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A DEEP TREE LIQUID STATE AND GREEDY STACKED AUTOENCODER FRAMEWORK FOR THYROID DISEASE PREDICTION

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ABSTRACT

Thyroid disease is a medical state of affairs in which the thyroid gland potentiality to be in action is affected. The thyroid gland being an endocrine organ positioned in front of neck that induces thyroid hormones and advances via the bloodstream to aid control a variety of other organs. On one hand when body induces too much thyroid hormone, hyperthyroidism is said to be developed whereas on the other hand insufficient hormone production results in hypothyroidism. Deep Learning (DL) algorithms, though analyze data in an automatic manner and constructing analytical models according to DL can also be utilized for thyroid disease diagnosis. Feature extraction is essential in DL to improve efficiency where features are extraction based on their significance. It means that the most important elements of the DL model have been extracted for prediction by discarding irrelevant features that have nothing to do with the disease prediction. In this work a method called Deep Tree Liquid State and Greedy Stacked Autoencoders (DTLS-GSA) based feature extraction for thyroid disease prediction. The DTLS-GSA based feature extraction for thyroid disease prediction is split into two sections, namely, efficient data handling and feature extraction. First, data handling employs thyroid raw datasets are performed using Deep Tree Liquid State Machine based architecture. The objective of employing the Deep Tree Liquid State Machine is the potential in handling data that are highly skewed without the loss of original information. Second, with efficient handling of data, Greedy Layerwise-Stacked Denoising Sparse Autoencoders is applied to extract the features required for thyroid disease detection. Also hereby employing both forward propagation (i.e., inputting sample instances) and backward propagation (i.e., fine tuning weights) therefore minimizes loss function convergence at an early stage, therefore improving overall precision and recall rate of extracted features. Experimental evaluation will be carried out using Thyroid Disease dataset with different factors such as, precision, recall, accuracy and training time.

Keywords: *Thyroid Disease Prediction, Deep Learning, Deep Tree Liquid State Machine, Greedy Layerwise, Stacked Denoising, Sparse Autoencoders*

I. INTRODUCTION

Thyroid disorder is regarded one of the frequent endocrine ailment issues globally. Thyroid disorder is one of the vital origins of heart disease, obesity, joint pain and infertility. Nevertheless, these thyroid diseases emanate at later stages, however some of the indications may also occur at an early stage. The thyroid hormone is accountable for thyroid disorder that may cause hypothyroidism or hyperthyroidism issues. Some of the tests conducted to diagnose the functioning of thyroid hormone is T3 (Triodothyronine), T4 (Thyroxine), TSH (Thyroid Stimulating Hormone) and Free Thyroxine (FT4). Nevertheless, manual analysis of these criterions for prediction and diagnosis is both laborious and time consuming.

This study on thyroid disease prediction focuses specifically on the development and evaluation of machine learning models for this purpose, rather than on new clinical testing methods. The scope is further delimited to the use of patient data—including clinical features like hormone levels (TSH, T3, T4), patient demographics (age, sex), and other symptoms—to build a predictive model. The research addresses persistent issues in existing computational approaches, such as limitations related to small datasets, data imbalance, and a lack of comparative analysis across different machine learning and deep learning algorithms.

In [1], DL-based Artificial Neural Network (ANN) was designed to construct predictive models, for dealing with text data with the objective of predicting hypo-thyroidism. The thyroid prediction employing DL-based ANN manifested both thyroid prediction and classification in four classes, namely primary hypothyroidism, secondary hypothyroidism, negative class and compensated hypothyroidism class respectively. The application of DL-based ANN for thyroid prediction shows thyroid prediction and classification in four classes namely negative class, compensated hypothyroidism class, primary hypothyroidism and secondary hypothyroidism with highest accuracy and few error rates. Though improvements were observed in terms of accuracy with few error rates, however, with features in the dataset being highly skewed, the training time involved in thyroid prediction was not focused.

In [2], Deep Neural Network for ensuring accurate thyroid disease prediction with dimension reduction techniques and reduced dimension data input to classifiers was proposed. In addition, data augmentation was also applied with the intent of generating adequate data for deep neural network model. In addition, using data augmentation using Gaussian distribution aided in generating sufficient data for deep neural network model with high accuracy of disease prediction. Despite improvements observed in terms of accuracy, however the measure of quality and measure of quantity were not made in an efficient manner for thyroid disease prediction.

Hyperthyroidism and hypothyroidism that have a high rate of incidence and misclassified diagnosis rate are said to be endocrine diseases arise due to abnormal thyroid hormone secretion and that in turn results in series repercussions. In [3] serum raman spectroscopy was combined with deep neural network with the intent of analyzing both hypothyroidism and hyperthyroidism in an accurate and precise manner.

Several research persons have designed numerous materials and methods for thyroid disease diagnosis. Aiming to provide solutions towards such disease, dimensionality reduction techniques was applied in [4] via deep neural network model to ensure high accuracy. However, in case of complicated data environments, correct handling of data is said to be pivotal for enhancing disease prediction rate. To this end, an information mining method employing association rule with dynamic threshold and weight optimization was proposed in [5] for early diagnosis of thyroid cancer. Though several research works have been focused for the employment of machine learning techniques for thyroid disease detection, however, robustness is said to be restricted by data imbalance nature. To address on this aspect, feature selection model employing filtering technique and stacking-based ensemble was presented in [6] for thyroid disease detection.

A review of machine learning technique for early thyroid disease prediction was proposed in [7] based on efficient feature selection model. Thyroid issues are becoming more and more prevalent and early detection only remains to be one of the solutions that in turn minimizes rate of mortality and complications. Owing to these different factors, early detection of thyroid has become more pivotal in the medical domain. Also evaluating the frequency and severity of disease are hence found to be critical for medical diagnosis and treatment.

Laboratory parameters pertinent of functioning of thyroid in addition to demographic features, with the objective of uncovering prospective correlations between thyroid function and metabolic phenotypes employing numerous machine learning methods was investigated in [8]. Yet another machine learning technique employing random forest classifier was presented in [9] to focus on the computational and space complexity aspects involved in prediction.

A thorough investigation of thyroid disease prediction in China along with prospective and retrospective was investigated in [10]. Nevertheless, machine learning techniques have ensured in detecting risk parameters for the thyroid disease. Five machine learning techniques were employed in [11] and the best features relevant to disease detection was selected via ensemble ML classifier technique. By employing this ensemble technique resulted in the accurate and precise detection of disease. Yet another ensemble method was proposed in [12] to focus on the precision and accuracy factor involved in thyroid disease prediction.

The problem is to develop an accurate, efficient, and automated system for predicting thyroid disease due to the increasing prevalence, complexity of diagnosis, and the potential for human error in manual analysis. Existing methods rely on time-consuming and sometimes ambiguous blood test results, and experienced doctors are needed for correct interpretation, highlighting the need for a machine learning-based approach to support early and precise diagnosis and reduce the workload on healthcare professionals.

1.1 Scope of the proposed work

The scope of thyroid disease prediction is huge, with its main focus being on early and accurate diagnosis using ML and big data analytics to enhance the patient results. It involves the classifying conditions such as, hyperthyroidism and hypothyroidism, and in cases like thyroid nodules, predicting the likelihood of malignancy. The field offers opportunities for increasing predictive models, creating accessible applications for risk assessment, and improving diagnostic tools to minimize the errors and avoid severe complications. In order to, DTLS-GSA) based feature extraction for thyroid disease prediction is introduced to enhance the precision, recall, accuracy with lesser time.

1.2 Novelty of the proposed contribution of this method

The novel contribution of the proposed DTLS-GSA method is utilized into thyroid disease prediction is listed in below

- A novelty of the Deep Tree Liquid State Machine is used to data handling employing thyroid raw dataset
- Greedy Layerwise-Stacked Denoising Sparse Autoencoder-based Feature Extraction algorithm is employed to extract the features with efficient handling of data.
- Obtain each forward propagation and backward propagation achieved to reduce the loss function convergence at an early stage, therefore improve the overall precision and recall rate of extracted features.

1.3 Contributing remarks

The contributions of the Deep Tree Liquid State and Greedy Stacked Autoencoders (DTLS-GSA) based feature extraction for thyroid disease prediction is listed as given below.

- To improve the precision, recall, accuracy and training time, the DTLS-GSA method is designed based on two major processes namely data handling and feature extraction.
- To reduce the training time, Deep Tree Liquid State Machine-based Data Handling algorithm is employed.
- To enhance precision and recall of thyroid disease prediction based on extracted features, Greedy Layerwise-Stacked Denoising Sparse Autoencoder-based Feature Extraction algorithm is applied to the data handled sample instances.
- To design forward propagation to extract significant features and backward propagation process to eliminate insignificant features ensures accurate extractions of features and therefore improving the overall thyroid disease prediction results.
- Finally, comprehensive experimental assessment is carried out with four distinct performance metrics, precision, recall, accuracy and training time to illustrate the proposed DTLS-GSA method over traditional methods.

1.4 Organization of the work

The rest of the paper is ordered as follows. Section 2 portrays the related works in the field of thyroid disease detection based on the features being extracted from the raw dataset. In Section 3 the proposed method, Deep Tree Liquid State and Greedy Stacked Autoencoders (DTLS-GSA) based feature extraction for thyroid disease is detailed with the aid of pseudo code representation. Section 4 provides the experimental setup and discussion followed by concluding remark in Section 5.

2. RELATED WORKS

Thyroid illnesses and disorders are extensive hormonal problems that exert influence on the major part world's population globally, to name a few being, thyroiditis and thyroid malignancy. In [13] to boost the diagnostic performance of nuclear medicine physicians' deep convolutional neural network (DCNN) model and following which the results were validated for thyroid disease by employing single-photon emission computed tomography (SPECT) image data. Empirical method using decision tree, random forest and artificial neural network for thyroid disease detection was presented in [14] with the intent of improving specificity and accuracy in an extensive manner.

Over the past few years, the utilization of artificial intelligence (AI) methods in health care domains has increased swiftly. In this context, early detection of diseases is the most common area of application. In this circumstance, thyroid diseases are an example of illnesses that can be efficiently looks on to if bring to light quite timely. Thyroid disease detection is pivotal with the intent of treating patients efficiently and rapidly by saving lives and minimizing healthcare costs.

Semi supervised machine learning techniques for predicting thyroid disease via logistic regression was presented in [15] employing FixMatch, Co-training and self-training. This in turn eases and boosted healthcare repercussions. An experimental comparative study on application of machine learning algorithms for thyroid disease risk prediction was investigated in [16]. A systematic review on artificial intelligence techniques for early thyroid disease detection was presented in [17].

Thyroid disease has been on the upswing in the course of past few years. As a consequence of its significance in metabolism, early thyroid disease detection is a mission of critical significance. In spite of numerous existing methods on thyroid disease detection, the issues of class imbalance were not investigated very well. To increase prediction accuracy for thyroid disease dimension reduction technique was applied in [18].

In spite of several existing methods on detecting thyroid disease the issue class imbalance was not investigated magnificently. Moreover, prevailing techniques for the most part concentrate on the binary-class issue. An optimization technique employing differential evolution algorithm with the objective of fine tuning the parameters using machine learning models was presented in [19] with improved accuracy. Yet another thyroid disease classification algorithm using several machine learning algorithms was designed in [20]. A combination of several scaling methods using Boruta, Recursive Feature Elimination (RFE) and Least Absolute Shrinkage and Selection Operator was presented in [21]. A detailed comprehensive review on thyroid disease prediction employing machine learning techniques was investigated in [22].

To circumvent the manual errors involved in prediction, the estimation of manual procedure consumed expertise domain and also consume a consideration amount of time. To detect disease at an early stage, a novel long short-term memory in addition to convolution neural network was used in [23]. With this type of heterogeneous mechanism resulted in the improvement of precision, recall, sensitivity and accuracy.

A plethora of machine learning technique for thyroid disease detection was presented in [24]. Distinct machine learning classification techniques [25] to name a few being, decision tree, random forest, logistic regression and naïve bayes were employed for classification of hyper and hypo thyroidism in an extensive manner.

With the scaling of medical data swiftly growing and also these data coming from distinct sources of data and also the amount of data being huge and the production speed being fast and different, knowledge graph technology was applied in [26] to assist in disease diagnosis. An in-depth analysis of machine learning techniques for classifying different types of thyroid disease was presented in [27]. Three different machine learning algorithms, support vector machine, naïve bayes and random forest were applied in [28] to focus on the computational complexity aspects. Yet another ensemble method for predicting thyroid disease was presented in [29] to focus on macro precision and macro recall. Selective features and machine learning technique for early disease prediction with improved precision and recall was proposed in [30].

Deep Transfer Learning was introduced in [31] for the precise diagnosis of thyroid nodules. But the time was higher. A residual and dilated convolution neural network (RED-Net) was employed in [33] for estimating the thyroid volume. But the huge dataset was not considered. A novel deep learning architecture was developed in [32] to perform thyroid segmentation with the Tri Attribute Hybrid Algorithm (TATHA). However, the accuracy was not enhanced. Deep learning methods were examined in [34] to find thyroid illnesses at an early stage. However, it failed to enhance the accuracy. Gaussian Process Regression was developed in [35] for a higher confidence level. Deep convolutional networks (DCNN) were designed in [36] for dissimilar classification methods. Also, the significant features were learned via networks to classify the characters. However, the precision was not concentrated.

Based on the above two traditional methods, DL-based ANN [1] and Deep Neural Network [2] for thyroid disease prediction detected disease with accuracy and minimal error rate, however the training time along with precision, recall involved were not concentrated. To address on this research gap, Deep Tree Liquid State and Greedy Stacked Autoencoders (DTLS-GSA) based feature extraction for thyroid disease prediction is

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proposed that with the aid of Deep Tree Liquid State Machine algorithm, keyword extraction can be performed in a computationally efficient manner. Also using Greedy Layer wise-Stacked Denoising Sparse Autoencoders the precision and recall can also be improved significantly. By employing Deep Tree Liquid State and Greedy Stacked Autoencoders (DTLS-GSA) based feature extraction for thyroid disease prediction not only minimizes training time and improves overall precision and recall involved in extracted features for thyroid disease prediction.

Motivated by the above research gaps, in this work, Deep Tree Liquid State and Greedy Stacked Autoencoders (DTLS-GSA) based feature extraction for thyroid disease prediction and Greedy Layerwise-Stacked Denoising Sparse Autoencoders are proposed to improve the precision as well as recall in a significant manner.

3.METHODOLOGY

Deep Learning (DL) has become a paramount part of human lives that bestows smart and reasonable solutions to several issues. By and of itself, healthcare is grabbing the consciousness of several research persons, as society depends upon healthy and performing individuals for its balanced functioning. This study targets at imparting solution with regard to such a thyroid disease prediction using a method called, Deep Tree Liquid State and Greedy Stacked Autoencoders (DTLS-GSA) based feature extraction for thyroid disease prediction. Figure 1 illustrates the block diagram of DTLS-GSA method.

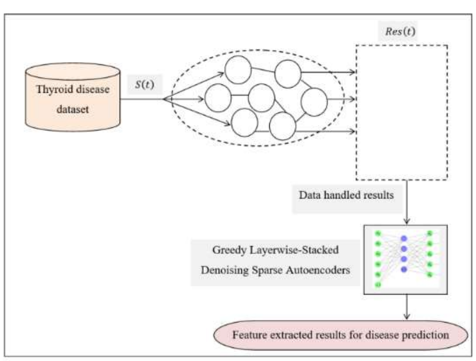

Figure 1 : Block diagram of Deep Tree Liquid State and Greedy Stacked Auto encoders (DTLS-GSA) based feature extraction for thyroid disease prediction

As shown in the above Figure 1, the DTLS-GSA based feature extraction for thyroid disease prediction is split into two sections. They are data handling and feature extraction. Also as given above the feature extraction for disease prediction employs thyroid disease dataset obtained from https://www.kaggle.com/datasets/emmanuelfwerr/thyroid-disease-data.

First, data handling using thyroid disease dataset is subjected to Deep Tree Liquid State Machine based architecture. The purpose behind the use of Deep Tree Liquid State Machine is handling highly skewed data to represent correlation between different features without loss of original information. Second with efficient handling of data, Greedy Layerwise-Stacked Denoising Sparse Autoencoders is applied with the intent of extracting features required for thyroid disease detection.

Finally, to ensure optimized results Greedy Layerwise-Stacked Denoising Sparse Autoencoders is introduced to build robust thyroid detection model using both forward propagation and backward propagation therefore minimizing loss function convergence at an early stage with improved precision and recall rate of extracted features.

3.1 Dataset description

The dataset created for our study are obtained from Thyroid disease dataset extracted via UCI Machine Learning Repository featuring both real and categorical data type by reconciling 10 separate databases from Garavan Institute from Health and Medicine domain. The dataset contains 9172 sample observations and each sample is denoted by 31 features. The size for the Thyroid disease dataset file featured within the Kaggle is provided below along with a list of features or attributes and their description summaries.

Table 1 : Thyroid disease dataset description summaries

S. No	Features or attributes	S. No	Features or attributes
1	Age	17	TSH_measured
2	Sex	18	TSH
3	On thyroxine	19	T3_measured
4	Query on thyroxine	20	T3
5	On antithyroid meds	21	TT4_measured
6	Sick	22	TT4
7	Pregnant	23	T4U_measured
8	Thyroid surgery	24	T4U
9	1131 treatment	25	FT1_measured
10	Query hypothyroid	26	FT1
11	Query hyperthyroid	27	TBG_measured
12	Lithium	28	TBG
13	Goitre	29	Referral_source
14	Tumor	30	Target

15	Hypopituitary	31	Patient ID
16	Psych		

The target prediction comprises of health conditions and diagnosis classes. The significance of the features has to be evaluated for selecting optimum number of features for thyroid disease classification via efficient data handling. As listed in the above table 1, the 31 features consist of float, integer, string and Boolean types. The feature-based analysis is initially performed using Deep Tree Liquid State Machine-based Data Handling to estimate the importance of the features. As described in the proposed methodology subsection, the data handling yield the correlation between different features without the loss of the original information. Table 2 given below lists the dataset containing 9173 patient records. Here, 6771 patient records were found to be normal patient records with no sign of thyroid disease, 233 patient records were found to be primary hypothyroid, 359 patient records were found to be compensated hypothyroid patients, 346 patients were found with increasing binding proteins and finally, 456 concurrent non-thyroidal illness patients.

Table 2: Class-wise target description

S. No	Patient records (diagnosis class)	Count
1	Normal patient records	6771
2	Primary hypothyroid patient records	233
3	Compensated hypothyroid patient records	359
4	Increasing binding protein patient records	346
5	Concurrent non-thyroidal illness patient records	456
6	Others	1008
	Total	9173

Incorrect diagnosis may result in erroneous medication and further difficulties. Hence, an automated method can be very considerate to aid medical experts in making automated thyroid disease predictions without any human mistakes. So this study follows a deep learning approach method called Deep Tree Liquid State and Greedy Stacked Autoencoders (DTLS-GSA) based feature extraction for thyroid disease prediction.

3.2 Deep tree liquid state machine-based data handling

Data Handling is the process of collecting, putting down and dispensing information in a manner that is considerate in analyzing, making predictions and possible course of actions. Due to the uneven distribution of sample instances across nodes influence the performance of parallel data processing resulting in consuming time for certain tasks than the others. Also, data handling is paramount for healthcare parallel data processing to make early decisions, rationalize processes and cohere to standards. In this work a model called, Deep Tree Liquid State Machine-based architecture for Data Handling is presented using thyroid raw dataset. The objective of employing the Deep Tree Liquid State Machine is the potentiality in handling data that are highly skewed with minimal loss of original information from dataset. The Deep Tree Liquid State Machine structure is appropriate to represent the correlation between different features that in turn prevents loss of temporal features of data without loss of original information. Figure 2 shows the structure of Deep Tree Liquid State Machine-based architecture for Data Handling.

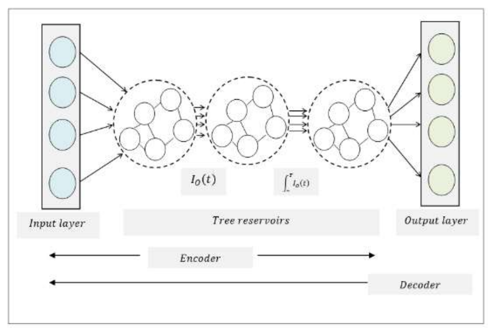

Figure 2 : Structure for Deep Tree Liquid State Machine-based architecture for Data Handling

As shown in the above Figure the Deep Tree Liquid State Machine-based architecture for Data Handling is split into two parts, encoder and decoder. On one hand encoder is performed via tree reservoirs using the sample instances from the input dataset. On the other hand decoder is done in the reverse side with the intention of handling data in an efficient manner. A standardized database permits all the sample instances to be clustered in a consistent space to conduct the necessitated processing steps. Hence, in this study, let '$S = \{S_1, S_2, \dots, S_N\}$' represent the medical examination data entered into dataset 'DS' and in 'S', let '$F = \{F_1, F_2, \dots, F_n\}$' represent a set containing all the features contained in the dataset and 'F_k' be one of the highly skewed resultant feature for a sample instance. In addition, let 'Res' be the corresponding target feature variable (i.e. the data handled result for that data piece). Then, '$Res = \{Res_1, Res_2, \dots, Res_l\}$' is a set containing all target variables and hence the input vector is mathematically represented as given below.

$$IV = \begin{bmatrix} S_1F_1 & S_1F_2 & \dots & S_1F_n \\ S_2F_1 & S_2F_2 & \dots & S_2F_n \\ \dots & \dots & \dots & \dots \\ S_NF_1 & S_NF_2 & \dots & S_NF_n \end{bmatrix} \quad (1)$$

From the above equation (1) the input vector 'IV' for data handling using thyroid raw dataset is formulated employing 'N' samples 'S_N' and 'n' features 'F_n'. The Deep Tree Liquid State Machine being a recurrent neural network, the associations between neurons define dynamic process and recurrence associations refer to the topology. The properties of artificial neurons (i.e. sample instances 'S') along with these recurrence associations (i.e., samples with respect to corresponding features 'S_NF_n') result in transforming any sequence of input into a spatiotemporal pattern activation of liquid.

The nomenclature come from probability of looking at the Deep Tree Liquid State Machine based recurrent neural network as a liquid like water in a pond (i.e. as a feature set like samples in a dataset), the stimuli are rocks thrown into the water (i.e. stimuli are the testing data from dataset for prediction) and the ripples on the pond (i.e. features in the dataset) are the spatiotemporal pattern.

The employment of a detector is conventional in the standard in the Deep Tree Liquid State Machine community where the idea behind the detectors remains in testing whether the information or features to be handled for prediction resides in the liquid and thus are not required to irrelevant. Hence, it is highly possible for detectors to extract any spatiotemporal feature fed into the liquid (i.e. present as features in the dataset).

A fundamental theory of the proposed Deep Tree Liquid State Machine lies in its potentiality of carrying out real time computations by transforming time varying input stream (i.e., sample instances using input vector 'IV') into a higher dimensional space employing three pivotal elements namely, an input layer, a reservoir or liquid and a memory-les readout circuit respectively. Here, initially, the sample instances using input vector 'IV' as an input layer, the reservoir has several neurons (i.e. sample instances) associated recurrently using dynamic synaptic connections.

The readout is also implemented by several neurons but they do not possess any inter-associations within them. The reservoir or liquid transforms lower dimensional input stream (i.e., sample instances) to a higher dimensional internal state (i.e., handling of sample data in an efficient manner by correlating between different features without loss of original information). This in turn act as an input to the memory-les readout circuit that is responsible for generating the final output of the Deep Tree Liquid State Machine (i.e., computationally efficient accurate data handled results.

The Deep Tree Liquid State Machine consists of two steps that are fundamental for the processing of raw input data. In the first instance, the raw input data '$S(t)$', are transformed into a higher dimensional state. The reservoir via plastic synapse is associated to the readout in the second phase. The readout neuron at any time 't' receives from the reservoir a file featured with a list of features is given by.

$$I_O(t) = \sum W_{Oi}.f_i(t) = \sum W_{Oi}.f_i[S(t)] \quad (2)$$

From the above equation (2) '$f_i(t)$' denotes the response from the '$i-th$' neuron in the reservoir with 'W_{Oi}' representing the synapse weight between '$i-th$'reservoir and '$O-th$' readout neuron respectively. Then, the consolidated file featured with a list of feature is then mathematically formulated as given below.

$$\int_0^T I_O(t) = \sum W_{Oi} \int_0^T f_i(t) = \sum W_{Oi} \int_0^T f_i\,[S(t)] \quad (3)$$

The inference of the above mathematical formulation obtained from (3) is that the readout neuron will be taken as linear predictor of the reservoir responses as the consolidated list of features from the readout neurons, a linear combination of consolidated outputs from reservoir neurons.

The readout neurons obtain generated computationally-efficient and accurate data handled results from the reservoir and interpret in linear form using Greedy Layerwise-Stacked Denoising Sparse Autoencoder-based Feature Extraction model for early thyroid disease prediction. The reservoir being a non-linear system with a network of artificial neurons or sample instances computed recurrently. Basically, it is used to encode the non-linear transformation of input stream (i.e., sample instances) by acquiring the past sample instances and translating into a high-dimensional activity state. On the other hand, the readout or the decoder retrieves the temporal information from reservoir and transforms it to a time-series output.

$$State\ (t) = \int_0^T I_O(t), State(t-1) \quad (4)$$
$$Res(t) = D\big(State(t)\big) \quad (5)$$

From the above equations (4) and (5) the network state '$State$' at time 't' is generated by combining the input value of '$I_O(t)$' sample instances at current time 't' with previous state at time '$t-1$' respectively. Followed by which the detector function results are arrived at using the Segmented Regression based on the set of data '$Res\ (t), State(t)$' where 'Res' denotes dependent variable and '$State(t)$' denotes independent variable.

The Segmented Regression when applied separately to each segment results in the following two equations.

$$FRes(t) = \begin{cases} a_1 State\ (t) + \alpha_1, for\ State\ (t) < BP \\ a_2 State\ (t) + \alpha_2, for\ State\ (t) > BP \end{cases} \quad (6)$$

From the above equation (6), network state '$State$' at time 't' is generated using the current time 't' with previous state at time '$t-1$'. Also Segmented Regression function is applied between observed '$State\ (t)$' and 'a_1, a_2', 'α_1, α_2' representing the regression coefficients and regression constants respectively. Finally correlation coefficient results for handling data efficiently is applied to the network state '$State$' at time 't' to obtain the computationally efficient and accurate data handling is represented as given below.

$$R_1^2 = 1 - \frac{\sum\big(Res(t) - FRe\ (t)\big)^2}{\sum\big(Res\ (t) - avg(FRes[seg1])\big)^2}, if\ State(t) < BP \quad (7)$$

$$R_2^2 = 1 - \frac{\sum\big(Res\ (t) - FRes(t)\big)^2}{\sum\big(Res\ (t) - avg(FRes[seg2])\big)^2}, if\ State(t) > BP \quad (8)$$

From the above equations (7) and (8), '$\big(Res(t) - FRes(t)\big)^2$' denotes the minimized sum of square of differences per segment with '$avg(FRes[seg1])$' and '$avg(FRes[seg2])$' representing the average values of '$FRes$' in the respective segments. Finally by obtaining the correlation coefficient results even highly skewed data (i.e. uneven curve distribution) are said to be handled in an efficient manner. The pseudo code representation of Deep Tree Liquid State Machine-based Data Handling is given below.

Input: Dataset 'DS', Samples '$S = \{S_1, S_2, \dots, S_N\}$', Features '$F = \{F_1, F_2, \dots, F_n\}$'
Output: Computationally-efficient and accurate data handling
1: **Initialize** '$N = 9172$', '$n = 31$' 2: **Begin** 3: **For** each Dataset 'DS' with Samples 'S' and Features 'F' 4: Formulate input vector as given in (1) **//Reservoir – encode non-linear transformation of input stream** 5: Obtain file featured with a list of feature as given in (2) 6: Formulate consolidated file featured with a list of features as given in (3) //Readout – decode 7: Retrieve temporal information from reservoir and transforms it to a time-series output as given in (4) and (5) 8: Apply Segmented Regression function separately to each segment results as given in (6) 9: Obtain correlation coefficient results for accurate data handling as given in (7) and (8) 10: **Return** data handled results '$DH = R_1^2\ or\ R_2^2$' 11: **End for** 12: **End**

Algorithm 1: Deep Tree Liquid State Machine-based Data Handling

As given in the above algorithm the objective behind the design remains in ensuring even distribution of sample instances across nodes that in turn would boost parallel data processing, therefore consuming minimal execution time. With this objective, with the sample instances and features obtained from raw thyroid dataset as input are subjected to Deep Tree Liquid State Machine. The Deep Tree Liquid State Machine consisting of input layer, reservoir (hidden layer) and readout (output layer) first, obtains the sample instances along with the features in the input layer. Second in the reservoir two operations, file featured with a list of features and consolidated file featured with a list of feature are obtained. The results are then passed in the form of encoder. Finally in the decoder stage, the readout operation initially obtains temporal information from reservoir and transforms it to a time-series output. Followed by which Segmented Regression function is applied separately to each segment results with high correlation coefficient results via breaking point for efficient data handling.

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3.3 Greedy layerwise-stacked denoising sparse autoencoder-based feature extraction

Second with efficient handling of data, Greedy Layerwise-Stacked Denoising Sparse Autoencoders is applied to extract the features required for thyroid disease detection. To ensure feature extraction optimized results Greedy Layerwise-Stacked Denoising Sparse Autoencoders is introduced to build robust thyroid detection model. Though it possess only one hidden layer, in our work layer-wise stacked sparse autoencoder is applied. Also as only with the application of backward propagation to directly train layer-wise stacked sparse autoencoder cannot get desirable results, in our work, both forward propagation (i.e., inputting sample instances) and backward propagation (i.e., fine tuning weights) are applied that in turn minimizes loss function convergence at an early stage, therefore improving overall precision and recall rate of extracted features. Figure 3 shows the structure of Greedy Layerwise-Stacked Denoising Sparse Autoencoder-based Feature Extraction.

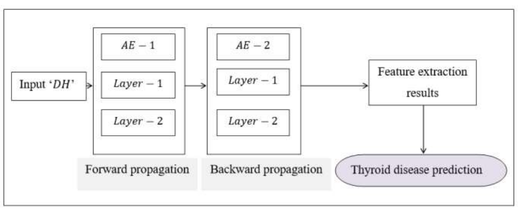

Figure 3: Structure of Greedy Layerwise-Stacked Denoising Sparse Autoencoder-based Feature Extraction

As illustrated in the above Figure , the data handled results forms the input to the Greedy Layerwise-Stacked Denoising Sparse Autoencoder-based Feature Extraction process. To obtain final extracted results it undergoes two distinct processes, namely, forward propagation and backward propagation. Let us consider we have training set '$\{(DH^{(1)}, Out^{(1)}), (DH^{(2)}, Out^{(2)}), \ldots . (DH^{(N)}, Out^{(N)})\}$' that has '$N$' data handled samples, inside '$Out^{(i)} \in \{1,2, \ldots l\}$' and '$l$' refers to the number of features being extracted to build robust thyroid detection model. Here, '$Prob(Out^{(i)} = j | DH^{(i)})$' indicates the probability when '$Out^{(i)}$'equal to 'j' given input '$DH^{(i)}$' parameters 'θ'.

Then for 'l' dimensions output vector '$h_\theta(DH^{(i)})$' the summation of elements of this resultant vector is then '1'. Then the absolute output using softmax function is written as given below.

$$h_\theta(DH^{(i)}) = \begin{bmatrix} Prob(Out^{(i)} = 1 | DH^{(i)}, \theta) \\ Prob(Out^{(i)} = 2 | DH^{(i)}, \theta) \\ \ldots \\ Prob(Out^{(i)} = l | DH^{(i)}, \theta) \end{bmatrix} \quad (9)$$

With the above obtained softmax output, both forward propagation (i.e., inputting sample instances) and backward propagation (i.e., fine tuning weights) are applied. This model is similar to forward feature extraction however when the new feature is extracted, the backward elimination process pushes it to compare with hitherto extracted features.

In our work two significance level values are determined with 'in' and 'out' of value ranges. Here '$p - value$' is used in our work so that the feature '$p - value$' should be less than the significance 'in' value to be included in the feature extraction process and greater than the significance 'out' value to be excluded in the feature extraction process. Let '$\{\emptyset\}$' denote an empty set. To start with a feature is extracted on the basis of the defined point of reference. Here, we use the forward propagation (i.e., inputting sample instances) to include the features in the list. This is written as given below.

$$Out_F = \{\emptyset\};\ Out_B = h_\theta(DH^{(i)}) \quad (10)$$

The next best feature is extracted using '$p - value$' comparison. Here, forward propagation is employed to extract the significant features. This is mathematically formulated as given below.

$$DH^+ = argmax\ J(Out_{F_l} + dh), where\ dh \in Out_{B_l}, dh \notin Out_{F_l} \quad (11)$$

$$Out_{F_{l+1}} = Out_{F_l} + DH^+ \quad (12)$$

The next best feature is extracted by employing the '$p - value$' comparison. Forward propagation feature extraction is employed to extract the next feature, backward propagation feature elimination eliminates any extracted features that are insignificant. The above process is continued until the 'l' reaches total number of features in given thyroid disease dataset.

$$DH^- = argmax\ J(Out_{B_l} - dh), where\ dh \in Out_{B_l}, dh \notin Out_{F_{l+1}} \quad (13)$$

$$Out_{B_{l+1}} = Out_{B_l} - DH^- \quad (14)$$

$$FE = \left(Out_{F_{l+1}}, Out_{B_{l+1}}\right) \quad (15)$$

As given above by using both forward propagation (i.e., inputting sample instances) and backward propagation (i.e., fine tuning weights) therefore minimizes loss function convergence at an early stage. This in turn improves overall precision and recall rate of extracted features. The pseudo code representation of Greedy Layerwise-Stacked Denoising Sparse Autoencoder-based Feature Extraction is given below.

Input: Dataset 'DS', Features '$F = \{F_1, F_2, \dots, F_n\}$'
Output: Accurate and precise feature extraction
1: **Initialize** data handled results 'DH', '$in = 0.05$', '$out = 0.05$' 2: **Begin** 3: **For**each Dataset 'DS' with Features 'F' and data handled results 'DH' **//Initial feature extraction process** 4: Formulate absolute output using softmax function as given in (10) **//Forward propagation** 5: Formulate forward propagation to extract significant features as given in (11) and (12) **//Backward propagation** 6: Formulate backward propagation process to eliminate insignificant features as given in (13) and (14) 7: **Return** feature extracted results 8: **End for** 9: **End**

Algorithm 2 Greedy Layerwise-Stacked Denoising Sparse Autoencoder-based Feature Extraction

As given in the above algorithm with the intent to extract the features required for thyroid disease detection absolute output using softmax function is generated via layer-wise stacked sparse autoencoder. Followed by which a greedy selection model is employed in extracting the combination of feature sets (i.e., forward propagation and backward propagation). Finally, evaluates the performance of combined feature set against the valuation criteria to extract significant features for thyroid disease prediction in an accurate and precise manner.

4. EXPERIMENTAL SETUP

In this section, experimental evaluation of the proposed, Deep Tree Liquid State and Greedy Stacked Autoencoders (DTLS-GSA) based feature extraction for thyroid disease prediction and two existing methods DL-based ANN [1] and Deep Neural Network [2] Deep Transfer Learning [31] and RED-Net [32] are implemented in Python high-level general-purpose programming language. In this work, Thyroid disease dataset extracted from https://www.kaggle.com/datasets/emmanuelfwerr/thyroid-disease-data is used in this experiment. The proposed work considers the experiment for a different set of samples. The experiment will be conducted on a computer Intel(R) Core (TM) i7-6700HQ CPU@2.60GHz with a RAM of 32 GB running Windows 10. Simulations are conducted with four performance metrics, precision, recall, accuracy and training time. To ensure fair comparisons same dataset is applied to the three methods by analyzing and validating with an average of 10 simulation runs.

4.1 Performance analysis of precision and recall

In feature extraction based thyroid disease prediction, precision and recall are performance metrics that apply to sample instances retrieved from a sample space. Precision on one hand refers to the ratio of relevant sample instance among the retrieved sample instance. On the other hand, recall refers to the ratio of relevant sample instances that were retrieved. Precision and recall are mathematically formulated as given below.

$$Pre = \frac{TP}{TP+F} \quad (16)$$

$$Rec = \frac{TP}{TP+FN} \quad (17)$$

From the above equations (16) and (17) precision 'Pre' and recall 'Rec' are measured based on the true positive rate (disease sample instances predicted as diseased) 'TP', false positive rate (non diseased sample instances predicted as diseased) 'FP' and the false negative rate (diseased sample instances predicted as non-diseased) 'FN'. Table 3 given below lists the tabulation results of precision and recall by substituting the values in equations (16) and (17) for two existing methods, DL-based ANN [1] and Deep Neural Network [2] Deep Transfer Learning [31] and RED-Net [32] and proposed DTLS-GSA method.

Table 3: Precision and recall rate for thyroid disease prediction based on features extracted

Samples	Precision					Recall				
	DTLS-GSA	DL-based ANN [1]	Deep Neural Network [2]	Deep Transfer Learning [31]	RED-Net [32]	DTLS-GSA	DL-based ANN [2]	Deep Neural Network [2]	Deep Transfer Learning [31]	RED-Net [32]
900	0.96	0.93	0.92	0.9	0.88	0.98	0.97	0.96	0.95	0.94
1800	0.94	0.89	0.79	0.75	0.73	0.95	0.9	0.82	0.78	0.75
2700	0.92	0.87	0.77	0.73	0.7	0.92	0.87	0.81	0.76	0.74
3600	0.9	0.85	0.75	0.71	0.69	0.9	0.85	0.77	0.73	0.71
4500	0.88	0.83	0.73	0.7	0.68	0.88	0.83	0.75	0.71	0.68
5400	0.91	0.87	0.77	0.74	0.72	0.85	0.8	0.72	0.68	0.65
6300	0.93	0.88	0.78	0.75	0.73	0.87	0.82	0.77	0.73	0.71
7200	0.94	0.89	0.79	0.76	0.74	0.89	0.84	0.86	0.77	0.75
8100	0.92	0.87	0.77	0.73	0.71	0.91	0.86	0.8	0.77	0.74
9000	0.95	0.92	0.82	0.78	0.74	0.88	0.83	0.75	0.72	0.7

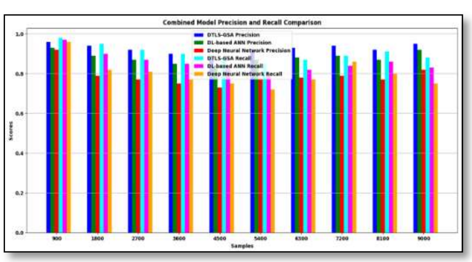

Figure 4 : Samples versus precision and recall

Figure 4 depict precision and recall rate respect to distinct numbers of sample instances ranging between 900 and 9000. With x axis representing the samples involved in simulation y axis represents the precision and recall rate arrived at for three different methods, DL-based ANN [1], Deep Neural Network [2], Deep Transfer Learning [31] and RED-Net [32] and proposed DTLS-GSA method. From the above graphical representation neither enhancing nor minimizing tendency in terms of precision and recall were observed for increasing numbers of samples. For example with 900 samples provided as input, 800 samples being detected with diseased and 100 samples being non detected with disease, the true positive rate using the three methods were observed to be, 770, 750, 740, 720 and 700 whereas false positive rate was 30, 50, 60, 80 and 100 the true negative rate was inferred to be 90, 80, 75, 65 and 60. With this the overall precision rate were observed to be 0.96 using DTLS-GSA method, 0.93 using [1], 0.92 using [2], 0.9 using [31] and 0.88 using [32] and the recall rate was found to be 0.98 for DTLS-GSA method, 0.97 for [1], 0.96 for [2], 0.95 for [31] and 0.94 for [32] respectively. With this results the precision and recall when applied with proposed DTLS-GSA technique was relatively superior than [1], [2], [31] and [32]. The reason behind the improvement was because of application of Greedy Layerwise-Stacked Denoising Sparse Autoencoder-based Feature Extraction method. Through utilizing this method, with the data handled results and features present in the dataset as input, initially, absolute output was obtained using softmax function. Followed by which forward and backward propagation were applied to extract the features. This in turn improved the precision using DTLS-GSA technique by 5%, 18%, 23% and 27% than the [1],[2], [31] and [32] and the recall was improved using DTLS-GSA techni.que by 5%, 13%, 19% and 23% than the [1], [2], [31] and [32].

4.2 Performance analysis of accuracy

The second factor considered for analysis towards thyroid disease prediction with the extracted features is accuracy. Disease prediction is significant because early the disease to be detected accordingly therapy can also be provided. Also, accuracy remains a major factor in disease prediction. Accuracy is mathematically represented as given below.

$$Acc = \frac{TP+}{TP+TN+FP+FN} \quad (18)$$

From the above equation (18) accuracy 'Acc' is measured based on the true positive rate (disease sample instances predicted as diseased) 'TP', false positive rate (non diseased sample instances predicted as diseased) 'FP', false negative

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rate (diseased sample instances predicted as non diseased) 'FN' and the true negative rate 'TN' (non diseased sample instances predicted as negative) respectively. Table 4 given below lists the tabulation results of accuracy by substituting the values in equation (18) for two existing methods, DL-based ANN [1] and Deep Neural Network [2] Deep Transfer Learning [31] and RED-Net [32]and proposed DTLS-GSA method.

Table 4 : Accuracy rate for thyroid disease prediction based on features extracted

Samples	Accuracy (%)				
	DTLS-GSA	DL-based ANN [1]	Deep Neural Network [2]	Deep Transfer Learning [31]	and RED-Net [32]
900	95	92	90	87	84
1800	92	87	80	76	74
2700	90	85	78	75	73
3600	88	83	76	73	71
4500	85	80	73	70	68
5400	88	83	77	74	72
6300	91	86	79	76	74
7200	93	88	81	79	75
8100	88	83	76	72	70
9000	90	85	78	75	73

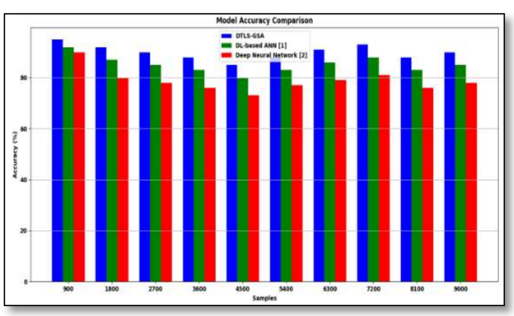

Figure 5: Samples versus accuracy

Figure 5 given above illustrates the graphical representation of accuracy with respect to distinct numbers of samples ranging between 900 and 9000. As of above graphical representation it is supposed which accuracy rate is neither inversely proportional nor directly proportional to sample instances given as input. Also, accuracy rate of proposed DTLS-GSA method is examined higher than the two conventional [1],[2]. This is evidence as of simulation with 900 samples involved, Acc rate using the three methods were examined 95%, 92%, 90%, 87% and 84% respectively. From this result it is obvious which Acc rate of DTLS-GSA method is said to be comparatively higher than [1] [2] [31] and [32]. The reason for the improvement was because of application of forward propagation to extract significant features and backward propagation process to eliminate insignificant features via Greedy Layerwise-Stacked Denoising Sparse Autoencoder-based Feature Extraction algorithm. This in turn improved the overall accuracy of proposed DTLS-GSA method by 6%, 14%, 19% and 27% than the [1], [2], [31] and [32].

4.3. Performance analysis of training time

Finally in this section the performance metrics, training time or the time consumed in extracting the features for thyroid disease prediction is discussed. The training time is mathematically represented as given below.

$$TT = \sum_{i=1}^{N} S_i * Time\ (FE) \qquad (19)$$

From the above equation (19), training time 'TT', is measured based on the samples considered for simulation 'S_i' and the time consumed in extracting the features '$Time\ (FE)$' for thyroid disease prediction. It is measured in terms of milliseconds (ms). Table 5 given below provides the tabulation results of training time by substituting the values in equation (19) for three different methods, DL-based ANN [1], Deep Neural Network [2]], Deep Transfer Learning [31] and RED-Net [32] and DTLS-GSA method respectively.

Table 5 : Training time for thyroid disease prediction based on features extracted

Samples	Training time (ms)				
	DTLS-GSA	DL-based ANN [1]	Deep Neural Network [2]	Deep Transfer Learning [31]	RED-Net [32]
900	31.5	36.9	43.2	33.45	47.3
1800	41.35	55.25	71.35	47.25	85.95
2700	48.25	65.35	82.45	58.65	88.85
3600	55.35	78.35	90.35	65.35	99.65
4500	71.35	85.25	108.95	75.85	115.5

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5400	84.35	95.25	115.25	90.45	125.5
6300	95.25	105.15	130.35	98.65	138.5
7200	108.35	125.35	145.25	116.5	155.5
8100	115.25	145.55	158.35	128.5	168.5
9000	128.35	163.15	175.25	142.5	185.5

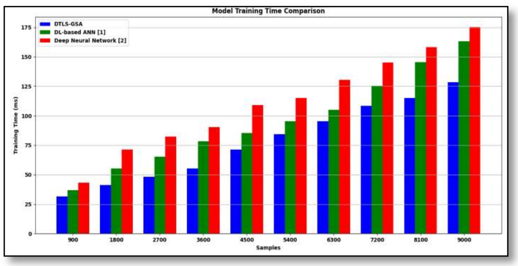

Figure 6 :Samples versus training time

Figure 6 given above shows the training time involved in extracting significant features for thyroid disease prediction. From the above Figure an increasing trend was observed using all the three methods for samples ranging between 900 and 9000. Also from Figure 6 it is supposed which training time using DTLS-GSA technique was comparatively lesser than [1], [2], [31] and [32]. It is evident from the sample instance of 900 where the training time for extracting significant features using DTLS-GSA method was observed to be 31.5ms, 36.9ms using [1] and 43.2ms using [2], 33.5ms using [31] and 47.3ms using [32]. The reason behind the training time improvement for feature extraction by DTLS-GSA method was owing to relevance of Deep Tree Liquid State Machine-based Data Handling method. By using this method, with Deep Tree Liquid State Machine comprising of input layer, reservoir (hidden layer) and readout (output layer) initially obtains the sample instances in the input layer. Followed by which in the reservoir two operations, file featured with a list of features and consolidated file featured with a list of feature were obtained and passed to the encoder. Finally in the decoder, the readout operation obtained temporal information from reservoir and transformed it to a time-series output. Finally, Segmented Regression function was applied and only with high correlation coefficient results via breaking point efficient data handling was made. This in turn reduced the training time for extracting features towards thyroid disease prediction using DTLS-GSA technique by 18%, 32%, 9% and 37% than the [1],[2], [31] and [32].

4.4 F1-score

It is a metric that combines precision and recall into. The F1-score is mathematically formulated as follows,

$$F - score = \left(2 * \left[\frac{Pre*Rec}{Pre+Rec}\right]\right) \tag{20}$$

Where, P indicates a precision, SN denotes a sensitivity. It is measured in percentage (%). Table 6 given below lists the tabulation results of F1-score by substituting the values in equation (20) for two existing methods, DL-based ANN [1], Deep Neural Network [2], Deep Transfer Learning [31] and RED-Net [32] and proposed DTLS-GSA method.

Table 6 : F1-score for thyroid disease prediction based on features extracted

Samples	F1-score				
	DTLS-GSA	DL-based ANN [1]	Deep Neural Network [2]	Deep Transfer Learning [31]	and RED-Net [32]
900	0.96	0.94	0.93	0.92	0.9
1800	0.94	0.89	0.8	0.76	0.73
2700	0.92	0.87	0.78	0.74	0.71
3600	0.9	0.85	0.75	0.71	0.69
4500	0.88	0.83	0.73	0.7	0.68
5400	0.87	0.83	0.74	0.7	0.68
6300	0.89	0.84	0.77	0.73	0.71
7200	0.91	0.86	0.79	0.76	0.74
8100	0.91	0.86	0.78	0.749	0.72
9000	0.91	0.87	0.783	0.74	0.71

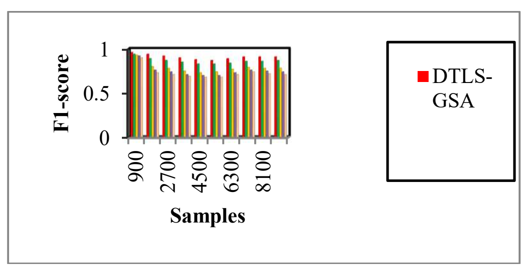

Figure 7 : Samples versus F1-score

Figure 7 given above demonstrate the F1-score involved in extracting significant features for thyroid disease prediction. From the above fig, samples ranging between 900 and 9000 considered. Also from Figure 7 it is supposed which F1-score using DTLS-GSA technique was comparatively lesser than [1], [2], [31] and [32]. It is evident from the sample instance of 900 where the F1-score for extracting significant features using DTLS-GSA method was observed to be 0.94, 0.94, 0.93 and 0.92 for [1], [2], [31] and [32]. The reason for higher F1-score is to apply forward propagation to extract important features and backward propagation process to eradicate insignificant features. This in turn reduced the training time for extracting features towards thyroid disease prediction using DTLS-GSA technique by 5%, 16%, 22% and 26% than the [1],[2], [31] and [32].

4.5 Comparative analysis of the proposed DTLS-GSA method with existing methods

The analysis of the proposed DTLS-GSAand the existing DL-based ANN [1], Deep Neural Network [2], Deep Transfer Learning [31] and RED-Net [32] are compared and executed in Python. Table 7 provides a detailed comparison result of the proposed DTLS-GSAwith the existing methods.

Table 7 : Overall performance analysis results

Methods	Precision	Recall	Accuracy (%)	Training time (ms)	F1-score
Proposed DTLS-GSA	0.92	0.9	90	77.93	0.91
DL-based ANN [1]	0.88	0.85	85	95.55	0.86
Deep Neural Network [2]	0.78	0.79	79	112.07	0.78
Deep Transfer Learning [31]	0.755	0.76	76	85.71	0.75
RED-Net [32]	0.73	0.73	73	121.07	0.72

Table 7 depicts the overall performance outcomes of precision, recall, accuracy, training time and F-1score for five different methods. DTLS-GSAmethod outperforms existing methods in terms of achieving higher precision, recall, accuracy and F-1score and lesser time. For experiment, DTLS-GSAmethod provided better performance of average precision, recall, accuracy and F-1score by 0.92, 0.9, and 90% than the existing methods. Also, the DTLS-GSAmethod reduces training time by 77.93ms compared to conventional methods

5.CONCLUSION

Analysis of thyroid disease prediction with significant feature extraction is one of the most prudent research areas that may assist by imparting lot of information for both analyzing and validating early detection and hence aid in overcoming the mortality rate. Past research works underscore thyroid disease prediction employing different traditional and non-traditional methods, including machine learning, deep learning. In this work, a Deep Tree Liquid State and Greedy Stacked Autoencoders (DTLS-GSA) based feature extraction for thyroid disease prediction (DTLS-GSA) is proposed. The individual procedures associated with the organization are data handling and feature extraction. Initially, a novel method of Deep Tree Liquid State Machine based architecture is applied to sample instances were acquired and provided as input for efficient data handling. After that, the Greedy Layerwise-Stacked Denoising Sparse Autoencoders was applied to obtain the robust and accurate feature extracted results that server for accurate thyroid disease prediction with efficient data handled results. The proposed DTLS-GSA method was experimented in Python high-level, general-purpose programming language using Thyroid disease dataset. The experimentation results validated that the DTLS-GSA method achieved to better results in performance of 18% of improved precision, 16% of recall and accuracy with 24% of minimum training time compared to the conventional methods.

REFERENCES

[1] Kalpna Guleria, Shagun Sharma, Sushil Kumar, Sunita Tiwari, "Early prediction of hypothyroidism and multiclass classification using predictive machine learning and deep learning", Measurement: Sensors, Elsevier, Vol. 24, Dec 2022 [DL-based ANN]

[2] Ritesh Jha, Vandana Bhattacharjee, Abhijit Mustafi, "Increasing the Prediction Accuracy for Thyroid Disease: A Step Towards Better Health for Society", Vol. 122, Feb 2022 [Deep Neural Network]

[3] Yizhe Li, Cheng Chen, Fangfang Chen, Chen Chen, Rui Gao, Bo Yang, Rumeng Si, Xiaoyi Lv, "Serum Raman spectroscopy combined with Deep Neural Network for analysis and rapid screening of hyperthyroidism and hypothyroidism", Photodiagnosis and

Photodynamic Therapy, Elsevier, Vol. 35, Sep 2021

[4] Pınar Karadayı Ataş, “A novel hybrid model to predict concomitant diseases for Hashimoto’s thyroiditis”, BMC Bioinformatics, Aug 2023

[5] Zhiwei Jia, Yuqi Huang, YanhuiLin, Min Fu, Chenhao Sun, “Multidimensional Prediction Method for Thyroid Cancer Based on Spatiotemporally Imbalanced Distribution Data”, IEEE Access, Vol. 12, Dec 2023

[6] George Obaido, OkechinyereAchilonu, Blessing Ogbuokiri, ChimeremmaSandra Amadi, Lawal Habeebllahi, Tony Ohalloran, Chidozie Williams Chukwu, EbikellaDomorMienye, Mikail Aliyu, Olufunke Fasawe, IbukunolaAbosede Modupe, ErepamoJob Omietimi, Kehinde Aruleba, “An Improved Framework for Detecting Thyroid Disease Using Filter-Based Feature Selection and Stacking Ensemble”, IEEE Access, Vol. 12, Jun 2024

[7] Zahrul Jannat Peya, Md. Shymon Islam, Mst. Kamrun Naher Chumki, “Thyroid Disease Prediction based on Feature Selection and Machine Learning”, National Library of Medicine, Aug 2022

[8] Hyeong Jun Ahn, Kyle Ishikawa, Min-HeeKimI, “Exploring the diagnostic performance of machine learning in prediction of metabolic phenotypes focusing on thyroid function”, Plos One, Jun 2024

[9] Viswanatha V, Ramachandra A.C, Rahul R Sankar, Chinmay Sanjay Mahulikar,”Thyroid disease detection using Machine Learning approach”, Journal of Xi'an University of Architecture & Technology, Jun 2023

[10] Jue Wang, Nafen Zheng, Huan Wan, Qinyue Yao, Shijun Jia, Xin Zhang, Sha Fu, Jingliang Ruan, Gui He, Xulin Chen, Suiping Li, Rui Chen, Boan Lai, Jin Wang, Qingping Jiang, Nengtai Ouyang, Yin Zhang, “Deep learning models for thyroid nodules diagnosis of fine-needle aspiration biopsy: a retrospective, prospective, multicentre study in China”, Digital Health, Lancet, Jul 2024

[11] Khandaker Mohammad Mohi Uddin, Abdullah Al Mamun, Anamika Chakrabarti, Rafid Mostafiz, “An ensemble machine learning-based approach to predict thyroid disease using hybrid feature selection”, Biomedical Analysis,Elsevier, Sep 2024

[12] Shengjun Ji, “SSC: The novel self-stack ensemble model for thyroid disease prediction”, Plos One, Jan 2024

[13] Huayi Zhao, Chenxi Zheng, Huihui Zhang, Maohua Rao, Yixuan Li, Danzhou Fang, Jiahui Huang, Wenqian Zhang and Gengbiao Yuan, “Diagnosis of thyroid disease using deep convolutional neural network models applied to thyroid scintigraphy images: a multicenter study”, Frontiers in Endocrinology, Aug 2023

[14] Tahir Alyas, Muhammad Hamid, Khalid Alissa, Tauqeer Faiz, Nadia Tabassum, Aqeel Ahmad, “Empirical Method for Thyroid Disease Classification Using a Machine Learning Approach”, BioMed Research International, Hindawi, Mar 2024

[15] Melih Agraz, “Semi-Supervised Machine Learning Approaches for Thyroid Disease Prediction and its Integration with the Internet of Everything”, International Journal of Interactive Multimedia and Artificial Intelligence, Jul 2024

[16] Saima Sharleen Islam, Md. Samiul Haque, M. Saef Ullah Miah, Talha Bin Sarwar and Ramdhan Nugraha, “Application of machine learning algorithms to predict the thyroid disease risk: an experimental comparative study”, Peer Journal of Computer Science, Mar 2022

[17] Lerina Aversano, Mario Luca Bernardi, Marta Cimitile, Andrea Maiellaro and Riccardo Pecori, “A systematic review on artificial intelligence techniques for detecting thyroid diseases”, Peer Journal of Computer Science, Jun 2023

[18] Ritesh Jha, Vandana Bhattacharjee, Abhijit Mustaf, “Increasing the Prediction Accuracy for Thyroid Disease: A Step Towards Better Health for Society”, Wireless Personal Communications, Springer, Aug 2021

[19] Punit Gupta, Furqan Rustam, Khadija Kanwal, Wajdi Aljedaani, Sultan Alfarhood, Mejdl Safran, Imran Ashraf, “Detecting Thyroid Disease Using Optimized Machine Learning Model Based on Differential Evolution”, International Journal of Computational Intelligence Systems, Springer, Jan 2024

[20] Khalid salman, Emrullah Sonuç, “Thyroid Disease Classification Using Machine Learning Algorithms”, International Conference on Physics and Applied Sciences, Oct 2021

[21] Azrin Sultana, Rakibul Islam, “Machine learning framework with feature selection approaches for thyroid disease classification and associated risk factors identification”, Journal of Electrical Systems and Information Technology, Springer, Oct 2023

ISSN: 1992-8645 www.jatit.org E-ISSN: 1817-3195

[22] Rakibul Islam, Azrin Sultana, Mohammad Rashedul Islam, “A comprehensive review for chronic disease prediction using machine learning algorithms”, Journal of Electrical Systems and Information Technology, Springer, Mar 2024

[23] E. Mohan, P. Saravanan, Balaji Natarajan, S. V. Aswin Kumer, G. Sambasivam, G. Prabu Kanna, Vaibhav Bhushan Tyag, “Thyroid Detection and Classification Using DNN Based on Hybrid Meta-Heuristic and LSTM Technique”, IEEE Access, Jul 2023

[24] Zhen-Tian Guo, Kun Tian, Xi-Yuan Xie, Yu-Hang Zhang, De-Bao Fang, “Machine Learning for Predicting Distant Metastasis of Medullary Thyroid Carcinoma Using the SEER Database”, International Journal of Endocrinology, Hindawi, Dec 2023

[25] Shanu Verma, Rashmi Popli, Harish Kumar, Atul Srivastava, “Classification of thyroid diseases using machine learning frameworks”, International Journal of Health Sciences, Apr 2022

[26] XuqingChai, “Diagnosis Method of Thyroid Disease Combining Knowledge Graph and Deep Learning”, IEEE Access, Aug 2020

[27] Sumya Akter, Hossen A. Mustafa, “Analysis and interpretability of machine learning models to classify thyroid diseass”, Plos One, May 2024

[28] Meghana G, R SireshaR Ajith Kumar, Ritika G M, Sathvika Patil, “Detection of Thyroid Disorder using Machine Learning Approach”, Journal of Emerging Technologies and Innovative Research, Vol. 10, Apr 2023

[29] Shengjun Ji, “SSC: The novel self-stack ensemble model for thyroid disease prediction”, Plos One, Jan 2024

[30] Rajasekhar Chaganti, Furqan Rustam, Isabel De La Torre Díez, Juan Luis Vidal Mazón, Carmen Lili Rodríguez, Imran Ashraf, “Thyroid Disease Prediction Using Selective Features and Machine Learning Techniques”, Cancers, Oct 2022

[31] Yan Xu, Mingmin Xu, Zhe Geng, Jie Liu and Bin Meng, “Thyroid nodule classifcation in ultrasound imaging using deep transfer learning”, Cancer, March 2025.

[32] Min-Ji Kim, Jin-A Kim, Naae Kim, Yul Hwangbo, Hyun Jeong Jeon, Dong-Hwa Lee, “RED-Net: A Neural Network for 3D Thyroid Segmentation in Chest CT Using Residual and Dilated Convolutions for Measuring Thyroid Volume”, IEEE Access, Dec 2024.

[33] Tathagat Banerjee, Davinder Paul Singh, Debabrata Swain, Shubham Mahajan, Seifedine Kadry &Jungeun Kim, “A novel hybrid deep learning approach combining deep feature attention and statistical validation for enhanced thyroid ultrasound segmentation”, Scientific Reports, July 2025.

[34] Dr. M. Gangappa, K. Bhargavasai, “Projection on Thyroid Diseases Detection Using Deep Learning”, International Journal Of Latest Technology In Engineering, Management & Applied Science (IJLTEMAS), July 2025.

[35] Zhen Li, Changfei Li, Liangyu Min, Dijia Lin, “Black-Litterman Portfolio Optimization Using Gaussian Process Regression”, IAENG International Journal of Applied Mathematics, Dec 2023

[36] Halima Begum, Muhammed Mazharul Islam, Humaira Sabira Eva, Naim Hossain Emon,Farhan Ahmed Siddique, “Deep Learning Networks for Handwritten BanglaCharacter Recognition”, IAENG International Journal of Applied Mathematics, Dec 2023