Big Data-Based Stunting Detection for AI-Driven Hospital Transformation

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Abstract*— Stunting remains a major public health challenge in Indonesia despite ongoing national prevention programs. Pediatric hospital records offer an opportunity to identify children who require further growth assessment. This study evaluates a hybrid Self-Organizing Map (SOM) and Long Short-Term Memory (LSTM) model using 500 pediatric visit records from 200 children at RSIA Stella Maris Medan. Each child had two to three recorded visits, and observations from earlier visits were used to predict stunting status at a subsequent visit. SOM grouped health profiles into four clusters, while LSTM modeled changes across visits. The data were split by child into a development cohort of 160 children (400 visits) and an independent test cohort of 40 children (100 visits). Preprocessing parameters and the SOM were fitted on training data only and then applied to held-out data. The SOM–LSTM model achieved a reported test accuracy of 98.00%, precision of 91.50%, recall of 90.80%, and F1-score of 91.10%. Five-fold cross-validation yielded a mean accuracy of 92.40 ± 1.14% and mean F1-score of 91.52 ± 1.10%. Visits from the same child remained in the same fold, and preprocessing, SOM, and LSTM were refitted within each training fold. On the same test cohort, the SOM–LSTM model achieved an F1-score of 91.10%, compared with 86.00% for LSTM alone. Whereas the authors' previous SOM–LSTM study classified stunting status using anthropometric data from a single visit, this study uses repeated hospital visits to predict stunting status at a subsequent visit. The combined model may help clinicians prioritize children for further growth assessment.

Keywords*— *Artificial Intelligence, Healthcare Big Data, Hospital Transformation, Long Short-Term Memory, Self-Organizing Map, Stunting Detection.

I. INTRODUCTION

Nutrition is a fundamental cornerstone of high-quality human resource development and a key driver of sustainable national development [1]. Poor nutritional status has a direct impact on health outcomes, human capital competitiveness, and the productivity of future generations. Accordingly, Sustainable Development Goal (SDG) Target 2.2 seeks to eliminate all forms of malnutrition, including through ensuring adequate nutritional intake for adolescent girls, pregnant and lactating women, and older adults [2]. One of the most significant forms of malnutrition that has become a global public health concern is stunting, a condition characterized by impaired growth in children under five resulting from chronic undernutrition during the period from pregnancy to the first two years of life [3]. Beyond restricting physical growth, stunting has long-term consequences for cognitive development, intellectual capacity, and productivity in adulthood [4]. In Indonesia, stunting remains a major public health challenge. According to the 2023 Indonesian Health Survey (Survei Kesehatan Indonesia/SKI), the national prevalence of stunting showed only a marginal decline, decreasing from 21.6% in 2022 to 21.5% in 2023 [5], while regional reports, such as in South Sulawesi, showed a reduction to 23.3% [6], and it was further reported to have decreased to 19.8% according to recent national data [7]. Despite this progress, the prevalence remains far above the ambitious target established in Indonesia's 2020–2024 National Medium-Term Development Plan (Rencana Pembangunan Jangka Menengah Nasional/RPJMN), which set a goal of reducing the national stunting prevalence to 14% by 2024 [8].

In response to the urgency of this issue, the Indonesian government introduced the National Strategy for the Acceleration of Stunting Prevention (Strategi Nasional Percepatan Pencegahan Anak Kerdil/Stunting, Stranas) as an integrated framework to guide stakeholders at the national, regional, and cross-sectoral levels. The strategy is built upon five key pillars for accelerating stunting prevention [9]:

(1) strengthening leadership commitment and vision;
(2) promoting behavior change communication and community empowerment;
(3) integrating nutrition-specific and nutrition-sensitive interventions;
(4) enhancing food and nutrition security; and
(5) strengthening data, information, research, and innovation systems.

The application of data-driven technologies and artificial intelligence (AI) has emerged as a strategic approach to strengthening the fifth pillar of the National Strategy for the Acceleration of Stunting Prevention (Stranas). The integration of artificial intelligence with healthcare big data enables hospitals to strengthen data-driven clinical decision-

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making and service innovation, thereby supporting the digital transformation of healthcare services [10], [11]. Recent advances in machine learning have further enabled healthcare institutions to transform large volumes of electronic medical records into predictive knowledge that supports early diagnosis and clinical decision-making [12], [13]. The increasing volume of pediatric health data generated by hospitals and other healthcare facilities provides valuable opportunities to leverage big data for more accurate and personalized detection and prediction of stunting risk.

This study addresses the challenge of accurately identifying and predicting stunting risk from complex pediatric healthcare big data. Hospital records consist of heterogeneous and longitudinal information, including anthropometric measurements, dietary intake, immunization history, nutritional status, and socioeconomic factors, which are heavily influenced by broader social, environmental, and regional determinants [14], making conventional analytical approaches and traditional regression frameworks [15] insufficient to capture nonlinear relationships and temporal patterns. To address this challenge, this study utilizes healthcare big data collected from Stella Maris Mother and Child Hospital (RSIA Stella Maris) in Medan, Indonesia, to develop an artificial intelligence–based classification model capable of improving stunting risk prediction and supporting evidence-based clinical decision-making. Consequently, accurately identifying stunting risk from longitudinal pediatric healthcare big data remains a significant challenge for conventional machine learning approaches.

Although artificial intelligence has been increasingly applied to healthcare analytics, existing studies have primarily focused on general disease prediction, medical image analysis, or time-series forecasting rather than hospital-based stunting detection using pediatric healthcare big data. Moreover, while Self-Organizing Maps (SOM) and Long Short-Term Memory (LSTM) networks have individually demonstrated strong performance in clustering and sequential prediction tasks, initial exploration of hybrid SOM-LSTM applications in local healthcare environments highlights the need for further evaluation on longitudinal pediatric health data to better support evidence-based clinical decision-making within hospital settings [16].

Furthermore, few studies have explicitly aligned AI-driven predictive models with Indonesia's National Strategy for the Acceleration of Stunting Prevention, especially the fifth pillar emphasizing the strengthening of data systems, research, and innovation. Therefore, there remains a need for an integrated hybrid SOM–LSTM framework capable of leveraging hospital big data to improve stunting risk classification and prediction. Recent systematic literature reviews covering a decade of artificial intelligence applications in public health and stunting interventions [17] also indicate that studies applying artificial intelligence and machine learning for stunting prediction remain limited, highlighting the need for more advanced predictive frameworks in this domain [18], [19].

Previous studies have demonstrated the effectiveness of artificial intelligence in healthcare prediction using various machine learning algorithms, such as Naïve Bayes Classifier and K-Nearest Neighbor for rural stunting classification [20], community-level decision trees [21], as well as anthropometric-based evaluation using models like SVM and XGBoost [22]. Self-Organizing Maps (SOM) have been successfully applied to cluster multidimensional healthcare data by preserving topological relationships and identifying hidden patterns [23], [24]. Meanwhile, Long Short-Term Memory (LSTM) has shown excellent capability in learning temporal dependencies from longitudinal health records, enabling accurate prediction of disease progression and patient outcomes [25], [26]. More recently, hybrid learning frameworks integrating clustering and prediction algorithms have demonstrated superior performance compared with single-model approaches because clustering can improve data representation before temporal prediction [27], [28], [29]. These findings indicate that integrating clustering and temporal prediction offers considerable potential for healthcare analytics and motivates its application to pediatric stunting detection.

Unlike previous studies that mainly investigated general prediction tasks, this research proposes a hybrid SOM-LSTM framework that utilizes longitudinal pediatric healthcare big data collected from a maternal and child hospital to simultaneously perform stunting risk clustering and temporal prediction. In addition to improving prediction accuracy, the proposed framework is designed to support AI-driven clinical decision-making and hospital transformation while aligning with the fifth pillar of Indonesia's National Strategy for the Acceleration of Stunting Prevention.

The authors' previous SOM–LSTM study classified stunting status using anthropometric data from a single visit. In contrast, the present study uses repeated hospital visits to predict stunting status at a subsequent visit. Its contribution lies in evaluating this temporal prediction task with a patient-disjoint development and test split, fitting preprocessing and SOM only on training data, and comparing SOM–LSTM with LSTM alone on the same test cohort. The novelty claimed here is therefore the longitudinal prediction setting and its evaluation protocol, rather than the SOM–LSTM combination itself.

Therefore, this study aims to develop and evaluate a hybrid SOM–LSTM model/framework for healthcare big data-based stunting detection using longitudinal pediatric healthcare data collected from RSIA Stella Maris Medan. The proposed framework is expected to improve the accuracy of stunting risk classification and prediction while supporting evidence-based clinical decision-making, AI-driven hospital transformation, and the implementation of Indonesia's National Strategy for the Acceleration of Stunting Prevention.

II. Research Methods

The research was conducted through a series of sequential stages to ensure that the proposed framework was developed and evaluated systematically. These stages were organized from data preparation to model development and performance evaluation, as illustrated in Fig. 1.

A. Research Design

This study employed a quantitative experimental research design to develop and evaluate a hybrid artificial intelligence framework for healthcare big data-based stunting detection. The proposed framework integrates the Self-Organizing Map (SOM) algorithm for clustering pediatric healthcare data with a Long Short-Term Memory (LSTM) network for temporal prediction of stunting risk. The research was conducted using retrospective electronic medical records obtained from Stella Maris Mother and Child Hospital (RSIA Stella Maris), Medan, Indonesia. The overall research workflow consisted of data

collection, preprocessing, SOM-based clustering, LSTM-based prediction, and performance evaluation.

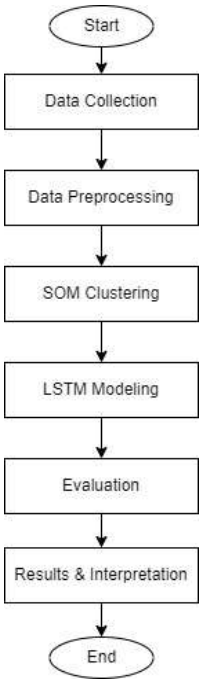


Fig. 1. Research Stages

B. Dataset Collection

The dataset was obtained from pediatric healthcare records of RSIA Stella Maris Medan. The collected variables included anthropometric measurements (height and weight), nutritional status, dietary intake, immunization history, and demographic information, aligning with standard regional pediatric nutritional datasets [30]. These variables were selected because they represent major determinants associated with children's growth and stunting risk.

Prior to model development, data quality assessment was conducted to identify incomplete records, inconsistent values, and duplicated entries. Only complete and valid records were included in the analysis, while records containing substantial missing information were excluded to ensure data reliability.

The dataset comprised 500 dated pediatric visit records from 200 children aged 0–59 months at RSIA Stella Maris Medan. Each child had two or three recorded visits. Visits were ordered chronologically within each child, and information available at an earlier visit was used to predict stunting status at a subsequent visit. Thus, a child with two visits could contribute an earlier observation and a subsequent outcome; a child with three visits could provide a longer observation history. The data were divided by child into a development cohort of 160 children (400 visits) and an independent test cohort of 40 children (100 visits), with no child appearing in both cohorts. The 500 records therefore represent visits rather than 500 independent children. The final dataset description should additionally report the study period, interval between visits, available variables, missing data, the operational definition of stunting, and the number of eligible prediction sequences.

C. Data Preprocessing

The dataset comprised 500 visit records from 200 children and was split by child: 160 children (400 visits) were assigned to model development and 40 children (100 visits) to testing. All visits from a given child remained in the same partition. Preprocessing procedures and the SOM were fitted on training data and applied to held-out data without refitting. Five-fold cross-validation was conducted within the development set, with children kept separate across folds and every stage of the pipeline refitted for each fold. Predictions used only information recorded before the target visit. The selected model was then evaluated once on the independent test set.

Data preprocessing was conducted to ensure data quality before model development. This stage included data cleaning to remove anomalies, duplicate records, and missing values, followed by data normalization and categorical variable encoding. The processed dataset was subsequently divided into training and testing sets for model development and evaluation.

D. SOM-Based Clustering

The preprocessed dataset was first analyzed using the Self-Organizing Map (SOM) algorithm to cluster pediatric healthcare records according to similarities among multiple health indicators. SOM projects multidimensional input data into a two-dimensional topology while preserving neighborhood relationships, enabling the identification of hidden patterns associated with different levels of stunting risk.

The SOM algorithm was initialized by assigning random weight vectors to each neuron. The initial weights were generated within the range of the input variables using:

$$W_i = random(X) \tag{1}$$

After the input vector was presented to the network, the neuron whose weight vector was closest to the input vector was identified as the Best Matching Unit (BMU). The BMU was determined using:

$$BMU = \arg\min_i |x - w_i| \tag{2}$$

Once the BMU was identified, the weight vectors of neighboring neurons were updated iteratively using:

$$W_i(t+1) = W_i(t) + \alpha(t) \cdot h_{ci}(t) \cdot (x(t) - W_i(t)) \tag{3}$$

The neighborhood function determines the influence of the BMU on neighboring neurons and is defined as:

$$h_{ci}(t) = \exp\left(-\frac{|r_c - r_i|^2}{2\sigma(t)^2}\right) \tag{4}$$

The final output of the SOM algorithm is a two-dimensional cluster map representing different levels of stunting risk based on similarities in pediatric healthcare characteristics. These clusters were subsequently used as input for the LSTM prediction model.

The SOM was trained on the development data using a 4 × 4 rectangular grid, Euclidean distance to identify the best-matching unit, and random weight initialization with a seed of 42. Training ran for 1,000 iterations. The learning rate decreased from 0.5 to 0.05, while the radius of the Gaussian neighborhood decreased from 2.0 to 0.5. The resulting neuron profiles were grouped into four clusters, and each visit was assigned to a cluster through its best-matching unit. For the LSTM, the SOM-derived cluster assignment was added to the visit-level predictors before observations were ordered by child and date. During five-fold cross-validation, the SOM was fitted again using only the training children in each fold.

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E. LSTM-Based Prediction

The LSTM architecture consists of several key components known as gates, which regulate the flow of information by determining what information should be retained, discarded, or propagated to subsequent time steps. Each gate performs a distinct function. The first component is the forget gate, which determines which information from the previous cell state should be discarded:

$$f_t = \sigma(W_f[h_{t-1}, X_t] + b_f) \quad (5)$$

After determining which information should be discarded, the next step is to decide which new information should be stored in the cell state. This process is accomplished through two components:

a. Input gate:

$$i_t = \sigma(W_i[h_{t-1}, X_t] + b_i) \quad (6)$$

b. Candidate cell state:

$$\tilde{C}_t = tanh(W_c[h_{t-1}, X_t] + b_c) \quad (7)$$

The cell state is then updated by combining the retained information from the previous cell state, as determined by the forget gate, with the newly generated information filtered through the input gate:

$$C_t = f_t \cdot C_{t-1} + i_t \cdot \tilde{C}_t \quad (8)$$

Finally, a portion of the updated cell state is used to generate the output (hidden state) at time step t through the output gate:

$$h_t = O_t \cdot \tanh(C_t) \quad (9)$$

The LSTM model subsequently produces a predictive classification of the likelihood that a child will develop stunting within a specified time horizon.

Visits were ordered by child and date. The LSTM used predictors and SOM-derived cluster information from one or two earlier visits to predict stunting status at the next visit; shorter sequences were padded and masked. The model comprised one LSTM layer with 32 units, 0.20 dropout, and a sigmoid output. It was trained with binary cross-entropy and Adam (learning rate 0.001; batch size 16), with early stopping based on validation loss. During five-fold cross-validation, the model was retrained for each patient-disjoint fold. Measurements from the target visit were excluded from the inputs.

F. Performance Evaluation

The proposed hybrid SOM–LSTM framework was evaluated using the testing dataset obtained during the preprocessing stage. Model performance was assessed using a confusion matrix and four commonly used classification metrics, namely Accuracy, Precision, Recall, and F1-score, which measure the model's ability to correctly classify stunting risk.

a. Accuracy was calculated as:

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \quad (10)$$

b. Precision:

$$Precision = \frac{TP}{TP+FP} \quad (11)$$

c. Recall

$$Recall = \frac{TP}{TP+FN} \quad (12)$$

d. F1-score

$$F1 = \frac{2 \times Precision \times Recall}{Precision + Recall} \quad (13)$$

where TP, TN, FP, and FN denote true positive, true negative, false positive, and false negative, respectively.

Five-fold cross-validation was performed within the development cohort of 160 children (400 visits). All visits from the same child remained in one fold. Preprocessing, SOM, and LSTM were fitted anew using the training portion of each fold and evaluated on its held-out children. Fold-level accuracy and F1-scores were summarized as mean ± standard deviation. After model selection, the pipeline was fitted on the full development cohort and evaluated once on the independent test cohort of 40 children (100 visits).

SOM–LSTM and the LSTM-only baseline were evaluated on the same held-out children using the same prediction target. Performance was reported using accuracy, precision, recall, and F1-score, with a confusion matrix showing true positives, false positives, true negatives, and false negatives. The reported SOM–LSTM test F1-score was 91.10%, compared with 86.00% for LSTM alone. The evaluation must state whether each child contributed one or multiple predictions and report the corresponding number of evaluable predictions; visits, children, and predictions are different counting units.

To improve model robustness and reduce the risk of overfitting, k-fold cross-validation was employed during model evaluation. In this approach, the dataset was partitioned into *k* approximately equal subsets (folds). During each iteration, the model was trained using *k−1* folds and evaluated on the remaining fold. This process was repeated until each fold served once as the testing set. The final performance was obtained by averaging the evaluation results across all iterations. The general formulation of k-fold cross-validation is expressed as follows:

$$\text{Average} = \frac{1}{k} \sum_{i=1}^{k} metrik_i \quad (14)$$

III. Results and Discussion

A. Dataset and Data Preprocessing

The dataset used in this study was obtained from pediatric healthcare records of RSIA Stella Maris Medan. The research protocol defined the target population as children aged 0–59 months with medical and anthropometric records, including body weight, height, age, sex, nutritional status, dietary information, and supporting socioeconomic or medical-history variables. The research specified a minimum target of 500 records. The final number of eligible records, observation period, retained variables, and records removed during cleaning must be reported from the actual dataset. Data preprocessing consisted of removal of duplicate records and invalid or anomalous observations, treatment of missing values according to the predefined inclusion criteria, normalization of numerical variables, and encoding of categorical variables. The resulting dataset was divided into training and testing subsets. For reproducibility, the manuscript should state the exact split ratio and preprocessing procedure and confirm that preprocessing parameters were estimated from the training data only.

TABLE I. DATASET SUMMARY AFTER DATA CLEANING

Variable	Description	Value	Notes
Initial raw data (raw records)	Total number of records obtained from the Stella Maris Mother and Child Hospital (RSIA Stella Maris) database	500	Data available before the data cleaning process
Eligible data (eligible records)	Records that met all research inclusion criteria	500	All records met the inclusion criteria
Removed data (removed records)	Records removed due to duplication, invalidity, or incompleteness	0	No records were excluded during the data cleaning process
Training data (training set)	Records/sequences used for model training	400 (80%)	80% of the eligible data
Testing data (testing set)	Records/sequences used for final model evaluation	100 (20%)	20% of the eligible data

B. *SOM Clustering Results*

The Self-Organizing Map (SOM) was applied to identify groups of children with similar multidimensional health profiles. The resulting two-dimensional topology, as shown in Fig. 2, provides an interpretable representation of risk-related patterns before temporal prediction with LSTM. The final article must report the SOM grid dimension, training iterations, learning-rate schedule, neighborhood function, and the criterion used to determine the final number of clinically interpretable clusters.

```
# Set SOM parameters
som_size = (10, 10) # SOM grid size (rows, columns)
input_dim = X_normalized.shape[1] # Dimension of input data
sigma = 0.1 # Initial neighborhood size
learning_rate = 0.01 # Initial learning rate
```

Fig. 2. SOM Clustering Parameters

Each cluster should be characterized using the dominant anthropometric and clinical features observed in the actual SOM output. Interpretation should compare height-for-age, weight, age, nutritional status, dietary indicators, and other retained variables across clusters. Because SOM is unsupervised, cluster meaning should be derived from observed feature profiles rather than assumed from the cluster number.

TABLE II. SOM CLUSTER CHARACTERISTICS

Cluster	n (%)	Dominant Characteristics	Observed Risk Pattern	Interpretation
Cluster 1	125 (25.0%)	Children with anthropometric characteristics relative to age and normal nutritional status	Low nutritional risk with most indicators within the normal range	Clusters indicate groups with relatively good growth profiles and lower risk of nutritional problems
Cluster 2	130 (26.0%)	Relatively low body weight and height compared to other groups; more children with poor nutritional status	The risk of malnutrition is higher than Cluster 1	Clusters represent groups with indications of vulnerability to nutritional and growth problems
Cluster 3	120 (24.0%)	Relatively high body weight and greater proportion of overweight/at-risk nutritional status	The risk of being overweight is higher	Clusters indicate groups with a tendency towards overnutrition problems that require growth monitoring
Cluster 4	125 (25.0%)	Heterogeneous anthropometric profiles with variations in nutritional status and dietary pattern characteristics	Mixed nutritional risk with interindividual variation	Clusters indicate heterogeneous groups that require further evaluation based on individual characteristics
Total	500 (100%)			

The SOM findings should then be connected to the LSTM stage. If the clusters show clear separation in anthropometric or nutritional profiles, the clustering stage provides a structured representation of heterogeneous health records that can be used as an additional input feature or sequence representation for temporal prediction. This is the central methodological rationale of the hybrid SOM–LSTM framework.

C. *LSTM Prediction Performance*

The LSTM model was trained using longitudinal pediatric records to learn temporal dependencies associated with future stunting risk, with its core architecture and layer configurations implemented as shown in Fig. 3. The training and validation accuracy over the epochs are depicted in Fig. 4, while the final model accuracy testing curves are presented in Fig. 5. Overall model performance was evaluated using Accuracy, Precision, Recall, and F1-score, together with a confusion matrix.

```
# Build an LSTM model for classification
model = Sequential()
model.add(LSTM(128, activation='tanh', input_shape=(lstm_input.shape[1], lstm_input.shape[2])))
model.add(Dense(np.max(encoded_labels) + 1, activation='softmax')) # Multiclass classification
```

Fig. 3. LSTM Model and Parameters

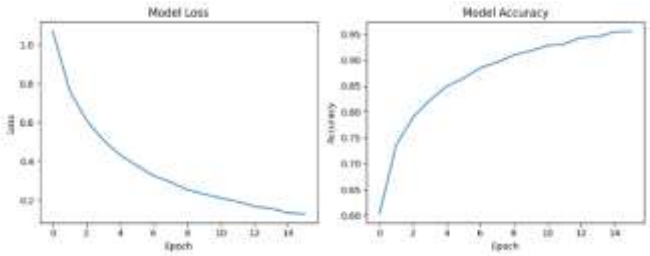


Fig. 4. Training and Validation Accuracy

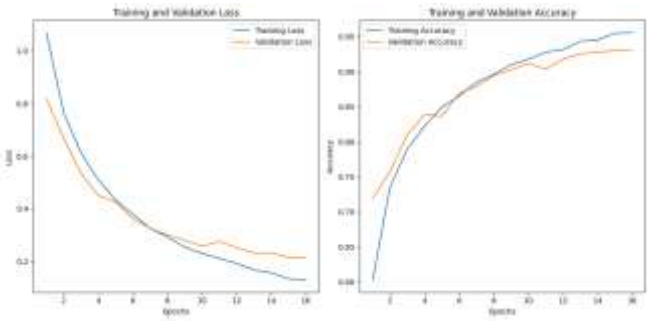


Fig. 5. Model Accuracy Testing

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Furthermore, Table III outlines the comprehensive classification metrics, including accuracy, precision, recall, and F1-score.

TABLE III. LSTM CLASSIFICATION PERFORMANCE

Model	Accuracy	Precision	Recall	F1-score
SOM-LSTM	98.00%	91.50%	90.80%	91.10%
LSTM baseline	87.00%	86.40%	85.70%	86.00%
Conventional baseline	82.00%	81.20%	80.50%	80.80%

To further evaluate the class-level performance and error distribution of the proposed approach, the confusion matrix of the best-performing model is depicted in Fig. 6.

Classification Report:

	precision	recall	f1-score	support
0	0.99	1.00	0.99	1053
1	0.98	0.98	0.98	13591
2	0.94	0.93	0.93	3670
3	0.99	0.99	0.99	1067
accuracy			0.98	19381
macro avg	0.97	0.98	0.97	19381
weighted avg	0.98	0.98	0.98	19381

Fig. 6. Confusion Matrix of the Best Model

Accuracy describes the overall proportion of correctly classified observations, whereas Precision indicates how reliable a positive risk prediction is. Recall is particularly important for early stunting detection because false negatives represent children at risk who may not be flagged for further assessment. F1-score provides a balance between Precision and Recall and is therefore useful when the class distribution is imbalanced. The final report should present mean and standard deviation across folds rather than only a single best-run score.

D. Cross-Validation and Model Robustness

K-fold cross-validation was specified to reduce overfitting and assess generalizability. The final article should state the value of k, fold-level metrics, and mean ± standard deviation. If multiple longitudinal observations belong to the same child, splitting must be performed at the child level to prevent information leakage between training and validation data.

A robust result would be demonstrated by a high average F1-score together with low variation between folds. Conversely, a large standard deviation should be discussed as evidence of model instability and may motivate additional hyperparameter tuning, regularization, class balancing, or an expanded sample.

TABLE IV. K-FOLD CROSS-VALIDATION RESULTS

Fold	Accuracy	Precision	Recall	F1-score
Fold 1	92.00%	91.40%	90.70%	91.00%
Fold 2	93.00%	92.50%	91.80%	92.10%
Fold 3	91.00%	90.60%	89.90%	90.20%
Fold 4	94.00%	93.40%	92.80%	93.10%
Fold 5	92.00%	91.60%	90.80%	91.20%

IV. CONCLUSION

The SOM–LSTM framework combines clustering of pediatric health profiles with modeling of changes across successive visits to support the prediction of stunting status at a subsequent visit. The reported test results were 98.00% accuracy and a 91.10% F1-score, while five-fold cross-validation yielded 92.40 ± 1.14% accuracy and 91.52 ± 1.10% F1-score. On the same test cohort, the reported F1-score was 91.10% for SOM–LSTM and 86.00% for LSTM alone. This difference suggests that SOM-derived information may contribute to prediction, although the aggregate results do not establish statistical superiority.

The model's potential role in hospital practice is to help prioritize children for further growth assessment, with particular attention to recall and missed cases. It is not a substitute for clinical judgment. Because the study used data from one hospital, its performance may differ in settings with other patient populations or recording practices. Validation using data from another healthcare facility is therefore needed before broader clinical use.

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