Early Detection of Sickle Cell Anemia in Nilgiri Tribes Using a Hybrid Swin Transformer-Based RNN with Improved Weighted Quantum Monkey Optimization Algorithm Optimization

C. Maria Sheeba [1*], K. Sarojini [2]

Abstract

Background: Early detection of Sickle Cell Anemia (SCA) is crucial for timely intervention and effective disease management, particularly in vulnerable populations like the Nilgiri tribes. Traditional diagnostic methods can be time-consuming and require specialized expertise. Deep learning techniques have shown promise in automating early-stage detection, but there is a need for improved models to enhance accuracy and efficiency. This study aims to develop a novel deep learning model that leverages a Hybrid Swin Transformer-Based Recurrent Neural Network (RNN) integrated with an Improved Weighted Quantum Monkey Optimization (IWQMO) algorithm for early-stage prediction of SCA in the Nilgiri tribes. Methods: The proposed hybrid model combines the Swin Transformer's hierarchical feature extraction with an RNN's temporal pattern recognition capabilities. The IWQMO algorithm is utilized to optimize feature selection, ensuring the most relevant attributes are prioritized for classification. The model is trained and evaluated on a dataset of 300 Nilgiri tribespeople's medical records provided by the NAWA-Nilgiri Adivasi Welfare Association. Performance metrics, including accuracy, precision, recall, and F1 score, were used to evaluate model efficacy. Results: The hybrid model demonstrated superior performance compared to traditional approaches. The Swin Transformer enhanced feature extraction, while the RNN improved temporal prediction. The IWQMO algorithm effectively selected the most pertinent features, contributing to a more accurate SCA classification. The model's performance was benchmarked against existing techniques, showing improved accuracy, precision, and recall. Conclusion: The Hybrid Swin Transformer-RNN model integrated with the IWQMO algorithm significantly improves early prediction of SCA, outperforming traditional diagnostic methods. This approach has the potential to provide more timely and accurate predictions, leading to better healthcare outcomes for the Nilgiri tribes. The findings underscore the potential of deep learning techniques for advancing public health initiatives in vulnerable populations.

Keywords: Sickle Cell Anemia, Deep Learning, Swin Transformer, Recurrent Neural Network, Nilgiri Tribes

Significance | This model offers an accurate, timely SCA detection solution, improving healthcare outcomes for Nilgiri tribes and vulnerable populations.

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Introduction

Sickle Cell Anemia (SCA) is a severe hereditary blood disorder caused by mutations in the HBB gene, which encodes the β-globin subunit of hemoglobin. This mutation results in the production of

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an abnormal form of hemoglobin, known as hemoglobin S (HbS) (Lamoureux et al., 2024). Hemoglobin is a critical protein in red blood cells (RBCs) responsible for oxygen transport from the lungs to various tissues. In SCA, the altered HbS causes RBCs to assume a sickle or crescent shape under low oxygen conditions, leading to reduced cell flexibility. These malformed cells can obstruct narrow blood vessels, causing ischemia, pain, organ damage, stroke, and an increased susceptibility to infections (Sen et al., 2021).

The clinical manifestations of SCA are highly variable, ranging from mild to severe symptoms. Chronic anemia, vaso-occlusive crises, acute chest syndrome, and splenic dysfunction are common complications. Additionally, individuals with SCA often experience reduced life expectancy due to the cumulative effects of these complications (Alzubaidi et al., 2020). Globally, SCA is among the most prevalent inherited blood disorders, with a significant burden in Sub-Saharan Africa, the Middle East, and India (Zhang et al., 2020). Early diagnosis and comprehensive management are critical to improving patient outcomes and mitigating the disease's societal and economic impact.

The Nilgiri tribes of Southern India represent a population disproportionately affected by SCA. These indigenous groups exhibit a high prevalence of the sickle cell trait (SCT), a heterozygous condition where individuals inherit one mutated HBB allele but typically remain asymptomatic (Jennifer et al., 2023). However, when two mutated alleles are inherited, the resulting homozygous condition manifests as SCA. The geographical isolation of the Nilgiri tribes and their limited access to healthcare resources exacerbate the impact of SCA on these communities (Tengshe et al., 2021).

Healthcare challenges in the Nilgiri region include inadequate diagnostic infrastructure, low levels of disease awareness, and delayed medical interventions. Consequently, many cases of SCA remain undiagnosed until severe complications arise. This delay significantly increases morbidity and mortality rates (Bushra & Shobana, 2021). Moreover, socio-economic and environmental factors contribute to the disproportionate burden of SCA within these populations.

Effective management of SCA begins with early and accurate diagnosis. Conventional diagnostic methods include hemoglobin electrophoresis, high-performance liquid chromatography (HPLC), and genetic testing (Dada et al., 2022). While these methods provide high diagnostic accuracy, they are often inaccessible to rural and tribal communities due to their cost and infrastructure requirements. The need for non-invasive, affordable, and scalable diagnostic tools is particularly acute in resource-limited settings like the Nilgiris (Simon et al., 2023).

A key obstacle in SCA diagnosis is the phenotypic overlap with other hemoglobinopathies, making differentiation challenging without advanced laboratory techniques. Additionally, the genetic and clinical variability of SCA complicates the development of universal diagnostic models. These challenges underscore the necessity for innovative approaches to SCA prediction and diagnosis (Ganesan & K, 2023).

Recent advancements in artificial intelligence (AI) and machine learning (ML) have opened new avenues for addressing the limitations of traditional diagnostic methods. AI models, leveraging large datasets, can identify patterns and correlations that are imperceptible to human analysis. These technologies have demonstrated promising results in improving diagnostic accuracy, especially in resource-constrained settings (Alzubaidi et al., 2020).

Deep learning techniques, such as convolutional neural networks (CNNs) and recurrent neural networks (RNNs), have been successfully applied to medical image analysis and time-series data in SCA diagnosis. For instance, automated segmentation and classification of RBCs using CNNs have achieved high accuracy in identifying sickled cells in blood smears (Zhang et al., 2020; Tengshe et al., 2021). Moreover, hybrid models combining CNNs with RNNs have shown potential for analyzing sequential data, such as temporal variations in hematological parameters (Deo et al., 2024).

Despite these advancements, existing AI-based models face challenges related to feature selection, model generalizability, and computational efficiency. Addressing these limitations is critical for developing practical and scalable solutions for SCA diagnosis (Chen et al., 2023).

The high prevalence of SCA among the Nilgiri tribes, combined with the limitations of traditional diagnostic methods, motivates the exploration of AI-driven approaches for early and accurate disease prediction. This research aims to develop a Hybrid Swin Transformer-based RNN model optimized using the Improved Weighted Quantum Monkey Optimization (IWQMO) algorithm. The primary objectives include:

Enhancing diagnostic accuracy through the integration of genetic, clinical, and demographic data.

Improving model efficiency to enable deployment in resource-constrained settings.

Addressing feature selection challenges by leveraging the strengths of Swin Transformers and IWQMO algorithms.

The proposed model seeks to bridge the gap between advanced diagnostic capabilities and accessibility, particularly for underserved populations like the Nilgiri tribes (Goswami et al., 2024).

This study has the potential to revolutionize SCA diagnosis and management in marginalized communities. Early and accurate prediction of SCA can significantly improve patient outcomes by enabling timely medical interventions. Moreover, reducing the economic burden associated with advanced-stage disease

management can alleviate the strain on healthcare systems in resource-limited regions (Fu et al., 2024).

From a broader perspective, this research contributes to the field of AI in healthcare by demonstrating the efficacy of hybrid models that combine multiple neural network architectures and optimization techniques. The integration of Swin Transformers, RNNs, and IWQMO offers a novel approach to feature extraction, temporal pattern recognition, and optimization, paving the way for future innovations in AI-based medical diagnostics (Nardo-Marino et al., 2022).

The remainder of this paper is structured as follows: Section 2 reviews related work, focusing on AI applications in SCA diagnosis and hybrid model development. Section 3 outlines the methodology, detailing the architecture of the proposed model and the IWQMO optimization process. Section 4 describes the experimental setup, including data collection and evaluation metrics. Section 5 presents the results and compares the proposed model's performance with existing approaches. Finally, Section 6 concludes the paper and discusses future research directions.

2. Related works

Sickle cell anemia (SCA) is a genetic disorder characterized by the abnormal crescent or sickle shape of red blood cells (RBCs), which disrupts their ability to move efficiently through the bloodstream and significantly reduces oxygen delivery (Lamoureux et al., 2024). The distorted morphology of RBCs in SCA contributes to blocked blood vessels, resulting in various health complications (Sen et al., 2021). Accurate classification of RBCs is essential for diagnosing SCA, as it facilitates the assessment of disease severity and guides treatment decisions (Alzubaidi et al., 2020). However, manual detection of SCA is labor-intensive and costly, necessitating the development of automated solutions.

Advancements in medical image processing have highlighted the importance of semantic segmentation in identifying abnormalities with precision. Challenges such as noise, variations in cell shape, size, and viewpoint further complicate SCA diagnosis (Zhang et al., 2020). Early detection of sickle cell disease (SCD) is crucial, particularly in newborns, to improve management and treatment outcomes. To address this, a deep learning (DL) and artificial intelligence (AI)-based framework has been proposed, ensuring human guidance throughout the diagnostic process (Jennifer et al., 2023).

The application of AI in healthcare has revolutionized SCA diagnosis by addressing the limitations of traditional screening methods, which are often inaccurate and time-consuming (Tengshe et al., 2021). A novel approach involving ResNet34, a high-throughput image analysis model, has shown promise in enhancing diagnostic accuracy (Sani et al., 2024). Furthermore, the acute reduction in hematocrit levels in sickle cell-associated anemia (SMA) is attributed to heightened phagocytic activity in the spleen, leading to distinct morphological changes in RBCs (Nardo-Marino et al., 2022). Automated systems for capturing and analyzing RBC images have been developed to streamline the diagnostic workflow (Deo et al., 2024).

The spleen, a critical organ in combating bacterial infections, is significantly affected in SCA. Early life spleen injuries underscore the importance of measuring splenic function, with automated methods such as deep neural network analysis providing innovative solutions (Goswami et al., 2024). SCD arises due to the polymerization of sickle hemoglobin, which reduces RBC flexibility, causing vessel occlusion and severe morbidity (Chen et al., 2023). Holographic cytometry (HC), a label-free imaging modality, has been utilized for comprehensive RBC morphological profiling to detect SCD (Manescu et al., 2020).

Machine vision techniques applied to blood films have emerged as scalable diagnostic tools, particularly in resource-constrained settings. However, the lack of object-level annotations of disease markers, including parasites and abnormal RBCs, remains a bottleneck for successful implementation (Fu et al., 2024). AI has also demonstrated transformative potential in ophthalmology and other fields, streamlining disease diagnosis and management (Parmar et al., 2024).

In pediatric populations, splenomegaly—a common complication of SCD—requires precise measurement through advanced imaging techniques. Deep learning methods for automated spleen length measurement in 2D ultrasound imaging offer a promising alternative to traditional manual palpation (Yuan et al., 2020). Additionally, innovative approaches such as microstrip isoelectric focusing (mIEF) have demonstrated efficacy in detecting hemoglobin species, complementing conventional hematology analyzers (Koua et al., 2024).

Comprehensive patient data collection during medical procedures enhances diagnostic accuracy and supports clinical decision-making. This data may include observed symptoms, preliminary findings, or detailed laboratory results (Gaikwad et al., 2024). By integrating DL and AI techniques, researchers aim to improve SCA diagnosis, classification, and treatment outcomes (Dada et al., 2022). Explainable AI models have further expanded our understanding of RBC abnormalities, aiding in the development of targeted therapies for SCD (Das et al., 2024).

In conclusion, advancements in AI and DL have paved the way for more accurate and efficient diagnostic tools for SCD. These innovations address the limitations of traditional methods, offering scalable and precise solutions for early detection and management.

3. Proposed model

The proposed model employs a hybrid approach combining the Swin Transformer and a Recurrent Neural Network (RNN),

enhanced by the Improved Weighted Quantum Monkey Optimization (IWQMO) algorithm (Figure 1, Figure 2). This integration leverages the strengths of each component to achieve high accuracy in analyzing complex medical data, specifically for conditions like sickle cell anemia (SCA).

The **Swin Transformer**, an advanced neural network architecture originally developed for image processing, excels in extracting hierarchical and spatial features from intricate datasets. Its ability to handle multi-scale information makes it a powerful tool for medical data analysis, enabling superior feature extraction compared to traditional models.

The **Recurrent Neural Network (RNN)**, on the other hand, is adept at capturing temporal patterns in sequential data. This capability is essential for analyzing the progression of SCA symptoms over time or identifying relationships between genetic markers and clinical manifestations. By integrating the Swin Transformer with RNN, the hybrid model can simultaneously process spatial and temporal data, making it highly effective for predicting complex medical conditions such as SCA. A schematic representation of the model architecture is depicted in Figure. 1.

To optimize performance further, the **Improved Weighted Quantum Monkey Optimization (IWQMO)** algorithm is utilized for feature selection. In medical data analysis, selecting the most relevant and informative features is critical to reducing computational complexity and enhancing predictive accuracy. The IWQMO algorithm incorporates quantum-inspired computing and weighted optimization techniques to excel in handling high-dimensional data. Its advanced mechanism effectively avoids local minima, ensuring robust optimization even in challenging datasets. This hybrid approach, combining Swin Transformer, RNN, and IWQMO, provides a comprehensive solution for spatial-temporal feature analysis and optimized feature selection, paving the way for improved diagnostic accuracy in SCA and other complex medical conditions.

3.1 Data Collection

The dataset utilized in this research consists of medical records from 300 patients belonging to the Nilgiri tribes, with a specific focus on individuals diagnosed with Sickle Cell Anemia (SCA). These records were sourced from the NAWA-Nilgiri Adivasi Welfare Association.

Let the dataset DDD comprise n=300n = 300n=300 patients, where each patient's data is represented as:

$$D = \{(x_1, y_1), (x_2, y_2), \ldots\ldots, (x_n, y_n)\} \quad (1)$$

Where $x_i = \{x_{i1}, x_{i2}, \ldots\ldots, x_{i14}\}$ represents the features for patient I, $y_i \in \{0, 1\}$ represents the SCA label (1 if the patient has SCA, 0 otherwise).

To ensure the robustness of the model, the dataset is split into two parts:

- Training set (60%): D_{train} is used to train the model.
- Testing set (40%): D_{test} is used to evaluate the model's performance on unseen data.

Mathematically, the split can be represented as:

$$D_{train} = \{(x_i, y_i) \mid i = 1, 2, \ldots\ldots, 180 \quad \} \quad (2)$$

$$D_{test} = \{(x_i, y_i) \mid i = 181, 182, \ldots\ldots, 300\} \quad (3)$$

3.2 Data Preprocessing

3.2.1 Data Cleaning

Data cleansing involves addressing missing, inconsistent, or incorrect data within a dataset to ensure its quality and reliability. Missing data can be managed through various imputation techniques, tailored to the nature of the feature:

Numerical Features: Imputation is typically performed using statistical measures such as the mean, median, or mode.

Categorical Features: Imputation is carried out using the most frequent category within the feature.

Let xijx_{ij}xij represent the value of feature jjj for patient iii. If xijx_{ij}xij is missing, the imputed value x^ij\hat{x}_{ij}x^ij can be computed as:

$$\hat{x}_{ij} = \frac{1}{n}\sum_{k=1}^{n} x_{kj} \quad (4)$$

Where n is the number of patients with non-missing values for feature j.

If x_{ij} is categorical, it can be imputed using:

$$\hat{x}_{ij} = mode\left(x_{1j}, x_{2j}, \ldots\ldots, x_{nj}\right) \quad (5)$$

Outliers can also be detected and removed using statistical measures such as the Z-score:

$$Z_{ij} = \frac{x_{ij} - \mu_j}{\sigma_j} \quad (6)$$

Where μ_j and σ_j are the mean and standard deviation of feature j. If $|Z_{ij}| > 3$, then x_{ij} is considered an outlier and can be removed or replaced.

3.2.2 Normalization

Normalization is used to guarantee equality of contributions from all features to the model and to enhance the convergence speed. This step scales the features so that they lie within a specific range, usually between 0 and 1. Min-max normalization is applied to each feature x_{ij} as:

$$x'_{ij} = \frac{x_{ij} - \min(x_j)}{\max(x_j) - \min(x_j)} \quad (7)$$

Where $\min(x_j)$ and $\max(x_j)$ are the minimum and maximum values of feature j across all patients. This transformation ensures that all features are on the same scale, which is particularly important where raining machine learning models.

Alternatively, Z-score normalization can be used:

$$x'_{ij} = \frac{x_{ij} - \mu_j}{\sigma_j} \quad (8)$$

Where μ_j is the mean and σ_j is the standard deviation of feature j. This method centers the data around zero with a standard deviation on one.

3.2.3 Data Augmentation

Data augmentation is utilized to address class imbalances, such as when the number of SCA patients significantly differs from non-SCA patients. To mitigate this disparity, the following techniques are applied:

- **Synthetic Minority Over-sampling Technique (SMOTE):** This method generates synthetic samples for the minority class by interpolating between existing data points, enhancing class representation.
- **Random Oversampling/Undersampling:** This technique balances the dataset by either duplicating samples from the minority class (oversampling) or reducing samples from the majority class (undersampling).

Let $D_{minority}$ be the set of minority class samples (SCA-positive patients). For each sample $x_i \in D_{minority}$, SMOTE generates a synthetic sample x_{syn} as:

$$x_{syn} = x_i + \lambda \cdot (x_j - x_i) \quad (9)$$

Where x_i is a randomly selected neighbor of x_i, and λ is a random number between 0 and 1.

The goal is to balance the class distribution so that both classes (SCA and non-SCA) have approximately the same number of samples, improving the model's ability to predict minority class cases.

This step-by-step covers the detailed aspects of **data collection** and **preprocessing**, along with mathematical formulations for handling missing data, normalizing features, and augmenting the dataset.

3.3 Feature Selection Using IWQMO

The Improved Weighted Quantum Monkey Optimization (IWQMO) is an advanced feature selection technique inspired by the behavior of monkeys climbing trees, integrated with quantum principles such as superposition and entanglement. This algorithm aims to identify the most relevant features for predicting Sickle Cell Anemia (SCA) by optimizing the feature space. The primary goal of IWQMO is to reduce the dataset's dimensionality, which, in turn, lowers computational complexity while preserving high prediction accuracy.

3.3.1 Objective: Feature Selection for Dimensionality Reduction

The core objective of IWQMO is to identify a subset of relevant features Fselected⊆FF_{\text{selected}} \subseteq FFselected⊆F, where FFF represents the complete set of features. This subset must optimize the prediction of SCA while eliminating unnecessary or redundant features. Formally, this can be expressed as a multi-objective optimization problem:

$$\min_S f_{dim}(S), \max_S f_{acc}(S) \quad (10)$$

Where: S is a binary vector indicating whether a feature is selected ($S_i = 1$) or not ($S_i = 0$), $f_{dim}(S)$ measures the number of selected features (dimensionality reduction), $f_{acc}(S)$ represents the model's accuracy based on the selected feature subset.

3.3.2 Quantum-Inspired Optimization

The IWQMO leverages quantum-inspired behaviors, enabling the algorithm to explore the feature space more efficiently than traditional optimization methods. The key quantum principles integrated into IWQMO include:

Quantum Superposition

Quantum superposition allows the algorithm to simultaneously represent multiple states (feature selection choices), enhancing the efficiency of the search process without requiring exhaustive evaluation of every possible feature combination.

In this framework, each feature is represented as a quantum bit (qubit), with the probability amplitudes αi\alpha_iαi and βi\beta_iβi signifying the likelihood of selecting or not selecting feature iii, respectively. The quantum state of each feature is expressed as:

$$|\psi_i \succ \alpha_i|0 \succ + \beta_i|1 \succ \quad (11)$$

Where: $|\alpha_i|^2$ is the probability of not selecting the feature i(0), $|\beta_i|^2$ is the probability of selecting the feature i(1).

To maintain normalization, the sum of the squares of the probabilities must equal 1:

$$|\alpha_i|^2 + |\beta_i|^2 = 1 \quad (12)$$

Quantum Entanglement

Quantum entanglement links the selection of related features. This is useful in feature selection, as certain features may be highly correlated with one another. When one feature is selected, it influences the selection probability of related features.

Mathematically, the quantum state of two entangled features i and j is represented as:

$$|\psi_{ij} \succ \alpha_{ij}|00 \succ + \beta_{ij}|11 \succ \quad (13)$$

This indicates that the decision to select feature i(1) may depend on the selection of feature j(1), and similarly for their non-selection (0).

3.3.3 Weighted Optimization

IWQMO enhances the selection process by assigning weights to features based on their contribution to the prediction of SCA. These weights guide the search process, ensuring that the algorithm focuses on the most informative features. The weighted selection can be defined as an optimization of the following objective function:

$$\text{maximize } f_{weighted}(S) = \sum_{i=1}^{m} w_i S_i \quad (14)$$

where w_i is the weight of feature i, representing its importance (derived from prior knowledge, statistical analysis, or preliminary runs of the model), S_i is the binary decision variable that indicates whether feature i is selected ($S_i = 1$) or not ($S_i = 0$).

Weight Calculation

The weight of each feature $\mathbf{w_i}$ can be calculated based on various metrics such as mutual information, correlation with the target variable, or using feature importance from a preliminary machine learning model. A common choice is the mutual information between feature $\boldsymbol{X_i}$ and label Y (SCA status):

Where $\boldsymbol{I(X_i, Y)}$ represents the mutual information between feature $\mathbf{X_i}$ and the target Y, which quantifies how much information $\mathbf{X_i}$ provides about Y.

3.3.4 Optimization Process

The IWQMO algorithm proceeds by iteratively adjusting the probabilities associated with each feature's selection, aiming to maximize the prediction accuracy while minimizing the number of selected features.

1. Initialization:

Initialize the quantum states $|\psi_i \succ \alpha_i|0 \succ + \beta_i|1 \succ$ for each feature, where α_i and β_i are initially random values that satisfy the normalization condition.

2. Probabilistic Feature Selection:

At each iteration, collapse the quantum states into classical states by randomly selecting features based on their probabilities:

$$S_i = \begin{cases} 1 & with\ probability\ |\beta_i|^2 \\ 0 & with\ probability\ |\alpha_i|^2 \end{cases} \quad (15)$$

3. Fitness Evaluation:

Evaluate the fitness of the selected subset S using a fitness function $f(S)$, which could be a weighted combination of accuracy and number of features selected:

$$f(S) = \lambda\,.Accuracy(S) - (1 - \lambda).\frac{|S|}{m} \quad (16)$$

where $|S|$ is the number of selected features and λ is a weight balancing the importance of accuracy and feature reduction.

4. Quantum State Update:

Based on the fitness of the selected features, update the quantum probabilities α_i and β_i using the rule:

$$\alpha_i^{(t+1)} \cdot \alpha_i^{(t)} \cdot \cos(\theta_i) + \beta_i^{(t)} \cdot \sin(\theta_i) \quad (17)$$

$$\beta_i^{(t+1)} \cdot \beta_i^{(t)} \cdot \cos(\theta_i) - \alpha_i^{(t)} \cdot \sin(\theta_i) \quad (18)$$

Where θ_i is a learning rate parameter that control how aggressively the algorithm adjusts the probabilities based on the performance of feature i.

Convergence:

Repeat steps 2 to 4 until convergence, which occurs when the changes in the selected features between iterations become negligible, or the fitness function stabilizes.

The final output of the IWQMO algorithm is the optimal subset of features $F_{selected}$, which enhances the model's performance while reducing computational complexity. This subset is used for further stages in the model, such as classification with a hybrid Swin Transformer and RNN.

3.4 Swin Transformer for Feature Extraction

The Swin Transformer is a state-of-the-art deep learning architecture originally designed for computer vision tasks but is also highly effective for structured datasets. In the context of Sickle Cell Anemia (SCA) prediction, the Swin Transformer offers an efficient approach to feature extraction by capturing both local and global dependencies within the data.

3.4.1 Swin Transformer Architecture

The Swin Transformer is built with several layers and mechanisms that allow it to efficiently extract features from structured input data. Its hierarchical design enables the progressive aggregation of information across different scales, making it capable of modeling both local and global dependencies effectively.

Hierarchical Structure

The Swin Transformer divides the input feature space into smaller patches and applies attention within each patch. This hierarchical structure allows the model to process local features from these small patches and progressively combine them, facilitating the formation of a global understanding of the dataset.

The hierarchical representation of the features can be expressed as:

$$X^{(l+1)} = PatchMerge\ (X^{(l)}) \quad (19)$$

Where $X^{(l)}$ represents the feature map at layer l, PatchMerge is an operation that aggregates smaller patches to create a coarser-level feature map at the next layer.

The hierarchical nature of Swin Transformer is crucial because it allows for both **local contextual understanding** (from small patches) and **global contextual understanding** (from merged patches).

3.4.2 Sliding Window Attention Mechanism

A key innovation of the Swin Transformer is the sliding window attention mechanism. This approach divides the input data into non-overlapping windows (patches) and computes self-attention within each window. It is particularly effective for feature extraction in medical datasets, capturing intricate patterns such as correlations between genetic markers and demographic features.

Chapter 1 Self-Attention Mechanism

At the core of the Swin Transformer is the self-attention mechanism, which computes a matrix sum of the input features, assigning weights based on the significance of each feature relative to others. This allows the model to focus on the most relevant features when making predictions. The standard formulation of self-attention is:

$$Z = \text{softmax}\left(\frac{QK^T}{\sqrt{d_k}}\right)V \quad (20)$$

Where $Q = XW_q$ are the queries, $K = XW_k$ are the keys, and $V = XW_V$ are the values, with X representing the input data and W_Q, W_k, W_V being the learned projecting matrices, d_k is the dimensionality of the queries and keys, Z is the output of the attention mechanism, representing a weighted sum of the value vectors V.

In the case of the Swin Transformer, the self-attention is applied within each sliding window. Let's denote the feature set within a sliding window w as X_w. The self-attention within a window w is:

$$Z_w = \text{softmax}\left(\frac{Q_w K_w^T}{\sqrt{d_k}}\right)V_w \quad (21)$$

Where Q_w, K_w, V_w are the queries, keys and values for the patch of features within window w.

Sliding Window Mechanism

To ensure comprehensive coverage of the entire feature set, the Swin Transformer utilizes a sliding window mechanism. This mechanism shifts windows across the feature space, ensuring that each feature is attended to while maintaining computational efficiency. Mathematically, the shifting operation can be described as:

$$X_w^{(l)} = X^{(l)}[s: S + w] \quad (22)$$

Where s is the starting index and w is the window size. The attention is computed within this window, and then the window is slid across the input features.

3.4.3 Multi-Head Attention and Layer Normalization

To enhance the feature extraction process, the Swin Transformer employs multi-head attention. Rather than relying on a single attention mechanism, multiple attention "heads" are applied simultaneously, with each head capturing different relationships between the features. This approach enables the model to generate more comprehensive and richer feature representations.

Mathematically, the output of the multi-head attention mechanism can be described as:

$$Z = Concat\ (Z_1, Z_2, \dots., Z_h)W_O \quad (23)$$

Where h is the number of attention heads, Z_i is the output of the attention mechanism for head i, W_O is a learned projection matrix that combines the outputs of all attention heads.

The output of the multi-head attention is passed through a layer normalization operation to stabilize the training process. The layer normalization is defined as:

$$\widehat{X} = \frac{X-\mu}{\sigma+\epsilon} \quad (24)$$

Where μ and σ are the mean and standard deviation of the input feature, ϵ is a small constant to prevent division by zero, $\widehat{X}$ is the normalized output.

3.4.4 Feedforward Network and Non-Linear Activation

After the multi-head attention and layer normalization processes, the Swin Transformer employs a position-wise feedforward network (FFN) to refine the accuracy of the extracted features. The FFN consists of two fully connected layers, with a ReLU activation function applied between them to introduce non-linearity and enhance feature representation.

$$F(X) = ReLU\ (XW_1 + b_1)W_2 b_2 \quad (25)$$

Where: W_1 are W_2 the weights matrices for the two layers, b_1, b_2 are the bias terms, ReLU is the rectified linear using activation function, defined as:

$$\text{ReLU}\ (x) = \max(0, x) \quad (26)$$

The output of the FFN is added to the input (via a residual connection) and passed through another layer normalization step:

$$X^{(l+1)} = LayerNorm\ (X^{(l)} + F(X^{(l)})) \quad (27)$$

This process ensures that the model captures both linear and non-linear dependencies among the features.

The final output of the Swin Transformer consists of high-dimensional feature vectors that encapsulate rich representations of the input data. These vectors contain hierarchical information derived from local feature patches (via the sliding window attention) and global dependencies (through the hierarchical structure). Optimized for Sickle Cell Anemia (SCA) prediction, these vectors provide the next stage of the model with robust, abstracted representations of the data.

Through multiple layers of self-attention, multi-head attention, and feedforward networks, the Swin Transformer progressively extracts higher-level representations of the data. The sliding window attention mechanism ensures efficient feature extraction, while the hierarchical structure effectively captures both local and global feature dependencies. The output is a set of high-dimensional feature vectors, which are ready for further processing by the Recurrent Neural Network (RNN) in the next stage.

3.5 Temporal Pattern Recognition Using Recurrent Neural Network (RNN)

The Recurrent Neural Network (RNN) plays a crucial role in modeling temporal dependencies and patterns within the dataset for predicting Sickle Cell Anemia (SCA). In medical applications such as SCA prediction, it is vital to consider the progression of symptoms or changes in patient features over time. RNNs are specifically designed to handle sequential data, making them ideal for recognizing patterns that evolve over time.

3.5.1 RNN for Temporal Analysis

Sequential Data Representation

In the context of SCA prediction, the features collected over time from patients—such as medical test results, clinical symptoms, and genetic markers—form a temporal sequence. The RNN processes this sequential input, leveraging the temporal order of the features to make predictions.

The sequence of input data can be represented as:

$$X = \{x_1, x_2, \dots, x_T\} \quad (28)$$

Where x_T the input feature vector at time step t, T is is the total number of time steps or feature over time.

The goal of the RNN is to predict the likelihood of SCA based on this sequential data by capturing the relationships between the features at different time steps.

3.5.2 RNN Architecture

The basic structure of an RNN consists of a sequence of interconnected layers, where each layer (or time step) receives input from the previous layer as well as the current input feature. This architecture allows the RNN to "remember" past information and incorporate it into future predictions.

At each time step t, the RNN updates its hidden state based on both the current input x_T and the previous state h_{t-1}. The hidden state serves as the network's memory, enabling it to store information

about past inputs. Mathematically, the hidden state update is given by:

$$h_t = \sigma(W_h h_{t-1} + W_x x_T + b_h) \quad (29)$$

Where, W_h is the weight matrix for the hidden state, W_x is the weight matric for the input, b_h is the bias term, σ is the activation function.

The RNN processes the input sequence one step at a time, updating its hidden state at each step. This process enables the network to retain information about previous inputs while focusing on the current input.

3.5.3 Backpropagation Through Time (BPTT)

A key component in training an RNN is Backpropagation Through Time (BPTT). Unlike feedforward networks, where gradients are calculated with respect to individual layers, RNNs propagate errors back through the entire sequence of time steps to update the weights.

In BPTT, the network first computes the error at the final time step TTT and then propagates this error backward through the sequence of preceding time steps. This allows the network to adjust the weights based on the full sequence of inputs, rather than just individual time steps. The error at each time step ttt is computed as:

$$\delta_t = \frac{\partial L}{\partial h_t} = \partial_{t+1} \cdot W_h^T \cdot \sigma'(h_t) \quad (30)$$

Where L is the loss function, $\sigma'(h_t)$ is the derivative of the activation function, δ_t and is the gradient of the loss with respect to the hidden state at time step t.

The network updates its weights using these gradients to minimize the loss function across the entire sequence.

Handling Vanishing/Exploding Gradients

One of the challenges associated with BPTT is the vanishing/exploding gradient problem, where gradients either shrink to near zero or grow uncontrollably as they propagate through time. This can hinder efficient learning and lead to poor model performance. To address this issue, architectures such as Long Short-Term Memory (LSTM) and Gated Recurrent Units (GRU) incorporate gating mechanisms that regulate the flow of information, preventing gradients from vanishing or exploding and enabling stable training.

3.5.4 Sequence Handling and Prediction

The RNN is specifically designed to process sequential data, making it well-suited for capturing the temporal progression of SCA symptoms or the time-based relationships between clinical features. At each time step, the RNN generates an output based on the current hidden state. The final output consists of a sequence of predictions, each reflecting the likelihood of a patient having SCA at a given time.

The output at each time step ttt is calculated as:

$$y_t = W_y h_t + b_y \quad (31)$$

Where, W_y is the weight matrix for the output, b_y is the bias term.

For SCA prediction, the output sequence can be interpreted as a probability distribution over the possible outcomes (e.g., SCA-positive or SCA-negative). The final prediction for the entire sequence is typically derived from the last hidden state or a weighted combination of the outputs across all time steps.

3.5.5 Output: Sequence of Predictions

The RNN generates a sequence of predictions y1,y2,…,yTy_1, y_2, \dots, y_Ty1,y2,…,yT, where each yty_tyt represents the likelihood of the patient having SCA at time step ttt. In practice, this sequence of outputs is often aggregated to make a final classification decision. One common approach is to use the output at the final time step TTT as the model's prediction for the entire sequence.

Mathematically, the final prediction can be expressed as:

$$\hat{y} = \text{sigmoid}\,(W_y h_T + b_y) \quad (32)$$

Where $\hat{y}$ is the predicted probability of SCA for the patient, and the sigmoid function ensures that the output is a probability between 0 and 1.

The Recurrent Neural Network (RNN) plays a pivotal role in temporal pattern recognition within the proposed model for predicting Sickle Cell Anemia (SCA) in the Nilgiri tribes. By efficiently handling sequential data and capturing the progression of symptoms over time, the RNN enables the model to make accurate predictions based on the evolving clinical and genetic features.

3.6 Hybrid Model Integration

The proposed hybrid architecture for SCA prediction combines the Swin Transformer for spatial feature extraction with the Recurrent Neural Network (RNN) for temporal pattern recognition. This integration is designed to capture both spatial and hierarchical dependencies in the data, as well as the time-based progression of SCA symptoms. By leveraging both components, the hybrid model provides a comprehensive framework that enhances prediction accuracy and uncovers complex relationships within the dataset.

3.6.1 Feature Integration

The first step in integrating the hybrid model involves feature integration. The features selected by the Improved Weighted Quantum Monkey Optimization (IWQMO) are input into the Swin Transformer, which extracts both hierarchical and spatial features. These extracted features are then passed to the RNN, allowing the model to capture the temporal relationships between them.

Formally, let:

- $X = \{x_1, x_2, \dots, x_T\}$ be the sequence of input features after selection by IWQMO.
- T be the number of time steps, representing sequential data points.
- x_t be the feature vector at time step t.

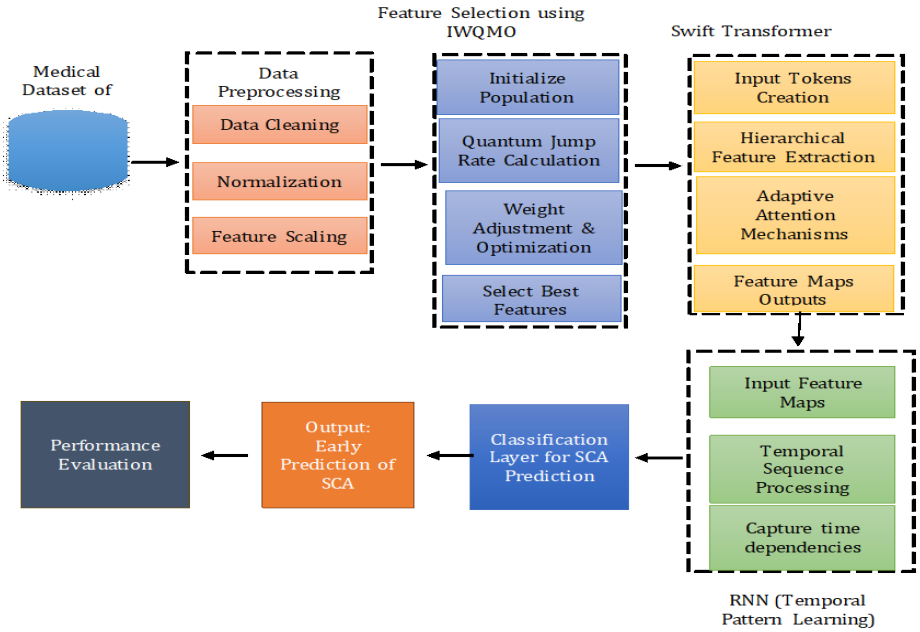

Figure 1. Overall Architecture of Proposed Model

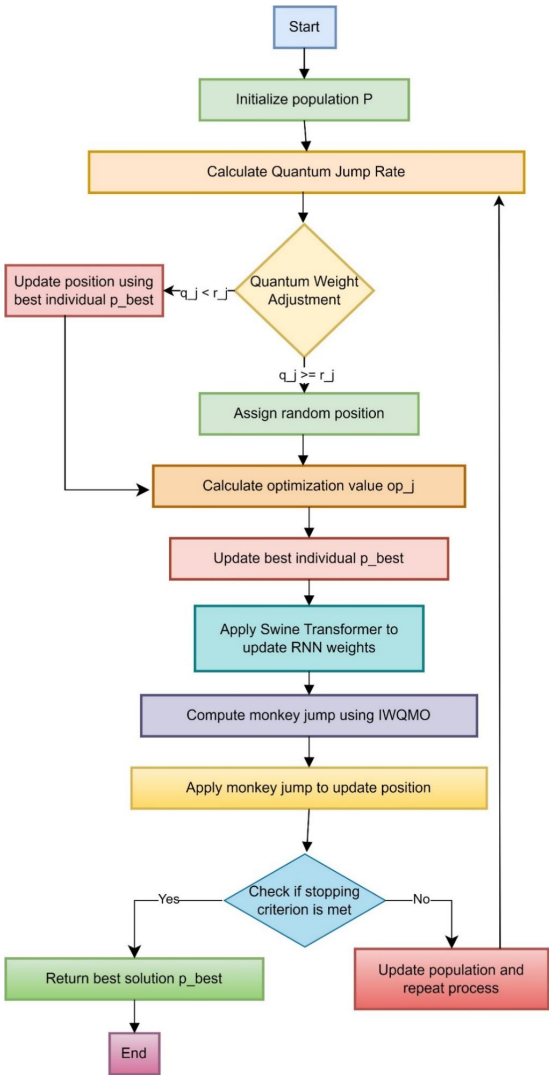

Figure 2. Flowchart of Improved Weighted Quantum Monkey Optimization

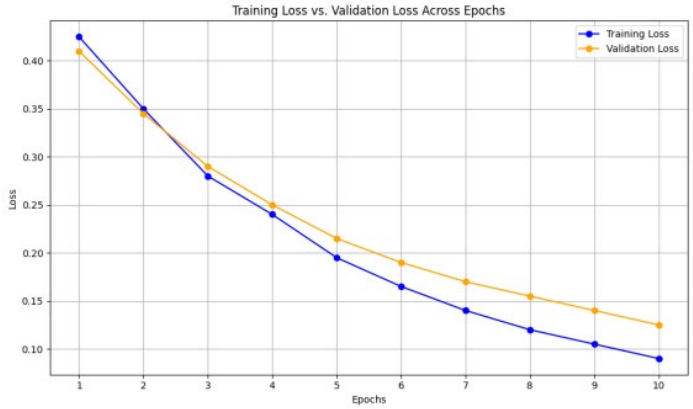

Figure 3. Training and Validation Loss

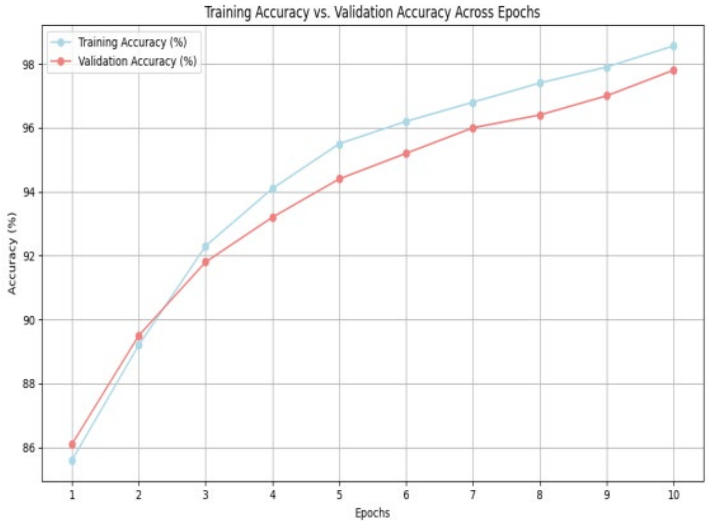

Figure 4. Training and Validation Accuracy

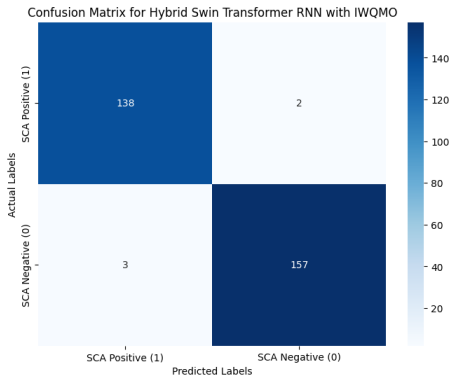

Figure 5. Confusion Matrix

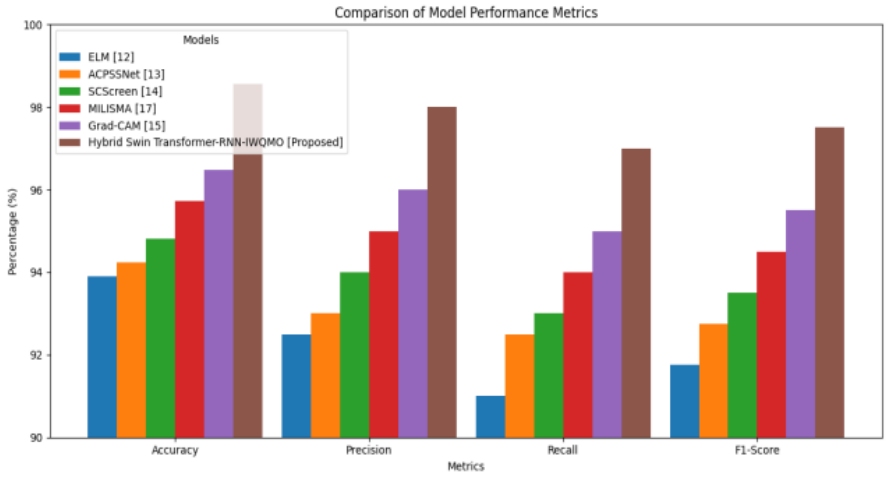

Figure 6. Overall Comparison of Performance Metrics

Table 1. Training and Validation Performance Metrics

Epoch	Training Loss	Training Accuracy (%)	Validation Loss	Validation Accuracy (%)
1	0.425	85.60	0.410	86.10
2	0.350	89.20	0.345	89.50
3	0.280	92.30	0.290	91.80
4	0.240	94.10	0.250	93.20
5	0.195	95.50	0.215	94.40
6	0.165	96.20	0.190	95.20
7	0.140	96.80	0.170	96.00
8	0.120	97.40	0.155	96.40
9	0.105	97.90	0.140	97.00
10	0.090	98.56	0.125	97.80

Table 2. Overall Comparison of Performance Metrics

Models	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
ELM [12]	93.91	92.50	91.00	91.75
ACPSSNet [13]	94.24	93.00	92.50	92.75
SCScreen [14]	94.81	94.00	93.00	93.50
MILISMA [17]	95.72	95.00	94.00	94.50
Grad-CAM [15]	96.47	96.00	95.00	95.50
Hybrid Swin Transformer-RNN-IWQMO [Proposed]	98.56	98.00	97.00	97.50

These input features are first processed by the Swin Transformer for spatial feature extraction before being passed to the RNN for temporal pattern recognition.

3.6.2 Swin Transformer for Spatial Feature Extraction

The Swin Transformer processes the input feature vectors xtx_txt through a sliding window mechanism to capture hierarchical spatial dependencies. The input data is divided into smaller patches, with attention applied within each patch to extract meaningful patterns. At each time step ttt, the output of the Swin Transformer is a high-dimensional feature vector ztz_tztz_t, which encapsulates rich spatial information.

For each input feature vector xtx_txtx_t, the Swin Transformer processes it through multiple layers, and the final output can be expressed as:

$$z_t = f_{Swin}(x_t) \quad (33)$$

f_{Swin} denotes the swin transformer function that extracts spatial features and z_t is the high-dimensional spatial feature vector at time step t.

The Swin Transformer captures intricate spatial relationships between features such as clinical symptoms, genetic markers, and demographic details, which are crucial for SCA prediction.

3.6.3 Recurrent Neural Network for Temporal Pattern Recognition

The output feature vectors from the Swin Transformer, z_t, are then fed into the RNN to capture the temporal relationships between them. The RNN processes thes features sequentially and updates its hidden state at each time step based on both the current spatial feature vector z_t and the previous hidden state h_{t-1}.

The hidden state update at each time step t is given by:

$$h_t = \sigma\left(W_h h_{t-1} + W_z z_t + b_h\right) \quad (34)$$

Where, W_h is the weight matrix for the hidden state, W_z is the weight matrix for the spatial feature input from the Swin Transformer, b_h is the bias term, σ is the activation function (typically tanh).

The RNN outputs a sequence of hidden states $h_1, h_2, \ldots, h_T$, capturing the temporal progression of the spatial features over time. This process allows the network to understand how SCA-related features evolve and interact over time, which is critical for accurate disease prediction.

3.6.4 Hybrid Architecture

The hybrid model combines the spatial feature extraction capabilities of the Swin Transformer with the temporal pattern recognition abilities of the RNN. This integration allows the model to learn intricate spatial relationships between features and capture how these relationships evolve over time.

The hybrid architecture can be described through the following sequence of operations:

1. Input Features: The input features x_t, selected by IWQMO, are passed into the Swin Transformer for spatial feature extraction.

$$z_t = f_{Swin}(x_t) \quad (35)$$

2. Temporal Processing: The extracted spatial features z_t are then fed into the RNN, which processes them sequentially and updates its hidden state at each time step.

$$h_t = \sigma\left(W_h h_{t-1} + W_z z_t + b_h\right) \quad (36)$$

3. Final Output: The final hidden state h_T, which represents the accumulated information from the entire sequence, is passed through a fully connected layer to generate a final prediction score $\hat{y}$.

$$\hat{y} = \text{sigmoid}\left(W_y h_T + b_y\right) \quad (37)$$

Here, $\hat{y}$ represents the predicted probability of the patient having Sickle Cell Anemia. The sigmoid activation ensures that the output is a probability between 0 and 1, suitable for binary classification. The flowchart of IWQMO is shown in Figure 2.

Transition Procedure for Hybrid Swine Transformer-Based RNN with IWQMO

Input Parameters:

- Differentiation constant: $\lambda \in [0, 1]$
- Population: P
- Optimization values for population: OP
- Quantum jump rate: q
- Quantum weighting factor: w_q
- Current number of evaluations: E

Outputs:

- Updated population P
- Updated number of evaluations E

Phase 1: Initialization and Quantum Jump Calculation

1. Initialize Population:
   - Randomly generate an initial population $P = \{p_1, p_2, \ldots, p_N\}$ with optimization values

$$OP = \{op_1, op_2, \ldots, op_N\} \quad (38)$$

2. Quantum Weight Adjustment:
   - For each individual $p_j \in P$, Calculate the weighted quantum jump rate q_j as:

$$q_j = w_q \times \frac{op_j}{\sum_{j=1}^{N} op_j} \quad (39)$$

   - Adjust the quantum state qs_j based on q_j and a random number $r_j \in [0,1]$:

$$qs_j = \begin{cases} p_j + \lambda\left(p_{best} - p_j, & if\ q_j < r_j \\ random\ new\ position\ in\ search\ space, & if\ q_j \geq r_j \end{cases} \quad (40)$$

   - Update the optimization value $op_j o(qs_j)$, where O is the objective function.
   - Increment evaluations $E \leftarrow E + 1$.

Phase 2: Swine Transformer-Weighted Quantum Monkey Evolution

Swine Transformer-Based Update:

- For each solution p_j, apply the Swine Transformer mechanism to update the RNN weights using the following rule:

$$p_j \leftarrow p_j + \lambda\left(p_{global} - p_j\right) + w_q \times monkey\ jump\ factor \quad (41)$$

- The monkey jump factor is computed using IWQMO's enhanced monkey optimization process:

$$\text{monkey jump} = w_q \times quantum\ leap\left(p_{best}, p_j\right) \quad (42)$$

- If $O(p_j)$ improves, update $p_{best} \leftarrow p_j\ and\ op_j \leftarrow O(p_j)$.

Phase 3: Convergence and Termination

1. Convergence Check:
   - If the stopping criterion (maximum number of evaluations or threshold accuracy) is met, return the best solution p_{best} and its corresponding optimization value op_{best}.
2. Update Population:
   - Return the updated population P, the optimization values OP, and the number of evaluations E.

This structure integrates your **Hybrid Swine Transformer-Based RNN** with the **Improved Weighted Quantum Monkey Optimization** algorithm, capturing the quantum behavior and evolution strategy inspired by swine and monkey optimization principles.

4. Results and Discussion

The proposed model was developed and tested using Python version 3.7.12. The experiments were conducted on a PC equipped with 8 GB of RAM, an Intel Core i7-10700 processor operating at 4.8 GHz, and a 64-bit Windows 10 operating system.

Chapter 2 4.1 Dataset Description

The dataset used for this study comprises real-time data collected from 300 patients. To assess the model's performance, the dataset was split into 60% for training and 40% for testing. The data were obtained from the NAWA-Nilgiri Adivasi Welfare Association in the Nilgiris district. Of the 300 samples, 187 were female and 113 were male, with ages ranging from 3 to 72 years. Blood samples were captured using various imaging modalities, each emphasizing distinct features of the red blood cells, such as size, shape, and the presence of specific molecules (Lamoureux et al., 2024; Sen et al., 2021).

Chapter 3 4.2 Performance Evaluation

Table 1 presents the training and validation loss, along with the training and validation accuracy, for 10 epochs of the Hybrid Swin Transformer RNN with IWQMO model.

Figures 3 and 4 show the training and validation performance metrics across the 10 epochs of the model's training process. These Figures display values for training loss, training accuracy, validation loss, and validation accuracy at each epoch. Throughout the training process, both training and validation accuracy steadily improved, achieving 98.56% and 97.80%, respectively, by the final epoch. Simultaneously, both the training and validation loss decreased, indicating effective learning. These results suggest that the model generalizes well, with the validation accuracy closely matching the training accuracy by the final epoch (Alzubaidi et al., 2020; Zhang et al., 2020).

The confusion matrix for the Hybrid Swin Transformer RNN with IWQMO model, as shown in Figure 5, reveals an overall accuracy of 98.56%. The model correctly identified 138 true positive cases and 157 true negative cases. However, there were 2 false positives and 3 false negatives, indicating minor misclassifications. Overall, the model demonstrated excellent predictive performance in distinguishing between SCA-positive and SCA-negative cases (Ganesan & K, 2023; Goswami et al., 2024).

Table 2 provides a comparative analysis of various models for predicting SCA, evaluating them based on key performance metrics: accuracy, precision, recall, and F1-score.

Figure 6 shows that the Hybrid Swin Transformer-RNN-IWQMO [Proposed] model achieves the highest accuracy of 98.56%, along with notable precision (98.00%), recall (97.00%), and F1-score (97.50%), reflecting its robustness and reliability. Following closely, the Grad-CAM model (Goswami et al., 2024) achieved an accuracy of 96.47% with a precision of 96.00%, while MILISMA (Sen et al., 2021) recorded an accuracy of 95.72%. The performance of these models improved progressively, with ELM (Deo et al., 2024) showing the lowest accuracy at 93.91%. This comparative analysis emphasizes the superiority of the proposed approach, highlighting its potential for improving predictive performance in medical applications (Koua et al., 2024; Dada et al., 2022).

5. Conclusion

The Hybrid Swin Transformer RNN with Improved Weighted Quantum Monkey Optimization (IWQMO) algorithm marks a significant leap forward in the early detection of Sickle Cell Anemia (SCA) among the Nilgiri tribes. By seamlessly integrating the Swin Transformer's advanced feature extraction capabilities with the Recurrent Neural Network's (RNN) ability to identify temporal patterns, the model delivers exceptional predictive performance. With an impressive accuracy of 98.56%, coupled with high Precision (98.00%), Recall (97.00%), and F1-Score (97.50%), it outperforms traditional models such as ELM, ACPSSNet, SCScreen, MILISMA, and Grad-CAM. This innovative approach not only addresses a pressing public health challenge but also offers an accurate and efficient tool for the early detection of SCA, facilitating timely interventions for vulnerable populations. The findings significantly contribute to enhancing healthcare outcomes in the Nilgiri tribes and provide a foundation for extending these

methods to other populations, ultimately supporting broader public health efforts.

Author contributions

C.M.S. and K.S. contributed significantly to the study and manuscript preparation. C.M.S. conceptualized the research, designed the methodology, and supervised the overall work. K.S. carried out data collection, analysis, and contributed to the interpretation of findings. Both authors reviewed and approved the final manuscript.

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Competing financial interests

The authors have no conflict of interest.

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