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SQUIRREL SEARCH GRADIENT OPTIMIZED DEEP BELIEF NETWORK CLASSIFIER FOR THYROID DISEASE PREDICTION

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ABSTRACT

Thyroid disease is a range of disorders that affect the thyroid gland, a butterfly-shaped organ located in the neck responsible for producing hormones that regulate metabolism, energy levels, and overall bodily functions. Early detection and management of thyroid disease are crucial, as untreated conditions leads to severe complications, including cardiovascular issues, infertility, and metabolic disorders. Advanced diagnostic methods, including machine learning and deep learning techniques, are increasingly used to improve the accuracy and timeliness of thyroid disease detection, facilitating better treatment outcomes. But, severity of thyroid disease prediction accuracy with minimal time is major challenging issues. In order to improve the accuracy of thyroid disease prediction, a novel Squirrel Search Gradient Optimized Deep Belief Neural Classifier (SSGODBNC) model is developed with minimal time consumption. The proposed Deep Belief Network (DBN) is a fully connected artificial feed-forward deep learning method comprising two visible layers such as the input and output layer and multiple hidden layers for processing the given input. In the layer-by-layer process, the first hidden layer receives weighted input and performs data preprocessing. Then extracting significant features and eliminates the insignificant features from the dataset using the Sparse Autoencoder model. These selected significant features are utilized to classify the severity level of thyroid disease using Sokal–Michener's simple matching method. During fine-tuning, error back-propagation algorithms adjust the hyperparameters using Squirrel Search Gradient Optimization to increase the accuracy of thyroid disease classification. This optimized fine-tuning process significantly enhances the performance of the deep belief network and improves overall learning efficiency in classification tasks. Finally, the accurate thyroid disease severity prediction results with minimal error are obtained at the output layer. Experimental assessment is conducted with different evaluation metrics such as Accuracy, Precision, Recall, F1-score, specificity and Thyroid disease prediction time. The observed result shows the effectiveness of the proposed SSGODBNC model with higher accuracy in thyroid disease prediction with minimum time than the existing methods.

Keywords: *Thyroid Disease Prediction, Deep Belief Network, Fine-Tuning, Adaptive Gradient Method, Squirrel Search Gradient Optimization, Sokal–Michener's Simple Matching Method*.

1. INTRODUCTION

Thyroid disease poses a substantial health risk, negatively impacting an individual's quality of life while also leading to increased medical expenses for diagnosis and treatment. Identifying thyroid disease particularly challenging, especially for less experienced healthcare professionals, as its symptoms often overlap with those of other conditions. Recent advancements in medical research have highlighted the potential of machine learning techniques as effective tools for diagnosing diseases. By analyzing patterns in clinical data, machine learning models supports practitioners in making accurate and timely diagnoses, thereby improving patient outcomes and reducing the burden on healthcare systems.

The scopes of the DBNs suggest the potential path for predicting thyroid diseases, with the aid of early diagnosis and modified treatment. Its context extends to enhance the accuracy and efficiency in identifying different thyroid conditions. The DBNs can be trained to forecast the entity patient responses to various treatments, allowing for further personalized and management of thyroid disorder and utilized to determine the medical images such as, X-rays and CT scans for thyroid abnormalities. It

classifies and diagnoses thyroid conditions based on thyroid scintigraphy images, offering another tool for diagnosis.

A Dynamic Selection Hybrid Model (DSHM) was proposed in [1] to predict thyroid disease and improve accuracy through robust feature selection. However, the DSHM model requires higher computational time for thyroid disease prediction. **A** Stacked Ensemble with IG feature selection model was designed in [2] with the aiming to enhance thyroid disease detection and reduce screening time and costs considering few clinical attributes. But it failed to predict the severity level of thyroid disease prediction.

Different machine learning models were developed in [3] for detecting thyroid disease, incorporating a differential evolution (DE)-based optimization algorithm to fine-tune parameters and minimize errors. But, it did not address increasing the dataset size, limiting the ability to further analyze the performance of deep learning models. A generalized deep learning-based decision support system was proposed in [4] to improve thyroid cancer diagnosis and enhance overall diagnostic performance. However, challenges related to precision and recalls in thyroid cancer detection remain unresolved. To enhance the performance of precision and recall, a novel random forest-based self-stacking classifier model was developed in [5] for efficient thyroid disease detection. However, the time complexity of thyroid cancer prediction remained unaddressed. Various machine learning approaches were developed in [6] for predicting papillary thyroid cancer. However, deep learning models were not utilized to enhance the accuracy of cancer prediction while minimizing time consumption. A Quantum Support Vector Machine classifier model was developed in [7] for more accurate classification of thyroid cancer by selecting significant features using the Quantum Particle Swarm Optimization method. However, it failed to apply effective feature selection and classification algorithms to improve the performance of thyroid disease prediction and achieve better accuracy rates.

Several machine learning techniques were proposed in [8] for classifying thyroid disease predictions, which include data preparation, feature selection, and hyperparameter tuning. However, these methods did not address the reduction of time complexity in thyroid disease prediction. A robust and effective machine learning-based method was developed in [9] for predicting thyroid disease by addressing class imbalance and performing feature selection. However, various feature selection techniques and robust handling of missing data were not adequately addressed. A fine-tuned Light Gradient Boosting Machine (LGBM) model was developed in [10] to achieve high accuracy in thyroid disease prediction. However, it did not incorporate deep learning models to further enhance the diagnostic performance for thyroid disease. Different machine learning algorithms were designed in [11] to predict hypothyroidism and hyperthyroidism by identifying the most significant features to distinguish thyroid diseases more accurately. However, it failed to develop a more effective feature selection scheme to further improve the results.

An ensemble learning model was developed in [12] for automatic, reliable, and accurate thyroid recognition with the aim of improving prediction accuracy. However, it failed to construct a multiclass thyroid classification model. A three-stage hybrid classifier (3SHC) model was developed in [13] for disease prediction by reducing the dataset dimension and performing feature selection. But, the designed classifier model requires higher computational resources and results in increased computational costs. An optimized extreme gradient boosting multiclass classifier model was introduced in [14] to classify patients with different types of thyroid disease. However, sophisticated deep learning models have not been applied to achieve even more accurate and effective outcomes. The regressor and classifier model developed in [15] aimed to predict the occurrence of hypothyroidism by analyzing the features required for classification. However, it failed to optimize the model hyperparameters to minimize the statistical loss functions.

1.1 A Novel Contribution of The SSGODBNC Method

The major contributions of the SSGODBNC model is listed as follows,

- To enhance the accuracy of thyroid disease prediction, the SSGODBNC model has been developed, incorporating preprocessing, data feature selection, and classification.
- A novelty of deep learning model performs data preprocessing and feature selection in the hidden layer using SSGODBNC model designed into minimize the training time of thyroid disease prediction

- A novel method of Sokal–Michener's simple matching technique is developed for analyzing the training and testing data samples and provides the multi class classification outcome to enhance the accuracy with minimum error.
- A novelty of squirrel Search Algorithm is obtained in fine-tuning process to optimize the error rate and improve the accuracy of thyroid disease prediction.
- Finally, an experimental evaluation is carried out to estimate the performance of the SSGODBNC model using various metrics and comparing it to other classification methods.

1.2 Problem Statement

The thyroid disease prediction is improving the occurrence of thyroid disorders and require for correct and early detection to enhance the patient results and minimum healthcare costs. The thyroid disease prediction [1] designed to enhance accuracy by robust feature selection. But, the DSHM model was not reducing the computational time. The feature selection model [2] introduced with improved thyroid disease detection with lesser screening time and costs. However, the severity level of thyroid disease prediction was not determined. The different machine learning methods are designed in [6] to thyroid cancer. But, it failed to improve accuracy of cancer prediction with reduced time consumption. To overcome this issue, the proposed SSGODBNC model achieved with better accuracy in thyroid disease prediction with lesser time than the existing methods.

1.3 Organization

The paper is structured as follows: Section 2 provides a review of related works in the field, highlighting issues. Section 3 introduces the proposed SSGODBNC model, offering a detailed explanation along with a diagram for better understanding. Section 4 outlines the experimental setup and provides a description of the dataset used for evaluation. In Section 5, the performance of the proposed model is compared with existing methods, considering various parameter configurations. Finally, Section 6 presents the conclusion.

2. RELATED WORKS

A Light Gradient Boosting Classifier model was developed in [16] to achieve high performance in thyroid cancer diagnosis. However, the designed model failed to be effectively applied in clinical practice to improve its predictive accuracy. A new combination of K-Neighbors (KN) and Random Forest (RF) classifier models was developed in [17] for the effective identification of thyroid syndrome. However, it did not incorporate more advanced neural network-based approaches to further enhance the performance scores for thyroid syndrome detection. An ensemble machine learning classifier model was introduced in [18] to improve classification performance with higher specificity. But, it failed to extend the classification of thyroid disease using an explainable machine learning approach, which could enhance accuracy, transparency, and outcomes. A machine learning (ML) integration was developed in [19] by applying multi-criteria decision-making for thyroid prediction. However, the time complexity of the thyroid prediction was higher. A hybrid model combining ensemble stacking and an advanced feature selection technique was developed in [20] to enhance the accuracy of thyroid disorder detection. However, the performance of sensitivity analysis in thyroid disorder detection was not addressed. An interpretable thyroid categorization approach was introduced in [21] using explainable AI, achieving the highest accuracy performance. However, it did not apply a multiclass classification approach.

A random forest model was developed in [22] to achieve improved prediction performance for thyroid papillary cancer. However, the issue of time consumption in predicting thyroid papillary cancer remained unresolved. A machine learning approach was developed in [23] to predict differentiated thyroid cancer based on hyper parameter tuning. However, it failed to explore these models on larger and more diverse datasets to validate the thyroid cancer prediction. In [24], machine learning algorithms were designed to predict medullary thyroid carcinoma. However, optimization and additional predictive factors were not incorporated into the carcinoma prediction. A convolutional neural network (CNN) prediction model was developed in [25] with the aim of detecting papillary thyroid cancer, achieving high sensitivity and specificity. But, an efficient optimization model was not applied to further enhance the thyroid cancer prediction. A machine learning model using eXplainable Artificial Intelligence (XAI) was introduced in [26] to improve thyroid disease prediction. However, multi-label thyroid disease prediction remained unaddressed. Risk prediction models were developed in [27] with the aim of predicting the cervical lymph node involvement in papillary thyroid carcinoma. However, the models

failed to validate the efficacy of these prediction models.

An efficient nomogram model was developed in [28] by utilizing visualized multipopulation data to accurately classify thyroid carcinoma. But, a deep learning classifier model was not applied to enhance the accuracy of thyroid carcinoma prediction. A binary logistic regression and Lasso regression model was developed in [29] for variable selection and risk factor analysis in thyroid disease prediction. However, the error rate in the risk factor analysis was not effectively addressed. A novel conditional generative adversarial network model was developed in [30] with the aim of detecting thyroid disease by extracting multi-scale features. But, it failed to perform an in-depth analysis of thyroid disease prediction.

3. PROPOSAL METHODOLOGY

Thyroid disease is a significant cause of mortality, highlighting the importance of early diagnosis to mitigate its impact. However, existing methods in healthcare diagnosis face challenges regarding performance consistency and accurate disease prediction within minimal time. This section introduces a novel methodology called SSGODBNC, developed for accurate thyroid disease prediction. The working methodology of the SSGODBNC model is divided into four primary processes namely data acquisition, data preprocessing, feature selection, and classification. Figure 1 provides an overview of the entire working process of the SSGODBNC model.

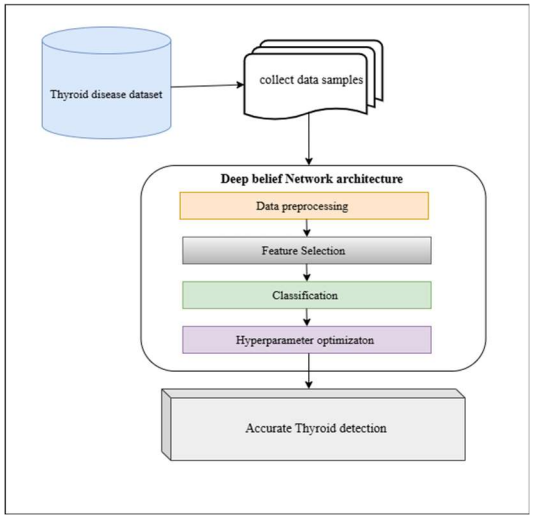

Figure 1: Architecture Diagram of SSGODBNC Model

Figure 1 above illustrates the architecture of the proposed SSGODBNC model, which aims to achieve accurate thyroid disease prediction in medical data processing. The SSGODBNC model integrates various fundamental processes that work collaboratively to enhance the prediction accuracy and efficiency. These processes include data preprocessing, feature selection, and evaluation, each playing a crucial role in refining the dataset and improving the performance of the disease prediction model. Through applying optimization, the model provides the better prediction results. In the following subsections, each of these processes is explained in detail, highlighting their significance in the overall framework of the proposed model.

3.1 Data Acquisition

Data acquisition is the crucial step in the SSGODBNC model that involves gathering relevant and reliable data from the healthcare databases namely Thyroid disease dataset extracted from https://www.kaggle.com/datasets/emmanuelfwerr/thyroid-disease-data. This step ensures that sufficient information is available to train and validate the model effectively. In the context of thyroid disease prediction, data acquisition focuses on collecting patient-related information, including clinical features, test results, and demographic details, to create a comprehensive dataset for further processing. Accurate and high-quality data acquisition plays a vital role in enhancing the reliability and performance of the proposed SSGODBNC model.

The dataset includes 9172 instances or records or data samples and 31 attributes or features for accurate thyroid disease prediction. The 31 attributes are listed as follows, age of the patient, sex of patient, on_thyroxine, query on thyroxine, on antithyroid meds, sick, pregnant, thyroid_surgery, I131_treatment, query_hypothyroid, query_hyperthyroid, lithium, goiter, tumor, hypopituitary, psych, TSH_measured, TSH, T3_measured, T3 level in blood from lab work (float), TT4_measured in the blood, TT4 level in blood, T4U_measured in the blood, T4U level in blood, FTI_measured , FTI level in blood, TBG_measured , TBG, referral_source, target, patient_id

Let us consider the dataset 'DS' and samples as well as features are arranged in the form of matrix. Therefore, the input matrix is formulated as given below,

$$IM = \begin{bmatrix} F_1 & F_2 & \dots & F_M \\ S_{11} & S_{12} & \dots & S_{1n} \\ S_{21} & S_{22} & \dots & S_{2n} \\ \vdots & \vdots & \dots & \vdots \\ S_{m1} & S_{m2} & \dots & S_{mn} \end{bmatrix} \quad (1)$$

Where, IM indicates an input matrix, each column indicates a number of features$F = \{F_1, F_2, \dots, F_n\}$, each row indicates a number of samples or instances or records '$S = \{S_1, S_2, \dots, S_N\}$' respectively.

3.2 Proposed Deep Belief Neural Network

The SSGODBNC model employs a Deep Belief Network (DBN), a specialized deep learning model designed to enhance the accuracy of thyroid diseases detection while reducing processing time. This approach improves the feature selection and classification, especially for handling the large volume of sequential data. A DBN architecture consists of multiple layers of Restricted Boltzmann Machines (RBMs) arranged hierarchically, functioning as a generative model. This layered architecture minimized the computational complexity while handling the large volume of data samples. Additionally, the proposed deep learning architecture effectively minimizes errors during training, leading to improved overall performance in the thyroid diseases prediction.

Figure 2 depicts the architecture of a Deep Belief Network for accurate thyroid disease prediction. The learning process is divided into two primary processes namely layer-by-layer training and fine-tuning.

During the layer-by-layer training phase, each layer of the Deep Belief Network processes weighted input data samples and transferred into the next layer. In the fine-tuning phase, error back propagation is

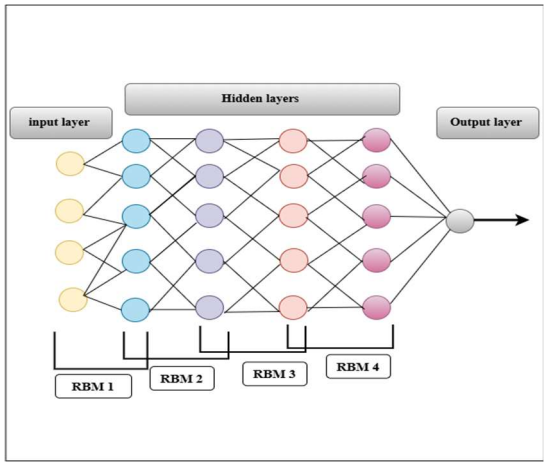

Figure 2 : Construction of Deep Belief Network

employed to adjust the network's hyper parameters, by applying a Squirrel Search Gradient Optimization method for enhanced performance.

In the layer-by-layer approach, Deep Belief Networks utilizes the Restricted Boltzmann Machines (RBMs), which are stochastic neural networks. Restricted Boltzmann Machines (RBMs) are a type of stochastic neural network used for unsupervised learning, particularly in feature extraction and dimensionality reduction tasks. An RBM consists of two layers such as a visible layer and a hidden layer. The visible layer represents the input data samples, while the hidden layer processes the data samples. The output generated by one RBM serves as the input to the visible layer of the next RBM, as illustrated in Figure 2.

As exposed in the figure 2, the DBNs consist of training set $\{S,Y\}$ where S denotes a input data samples $S_i = \{S_1, S_2, S_3, \dots S_n\}$' collected from the dataset and a label or output 'Y' representing its category which belongs to the different classes($Y_k \in 1,2,3 \dots k$). The input data samples is associated to a weight ' $\vartheta_1, \vartheta_2, \dots, \vartheta_n$' and added with bias '$B_v$'. The probability of the neuron activation in the visible layer is given below,

$$P_{vl} = F\left(\sum_{i=1}^{n} S_{i\square} * \vartheta_{vl}\right) + B_v \quad (2)$$

Where, P_{vl} denotes a neuron activation probability in visible layer, F symbolizes a sigmoid activation function, 'S_i' indicates an input patient data samples, ϑ_{vl} represents a weights in visible layer B_v indicates a bias of visible layer. If the neuron activation probability $P_{vl} = 1$, then the input data

samples are sent into the hidden layer. In that layer, data preprocessing is carried out by significantly improve the performance of predictive models by addressing issues of missing values in the given dataset.

3.2.1 Data Preprocessing

Data preprocessing is essential for ensuring that the machine learning model learns from high-quality, structured, and relevant dataset, leading to more reliable and accurate disease predictions. In the preprocessing step, the proposed SSGODBNC model addresses the missing data in the given dataset through the nearest neighbor imputation method.

The first step involves analyzing the dataset to recognize the distribution of missing values. After that, the nearest neighbor imputation method is then applied for finding the missing values. The values of the nearest neighbors are averaged to fill in the missing entries. The missing data imputation process is expressed as follows,

$$S_{miss} = \frac{\sum_{v=1}^{K} S_v \delta_v}{\sum_{v=1}^{K} \delta_v} \quad (3)$$

Where, S_{miss} indicates a missing data values, S_v denotes an observed neighboring known data sample values available in dataset, δ_v designates a weights assigned to the neighboring known data sample values.

After finding the missing data, the determined values are refined by applying a normalization process. It is used to reduce the dimensionality of the dataset and capture the most significant values that explain the variance in the data. This refinement process stabilizes the effect of both continuous and categorical variables which capture the underlying structure and relationships within the data. In this step, the mean of each known value is computed as follows,

$$\mu = \frac{1}{K} \sum_{v=1}^{K} S_v \quad (4)$$

Where, μ denotes a mean of each value, K denotes a number of neighboring data samples. After that, the normalization method is applied to rescales data into standard normal distribution.

$$S_{Norm} = \frac{(S_{miss} - \mu)}{\sigma} \quad (5)$$

Where, S_{Norm} denotes a normalization of the respective missing values 'S_{miss}' and μ denotes a mean, σ denotes a standard deviation. The missing values, imputed with the mean value to minimize deviation, ensure that the underlying structure of the data is accurately reflected. Finally, these imputed values refine the dataset, enhancing the accuracy of disease prediction while minimizing time consumption.

3.2.2 Feature Selection

After the preprocessing, the feature selection process is performed to reduce its dimensionality. This step involves identifying and retaining the most important features while discarding less relevant or redundant ones. By focusing on the most informative attributes, feature selection not only simplifies the dataset but also enhances the efficiency and accuracy of subsequent modeling tasks. This process ensures that the model operates on a refined set of features, reducing computational complexity and improving predictive performance. The proposed SSGODBNC model utilizes the Convergent Propagated Sparse Auto encoder model for selecting the significant features by removing the other features. The Sparse Auto encoder is a variation of an auto encoder neural network that helps to enhance the learning of input samples and provides the output in terms of compact and meaningful representation.

A Sparse Auto encoder performs two major processes namely forward propagation and backward propagation to minimize the dimensionality of the input dataset. The proposed auto encoder model consider the preprocessing output 'PO' as input for feature selection. Forward propagation is used to find the most significant feature that maximizes the objective function' J' as expressed as follows,

$$F^{+} = argmax\, J\big(Out_{F_l} + PO\big), where\ PO \in Out_{B_l},\ PO \notin Out_{F_l} \quad (6)$$

Where, F^{+} features selection at the forward propagation, $argmax$ denotes argument of maximum function, Out_{F_l} denotes a forward propagation of the features combined with the preprocessing output 'PO' during the feature selection process. After the forward propagation identifies significant features, backward propagation is employed to eliminate insignificant features from the selected set. This ensures that the feature set is refined to retain only the most relevant and impactful features.

$$F^{-} = argmax\, J\big(Out_{B_l} - PO\big), where\ PO \in\ Out_{B_l}, PO \notin Out_{F_l} \quad (7)$$

$$FS = (F^{+}, F^{-}) \quad (8)$$

Where, F^{-} features elimination at the backward propagation, $argmax$ denotes argument of maximum function, Out_{B_l} denotes a backward propagation output combined with the preprocessing output 'PO' during the feature selection process, J denotes a objective function, FS indicates a final dimensionality feature set output which includes the significant feature selection and elimination. The process converges when the total number of features in the thyroid disease dataset is fully evaluated (both selected and eliminated), ensuring that the final feature set 'FS' contains only the most relevant features. This approach enhances the model's performance by optimizing the feature set through iterative refinement. The selected significant features are transferred into the third hidden layer.

3.2.3 Classification

After the feature extraction phase, the classification process is performed to analyze the extracted features from the training and testing datasets. This phase is crucial for building and validating the predictive model. The Sokal–Michener's simple matching method is a statistical method which applied to analyze the training and testing data samples based on the correlation measure. It is mathematically computed as follows,

$$corr\ (S_{tr}, S_{ts}) = 1 - \frac{|S_{tr}\,\Delta\, S_{ts}|}{n} \quad (9)$$

$$Y = corr\ (S_{tr}, S_{ts}) \quad (10)$$

Where, Y denotes an analysis outcomes, $corr\ (S_{tr}, S_{ts})$indicates a correlation between the testing data samples 'S_{ts}' and training samples 'S_{ts}',' n' denotes a number of samples,$S_{tr}\,\Delta\, S_{ts}$ denotes a deviation between the samples. Based on the Sokal–Michener's simple matching method, the correlation provides the similarity outcomes from '0' to '1. The maximum correlation results provide the final classification outcomes.

3.2.4 Fine Tuning

Fine-Tuning is a vital process in deep learning where a classifier model is further optimized to perform a specific task. It is used to refine the weights of the network for improved classification performance. In fine tuning process, the error rate is measured based on squared difference between the actual and predicted classification output as follows,

$$ER = \left[Y_{act} - Y_{pre}\right]^2 \quad (11)$$

Where, 'ER' symbolizes the error rate, Y_{act}signifies the actual classification output, Y_{pre} symbolizes the predicted classification output. In order to minimize the error, the adaptive Gradient method is employed to update the weight.

$$\vartheta^{new} = \vartheta^{old} - \eta \left[\frac{\partial E}{\partial \vartheta^{old}}\right] \quad (12)$$

Where, ϑ^{new} indicates a new weight, ϑ^{old}specifies a current weight, η indicates a learning rate, $\frac{\partial ER}{\partial \vartheta^{old}}$signifies the first-order derivative to find out a local minimum of a function (i.e. error rate) by updating the current weight 'ϑ^{old}'

In order to find optimal weight value, Squirrel Search Optimization algorithm is employed to reduce the error and enhance the accuracy of thyroid disease prediction. Squirrel Search Optimization (SSO) is a meta-heuristic algorithm inspired by the adaptive foraging behavior of squirrels. During warm weather, squirrels actively glide between trees in search of food resources, showcasing dynamic exploration patterns. In this optimization algorithm, squirrels symbolizes weights, while food resources represented by a fitness function. In colder periods, their activity decreases as they conserve energy to meet their basic needs. When the weather becomes constructive again, the squirrels resume their active foraging and exploration behaviors. This cyclic pattern continues throughout the lifespan of the squirrels, forming the basis of the optimization process.

First, populations of squirrels (i.e. weights) are initialized in search space,

$$\vartheta_b = \vartheta_1, \vartheta_2, \vartheta_3, \ldots . \vartheta_b \quad (13)$$

Where, ϑ_b denotes a 'b' number of updated weighs. For each squirrel (i.e. weight), the fitness is measured based on the error rate.

$$f(\vartheta_b) = arg\ min\ ER (14)$$

Where,$f(\vartheta_b)$ represents a fitness of weight, $arg\ min$ indicates an argument of minimum function,

ER indicates an error rate of the classifier model. Based on the fitness estimation, the current best weight is selected among the population. Then executes a different behaviors of the squirrels as follows,

- **New Locations Generation Through Gliding**

In this behavior, new locations are generated by mimicking the gliding behavior of squirrels, which reflects their natural foraging habits. This gliding mechanism enables the algorithm to efficiently explore the solution space in detection of optimal results.

$$X_i^{new} = X_i + D_k G_C * \frac{1}{2}|X_i - X_{best}| \quad (15)$$

Where, X_i^{new} indicates a new location of the squirrels, X_i indicates old location of the squirrel, D_k denotes a random gliding distance, G_C indicates a gliding constant, $|X_i - X_{best}|$ indicates a deviation between the current position of squirrel 'X_i' and X_{best}' indicates a best position of the squirrel.

- **Verify Seasonal Monitoring Condition**

The foraging patterns of flying squirrels are significantly influenced by seasonal variations. To address this, a seasonal monitoring mechanism is implemented, ensuring the algorithm avoids becoming stuck in local optima.

$$ZS = \sqrt{(X_i^t - X_{best})^2} \quad (16)$$

Where, ZS denotes a seasonal constant, X_i^t indicates a current solution, X_{best} designates an best position of squirrel.

$$ZS_{min} = \frac{10\,[e^{-6}]}{365^{\left(Iter/Iter_{mx}\right)*2.5}} \quad (17)$$

WhereZS_{min}indicates a minimum seasonal constant, $Iter$indicates an iteration, $Iter_{mx}$designates a maximum iteration. When $ZS < ZS_{mn}$ indicating the end of winter, flying squirrels lose their ability to navigate the forest efficiently and instead begin randomly exploring new locations in search of food. This cycle continues until the maximum number of iterations is achieved. If not, the process of generating new positions and evaluating seasonal monitoring conditions is repeated.

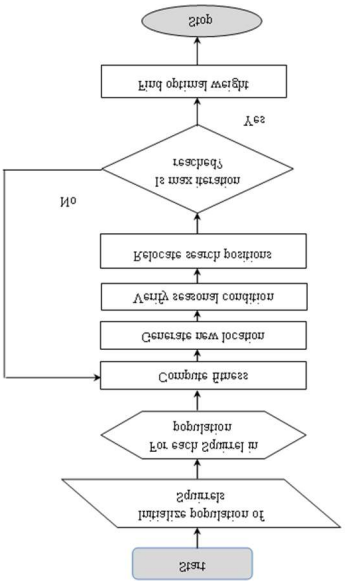

Figure 3 : Flow Chart of Squirrel Search Optimization

Figure 3 demonstrates the flow diagram of the squirrel search optimization for selecting the optimal weight with minimum error. As a result, then the optimally selected weights are used to enhance the disease prediction. Finally, the disease prediction results are obtained at the output layer as follows,

$$Y_{final} = F_{soft}\,(\,\delta_{ho} * h_t) \quad (18)$$

Where Y_{final} indicates a multiclass classification output, F_{soft} indicates a softmax activation function, h_t indicates an output of the previous hidden layer, δ_{ho} denotes a weight between the hidden and output layer. A softmax activation function 'F_{soft}' in the output layer for multi class classification output is formulated as follows.

$$F_{soft} = \frac{\exp(Y_K)}{\sum_{K=1}^{C}\exp(Y_K)} \quad (19)$$

From the above (19), the softmax activation function is used to make a multiple classification results, Y_K denotes a raw output for the K^{th} class, C denotes a total number of classes. The algorithmic process of Squirrel Search Gradient Optimized Deep Belief Neural Classifier model is given below.

// Algorithm 1: Squirrel Search Gradient Optimized Deep Belief Neural Classifier model
Input: dataset 'DS' , number of features$F = \{F_1, F_2, \ldots, F_n\}$, samples '$S = \{S_1, S_2, \ldots, S_N\}$'
Output: Increase the disease prediction accuracy

Begin

1. **Collect n**umber of features$F = \{F_1, F_2, \dots, F_n\}$ and samples '$S = \{S_1, S_2, \dots, S_N\}$--- **input layer**
2. **For each** sample S
3. Formulate the neuron activation probability using (1)
4. **End For**
5. Preprocessing **the data samples using (3) (4)** (5)–**[hidden layer 1]**
6. **For each preprocessing samples 'PO'**
7. Perform forward propagation to extract significant features as given in (6)
8. Perform backward propagation process to eliminate insignificant features (7)
9. Obtain the feature set 'FS' using (8)
10. **End for**
11. **End for**
12. **For each** training and testing data samples
13. Apply Sokal–Michener's simple matching method using (9)
14. Obtain the classification results (10)
15. **End for**
16. **For each classification outcomes--**
17. Compute the error rate 'ER' using (11)
18. **Apply** adaptive Gradient method to update weight using (12)
19. **End for**
20. Initialize the population of the weights $\vartheta_b = \vartheta_1, \vartheta_2, \vartheta_3, \dots . \vartheta_b$
21. **For each** weight in populations
22. Compute the fitness 'F' using (14)
23. **While (**$Iter < Iter_{mx}$**)**
24. Select the current best using
25. Generate new location using (15)
26. Verity Seasonal Monitoring Condition using (16) (17)
27. $\boldsymbol{if}(ZS < ZS_{min})$**then**
28. Relocate the search space
29. $Iter = Iter$ **+1**
30. go to step 23
31. **Else**
32. Find the optimal weight
33. **End if**
34. **End while**
35. Obtain the final classification results using (18) (19) with softmax activation function **at output layer**

End

Algorithm 1 outlines the process for predicting different types of thyroid diseases with minimal time consumption. For each input data sample, weights and biases are assigned to the visible layer of the deep belief network (DBN) architecture. The input is then transferred to the neurons in the hidden layer, where data preprocessing is performed to handle missing values within the dataset. Next, significant features are selected in the subsequent hidden layer. Classification is carried out in third hidden layer using the Sokal–Michener's simple matching method to compare training and testing data samples. Based on this similarity, different types of thyroid diseases are classified. After classification, a fine-tuning process is performed using the Squirrel Search optimization algorithm. Initially, the number of weights is determined, and a population of squirrels (representing the weights) is initialized within the search space. The fitness of each squirrel is computed based on the classification error. The position of each squirrel is then updated iteratively. This process continues until the maximum number of iterations is reached. Through this iterative approach, the Squirrel Search algorithm identifies the optimal weight values that minimize the classification error. Finally, the prediction outcomes are determined by minimizing the classification error at the output layer.

4. Experimental Settings

In this section, experimental evaluation of the proposed, SSGODBNC and two existing methods DSHM [1] and Stacked Ensemble with IG feature selection [2] are implemented in Python high-level general-purpose programming language. In order to conduct the experiment, Thyroid disease dataset is applied and it taken from the https://www.kaggle.com/datasets/emmanuelfwerr/thyroid-disease-data. This step ensures that sufficient information is available to train and validate the model

effectively. The dataset consists of 9172 instances or records or data samples and 31 attributes or features for accurate thyroid disease prediction.

5. Performance Comparative Analysis

In this section, the performance of the proposed SSGODBNC and two existing methods DSHM[1] and Stacked Ensemble with IG feature selection [2] are analyzed using various metrics, such as accuracy, precision, recall, F1 score, Specificity and thyroid disease prediction time across different data samples are discussed with the help of table and graphical representation.

Accuracy: Accuracy in thyroid disease prediction refers to the measure of correctly a model predicts the thyroid diseases based on input data samples. Mathematically, it is calculated as the ratio of the number of correct predictions (true positives and true negatives) to the total number of predictions (including false positives and false negatives).

$$Acc = \frac{TP+TN}{TP+TN+FP+F} \quad (20)$$

Where, accuracy 'Acc' is measured based on the true positive rate (TP), which reflects the number of diseased samples correctly predicted as diseased, the false positive rate (FP), representing non-diseased samples incorrectly predicted as diseased, the false negative rate (FN), indicating diseased samples incorrectly predicted as non-diseased, and the true negative rate (TN), which denotes the correct identification of non-diseased samples as negative.

Precision: it is a measure of the accuracy of positive predictions made by the model. It is defined as the ratio of true positive predictions (TP) to the total number of predicted positive instances, which includes both true positives (TP) and false positives (FP). Mathematically, precision is expressed as follows,

$$Pre = \frac{TP}{TP+FP} \quad (21)$$

Where, precision 'Pre' is measured based on the true positive rate (TP), which reflects the number of diseased samples correctly predicted as diseased, the false positive rate (FP).

Recall:it, also known as the sensitivity, measures the model's ability to correctly identify positive instances. It is the ratio of true positive predictions (TP) to the total number of actual positive instances, including both true positives (TP) and false negatives (FN). Mathematically, recall is expressed as follows,

$$Rec = \frac{TP}{TP+FN} \quad (22)$$

Where recall 'Rec' are measured based on the true positive rate (disease sample instances predicted as diseased) 'TP', FN'denotes a false negative rate (diseased sample instances predicted as non diseased)

F1 score: it is the harmonic mean of precision and recall, providing a single metric that balances both concerns. The F1 score is calculated using the following formula:

$$F1\ score = 2 * \left[\frac{Pre*Rec}{Pre+R}\right] \quad (23)$$

Where, Pre denotes a precision, Rec' indicates a recall .

Specificity: it measures the proportion of actual negative cases that are correctly identified as negative by the model. Mathematically, specificity is expressed as follows,

$$Specificity = \frac{TN}{TN+FP} \quad (24)$$

Where, the false negative rate (FN), indicating diseased samples incorrectly predicted as non-diseased, and the false positive rate (FP), representing non-diseased samples incorrectly predicted as diseased.

T**raining time:** it is the amount of time taken by algorithm for thyroid disease prediction. The training time is mathematically represented as given below.

$$TT = \sum_{i=1}^{n} S_i * Time\ (TDP) \quad (25)$$

Where, training time 'TT', is measured based on the samples considered for simulation 'S_i' and the time consumed in thyroid disease prediction '$Time\ (TDP)$'. It is measured in terms of milliseconds (ms).

Table 1: Comparison of Accuracy

Number of data samples	Accuracy (%)		
	SSGODBNC	DSHM	Stacked Ensemble with IG feature selection

900	97.22	93.55	91.66
1800	96.45	91.32	88.52
2700	95.05	89.05	86.23
3600	93.56	89.26	85.12
4500	94.56	90.05	86.32
5400	97.05	91.45	87.05
6300	96.45	90.45	87.56
7200	95.12	91.36	88.46
8100	94.56	87.56	85.56
9000	96.45	89.05	87.78

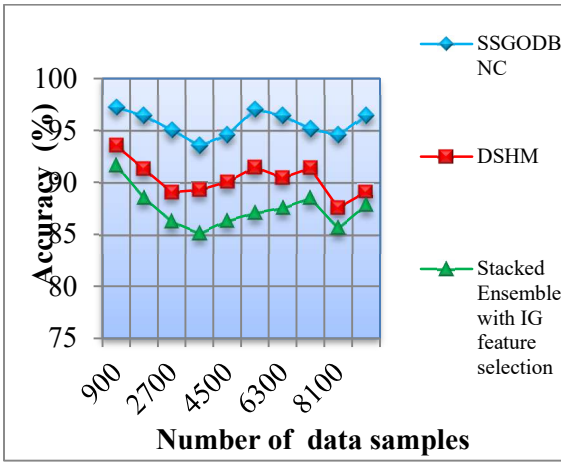

Figure 4: Graphical Results of Accuracy

Figure 4 illustrates the accuracy of thyroid disease prediction results achieved by three methods namely SSGODBNC model and two existing methods DSHM[1] and Stacked Ensemble with IG feature selection [2]. The horizontal axis represents the number of data samples, ranging from 900 to 9000, while the vertical axis depicts the prediction accuracy. The SSGODBNC model demonstrates obviously higher accuracy compared to the other approaches. For instance, in the first iteration with 900 samples, the SSGODBNC model achieved an accuracy of 97.22%, outperforming the existing models [1] and [2], which recorded accuracies of 93.55% and 91.66%, respectively. Ten dissimilar results were generated for each method by varying the number of input data samples, allowing a comprehensive comparison of their performance. The comparative analysis exposes that the SSGODBNC model outperformed [1] and [2] by 6% and 9%, respectively. This improvement is achieved due to the proposed deep belief network, which analyzes training and testing data samples using Sokal–Michener's simple matching method. This approach enhances classification accuracy by effectively distinguishing between different types of thyroid cancer. Furthermore, the fine-tuning process of the SSGODBNC model, utilizing the squirrel search optimization algorithm, reduces the classification error rate. This results in minimized false positives and false negatives, while significantly improving the true positive and true negative rates. Consequently, the accuracy of the SSGODBNC model is greatly enhanced for thyroid disease prediction.

Table 2: Comparison of Precision

Number of data samples	Precision		
	SSGODBNC	DSHM	Stacked Ensemble with IG feature selection
900	0.975	0.95	0.933
1800	0.965	0.932	0.921
2700	0.961	0.918	0.908
3600	0.955	0.916	0.895
4500	0.966	0.922	0.887
5400	0.958	0.927	0.896
6300	0.967	0.932	0.907
7200	0.966	0.935	0.906
8100	0.963	0.937	0.911
9000	0.967	0.928	0.909

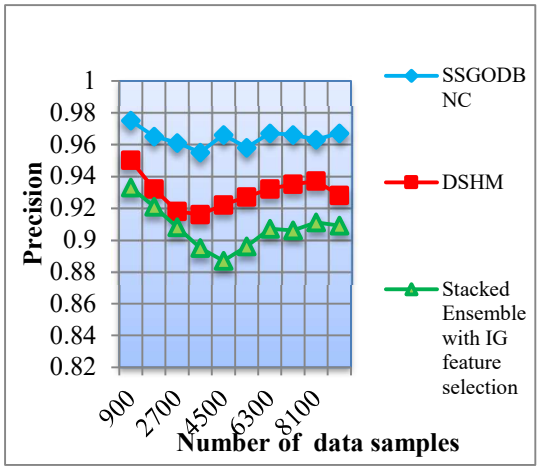

Figure 5: Graphical Results of Precision

Figure 5 illustrates the graphical illustration of precision in relation to the number of data samples, which range from 9000 to 9000. Three methods were evaluated namely SSGODBNC model and two existing methods DSHM[1] and Stacked Ensemble with IG feature selection [2], to evaluate precision during thyroid disease prediction. The horizontal axis represents the data sample count, while the vertical axis indicates precision performance. The experimental findings reveal that the SSGODBNC model consistently achieved superior precision compared to the other two approaches. For instance, with 900 samples from the dataset, the SSGODBNC model recorded a precision of 0.975, outperforming [1] and [2], which achieved precisions of 0.95 and 0.933, respectively. A range of precision results were observed for all three methods with varying data sample, enabling a comprehensive comparison. The overall analysis indicates that the SSGODBNC model improved precision by 4% over [1] and 6% over [2] in accurately identifying different types of thyroid disease conditions. This enhanced performance is achieved to the use of a Deep Belief Network for analyzing training and testing samples which maximizing the true positive rate. Furthermore, the integration of the Squirrel Search Optimization Algorithm reduces classification errors, thereby enhancing accuracy by minimizing false positives. As a result, the SSGODBNC model outperforms existing methods by achieving higher precision.

Table 3: Comparison of Recall

Number of data samples	Recall		
	SSGODBNC	DSHM	Stacked Ensemble with IG feature selection
900	0.983	0.953	0.941
1800	0.975	0.937	0.924
2700	0.967	0.92	0.911
3600	0.96	0.918	0.907
4500	0.972	0.93	0.912
5400	0.968	0.929	0.908
6300	0.973	0.933	0.913
7200	0.975	0.936	0.912
8100	0.969	0.941	0.923
9000	0.972	0.931	0.918

Figure 6 provide a graphical representation of the graphical outcomes of recall with respect to number of data samples, ranging from 900 to 9000 for three methods namely the SSGODBNC model, DSHM [1] and Stacked Ensemble with IG feature selection [2]. The horizontal axis denotes the number of samples, while the vertical axis represents recall performance. The SSGODBNC model, exhibits relatively higher performance in achieving recall than [1] and [2], as shown through statistical analysis.

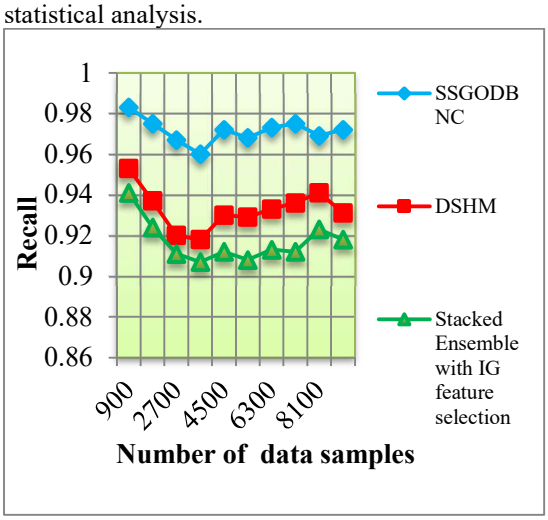

Figure 6: Graphical Results of Recall

For first run, with 900 samples, the SSGODBNC model, achieved a recall performance of 0.983, whiles the existing methods [1] and [2] were achieved to be 0.953 and 0.941, respectively. Comparing the SSGODBNC model, with the existing methods, the recall performance is significantly improved by 4% and 6% over [1] and [2], respectively. The proposed deep belief network model reduces the squared difference between the actual and predicted disease classification outputs by applying squirrel search optimization to determine the optimal weights for training the layers. This process is repeated until a minimal error rate is achieved, thereby minimizing the false-negative rates in thyroid disease prediction.

Table 4: Comparison of F1score

Number of data samples	F1score (%)		
	SSGODBNC	DSHM	Stacked Ensemble with IG feature selection
900	0.978	0.951	0.936
1800	0.969	0.934	0.922
2700	0.963	0.918	0.909
3600	0.957	0.916	0.900
4500	0.968	0.925	0.899

5400		0.962	0.927	0.901
6300		0.969	0.932	0.909
7200		0.970	0.935	0.908
8100		0.965	0.938	0.916
9000		0.969	0.929	0.913

5400	0.935	0.875	0.856
6300	0.945	0.875	0.853
7200	0.937	0.893	0.874
8100	0.943	0.887	0.861
9000	0.936	0.892	0.872

igure 7 presents the experimental analysis of the F1-score across a sample range of 900 to 9000. The results indicate that the proposed SSGODBNC model considerably improved F1-score performance.

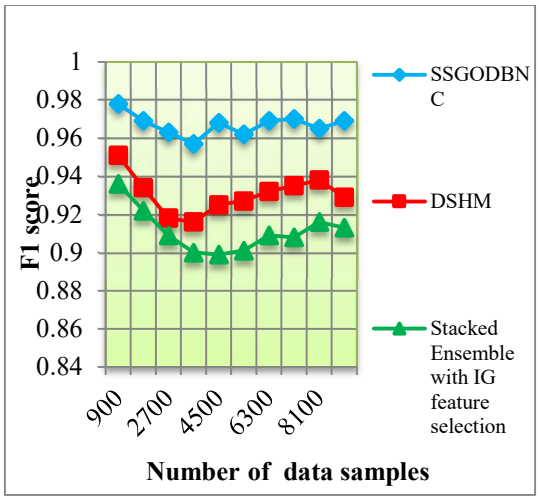

Figure 7: Graphical Results of F1 Score

For instance, with 900 samples in the first run, the SSGODBNC model achieved an F1-score of 0.978, outperforming the methods [1] and [2], which recorded F1-scores of 0.951 and 0.936, respectively. This analysis highlights that the SSGODBNC model achieved superior performance in thyroid disease prediction. On average, across ten comparisons, the SSGODBNC model improved the F1-score by approximately 4% and 6% compared to methods [1] and [2], respectively. This improvement is attributed to the SSGODBNC model ability to enhance both precision and recall in thyroid disease prediction.

Table 5: Comparison of Specificity

Number of data samples	Specificity		
	SSGODBNC	DSHM	Stacked Ensemble with IG feature selection
900	0.949	0.9	0.866
1800	0.942	0.895	0.862
2700	0.94	0.892	0.858
3600	0.937	0.885	0.855
4500	0.933	0.883	0.863

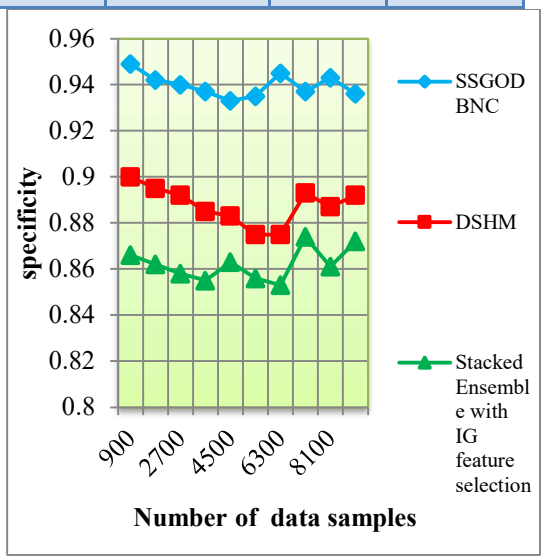

Figure 8: Graphical Results of Specificity

Figure 8 exhibits the performance results of the specificity using three methods namely SSGODBNC model, DSHM [1] and Stacked Ensemble with IG feature selection [2]. The specificity performance results were evaluated based on number of samples. It is evident from these results that the SSGODBNC model outperforms the existing methods in terms of achieving higher specificity. The application of the SSGODBNC model improves the specificity in the thyroid disease prediction. This improvement is achieved to the effective application of the deep learning classifier, which directs to a higher specificity. Overall, the performance results demonstrate that the specificity of the SSGODBNC model is enhanced by 6% compared to [1] and by 9% compared to [2].

Table 6: Comparison of Training Time

Number of data samples	Training time (%)		
	SSGODBNC	DSHM	Stacked Ensemble with IG feature selection
900	27	34.2	38.7
1800	28.23	47.25	52.32
2700	35.52	53.65	60.41
3600	48.32	65.56	72.04
4500	52.56	80.06	88.42

5400	70.23	88.34	93.05
6300	78.45	98.05	105.41
7200	83.56	112.56	120.05
8100	99.45	118.04	127.56
9000	108.52	130.45	138.65

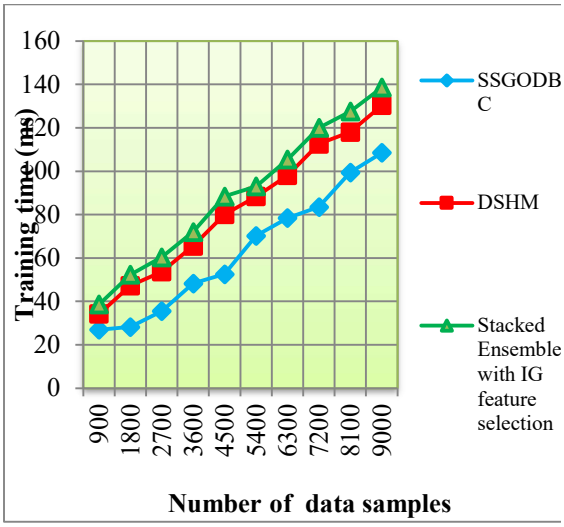

Figure 9: Graphical Results of Training Time

Figure 9 highlights the training time performance relative to the number of data samples. As the number of samples increases, the overall training time also increased. However, the SSGODBNC model demonstrates lower training times compared to other existing techniques. For experimentation with 900 data samples, the training time for SSGODBNC model was recorded as $27ms$, whereas the existing [1] and [2] methods required $34.2ms$ and $38.7ms$, respectively. Different volumes of input data samples provided better performance across all three approaches. The results indicate that the SSGODBNC model achieved a significant reduction in training time by 25% and 32% compared to [1] and [2], respectively. This reduction is achieved through the integration of data preprocessing within the hidden layers of the deep belief network architecture. Additionally, the automatic feature selection operations of the SSGODBNC model identify significant features while eliminating irrelevant ones. With the selected significant features, classification is performed, resulting in enhanced thyroid disease prediction while optimizing time efficiency.

6. Conclusion

The thyroid gland is a vital organ in the human body responsible for regulating metabolic processes. An imbalance in thyroid hormone production leads to various health issues. Therefore, early detection of thyroid disease is crucial for effective management and treatment. In this paper, a novel deep learning model called SSGODBNC has been developed to enhance thyroid disease prediction accuracy while minimizing time consumption. The proposed SSGODBNC model incorporates data preprocessing and feature selection within the hidden layer of the deep learning architecture, effectively reducing the time required for thyroid disease prediction. With the selection of significant features, the classification process is performed to predict different types of thyroid diseases. Additionally, the hyperparameter optimization process reduces the error rate in thyroid disease prediction.

An experimental evaluation was conducted to assess the performance of the SSGODBNC model and compare it with conventional methods using various metrics, including accuracy, precision, recall, F1 score, specificity, and training time. The results demonstrate that the proposed SSGODBNC model significantly outperforms conventional methods, showing notable improvements in accuracy, precision, recall, F1 score, and specificity. Furthermore, the SSGODBNC model reduces the training time for thyroid disease prediction compared to traditional approaches. The comparative analysis for strengths are involves the robust to perceive early diseases detection, personalize treatment plans, and improves the diagnostic accuracy compared to existing methods, mainly when collective with advanced techniques like feature selection and classification. The weakness of their proposed work is overfit the training data, to reduce the performance on novel data and scalability as well as integration with different existing healthcare systems can be difficult.

The limitations of their proposed method using DBNs comprise the issues with dataset size and generalizability and require to focus on specific disease types, prevalence of imbalanced datasets. Moreover, a need to importance on model tuning and traditional tuning inefficiencies hinder performance. In addition, the deep learning models can limit their acceptance with healthcare systems.

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