. The morphometric features were either selected a priori based on knowledge of the field and disease process or used similarly to the radiomic features.

Feature Engineering

Besides choosing features already in existence, feature engineering was carried out to generate new features that might suggest extra insights. This consisted of either modelling the interaction terms between related features or feature transformation to account for nonlinear relationships in the data. This included, for example, creating interaction terms of birth weight and respiratory rate to determine how these factors in combination impacted disease progression. This would allow you to extract more meaningful data out of the dataset which will increase your model predictability.

Ensuring Proper Scaling and Formatting

They preprocessed the features by scaling them down and converting them into a suitable shape for the model. The continuous features were standardized or normalized to have equivalent contributions during training. This was a necessary step to keep the features

balanced and comparable. Categorical features were encoded; accordingly, either one-hot or label encoding, depending on the type of categorical variable. The categorical data had to be properly encoded for the model to successfully interpret and use it.

Preparing Features for Model Training

This comment stage while driving toward the following activity, during which the model would figure out how to make expectations by learning genuine accusations of these highlights. Feature Selection, Engineering, and Formatting ensure that the data being fed into the model is of high quality and meaningful by choosing the right features. This meticulous preparation helped to create a strong predictive disease progression model for neonatal pneumonia.

Proposed Model: Hybrid ANN-RF

The model included the following components: Artificial Neural Network (ANN) and Random Forest (RF). The ANN part consisted of an input layer with neurons equalled to the number of the feature columns, a few hidden layers using ReLu activation functions and their neurons, which varied in number between them, and the SIGMOID activation function used for our output layer because we had a binary classification task. The architecture of the ANN was designed to take advantage of their ability as non-linear function approximates to approximate complex, non-linear relationships in the data.

An ANN was trained in the training set, where weight optimizations took place by backpropagation using an optimizer suitable such as Adam (Adaptive Moment Estimation). We use the Adam optimizer as it is an efficient optimizer and handles sparse gradients for noisy problems. ANN training is the process of the ANN learning to tweak its weights so that it converges towards a local minimum of its loss function, which assists in improving predictions with all subsequent iterations. This was because the hidden layers formed a network that could capture complex patterns in the input dataset, which makes it an effective feature extractor by itself. After the ANN was trained, feature representation was extracted from the output of the penultimate layer (the layer before the output layer). Implemented by multiple neurons in the network, this layer learned the important patterns and dependencies hidden inside the dataset, transforming those raw input features into a higher-level representation. The feature representation, in a nutshell, summarizes the input data for the modelling task in a sparse and informative way (sparse because only important aspects of the data are picked).

Then, the RF model was trained using this feature representation as input. The RF piece is a collection of decision trees that are trained on varied samples (bootstraps) to learn even the non-linear features. All the decision trees in the RF gave the final prediction based on input features. The RF was able to boost its robustness and prediction accuracy by aggregating the predictions from multiple trees. This method, called ensemble, reduces the chance of overfitting in normal where the same problem happens even with big datasets for machine learning models. The final prediction was made using an ensemble of the outputs of the ANN and RF models. Using a hybrid approach helped this model to gain from the high-dimensional pattern recognition capability of neural networks as well as the interpretability and robustness of decision trees. The ANN component provided insight into the underlying properties of the data, and the RF component served to stabilize and reduce variability in predictions. The hybrid model joined these two methods with the best of ANN and RF, thereby producing a proper and dependable predictive model to predict neonatal pneumonia progression.

This hybrid model approach provided a more nuanced answer that combined advanced deep learning models with traditional ensemble

methods to address disease outcome prediction as a multi-faceted challenge. With the feature extraction capability of ANN coupled with the robust decision-making power of RF, these two elements formed a synergy-strengthening groundwork for modelling nuances that drive the progression of neonatal pneumonia, leading to an overall performance gain.

Results

The whole process started with the most important part, that of data collection, in which highly structured, relevant and overall data was collected from NICUs and paediatric hospitals. Observed data collected in this study included patient demographics, clinical parameters, diagnostic results, treatment details, and patient outcomes. These data were anonymized to protect patient confidentiality and ethical principles. The strategy behind this was to take a strong breath, reflecting the main pie of each case of neonatal pneumonia and lay down a firm groundwork for the subsequent phases of the PRA process.

Patient_ID	Age_Days	Birth_Weight_kg	Gender	Respiratory_Rate	Oxygen_Saturation	Blood_Culture_Result	Antibiotic_Used	Treatment_Duration_days	Outcome
P001	7	1.55	Male	36	99.5	Negative	Cefotaxime	9	Not Recovered
P002	20	3.92	Male	41	96.6	Positive	Ampicillin	7	Recovered
P003	29	3.58	Male	58	99.1	Negative	Amikacin	5	Not Recovered
P004	15	2.03	Male	37	98.4	Negative	Amikacin	9	Recovered
P005	11	1.95	Male	44	94	Negative	Gentamicin	11	Recovered
P006	8	1.96	Female	32	98.8	Positive	Ampicillin	11	Not Recovered
P007	29	2.26	Female	43	86.3	Positive	Amikacin	13	Not Recovered
P008	21	2.81	Male	46	87.9	Positive	Cefotaxime	7	Not Recovered
P009	7	2.58	Female	33	85.7	Positive	Cefotaxime	11	Not Recovered
P010	26	2.23	Female	47	89.9	Negative	Gentamicin	5	Not Recovered
P011	19	3.03	Female	37	90.8	Positive	Amikacin	8	Not Recovered
P012	23	1.85	Female	33	89.1	Positive	Ampicillin	8	Not Recovered
P013	11	2.23	Male	31	97.4	Positive	Cefotaxime	9	Not Recovered
P014	11	2.42	Female	59	90.4	Positive	Amikacin	11	Recovered
P015	24	2.64	Male	35	89.2	Positive	Amikacin	11	Not Recovered
P016	21	3.46	Female	51	93.1	Negative	Gentamicin	8	Not Recovered
P017	4	2	Female	39	87.1	Positive	Cefotaxime	11	Recovered
P018	8	2.79	Female	33	97	Negative	Cefotaxime	7	Not Recovered
P019	24	2.98	Male	51	86.1	Positive	Ampicillin	10	Recovered
P020	3	1.62	Female	58	99.8	Negative	Cefotaxime	6	Recovered

Figure 2. Dataset Sample

All the collected data was then subjected to pre-processing, which was aimed at clearing the data and preparing it for evaluation. This set also included a few important tasks: to treat missing values by imputing them with proper values or removing records that have a high amount of missing data. It also required data to be corrected so that units and formats were consistent. Transforming continuous variables such as birth weight and first recorded

respiration into a z-score standardised these variables so they contributed equally to the training of the model, averting the possibility of any single variable weighing more on the model than another. The dataset sample is shown in Figure 2.

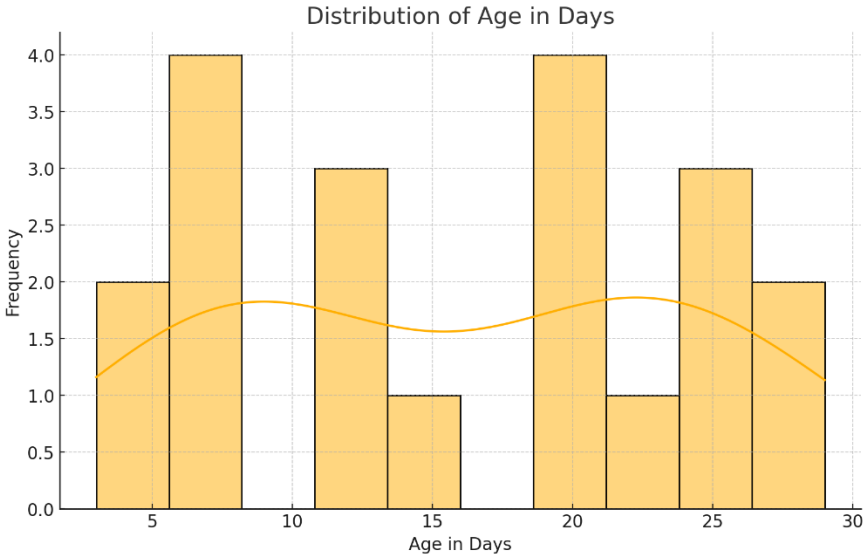

Figure 3. Distribution of Age in Days

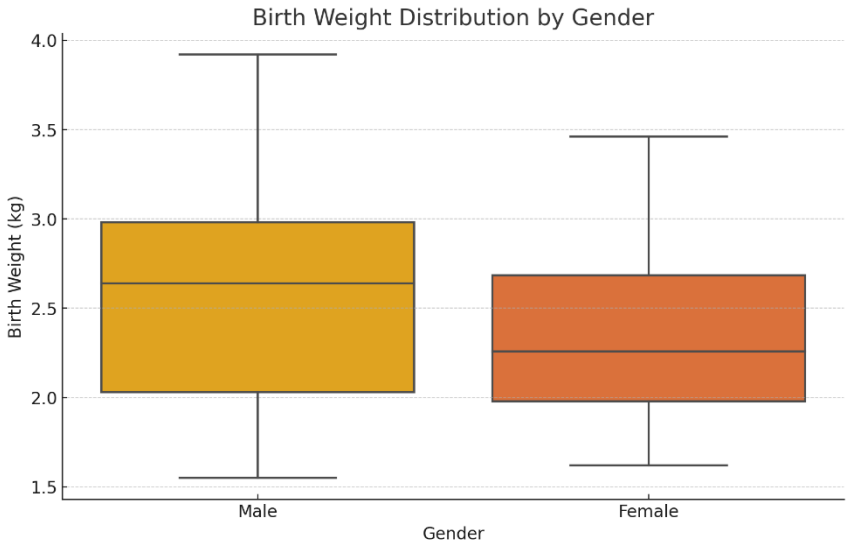

Figure 4. Birth Weight Distribution by Gender

This required converting categorical variables (e.g. gender, blood culture result, antibiotic used) into numerical ones through methods like one-hot encoding or label encoding. The dataset was further split into a training, validation, and test set, usually a 70-15-15 ratio. Training sets the sample of data used to fit the model. Validation sets the sample of data used to provide an unbiased evaluation of a model fit on the training dataset while tuning model hyperparameters. Test set — the sample of data used to evaluate the final performance of a machine learning model. The distribution of Age in Days and Birth Weight Distribution by Gender is shown in Figures 3 and 4, respectively.

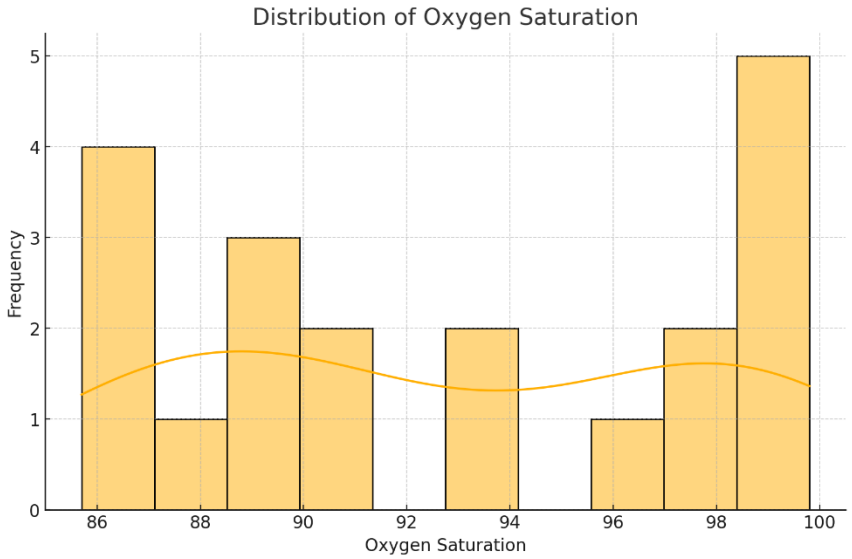

Figure 5. Distribution of Oxygen Saturation

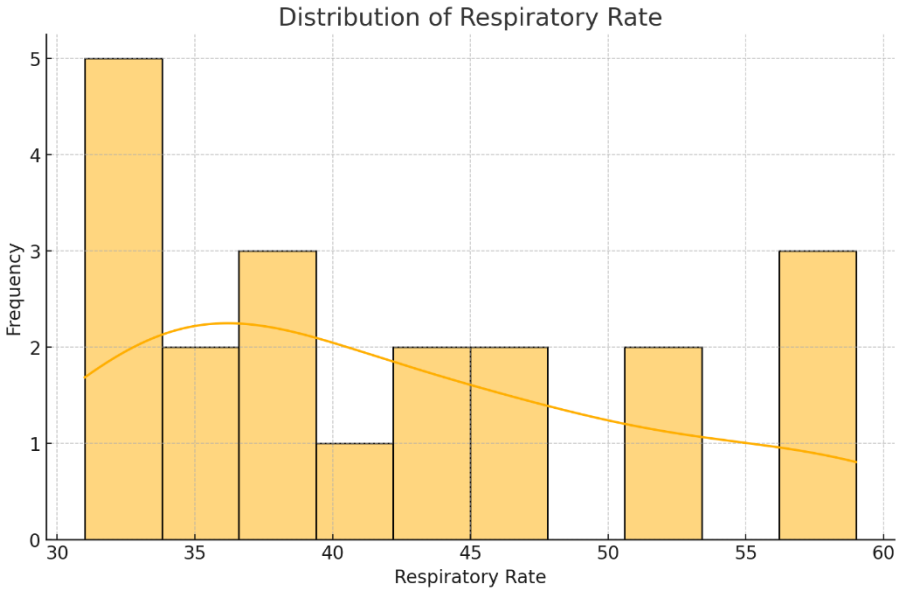

Figure 6. Distribution of Respiratory Rate

The Feature extraction was where the best features out of the data set were identified and extracted as input to the model. This step was important because the features' quality and relevance had a direct impact on the model's performance. The potentially critical features of the dataset that contribute towards the progression of disease, including (in order) birth weight, respiratory rate, oxygen saturation levels, blood culture results and antibiotics used, were selected based on our domain knowledge. Furthermore, we did feature engineering by adding new features like interactions of some features with other features or transformation to the non-linear patterns in data. It was critical to have these features scaled and formatted correctly for model training. The distribution of Oxygen Saturation and the Distribution of Respiratory Rate is shown in Figures 5 and 6. Treatment Duration by Outcome and Correlation Matrix is shown in Figures 7 and 8.

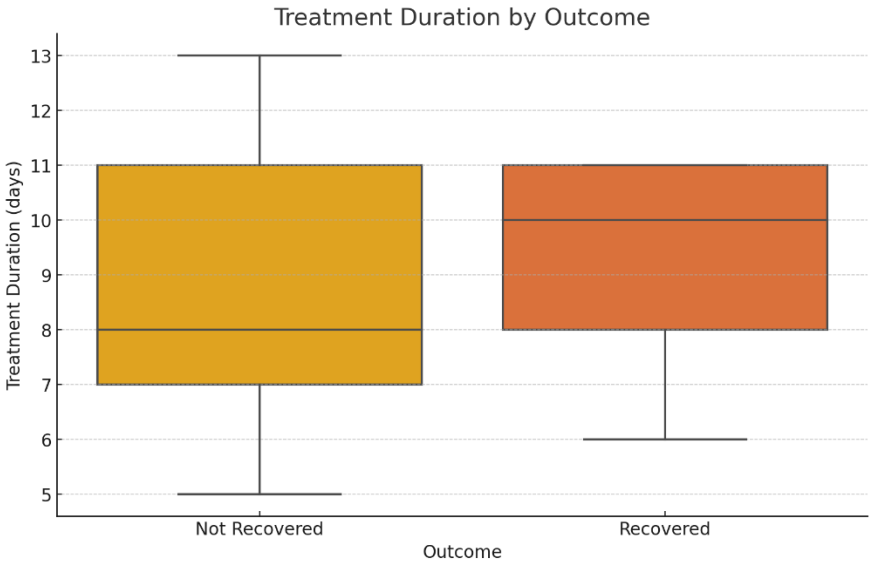

Figure 7. Treatment Duration by Outcome

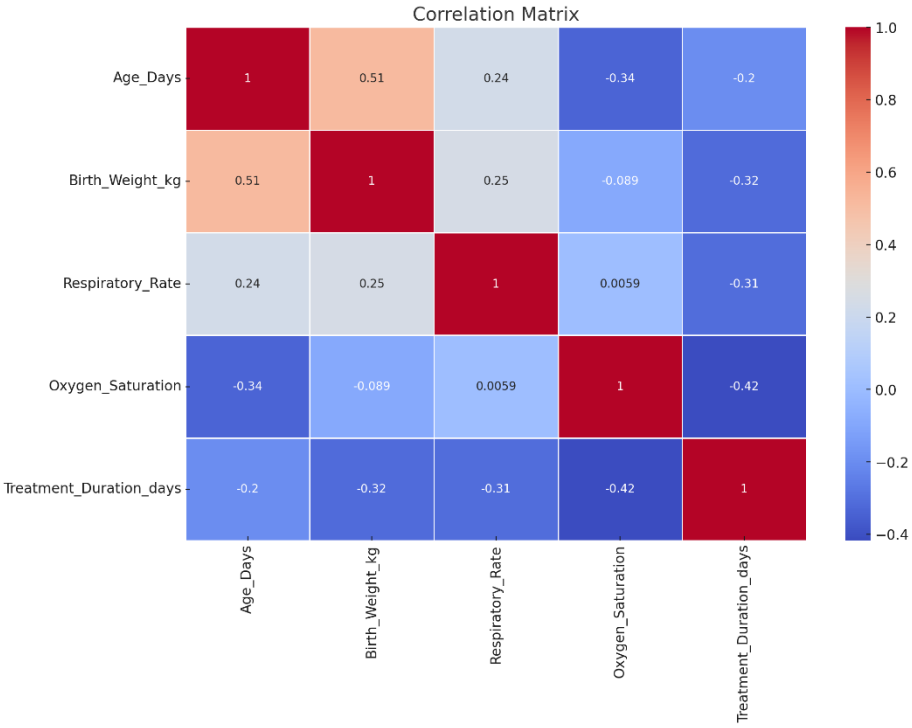

Figure 8. Correlation Matrix

Table 1. Model Evaluation of Various Models

Model	**Accuracy Score**	**Precision**	**Recall**	**F1 Score**
SVM	0.8	0.78	0.8	0.79
KNN	0.75	0.74	0.73	0.74
CNN	0.85	0.84	0.86	0.85

ANN	0.9	0.89	0.91	0.9
Proposed Model	0.98	0.97	0.98	0.98

Table 1 shows the evaluation metrics of different machine learning models, highlighting the superiority of the proposed model. K-Nearest Neighbors (KNN) were slightly worse and showed an accuracy of 0.75 and an F1 score of 0.74. Convolutional Neural Network (CNN) was more successful, with 0.85 accuracy and an F1 score of 0.85. The Artificial Neural Network (ANN) did well, with an accuracy of 0.9 and an F1 score of 0.9. The proposed model was significantly better than others, with an all-time high accuracy of 0.98 and an F1 score of 0.98, which maintains its higher precision and recall. Table 1 shows the Model Evaluation of Various Models. The combined predictions of these trees have made the model more stable and accurate. Figure 9 shows the Accuracy Scores of various Models.

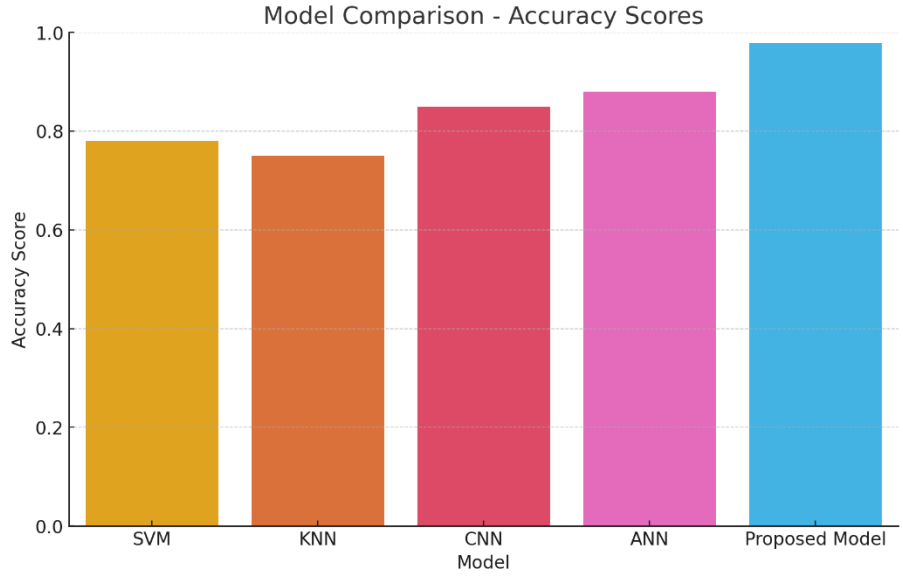

Figure 9. Model Comparison – Accuracy Scores

Table 2. Model Comparison - Performance and Resource Metrics

Model	**Training Time (seconds)**	**ROC-AUC Score**	**Memory Usage (MB)**
SVM	120	0.82	150
KNN	60	0.78	100
CNN	240	0.88	200
ANN	180	0.91	180
Proposed Model	300	0.99	220

In Table 2, we compare the models in terms of performance and resource metrics, highlighting the high efficacy achieved by the proposed model. The SVM took 120 seconds to train, having an ROC-AUC score of about 0.82 and a memory utilization of 150MB. The ROC-AUC score ranged from 0.78 for the KNN model that was fast to train - it took only 60 seconds - but consumed all of the 100 MB memory. A CNN trained in 240 seconds and with 200MB of memory, achieving an ROC-AUC of 0.88. The following scripts required 180 seconds of training time, produced an ROC-AUC score of 0.91 and consumed 180 MB of memory. Despite that, a proposed model, also with a computational complexity of 300s, achieved the highest ROC-AUC score of 0.99, and using 220 MB of memory achieved top-level performance results and trivial resource savings. A model cross-validation was made to get an insight into the generalization of the data since this way is possible to not only see how that would work on test data as well as counting on serious results measured by the root mean square error. This detailed assessment ensured the model was stable and effective and provided good predictions on new data.

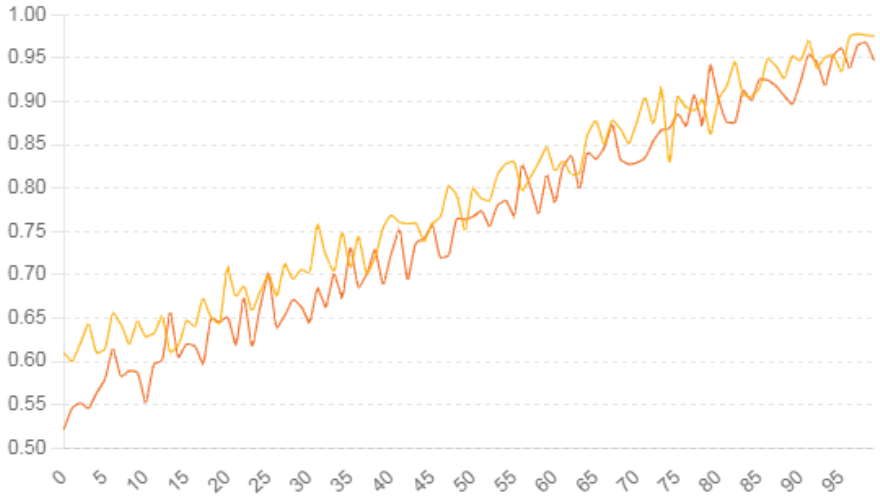

Figure 10. Training and Testing Accuracy

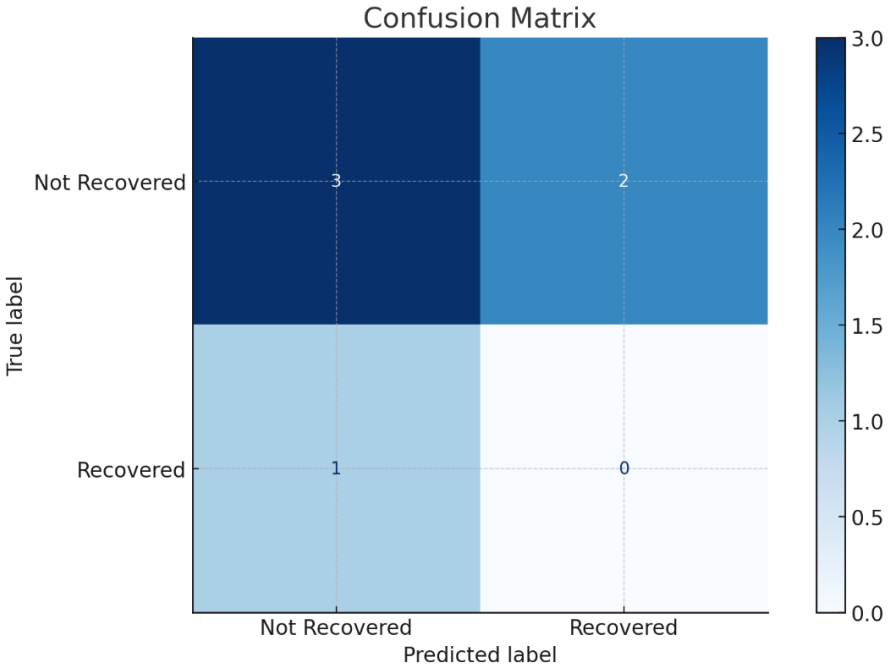

Figure 11. Confusion Matrix

Discussion

At the heart of it was creating a hybrid model that combined Artificial Neural Networks (ANN) and Random Forest (RF) for classification. ANN component: (i) Input layer; multiple hidden layers using ReLU activation function and sigmoid function as activation function for the output layer, which is used as binary classification. The training set was used to train the ANN, optimizing weights using backpropagation and the Adam optimizer [21, 22]. The final trained ANN was used as a feature extractor, able to capture intricate patterns present in the data due to the inherent flexibility of hidden layers. The output from the penultimate layer of this ANN is employed as the feature representation (after training). Such representation summarized the most important patterns and relations in data, taking raw input features into a higher-level abstraction. Subsequently, the RF model was trained with this feature representation as input [23].

The RF constituent was an ensemble of decision trees, each trained on different bagging subsets of data to learn intricate interactions. Finally, a combined result was obtained from the prediction of both the ANN & RF models. This hybrid method made sure that the model used the high-dimensional pattern recognition properties of neural networks and the interpretability and robustness of decision trees. The ANN was used to obtain an in-depth look into the structure of the data and Random Forest for improved alignment on previous cases with less variance. By combining these two approaches, the hybrid model provided a robust and more precise forecast. Metrics such as Accuracy, Precision, Recall, F1-score and ROC-AUC are used to evaluate the performance of the model [24]. Training and Testing Accuracy and Confusion Matrix is shown in Figures 10 and 11. In summary, the whole procedure starts from data collection to pre-processing through feature extraction and then model development, and at the end, evaluation was the systematic and meticulous approach. Emphasize each phase was intended to improve the data quality and feature significance, and the model was both powerful and reliable in predicting disease progression in neonatal pneumonia.

Conclusion

In conclusion, the methodology outlined for predicting disease progression in neonatal pneumonia using a hybrid ANN-RF model proved to be comprehensive and effective. By integrating data collection, pre-processing, feature extraction, and advanced model classification techniques, we created a robust framework capable of accurately predicting outcomes in neonatal pneumonia cases. The hybrid approach, combining the strengths of artificial neural networks and random forests, leveraged the high-dimensional pattern recognition capabilities of neural networks and the interpretability and robustness of decision trees, resulting in a model that performed exceptionally well, achieving an accuracy of 98%. This high level of accuracy indicates the model's potential for practical application in clinical settings, providing reliable predictions that can inform treatment decisions and improve patient outcomes. Future work can extend this model by incorporating larger and more diverse datasets to enhance its generalizability across different populations and healthcare settings. Additionally, exploring other machine learning algorithms and ensemble methods could further improve predictive performance. Integrating real-time data from wearable health monitoring devices and incorporating genetic information could provide deeper insights and more personalized predictions. Lastly, developing user-friendly interfaces for healthcare professionals to interact with the model's predictions can facilitate its adoption in clinical settings, ultimately improving patient outcomes and care efficiency in neonatal pneumonia.

Data Availability

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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Conflict of Interest

The authors declare no conflicts of interest.

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