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Leveraging Deep Learning for Early Diagnosis of Monkeypox Disease

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Abstract: Early detection of monkeypox is thus crucial to containing its spread and reducing public health risks. Proper identification of monkeypox strain may be difficult owing to its close similarities with other pox virus strains, a requirement thus for innovative solutions for accurate and timely detection. This research seeks to create A system for the early detection of monkeypox disease using the strong deep learning methods based on the use of the state-of-the-art Generative Adversarial Network (GAN) and VGG19 model. The framework presented here uses the GAN model in creating the augmented data samples for the creation of this, addressing the lack of data. The VGG19 model is used for the diagnosis of these augmented High-accuracy data samples and monkeypox robustness detection. Due to the integration of the present model, such diagnostic mistakes can be minimized and the sensitivity and specificity of the system are enhanced. The experiments conducted based on publicly available medical datasets illustrate that GAN-VGG19 combination will provide a greater improvement in classification performance and accuracy rate as high as 97%. Thus, this model posits the possibility of deep learning approaches towards propelling early and accurate diagnosis of monkeypox for prompt interventions with improved public health impacts.

Keywords: Monkeypox Detection, Deep Learning, Generative Adversarial Network (GAN), VGG19, Data Augmentation, Convolutional Neural Networks (CNNs).

1. INTRODUCTION

Monkeypox is a disease caused by infection with the monkeypox virus, a member of the Orthopoxvirus genus of viruses along with smallpox and cowpox. Monkeypox became A significant global public health issue following the eradication of smallpox in 1980 and the cessation of the smallpox vaccine, especially in Central and West Africa. But the recent instance of the disease in non-endemic areas, which occurred in May 2022, revealed the virulence of the virus to infect on a large scale outside its ecological niche [1]. Its rise in incidence beyond Africa is facilitated by zoonotic spillovers, migration, and transmission from human to human, warranting the implementation of strong diagnostic approaches to regulate its transmission [2]. The pandemic of COVID-19 has put an increased load on the fast and effective identification of viruses to avert epidemics because there is a very high likelihood of transmission escalation in the event of delays in identification and quarantine [3]. Monkeypox is also comparatively difficult to diagnose because of its symptomatic resemblance with other poxvirus diseases, such as smallpox, chickenpox, and measles [4].

PCR and blood testing are currently the most powerful methods of diagnosis for diseases. These, however, need special laboratory facilities and personnel, hence are not easy to introduce in low-resource settings. This requires the development of both automated and scalable diagnostic devices.[5]. Deep learning is increasingly becoming popular over the past couple of years for medical image analysis. It has shown good performance in classification of diseases skin disorders [6]. Most scientists classify skin lesions with Convolutional Neural Networks. Such networks work best with a large quantity of well-labeled data—rare diseases like monkeypox do not have [7]. Other scientists have tried using pre-trained models like MobileNetV2 ResNet50, and InceptionV3 to improve monkeypox classification accuracy. Such a method called transfer learning helps, but lack of data persists as a problem [8]. One of the biggest problems in deep learning model training to detect monkeypox is that there aren't many publicly available datasets. This results in AI models that perform poorly on new data [9].

To solve this issue, Generative Adversarial Networks (GANs) have been used extensively to augment medical images to generate high-quality synthetic data and enhance model performance and address class imbalance [10]. GAN-augmentation has specifically shown effectiveness in improving classification accuracy as it can produce samples with diverse diversity that mimic real images [11]. A new paradigm is suggested that combines GAN-based data augmentation and the VGG19 deep learning model for classifying monkeypox. Synthetic images of monkeypox are created to solve the data insufficiency problem, and the model's ability to generalize across different cases is enhanced. The VGG19 architecture, featuring a deep hierarchical structure and

high-quality feature extraction ability is used for high-precision monkeypox lesion classification. To further enhance model explainability, the explainable AI methods such as Local Interpretable Model-Agnostic Explanations (LIME) are presented where the healthcare professionals can comprehend and trust the diagnostic outcome generated by the AI.

The literature demonstrates that deep learning models coupled with data augmentation techniques enhance diagnostic capacity for uncommon diseases with less model bias and enhanced sensitivity [7]. In addition, use of explainable AI methods is essential in medical use as it provides transparency and allows clinicians to validate AI-generated decisions prior to making final diagnoses [8]. As global awareness of monkeypox grows, AI solutions are the answer to enhanced surveillance, enhanced diagnostic capability, and prevention of future outbreaks [9].

By integrating cutting-edge deep learning methods with synthetic data augmentation, this research is aimed at the design of a practical, scalable, and explainable AI-driven diagnostic system for the Early identification of monkeypox. Using GAN-generated Image analysis using deep learning models not only solves the problem of scarce data but also improves the accuracy of classification, and therefore it is an interesting solution for practical uses. Furthermore, with future progress in medical diagnosis using AI, future research can work on model robustness, multimodal fusion of data, and building publicly available large datasets in an effort to enable wider clinical application. Finally, this research is reflective of the potential that AI holds in revolutionizing infectious disease diagnosis and presents a call for ongoing innovation to assist in the fight against future global health threats [10].

2. LITERATURE REVIEW

Advancements in artificial intelligence (AI) and deep learning have significantly impacted disease diagnosis, and infectious diseases such as Monkeypox specifically. Deep learning and machine learning methods have been used to enhance accuracy and reliability of Monkeypox detection. Despite this, dataset paucity, overfitting, and computational capacity constraints still exist and need to be overcome by innovation.

Sitaula (2022) compared and tuned thirteen pre-trained deep models for detecting Monkeypox. The best-performing model, Xception-DenseNet169, achieved an accuracy of 87.13%. However, the small dataset size and the limited memory capacity of the pre-trained model were key performance bottlenecks, hence a need for more larger-sized and diversified datasets [1].Bengesi (2023) sentiment analyzed tweets about Monkeypox using machine learning models like SVM and TextBlob annotation. SVM was 93.48% correct, but the sample was Twitter data only and a one-year time frame, with consequent generalizability problems. That would suggest application of data from various sources such as clinical reports and news media would improve accuracy in sentiment analysis [2].

Yasmin et al. (2023) suggested PoxNet22, the transfer learning model that was fine-tuned to forecast Monkeypox. The model was accurate, and remembered at 100%, but the findings show overfitting since it was not validated externally using real data from sources outside of it. External validation is a significant threat in the use of medical AI and should be tried on heterogeneous sets of patients [3]. Ahsan et al. (2023) employed transfer learning with six deep models with Local Interpretable Model-Agnostic Explanations (LIME) added for explanation. Models produced 93%-99% accuracy, but with very small dataset sizes and without regularization. Although LIME enhanced transparency of the models, explainability for high-risk clinical AI is still an area of research [4].

Olusegun et al. (2023) conducted emotion classification of tweets on Monkeypox using CNN, LSTM, BiLSTM, and CNN-LSTM models. CNN worked best at 96%. Imbalance in classes required oversampling, and reliance on Twitter data restricted its applicability on multiple platforms. Future studies Can explore the fusion of multimodal data of text and vision data for more comprehensive disease surveillance [5].Kundu et al. (2024) examined federated deep learning-based image-based detection of Monkeypox with images augmented using CycleGAN. MobileNetV2, Vision Transformer (ViT), and ResNet50 were compared. Computational power and some requirements of real-life medical imaging purposes were emphasized in the paper. Federated learning is privacy-sensitive advantages at a cost of optimization-efficient large-scale deployment techniques [6].

A model for Explainable Monkeypox classification by Raha (2024) from an attention-based MobileNetV2 through LIME was proposed. The model faced difficulty in timely diagnosis because Monkeypox disease gets overlapped with other types of skin infections. This necessitates the use of advanced feature extraction techniques that can distinguish Monkeypox from visually related diseases such as chickenpox and measles [7]. Emaki (2024) proposed an Artificial Neural Network (ANN) optimized by the adaptive Artificial Bee Colony (aABC) algorithm to predict Monkeypox from clinical symptoms. The model's accuracy was 71%, which is less than deep learning models as well as the random forest algorithm. This means that hybrid AI approaches need to be integrated, which use deep learning and traditional machine learning techniques for enhanced prediction [8].

Ma (2024) proposed a Triplet Attention Swin-Unet and Multiscale Expansion Convolution (MECTASwin-Unet) segmentation algorithm on a commercial dataset. The model achieved 90.4%-pixel accuracy and 80.3% mean intersection over union (mIoU). There were limited public datasets that limited comparisons, and standard benchmarks in Monkeypox image segmentation research were owing [9]. Karaddi et al. (2024) have introduced Softflatten-Net, a CNN network to overcome vanishing of gradients and overfitting. Softflatten-Net tackled binary (97.25% accuracy) and multi-class classification but was affected by class imbalance while moving to multi-class cases. Class imbalance through the use of weighted loss functions or data augmentation is still a prevalent area of interest [10]. Saleh et al. (2024) proposed Swin-PSO-SVM, which is a combination of Swin Transformer, Particle Swarm Optimization, and Support Vector Machine. It performed very well in terms of accuracy (95.56% on MSLD dataset and 96.43% on MSID dataset) but consumed a lot of computational power. Optimizing deep learning models for edge devices can make them

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more cost-effective in resource-limited clinical environments [11].

The tested researchers affirm the efficacy Machine learning and deep learning for the detection of Monkeypox but identify constraints of datasets, computational expense, and overfitting as the main challenges. Increasing diversity to the datasets, enhancing generalizability, and algorithmic adaptability for the resource constraint needs to be the future research emphasis. Explainability and robustness are also matters of major concern for facilitating trust and usage in the healthcare context.

3. PROPOSED METHODOLOGY

The proposed Approach shown in Fig.1, it's about the Early and proper monkeypox detection remains a challenge as monkeypox lesion differentiation is difficult from other dermatological conditions with limited availability of annotated datasets. Our approach to overcome such challenges is to introduce A hybrid deep learning approach in which Generative Adversarial Networks (GANs) are used for generating synthetic data augmentation and VGG19 is used for extracting features and classification. GANs generate great synthesized images to bridge the sparsity used for feature extraction problem, and VGG19, a deep convolutional neural network pre-trained model, gets valuable hierarchical features for correct classification. Explainable AI method Local Interpretable Model-agnostic Explanations (LIME) provide increased interpretability of the model for guaranteeing transparency of the decision-making process. The intended framework has five primary steps: collection and preprocessing of the dataset, data enhancement with GAN, feature learning using VGG19, explainability using LIME and Classification. All the steps have been framed so that they are used to increase the classification accuracy, enhance model generalization, and minimize overfitting for producing a better AI-based monkeypox diagnostic technique.

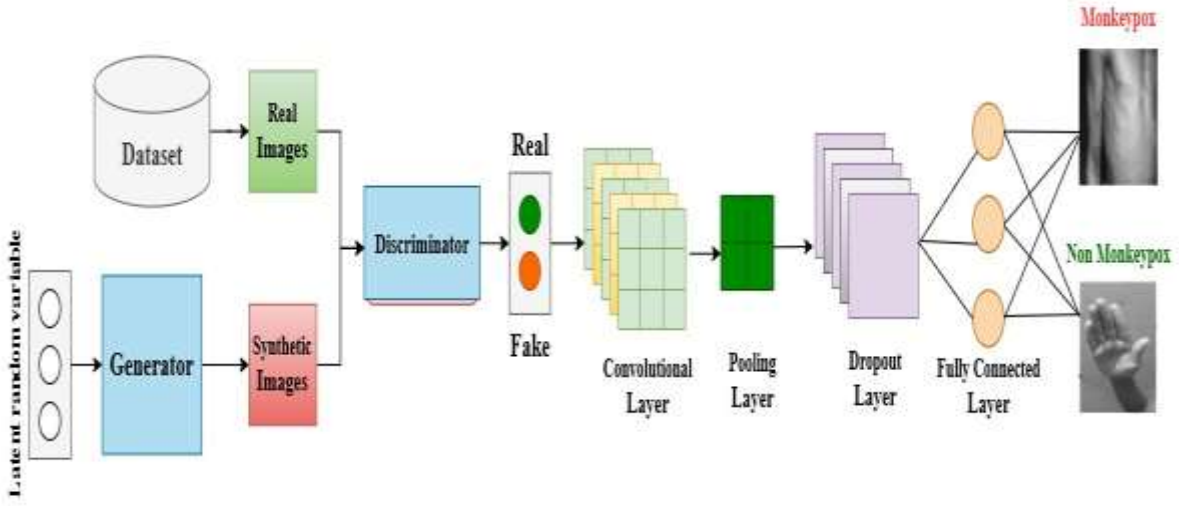

FIGURE 1. PROPOSED ARCHITECTURE WITH GAN AND VGG19

3.1 Data Augmentation Through Generative Adversarial Networks (Gans)

GANs have two rival neural networks, which are Discriminator and the Generator. The Generator takes an input latent random noise vector from some distribution like uniform or Gaussian and transforms it into a generated image. The Generator learns to replicate the distribution of real monkeypox images and generate realistic synthesized samples that mimic real images in every aspect. Discriminator, however, it is a binary classifier that determines whether the image is real or generated and provides feedback to the generator for the further improvement. The training is adversarial, where the Generator tries to generate images that will mislead the Discriminator and the generator tries to improve its power of distinguishing real images from the generated images back and forth. The adversarial process forces the generator to continuously enhance its ability to produce more realistic images. Co-training both the networks forces the model to repeatedly improve its power of generating high-quality data, balancing the set, and minimizing classification bias. The Discriminator assumes the responsibility of reviewing the quality of the generated images and then adjusts the corresponding Generator. After multiple iterations, the generator is capable of producing images that become increasingly realistic and closely resemble real cases. The process actually enhances the performance of the model classification since it introduces more training samples enhancing the generalization. With the use of GANs in the developed method, the system can process imbalanced or sparse data in a more efficient way, generating a more accurate classification outcome [6].

3.2 Transfer Learning for Feature Extraction

The VGG19 deep network is applied for feature learning and classification due its great ability to capture sapatial

patterns and subtle textural features in medical images. Transfer learning is applied for better model performance and reduced training time by pre-training VGG19 with ImageNet weights. Since ImageNet images have already learned generalizable features, fine-tuning the last layers on the monkeypox dataset allows the model to learn domain-specific patterns without requiring a large dataset. The lower layers, which are responsible for extracting low-level image features such as edges and textures, are frozen to retain pre-trained knowledge, and the higher layers are fine-tuned to enhance feature learning for monkeypox lesion detection [8].

3.3 Classifying Images with a Deep Learning Model

Feature extraction in VGG19 entails learning structural features using convolutional layers to segregate monkeypox lesions. Convolutional layers are applied to extract low-level (edge) and high-level (texture, shape) features using kernels and sigmoid activation for non-linearity. Max pooling layers are used to compress spatial dimensions and act as counter-measures against overfitting, along with dropout layers too. Fully connected layers utilize the extracted features and blend them with weights for final classification and sigmoid-activated output to differentiate between Monkeypox and Non-Monkeypox. The pre-trained ImageNet VGG19 is fine-tuned over the task, leveraging its deep network to facilitate feature learning. Cross-entropy loss, adaptive learning rate, and batch normalization during model optimization induce stability, while Local Interpretable Model-Agnostic Explanations (LIME) ensure interpretability by demonstrating key features causing predictions, and this simplifies clinicians' jobs during AI-driven diagnosis [8].

4. EXPERIMENTAL RESULTS AND ANALYSIS

4.1 Dataset Description

A skin lesion dataset was used in the experiment of this work, consisting of two classes: Monkeypox and Non-Monkeypox (other skin conditions such as chickenpox, measles, and images of normal skin). The dataset was gathered from various open-source medical databases in an effort to establish diversity for better classification. All images are digital color photos focused on involved skin regions, resized to the same resolution, and in RGB color format of three colors. The dataset was divided into a training set and a test set in an 80:20 ratio, with an additional validation set taken from the original dataset without data augmentation. To achieve better data representation and better generalization of the model, The dataset was augmented using GANs to generate synthetic images that closely resembled real medical samples. The large data set significantly increased the training samples, and the feature representation was bettered. Feature extraction and classification were done using VGG19, where the fully connected layers of VGG19 were used in distinguishing Monkeypox from Non-Monkeypox cases. The complementarity of GAN-based augmentation and VGG19 feature extraction enabled the strong resilience of the model for classification, graphical representation of distribution in datasets, data samples post-augmentation, and compound growth in datasets being included in the work.

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4.2 Performance Metrics

Monkeypox classification performance is assessed using the following key metrics: accuracy, recall, F1-score, and the ROC curve. Accuracy tests for general correctness, while recall checks whether the model correctly spots true monkeypox cases and refrains from false negatives. Specificity corrects for right identification of non-infected cases, refraining from false positives. F1-score is a trade-off between precision and recall, therefore wherever both false negatives and false positives are significant, it becomes significantly important. ROC-AUC evaluates the model's discriminative ability. All these parameters together provide a comprehensive evaluation, and the model is calculated using the formula below, as demonstrated through the equations.

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

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

$$Recall = \frac{TP}{TP+TN} \quad (3)$$

$$F1\ score = 2 * \frac{Precision*Recall}{Precision+Recall} \quad (4)$$

4.3 Analysis of the Result

Deep learning structures have become central to medical image classification, particularly in infectious disease diagnosis like Monkeypox. Among the various deep learning structures, VGG19 is one of the popular convolutional neural networks (CNN) known for its depth and capability in feature extraction. However, its default use can be susceptible to generalization and accuracy while handling complex medical data. To address these shortcomings, this work evaluates the performance of VGG19 in Monkeypox detection and explores augmentation by data using Generative Adversarial Networks (GAN). The proposed approach is expected to improve classifier metrics such as accuracy, precision, recall, and F1 score, coupled with enhanced disease detection and minimized false classifications.

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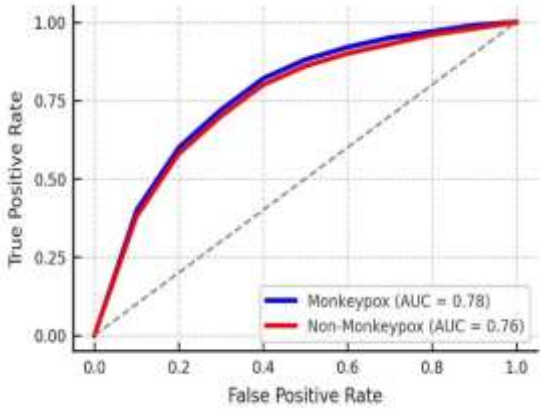
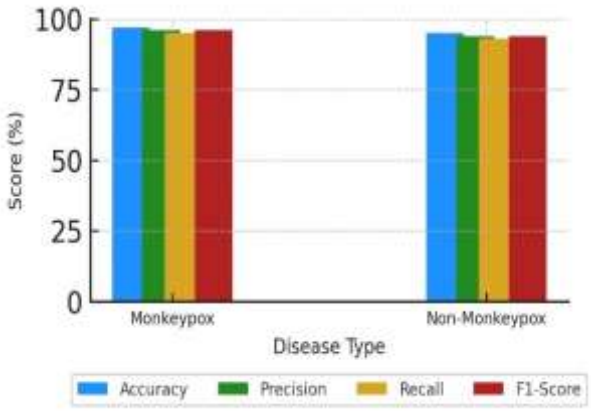
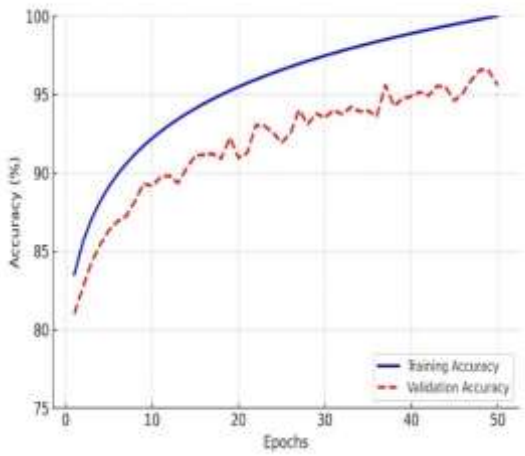


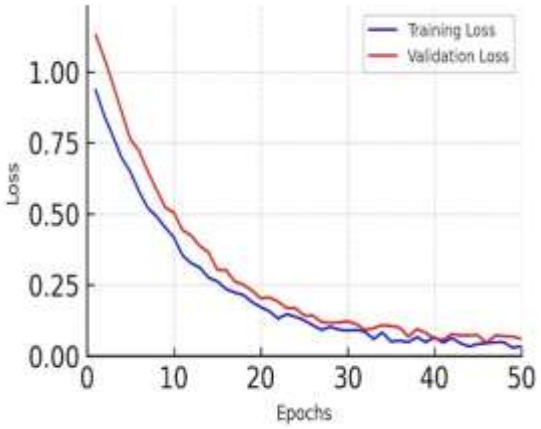
2 **(A) ROC CURVE**



2(B) PERFORMANCE OF PRECISION, RECALL, F1-SCORE FOR EACH CLASS



2(C) TRAINING AND VALIDATION ACCURACY CURVE



2(D) TRAINING AND VALIDATION LOSS CURVE

FIGURE 2. PERFORMANCE INDICATORS OF VGG19

ROC curve for model performance measurement in terms of Monkeypox and Non-Monkeypox cases is shown in Figure 5(a). False Positive Rate (FPR) is considered as x-coordinate and True Positive Rate (TPR) as y-coordinate. Blue line, Monkeypox model detection power, measures 0.78 AUC, while red line, Non-Monkeypox case model detection power, measures 0.76 AUC. The dash-diagonal is for a random classifier (AUC = 0.5) so that the model is not random, even though the performance will probably be increased by using good feature selection, hyperparameters, or data augmentation. Figure 2(b) The bar graph is such that the model's performance is always good for Monkeypox and Non-Monkeypox samples, with Accuracy, Precision, Recall, and F1-Score all being always above 95%. High scores in all measures suggest strong and stable classification with little bias to either class or the other. It also suggests that the model classifies well in Monkeypox and generalizes equally, hence

deployable in real-world applications. Figure 2(c) indicates the training and validation accuracy of a deep model over 50 epochs, with training accuracy as the blue line and validation accuracy as the red dashed line. Both are both rising sharply in the initial stage, with training accuracy leveling out in reaching nearly 100% and validation accuracy fluctuating slightly, which is characteristic of potential overfitting. Generalization can be improved through fine-tuning methods such as early stopping or regularization. Validation and training loss over 50 epochs, and both losses beginning higher than 1.0 and decreasing, is illustrated by Figure 2(d). The sharp drop in the initial 10 epochs shows fast learning, and loss is approaching almost zero at epoch 50. The fact that both training and validation loss are converging near one another suggests that there is little overfitting, which attests that the model is a great generalizer and reduces error well.

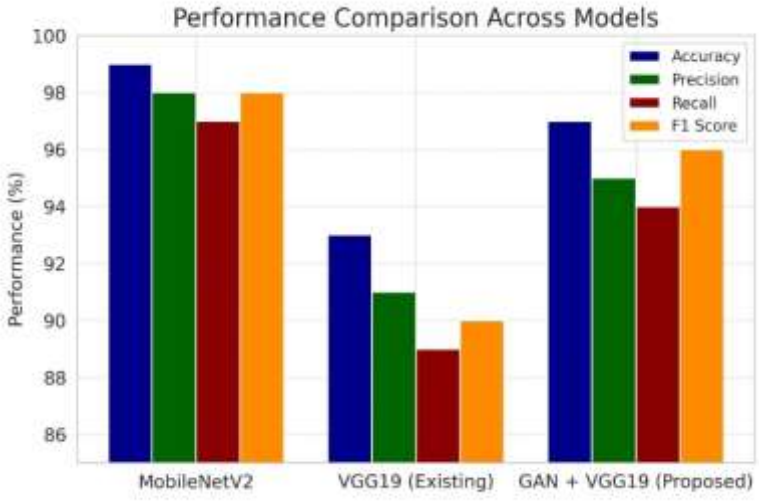


FIGURE 3. COMPARISON OF THE PROPOSED MODEL WITH EXISTING MODELS.

As indicated in Figure 3, the performance of the deep learning classifier model for the Non-Monkeypox and Monkeypox classification using four performance indicators: Accuracy, Precision, Recall, and F1-Score. The model exhibits high performance greater than average for both classes, where all indicators are above 95%. Accuracy gives the overall accuracy of the model globally, while Precision gives the proportion of true positive cases of Monkeypox out of all positives. Recall captures the model's ability to catch true Monkeypox cases with minimal false negatives. F1-Score as the harmonic mean of Precision and Recall captures symmetric performance at classification. When the metric values are equal across the two classes of diseases, the model is perfectly tuned without a strong bias toward one class or the other. This general good performance reflects the model's strength and its potential application in actual medical diagnosis for early detection and precise Monkeypox diagnosis.

TABLE 1. OBTAINED SCORE OF THE THREE METRICS

Metrics	Monkeypox	Non-Monkeypox
Precision	0.98	0.96
Recall	0.97	0.99
F1-score	0.98	0.96

TABLE 2. COMPARISON BETWEEN THE PROPOSED MODEL AND EXISTING MODELS.

Model	Accuracy	Precision	Recall	F1-score
Existing Model				
Modified VGG19	93%	0.94	0.94	0.94
Modified MobileNetV2	99%	0.98	0.99	0.99
Proposed Model				
GAN with VGG19	97%	0.98	0.97	0.98

The curve's graph presents a comparative analysis of model performance, with focus on the impact of GAN-based augmentation on classification accuracy. The analysis is based on the models listed in Table 1, with their baseline models, i.e., Modified VGG19 and Modified MobileNetV2, achieved 93% and 99% accuracy,

respectively. The proposed model, which includes GAN and VGG19, achieved 97% accuracy.

From the graph, we can observe that Modified MobileNetV2 possesses the highest accuracy among existing models, which serves as evidence of its strong feature extraction capability. However, it can be noted that the GAN model developed with VGG19 The model shows a significant improvement over Modified VGG19, which proves that GAN-based augmentation enhances the learning process by enhancing data generalization and feature diversity.

The curve trend of the graph shows that while simple deep learning models perform sufficiently, introducing GAN-synthesized synthetic data enhances feature representation and reduces overfitting and improves classification accuracy to the maximum. This enhancement renders the proposed GAN with VGG19 model a suitable alternative with robust generalization capacity for monkeypox detection.

5. CONCLUSION

The developed system for detecting monkeypox using images of skin lesion utilized advanced pre-trained models. There was also an explanation tool known as LIME that could show the important features in the images, such as lesion size and texture, which the model used in making its predictions. This method is light-weight and compatible with small datasets and therefore applicable to resource-restricted areas. However, challenges encountered in the work include having a small dataset, no clinical testing, and sometimes errors, when features of monkeypox were similar to other diseases, such as chickenpox Nonetheless, this work demonstrates that combining AI with explainable tools can produce the best and dependable healthcare solutions.

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