The Scientific Temper (2025) Vol. 16 (5): 4260-4269
E-ISSN: 2231-6396, ISSN: 0976-8653
Doi: 10.58414/SCIENTIFICTEMPER.2025.16.5.11
https://scientifictemper.com/

RESEARCH ARTICLE

Hybrid pigeon optimization-based feature selection and modified multi-class semantic segmentation for skin cancer detection (HPO-MMSS)

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Abstract

Skin Cancer is among the most serious medical conditions in the worldwide, and curative results are better when detected early. Some of the challenges with conventional skin cancer detection methods, such as genetic algorithms, particle swarm optimization, and U-net-based segmentation models, include selecting the appropriate characteristics and accurately identifying skin lesions. This paper proposes a unique method that combines a Hybrid Pigeon Optimization Algorithm (HPOA) for feature selection with a Modified Multi-Class Semantic Segmentation (MMSS) model for lesion segmentation. The precise feature selection of the proposed HPOA improves the performance of the segmentation and classification models. Based on an enhanced U-Net architecture, the MMSS model uses skip connections and boundary detection techniques to improve segmentation accuracy. This approach integrates information from multiple feature spaces to produce a more informative structure for segmenting the skin lesions. The ISIC 2020 dataset counts considered are 2000, 4000, 6000, 8000, and 10000 for testing the proposed methodology. The experimental results with segmentation accuracy (ranging from 91–96%), precision (ranging from 89–94%), and recall (ranging from 88–94%) show that the proposed methodology gives a strong foundation for detecting skin cancer automatically.

Keywords: Skin cancer detection, Deep learning, hybrid pigeon optimization (HPOA), Semantic segmentation, ISIC 2020 dataset.

Introduction

Among the most widespread and deadly types of cancer worldwide, skin cancer has become more common in recent years. The early detection of skin cancer is essential for decreasing the mortality rate in humans and reducing risks associated with treatment. Among the serious cancer types, Melanoma is considered a dangerous one, of about 75% and only 30% of all skin cancer diagnoses (2017). This will be particularly helpful for dermatologists in detecting skin cancer using Computer-Aided Diagnosis (CAD). There are some parameters, such as skin texture, lesion size, and distribution of pigment color, which will face issues in the accurate segmentation and classification of lesions (2017). This becomes a more challenging factor for accurately identifying the exact boundary and extracting features from skin lesions due to the uneven distribution of boundaries and skin lesion features, which exhibit a variety of visual patterns in the skin. This will lead to a trouble stage for the automated diagnostic tools, which make the system less reliable.

Data Preprocessing

The essential stage is the preprocessing of data for diagnosing the skin cancer types. This stage ensures the accurate prediction of skin cancer and improves the standardization of input images for efficient model training. Model performance may be hampered by biases introduced by variations in dermoscopic picture brightness, contrast, and resolution. This enhances the feature extraction process by letting the

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How to cite this article: Fouzia, F.J., Surputheen, M.M., Rajakumar, M. (2025). Hybrid pigeon optimization-based feature selection and modified multi-class semantic segmentation for skin cancer detection (HPO-MMSS). The Scientific Temper, **16**(5):4260-4269.

Doi: 10.58414/SCIENTIFICTEMPER.2025.16.5.11

Source of support: Nil

Conflict of interest: None.

Received: 01/04/2025 **Accepted:** 03/05/2025 **Published** : 31/05/2025

model focus on relevant lesion characteristics rather than noise or artifacts. Normalization is a preprocessing technique that helps to reduce variability and ensure consistent data input by scaling pixel values. The effectiveness of the preprocessing stage balances the classification stage and model generalization enhancement upon differentiating skin lesions by non-representative class enhancement. Finally, this helps in improving the performance metrics of the proposed methodology. Metrics, such as precision, robustness, and reliability, play a significant role in various types of skin cancer detection (2018).

Feature Selection

The improvement of the efficiency of the CAD system for detecting skin cancer by Feature selection and segmentation process. After removing unwanted information, the choice of efficient feature selection focuses on the most characteristic characteristics of skin lesions (2017). Additionally, accurate segmentation ensures that only the regions are analyzed for categorization, increasing the diagnosis's precision (2018). The representation of a novel hybrid framework with the usage of the MMSS model for lesion segmentation, accurate prediction, and HPOA for predominant feature selection. Normalization technique is used for consistent scaling of input image features, which leads to the crucialness of the preprocessing stage. The proposed system aims to address current challenges in skin cancer detection and significantly enhance diagnostic findings by utilizing advanced feature selection and segmentation approaches (2017, 2018).

Segmentation

Regarding the analysis of medical images, especially in skin cancer prediction, segmentation is the most predominant stage. Skin tissue is covered by healthy tissue which have a relationship with the lesion. This is separated and detected by meticulous segmentation, which is considered as most critical stage in image processing. The accuracy of conventional segmentation techniques is reduced due to their inability to handle irregular lesion shapes, variations in skin tone, and unclear boundaries. Advanced methods, such as semantic segmentation models, have demonstrated promise in pixel-level classification, enabling the overcoming of these restrictions and ensuring that every pixel in an image is accurately classified into either skin lesion or skin non-lesion regions. Generally, the available methodologies utilize boundary-aware loss functions, encoding-decoding models, and a connection skipping accuracy enhancement factor for the segmentation stage, while considering the ISIC 2020 dataset, which exhibits significant variations in lesion characteristics. The improvement of classification performance and early detection of melanoma utilizing precise segmentation, which helps in the significant improvement of patient outcomes by reducing false negatives and false positives (2021).

Classifiers

The classification of lesions between benign and malignant types is done using Classifiers. This is an essential stage in the skin cancer detection process. Currently, the most prevalent deep learning classifier model is the convolutional neural network (CNN). Random Forest and Support Vector Machine classifiers are used in the diagnostic process for the keen extraction of construction features from dermatological photographs.

Convolutional Neural Network

The significant classifier CNN, is used at the initial stage for image segmentation. Because CNN has the capability of automatically extracting spatial features from the imputed images by utilizing its different layers. CNN layers consist of convolution layers, pooling layers, hidden layers, and an activation function. Skin lesion type differentiation based on lesions, texture variation feature, shape, and color of skin. The CNN carefully extracts these features from the segmented lesion. Then, the normalised and segmented images are at usage for training the CNN models after splitting skin lesions into many groups. Achieving high accuracy in intricate pattern identification in input images is easily handled by CNN.

Support Vector Machine

SVM is a supervised learning algorithm that effectively classifies using the hyperplane technique. SVM helps improve the accuracy metric by employing nonlinear separation management within skin lesion types. By following up the feature extraction process, it is considered a promising method for fine-tuning the model for classification. SVM plays a role in handling high-dimensional feature spaces in input images. The overall accuracy, performance, and misclassification reduction are enhanced by SVM incorporated along with CNN's learned features, especially when concluding the differentiation of similar visualizations of skin lesion types.

Random Forest

The decision tree methodology serves as the underlying framework for the random forest algorithm, enabling efficient classification and determining the significance of minute features in the classification process. That's why random forest is considered the most complex ensemble learning algorithm. The skin features, such as skin tone, texture, and boundary characteristics, enhance the precision of skin cancer prediction by utilizing the random forest algorithm. Based on how often a feature occurs in the decision trees and the extent to which it enhances the model's classification performance, the Random Forest algorithm gives each feature an importance score. Understanding how the model makes decisions and ensuring that the most relevant features are prioritized during classification depends on this step.

Related work

Arshaghi *et al*. (2020) proposed a hybrid framework of feature selection methodology that combines SVM with the buzzard optimization algorithm (BUZO). The BUZO algorithm enhances the performance of the classification process and reduces dimensionality by selecting pertinent features from dermatology images. The accuracy of the classification process is 94.3%, attained by using the publicly available ISIC dataset. However, the accuracy was compromised; there is a limitation in handling multi-class skin cancer detection because of focusing on binary classification of images, i.e., benign vs. malignant. Moreover, the proposed model's computational efficiency was not discussed, raising concerns about its practicality in real-time clinical environments.

Doma *et al*. (2021) highlighted the framework with the hybrid combination of deep convolutional inverse graphics network (DCIGN), a hybrid deep Kohonen network (HDKN), and a pelican optimization algorithm (SPOA) for skin cancer diagnosis. This hybrid novelty framework contains a segmentation stage, a feature extraction stage, and a feature selection stage. The main focus of the model is on classification accuracy, with limited evaluation of the segmentation phase. This becomes particularly critical for the precise identification and classification of skin lesions.

Alazzam *et al*. (2020) proposed a Pigeon-Inspired Optimizer (PIO) for a feature selection algorithm for intrusion detection systems. The new method was introduced for binarizing a continuous PIO along with cosine similarity. This helps improve convergence speed compared to conventional sigmoid methods. The datasets, such as KDDCUP99, NLS-KDD, and UNSW-NB15, are used to assess the model's performance. It achieves promising outcomes, including TPR, FPR, accuracy, and F-score, compared to traditional AI-driven methods. Although this method was initially specific to intrusion detection systems, it is also generalizable to other domains.

Moradi *et al*. (2021) presented a model with superior results in segmenting various types of lesions. It becomes increasingly challenging for real-time clinical applications to overcome high computational complexity. Additionally, the study ignored feature selection, which could improve classification accuracy in favor of segmentation tasks.

A better binary version of the Pigeon-Inspired Optimization (PIO) algorithm was created by Pan *et al*. (2021) for feature selection tasks. The authors improved the speed update scheme and proposed novel transfer functions in four categories to enhance performance quality. The better classification performance is achieved with fewer features, as evaluated using UCI datasets. There is no investigation of multi-class classification, as it was only concentrated on binary classification methodology. Reddy and Gopinath (2022)proposed a CNN-based model for the enhancement of segmentation and skin lesion classification. The image quality enhancement and data augmentation strategy are implemented using preprocessing techniques and segmentation techniques. The achievement of 90.2% segmentation process accuracy and 88.7% classification process accuracy by the use of the ISIC 2018 dataset. However, the study lacked a robust feature selection technique that could improve classification performance. The absence of a multi-class classification framework was a significant drawback of the proposed model, which also led to overfitting due to the use of sparse data.

Baygin *et al*. (2022) proposed a hybrid model that combines textural features, such as Local Binary Patterns, with deep features from the DarkNet architecture. The model achieved a classification accuracy of 91.54% using a collection of colorful skin cancer images. This framework focuses on a binary classification model, but fails to validate the model with diverse datasets, thereby limiting its generalizability. The incorporation of neighborhood component analysis (NCA) is employed as a feature selection strategy to enhance accuracy and reduce computational cost.

To improve feature extraction capabilities and refine segmentation by optimizing the selection of pertinent features, Sarwar *et al*. (2024) proposed a framework for skin lesion segmentation that combines the Hybrid Residual U-Net (ResUNet) model with Ant Colony Optimization (ACO). The primary objective is to improve the accuracy and efficiency of the framework's performance in diagnosing skin lesions. However, this methodology affects processing time when dealing with large datasets.

Taghizadeh and Mohammadi (2022) developed a two-step pipeline using a fine-tuned YOLOv3 model for skin lesion detection and a SegNet model for segmentation. The study achieved a mean Average Precision (mAP) of 96% on the ISIC 2018 dataset. Despite its high accuracy, the model was primarily focused on melanoma detection, which limited its utility for other skin cancer types. The computational cost of running two separate models also raised concerns about the framework's efficiency in real-time applications.

Liu *et al*. (2023) introduced a dual-path network to integrate local and global features for better skin lesion segmentation. The local path captured detailed lesion features, while the global path accounted for larger contextual information. The model was assessed on the PH2 dataset, achieving an IoU of 89.6%. Despite its promising results, the study did not address multi-class classification, and the dataset used was relatively small and imbalanced, affecting the model's generalizability.

Omneya Attallah (2024) proposes a hybrid model (HTDFFM) to enhance skin cancer classification in two types of images. By applying DCT, the image quality is enhanced, and CNNs are used for feature extraction. The approach employs a three-stage fusion process to merge features from both original and DCT-enhanced images, resulting in a robust feature vector for classification. The method's computational complexity due to multi-stage fusion and multiple CNNs could limit its real-time clinical applicability.

Zhao *et al*. (2023) proposed a lightweight segmentation model designed for real-time clinical applications. Depth-wise separable convolutions were used in the model to speed up inference and lower computing costs. An accuracy achievement of 93.7% on the ISIC 2021 dataset. Despite its efficiency, the model showed limited performance on more complex lesion types, and the authors did not explore feature selection techniques, which could have further enhanced accuracy.

A deep learning framework called EOSA-Net for multi-class skin cancer classification is proposed by Purni and Vedhapriyavadhana (2024). The ebola optimization search algorithm (EOSA) is used for model integration of the enhanced Canny Edge Detection technique, which optimizes preprocessing and hyperparameters. ISIC 2018 and ISIC 2019 are the datasets used to train and evaluate the model for categorizing 8 types of skin cancer. A classification accuracy of 99% is achieved. While handling a smaller dataset, it faces overfitting problems, rather than dealing with large datasets, and is also in need of increased processing power. Additionally, the essential component for segmentation, which is necessary for the precise identification of lesion boundaries, is also lacking in this methodology.

Imran *et al*. (2024) highlighted the methodology for identifying various inflammations in skin tissues and carcinomas using a transformer-based multi-class segmentation of immunohistochemistry images. A self-attention mechanism captures global and local interdependence in skin pictures. An average of 83.1% accuracy, 90.8% of F1 score, and 65.3% of mean IoU is achieved by using the publicly available ISIC 2016 dataset. Feature selection is absent is a limitation of this model for improving the classification task. It primarily focuses on histopathological images, which limits the model's real-time applicability.

Yaqoob *et al*. (2024) proposed a framework called HRDOXGB, which integrates random drift optimization (RDO) with the XGBoost algorithm. This hybrid approach attains enhancement in accuracy and efficiency by identifying a minimal subset of pertinent genes from high-dimensional datasets. It only operates on microarray data, which is a major limitation of this approach, but it does not affect the system's performance. Rather, it may not directly reflect on complexity of cancer genetics when compared with future technologies.

Proposed Methodology

The combination of the MMSS model and HPOA model for exact lesion segmentation and feature selection, respectively, for accuracy improvement and robustness enhancement. The hybridization work model helps address current model issues, such as uneven feature selection, computational efficiency, and enhancement of segmentation phase accuracy.

Normalization

Normalization is a crucial step in image preprocessing, as it involves converting pixel values to a standard range by handling the consistency of input data, which helps reduce image variability. Generally, there will be variation in image brightness, contrast, and distribution of color in Skin lesion images in dermoscopic image datasets due to the capturing conditions of pictures. The proposed HPO-MMSS methodology combines batch normalization (BN) and instance normalization (IN) techniques to enhance robustness and accommodate image variations.

Instance Normalization

To handle variations in the images, IN is used in the preprocessing stage to minimize brightness variations and contrast variations, and creates a relationship between the images through independent normalization. Uniformity enhancement of the input images facilitates pixel modification of intensity values with a mean of 0 and a standard deviation of 1. The mathematical formulation of IN can be given as follows,

$$x' = \frac{x - \mu'}{\sigma'} \qquad \textit{Eq.(1)}$$

Where,
x' - normal pixel value
x - original pixel value
μ' - mean
σ'- standard deviation

Eq. (1) is applied to every pixel in the ISIC 2020 dataset images for image standardization. By adjusting the pixel values to have a 0 mean and 1 standard deviation to maintain a consistent factor in pixel intensity of the images. This leads to affecting the factors of variation in the image's illumination and color factor throughout the whole dataset.

Batch Normalization

BN normalizes the network's intermediate activation function after the modification of each output from each layer to have a mean value of 0 and a standard deviation value of 1. This BN is used to train the MMSS model for enhancement purposes. This method reduces the likelihood of overfitting while improving the model's stability and convergence. The mathematical expression for Batch Normalization is:

$$y = \gamma . \frac{x - \mu}{\sigma} + \beta \qquad \textit{Eq.(2)}$$

Where,

y - batch normalized output

x - input activation

μ – mean average of the small batch's activations

σ - standard deviations of the activations in the mini batch

γ. β - Learnable settings to change and scale the output that has been standardized

Eq. (2) is applied to each mini-batch and improves the model's generalization capability by ensuring that the activations remain stable throughout the training process.

Feature Selection Using Hybrid Pigeon Optimization Algorithm (HPOA)

The subsequent phase in the proposed initiative pertains to HPOA, a metaheuristic optimization algorithm derived from the navigational behavior of pigeons, specifically their remarkable ability to interpret environmental indicators. By selecting the most prominent features from dermoscopic images, the HPOA is used for feature selection in skin cancer diagnosis, reducing the dimensionality of the input data. The efficacy of feature selection is crucial for enhancing the machine learning model's performance, as redundant or irrelevant features can significantly undermine classification accuracy. The HPOA optimizes the selection process by balancing exploration and exploitation during the search for the optimal feature subset. The result is a more compact feature set that retains the most relevant information for classification, thereby enhancing both classification accuracy and computational efficiency.

Pseudo Code for HPOA

```
Initialize pigeon population (positions and velocities)
Evaluate initial fitness for each pigeon
While (iteration < max iterations):
  If (iteration < max iterations / 2):
    Apply Map and Compass Operator
  Else:
    Apply Landmark Operator
  Update positions and velocities
  Evaluate fitness for each pigeon
End While
Select the best pigeon as the optimal feature subset
```

Initially, the hybrid pigeon optimization algorithm (HPOA) creates a population of pigeons, which in the feature space represent possible solutions. The pigeons' starting locations and speeds are chosen at random. The Map and Compass Operator is the next step in the algorithm, which allows pigeons to systematically explore the feature space on a global scale by adjusting their placements based on their velocity, personal best position, and the global best position. Subsequently, in the subsequent phase, the Landmark Operator is implemented, whereby pigeons refine their positions towards the centroid of the population to engage in local exploitation. The best-performing pigeon is chosen as the ideal feature subset after its fitness is assessed using a classification accuracy score in each iteration. The ideal feature subset for skin cancer detection is returned when the algorithm reaches convergence or the maximum number of iterations has been reached. The location of each pigeon is updated in response to its velocity and direction:

$$X_i^{t+1} = X_i^t + V_i^t \quad Eq.(3)$$

Where, X_i^t - position of pigeon i at iteration t

V_i^t - velocity of pigeon i at iteration t

The pigeon's best-known position and the population's worldwide best position both affect velocity:

$$V_i^{t+1} = w.V_i^t + c_1 r_1 (P_{best} - X_i^t) + c_2 r_2 (G_{best} - X_i^t) \quad Eq.(4)$$

Where:

w - inertia weight,

c_1 and c2 - learning factors,

r_1 and r_2 - random values between 0 and 1,

P_{best} - personal best position,

G_{best} - global best position.

Each pigeon is a possible subset of features chosen from the dermoscopic images in the context of the ISIC 2020 dataset. This dataset has a high-dimensional feature space with many features based on color, texture, and shape. During each iteration, *Eq.(3)* and *Eq.(4),* Pigeons adjust their velocity and position to explore the feature space, respectively. The personal best (P_best) position represents the best feature subset a pigeon has found so far based on classification accuracy, the global best (G_best) position is the best feature subset found by the entire population, and the updated position reflects a new combination of features for the next iteration. Landmark Operator Focuses on local exploitation to refine the feature selection process. In this phase, the pigeons' positions are adjusted based on the average position of the population:

$$X_i^{t+1} = \frac{1}{N} \sum_{j=1}^{N} X_j^t \quad Eq.(5)$$

Where,

N - No. of pigeons in the population.

Eq.(5) calculates the center position of the pigeon population by averaging the positions of all pigeons at a given iteration, and it represents the average position, indicating the consensus about promising features across all pigeons.

$$X_i^{t+1} = \frac{X_i^t + X_{center}}{2} \quad Eq.(6)$$

Eq. (6) updates the position of each pigeon by moving it closer to the center point, and it adjusts the pigeon's position by averaging its current position. X_i^t With the calculated center position, X_{center} Refining the feature selection process.

Modified Multi-Class Semantic Segmentation (MMSS)

The third step in the proposed work is the MMSS model is an enhanced encoder-decoder architecture designed to perform pixel-wise segmentation of dermoscopic images into melanoma, basal cell carcinoma, and benign keratosis. Traditional segmentation models often face challenges in accurately detecting irregular lesion boundaries and handling class imbalance in multi-class datasets, particularly in ISIC 2020. The proposed MMSS model addresses the above challenges through the following modifications.

Pseudo code for MMSS

Initialize the encoder-decoder network
For each image in the training set:
  Extract feature maps using the encoder
  Apply skip connections to preserve spatial details
  Perform upsampling in the decoder to reconstruct the segmentation mask
  Apply class balancing using weighted loss functions
  Enhance boundary detection using edge filters
  Calculate total loss (Dice Loss + Boundary Loss)
  Update model weights using backpropagation
End For
Evaluate the model on the validation set
Use the trained model for final prediction on test images

Encoder-Decoder Architecture with Skip Connections

The segmentation map is reconstructed by the decoder after the encoder has extracted hierarchical features from the input images. The use of skip connections ensures that spatial details are preserved during the decoding process, improving the accuracy of segmentation, especially for lesions with irregular borders. Mathematically, skip connections can be represented as:

$$F_{decoder} = F_{decoder} + F_{encoder} \quad \textit{Eq. (7)}$$

The *Eq. (7)* allows the decoder to receive feature maps directly from the encoder, bypassing the downsampling process. This skip connection helps the decoder to retain the exact shape, size, and boundaries of lesions in the ISIC 2020 dataset.

Class Balancing Techniques

To solve the problem of imbalanced datasets, where specific skin lesion types are underrepresented, the MMSS model integrates class-balancing techniques. Dice loss function or weighted cross-entropy loss can be used to address class imbalance in multi-class segmentation. Depending on how frequently each class appears in the dataset, the weighted cross-entropy loss gives it a different weight:

$$L_{WCE} = -\sum_{c=1}^{C} w_c \cdot y_c \log(\hat{y}_c) \quad \textit{Eq.(8)}$$

Where:

- C - No. of classes,
- y_c - actual classification for class C,
- $\hat{y}_c$ - anticipated likelihood for class C.
- w_c - weight assigned to class C.

The *Eq. (8)* assigns higher penalties to underrepresented classes in the ISIC 2020 dataset and ensures that the MMSS model pays equal attention to all classes. An increased accuracy of the segmentation phase for uneven skin lesion types leads to a dependable nature of the model while dealing with multi-class skin cancer detection.

Boundary Detection Enhancements

The combination of boundary detection filter mechanism and boundary-aware loss function in the MMSS model is used for skin lesion border segmentation enhancement. For classifying the differentiation between benign and malignant lesions, the important characteristics such as form and lesion texture are considered. The mathematical formulation of the Dice loss function is represented as follows:

$$L_{dice} = 1 - \frac{2 X |P \cap G|}{|P| + |G|} \quad \textit{Eq.(9)}$$

Where:

P - segmentation mask for predicted

G - segmentation mask for ground truth

Increasing the overlapping factor between the segmentation mask of ground truth and the segmentation mask for the predicted image is the primary duty of the Dice loss function. The value of L_{dice} = 1 when there is no overlapping, else L_{dice} = 0. It shows that the MMSS model shows more interest in overlapping optimization between predicted mask and ground truth mask, which results in accuracy enhancement in skin lesion segmentation while using the ISIC 2020 dataset images.

Boundary-aware loss functions and edge detection filters can improve boundary detection. For edge detection, the Sobel operator is frequently employed and is expressed as follows:

$$G_x = \begin{matrix} -1 & 0 & 1 \\ -2 & 0 & 2 \\ -1 & 0 & 1 \end{matrix} * I, \quad G_y = \begin{matrix} -1 & 0 & 1 \\ -2 & 0 & 2 \\ -1 & 0 & 1 \end{matrix} * I \quad \textit{Eq.(10)}$$

Where:

G_x and G_y - the gradients in the horizontal and vertical directions,

I - input image

*denotes the convolution operation

The combined gradient magnitude is computed as:

$$G = \sqrt{G_x^2 + G_y^2} \qquad \text{Eq.(11)}$$

Eqs. (10), (11), and (12), which apply convolution filters to the input image, highlight regions with sharp changes in intensity that correspond to lesion boundaries and detect edges in the vertical as well as horizontal directions. Inaccurate boundary predictions can be penalised using boundary-aware loss functions.

$$L_{Boundary} IoU = 1 - \frac{|B_{pred}| \cap |B_{true}|}{|B_{pred}| \cup |B_{true}|} \qquad \text{Eq.(12)}$$

Where:

B_{pred}- predicted boundary,

B_{true}- ground truth boundary.

The *Eq. (12)* measures the overlapping factor between predicted and ground truth boundaries, penalizing incorrect boundary predictions to ensure sharp and accurate segmentation of skin lesions.

Experimental Setup

The experimental setup involves training and testing the proposed HPOA combined with the MMSS model on the publicly available skin cancer dataset ISIC 2020. The dataset images are normalized to ensure uniformity across input data. The experiments are conducted on a high-performance computing system to accelerate deep learning computations. Accuracy, Recall, Dice Coefficient, Precision, and IoU are the evaluation measures that analyze the performance of the model. The proposed model is compared against baseline methods like YOLOv3, SegNet, and Vision Transformers to demonstrate its superior performance in multi-class skin lesion detection and image segmentation.

Dataset Description

The data set used is the International Skin Imaging Collaboration (ISIC) 2020, which is used to train the proposed framework. This dataset is considered as most predominant, which has a large collection of derma images of skin lesions. The dataset contains 33,126 images with both benign and malignant skin lesions. The ISIC 2020 dataset includes a wide range of skin lesions, such as vascular lesions, benign keratosis, basal cell carcinoma, actinic keratosis, and melanoma. It also contains the metadata inclusion of lesion diagnosis and patient demographics, which leads to an efficient path for multiclass classification and image segmentation process. A 70:30 ratio is used to partition the ISIC 2020 dataset. 30% of the data is divided as 15:15 and utilized for testing and validation, respectively, while 70% of the data is used for model training. To preserve the class distribution across all sets, stratified sampling is used for the splitting process. The model is trained using 70% of the information to identify the underlying patterns and characteristics of various skin lesions (training set). The ratio of 15 % dataset is used for validation, and 15% dataset is used for testing the model, respectively. Validation helps to improve the model's performance and prevent overfitting by utilizing the input given during the training process. The generalizability of the model is assessed throughout the testing phase.

Implementation Tools and Libraries

Python is used as the primary language for implementation. Libraries such as TensorFlow and Keras are used for building and training the AI-driven model. For data manipulation NumPy and Pandas packages are used. Image processing tasks like augmentation and segmentation, OpenCV is used. Data visualization is done using Seaborn and Matplotlib. Scikit-learn is for accessing the performance metrics like Accuracy, Recall, Dice Coefficient, Precision, and IoU.

Results and Discussion

The proposed methodology is the combination of HPOA and MMSS models that provides better working for skin cancer detection when compared to other available models. By considering various sizes of datasets, the proposed framework outperforms the related models, such as YOLOv3, SegNet, and Vision Transformers, in terms of accuracy, precision, recall, dice coefficient, and IoU. The robustness of the HPO-MMSS methodology is also efficient in managing multi-class lesion classification and image segmentation. The discussion section demonstrates that the proposed framework improves accuracy in clinical applications by focusing on boundary detection and feature selection of skin lesions, outperforming previous related methodologies.

Performance Metrics

The performance metrics are considered as Accuracy, Recall, Dice Coefficient, Precision, and IoU. The performance of the suggested model is assessed using these metrics. It provides a thorough evaluation of segmentation and skin lesion categorization. The proposed framework's performance is compared with the related works such as ESCCHOA[7], SLSACO[13], HTDFFM[16], and HRDOXGB[20]. This comparison depicts the outperformance of the hybrid integration of HPOA-MMSS methodology for multi-class segmentation and feature selection. Table 1 describes the accuracy metric result of the proposed framework and the previous related works. It demonstrates that the HPO-MMSS model achieves accuracy enhancement through feature selection and the segmentation phase, identifying relevant features that differentiate skin lesion types. Figure 1. Shows the data visualization of the accuracy obtained.

Table 1: Accuracy Comparison of HPO-MMSS(%)

DATASET	*ESCCHOA*	*SLSACO*	*HTDFFM*	*HRDOXGB*	*HPO-MMSS*
2000	85.2	88.5	86.1	89.3	91.1
4000	87.5	89.9	87.4	90.5	92.6
6000	89.1	91.2	89.0	91.8	94.0
8000	90.4	92.4	90.7	93.0	95.3
10000	91.8	93.1	92.0	94.2	96.7

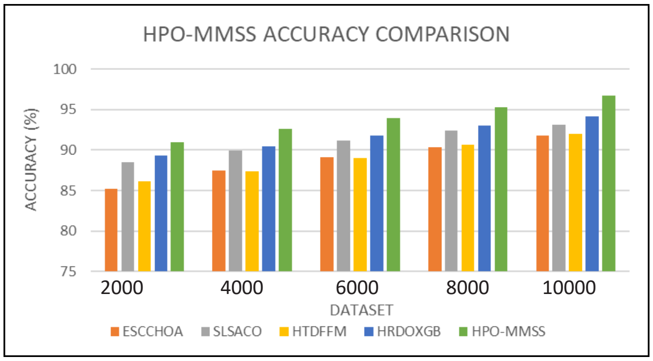

Figure 1: Accuracy (%) of HPO-MMSS and related works

Table 2: Precision Comparison of HPO-MMSS(%)

DATASET	*ESCCHOA*	*SLSACO*	*HTDFFM*	*HRDOXGB*	*HPO-MMSS*
2000	83.9	85.6	84.3	86.7	89.0
4000	85.4	87.1	85.8	88.2	90.5
6000	87.0	88.6	87.3	89.8	91.9
8000	88.3	89.9	88.6	91.3	93.3
10000	89.5	91.3	90.0	92.7	94.7

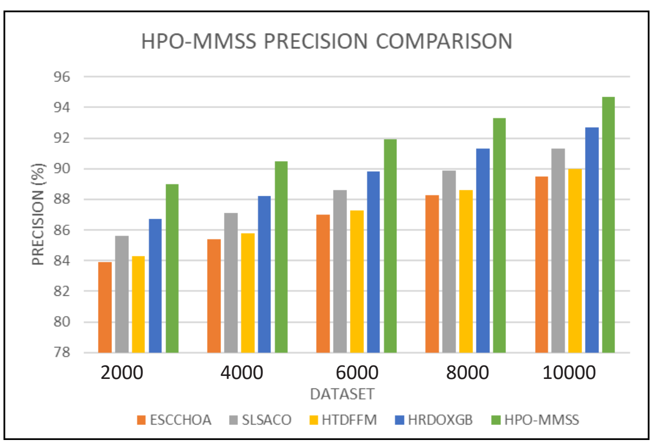

Figure 2: Precision comparison (%)

Table 2 illustrates the extent to which incorporating HPOA for feature selection and Instance Normalization (IN) improves the precision metric. By ensuring that discriminative features are chosen, HPOA lowers the number of false positives in classification. By ensuring consistent feature extraction, IN helps stabilize the model's performance across a variety of lesion images, particularly when lesions are unclear and difficult to distinguish. Figure 2 represents the graphical representation of the comparative analysis of HPO-MMS with other models.

Table 3 compares the recall value to the existing works. The MMSS framework's boundary detection capability helps the recall metric by precisely segmenting lesions with asymmetrical shapes and hazy borders. To reduce false negatives and improve the detection of malignant lesions in the ISIC datasets, IN makes sure the model captures fine-grained details. Figure 3 represents the graphical representation of recall comparison.

Table 4 illustrates the extent to which the MMSS method improves the dice coefficient (Figure 3). The model's ability to accurately describe lesion borders is enhanced by this technique, especially when lesions have overlapping areas or unusual shapes. To improve this metric, the refined

Table 3: Comparison of the Recall metric of HPO-MMSS (%)

DATASET	*ESCCHOA*	*SLSACO*	*HTDFFM*	*HRDOXGB*	*HPO-MMSS*
2000	84.7	86.3	85.2	87.6	88.4
4000	86.2	87.8	86.7	89.1	89.9
6000	87.7	89.2	88.2	90.5	91.3
8000	89.0	90.5	89.5	92.0	92.7
10000	90.4	91.9	90.9	93.4	94.1

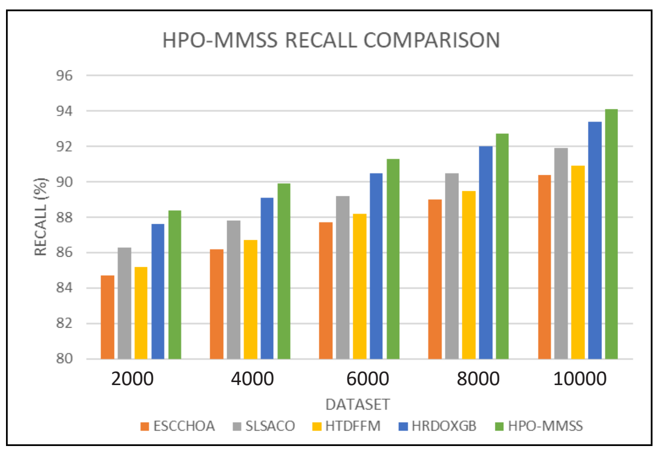

Figure 3: Comparison of recall(%)

Table 4: Dice Coefficient Comparison of HPO-MMSS(%)

DATASET	*ESCCHOA*	*SLSACO*	*HTDFFM*	*HRDOXGB*	*HPO-MMSS*
2000	86.2	87.5	86.9	88.7	89.5
4000	87.8	89.0	88.4	90.2	91.0
6000	89.3	90.5	89.9	91.7	92.5
8000	90.7	91.9	91.2	93.2	93.9
10000	92.0	93.3	92.6	94.6	95.3

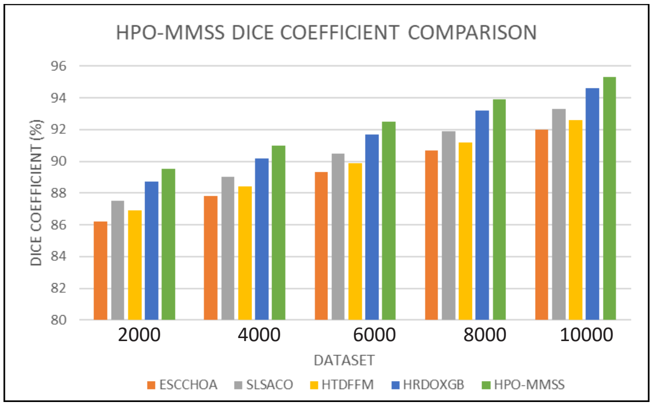

Figure 4: Comparison of dice coefficient (%)

Table 5: Intersection over union comparison of HPO-MMSS(%)

DATASET	*ESCCHOA*	*SLSACO*	*HTDFFM*	*HRDOXGB*	*HPO-MMSS*
2000	82.4	84.0	83.6	85.3	86.5
4000	84.2	85.6	85.2	86.9	88.1
6000	85.5	87.1	86.7	88.4	89.6
8000	86.9	88.5	88.1	89.9	91.1
10000	88.2	89.9	89.4	91.3	92.5

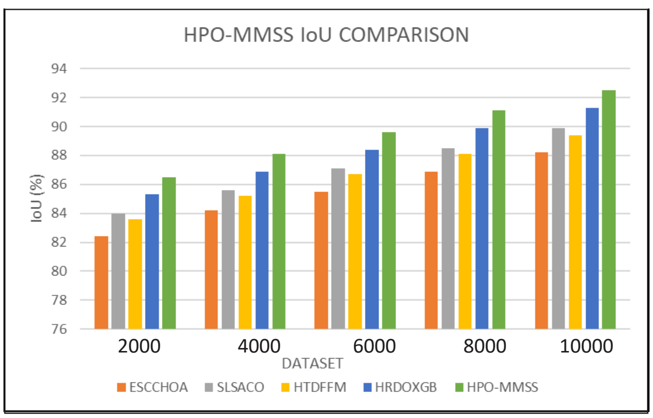

Figure 5: Comparison of IoU(%)

segmentation process minimizes under-segmentation errors.

The overlap between the anticipated ground truth and predicted segmentation mask is explained by the metric called IoU is represented in Table 5. It depicts that the proposed framework outstrips with superior IoU results when compared to other works. IN is responsible for this because it confirms that small lesion patterns do not overlap when dealing with different skin lesions. The suggested framework's relative comparison representation with other studies is displayed in Figure 5.

The proposed HPO-MMSS methodology shows the incredible performance even when dealing with multi-class skin cancer detection and segmentation in the ISIC 2020 data images. And the metrics percentage shows that it outperforms the related works such as MSCDN, HDEF, HAVT, and ViTMCS in terms of accuracy, precision, recall, Dice coefficient, and IoU. HPOA is mainly responsible for noise reduction and classification boosting for the relevant features. Boundary details are maintained seamlessly, which is essential in differentiating the types of skin lesions, which leads to segmentation factor enhancement. When increasing the count of dataset images, there is a consistent increase in performance gain. It shows that HPO-MMSS acts efficiently in dealing with large datasets. Irregular boundaries are segmented precisely, as understood by the outperformance of recall and IoU metrics. It results conclude that the proposed framework is more scalable, dependable, reliable, and accurate for multi-class skin cancer detection in a real-world scenario.

Conclusion

The proposed HPO-MMSS framework offers a fresh and practical perspective on multi-class skin cancer detection and segmentation by comparing it with current related techniques. The improvement in diagnostic accuracy while dealing with the increase in dataset size is outperformed. The combination of HPOA for feature selection and MMSS for boundary segmentation is carried out in a novel manner, proving excellent outperformance in detecting skin cancer efficiently. The experimental results, considering the ISIC 2020 dataset, show a consistent increase in dataset count, indicating the seamless enhancement of the system's performance. The framework also outperforms, with a superior increase in performance, when the dataset size is consistently increased. Compared to existing models that suffer from irregular lesion borders and multi-class classification, the HPO-MMSS framework is more efficient and scalable, achieving higher accuracy (96.7%) and a higher Dice coefficient (95.3%) on larger datasets. The experimental results on the ISIC 2020 dataset demonstrate consistent performance improvements, particularly in challenging metrics such as the Dice coefficient and IoU, which are crucial for precise lesion boundary detection.

In real-world clinical applications, the framework's outstanding performance paves the way for early diagnosis of skin cancer, which will become an increasingly essential part of the medical field. The future consideration primarily focuses on enhancing real-time capabilities and applying the current scenario-based augmentation methodology to expedite the diagnosis process in the dermatology field. Future enhancements of the HPO-MMSS framework concentrate on advanced data augmentation techniques to enhance real-time usability, addressing class imbalance and improving model generalization. The efficacy of the framework is enhanced by Self-supervised learning, which reduces its reliance on large labeled datasets.

Acknowledgement

We acknowledge the support of the PG & Research Department of Computer Science, Jamal Mohamed College (Autonomous), Trichy for providing computational resources. This research was not supported by any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

References

Alazzam, H., Sharieh, A., & Sabri, K. E. (2020). A feature selection algorithm for intrusion detection system based on pigeon inspired optimizer. *Expert Systems with Applications, 148*, 113249.

Arshaghi, A., Ashourian, M., & Ghabeli, L. (2020). Detection of skin cancer image by feature selection methods using new Buzzard Optimization (BUZO) algorithm. *Traitement du Signal, 37*(2), 255–262.

Attallah, O. (2024). A hybrid trio-deep feature fusion model for improved skin cancer classification: Merging dermoscopic and DCT images. *Technologies, 12*(10), 190. https://doi.org/10.3390/technologies12100190

Baygin, M., Tuncer, T., & Dogan, S. (2022). New pyramidal hybrid textural and deep features-based automatic skin cancer classification model: Ensemble DarkNet and textural feature extractor. *arXiv preprint arXiv:2203.15090*.

Esteva, A., Kuprel, B., Novoa, R. A., Ko, J., Swetter, S. M., Blau, H. M., & Thrun, S. (2017). Dermatologist-level classification of skin cancer with deep neural networks. *Nature, 542*(7639), 115–118.

Green, A. C., & Olsen, C. M. (2017). Cutaneous squamous cell carcinoma: An epidemiological review. *British Journal of Dermatology, 177*(2), 373–381.

He, Z., Li, X., Chen, Y., Lv, N., & Cai, Y. (2023). Attention-based dual-path feature fusion network for automatic skin lesion segmentation. *BioData Mining, 16*(1), 28.

Hu, M., & Yang, X. (2023). Attention-driven lightweight model for pigmented skin lesion detection. *arXiv preprint arXiv:2308.02119*.

Imran, M., Tiwana, M. I., Mohsan, M. M., Alghamdi, N. S., & Akram, M. U. (2024). Transformer-based framework for multi-class segmentation of skin cancer from histopathology images. *Frontiers in Medicine, 11*, 1380405.

Isensee, F., Jaeger, P. F., Kohl, S. A. A., Petersen, J., & Maier-Hein, K. H. (2021). nnU-Net: A self-configuring method for deep learning-based biomedical image segmentation. *Nature Methods, 18*, 203–211.

Krishna, D. M., Sahu, S. K., & Raju, G. (2023). Enhanced skin cancer classification through a hybrid optimized approach: Deep echo network machine utilizing pelican-optimized deep Kohonen features. *Traitement du Signal, 40*(6), 2455–2469. https://doi.org/10.18280/ts.400611

Liu, Y., Jain, A., Eng, C., Way, D. H., Lee, K., Bui, P.,... & Coz, D. (2020). A deep learning system for differential diagnosis of skin diseases. *Nature Medicine, 26*(6), 900–908.

Moradi, N., & Mahdavi-Amiri, N. (2021). Multi-class segmentation of skin lesions via joint dictionary learning. *Biomedical Signal Processing and Control, 68*, 102787.

Pan, J. S., Tian, A. Q., Chu, S. C., & Li, J. B. (2021). Improved binary pigeon-inspired optimization and its application for feature selection. *Applied Intelligence, 51*(12), 8661–8679.

Purni, J. T., & Vedhapriyavadhana, R. (2024). EOSA-Net: A deep learning framework for enhanced multi-class skin cancer classification using optimized convolutional neural networks. *Journal of King Saud University – Computer and Information Sciences, 36*(3), 102007.

Reddy, A. S., & Gopinath, M. P. (2022). A comprehensive review on skin cancer detection strategies using deep neural networks. *Journal of Computer Science, 18*(10), 940–954.

Sarwar, N., Irshad, A., Naith, Q. H., Alsufiani, D. K., & Almalki, F. A. (2024). Skin lesion segmentation using deep learning algorithm with ant colony optimization. *BMC Medical Informatics and Decision Making, 24*(1), 265. https://doi.org/10.1186/s12911-024-02686-x

Taghizadeh, M., & Mohammadi, K. (2022). The fast and accurate approach to detection and segmentation of melanoma skin cancer using fine-tuned YOLOv3 and SegNet based on deep transfer learning. *arXiv preprint arXiv:2210.05167*.

Tschandl, P., Rosendahl, C., & Kittler, H. (2018). The HAM10000 dataset, a large collection of multi-source dermatoscopic images of common pigmented skin lesions. *Scientific Data, 5*, 180161.

Yaqoob, A., Verma, N. K., Aziz, R. M., & Shah, M. A. (2024). Optimizing cancer classification: A hybrid RDO-XGBoost approach for feature selection and predictive insights. *Cancer Immunology, Immunotherapy, 73*(12), 261. https://doi.org/10.1007/s00262-024-03843-x