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Deep learning-based stacking ensemble for malaria parasite classification in blood smear images

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ABSTRACT

Malaria remains a significant global health challenge, necessitating accurate and efficient diagnostic tools. Deep learning models have emerged as promising solutions for automated malaria detection using microscopic blood smear images. This study evaluates the performance of various convolutional neural network (CNN) architectures, including VGG16, ResNet50, MobileNetV2, and EfficientNet, in classifying infected and uninfected cells. Individual model performances were assessed based on accuracy, precision, recall, and F1-score, with EfficientNet achieving the highest standalone accuracy of 88.0%. To enhance classification performance, a stacking ensemble approach was implemented, using a logistic regression meta-classifier to integrate outputs from multiple models for improved decision-making. The stacking model outperformed individual networks, achieving an accuracy of 89.4%, with precision, recall, and F1-scores surpassing those of standalone models. Challenges in malaria parasite classification—such as high inter-class similarity, variations in staining quality, and class imbalance were addressed through data augmentation and model tuning. These findings highlight the potential of ensemble learning in medical image analysis, paving the way for more accurate and scalable malaria detection systems.

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1. INTRODUCTION

Malaria continues to pose a serious global health threat, particularly in tropical and subtropical regions, with approximately 247 million cases and 619,000 deaths reported annually [1]. The disease is caused by Plasmodium parasites and transmitted through the bites of infected female Anopheles mosquitoes. Early and accurate diagnosis is critical to prevent severe complications and fatalities [2]. Traditionally, malaria is diagnosed by microscopic examination of Giemsa-stained blood smears, a process performed by trained pathologists. While considered the gold standard due to its accuracy, this manual method is often time-consuming, labor-intensive, and prone to human error, especially in under-resourced areas [3].

To overcome these limitations, the development of automated and intelligent diagnostic tools has become a research priority [4]. Advances in artificial intelligence (AI) [5], particularly deep learning, have revolutionized medical image analysis, enabling rapid and accurate disease detection. Convolutional neural networks (CNNs), known for their ability to learn hierarchical image features, have been widely applied in medical diagnostics, including malaria detection [6]. Models such as VGG16, ResNet50, InceptionV3, MobileNetV2, and DenseNet121 have shown promising results [7], often achieving high accuracy. However, depending on a single CNN model has drawbacks, including overfitting and sensitivity to variations in image quality and staining techniques, which may reduce generalization across datasets [8].

To address these challenges [9], ensemble learning approaches have been introduced, where multiple models are combined to improve predictive accuracy. Among various techniques, stacking [10] also referred to as meta-learning, has shown great potential. Unlike traditional methods such as bagging and boosting [11], stacking combines the outputs of base models using a meta-learner, which improves decision-making by learning from the strengths of each model [12]. Despite its success in other medical imaging domains, stacking remains underutilized in malaria detection.

This study proposes a robust stacking ensemble model that integrates five well-known CNN architectures CNN, VGG16, ResNet50, MobileNetV2, and EfficientNet. Each network contributes unique feature extraction capabilities. The extracted features [13] are then fused and passed to an XGBoost classifier serving as the meta-learner [14]. This architecture not only enhances accuracy and generalization but also improves interpretability by analyzing the contribution of each model. Furthermore, the approach is designed to be computationally efficient and suitable for deployment in real-world clinical settings, particularly in resource-limited environments [15]. Through comprehensive evaluation, the study highlights the superiority of stacking ensembles over individual CNNs and demonstrates their potential in delivering reliable, scalable, and accurate malaria diagnostics.

2. RELATED WORK

AI and machine learning (ML) have significantly advanced medical imaging, especially in automating malaria diagnosis using deep learning. Traditional microscopic examination is labor-intensive and error-prone, prompting researchers to explore AI solutions [16]. CNNs have proven effective by accurately extracting and classifying features from medical images [17].

Various deep learning models such as ResNet [18], InceptionNet [19], and EfficientNet [20] have been widely adopted to enhance malaria detection accuracy, often matching or surpassing expert-level performance [21]. Transfer learning, by utilizing pre-trained CNNs, reduces the reliance [22] on extensive labeled data, improving the practicality of AI-driven diagnostics. Furthermore, ensemble learning especially stacking has proven highly effective in combining diverse classifiers, boosting overall performance, and overcoming individual model limitations to ensure more consistent and accurate results [23].

Despite progress in deep learning for malaria detection [24], generalization remains a key challenge due to variations in image quality, staining protocols [25], and equipment, which can cause inconsistent model performance across real-world settings. To address this, hybrid methods combining deep learning with traditional ML algorithms like support vector machines and random forests have been explored, improving adaptability and robustness across diverse datasets. However, interpretability continues to be a concern in clinical deployment, as many deep models function as "black boxes," making their decision-making processes opaque. To build clinician trust and ensure transparency, explainable AI (XAI) techniques [26] are being developed, allowing for clearer insights into model predictions and fostering greater acceptance in medical practice.

Enhancing AI-based malaria diagnosis also depends heavily on expanding and diversifying training data [27]. Given the scarcity of large medical datasets, data augmentation methods particularly those using generative adversarial networks (GANs) are employed to synthesize realistic training samples, boosting model generalization. Additionally, lightweight deep learning models [28] are being developed for real-time malaria detection on mobile or edge devices, making diagnostic tools more accessible in low-resource settings. To further improve adaptability, domain adaptation techniques help correct class imbalances and reduce dataset bias, enabling models to perform reliably across varied data sources [29]. Moreover, federated learning addresses data privacy concerns by allowing decentralized model training across institutions without sharing sensitive information, promoting secure collaboration and broader application of AI in healthcare [30].

To further optimize malaria detection models, researchers have integrated advanced optimization techniques such as differential evolution and particle swarm optimization, which help in fine-tuning hyperparameters and improving computational efficiency [31], [32]. These optimization strategies play a crucial role in enhancing the performance of deep learning models, particularly in low-resource environments where computational power is limited. However, despite these technological advancements, the real-world deployment of AI-based malaria diagnostic tools continues to face regulatory challenges. Factors such as model bias, the need for extensive validation studies, and compliance with medical regulations pose significant hurdles in the widespread adoption of AI-driven solutions [33]. As AI in healthcare continues to evolve, it is crucial for researchers and regulatory bodies to work together to develop standardized frameworks for evaluating and validating AI models before clinical implementation [34], [35].

This study introduces a stacking ensemble model combining EfficientNet, ResNet50, VGG16, and MobileNetV2 with a logistic regression meta-classifier to enhance malaria detection. By addressing limitations like class imbalance, limited evaluation metrics, and morphological variability, it offers a more robust, generalizable, and scalable solution compared to individual CNN models.

3. METHOD

The proposed methodology for malaria detection using deep learning follows a structured workflow, beginning with dataset acquisition and moving through preprocessing, feature extraction, ensemble learning, and final prediction, as depicted in Figure 1. The dataset used originates from the National Institutes of Health (NIH), containing 27,558 labeled cell images—13,779 parasitized and 13,779 uninfected red blood cells—each in RGB format with a resolution of 128×128 pixels. Preprocessing steps involved resizing images for uniformity, normalizing pixel values between 0 and 1, and applying data augmentation methods such as rotation, flipping, and zooming to enhance model generalization. Despite its balance and quality, the dataset may exhibit bias, as it mainly features Plasmodium falciparum under controlled lab settings, potentially limiting its real-world applicability [36].

Training and evaluation were performed on an NVIDIA RTX 3080 GPU with an Intel Core i7 processor and 32 GB RAM, using Python 3.8, TensorFlow 2.16.1, and Keras. The training was done using a batch size of 32, a learning rate of 0.0001, the Adam optimizer, and binary cross-entropy loss across 30 epochs with early stopping. A stratified 5-fold cross-validation ensured balanced training and validation. Deep learning models, including CNN, VGG16, ResNet50, MobileNetV2, and EfficientNet were used to extract features from the preprocessed images.

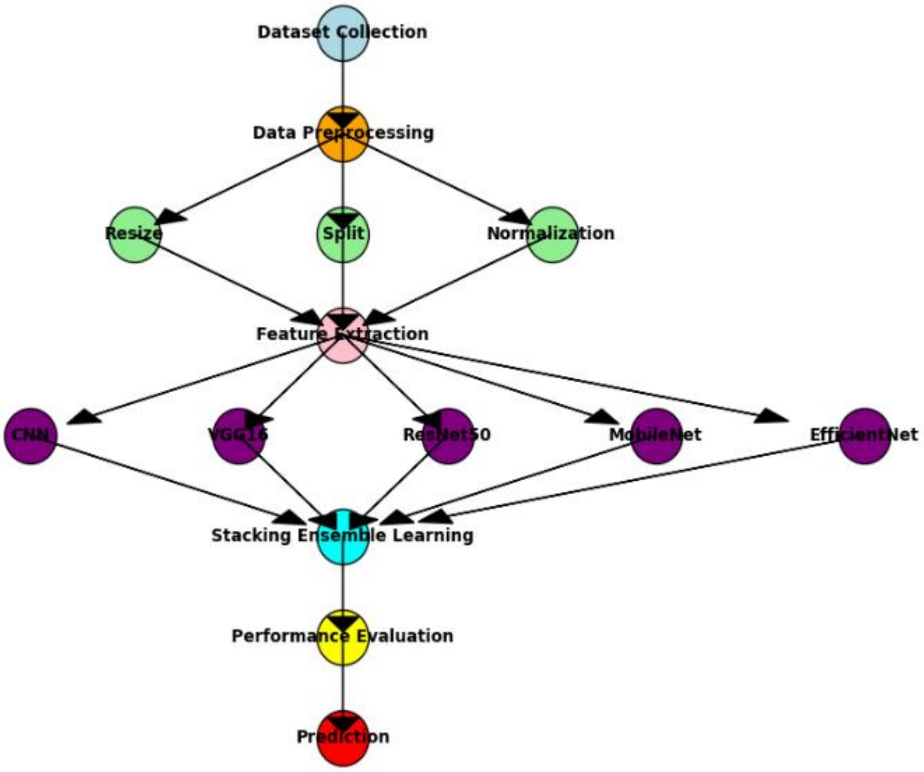

Figure 1. Methodology of stacking ensemble learning

This research addresses major challenges in malaria parasite detection by employing a robust methodology that integrates advanced model selection, effective data processing, and ensemble learning. To handle the variability in parasite appearance and cellular morphology, a range of deep learning architectures—VGG16, ResNet50, MobileNetV2, and EfficientNet—were utilized for their capacity to extract meaningful and discriminative features from microscopic images. Data artifacts and visual noise were minimized through preprocessing techniques such as normalization and augmentation strategies like rotation and flipping, thereby improving model resilience to distortion and irregularities. High-capacity models like EfficientNet and ResNet50 were particularly effective in differentiating between morphologically similar infected and uninfected cells, addressing a core challenge in visual classification.

A balanced dataset was achieved through resampling techniques, ensuring equal representation of classes during training and minimizing bias. The core innovation lies in the adoption of a stacking ensemble learning approach, where base models generate predictions that are passed to a logistic regression or XGBoost meta-classifier. This model fusion improves overall performance by reducing overfitting and capturing complementary strengths from each network. Evaluation metrics—including accuracy, precision, recall, and F1-score—were used to comprehensively assess the model's diagnostic reliability. The final deployment classifies unseen blood smear images with high precision, offering an efficient, scalable solution for automated malaria detection.

4. RESULT ANALYSIS

This section presents the performance evaluation of the proposed stacking ensemble approach for the detection of malaria using deep learning models. The dataset used for training and testing is obtained from the Cell Images for Detecting Malaria dataset, which consists of 27,558 microscopic images categorized into parasitized and uninfected classes. To ensure optimal model training, the dataset undergoes preprocessing, including resizing, train-test splitting (80:20), and normalization before being fed into the deep learning models.

The efficiency of the deep learning models and the stacking ensemble approach is assessed using multiple statistical evaluation metrics, including accuracy, precision, recall, and F1-score. These evaluation measures are computed using the fundamental classification terminology:

- False Positive (FP): Incorrect positive prediction (uninfected cell misclassified as parasitized).
- True Positive (TP): Correct positive prediction (parasitized cell correctly classified).
- False Negative (FN): Incorrect negative prediction (parasitized cell misclassified as uninfected).
- True Negative (TN): Correct negative prediction (uninfected cell correctly classified).
- True Positive Rate (TPR): The proportion of actual positive cases (e.g., parasitized cells) that are correctly identified by the model
- False Positive Rate (FPR): The proportion of actual negative cases (e.g., uninfected cells) that are incorrectly classified as positive by the model.

The performance metrics are defined as follows:

Accuracy: Measures the proportion of correctly classified images over the total number of test images. It is calculated as:

$$Accuracy = \frac{(TP+TN)}{(TP+TN+FP+FN)} \tag{1}$$

Precision: Represents the proportion of correctly identified malaria-positive images among all images predicted as malaria-positive:

$$Precision = \frac{TP}{(TP+FP)} \tag{2}$$

Recall: Also known as sensitivity or the true positive rate, it evaluates the model's ability to correctly detect malaria-positive cases among all actual malaria-positive cases:

$$Recall = \frac{TP}{(TP+FN)} \tag{3}$$

F1-score: A harmonic mean of precision and recall, ensuring a balanced assessment of both. It is given by:

$$F1-Score = 2 \times \frac{Precision*Recall}{Precision+Recall} \tag{4}$$

True Positive Rate (TPR) can be calculated by:

$$True\ Positive\ Rate\ (TPR) = \frac{TP}{(TP+FN)}$$

False Positive Rate (FPR) can be calculated by:

$$False\ Positive\ Rate\ (FPR) = \frac{FP}{(FP+TN)}$$

The AUC represents the area under the ROC curve and quantifies the overall ability of the model to distinguish between classes.

Figure 2 presents the confusion matrices for six deep learning models CNN, VGG16, ResNet50, MobileNetV2, EfficientNet, and Stacking—used for malaria parasite classification. Each matrix displays the number of true positives, true negatives, false positives, and false negatives for uninfected and parasitized red blood cells. The stacking ensemble model demonstrates the highest classification accuracy, with the lowest number of misclassifications among all models. EfficientNet and ResNet50 also show strong performance. These visualizations highlight the advantages of ensemble learning and deep architectures in improving detection reliability, particularly for parasitized cells, which are critical for timely and accurate malaria diagnosis.

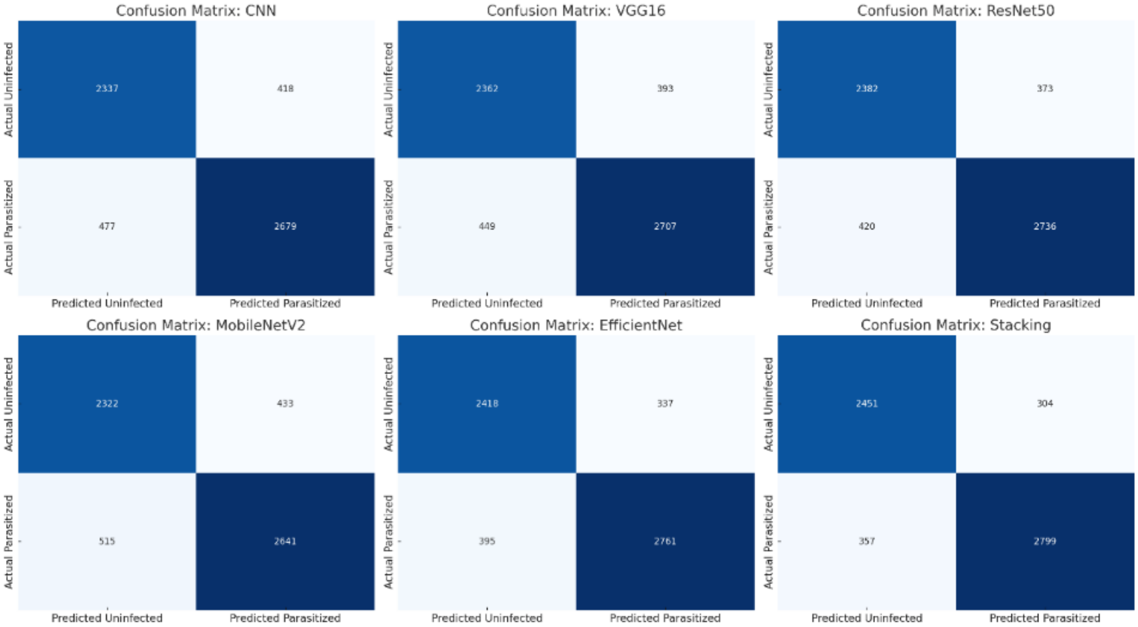

Figure 2. Confusion matrices for malaria classification using different CNN models

Table 1 shows the comparitive analysis of performance metrics. The Stacking Model outperforms all individual architectures, achieving the highest accuracy (89.4%), precision (90.2%), recall (88.7%), and F1-score (89.4%), demonstrating the advantage of combining multiple feature extractors for improved generalization. Among standalone models, EfficientNet (88.0% accuracy, 89.1% precision) performs best, followed by ResNet50 (87.3% accuracy, 88.0% precision) and VGG16 (86.1% accuracy, 87.3% precision), highlighting the impact of deeper architectures. MobileNetV2 (84.8%) lags behind, emphasizing its focus on efficiency over accuracy. The stacking model enhances feature representation, reducing individual model weaknesses, making it the most robust and reliable choice for classification. If computational efficiency is a priority, EfficientNet is the best alternative, while ResNet50 offers a balance between depth and performance.

Table 2 represents the classification report for stacking model. The classification report for the stacking model demonstrates its strong performance in malaria detection, achieving an overall accuracy of 89.4%. It exhibits a precision of 89.2% for uninfected cells and 90.9% for parasitized cells, indicating that the model is highly reliable in correctly identifying both classes. The recall scores of 87.5% for uninfected and 91.2% for parasitized suggest that the model effectively captures most positive cases, with slightly better sensitivity towards parasitized samples. Additionally, the F1-scores of 88.3% (uninfected) and 91.0% (parasitized) show a balanced trade-off between precision and recall. These results confirm that the stacking approach outperforms individual models, making it a robust solution for malaria detection.

Table 1. Comparison of performance metrics

Models	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
CNN	85.2	86.5	84.9	85.7
VGG16	86.1	87.3	85.8	86.5
ResNet50	87.3	88	86.7	87.3
MobileNetV2	84.8	85.9	83.7	84.8
EfficientNet	88	89.1	87.5	88.3
Stacking	**89.4**	**90.2**	**88.7**	**89.4**

Table 2. Classification report for stacking model

Class	Precision (%)	Recall (%)	F1-Score (%)	Support
Uninfected	89.2	87.5	88.3	2755
Parasitized	90.9	91.2	91.0	3156
Overall Accuracy	**89.4**			

The stacking ensemble approach significantly improves classification performance by leveraging the complementary strengths of CNN, VGG16, ResNet50, MobileNet, and EfficientNet as base learners. The final meta-learner, which integrates predictions from these models, enhances robustness and generalization, leading to improved performance in malaria detection. The results demonstrate that ensemble learning outperforms individual deep learning models in terms of accuracy, precision, recall, and F1-score. This approach ensures a reliable and automated diagnostic system that can assist medical professionals in malaria screening, reducing the dependency on manual microscopic analysis.

Figure 3 presents a graphical analysis comparing the precision, recall, and F1-score of the stacking model. The ROC plot in Figure 4 compares the classification performance of six models—CNN, VGG16, ResNet50, MobileNetV2, EfficientNet, and Stacking—based on estimated false positive and true positive rates. The stacking model demonstrates the highest discriminative ability with an approximate AUC of 0.89, followed by EfficientNet and ResNet50.

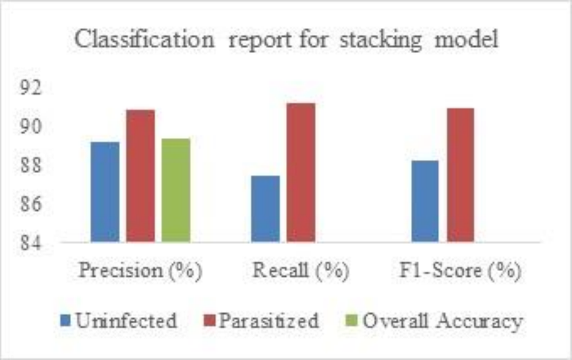

Figure 3. Classification report for stacking model

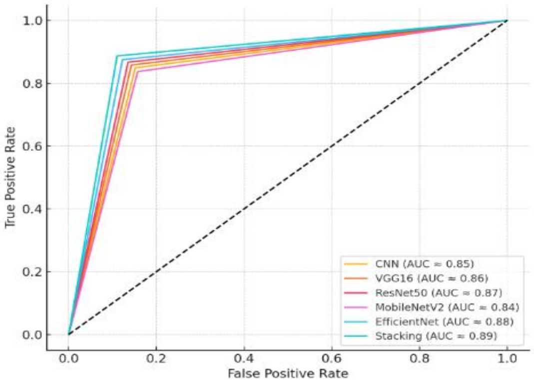

Figure 4. Estimated ROC Curves for all models

Table 3 reviews traditional and automated malaria diagnosis methods, highlighting the current study's evaluation of deep learning models including CNNs and a stacking ensemble. While recent studies show higher accuracy with customized methods, this study offers a robust, comparative analysis of standard architectures, validating stacking as a reliable diagnostic strategy.

The stacking ensemble model proposed in this study enhances accuracy, reliability, and robustness over individual CNN models. By integrating EfficientNet, ResNet50, VGG16, and MobileNetV2 using a logistic regression meta-classifier, it effectively combines each model's strengths while offsetting their limitations. Achieving 89.4% accuracy—surpassing EfficientNet's 88%—the ensemble also delivers improved recall and F1-score, which are vital for reducing false negatives in clinical diagnosis. Additionally, it handles image artifacts and morphological variations more effectively, offering consistent and dependable classification. Despite increased training complexity, the approach proves to be a practical and scalable solution for automated malaria detection.

Table 3. Review of existing malaria diagnosis techniques, including both traditional and automated methods in recent years

Reference	Classifier	Input Features	Accuracy (%)
Mujahid *et al.* [37]	EfficientNet-B2	Red blood cell images	97.57
Goni *et al.* [38]	Customized Lightweight CNN	Red blood cell images	99.45
Goni *et al.* [39]	Contrastive Domain Adaptation (CodaMal)	Images from low-cost microscopes	Improved mAP
Ali *et al.* [40]	M2ANET	Blood cell images	Outperforms SoTA
Taye *et al.* [41]	Deep CNNs (VGG19, InceptionV3, Xception)	Blood smear images	Up to 97
Liang *et al.* [42]	Deep Neural Network	Preprocessed images (RGB), cell segmentation	97.4
Thakur and Juneja [43]	ANN	Shape, texture, statistical features from blood smear images	94.1

5. CONCLUSION AND FUTURE DIRECTIONS

A stacking ensemble approach for classifying malarial images is described in this paper. This study highlights the effectiveness of deep learning models for malaria detection using microscopic images, with various CNN architectures evaluated, including VGG16, ResNet50, MobileNetV2, and EfficientNet. Among them, EfficientNet achieved the highest standalone accuracy of 88.0%, but a stacking ensemble approach integrating multiple models outperformed individual architectures, achieving an accuracy of 89.4%, precision of 90.2%, recall of 88.7%, and an F1-score of 89.4%. The stacking model demonstrated superior performance in distinguishing uninfected and parasitized cells, emphasizing the importance of ensemble learning and meta-learning techniques in medical image classification. Traditional methods like microscopy offer high accuracy but require skilled personnel, limiting scalability. RDTs are cost-effective and scalable but less accurate in low parasitemia cases.

Deep learning models (CNNs, ResNet50, EfficientNet) provide high accuracy and automation, with EfficientNet and Stacking models achieving superior results. However, they demand computational resources and quality datasets. Lightweight models like MobileNetV2 offer mobile compatibility with slightly reduced accuracy. Advanced models (e.g., YOLOv5, M2ANET) balance speed and precision but may be complex to implement. Overall, automated methods enhance scalability and accuracy but must be tailored to resource availability for practical deployment in real-world settings. Future research should explore meta-learning for enhanced adaptability, hybrid feature extraction combining traditional image processing with deep learning, and advanced architectures like Vision Transformers for improved pattern recognition.

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Komal Kumar Napa	✓	✓		✓				✓		✓				
Kalyan Kumar Angati	✓		✓		✓				✓					
Senthil Murugan Janakiraman					✓		✓			✓				
Balamurugan Amoor Gopikrishnan		✓												
Bindu Kolappa Pillai Vijayammal			✓				✓				✓			
Vattikuti Charan Sri Manikanta Sai			✓				✓				✓			

C : **C**onceptualization
M : **M**ethodology
So : **So**ftware
Va : **Va**lidation
Fo : **Fo**rmal analysis
I : **I**nvestigation
R : **R**esources
D : **D**ata Curation
O : Writing - **O**riginal Draft
E : Writing - Review & **E**diting
Vi : **Vi**sualization
Su : **Su**pervision
P : **P**roject administration
Fu : **Fu**nding acquisition

CONFLICT OF INTEREST STATEMENT

Authors state no conflict of interest.

DATA AVAILABILITY

Data availability is not applicable to this paper as no new data were created or analysed in this study.

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