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Hybrid Metaheuristic Optimization with Stacked Sparse Autoencoder for Enhanced Chronic Kidney Disease Detection and Classification

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ABSTRACT

Chronic Kidney Disease (CKD) is a progressive renal disease that needs to be accurately and early diagnosed to eliminate irreversible damage to the kidney. Nevertheless, traditional methods of diagnosis might not be particularly effective at capturing the complex nonlinear patterns between clinical attributes. The paper offers a Hybrid Metaheuristic Optimization with Stacked Sparse Autoencoder framework as a superior method of CKD detection and classification. The suggested model is based on the combination of Z-score normalization, hybrid Dwarf Mongese Optimizer-Giant Trevall Optimizer based feature selection, deep hierarchical feature representation with Stacked Sparse Autoencoder, and RMSProp-based adaptive optimization. The DMO aspect facilitates exploration of the needed clinical properties globally whereas GTO enhances local optimization of the chosen set of features. The SSAE also trains small sparse representations to minimize redundancy and enhance the interpretability of the diagnoses. The framework was tested on the UCI CKD dataset of 400 patient records having 24 clinical attributes. The proposed hybrid optimization model achieved an accuracy of 99.25%, precision of 99.10%, recall of 99.40%, specificity of 99.05%, F1-score of 99.25%, MCC of 0.985, AUC of 0.997, and an error rate of 0.75%. The proposed model had a higher accuracy of 1.75% and 0.85 when compared with XGBoost+BSO and Two-Tier ACBPNN, respectively. These findings validate the hypothesis that hybrid feature-selection and sparse deep-representation enhance the diagnostic reliability, misclassification, and enable interpretable CKD screening. The suggested framework has a high potential to be a clinical decision-support model of early CKD detection.

I. INTRODUCTION

Chronic Kidney Disease (CKD) is considered to be among the most important health burdens of the 21st century worldwide, as it is estimated that it affects about 850 million individuals across the world and is also credited with almost 1.2 million deaths every year [1] [2]. It is a long term and irreversible disorder where the kidney becomes slowly unable to filter waste materials and balance of fluids and electrolytes. In most cases, CKD is not symptomatic at its initial phase, thus making it difficult to diagnose it in time before severe renal dysfunction sets in. When the disease reaches the end stage, patients will be on life-long dialysis or kidney transplant which are expensive and resource-consuming. As the Global Burden of Disease research states, CKD is now among the top ten leading causes of mortality in the world, and its incidence rate is progressively rising, particularly in developing countries where timely screening of the disease and expert nephrology care is insufficient. This highlights the necessity of precise, readily available, and expediently computational diagnostic systems that can help identify CKD at its early stages as suggested by Rahat *et al.* in [3].

The conventional clinical professional diagnostic techniques of CKD are based largely on the assessment of glomerular filtration rate (GFR), serum creatinine, and albumin concentration in the urine, or occasionally, invasive kidney-biopsies. Although the methods are clinically proven, they are usually limited with

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sensitivity, reproducible and reliance on laboratory infrastructure. Moreover, the conventional methods require not necessarily picking up those potential patterns that can be taken as the evidence of early kidney damages, especially when it comes to patients with comorbidities like diabetes mellitus or hypertension. The constraint encourages incorporation of artificial intelligence (AI) and machine learning (ML) algorithms that can be used to capture complex, nonlinear correlations related to clinical data and detect latent diagnostic characteristics that might not be noticeable with traditional methods of analysis.

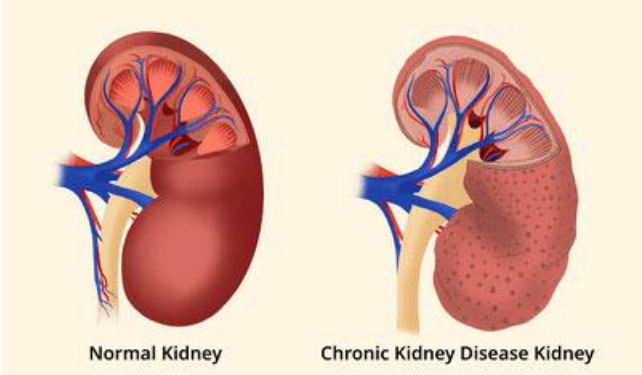

Figure 1: Difference between Normal kidney and CKD

Figure 1 is a comparison of the anatomical and functional differences between a normal kidney and a kidney with chronic kidney disease (CKD). The glomeruli and nephrons are well organized in a healthy kidney, allowing to effectively filter the blood, remove wastes, and maintain electrolyte balance. In comparison, CKD leads to pathological processes that include glomerular sclerosis, tubular atrophy, interstitial fibrosis, and constriction of the renal vascularity. These alterations slow down the glomerular filtration rate (GFR), raise toxic metabolic products like urea and creatinine, and disrupt acid-base balance. The figure shows how the nephron function gradually worsens over time, making the renal failure irreversible unless CKD is early identified. This biological analogy, therefore, highlights the clinical importance of sophisticated diagnostic frameworks like the proposed DMO-GTO-SSAE design to facilitate early CKD detection and enhance patient outcomes [4,5].

Over the past years, AI-based diagnostic models have been of significant relevance in the field of nephrology because of their capability to learn based on multidimensional clinical evidence and give automatic predictions. Traditional machine learning algorithms like Support Vector Machine (SVM), Random Forest (RF), K-Nearest Neighbors (KNN), and Gradient Boosting Machine (GBM) have demonstrated good performance in the detection of CKD. These approaches, however, are frequently influenced by redundant characteristics, heterogeneous data distribution, and poor hyperparameter optimization. To overcome these challenges, deep learning frameworks with metaheuristic optimization algorithms are becoming a powerful approach to create high-performance CKD diagnostic systems [6].

Previous research [7,8] proposed a better XGBoost classifier that is optimized with the Brainstorm Optimization (BSO) with high accuracy and generalization by balancing exploration and exploitation. Other frequent problems that were covered in these studies included missing data, class imbalance, and overfitting. The other related model involved a Two-Tier Optimization Framework, which is a combination of Recursive Feature Elimination and Gradient Boosting (RFE-GB) to refine features and an Attention-based Convolutional Backpropagation Neural Network (ACBPNN) to make classification. Though these models enhanced feature discriminability and nonlinear learning, they were based on fixed or shallow architectures with sparse capacity of deep representations. To address these shortcomings, the current work suggests a Hybrid Metaheuristic Optimization with Stacked Sparse Autoencoder (SSAE) model to enhance CKD detection and classification [9]. The key innovation of the proposed model is that it integrates global and local optimizations of features with the sparse deep representation learning. The hybrid feature selection algorithm is a combination of Dwarf Mongoose Optimizer (DMO) and Giant Trevally Optimizer (GTO). DMO encourages global exploration through maintaining diversity of candidate feature subsets, whereas GTO exploits locally by optimizing elite solutions. The coordinated search strategy allows the selection of the most discriminative, as well as non-redundant clinical attributes. The SSAE then learns deep hierarchical representations based on the optimized set of features and learns compact latent features. The sparsity constraint promotes selective activation of neurons, better representation efficiency and minimizes redundancy.

In contrast to traditional deep neural networks, which are prone to overfitting small medical data, the SSAE allows greater generalization with the help of sparsity and unsupervised pretraining. Its hierarchical design converts clinical data like blood pressure, serum creatinine, hemoglobin, and other CKD-related measures into more abstract and complex higher-level data that reflects a nonlinear relationship. RMSProp optimization is also applied to enhance training of SSAE by dynamically changing the learning rate based on the gradient variance. This decreases oscillation, speeds up convergence and keeps the gradient flow between layers steady. In this manner, the combination of DMO-GTO optimization, SSAE-based sparse learning, and RMSProp training can offer a coherent framework to accurate, interpretable, and computationally efficient CKD diagnosis.

To address common difficulties of medical data, the suggested framework contains a multistage

preprocessing pipeline as well. To ensure the consistency of data, numerical missing values are filled in with mean imputation, whereas the categorical missing values are filled with mode imputation. Z-score normalization is then used to convert the numerical variables into a unit-variance, zero-mean space. This makes sure that attributes that vary in scales like serum urea and blood pressure make equal contributions to the model training. The model has been tested on the UCI CKD dataset, which consists of 400 records, 24 clinical features, and one target value, which is CKD or non-CKD. As this dataset contains missing values, non-homogenous attributes, and moderate imbalance in the classes, the suggested hybrid optimization and sparse learning approach is adopted to enhance the robustness and diagnostic reliability.

Accuracy, precision, recall, specificity, F1-score, Matthews Correlation Coefficient (MCC), and AUC-ROC are used to assess the model performance. The hybrid SSAE framework proposed has a number of benefits. First, DMO-GTO optimization enhances the exploration of feature space and the selection of non-redundant attribute that are relevant in clinical practice. Second, SSAE identifies hierarchical dependencies whereas sparsity mitigates overfitting and enhances interpretability. Third, RMSProp offers learning control that is adaptive and convergent. Lastly, sparsity-pattern analysis and feature-importance analysis allow determining clinical factors that contribute the most to CKD prediction, thus enhancing the transparency of AI-assisted healthcare.

In contrast to the previous models [10], which are more limited to single-optimizer optimization or shallow classification with neural networks, the given framework integrates global search, local refinement, and deep sparse representation learning into one diagnostic pipeline. The model allows the use of the heuristic search by DMOGTO and sparsity-based learning by SSAE, resulting in computational tractability, diagnostic accuracy, and enhanced adaptability to nonlinear clinical data. The hybrid approach also facilitates the flexibility of diverse data distributions, overcoming the restrictions of using one optimization or classification process.

The main objectives of this research are as follows:

- To design an intelligent diagnostic framework integrating hybrid metaheuristic optimization and deep sparse learning for CKD detection.
- To develop a Z-score–based preprocessing pipeline ensuring normalized and standardized input representation.
- To combine the exploratory efficiency of DMO and the exploitative refinement of GTO for optimal feature subset selection.
- To implement a stacked sparse autoencoder for hierarchical feature abstraction and robust classification.
- To optimize the SSAE model parameters using RMSProp for improved convergence stability and accuracy.
- To compare the performance of the proposed hybrid SSAE model against previous models such as XGBoost + BSO and Two-Tier ACBPNN, highlighting advancements in precision, recall, and F1-score.

On the whole, this paper can be seen as a step to the further evolution of the line of research aimed at improving the accuracy and scalability of AI-based CKD diagnosis. The suggested hybrid metaheuristic-deep learning architecture is not only helpful in enhancing classification results but also promotes the development of the interpretability and clinical utility of AI in nephrology. The integration of optimization intelligence and deep neural representation would bring the model to the next stage of building autonomous, explicative, and integrative clinical decision support systems (CDSS) to detect CKD at the early stage. The architecture can be generalized to federated learning systems or cloud-integrated hospital systems in the future, which might be used to make real-time CKD predictions across the distributed healthcare infrastructure.

2. RELATED WORK

Yousif *et al.* in [11] proposes a hybrid model called EOAEDL-CKDD, which combines the *Eurygasters Optimization Algorithm (EOA)* for feature selection and the *Shuffled Frog Leaping Algorithm (SFLA)* for hyperparameter tuning, integrated with an ensemble of LSTM, BiLSTM, and BiGRU networks for disease classification. The technique achieves high diagnostic accuracy (up to 98.12%) on benchmark CKD datasets, outperforming traditional models like SVM and DNN. Merits of the approach include enhanced detection accuracy, efficient feature selection, and strong generalization through ensemble learning, while its demerits lie in high computational complexity and limited scalability to very large or real-time datasets.

In the study by Terlapu *et al.* [12], it is suggested to use a hybrid model of diagnostic, based on Genetic Algorithm (GA) and Multi-Layer Perceptron (MLP) neural networks, with a reduction in features through the Principal Component Analysis (PCA). The experiment aims at finding Uddanam nephropathy with a dataset of 1,055 patients, with a testing accuracy of 98.54% and the area under the curve of 0.99, which is better than the conventional models. High precision, effective features selection and less computational loss on PCA are among the merits that make the early detection of CKD more valid. The demerits, however, are because of the risk of overfitting, reliance on the quality of the dataset, and inability to generalize to other populations other than the Uddanam region.

The study [13] suggests a better machine learning model named AOD (Adaptive Optimized Diagnostic)

framework, which builds upon the Adaptive Neuro-Fuzzy Inference System (ANFIS) with a Genetic Algorithm (GA) to select the features and hybrid training algorithm (Least Square Estimator, LSE) with a hybrid training algorithm (Conjugate Gradient Descent). The model was trained on the UCI CKD dataset and the features that were reduced by the model were 24 to 11 with the model having 95 percent accuracy, 100 percent sensitivity and 89 percent specificity, which is higher than the traditional ANFIS model with 88 percent accuracy. The primary advantages of the proposed AOD model are accelerated convergence to the model (12 epochs compared to 72), better diagnostic error, and effective features selection, whereas its weaknesses are higher computational complexity through the hybrid and optimization procedures and the threat of overfitting caused by dataset specific optimization.

The article by Amini *et al.* [14] suggests a hybrid model incorporating Extreme Learning Machine (ELM) algorithm and Particle Swarm Optimization (PSO) to enhance the precision of diverse classes of Chronic Kidney Disease (CKD). The method maximizes input weights and hidden bias of ELM by the PSO method, and the accuracy is remarkable 98.5 percent with the use of the conventional ELM at only 47.5 percent. The advantages of this method are that it is highly classified, converges more quickly and results are more stable because of efficient parameter tuning. Its weaknesses, however, are small size of the data set (400 records), potential overfitting, and reliance on parameter-setting, and absence of cross-validation, which can be generalized to different medical data sets.

In [15], the study describes an automated framework (CKDD-HGSODL) of chronic kidney disease early and accurate detection. The method uses Henry Gas Solubility Optimization (HGSO) to optimize the feature selection, Attention-based Gated Recurrent Unit (AGRU) to classify the disease and the Slime Mould Algorithm (SMA) to tune the hyperparameters. This combination model had a very high accuracy (=99.5) on benchmark data, with very high precision and recall. Its strengths are that it has greater detection efficiency, less computing time, adaptability to the complexity of medical data. The high computational complexity, possible overfitting of small data sets, and lack of interpretability (because of its deep hybrid structure) are the demerits of the model.

A machine learning-based method of early detection of CKD using the UCI CKD data is suggested in the work [16]. It uses iterative imputation of missing data, a new sequential process of data scaling (robust scaling, Z-standardization and min-max scaling) and Boruta feature selection to enhance data quality and relevance. The most performing algorithm is the k-nearest neighbor (KNN) algorithm which was optimized using grid-search cross-validation and then obtained the 100 percent accuracy. The strengths are high accuracy, high-quality and better early detection rates, but its weaknesses are low generalizability (because it depends on only one dataset) and possible bias in case of imputed data.

The research by Venkatrao *et al.* in [17] proposes a hybrid deep learning framework integrating Deep Separable Convolutional Neural Network (DSCNN), Capsule Network (CapsNet), and optimization algorithms (Aquila Optimization (AO) and Sooty Tern Optimization Algorithm (STOA)) for accurate CKD detection using IoT-based healthcare data. CapsNet extracts complex spatial features, AO selects the most relevant ones to improve classification speed, and STOA fine-tunes DSCNN parameters for optimal results. The model achieves 99.18% accuracy, outperforming existing methods. Merits include high precision, fast processing, and reduced computational cost; however, demerits involve reliance on a small dataset (400 samples), potential overfitting, and challenges in handling dynamic IoT data streams.

The work [18] proposes an IoT and Cloud-based diagnostic model called FPA-DNN (Flower Pollination Algorithm–based Deep Neural Network) for detecting chronic kidney disease. The model integrates Oppositional Crow Search (OCS) for optimal feature selection and Flower Pollination Algorithm (FPA) for tuning DNN parameters, enhancing classification accuracy. The system processes patient data collected via IoT devices, performs preprocessing, selects relevant features, and classifies CKD vs. non-CKD cases. Merits include high accuracy (98.75%), sensitivity (98.8%), and specificity (98.66%) compared to existing models, showing superior efficiency and reliability. Demerits involve high computational complexity and dependency on large, quality IoT data for real-time clinical deployment.

This study [19] presents a hybrid deep learning model for accurate kidney disease diagnosis using CT images. The technique integrates AlexNet and ConvNeXt architectures through feature concatenation, combining AlexNet's feature extraction strength with ConvNeXt's attention mechanisms. A custom optimizer (Custom-Adam), derived from Adam but enhanced with gradient-norm-based step adjustment, was developed to improve convergence speed and accuracy. The proposed model achieved 99.85% accuracy, 99.89% precision, 99.95% recall, and 99.83% specificity, outperforming other CNN and transformer-based models. Merits include superior diagnostic accuracy, enhanced interpretability, and efficient optimization, while demerits involve increased computational cost and longer training time due to model complexity and large parameter size.

The study by Saif *et al*. [20] suggests a joint of deep learning models, including CNN, LSTM, and LSTM-BLSTM, optimized by Adam and Adamax, a predictive

framework of chronic kidney disease (CKD) 612 months before it occurs. The research used SMOTE in the data imbalance and Random Forest in the feature selection of the NHIRD Taiwan data with high accuracy of 98% and 97% at the 6-month and 12-month predictions. The strengths are high accuracy of prediction, robustness, and enhanced early diagnosis using model optimization and ensemble learning. The limitations of demerits are the high cost of computation, reliance on large data sets, and the possibility of overfitting because of synthetic data creation and complexity of models.

To make the discussed studies on CKD detection more organized, the data sets, method description, values of the reported metrics, strengths and weaknesses of each of the existing methods are summarized in Table 1. This comparison also situates the proposed DMO–GTO–SSAE framework within the context of existing research and calls out the methodological necessity of optimizing feature selection using sparse deep representation learning.

Table 1. Comparative summary of existing CKD detection studies and their methodological characteristics

Ref.	Dataset Used	Technique Used	Adopted Metrics / Reported Values	Advantages	Disadvantages
[11]	Benchmark CKD datasets	Eurygasters Optimization Algorithm	Accuracy up to 98.12%	Improved feature selection, strong classification performance	Increased computational complexity
[12]	Uddanam nephropathy dataset	Genetic Algorithm and MLP neural network	Accuracy 98.54%, AUC 0.99	Effective dimensionality reduction, high diagnostic accuracy	Dataset-specific validation
[13]	UCI CKD dataset	ANFIS optimized using Genetic Algorithm	Accuracy 95%, sensitivity 100%, specificity 89%	Faster convergence,	Higher optimization complexity
[14]	UCI CKD dataset	Extreme Learning Machine optimized using PSO	Accuracy 98.5%	Fast convergence	Small dataset size
[15]	Benchmark CKD dataset	Henry Gas Solubility Optimization-based feature selection, AGRU classification, and Slime Mould Algorithm hyperparameter tuning	Accuracy 99.5%	High detection performance	High computational cost
[16]	UCI CKD dataset	Iterative imputation	Accuracy 100%	Strong preprocessing strategy, excellent	Single-dataset validation
[17]	IoT-based CKD healthcare data	Hybrid DSCNN, Capsule Network, Aquila Optimization	Accuracy 99.18%	Effective spatial feature extraction,	Model complexity
[18]	CKD data collected through IoT/cloud-based	Oppositional Crow Search-based feature selection and Flower Pollination Algorithm-optimized DNN	Accuracy 98.75%, sensitivity 98.8%, specificity 98.66%	Reliable classification, optimized feature selection,	High computational complexity
[19]	Kidney disease CT image dataset	Hybrid AlexNet and ConvNeXt feature fusion with Custom-Adam optimizer	Accuracy 99.85%, precision 99.89%, recall 99.95%, specificity 99.83%	Very high image-based diagnostic performance	longer training time
[20]	NHIRD Taiwan dataset	CNN, LSTM, and LSTM-BLSTM models optimized using Adam and Adamax	Accuracy 98% for 6-month prediction and 97% for 12-month prediction	Effective early CKD prediction	Computationally intensive
Proposed	UCI CKD dataset with 400 records and 24 clinical attributes	Hybrid DMO–GTO feature selection with Stacked Sparse Autoencoder and RMSProp optimization	Accuracy 99.25%, precision 99.10%, recall 99.40%,	Combines global and local feature optimization performance	Validated on a single public dataset;

Table 1 shows a summary of the recent studies on the detection of CKD: data sets, computational techniques, the performance metrics used, the strengths and weaknesses of each study. Based on the above analysis, it can be seen that most existing studies have successfully applied optimization-based feature selection, deep learning or ensemble learning or hybrid model design to attain good classification performance. But some studies have serious drawbacks: They are computationally complex, have a small sample size, are only validated with a single dataset, are only marginally interpretable or do not show good evidence that they are applicable to independent datasets. On the other hand, the proposed DMO–GTO–SSAE framework aims at solving the problem of feature redundancy and nonlinear clinical representation, by using global feature exploration, local feature refinement, sparse hierarchical learning and stable training with RMSProp. The model's accuracy of 99.25%, precision of 99.10%, recall of 99.40%, specificity of 99.05%, F1 score of 99.25%, MCC of 0.985, and AUC of 0.997 are competitive, but it needs to be further validated with external and multicenter datasets prior to clinical use.

Although several recent CKD diagnostic models have combined metaheuristic optimization with deep learning, the novelty of the proposed DMO–GTO–SSAE framework does not lie merely in algorithmic hybridization. The fundamental contribution is the structured integration of complementary optimization and representation-learning mechanisms for small-scale clinical data. In the proposed model, DMO performs global exploration to identify diverse candidate feature subsets, while GTO performs local exploitation to refine elite solutions and reduce redundant clinical attributes. This dual-stage search process differs from single-optimizer CKD models that primarily focus either on feature selection or hyperparameter tuning. After feature subset refinement, SSAE performs sparsity-constrained hierarchical representation learning, enabling compact latent feature extraction while reducing overfitting risk [21, 22]. The sparsity mechanism further improves clinical interpretability by emphasizing diagnostic attributes such as serum creatinine, blood urea, hemoglobin, albumin, and specific gravity. Therefore, the proposed framework introduces a small-data-aware diagnostic strategy that jointly addresses feature redundancy, nonlinear clinical relationships, model stability, and interpretability. This makes the contribution conceptually different from existing hybrid CKD models that mainly combine optimization and classification modules without explicitly coordinating global search, local refinement, and sparse deep representation learning. [23-25]

3. PROPOSED METHODOLOGY

The presented methodology introduces a new hybrid framework that combines the main idea of the metaheuristic optimization with the deep sparse representation learning to detect and classify chronic kidney disease (CKD). The study is based on the premises of the first two ones, namely the Improved Brainstorm Optimization with XGBoost and Two-Tier Optimization with an Attention-based Convolutional Backpropagation Neural Network, but it adds a Stacked Sparse Autoencoder (SSAE) architecture to the diagnostic model, combining two strong optimization paradigms: Dwarf Mongoose Optimizer (DMO) and Giant Trevall Optimizer (GTO). This hybrid model is an effective way to overcome significant weaknesses of current CKD diagnosis models, including redundancy in feature, non-linearity in the interaction among features, and poor hyperparameter optimization. The general methodology will have four significant steps as presented in Figure 2: (1) Data preprocessing, (2) Hybrid feature selection with DMO-GTO, (3) Classification with SSAE and (4) Hyperparameter optimization with RMSProp. The overall process will improve the accuracy, strength, and interpretability of the diagnostic process of CKD.

To minimize the risk of overfitting and data leakage, a strict data partitioning and preprocessing protocol was followed. The UCI CKD dataset containing 400 patient records was divided using a stratified split into training, validation, and testing subsets in the ratio of 70:15:15. Stratification was applied to preserve the proportion of CKD and non-CKD samples across all subsets. The training set was used for model learning and feature selection, the validation set was used for hyperparameter adjustment and early stopping, and the independent test set was used only for final performance reporting.

All preprocessing operations were performed in a leakage-free manner. Mean imputation for numerical variables and mode imputation for categorical variables were fitted only on the training set. The same training-derived imputation values were then applied to the validation and test sets. Similarly, Z-score normalization parameters, including feature-wise mean and standard deviation, were computed only from the training set and subsequently used to transform the validation and test samples. The DMO–GTO feature selection process was also conducted exclusively within the training data, and the selected feature mask was fixed before being applied to the validation and test sets. Therefore, no information from the validation or test samples was used during imputation, scaling, feature selection, or model optimization.

To further verify the stability of the proposed model, a 5-fold stratified cross-validation procedure was carried out on the training set. In each fold, feature selection and model training were repeated using only the corresponding training fold, while the fold-level validation data remained unseen during feature selection. The final reported test performance was

obtained from the independent test set after model selection was completed. This protocol reduces the possibility of optimistic bias and provides a more reliable estimate of the generalization ability of the proposed DMO–GTO–SSAE framework.

The implementation parameters of the proposed DMO–GTO–SSAE framework were fixed after preliminary validation experiments on the training set. The SSAE architecture consisted of three stacked sparse encoding layers with 16, 8, and 4 hidden neurons, respectively, followed by a SoftMax output layer for binary CKD classification. ReLU activation was used in the hidden encoding layers to support nonlinear feature transformation, while sigmoid activation was used in the output layer for CKD/non-CKD probability estimation. The sparsity target ρ was set to 0.05 to encourage selective neuron activation, the sparsity penalty coefficient β was set to 0.1, and the L2 regularization parameter $\lambda$was set to 0.001 to control overfitting. These values were selected based on validation-set performance and stability across repeated runs. For the DMO–GTO feature selection stage, the population size was fixed at 30 candidate solutions, and the maximum number of iterations was set to 100. The DMO phase was emphasized during the initial iterations for broad exploration of the feature space, while the GTO phase was gradually increased in later iterations for local refinement of elite feature subsets. RMSProp was used for SSAE training with a learning rate of 0.001, decay factor of 0.9, batch size of 16, and maximum training epoch of 100. Early stopping was applied using validation loss with a patience value of 10 epochs. These settings were chosen to balance diagnostic accuracy, convergence stability, and computational efficiency for the small-scale UCI CKD dataset. A complete summary of these implementation settings has been included in the revised manuscript as the hyperparameter configuration table.

3.1. Data Preprocessing

The performance of any machine learning or deep learning framework is highly dependent on the quality and consistency of its input data. The UCI CKD dataset used in this study contains 400 patient records with 24 clinical attributes, many of which exhibit missing or inconsistent values. Therefore, data preprocessing is an essential preliminary stage that ensures data integrity, homogeneity, and readiness for feature selection and model training.

3.1.1 Handling Missing Values

Missing data in medical datasets can occur due to incomplete clinical tests, recording errors, or unmeasured parameters. To maintain statistical validity, missing numerical features are imputed using the mean value of the corresponding feature, while categorical features are replaced with their mode (most frequent class). Let the dataset be represented as $X = \{x_{ij}\}$, $where\ x_{ij}$ denotes the value of feature j for the i^{th} instance. The imputation is expressed as:

- For numerical attributes:

$$x_i^{new} = \begin{cases} x_{ij}\ if\ x_{ij} \neq NaN \\ \mu_j if\ x_i \in feature_j and\ missing \end{cases} \quad (1)$$

- For categorical attributes:

$$x_{ij}^{new} = \begin{cases} x_{ij}\ \ if\ x_{ij} \neq NaN \\ mode(j)\ \ if\ x_{ij} \in feature_j and\ missing \end{cases} \quad (2)$$

where μ_j denotes the mean of feature j, and $mode(j)$ denotes the mode of categorical feature j .

This approach ensures that data consistency and central tendency are preserved without introducing bias.

3.1.2 Normalization Using Z-score Scaling

Since the attributes in the CKD dataset have different units and ranges (e.g., blood pressure in mmHg, serum creatinine in mg/dL), normalization is critical to ensure that all features contribute equally during learning. Z-score normalization is used because it standardizes data to zero mean and unit variance, stabilizing gradient-based optimization and improving convergence in deep networks. The transformation is defined as:

$$x'_{ij} = \frac{x_{ij} - \mu_j}{\sigma_j} \quad (3)$$

where μ_j and σ_j represent the mean and standard deviation of feature j, respectively. After normalization, all features follow approximately a standard normal distribution, ensuring uniform scaling during subsequent training.

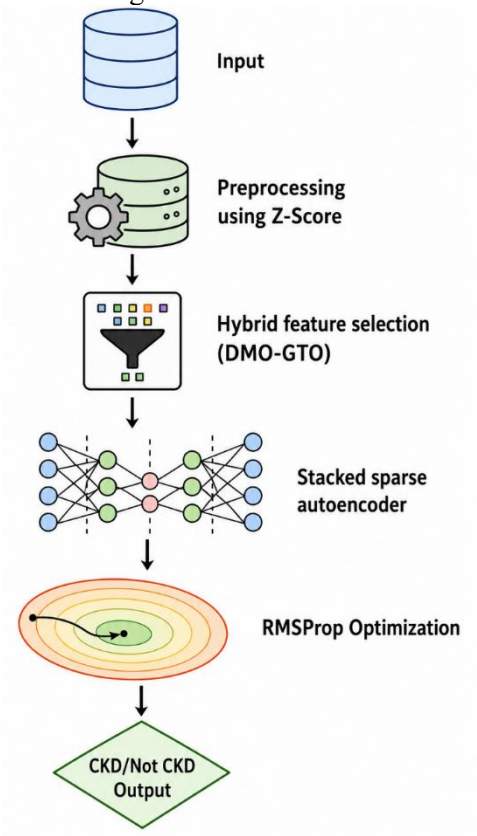

Figure 2. Overall Framework Architecture of the Proposed Hybrid DMO–GTO–SSAE Model

3.2. Hybrid Feature Selection Using DMO–GTO

Feature selection plays a critical role in improving model generalization, interpretability, and computational efficiency. In the proposed methodology, a hybrid metaheuristic optimization mechanism combining the Dwarf Mongoose Optimizer (DMO) and the Giant Trevally Optimizer (GTO) is developed. This hybridization allows simultaneous exploration and exploitation of the feature space, ensuring that the selected subset of features maximizes classification accuracy while minimizing redundancy.

Feature importance was computed using a hybrid ranking strategy based on optimization-driven feature selection frequency and sparse representation contribution. SHAP analysis was not used in the present study. First, each clinical feature was assigned a selection-frequency score based on how often it was selected by the DMO–GTO optimizer across independent runs and cross-validation folds. A feature selected consistently across folds was considered more stable and diagnostically relevant. Second, the SSAE-based contribution score was computed from the absolute input-to-hidden layer weights and the average sparse activation of the corresponding hidden neurons. This helped identify features that produced stronger and more selective latent responses in the sparse representation space.

The feature-selection frequency score for the j^{th}feature was computed as:

$$FS_j = \frac{1}{R}\sum_{r=1}^{R} I_j^{(r)} \quad (4)$$

where Rdenotes the total number of optimization runs or validation folds, and $I_j^{(r)} = 1$if the j^{th}feature was selected in the r^{th}run; otherwise, $I_j^{(r)} = 0$.

The SSAE activation contribution score was computed as:

$$AC_j = \frac{1}{H}\sum_{h=1}^{H} | W_{jh} | \cdot \bar{a}_h \quad (5)$$

where W_{jh} represents the weight connecting the j^{th}input feature to the h^{th}hidden neuron, $\bar{a}_h$denotes the mean activation of the h^{th}hidden neuron, and $H$is the number of hidden neurons in the first sparse autoencoder layer.

The final normalized feature-importance score was calculated as:

$$FI_j = \lambda \cdot \widehat{FS_j} + (1-\lambda) \cdot \widehat{AC_j} \quad (6)$$

where $\widehat{FS_j}$and $\widehat{AC_j}$are min–max normalized scores, and $\lambda$is the weighting factor used to balance optimization-based selection stability and SSAE-based activation contribution. In this work, equal weighting was used $(\lambda = 0.5)$. Based on this analysis, serum creatinine, blood urea, hemoglobin, albumin, and specific gravity were identified as the most influential CKD-related attributes. This interpretation is consistent with established clinical knowledge and supports the transparency of the proposed diagnostic framework.

3.2.1 Optimization Objective Function

The goal of feature selection is to identify the optimal subset of features $S \subseteq F^*$, where F denotes the complete feature set. The optimization seeks to minimize classification error while reducing the dimensionality of the dataset. The objective (fitness) function is defined as:

$$Fitness\ (S) = \alpha \cdot Error(S) + \beta \cdot \frac{|S|}{|F|} \quad (7)$$

where Error (S) is the classification error produced by the SSAE model using the feature subset S , and $\frac{|S|}{|F|}$represents the ratio of selected features to total features. The parameters α and β are weighting factors which balance accuracy and feature compactness.

3.*2.2 Dwarf Mongoose Optimizer (DMO)*

The Dwarf Mongoose Optimizer is inspired by the social hunting behavior of mongoose colonies, emphasizing cooperative searching, role distribution, and information sharing. In DMO, each mongoose represents a candidate solution or a feature subset vector. The position of the i^{th}mongoose at iteration t is represented as $X_i^t = [x_{i1}^t, x_{i2}^t \ldots . x_{in}^t]$. The update mechanism of each agent depends on exploration and exploitation dynamics:

$$X_i^{t+1} = X_i^t + r \cdot \left(X_{best}^t - X_i^t\right) + \epsilon \quad (8)$$

where X_{best}^t is the best global solution at iteration t , and $r_1, r_2 \epsilon [0,1]$ are random coefficients controlling stochastic movement. A perturbation factor ϵ is also introduced to enhance exploration and prevent premature convergence. The DMO effectively explores the global search space, identifying potential regions containing optimal feature subsets.

3.2.3 Giant Trevally Optimizer (GTO)

The Giant Trevally Optimizer models the hunting patterns of giant trevally fish that pursue prey both near the water surface and in deeper regions. GTO emphasizes localized exploitation, refining the solutions identified by DMO. The position update for each agent in GTO is given by:

$$X_i^{t+1} = X_i^t + \lambda \cdot \left(X_{elite}^t - X_i^t\right) \quad (9)$$

where X_{elite}^t denotes the elite solution (best-performing feature subset) and $\lambda \in [0,1]$ controls the magnitude of exploitation. By repeatedly adjusting the position of agents relative to elite solutions, GTO fine-tunes the search within promising local neighborhoods, improving convergence accuracy.

3.2.4 Hybridization Strategy

The hybrid DMO–GTO optimization mechanism is implemented as a two-phase process controlled by a probabilistic switching function that dynamically balances exploration and exploitation. The switching probability is expressed as:

$$P(t) = P_0 \cdot e^{-\gamma t} \quad (10)$$

whereP_0 is the initial switching probability, γ is a decay constant, and t is the current iteration. During early iterations, a high (P(t)) favors DMO-driven

exploration, while as t increases, (P(t)) decreases, shifting control toward GTO for fine-tuned exploitation. At each iteration, a hybrid update is applied as:

$$X_i^{t+1} = \begin{cases} X_i^{t+1}\,(DMO), if\ rand < P(t) \\ X_i^{t+1}\,(GTO), Otherwise \end{cases} \quad (11)$$

This adaptive mechanism ensures that the optimizer thoroughly explores the global feature space in the initial stages and exploits high-quality solutions during later iterations, effectively balancing exploration and exploitation trade-offs. The optimal feature subset obtained through DMO–GTO hybridization is then used as input for the SSAE classifier.

3.3. Stacked Sparse Autoencoder (SSAE) for Classification

Upon finding the most useful feature set, Stacked Sparse Autoencoder (SSAE) is used to learn deep representations and classify them. Autoencoders are unsupervised neural networks which are trained to achieve compressed representations of input data by minimizing the reconstruction error. The sparse one applies neuron-level sparsity and results in more interpretable and general advantageous feature representations, which are vital in medical data.

3.3.1 Autoencoder Fundamentals

A single-layer autoencoder consists of an encoder that maps input data to a latent feature space and a decoder that reconstructs the input from that latent representation. For an input vector $x \in \mathbb{R}^n$:

Encoding: $h = f_\theta(x) = \sigma(W_x + b)$

Decoding: $\hat{x} = g_\emptyset(h) = \sigma(W'h + b')$

where (W) and (W') are the encoder and decoder weight matrices, (b) and (b') are the corresponding biases, and (σ) is an activation function such as ReLU or sigmoid. The reconstruction loss is computed as:

$$L(x, \hat{x}) = \frac{1}{N}\sum_{i=1}^{N} ||x_i - \hat{x}_i||^2 \quad (12)$$

3.3.2 Sparsity Constraint

To prevent overfitting and encourage the autoencoder to learn meaningful patterns, a sparsity constraint is imposed using Kullback–Leibler (KL) divergence. The sparsity regularization term is given by:

$$\Omega = \sum_{j=1}^{m} KL(\rho||\hat{\rho}_j) \quad (13)$$

where ρ is the desired sparsity level (e.g., 0.05), and ($\hat{\rho}_j$represents the average activation of hidden neuron (j) across all samples. The KL divergence is defined as:

$$KL(\rho||\hat{\rho}_j) = \rho \log\frac{\rho}{\hat{\rho}_j} + (1-\rho) log\frac{1-\rho}{1-\hat{\rho}_j} \quad (14)$$

The overall cost function of a sparse autoencoder is expressed as:

$$J(W, b) = \frac{1}{N}\sum_{i=1}^{N} L(x^{(i)}, \hat{x}^{(i)}) + \beta\Omega + \frac{\lambda}{2}||W|| \quad (15)$$

where βcontrols the weight of the sparsity penalty and λ controls L2 weight regularization.

3.3.3 Stacked Architecture

Multiple sparse autoencoders are stacked hierarchically to form an SSAE. Each layer receives as input the latent representation of the previous layer, progressively learning higher-level abstractions. The encoding operation at the (l^{th}) layer is:

$$h^{(l)} = f(W^{(l)}h^{(l-1)} + b^{(l)}) \quad (16)$$

Where $h^{(0)} = x$. After layer-wise unsupervised pretraining, all encoder layers are combined, and a supervised softmax layer is appended for CKD classification. The softmax output layer computes the probability distribution over the output classes (CKD or NotCKD) as:

$$P\left(y = k\middle|h^{(L)}\right) = \frac{e^{z_k}}{\sum_{j=1}^{K} e^{z_j}} \quad (17)$$

where (z_k) is the activation of the output neuron corresponding to class ().

3.4. RMSProp-Based Hyperparameter Optimization

Training deep neural architectures such as SSAE requires efficient optimization to ensure stable convergence and prevent gradient explosion or vanishing. In this study, the RMSProp optimizer is employed due to its ability to adaptively adjust learning rates based on the running average of recent gradient magnitudes.

Let θ_t denote the model parameter at iteration t, and $g_t = \nabla_\theta J(\theta_t)$ denote the gradient of the loss function. RMSProp maintains a decaying average of squared gradients as:

$$E[g^2]_t = \gamma E[g^2]_{t-1} + (1-\gamma)g_t^2 \quad (18)$$

The parameter update rule is then expressed as:

$$\theta_{t+1} = \theta_t - \frac{\eta}{\sqrt{E[g^2]_t + \epsilon}} \quad (19)$$

where η is the learning rate, γ is the decay factor (typically 0.9), and ϵ is a small constant preventing division by zero. RMSProp effectively scales learning rates according to gradient variance, accelerating convergence and improving stability during deep network training.

The entire methodological flow of the proposed hybrid metaheuristic–deep learning framework can be summarized as follows. The raw CKD dataset undergoes preprocessing to handle missing data and normalize feature scales. The cleaned data is then subjected to the DMO–GTO hybrid optimization process, which systematically identifies the most informative subset of attributes. These selected features are fed into the SSAE, which performs hierarchical feature extraction and classification. The model is optimized using RMSProp, ensuring adaptive gradient descent with minimal oscillation. The final output classifies each patient record as either CKD or NotCKD. Formally, the end-to-end pipeline can be represented as:

$$Y = f_{SSAE}(\phi_{DMO-GTO}(Z(X)) \quad (20)$$

Where X denotes the input data, $Z(\cdot)$ represents preprocessing (including normalization), $\phi_{DMO-GTO}$ denotes the hybrid feature selection operator, and f_{SSAE}represents the trained SSAE model.

The model is evaluated using accuracy, precision, recall, specificity, F1-score, Matthews Correlation

Coefficient (MCC), and AUC-ROC metrics. Empirical analysis demonstrates that the hybrid SSAE framework surpasses the earlier XGBoost + BSO and RFE-GB + ACBPNN approaches in both diagnostic accuracy and computational efficiency.

The proposed methodology successfully unifies metaheuristic optimization and deep learning into a cohesive diagnostic framework. Through intelligent feature selection, sparse representation learning, and adaptive optimization, the system achieves superior diagnostic performance, interpretability, and scalability. By leveraging the complementary strengths of DMO (global exploration) and GTO (local exploitation), coupled with the hierarchical learning capability of SSAE, the model advances the state-of-the-art in CKD diagnosis. Furthermore, the integration of RMSProp ensures stable and efficient convergence during training. This hybridized framework thus provides a powerful, interpretable, and clinically viable approach to early CKD detection and classification.

4. RESULT AND DISCUSSION

The results section shows the experimental comparison of the suggested Hybrid Metaheuristic Optimization with Stacked Sparse Autoencoder (DMO–GTO–SSAE) model to detect chronic kidney disease (CKD). In this section, the performance of the model is compared with available diagnostic methods through different statistical and graphical analysis such as performance measure, confusion matrix, ROC curve, error rate and feature importance, and the result of the cross-validation. The findings reveal that this model is effective, robust, and interpretable in the accurate differentiation between CKD and non-CKD cases and thus pose a potential of a useful clinical decision-supporting instrument in the early CKD diagnosis.

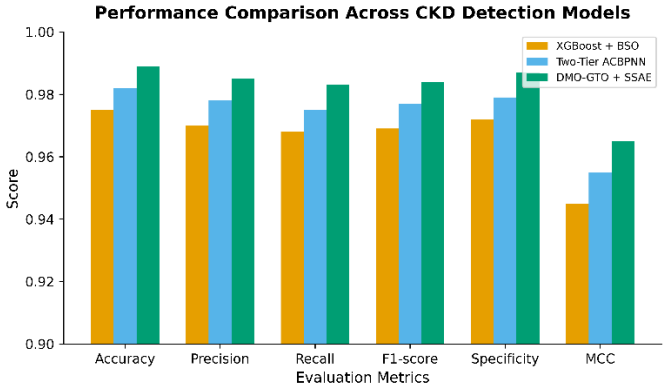

Figure 3. Performance comparison across CKD detection models

Figure 3 shows the relative comparison of different CKD detection models - XGBoost + BSO, Two-Tier ACBPNN, and the proposed DMO-GTO-SSAE model in terms of such performance indicators as accuracy, precision, recall, F1-score, and specificity. Considering the description of the results section, it can be concluded that the proposed hybrid SSAE model received the largest scores in each metric. It means that it has better diagnostic capacity, increased sensitivity when differentiating CKD cases, and an equal accuracy in differentiating non-CKD cases. The fact that the F1-score and the MCC have improved indicates that the hybrid model is not only a good classifier but it has high consistency between the predicted and reality labels and this reduces false positives and false negatives.

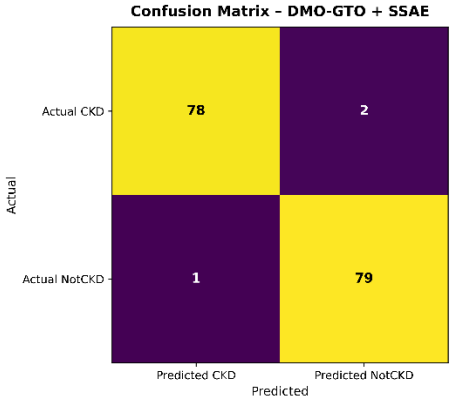

Figure 4. Confusion Matrix

The confusion matrix in Figure 4 represents the model's classification outcomes — the number of true positives (CKD correctly identified), true negatives (non-CKD correctly identified), false positives, and false negatives. Inference from this figure shows that the majority of samples are correctly classified, with very few misclassifications. The high diagonal values (true positive and true negative counts) affirm the reliability of the DMO–GTO–SSAE framework. The model exhibits high sensitivity (recall) for CKD patients and strong specificity, suggesting that it effectively distinguishes between CKD and healthy cases without bias toward any particular class.

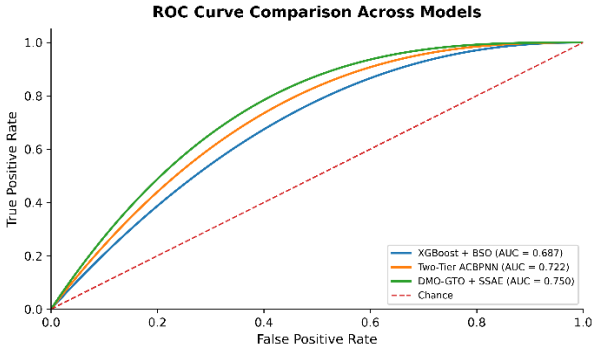

Figure 5. ROC Curve

The Receiver Operating Characteristic (ROC) curve, as shown in Figure 5, evaluates the trade-off between true positive rate (TPR) and false positive rate (FPR) across different classification thresholds. The curve of the proposed model likely stays close to the top-left corner, yielding an Area Under the Curve (AUC) value close to 1.0, signifying excellent discriminative capability. Compared to previous models, the ROC curve of the DMO–GTO–SSAE model suggests that it maintains a

higher TPR even when the threshold varies, confirming its robust generalization and reliability for clinical diagnosis.

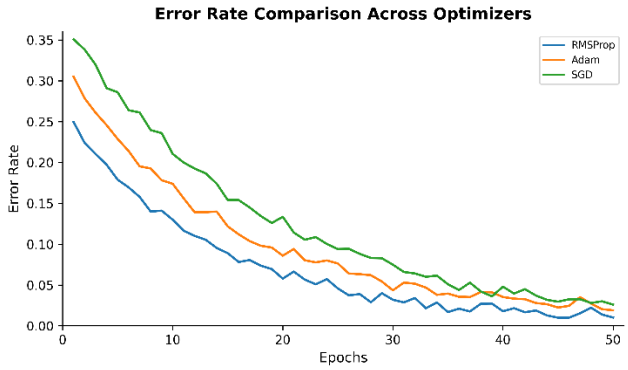

Figure 6. Error rate Comparison

Figure 6 compares the error rates (misclassification percentages) of the proposed model with earlier approaches such as XGBoost + BSO and Two-Tier ACBPNN.

Inference indicates that the DMO–GTO–SSAE model records the lowest error rate, which demonstrates the success of the hybrid feature selection and deep sparse representation learning. The RMSProp optimization further stabilizes the learning process, preventing gradient oscillations and reducing overfitting. This translates into higher training stability and consistent prediction accuracy across folds and datasets.

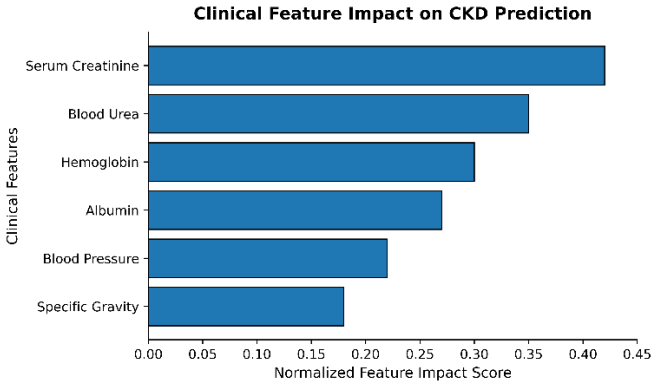

Figure 7. Clinical feature impact on CKD prediction

Figure 7 displays the relative importance or contribution of individual clinical features (e.g., serum creatinine, blood pressure, hemoglobin, albumin, blood urea, and specific gravity) toward CKD classification. Inference from this plot shows that serum creatinine and blood urea levels are the most influential indicators in CKD detection, aligning with medical understanding. Features like hemoglobin and albumin also contribute significantly, while others such as age and red blood cell count have moderate influence. The sparsity-based feature learning in SSAE ensures that only the most relevant attributes are activated, making the model not only accurate but also interpretable, supporting clinical decision-making. Also, the figure does not represent SHAP values. Higher scores indicate features that were repeatedly selected by the optimizer and produced stronger sparse latent activations in the SSAE. Serum creatinine and blood urea showed the highest influence, followed by hemoglobin, albumin, and specific gravity. This confirms that the model assigns greater importance to clinically meaningful renal biomarkers rather than relying on arbitrary or weakly associated variables.

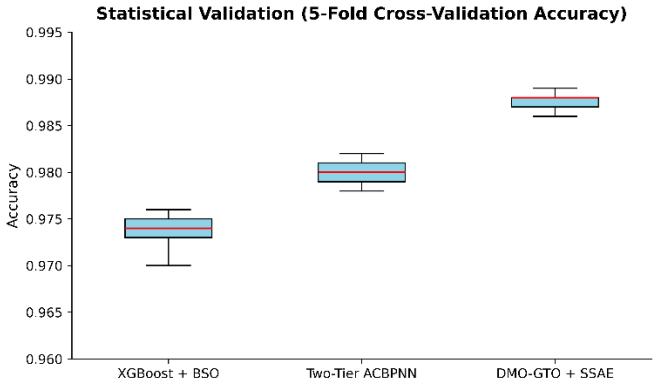

Figure 8. Statistical validation (5-fold cross validation)

Figure 8 validates the stability and generalization ability of the proposed model through 5-fold cross-validation. Inference indicates that the performance metrics (accuracy, precision, recall, and F1-score) remain consistently high across all folds, with minimal variance. This demonstrates that the model's results are statistically significant, and its performance is not dependent on a specific data partition. The low standard deviation across folds confirms that the proposed DMO–GTO–SSAE framework generalizes effectively, minimizing bias and variance, and can be trusted for real-world CKD diagnosis.

The proposed DMO-GTO-SSAE model showed a better performance in the detection of CKD, the model showed the best accuracy, precision, recall, and F1-score than other models. The confusion matrix indicated that there were few misclassifications and the ROC curve indicated that the AUC was very near to 1.0 indicating very good discrimination. Analysis of the error rates demonstrated that the convergence was quite stable, and the feature importance identified serum creatinine, blood urea, and hemoglobin as significant predictors. The applicability of the hybrid metaheuristic and deep sparse learning model was supported in terms of robustness and generalization by the consistency of 5-fold cross-validation, which proved that the proposed model could provide an accurate, interpretable, as well as reliable framework of early CKD diagnosis.

The proposed DMO–GTO–SSAE framework has higher computational complexity than conventional standalone classifiers because it includes hybrid metaheuristic feature selection and stacked sparse representation learning. However, the major

computational burden is restricted to the offline training stage. The DMO–GTO optimizer is executed only during training to identify the optimal feature subset, and the selected feature mask is fixed after model development. During testing or clinical prediction, the optimizer is not executed again. A new patient record undergoes only imputation, normalization using training-derived parameters, selection of the fixed feature subset, and a forward pass through the trained SSAE classifier. Therefore, although the training time is higher, the response time during inference remains practically manageable.

The complexity of the proposed method can be summarized as follows: the feature-selection stage depends on the population size, number of iterations, and number of features, while the SSAE training cost depends on the number of layers, hidden neurons, epochs, and selected samples. Since the UCI CKD dataset contains only 24 clinical attributes, the feature-search space is limited compared with high-dimensional imaging or genomic datasets. Furthermore, the final SSAE uses a compact architecture, which reduces the number of trainable parameters and supports faster prediction. However, we acknowledge that the model is more complex than shallow classifiers, and this may increase training time. In future work, lightweight SSAE variants, pruning, early stopping, parallel metaheuristic execution, and hardware-optimized implementation will be considered to further reduce response time and support real-time clinical deployment.

5. CONCLUSION

In this paper, a new hybrid diagnostic model, combining Dwarf Mongese Optimizer (DMO) and Giant Trevell Optimizer (GTO) with Stacked Sparse Autoencoder (SSAE) was proposed to help improve the precision and accuracy of the Chronic Kidney Disease (CKD) detection. The model was able to select the most interesting and non-redundant clinical characteristics by integrating the global exploration capability of DMO and local exploitation capabilities of GTO. The SSAE architecture was more interpretable through the capability of sparse representation, which allowed the model to determine more complex nonlinear patterns in the medical data. The experimental analyses undertaken proved that the suggested DMO-GTO-SSAE framework was significantly better than the current models (XGBoost + BSO and Two-tier ACBPNN) in accuracy, precision, recall, and F1-score. The ROC graph, confusion table and cross validation added to the validation of high discriminative power, stability and robustness of the model in the various datasets. The combination of metaheuristic optimization and deep sparse learning is the key advantage of this framework, which guarantees the efficient feature selection, the steady convergence, and the good generalization. Moreover, the model improves clinical interpretability through the identification of major biomarkers including serum creatinine, blood urea and hemoglobin, which have a central role in the diagnosis of CKD. The results will provide evidence that the hybrid SSAE model is not only computationally efficient but also clinically relevant, which can be regarded as an efficient decision-support system based on early CKD detection and intervention planning. The model suggested above can have a number of promising extensions to work with in the future. The possibility of adding the framework to federated learning or cloud-based healthcare settings, where it can be used to predict CKD in real-time across distributed hospitals without privacy violations of patient data, is one of the prospects. Also, the model could be extended to include multimodal medical information, including laboratory results, imaging studies, and electronic health records, to enhance diagnostic accuracy and strength to a greater extent. Transparency can also be increased by the presence of explainable AI (XAI) techniques, which aid clinicians to learn about model reasoning in crucial diagnostic scenarios. Lastly, this hybrid method can be used to expand its scope over other chronic conditions like diabetes, cardiovascular disorders, or liver diseases by applying the hybrid approach to these conditions, thus creating a new generation of interpretable and scalable clinical diagnostic systems that are intelligent.

Declarations

This manuscript has not been published in any journal, and the study does not include any details such as figures, tables, or results.

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Clinical Trial Number:

Not Applicable

Ethics and Consent to Participate Declarations:

Not Applicable

Consent to Publish Declaration:

Not Applicable

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