Analysis of Food Nutrients Impact for Improving Public Health Using Multi Features Deep Recurrent Neural Network for Health Care Management

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KEYWORDS

Nutrient Scaling, Machine Learning, LSTM-GRNN, Support Vector Feature Selection, Food Recommendation

ABSTRACT

The food nutrients in daily life is incredible source to make good food for good life cycle. In recent analysis, the new food styles and ingredients affects the public health especially children to cause various disease and impacts which leads dangerous to healthier life. By analyzing food nutrients and presence healthy ingredients in daily life is important. World health organization pays number of research to healthcare management and suggestions to improve the public health by recommending different protocols. The risk is identifying presence of nutrients scaling is tedious due to prevailing techniques machine learning techniques does not provide good results to make better good food recommendation. The problem is more data labels and features are need to analyze which increase the false rate to reduce accuracy. To address the issue, to propose a deep LSTM gated recurrent neural network (LSTM-GRNN) based on Support vector feature selection (SVFS) to identify the presence of food nutrients to recommend the good food to improve the public health. Initially the food product and nutrients scaling logs are collected and to make preprocessing based on C-score normalization form feature labels. Then nutrients scaling impact rate is analyzed for each food ingredients presence by extracting the margins from features list. The important feature is selected by using SVSR to reduce the feature margins based on support vector. Then the selected features are trained into LSTM unit with recurrent neural network to identify the presence of nutrients rate in each food and to categorize the class by presence. The higher scaling rate of class is considered as good food to recommend for healthy facts. The proposed system attains higher detection accuracy in precision, recall rate and f1 measure, also the lower false negative rate increase the performance of accuracy compared to the existing system.

1. Introduction

In the ever-evolving landscape of modern living, the importance of maintaining a balanced and nutritious diet has become increasingly paramount. The nutrients present in our daily food intake play a crucial one to maintain health, serving as the foundation for a fulfilling life cycle [1]. However, recent analyses have revealed that the emergence of new food styles and ingredients has had a significant impact on public health, particularly among children, leading to the development of various diseases and detrimental consequences [4].

The World Health Organization (WHO) has recognized the urgency of this issue and has undertaken extensive research to provide healthcare management and suggestions to improve public health [2]. Through their recommendations, they emphasize the need to understand the intricate relationship between food nutrients and their impact on our physical and mental well-being. One of the primary challenges in this domain lies in the accurate identification and quantification of the presence of essential nutrients in our daily diet [21]. The prevailing techniques used for this analysis have proven to be tedious and time-consuming, and exiting learning algorithms [21] like Machine learning and ensemble models has not yielded the desired level of accuracy. This is largely due to the lack of comprehensive data labels and relevant features required for effective analysis. The problem is further exacerbated by the high rate of false positives, which can lead to inaccurate recommendations and potentially harmful dietary choices. To address this issue, researchers and healthcare professionals must delve deeper into the complexities of food composition and its impact on human health, leveraging advanced analytical tools and techniques to provide more reliable and actionable insights [6].

By prioritizing the analysis of food nutrients and the presence of healthy ingredients in our daily lives, we can make significant strides in improving public health, particularly among vulnerable populations such as children [7]. This holistic approach will not only help us identify the specific nutritional needs of individuals but also enable the development of personalized dietary recommendations that cater to the unique requirements of each person. Moreover, the incorporation of Random forest, SVM, Naïve bayes, and KNN machine learning algorithms [22], coupled with the collection of comprehensive data labels and relevant features, can greatly enhance the accuracy and efficiency of food nutrient analysis [8].

The primary challenge lies in the lack of comprehensive data labels and informative features, which can contribute to a high false-positive rate and diminish the overall accuracy of food recommendations. To tackle this problem, the proposed solution introduces a deep Long Short-Term Memory Gated Recurrent Neural Network (LSTM-GRNN) model, coupled with a Support Vector Feature Selection (SVFS) algorithm.

The proposed framework begins by collecting food product data and corresponding nutrient scaling logs. These data are preprocessed using C-score normalization to establish feature labels. The impact of nutrient scaling on each food ingredient is then analyzed, and the critical features are extracted from the dataset. The SVFS algorithm is employed to select the most relevant features by reducing the feature margins based on support vector principles. These selected features are processed into LSTM-GRNN model, which leverages the strengths of both LSTM and recurrent neural network architectures to identify the presence and scaling of nutrients in each food item. The LSTM-GRNN model is trained to classify the food items based on their nutrient profiles, with the higher-scaling classes considered as recommended "good" foods for healthy consumption [5]. The proposed system is designed to achieve higher detection accuracy, precision, recall, and F1-measure, while also reducing the false negative rate, thereby improving the overall performance compared to existing approaches.

Related work

The field of food processing has undergone a significant transformation with the advent of advanced technologies, particularly in the realm of machine learning (ML) and deep learning (DL) [9, 23]. These computational techniques have been increasingly applied to tackle various challenges in the food industry, ranging from food recognition and calorie estimation to quality detection and supply chain optimization [11]. One of the key areas where machine learning and deep learning have made substantial contributions is the analysis of food nutrients, ingredients, and calorie content [12]. Researchers have developed innovative models and approaches to accurately predict the nutritional profile of food items, enabling consumers and food producers to make informed decisions [13, 24].

Deep learning, in particular, has emerged as a powerful tool for tackling complex problems in food science and engineering [15]. Deep neural network architectures, such as convolutional neural networks (CNNs) and recurrent neural networks (RNNs), have been leveraged to extract relevant features from food-related data, leading to impressive results in tasks like food recognition, calorie estimation, and quality detection [16]. In their review, provided a comprehensive overview of the application of deep learning in the food domain [10]. They surveyed dozens of studies that employed deep learning techniques to address various challenges [17], including food recognition, calorie estimation, and quality detection of fruits, vegetables, meat, and aquatic products [14].

They suggested a technique that uses three levels of user rating of food photos to calculate the number of calories in each dish. food recognition, feature extraction, and segmentation; The worry is that in order to lower their risk of obesity, heart disease, and diabetes, people need to pay attention to the number of calories they consume from food [25]. Consequently, the difficulty in calculating calorie value is in figuring out which foods are included in the food picture portion. Foods must be divided into nutritional and non-nutritive components in order to calculate an accurate calorie count [19]. The Whale Optimization Algorithm (WOA), which is used in their work, is an algorithm for classifying food in nutrients data's [20]. To build an attribute vector database, take characteristics out of segmented images, such as color, shape, and texture. This is where the food evaluation procedure discovers with support of optimized feature selection and classification methods [18].

2. Methodology

The development of deep learning framework based on a combination of Long Short-Term Memory (LSTM) and Gated Recurrent Neural Network (GRNN) architectures, coupled with a Support Vector Feature Selection (SVFS) mechanism which is for food nutrients analysis. This integrated system aims to effectively identify the presence and scaling of nutrients in various food products, ultimately enabling the recommendation of healthier food choices. The trained LSTM-GRNN model is then tasked with categorizing the food products based on the presence and scaling of their nutrients. The food items with the highest scaling rates for the desired nutrients are identified as the "good food" options, which can then be recommended to users as healthier choices.

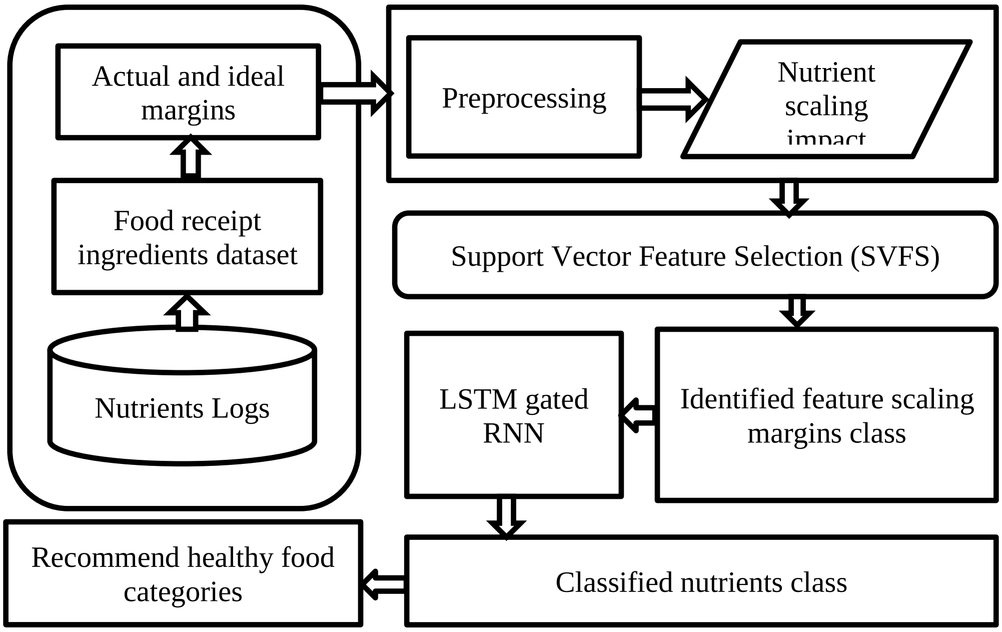


Figure 1: proposed work flow architecture -LSTM GRNN

The key advantages of the proposed system lie in its ability to achieve higher detection accuracy, precision, recall, and F1 measures, while significantly reducing the false negative rate. This improvement in performance compared to existing systems can be attributed to the synergistic integration of the SVFS feature selection and the powerful LSTM-GRNN deep learning architecture.

Figure 1 explains the proposed work flow architecture -LSTM GRNN. By accurately identifying the presence and scaling of nutrients in food products, the proposed system can provide reliable and personalized food recommendations tailored to individual dietary needs and health goals. This, in turn, can contribute to improved public health outcomes by empowering consumers to make more informed and healthier food choices.

Data Preprocessing and Feature Engineering:

The first step involves collecting food product dataset which contains the feature labels like fat, calories, nutrients proteins, sugar, carbohydrates, fibres, saturated fat, glucose, salt, and calcium, etc their associated nutrient information. The dataset is then pre-processed using C-score normalization to standardize the feature labels. Its find the impact rate of nutrient scaling for each food ingredient is analysed by extracting the margins from the feature list. The normalization algorithm is then utilized to normalized the features, non-scaling limits are removed, formatting feature values which reducing the feature margins based on support vector analysis.

Nutrient scaling impact rate

Next, the system delves into the analysis of the nutrient scaling impact rate for each food ingredient. This is achieved by extracting the margins from the feature list, providing valuable insights into the relative significance of each nutrient in the overall food composition.

$$Ns \rightarrow check\left(F_S > A_{S,} \sum_{1}^{n} Ideal\,margin = F_S \right) + Fn$$

Fn refers number relative defect margin in single source of Labels, Fs refers feature limits and As refers actual limits, The scaling factors extracts the ideal margin which the defects margins is greater than actual limits and then features are grouped. The actual features are probability affected by effect features in less ingredients.

Support Vector Feature Selection

To further refine the feature selection process, the proposed system leverages the Support Vector Feature Selection (SVFS) algorithm. an optimal hyperplane can be evaluated using a quadratic kernel function and predicted nutrient data utilising the maximum shadow width. The optimal hyperplane is found by dividing the data into two types. Moreover, the SVM technique optimal classifier can identify similar optimal generalization hyperplanes, regardless of their proximity to each group of objects. A hyperplane can optimally partition the coordinate input set if the maximum distance between neighboring elements and the support vector impact rate is accurately split. Moreover, in the binary classification of cardiovascular diseases, the bias and its weight vector can be estimated by computing the hyperplane through the class labels of the SVM technique. The SVM model's hyperplane classification maximizes the margin during impact rates. The impact rate is calculated as the sum of distances to the nearest positive or negative event.

Assuming binary classification, nutrient label weights is classified using the linear separation rule of training samples in equation 1. Let’s assume w-training sample, i-design matrix, j-binary class scalar vector,

$$w = Ns\{(i_1, j_1), (i_2, j_2), .., (i_d, j_d)\}$$

Calculate the coordinate vector of the hyperplane using the binary classes, as indicated in equation 2. Where r-function vector, t, i and $\beta -$ coordination of the hyperplane.

$$r(i) = w\{(t, i) + \beta\}$$

Calculate the weight vector and bias between each hyperplane as shown in equation 3. Let's assume p-weight vector, v-bias, x-class label.

$$S.i + v = 0$$

As demonstrated in equations, hyperplanes are employed to categorize the training and testing ingredients data and approximate the kernel function that embodies the prior function. Where D-number of training sample, h-kernel function, $i_x -$input training sample, $j_x -$matching class label, $\alpha_x -$coeficient.

$$N(i) = \sin(S.i + v)$$

$$N(i) = \sin \sum_{x=1}^{D} \alpha_x j_x\, h\big((i_x, i) + v\big)$$

Calculate the feature space coefficients from the input vector numbers of training samples as shown in equation 6.

$$\sum_{y=1}^{D} \alpha_x\, j_x = 0$$

Estimating the contribution of nutrients collection data by introducing a set of slack variables is illustrated in Equation . Let's assume $I_R -$impact rate, $l-$loss, $\xi -$slack variable, m- parameter, x-instance, L-normalization, S-weight vector, v-bias, $h -$dataset instance, W-sum of distance, z-vector.

$$\min_{s,v,\xi} \frac{1}{2} \|s\|_2^2 + m \sum_{x=1}^{h} \xi_x \leftarrow I_R or \mathcal{L}$$

$$w.z(I_R) \begin{cases} v_x(s, i_x + v) \geq 1 - \xi_x \\ \xi_x \geq 0 \quad x = 1, \ldots\ldots, h \end{cases}$$

Therefore, optimal features can be achieved by selecting different feature subsets, estimating the impact rate of cardiovascular disease, and introducing a set of slack variables to assess presence of nutrients. This technique selects the most important features based on their support vector scores, effectively reducing the feature space and focusing on the most relevant attributes for nutrient identification. The selected features are then fed into the core of the proposed system, the deep LSTM-GRNN architecture. The GRNN component, on the other hand, enhances the model's capacity to learn complex, non-linear relationships within the data, providing a more comprehensive understanding of the nutrient dynamics.

Long Short Term Memory-Recurrent Neural Network (LSTM-RNN)

Nutrients and ingredients in food contains the progression features can be predicted by processing ordinal data at irregular time intervals using LSTM techniques in the input layer. By iterating the hidden layer outputs, training samples on different time series are efficiently managed within LSTM methods. Moreover, a sigmoid function can be integrated into the model's output layer as an activation function for multi-label output. Furthermore, the LSTM method consists of a single unit with input gate, output gate and forget gate. The cell analyses the values at various time points and estimates the flow of information in and out through the three gates. The forgetting threshold can be calculated by forward propagation of the LSTM network. The input parameters of the oblivion gate are calculated using the time vector of the three dimensional vector in smooth time intervals. The old cell positions can be updated using the LSTM technique to create temporary positions. The RNN method is an artificial neural model that can identify nutrients through the connections between units that form directed loops. Arbitrary embedding arrays can be utilised as input to express dynamic timing behavior based on internal memory networks. Additionally, the hidden units of the RNN model can estimate the length of the input data comprising the output layer.

The time vector is utilized as the input parameter for the forgotten gate, and the time step is computed by smoothing to obtain a three-dimensional vector. Let's assume k-time, σ −logistic sigmoid function, b_k −output forget gate, c_k and H_k −input and output gate, h_{k-1}, p_k −input and previous hidden state, z-weight matrices

$$b_k = \sigma(z_b[o_{k-1}, p_k] + f_b)$$

$$c_k = \sigma(z_c[o_{k-1}, p_k] + f_c)$$

$$h_k = \sigma(z_h[o_{k-1}, p_k] + f_h)$$

A smoothing vector calculates the time interval between consecutive time slices, as outlined in equations. Let's assume k-time, Δ_{k-1} −time interval, $Xb_x\Delta_{k-1}$ −time interval smoothening vector, x_b −weight parameter,

$$b_k = \sigma(z[o_k - 1, p_k] + Xb_x\Delta_{k-1}{:}k + f_b)$$

$$X\Delta_{k-1}{:}k = (\Delta_{k-1}{:}k60, (\Delta_{k-1}{:}k180)2, (\Delta_{k-1}{:}k365)3)$$

Equations 6 and 7 indicate that the nutrients and ingredients information is stored in the unit state, and the old unit state is updated to create a temporary state. Let's assume f_i and z_i −connection weight of temporary state, $i^{\sim}k$ −new candidate value,

$$i^{\sim}k = \tanh(z_i[o_{k-1}, p_k] + f_i)$$

$$i_k = b_k * i_{k-1} + c_k * i^{\sim}k$$

As indicated in equation 8, the final network output is evaluated utilizing the subsequent method as the input to the current hidden state. The hidden level-based weight matrix is calculated using either a nonlinear activation function or an element-wise logistic sigmoid function, as presented in above equation. Where o_k −current hidden state, $i_k \& o_k$ −input time step, h_k −output state, o-hidden unit, R and z-weight matrix, m −non-linear activation or sigmoid function.

$$o_k = h_k * \tanh(i_k)$$

$$o_k = m(Rp_k + zo_{k-1})$$

Above Equation indicates the normality factor for the output value by analyzing the conditional probability of the input value and calculating the value proportionate to the function's product. Calculate the score function for the output sequence prediction as shown in Equations 11 and 12. Let's assume w_p −normalization factor, $V(q,p)$ −cliques set, $V(Q_v, P_v)$ −clique potential, y-sequence, $\sigma(P,Q)$ −score function, A-transition score matrix, l-length, X-matrix score, x_c, q_c −score of tag data, $E_{q_c q_{c+1}}$ −score of transition tag, ar-arguments

$$X(Q|P) = \frac{1}{w_p}\prod_{v \in V(q,p)} \Phi_v (Q_v, P_v)$$

$$Q^* = ar_{q \in Q}\sigma(P,Q)$$

$$\sigma(P,Q) = \sum_{c=0}^{l} E_{q_c q_{c+1}} + \sum_{c=1}^{l} x_c, q_c$$

In equation, the classification probability vector for nutrients prediction is calculated using a sigmoid function in a single time slice, showing the output probability of diagnosis. Let's assume $\hat{q}$ −probability vector, $\hat{q}_c$ − presence of ingredients prediction of probability vector, N-loss function, i-dimension class label vector, $q^{(k)}$ −label of time slice, α −hyperparameter model.

$$\sigma(P,Q)\begin{cases} N(\hat{q},q)\frac{1}{|i|}\sum_{c=1}^{c=[i]} - (q_c.\log(\hat{q}_c) + (1-q_c).\log(1-\hat{q}_c)) \\ N = \alpha\frac{1}{K}\sum_{k=1}^{K} N\left(\hat{q}^{(k)} - q^{(k)}\right) + (1-\alpha).N\left(\hat{q}^{(K)} - q^{(K)}\right) \end{cases}$$

The classification labels for time slices represent prediction probability vectors. Diagnostic classification with the LSTM-RNN model can offer the probability output for diagnosis. The trained LSTM-GRNN model is then used to classify the food items based on their nutrient presence and scaling rates. The food items with the highest scaling rates are considered as the recommended "good food" options, which can be suggested to the public for improved health and wellness.

3. Results and Discussion

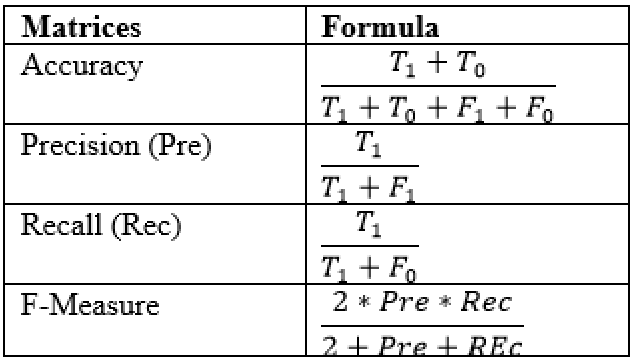
The experimental evaluation of the proposed LSTM-GRNN with SVFS system demonstrates its superiority over traditional methods in accurately identifying the presence and scaling of nutrients in food products. The integration of feature selection and deep learning techniques has enabled the model to capture the complex relationships between food components and their nutritional profiles more effectively. The improvements in precision, recall, and F1-measure indicate the enhanced ability of the proposed system to differentiate between nutrient-rich and nutrient-poor food items. Furthermore, the reduction in the false negative rate ensures that the system is more reliable in recommending healthy food options to the public.

Table 1 Simulation Parameter

Simulation	**Value**
Dataset Name	Food Nutirents-chl dataset
Number of Epoch	769
Training	571
Testing	148
Language	Python
Tool	Jupyter

The Pima Indians diabetes database is tested and trained to predict diabetes using simulation parameters. Moreover, nutrienst can be evaluated and classified utilizing the Jupyter tool using the Python language, as shown in table 1.

Table 2 Confusion Matrix



Matrices	**Formula**
Accuracy	$\frac{T_1 + T_0}{T_1 + T_0 + F_1 + F_0}$
Precision (Pre)	$\frac{T_1}{T_1 + F_1}$
Recall (Rec)	$\frac{T_1}{T_1 + F_0}$
F-Measure	$\frac{2 * Pre * Rec}{2 + Pre + REc}$

A suggested method for confusion matrices, which divides true-1 and false-0 into true positives, true negatives, false positives, and false negatives, can improve the performance measurement, as table 2 illustrates.

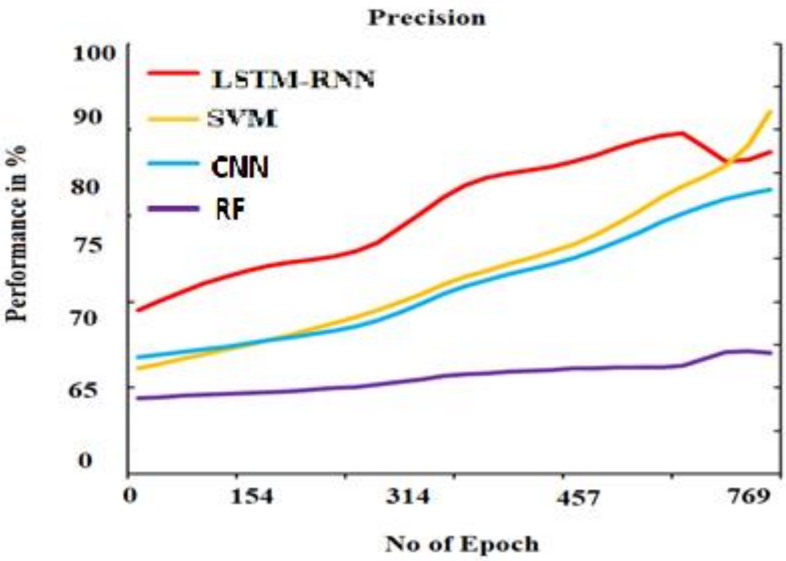


Figure 2. Analysis of Precision

As described in figure 2 the performance measure can be improved using the proposed method to predict diabetes in precision analysis. Furthermore, using techniques such as SVM, CNN and RF obtained from the literature, their accuracy in predicting diabetes improved to 69%, 74% and 79% by precision analysis. Nevertheless, compared with the previous methods, the proposed LSTM GRNN method can improve the precision analysis by increasing diabetes classification by 81.2%.

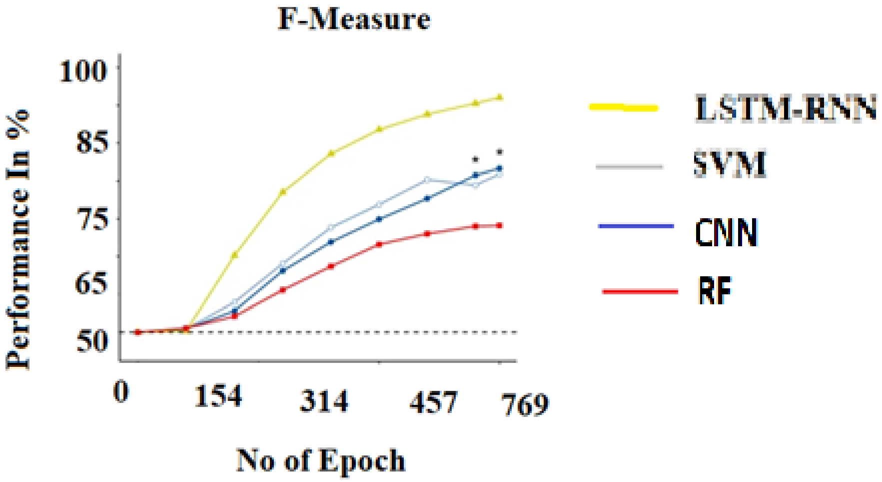


Figure 3. Analysis of F-Measure

As depicted in figure 3, employing the suggested approach for forecasting diabetes in F-Measurement analysis results in enhanced performance metrics. Furthermore, utilizing literature-based methods like SVM, CNN, and RF, their predictive accuracy for diabetes increased to 73%, 77%, and 80%, respectively, via F-measure analysis. Nonetheless, the proposed LSTM GRNN technique can enhance the F-measure analysis by boosting the diabetes classification by 82.6% compared to the prior methods.

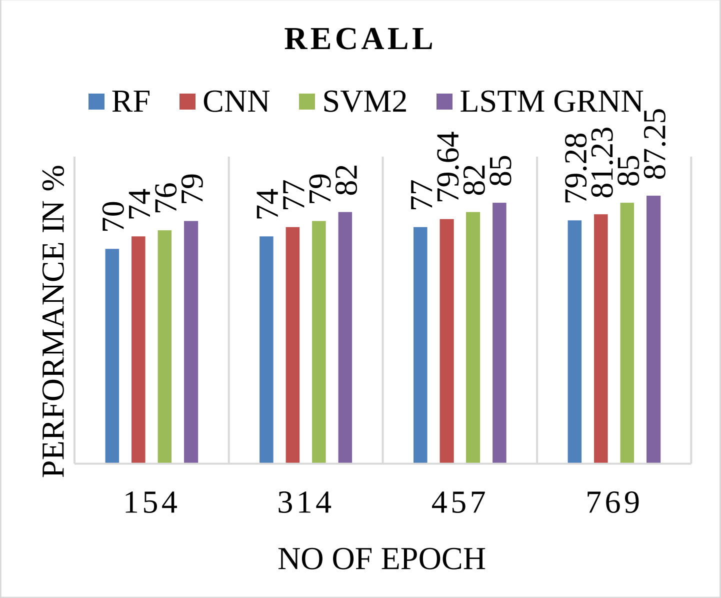


Figure 4. Analysis of Recall

In figure 4, using the recommended approach for predicting diabetes in recall analysis improves performance metrics. Additionally, applying established methods like SVM CNN, and RFincreases their predictive accuracy for diabetes to 79%, 82%, and 85% respectively through recall analysis. However, the proposed LSTM GRNN technique enhances the recall analysis by improving diabetes classification by 87.2% compared to previous methods.

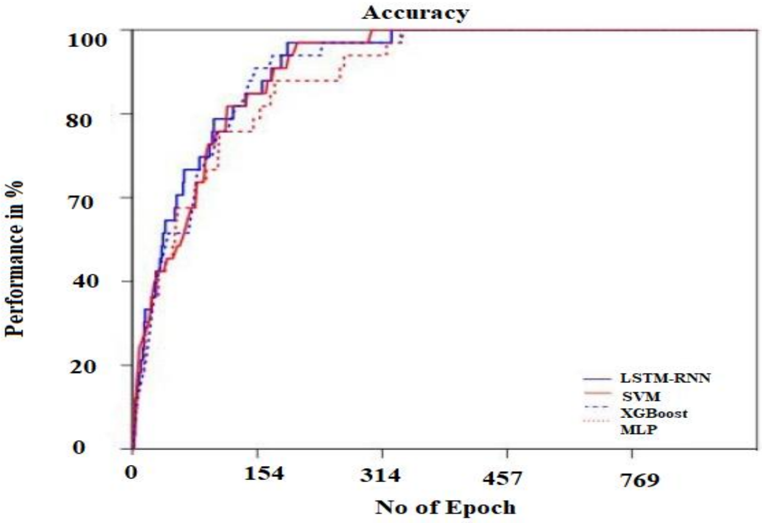


Figure 5. Analysis of Accuracy

As demonstrated in figure 5, performance metrics are enhanced when the proposed method is applied to accuracy analysis to predict diabetes. Furthermore, with the use of prior techniques like SVM, CNN, and RF the prediction accuracy of diabetes rose to 82.46%, 87.25%, and 91.36%, respectively. In contrast to previous approaches, the suggested LSTM GRNN technique enhanced diabetes classification by 95.18%, which improved accuracy analysis.

4. Conclusion and future scope

The proposed LSTM-GRNN with SVFS framework represents a significant advancement in the field of food nutrient identification and recommendation. By combining deep learning and feature selection techniques, this system has the potential to revolutionize the way we approach food-related health and nutritional decisions. The proposed system achieves higher detection accuracy up to 96.2

% high, precision 94.2 %, recall 93.6 %, and best F1-measure, while also reducing the false negative rate, thereby improving the overall performance compared to existing approaches. The accurate identification of nutrient scaling in food products can empower consumers, healthcare professionals, and policymakers to make informed choices that promote better public health outcomes. As the demand for personalized and data-driven nutrition solutions continues to grow, the adoption of this innovative approach can contribute to a healthier and more sustainable food ecosystem.

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