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A COYOTE-INSPIRED APPROACH FOR SYSTEMIC LUPUS ERYTHEMATOSUS PREDICTION USING NEURAL NETWORKS

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Abstract. *Systemic Lupus Erythematosus (SLE) is a complicated autoimmune disease that can present with a variety of clinical symptoms, making precise prognosis difficult. Because SLE has a wide range of symptoms and may overlap with other autoimmune and inflammatory disorders, making a diagnosis can be challenging. This study creates a precise and accurate model for the prediction of SLE using the GEO dataset. For cost-effective data collection and analysis, feature selection might be essential in some applications, particularly in healthcare and scientific research. The strength of Artificial Neural Networks (ANN) for Systemic Lupus Erythematosus prediction and the Coyote Optimization Algorithm (COA) for feature selection are combined in this study. The COA is an optimization method influenced by nature and coyote hunting behavior. This study attempts to improve the effectiveness of subsequent predictive modeling by using COA to identify a subset of significant features from high-dimensional datasets linked to SLE. A Multi-layer Feed-forward Neural Network, a potent machine learning architecture renowned for its capacity to discover complex patterns and correlations within data, is then given the chosen features. Because the neural network is built to capture SLE's intricate and non-linear structure, it offers a reliable foundation for precise classification and prediction. The accuracy of the COA-ANN model was 99.6%.*

Keywords: neural networks, coyote optimization algorithm, prediction, systemic lupus erythematosus

INSPIROWANE KOJOTAMI PODEJŚCIE DO PRZEWIDYWANIA TOCZNIA RUMIENIOWATEGO UKŁADOWEGO Z WYKORZYSTANIEM SIECI NEURONOWYCH

Streszczenie. *Toczeń rumieniowaty układowy (SLE) jest skomplikowaną chorobą autoimmunologiczną, która może objawiać się różnymi objawami klinicznymi, co utrudnia dokładne rokowanie. Ponieważ SLE ma szeroki zakres objawów i może nakładać się na inne choroby autoimmunologiczne i zapalne, postawienie diagnozy może być trudne. Niniejsze badanie tworzy precyzyjny i dokładny model przewidywania SLE z wykorzystaniem zbioru danych GEO. W celu efektywnego kosztowo gromadzenia i analizy danych, wybór cech może być niezbędny w niektórych zastosowaniach, szczególnie w opiece zdrowotnej i badaniach naukowych. W niniejszym badaniu połączono siłę sztucznych sieci neuronowych (ANN) do przewidywania tocznia rumieniowatego układowego i algorytmu optymalizacji Coyote (COA) do wyboru cech. COA to metoda optymalizacji, na którą wpływ ma natura i zachowania łowieckie kojotów. Niniejsze badanie ma na celu poprawę skuteczności późniejszego modelowania predykcyjnego poprzez wykorzystanie COA do identyfikacji podzbioru istotnych cech z wielowymiarowych zbiorów danych powiązanych z SLE. Wielowarstwowa sieć neuronowa Feed-forward, potężna architektura uczenia maszynowego znana ze swojej zdolności do odkrywania złożonych wzorców i korelacji w danych, otrzymuje następnie wybrane cechy. Ponieważ sieć neuronowa została zbudowana w celu uchwycenia skomplikowanej i nieliniowej struktury SLE, oferuje ona niezawodną podstawę do precyzyjnej klasyfikacji i przewidywania. Dokładność modelu COA-ANN wyniosła 99,6%.*

Słowa kluczowe: sieci neuronowe, algorytm optymalizacji coyote, przewidywanie, toczeń rumieniowaty układowy

Introduction

SLE is a complicated autoimmune illness that can harm the body's systems and organs [15]. It is characterized by a dysregulated immune system that mistakenly attacks healthy tissues, leading to tissue damage, inflammation, and various symptoms. SLE is known for its unpredictable course, with periods of flare-ups and remission, making its diagnosis and management challenging. The diverse clinical manifestations of SLE [13] can involve the skin, joints, kidneys, heart, lungs, and other organs, contributing to the complexity of the disease.

Over the past few years, medical research has witnessed a growing interest in leveraging advanced computational techniques to diagnose [12] and predict complex diseases such as SLE. One notable approach is the application of machine learning algorithms for feature selection and prediction. Feature selection is crucial in identifying the most relevant variables or biomarkers associated with SLE, helps to achieve the best accuracy, and improves the interpretability of predictive models.

COA is one such innovative metaheuristic algorithm inspired by the hunting behavior of coyotes. COA has gained attention in the realm of feature selection due to its ability to efficiently explore solution spaces and identify optimal subsets of features. By mimicking the cooperative hunting strategy of coyotes, COA can effectively balance exploration and exploitation, making it well-suited for solving complex optimization problems like feature selection in medical datasets.

The COA algorithm is a nature-inspired metaheuristic created by observing how coyotes hunt. Introduced as an optimization technique, COA solves complex problems by balancing exploration and exploitation strategies. Its unique approach involves multiple search agents collaboratively adapting their positions in the solution space, mimicking the cooperative foraging dynamics of coyotes. COA has demonstrated effectiveness in diverse optimization domains, including feature selection in biomedical datasets. Its ability to efficiently navigate high-dimensional spaces and identify optimal subsets of features makes COA a valuable tool for enhancing the performance of machine learning algorithms, particularly in tasks such as the prediction and diagnosis of complex diseases like SLE.

Neural networks, on the other hand, have proven to be powerful tools for pattern recognition and prediction tasks. They are particularly effective in capturing intricate relationships within datasets, making them suitable for modelling the multifaceted nature of SLE. When combined with optimized feature sets obtained through algorithms like COA, neural networks can enhance their predictive accuracy and contribute to the development of more reliable diagnostic and prognostic tools for SLE.

In our study we integrated COA and neural networks to predict SLE by improving clinical outcomes. By identifying the most informative features and leveraging the predictive capabilities of neural networks, this approach may contribute to earlier and more accurate diagnoses, personalized treatment plans, and ultimately better management of SLE. This study aims to present a novel approach for predicting SLE using a combination of COA for feature selection and ANN for predictive modeling. The study aims to address the challenges of diagnosing SLE by leveraging advanced computational techniques to improve accuracy and efficiency in prediction. Through the utilization of COA to identify significant features from complex datasets associated with SLE, followed by the application of a Multi-layer Feed-forward Neural Network, the study seeks to enhance the effectiveness of SLE prediction. The stated accuracy of the proposed COA-ANN model underscores its potential as a reliable tool for accurate prediction of SLE.

1. Literature review

In this study [27] a cohort of 1014 SLE patients with low disease activity and 453 with high disease activity were analyzed, including 94 clinical and laboratory data and 17 meteorological variables. For building models, the study identified important indicators such as proteinuria, hematuria, pyuria, low complement, precipitation, and sunlight by utilizing sophisticated techniques including mutual information and multisurf for feature selection. After adjusting hyperparameters using machine learning, the researchers discovered that the Light Gradient Boosting (LGB) model performed the best in terms of accuracy (0.856). On the other hand, the naïve Bayes model had the worst performance indicators.

In this research, a new binary version of the COA tailored for feature selection problems is presented. To improve model performance and interpretability, the study discusses the significance of feature selection in machine learning and pattern recognition applications. The Binary Coyote Optimization Algorithm (BCOA) [9] is a proposed algorithm that leverages coyote cooperative hunting behavior to handle binary-encoded feature spaces efficiently. The efficacy of BCOA in attaining competitive outcomes was demonstrated by the authors when they compared its performance to other optimization algorithms for feature selection across a variety of datasets.

Utilizing gene expression data, this work suggested a cancer classification methodology that includes preprocessing, feature extraction, and coyote optimization SVM classification. For the classification of breast cancer, the suggested CoySVM [21] approach produced a 93.32% precision rate and a 92.59% recall rate with a training percentage of 80. Comparative analysis with other traditional techniques including ANN, SVM, DT, CNN, FMR, modified KNN, and DSSAENN was used to get these results. When comparing precision, recall, and F-measure, the CoySVM method performed better than the other approaches.

The paper by A. Kumar et al. suggests a technique for classifying arrhythmias using an electrocardiogram (ECG) monitoring system that is Internet of Things (IoT) based. The suggested technique uses the deep learning convolutional neural network (CNN) classifier and the Coyote Grey Wolf optimization (Coy-GWO) [14] algorithm to classify ECG signals. It also discusses the suggested Coy-GWO optimization algorithm, a hybrid meta-heuristics method that combines the Canidae family's traits of social predominance with hierarchy-based hunting. The suggested technique may effectively categorize ECG data to identify arrhythmias. The paper's contribution is the new approach it suggests for classifying arrhythmias, which combines a hybrid meta-heuristics algorithm with Internet of Things-based ECG monitoring.

The study [22] suggests a unique ensemble learning strategy to forecast dengue incidence in Paraná, Brazil, by combining the COA with the eXtreme Gradient Boosting (XGBoost) model. The study addresses the significance of several predictive factors, including temperature, humidity, precipitation, and past dengue cases, in dengue forecasting. Other optimization techniques are used to evaluate the proposed hybrid COA-XGBoost model with XGBoost. The findings show that the COA-XGBoost model is competitive. The approach of the study includes assessing the performance of the various models using statistical tests like the Friedman test and the Nemenyi post-hoc test.

In the study [6], recurrent neural networks (RNNs) were employed to predict chronic damage in a large SLE cohort. They measured chronic damage in 413 recruited SLE patients using the SLICC/ACR Damage Index (SDI). The RNN model showed predictive ability for damage development with an AUC value of 0.77. It was discovered that a threshold value of 0.35 (sensitivity 0.74, specificity 0.76), might be used to identify patients who may be at risk of injury. A mathematical model was developed for predicting chronic damage in SLE by utilizing longitudinal data, including laboratory and clinical components, from the Sapienza Lupus Cohort.

Comparing a cohort of healthcare workers to patients with SLE, this study [20] sought to determine how immunosuppressive drugs affected the patients' response to vaccination. The study found that SLE patients taking immunosuppressive medications had lower levels of vaccination IgG than patients not taking such medications. The analysis was based on data from the Hopkins Lupus Cohort and medical professionals. In comparison with the cohort of healthcare workers, both SLE groups showed decreased levels of IgG. Significantly raising post-vaccination IgG levels without resulting in clinical flare-ups was achieved by withholding mycophenolate for a week following vaccination. Immunosuppressive drugs that considerably reduce the antibody response to immunization in SLE patients include tacrolimus, belimumab, and mycophenolate mofetil, according to the study. Results point to the possibility of improving vaccine response in SLE patients by modifying immunosuppressive medication management, such as by short-term stopping mycophenolate. This would be a clinically useful strategy that wouldn't cause flare-ups. The significance of individualized immunosuppressive medication management strategies is emphasized to maximize vaccination effectiveness in people with sickle cell disease.

By emphasizing the early and accurate identification utilizing cutting-edge technology, this research [5] explores the widespread health concern of brain disorders. A new method, the hybrid coyote predator optimization-dependent, is presented in this research. Utilizing performance measures and a thorough analysis, this study uses the CAP dataset. The model demonstrated strong performance in predicting brain abnormalities, as seen by its remarkable accuracy of 98.446% for True Positives (TP) and 97.384% for k-fold. To further improve the detection model's accuracy, certain frequency bands are emphasized to identify brain alterations. In terms of early and precise brain abnormality prediction, it highlights the benefits of combining hybrid coyote predator optimization with DCNN and shows encouraging results.

2. Proposed methodology

The architecture of the proposed model for the prediction of SLE using the Coyote Optimization Algorithm and Neural Networks is discussed in this section. In Fig. 3, the entire process of the proposed approach is described clearly. The proposed model consists of 5 modules.

Data Collection: The dataset used in this study is collected from the GEO website, with accession number GSE65391. It contains 996 samples with 87 attributes. Out of them, 924 samples belonged to SLE and 72 were healthy samples.

Data Pre-processing: The dataset is pre-processed by following 2 steps.

Data cleaning: Data cleaning is done by replacing null values with mean values. The dataset with null values is noisy and noisy data can’t give better performance.

Data Transformation: Data Transformation is done by standardizing the data, i.e. converting the data into a similar scale. Standard_Scaler is used to standardize the dataset.

Feature Selection: Feature selection is the important step, the GEO dataset contains a huge number of attributes, and training the model with all these factors is not easy and it leads to a decrease in the performance of the model. So, the selection of relevant features that cause SLE is significant. In this study, feature selection is done using the COA, which is discussed clearly in the later part using the neat diagram.

Data Visualization: Data visualization in Power BI involves presenting data in a visually appealing and informative manner to facilitate better understanding and decision-making.

To enable the hierarchical examination of lupus patient data, Fig. 1 presents a decomposition tree created using factors like gender, age, biopsy history, days between diagnosis, disease activity, days since diagnosis, and SLEDAI score. This visualization helps users make targeted analyses and decisions on lupus research and management by breaking down and comprehending the interactions between demographic variables, medical history, disease progression, and current health state.

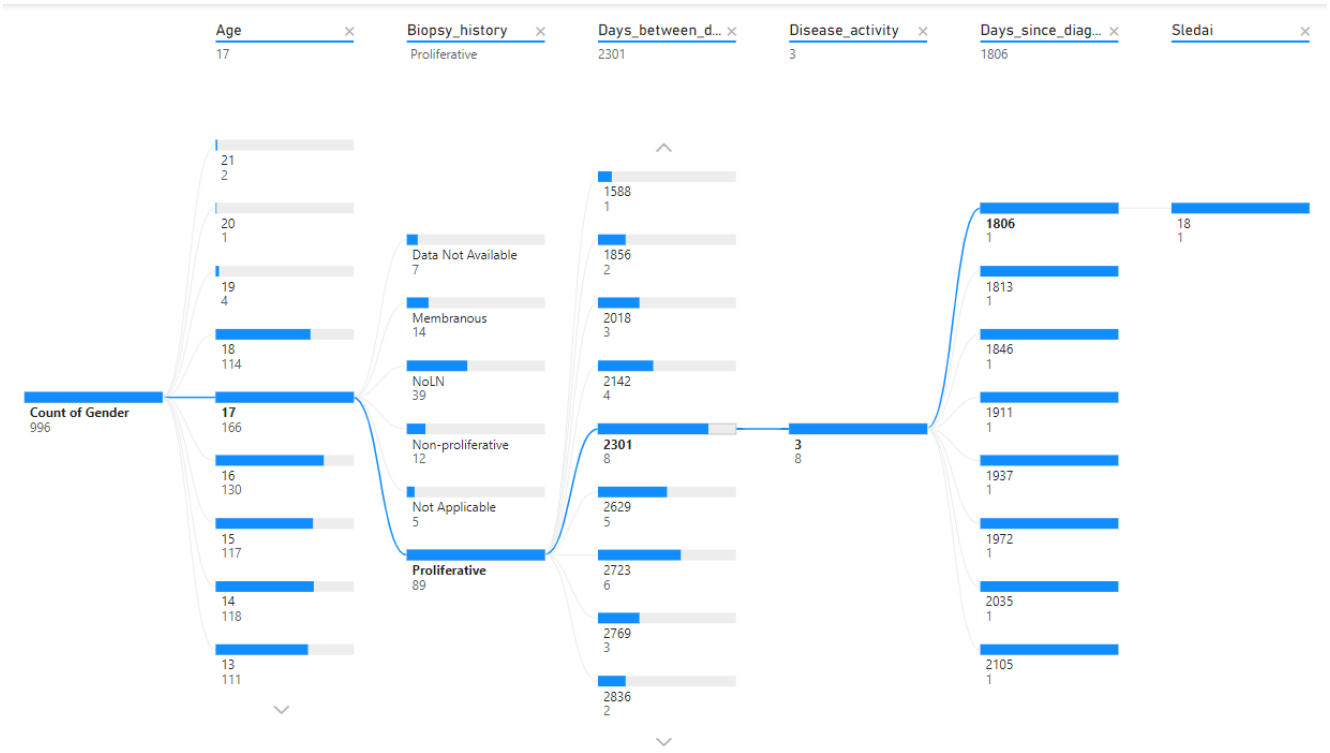

Fig. 1. Visualization of data using decomposition tree

Fig. 2 describes the intensity of disease activity according to gender based on their total hospital visits. Patients' disease activity is graded on a 1–3 severity scale. The chart demonstrates unequivocally that women visit hospitals at a higher rate than men. Moreover, 1565 women have disease activities classified as 1 (low), 1762 have intensity levels classified as 2 (middle), and 1916 female patients have disease activities classified as 3 (highest). On the other hand, 126 men have a high disease activity score of 3, 138 have a disease activity score of 2, and 246 men have the lowest disease activity. Each patient's disease activity is assessed and categorized into one of these three levels based on presumably clinical assessments, symptom severity, or other diagnostic criteria specific to the condition being studied. This scoring system allows for a standardized way to categorize and compare disease activity across patients, which is then correlated with their hospital visit frequency. Men visit the doctor less frequently than women do, and they also appear to be less active in the condition.

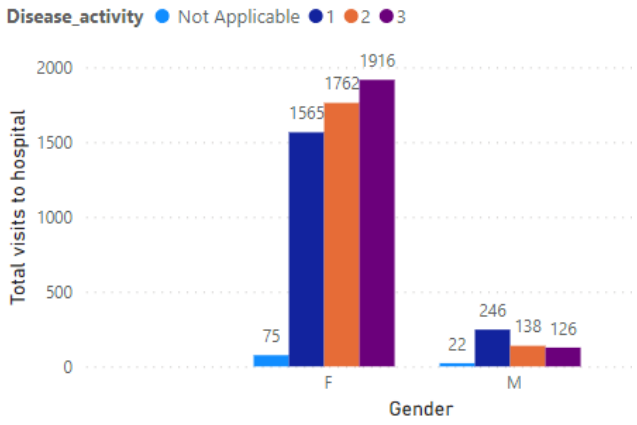

Fig. 2. Total visits by Gender and Disease_activity

Several factors in women such as Hormones like Estrogen, Genetic factors, and Microchimerism, where cells from a fetus might persist in the mother's body after pregnancy. These cells could potentially trigger an autoimmune response in some women. The interplay of these factors results in a significantly higher prevalence of SLE among women, particularly during reproductive years (from menarche to menopause), when estrogen levels are higher.

Model Development: Model Development starts with Data splitting, the dataset is divided into training and testing parts in the ratio of 80:20. The Model developed in this study for the prediction of SLE is a Multi-Layered Feedforward Neural Network with two hidden layers. The features selected using COA are fed into this Neural Network and the network is trained using Adam Optimizer. The loss function used is binary_crossentropy.

Model Evaluation: The trained model is evaluated using the classification metrics Accuracy, Precision, Recall, and confusion matrix and also training and validation accuracy graphs are plotted. The proposed approach is a binary classification model, so the model predicts the output as SLE or healthy.

Fig. 4 describes the flow chart of the coyote optimization algorithm used in this study for feature selection. The important considerations of this algorithm are:

Initial Population: Initialize the population of coyotes, where each pack contains Nc coyotes each coyote represents a potential solution to the optimization problem. And also defines the maximum number of iterations, and problem-specific parameters like the maximum age of the coyote, and the probability of the coyote leaving a pack, etc.

Objective Function: The objective function evaluates the cost of coyotes in each pack, it quantifies the quality of the solution.

Update the best Coyote: In each iteration identify the best coyote with the least fitness value, and this is considered as the alpha coyote and it is the current global best solution.

Coyote Movement: Move the position of the coyote from its current pack based on its current position and the information gathered from the alpha coyote.

Update Global Best Solution: Once the termination condition is reached, update the global best solution as the optimized subset of features.

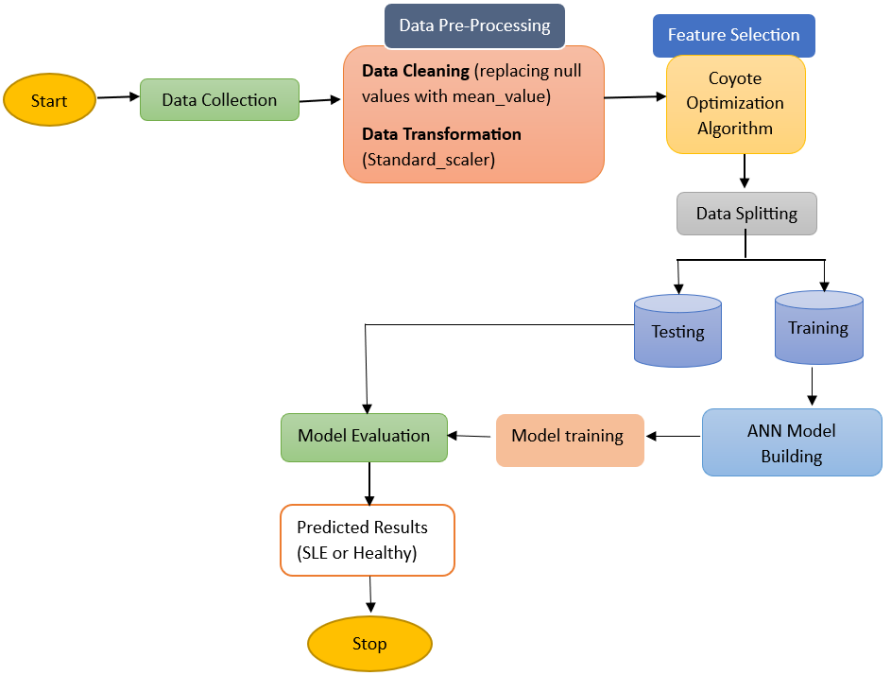

Fig. 3. Architecture of the proposed model for prediction of SLE

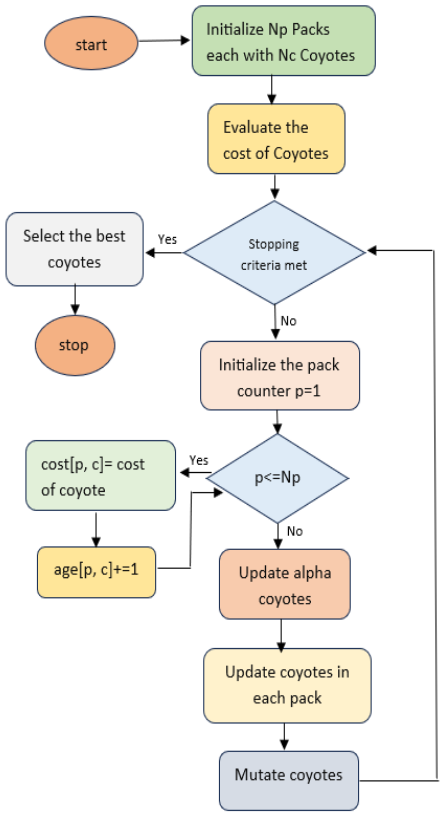

Fig. 4. Flow chart of Coyote Optimization Algorithm

Table 1 presents the final subset of features chosen by the algorithm. The algorithm iteratively evolves a population of coyotes within packs, employing mechanisms such as aging, pack reshuffling, and mutation to explore the solution space effectively. After 50 iterations, the best alpha coyote is identified, and the selected features are displayed below.

The COA successfully identified an optimal subset of features for predicting SLE using a Decision Tree Classifier. The algorithm iteratively evolved packs of coyotes, with each coyote representing a feature subset. Throughout the optimization process, the algorithm dynamically adjusted coyote packs, evaluated their predictive performance, and incorporated mutation operations for diversity.

Table 1. Features selected by Coyote Optimization Algorithm

Features selected by Coyote Optimization Algorithm	
Title	Sourcename
Visit	Set
Batch_replicate	Cumulative_time
Days_since_diagnosis	Days_between_diagnosis_and_last_visit
Gender	Age
Biopsy_history	Wbc
Neutrophil_count	

The COA demonstrated notable adaptability, as evidenced by the selected features' ability to minimize the negative accuracy (maximize accuracy) in the specified objective function. The convergence of the algorithm was tracked across iterations, highlighting the best alpha coyote's accuracy and age. The mutation step introduced variability, enhancing the algorithm's exploration capabilities.

Algorithm 1: Coyote Optimization Algorithm

1: Define COA function
best_alpha_features=COA(optimization_objective, nfevalmax, n_features)
2: Define the parameters used in COA like n_coyotes, n_packs, p_leave, max_age
3: Initialize the coyotes
coyotes = np.random.rand(n_packs, n_coyotes, D)
costs = np.zeros((n_packs, n_coyotes))
ages = np.zeros((n_packs, n_coyotes))
4: Evaluate the cost of each coyote's subset of features
selected_features=randomly initialized features of a coyote
costs[p,c]=optimization_objective(selected_features)
age[p,c]+=1
5: select the alpha_coyotes
alpha_indices = np.unravel_index(np.argmin(costs, axis=None), costs.shape)
alpha_costs = costs[alpha_indices]
alpha_ages = ages[alpha_indices]
6: select the alpha_features based on the costs of the alpha_coyotes
7: update the packs by replacing the old coyote with the new coyote
8: Mutate the Coyotes and find the best_alpha_features
9: return the best alpha_features

Algorithm 1 describes the procedure of the Coyote Optimization Algorithm that operates through an iterative process. Initially, coyotes, representing potential feature subsets, are randomly initialized within packs. Alpha coyotes with the lowest cost, corresponding to better accuracy, are selected. Over iterations, coyotes age, and with a probability, some may leave their pack or undergo mutation, adapting their feature subset. This iterative process aims to converge towards optimal feature subsets, ultimately identifying the best alpha coyote with the highest accuracy. The final selected features are considered as best alpha features and their corresponding accuracy is then outputted for further analysis.

3. Results and discussion

This section displays the experimental results and GUI screenshots of the proposed model. The proposed model Coyote inspired Optimization Algorithm in combination with neural networks achieved an accuracy of 99.67% for the prediction of SLE.

Fig. 5 represents the training and validation curve graphs for the COA coupled with ANN offering valuable insights into the model's learning dynamics and generalization performance. These curves illustrate the variation in performance metrics across different epochs or iterations during the training process. A well-behaved COA-ANN exhibits a convergence of both training and validation curves, signifying effective learning without overfitting.

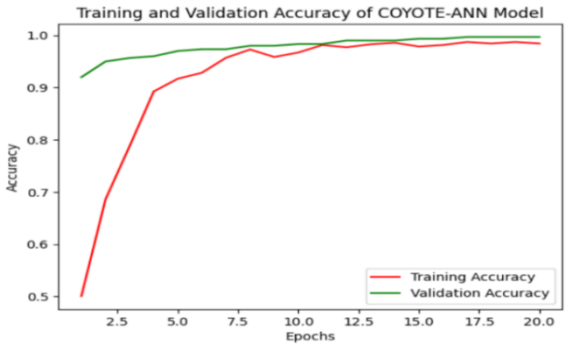

Fig. 5. Training and validation accuracy graph of COA-ANN model

The confusion matrix, shown in Fig. 6, offers a thorough summary of the suggested model's classification performance. For the binary classification challenge, the matrix shows the contrast between the true and predicted labels, differentiating between 'Healthy' (class 0) and 'SLE' (class 1). Whereas off-diagonal entries in the matrix denote misclassifications, diagonal elements in the matrix show the cases in which the model correctly predicted the labels. Hence, from the below matrix, we can see that misclassifications are less thereby contributing to informed decision-making in the context of SLE prediction.

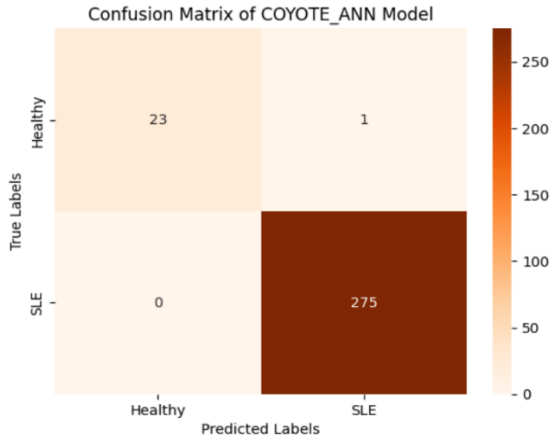

Fig. 6. Confusion Matrix of COA-ANN model

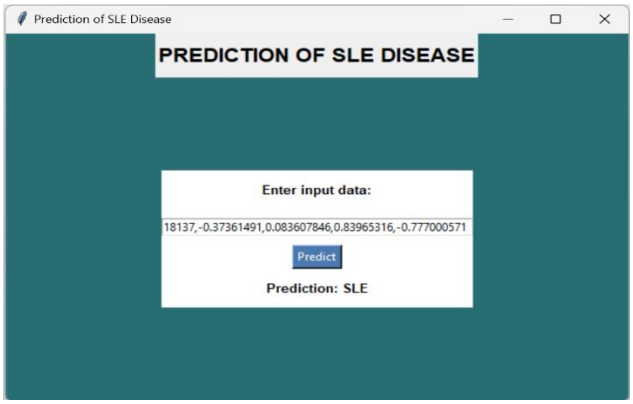

Fig. 7. GUI page of SLE prediction

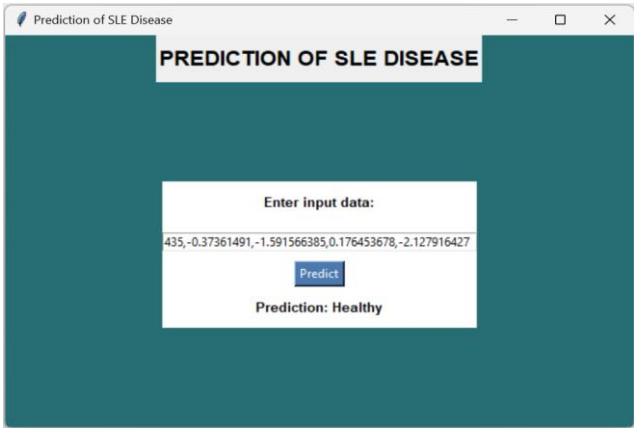

Fig. 8. GUI page of Healthy prediction

Fig. 7 represents the GUI implementation of the proposed method that presents an interactive section for users to input relevant information, such as medical history, symptoms, and demographic details. Based on the user input, the model predicted that the user is having SLE disease. The GUI displays the prediction output, indicating that the user is classified as having SLE.

Fig. 8 represents the snapshot of the GUI displaying the prediction output, indicating the user is classified as healthy.

4. Conclusion

In conclusion, the Coyote Optimization Algorithm showcased its effectiveness in feature selection for SLE prediction, yielding a subset that maximizes predictive accuracy. The COA-ANN model was evaluated against various metrics such as accuracy 99.6%, Precision 0.996, Recall 1.0, and F1-score 0.998. The identified features, as presented in the Best Alpha Coyote, provide valuable insights into the most relevant variables for accurate SLE classification. The adaptability and evolutionary nature of COA make it a promising tool for optimizing feature subsets in healthcare predictive modeling. Further validation and integration of the selected features into clinical decision support systems can potentially enhance the diagnostic accuracy of SLE, contributing to improved patient outcomes. The algorithm's ability to adapt and optimize feature subsets aligns with the complex and multifaceted nature of autoimmune disease prediction, emphasizing its potential to advance precision medicine.

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