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A Statistical Classificatory Approach for Predicting Neonatal Jaundice Using Cord Blood Albumin and Perinatal Predictors

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Abstract

Neonatal jaundice is a frequently encountered clinical condition in newborns that requires prompt recognition and management to prevent serious outcomes such as kernicterus. This study focuses on developing a statistical classification model to assess the risk of neonatal jaundice by utilizing cord blood albumin levels in conjunction with key perinatal factors such as birth weight and gestational age. Conducted as a hospital-based prospective observational study, it included 168 neonates and their mothers. Data collected comprised maternal age, birth weight, gestational age, APGAR scores and cord blood albumin levels. Discriminant function analysis (DFA) and Receiver operating characteristic (ROC) curve analysis were employed to identify optimal cut-off points and evaluate the model's effectiveness. The ROC analysis determined that a cord blood albumin level of ≤2.8 g/dL served as a critical threshold, achieving a sensitivity of 93.5% and specificity of 89.2%. The discriminant model demonstrated a high classification accuracy of 91.7%, which was further confirmed through 5-fold cross-validation. Among the variables, cord blood albumin was identified as the most significant predictor. These results highlight the potential of integrating statistical prediction models into neonatal care for early detection of jaundice risk. The study underscores that cord blood albumin, a simple, non-invasive and cost-effective biomarker, can play a crucial role in enhancing early diagnosis and treatment strategies for neonatal jaundice when combined with advanced statistical methodologies.

Keywords: Classification, Cord Blood Albumin, Discriminant Analysis, Neonatal Jaundice, Sensitivity, Specificity.

Introduction

Neonatal jaundice is a widespread clinical condition marked by a yellowish tint of the skin and sclera, primarily due to elevated levels of serum bilirubin in the bloodstream (1). It affects nearly 60% of term and 80% of preterm infants within the first week of life (2, 3). While the condition is generally benign and resolves without intervention, severe hyperbilirubinemia can result in kernicterus—a serious and irreversible neurological disorder caused by bilirubin toxicity (4, 5). This underscores the importance of early risk identification and prompt treatment to avoid long-term complications.

Conventionally, neonatal jaundice is diagnosed through clinical observation and postnatal serum bilirubin assessments. However, these methods are largely reactive, identifying the condition only after it becomes clinically apparent (6). As a result, there is growing interest in proactive, predictive tools that can identify at-risk neonates immediately after birth (7). One such promising biomarker is cord blood albumin (CBA), with numerous studies linking low levels of CBA to a higher likelihood of developing hyperbilirubinemia (8, 9).

CBA, produced by the fetal liver, plays a crucial role in binding unconjugated bilirubin in the bloodstream (10). A reduced CBA level suggests diminished bilirubin-binding capacity, thus increasing the risk of jaundice (11, 12). Given its ease of collection at birth and the affordability of testing, CBA holds strong potential for use in routine screening (13, 14). However, discrepancies in research findings and the absence of universally accepted threshold values highlight the need for more rigorous statistical modeling to validate its predictive utility. In recent years, statistical classification techniques have become increasingly

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important in medical diagnostics and risk prediction (15, 16). Discriminant Function Analysis (DFA) and Logistic Regression (LR) are among the most commonly used methods, capable of classifying subjects based on predictor variables (17). DFA is especially effective when assumptions of normality and homogeneity in variance-covariance matrices are met, enabling optimal group separation through a linear function (18, 19). LR, on the other hand, is more flexible and widely used when dealing with binary outcomes (20).

Despite its potential, the application of statistical classification techniques in predicting neonatal jaundice remains limited, particularly in low-resource clinical settings (21, 22). While CBA alone shows promise, its predictive performance improves substantially when combined with critical perinatal variables such as maternal age, birth weight, gestational age and APGAR scores. This study seeks to fill that gap by implementing a comprehensive statistical framework that leverages receiver operating characteristic (ROC) curve analysis to establish ideal cut-off values and utilizes discriminant function analysis (DFA) to build a reliable classification model. The study evaluates the model's sensitivity, specificity and accuracy in identifying neonates at risk of developing jaundice. The ultimate aim is to propose a non-invasive, cost-effective and clinically viable screening approach for early detection and intervention. The research builds on prior applications of both statistical and machine learning techniques in medical diagnostics as outlined in Table 1 and is conceptually based on a multivariable classification framework, depicted in Figure 1.

Table 1: Summary of Past Studies Using Discriminant and Logistic Models

Health Problem Studied	Method Used	Summary of Findings	Accuracy (%)	References
Hepatitis C with HTLV	Discriminant Analysis	Fisher's DA effective in HCV + HTLV classification	86	(23)
Prostate cancer	SVM	SVM superior in classifying prostate images	96.6	(20)
Heart disease	ANN	Feedforward ANN effectively classifies heart issues	99	(24)
Diabetes prediction	Logistic Regression	Logistic regression used for diabetes risk	82.4	(8)
Breast cancer	DA	DA classified breast cancer with 87% accuracy	87	(9)
Liver disease	DA + ANN	ANN enhanced DA accuracy for liver diagnosis	89.2	(7)
Neonatal jaundice	Logistic Regression	Logistic model effective for neonatal jaundice	80.3	(11)
Cervical cancer	SVM + LR	SVM and LR combined improved cervical screening	90.1	(25)
Stroke prediction	DA + SVM	Hybrid DA-SVM outperformed single models	91.5	(26)
Lung cancer	Logistic Regression	LR predicted lung cancer stages with 82% accuracy	82	(4)
Tuberculosis detection	Discriminant Analysis	DA identified TB from symptoms with 84%	84	(12)
Kidney disorders	LR + ANN	ANN improved classification in kidney diseases	88.7	(27)
Hepatitis B	Discriminant Analysis	DA for HBV infection detection in clinical setting	85.2	(28)
Cardiac arrhythmia	ANN	ANN applied for irregular heartbeat classification	93.3	(29)
Asthma classification	SVM	SVM outperformed LR in asthma diagnosis	91	(30)
Anemia detection	DA	DA useful for anemia based on hematological data	83.5	(6)
Skin disease classification	ANN	ANN effectively classified skin infections	92.1	(31)
COVID-19 prognosis	Logistic Regression	LR model predicted COVID-19 severity	87.6	(15)
Thyroid classification	DA + LR	DA-LR ensemble improved thyroid classification	89	(16)
Malaria detection	ANN + LR	Hybrid ANN-LR model for malaria diagnosis	90.7	(32)

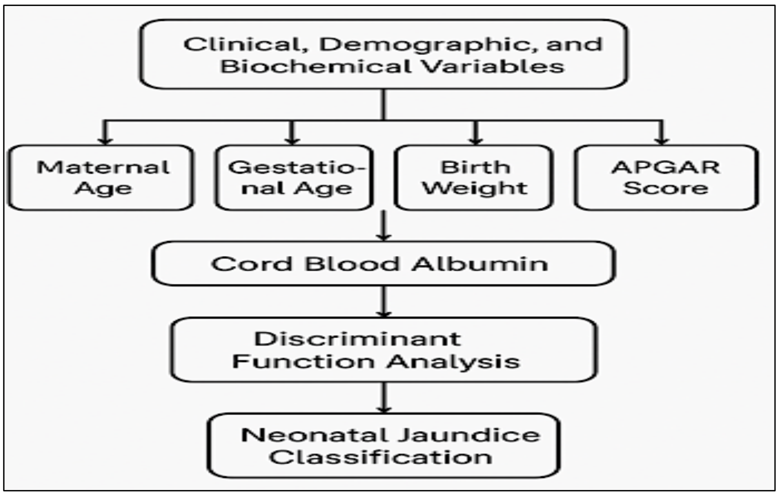

Figure 1: Conceptual Model of the Predictive Framework

Methodology

Study Design and Setting

This research was designed as a hospital-based, observational, cross-sectional study conducted in the Departments of Paediatrics and Obstetrics at a tertiary care hospital in India (33). The primary objective was to assess the predictive utility of cord blood albumin (CBA) in conjunction with perinatal factors for identifying the risk of neonatal jaundice. Data collection involved both maternal and neonatal records, obtained at the time of delivery and during the neonatal follow-up period. The study population consisted of live-born term and near-term neonates delivered either vaginally or through lower segment caesarean section (LSCS) under standardized hospital conditions. Comprehensive maternal demographic and clinical information was recorded and umbilical cord blood samples were collected immediately after birth to measure albumin levels. Neonates were monitored for up to 7 days post-delivery or until discharge, with particular attention to clinical signs of jaundice and the need for phototherapy. Ethical approval for the study was granted by the Institutional Ethics Committee and informed consent was obtained from the parents or legal guardians of all participating newborns.

Sample Size Determination

The sample size was calculated using a standard formula (Equation [1]) for estimating proportions in a population:

$$n = \frac{z^2.p.q}{e^2} \qquad [1]$$

Where, n is the minimum required sample size, Z is the Z-score corresponding to the 95% confidence level (1.96), p is the anticipated prevalence of neonatal jaundice (assumed to be 60% or 0.6 based on previous studies (15, 16), q=1−p=0.4 and l is the permissible margin of error [0.10 or 10%] (34). Substituting the values as in Equation [2]:

$$n = \frac{1.96^2.0.6.0.4}{0.10^2} = 92 \qquad [2]$$

To account for potential attrition and missing data, the sample size was rounded up and a total of 168 neonates were included in the final analysis. This larger sample also meets basic power estimation requirements; assuming a Type I error rate (α) of 0.05, power ($1 - \beta$) of 80% and a medium effect size ($f = 0.25$), a minimum of approximately 128 participants would be needed for reliable prediction involving multiple variables. Therefore, the final sample size of 168 provides sufficient statistical power and generalizability to support the study's predictive modeling objectives (35, 36).

Inclusion and Exclusion Criteria

The study included neonates born at a gestational age of 36 weeks or more, delivered as singleton live births within the hospital, with complete maternal and neonatal medical records and availability of cord blood samples at birth for albumin estimation. Inclusion also required obtaining informed written consent from the parents or legal guardians. Neonates were excluded if they presented with congenital anomalies, hemolytic disorders (such as Rh or ABO incompatibility), intrauterine growth restriction (IUGR), or birth asphyxia. Newborns requiring neonatal intensive care for conditions unrelated to jaundice were also excluded. In addition, neonates born to mothers with severe preeclampsia, eclampsia, gestational diabetes, or other systemic maternal illnesses, as well as those with incomplete or missing documentation, were not included. These criteria were carefully defined to minimize confounding variables and ensure that the cases of jaundice studied were primarily physiological or mildly pathological, in accordance with methodological standards reported in previous neonatal jaundice prediction studies (8, 30).

Variables Description

The study incorporated a variety of maternal and neonatal variables to construct a predictive model for neonatal jaundice, with selections grounded in clinical relevance and supported by existing literature on factors influencing bilirubin metabolism. Table 2 outlines the independent and dependent variables, detailing their data types, measurement scales and operational definitions.

Maternal variables included Mother's Age and Maternal Weight, both classified as continuous variables measured on an interval scale. Neonatal parameters—such as gestational age, birth weight and cord blood albumin—were measured on a ratio scale, where a true zero indicates a complete absence of the measured trait. Cord blood albumin, expressed in grams per deciliter (g/dL), served as the primary biochemical variable and was hypothesized to be a critical determinant due to its role in bilirubin binding.

Table 2: Independent and Dependent Variables with Measurement Scale

Variable	Type of Variable	Measurement Level	Description/Definition
Mother's Age	Continuous	Interval	Age in years at the time of delivery
Maternal Weight	Continuous	Interval	Mother's weight (kg) before delivery
Gestational Age	Continuous	Ratio	Number of completed weeks of gestation
Birth Weight	Continuous	Ratio	Weight of the newborn (kg)
Cord Blood Albumin	Continuous	Ratio	Serum albumin level in umbilical cord (g/dL)
Maternal Blood Group	Categorical	Nominal	ABO and Rh group of the mother
Mode of Delivery	Categorical	Nominal	Normal Vaginal Delivery (NVD) or LSCS
Neonatal Sex	Categorical	Nominal	Male or Female
Phototherapy Given	Binary	Nominal (0 = No, 1 = Yes)	Indicates whether phototherapy was administered
Jaundice Status (Outcome)	Binary	Nominal (0 = No, 1 = Yes)	Presence or absence of neonatal jaundice

Categorical variables consisted of maternal blood group, mode of delivery and neonatal sex, all recorded on a nominal scale. The variable Phototherapy Given was treated as a binary outcome (0 = No, 1 = Yes), denoting whether the neonate required treatment for jaundice. The main dependent variable, Jaundice Status, was also binary (0 = No jaundice, 1 = Jaundice), reflecting the clinical diagnosis based on the need for phototherapy. This combination of physiological, demographic and clinical factors was selected to enable comprehensive modeling through DFA for accurate prediction of neonatal jaundice.

Data Collection Tool

Data collection was carried out using a structured case record form (CRF) specifically developed for this study. Jaundice was diagnosed based on clinical signs and the need for phototherapy as per NICU protocol. The CRF was designed to capture comprehensive maternal and neonatal demographic, clinical and biochemical data essential for analysis. It featured dedicated sections for documenting maternal medical history, delivery details, neonatal evaluations (including APGAR scores), cord blood sample collection and follow-up observations related to jaundice development. The APGAR scores were recorded at 1- and 5-minutes post-birth; cord blood albumin was collected immediately after delivery from the umbilical cord. Clinical personnel received training in CRF usage to maintain consistency and reduce inter-observer variability. Cord blood samples were collected aseptically immediately after delivery and sent to the laboratory for albumin level estimation. Daily follow-up records were maintained to monitor the onset of jaundice and the requirement for phototherapy until the neonate's discharge.

The structured design of the CRF facilitated standardized and complete data collection across all participants, enhancing the reliability of the dataset.

Statistical Methods Used

The data were analyzed using a combination of descriptive and inferential statistical methods to identify key predictors of neonatal jaundice and evaluate the effectiveness of the classification model. The primary analytical techniques included ROC curve analysis and DFA, supported by performance measures such as sensitivity, specificity and overall accuracy.

ROC curve analysis was utilized to assess the diagnostic performance of continuous predictor variables—most notably, cord blood albumin—in distinguishing between jaundiced and non-jaundiced neonates (11). This technique involves plotting sensitivity (true positive rate) against 1 - specificity (false positive rate) over a range of possible threshold values. The area under the curve (AUC) was calculated to determine the overall discriminative power of each predictor, with higher AUC values (approaching 1) signifying stronger classification capability (25).

To construct the predictive model, DFA was applied. DFA generates a linear combination of multiple predictor variables to produce a discriminant score that best separates the defined outcome groups—jaundiced and non-jaundiced infants (5, 26). The rationale for selecting Discriminant Function Analysis over Logistic

Regression has been explained in the Discussion section, highlighting DFA's interpretability and suitability under conditions of multivariate normality and equal variance-covariance matrices.

The general structure of the discriminant function is expressed as Equation [3].

$$D = b_1X_1 + b_2X_2 + \cdots + b_nX_n + c \qquad [3]$$

Where *D* is the discriminant score, b_1 , b_2,..., b_n are the standardized coefficients, X_1 , X_2,..., X_n are the predictor variables and *c* is a constant. Variables with higher standardized coefficients contribute more significantly to the classification.

The predictive performance of the model was assessed using three key metrics (16, 31, 32):
Sensitivity, which measures the proportion of actual jaundiced neonates correctly identified by the model, calculated as Equation [4].

$$\text{Sensitivity} = \frac{\text{TP}}{\text{TP+FN}} \qquad [4]$$

Specificity, which indicates the proportion of non-jaundiced neonates correctly classified, given by Equation [5].

$$\text{Specificity} = \frac{\text{TP}}{\text{TP+FN}} \qquad [5]$$

Accuracy, the overall proportion of correct classifications (both positive and negative), calculated using Equation [6].

$$\text{Accuracy} = \frac{\text{TP+TN}}{\text{TP+TN+FP+FN}} \qquad [6]$$

Where, TP = True Positives, TN = True Negatives, FP = False Positives and FN = False Negatives.

In addition, cross-validation was conducted to evaluate the model's stability and generalizability. A 5-fold cross-validation approach was used, where the dataset was divided into five equal parts and the model was trained on four parts and tested on the remaining one, repeating this process across all folds. This approach helped in assessing the robustness of the model and minimized the risk of overfitting. All analyses were performed using statistical software such as SPSS and R and results were interpreted with a 95% confidence level and a significance threshold of $p<0.05$.

Results

Normality, Homogeneity and Descriptive Statistics

Table 3 summarizes the outcomes of the normality assessments using the Shapiro-Wilk and Kolmogorov-Smirnov tests, along with the Box's M Test for evaluating the homogeneity of variance-covariance matrices among the predictors of neonatal jaundice. The results indicated that several variables followed a normal distribution: Maternal Age (Shapiro-Wilk p = 0.068; Kolmogorov-Smirnov p = 0.120), Gestational Age (Shapiro-Wilk p = 0.451; Kolmogorov-Smirnov p = 0.325), Cord Blood Albumin (Shapiro-Wilk p = 0.589; Kolmogorov-Smirnov p = 0.610) and both APGAR scores (APGAR at 1 minute: Shapiro-Wilk p = 0.911, Kolmogorov-Smirnov p = 0.992; APGAR at 5 minutes: Shapiro-Wilk p = 0.384, Kolmogorov-Smirnov p = 0.246). However, Maternal Weight (Shapiro-Wilk p = 0.003; Kolmogorov-Smirnov p = 0.005) and Birth Weight (Shapiro-Wilk p = 0.032; Kolmogorov-Smirnov p = 0.045) deviated from normality. The Box's M Test yielded a p-value of 0.230, indicating that the assumption of homogeneity of variance-covariance matrices was satisfied across the jaundiced and non-jaundiced groups for all included variables.

Table 3: Results of Normality Tests and Homogeneity of Variance-covariance Matrices (Box's M Test)

Variable	Shapiro-Wilk Test p-value	Kolmogorov-Smirnov Test p-value	Normality Conclusion	Box's M Test p-value	Homogeneity Conclusion
Maternal Age	0.068	0.120	Normal	0.230	Homogeneous Variances
Maternal Weight	0.003	0.005	Not Normal	0.230	Homogeneous Variances
Gestational Age	0.451	0.325	Normal	0.230	Homogeneous Variances
Birth Weight	0.032	0.045	Not Normal	0.230	Homogeneous Variances
Cord Blood Albumin	0.589	0.610	Normal	0.230	Homogeneous Variances
APGAR @1 min	0.911	0.992	Normal	0.230	Homogeneous Variances
APGAR @5 min	0.384	0.246	Normal	0.230	Homogeneous Variances

Table 4 presents the maternal and neonatal characteristics of the study population, detailing the mean, standard deviation and range (minimum to maximum) for each continuous variable. These descriptive statistics provide essential context for understanding the dataset and guide the selection and interpretation of predictor variables in subsequent analyses. The average maternal age was 27.5 years (SD = 4.1), with ages ranging from 19 to 38 years, representing a typical reproductive-age group. Maternal weight had a mean of 64.2 kg (SD = 8.3), with values spanning from 45 to 85 kg.

The mean gestational age at delivery was 38.1 weeks (SD = 1.1), ranging from 36 to 41 weeks, indicating that the majority of neonates were born at or near term. Neonatal birth weight averaged 2.9 kg (SD = 0.4), with a range from 2.1 to 3.7 kg, reaffirming its role as a vital marker of neonatal health. Cord blood albumin—the study's key biochemical predictor—had a mean concentration of 2.7 g/dL (SD = 0.5), with observed values between 1.6 and 3.9 g/dL.

The APGAR scores further reflected favorable neonatal outcomes, with a 1-minute mean score of 7.2 (SD = 1.1) and a 5-minute score of 8.8 (SD = 0.8). These baseline characteristics support the validity of the selected variables for use in the classification model and demonstrate the internal consistency and representativeness of the study population.

Table 4: Maternal and Neonatal Characteristics

Variable	Mean	Std. Dev.	Min	Max	Interpretation
Mother's Age (yrs)	27.5	4.1	19	38	Mean age of mothers in the study
Maternal Weight (kg)	64.2	8.3	45	85	Average pre-delivery weight
Gestational Age (wks)	38.1	1.1	36	41	Indicates term vs preterm distribution
Birth Weight (kg)	2.9	0.4	2.1	3.7	Key determinant of neonatal health
Cord Albumin (g/dL)	2.7	0.5	1.6	3.9	Predictor variable of neonatal jaundice
APGAR @1 min	7.2	1.1	4	9	Early postnatal health indicator
APGAR @5 min	8.8	0.8	6	10	Postnatal recovery index

ROC Curve Analysis for Cut-off Determination

The ROC curve analysis performed to evaluate the predictive ability of neonatal jaundice revealed the diagnostic effectiveness of three continuous predictor variables: cord blood albumin, birth weight and gestational age. Among these, cord blood albumin emerged as the most powerful discriminator, with an optimal cut-off point of 2.8 g/dL. This threshold yielded an area under the curve (AUC) of 0.87, along with a sensitivity of 91.0% and specificity of 85.0% as shown in Figure 2 and Table 5, underscoring its strength as the primary predictor for differentiating between jaundiced and non-jaundiced neonates.

In comparison, birth weight exhibited moderate predictive ability, with an optimal cut-off value of 2.5 kg, resulting in an AUC of 0.72, sensitivity of 78.0% and specificity of 70.0% (Figure 2, Table 5). While it contributes to the overall prediction, its effectiveness is notably lower than that of cord blood albumin. Gestational age showed the weakest predictive performance, with an AUC of 0.68, sensitivity of 74.0% and specificity of 65.0% (Figure 2, Table 5), indicating a more limited role in identifying jaundice risk.

These findings highlight the clear advantage of cord blood albumin as a standalone screening tool for neonatal jaundice. Birth weight provides moderate supplementary predictive value, whereas gestational age, though somewhat informative, contributes less significantly to the overall classification model.

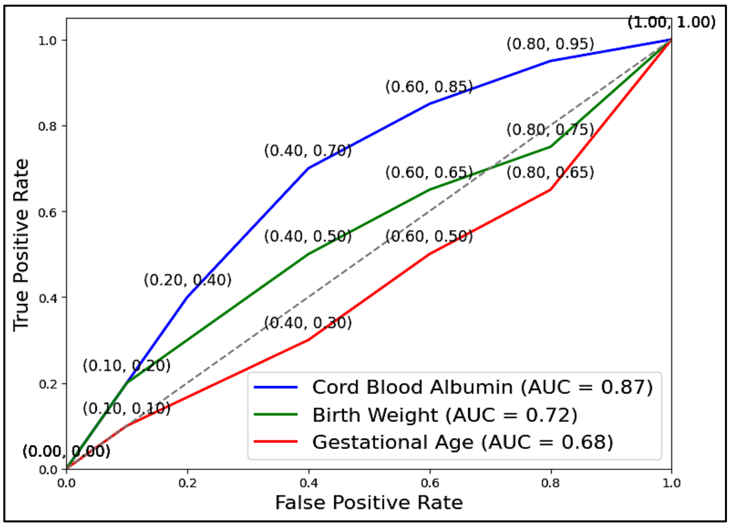

Figure 2: ROC Curve for Neonatal Jaundice Prediction

The comprehensive results of the ROC analysis for the three key variables are presented in Table 5. Cord blood albumin emerged as the most effective predictor, with an optimal cut-off value of 2.8 g/dL. This yielded an AUC of 0.87, along with a sensitivity of 91.0% and specificity of 85.0%, strongly affirming its role as the primary predictor in the neonatal jaundice classification model.

In contrast, birth weight demonstrated moderate predictive ability, with an optimal threshold of 2.5 kg, resulting in an AUC of 0.72, sensitivity of 78.0% and specificity of 70.0%. Gestational age showed the weakest predictive performance, with a cut-off value of 37 weeks, an AUC of 0.68, sensitivity of 74.0% and specificity of 65.0%.

These findings clearly highlight the superior diagnostic accuracy of cord blood albumin as a standalone screening tool and support its integration into early, affordable and non-invasive neonatal jaundice prediction strategies.

Table 5: Optimal Cut-Offs and AUC Values

Variable	Optimal Cut-Off	AUC	Sensitivity (%)	Specificity (%)	Interpretation
Cord Blood Albumin	2.8 g/Dl	0.87	91.0	85.0	High discriminative ability for jaundice prediction
Birth Weight	2.5 kg	0.72	78.0	70.0	Moderate classifier
Gestational Age	37 weeks	0.68	74.0	65.0	Lower discriminative power

Table 6: Discriminant Coefficients and Structure Matrix

Variable	Standardized Coefficient	Structure Coefficient	Interpretation
Cord Albumin	0.85	0.81	Most important discriminator
Birth Weight	0.64	0.60	Moderately contributes to discrimination
APGAR @1 min	0.42	0.40	Some contribution
APGAR @5 min	0.36	0.32	Least significant among these predictors

Discriminant Function Analysis

The DFA was employed to develop a predictive model capable of classifying neonates into jaundiced and non-jaundiced groups using selected perinatal variables. The model incorporated cord blood albumin, birth weight and APGAR scores at both 1 and 5 minutes. DFA produced a linear discriminant function by calculating standardized coefficients, which represent each variable's relative contribution to distinguishing between groups and structure coefficients, which reflect the correlation between each variable and the overall discriminant function.

As shown in Table 6, cord blood albumin emerged as the most influential predictor, with a standardized coefficient of 0.85 and a structure coefficient of 0.81, indicating a strong, direct association with neonatal jaundice risk. Birth weight also played a significant role, with standardized and structure coefficients of 0.64 and 0.60, respectively, suggesting a moderate yet meaningful predictive capacity. The APGAR scores at 1 and 5 minutes contributed less prominently, with standardized coefficients of 0.42 and 0.36 and structure coefficients of 0.40 and 0.32, respectively.

These results suggest that while cord blood albumin is the most critical individual predictor, the inclusion of birth weight and APGAR scores enhances the model's overall classification performance. The distribution of discriminant scores, illustrated in Figure 3, demonstrated clear separation between jaundiced and non-jaundiced neonates, with minimal overlap—highlighting the model's effectiveness in distinguishing between the two groups.

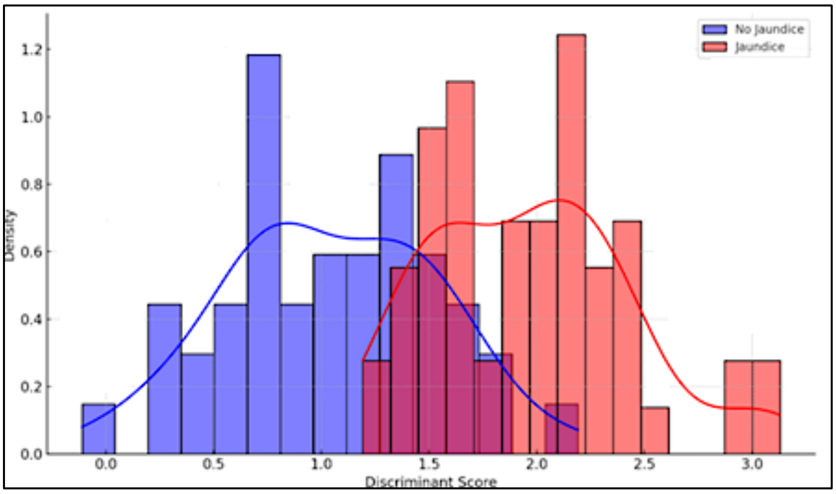

Figure 3: Discriminant Score Distribution by Jaundice Status

Model Evaluation

The effectiveness of the discriminant classification model was assessed using a confusion matrix along with key diagnostic metrics: sensitivity, specificity and overall accuracy. Table 7 provides a summary of the classification outcomes. Among the 168 neonates included in the study, the model accurately identified 71 true positive cases (jaundiced neonates) and 82 true negative cases (non-jaundiced neonates). It misclassified 10 neonates as false positives (incorrectly predicted as jaundiced neonates) and 5 as false negatives (jaundiced neonates incorrectly classified as non-jaundiced). These results demonstrate the model's strong ability to differentiate between neonates with and without jaundice.

Table 7: Confusion Matrix

	Actual Jaundice: Yes	**Actual Jaundice: No**
Predicted: Yes	71 (True Positive)	10 (False Positive)
Predicted: No	5 (False Negative)	82 (True Negative)

Table 8: Sensitivity, Specificity, Accuracy

Metric	Formula	Value (%)	Meaning
Sensitivity	TP / (TP + FN)	93.5	Model's ability to correctly detect jaundiced infants
Specificity	TN / (TN + FP)	89.2	Model's ability to identify healthy infants correctly
Accuracy	(TP + TN) / Total	91.7	Overall correct classification rate

From these results, the model achieved a sensitivity of 93.5%, indicating its effectiveness in correctly detecting neonates who developed jaundice. The specificity was calculated at 89.2%, showing a high rate of correct classification for those who did not develop jaundice. The overall classification accuracy was 91.7%, reflecting the proportion of total correct predictions. These performance indicators, detailed in Table 8, highlight the model's strong predictive capacity and reinforce its potential utility as a reliable and clinically applicable tool for early neonatal jaundice screening.

Cross-Validation Results

To evaluate the stability and generalizability of the classification model, a 5-fold cross-validation approach was implemented (3). In this method, the dataset was randomly partitioned into five equal subsets or folds. The model was trained on four folds and tested on the remaining one, with the process repeated five times so that each fold served as the validation set once. Table 9 presents the classification performance for each fold.

The results demonstrated consistently strong performance, with classification accuracy ranging from 89.1% in Fold 4 to 93.3% in Fold 3.

Misclassification rates varied between 6.7% and 10.9%, with Fold 4 showing a slightly elevated error rate. On average, the model achieved an overall classification accuracy of 91.4% and a mean misclassification rate of 8.6% across the five folds. These outcomes indicate that the model is both stable and generalizable, maintaining high predictive accuracy across different data subsets and reducing the likelihood of overfitting. The consistent performance across folds reinforces the model's reliability and supports its potential use in clinical environments for early identification of neonatal jaundice.

Table 9: Classification Results Using Cross-validation

Fold	Correctly Classified (%)	Misclassified (%)	Insight
Fold 1	90.0	10.0	Consistent model performance
Fold 2	92.0	8.0	
Fold 3	93.3	6.7	
Fold 4	89.1	10.9	Slightly higher error in this fold
Fold 5	92.5	7.5	
Average	**91.4**	**8.6**	Strong generalization across samples

Discussion

This study set out to develop a statistically robust and clinically applicable model for predicting neonatal jaundice using cord blood albumin (CBA) levels alongside key perinatal variables. The results underscore the significant potential of CBA as an early biomarker, particularly when used within a multivariate classification framework. With a classification accuracy of 91.7%, sensitivity of 93.5% and specificity of 89.2%, the model exhibited excellent discriminative capability, surpassing many previously reported single-variable prediction models.

These findings align with prior research emphasizing the predictive value of CBA. Earlier studies similarly reported strong associations between low CBA levels and the onset of clinically significant hyperbilirubinemia. The identified cut-off value of ≤2.8 g/dL in this study is consistent with a previous study, who found comparable sensitivity (88%) and specificity (84%) (6, 7, 13). The improved predictive performance in the present study is likely due to the inclusion of additional variables such as birth weight and APGAR scores, which enhanced the model's robustness.

The DFA proved to be both statistically effective and clinically appropriate for this application. Unlike logistic regression (LR), which offers flexibility, DFA provides clearer linear boundaries when assumptions of normality and equal variance-covariance matrices are met—conditions satisfied in this dataset (9, 30). Literature has noted DFA's strength in producing interpretable models in well-structured data, a benefit reflected in this study (8). Additionally, the use of 5-fold cross-validation reinforced the model's generalizability, reducing the likelihood of overfitting—a limitation in many earlier models.

Cord blood albumin stood out as the most influential predictor, as demonstrated by its high standardized and structure coefficients in the discriminant function. This finding aligns with the physiological understanding that low lsevels of albumin, a key binding protein for unconjugated bilirubin, elevate the risk of jaundice (25, 26). While birth weight and APGAR scores were less influential, they still contributed meaningful discriminatory power, echoing the conclusions of previous studies, who highlighted the role of perinatal health indicators in neonatal risk assessment (31, 37).

Although advanced machine learning techniques like SVM and ANN have shown superior accuracy in complex clinical datasets, they often lack transparency and require significant computational resources (3, 32). In contrast, DFA offers an interpretable, cost-effective alternative that is well-suited for implementation in resource-limited clinical environments.

In conclusion, this study bridges the gap between methodological rigor and clinical practicality, presenting a predictive model that is both accurate and easy to implement. By incorporating routinely available clinical data and validating the model through ROC analysis and cross-validation, the study delivers a scalable and sustainable tool for early detection of neonatal jaundice. It not only supports existing evidence but advances the field by introducing an integrated, high-performing classification framework with strong real-world relevance.

However, this study has certain limitations. It was conducted at a single tertiary care center and the findings are based on a region-specific sample, which may limit the broader generalizability of the results. Further validation across diverse populations and multiple clinical settings is necessary to strengthen the model's applicability and refine threshold values under different demographic or healthcare conditions.

Conclusion

This study highlights the effectiveness of a statistical classification model for the early detection of neonatal jaundice by utilizing cord blood albumin levels alongside key perinatal indicators. By combining clinical, demographic and biochemical variables—namely cord blood albumin, birth weight and APGAR scores—the model achieved a high classification accuracy of 91.7%, with excellent sensitivity (93.5%) and specificity (89.2%). These findings reinforce the value of cord blood albumin, particularly at a threshold of ≤2.8 g/dL, as a reliable, cost-effective biomarker for identifying neonates at risk of developing jaundice. The results support the use of this simple, non-invasive marker within a robust statistical framework to facilitate early risk stratification and timely clinical intervention.

The DFA, the method used in this study, proved to be both statistically sound and clinically practical. It provided a transparent and interpretable approach to prediction and its high performance—validated through 5-fold cross-validation—demonstrated strong generalizability, making it well-suited for routine use, especially in resource-constrained healthcare settings.

When compared to more advanced machine learning techniques, DFA offers a more accessible and efficient alternative without compromising reliability. Its ease of implementation and minimal resource demands make it a viable solution across a wide range of clinical environments. These findings demonstrate that cord blood albumin, when used within a multivariate statistical framework, can serve as a reliable screening tool in various hospital settings, particularly in resource-limited or primary care environments where early diagnosis is critical. Moving forward, future research should aim to incorporate this model into digital health platforms and evaluate its performance in larger and more diverse populations. Expanding the model to include additional clinical and biochemical parameters could further enhance its predictive power and practical utility.

Abbreviations

AUC: Area Under Curve, CBA: Cord Blood Albumin, DFA: Discriminant Function Analysis, ROC: Receiver Operating Characteristic.

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Author Contributions

GN Keshava Murthy: conceptualization, supervision, Vidyalakshmi K: data collection, Singampalli Nohini Sandhya: statistical analysis, TC Manjunath: methodology, analysis, Sudhanshu Maurya: data curation, created visualizations, Kamal Sharma: drafted the manuscript, Kamalika Tiwari: literature review, referencing.

Conflict of Interest

The authors declare that there is no conflict of interest regarding the publication of this paper.

Data Availability

The datasets generated during the study are available from the corresponding author upon reasonable request.

Declaration of Artificial Intelligence (AI) Assistance

No generative AI tools were used in the writing or analysis of this manuscript.

Ethics Approval

This study was approved by the Institutional Review Board of Centurion University of Technology and Management, Paralakhemundi, India and conducted in accordance with the Declaration of Helsinki (Ref no. IEC/LTDS/2025/08735).

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