



Hybrid Machine Learning for Classifying Ringworm, Chickenpox, and Shingles from Image Embeddings

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Abstract

Background: Skin diseases caused by fungal and viral infections, such as ringworm, chickenpox, and shingles, often exhibit similar visual patterns in their early stages, making manual classification difficult and potentially leading to misdiagnosis.

Objective: This study proposes an image-based skin disease classification approach that combines visual feature extraction with machine learning algorithms.

Methods: Feature extraction is performed using pretrained models (Inception-v3, VGG-16, and VGG-19) to generate image embeddings. The extracted features are classified using logistic regression, support vector machine (SVM), and neural network models via the Orange Data Mining platform.

Results: Performance evaluation using AUC, classification accuracy (CA), F1 score, precision, recall, and Matthews correlation coefficient (MCC) shows that the combination of Inception-v3 and SVM achieves the best performance. Pretrained feature extraction effectively improves the accuracy of machine learning-based classification.

Conclusion: Combining pretrained feature extraction with machine learning provides an efficient and accurate approach to skin disease classification, with strong potential for development into an early-stage clinical decision-support system.

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INTRODUCTION

Skin diseases are a substantial global public health burden, and visually similar inflammatory or infectious lesions can complicate timely triage. Ringworm, chickenpox, and shingles may share lesion color, distribution, and texture, especially at early presentation; therefore, image-based classification should be treated as a decision-support task rather than a replacement for clinical diagnosis (Bologna et al., 2018; Collaborators, 2020; Ramos-e-Silva et al., 2026).

Recent advances in image processing and machine learning have enabled the automated analysis of dermatological images using numerical visual features. Nevertheless, robust performance depends on the data distribution, feature representation, and validation procedure; performance estimates from small datasets should not be interpreted as evidence of clinical effectiveness (Azarkaman & Nazari, 2026; Barata et al., 2019; Mujahid et al., 2025; Tschandl et al., 2020).

Transfer learning through pretrained deep-learning models is useful when labeled dermatology datasets are limited. Inception-v3, VGG-16, and VGG-19 can generate image embeddings that are subsequently evaluated by conventional classifiers, enabling a controlled comparison of feature representations without retraining the backbone models (Simonyan & Zisserman, 2015, 2026; Szegedy et al., 2016).

Logistic Regression, Support Vector Machine (SVM), and Neural Network classifiers offer complementary decision functions for high-dimensional image embeddings. Earlier studies have often reported promising accuracy for individual deep-learning architectures or end-to-end systems, but they do not consistently compare multiple pretrained embeddings and conventional classifiers using the same disease classes and evaluation protocol. This limits the evidence regarding whether observed performance stems primarily from the feature extractor or the classifier.

Accordingly, this study benchmarks three pretrained image-embedding models (Inception-v3, VGG-16, and VGG-19) in combination with Logistic Regression, SVM, and Neural Network classifiers for images of ringworm, chickenpox, and shingles. The workflow is implemented in Orange Data Mining to provide a transparent, low-code experimental baseline.

This study aims to compare the predictive performance and feature-space separation of nine image-embedding/classifier combinations for three visually similar skin diseases. Its contribution is a reproducible comparative baseline that distinguishes the contribution of the feature extractor from that of the classifier in a balanced three-class dataset; practically, the results can inform the design of future clinical decision-support research, subject to external validation.

METHOD

This study used a comparative experimental design. The same labelled image set was processed by three fixed pretrained image-embedding models and classified by Logistic Regression, SVM, and Neural Network algorithms. Performance was compared under one evaluation workflow in Orange Data Mining; the study therefore evaluates an experimental benchmark rather than a clinically deployed diagnostic system.

Research Data

The data used in this research consists of skin disease images comprising three classes:

1. *Ringworm* (fungal infection)



Figure 1. Ringworm (fungal infection)

2. *Chickenpox* (virus infection)



Figure 2 Chickenpox (virus infection)

3. *Shingles* (virus infection)

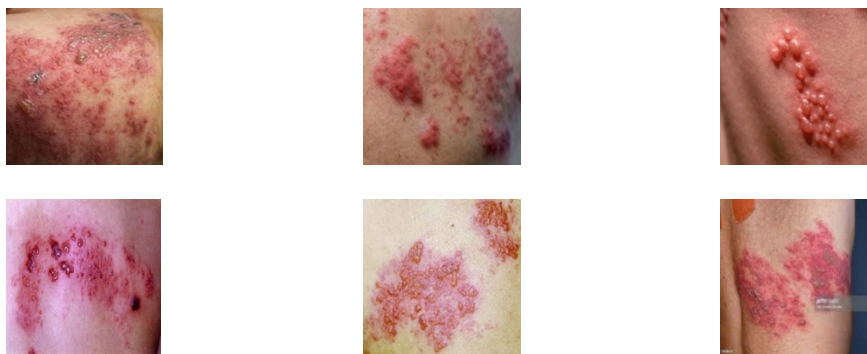


Figure 3 Shingles (virus infection)

The dataset comprised 300 labelled images: 100 ringworm, 100 chickenpox, and 100 shingles images. The balanced class allocation reduces class-frequency bias in the reported aggregate metrics; however, the sample remains limited and is suitable only for an exploratory benchmark. Because images were obtained from a public dataset, the results require external validation on independent and clinically curated images before generalisation.

Research Flow

The research flow is arranged sequentially from data preprocessing to classification result analysis. The research stages include:

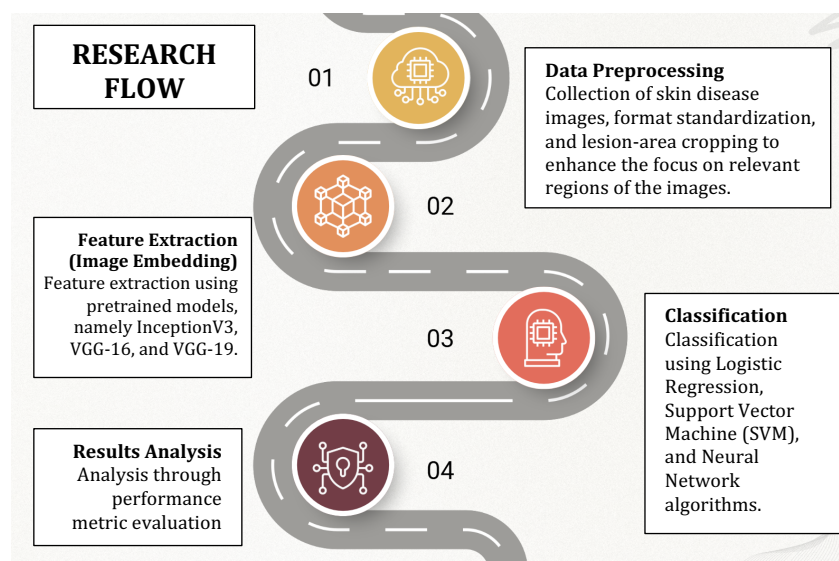


Figure 4. Research Flow

This flow structure is adapted from feature-based image-classification research ([Bishop, 2006](#); [Bishop & Bishop, 2024](#)).

Data Preprocessing

Images were obtained from the public Skin Disease Dataset on Kaggle ([Biswas, 2020](#); [Sasithradevi et al., 2025](#); [Sumaiya et al., 2025](#)). The analysis was restricted to ringworm, chickenpox, and shingles because these conditions can present overlapping visual characteristics. Labels supplied with the dataset were used as class labels; no patient-level clinical information was available.

The dataset contains a collection of skin disease images covering various types of infections with variations in visual conditions, such as differences in skin color, lighting, lesion size, and disease severity. In this research, the data used was focused on three classes of skin diseases, namely ringworm, chickenpox, and shingles, which were chosen because they have similar visual characteristics and pose challenges in the classification process.

Preprocessing involved selecting the three target classes, checking image readability, adjusting files to the input requirements of the Orange Image Embedding widget, and cropping the lesion area where needed to reduce irrelevant background. The widget applied its model-specific internal preprocessing before embedding. No additional data augmentation or lesion-segmentation procedure was used; this restriction should be considered when interpreting generalisability.

- 1) Data Selection, namely selecting images relevant to the three classes of skin diseases studied.
- 2) Image Format and Size Adjustment, so that images can be optimally processed in the image embedding stage in Orange Data Mining.
- 3) Lesion Area Cropping, to focus analysis on the infected skin area and reduce interference from irrelevant background areas.
- 4) Implicit Visual Normalization, performed internally by the image embedding module in Orange Data Mining during the feature extraction process.

This preprocessing stage aims to improve the quality of the visual feature representation produced and reduce irrelevant variations in the image data. Data preprocessing is an important step in medical image classification research because it greatly affects the performance of the classification models used ([Abbadi et al., 2026](#); [Gonzalez & Woods, 2018](#)).

Feature Extraction Using Image Embedding

Image embeddings were generated with the Orange Image Embedding widget using pretrained Inception V3, VGG-16, and VGG-19 models. The pretrained backbones were used only as fixed feature extractors; no fine-tuning was performed on the 300 study images. The resulting numerical embeddings were passed unchanged to the downstream classifiers, allowing the feature-extractor/classifier combinations to be compared under a common workflow.

The pretrained model-based feature extraction approach enables the utilization of high-level visual representations that have been learned from large-scale datasets, making it effective for use on limited-sized datasets ([Simonyan & Zisserman, 2015, 2026](#); [Szegedy et al., 2016](#)). The extracted features were then used as input for the classification stage.

Classification

Each embedding set was classified separately with Logistic Regression, SVM, and Neural Network models in Orange Data Mining. Logistic Regression provided a linear baseline, SVM represented a margin-based classifier suitable for high-dimensional features, and Neural Network captured nonlinear decision boundaries. To minimise selective reporting, all nine combinations were retained in the comparison.

- 1) Logistic Regression, used as a simple and interpretative linear model.
- 2) Support Vector Machine (SVM), used for its ability to handle high-dimensional data and build optimal decision boundaries ([Lutfiansyah, 2026](#)).
- 3) Neural Network, used to model nonlinear relationships between features and skin disease classes ([Leonardo, 2026](#)).

Each algorithm receives input in the form of extracted features and produces skin disease class predictions. The classification process was conducted separately for each type of feature extraction model to obtain objective performance comparisons. Figure 5 is the display of the data process through Orange Data Mining:

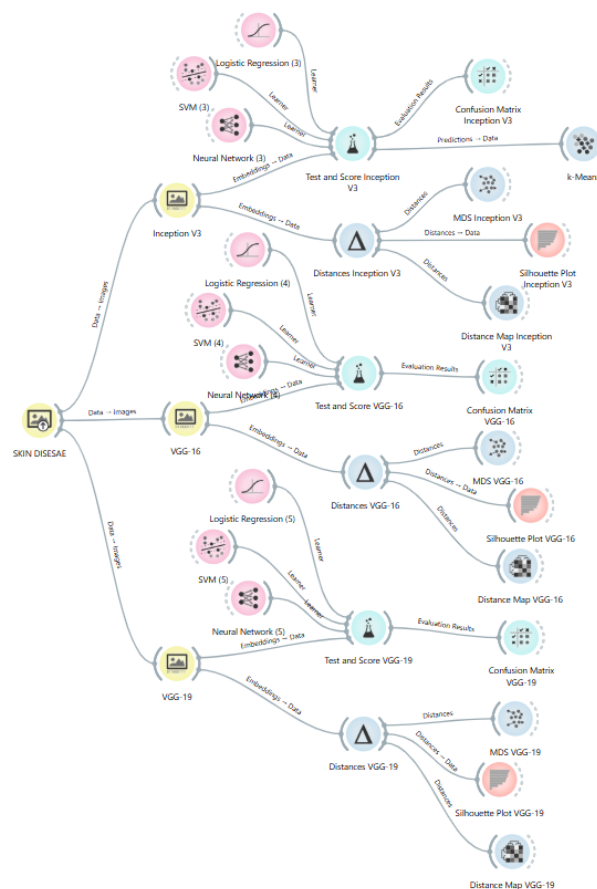


Figure 5. Data Process Display through Orange Data Mining

Analysis of Model Performance Evaluation Results

Model performance was evaluated in Orange Data Mining using the Test and Score workflow with stratified 10-fold cross-validation, so that each image was used for both training and validation across folds while preserving the balanced class distribution. AUC, Classification Accuracy (CA), F1-score, Precision, Recall, and Matthews Correlation Coefficient (MCC) were reported because they capture complementary aspects of multiclass discrimination and prediction agreement ([Kamalraj et al., 2026](#); [Powers, 2011](#)).

- 1) Area Under the Curve (AUC),
- 2) Classification Accuracy (CA),
- 3) F1-score,
- 4) Precision,
- 5) Recall,
- 6) Matthews Correlation Coefficient (MCC).

These metrics were interpreted jointly rather than through accuracy alone. The reported results are descriptive cross-validation estimates; no formal between-model significance test was performed, so small numerical differences should not be treated as statistically confirmed superiority.

Visualization Analysis

In addition to numerical evaluation, visual analysis was performed to understand the characteristics of class separation in the feature space. Several visualization techniques used include:

- 1) Confusion Matrix, to analyze classification errors between classes,
- 2) Distance Analysis and Multidimensional Scaling (MDS), to project high-dimensional data into two-dimensional space,
- 3) Silhouette Analysis, to measure the quality of cluster separation between classes.

This visual analysis helps in evaluating the extent to which the extracted features are able to effectively distinguish each skin disease class (Rousseeuw, 1987).

RESULTS AND DISCUSSION

Results

The experimental results show a comparison of skin disease classification performance using three pretrained deep learning-based feature extraction models, namely Inception V3, VGG-16, and VGG-19, combined with Logistic Regression, Support Vector Machine (SVM), and Neural Network machine learning algorithms. Evaluation was conducted using Area Under the Curve (AUC), Classification Accuracy (CA), F1-score, Precision, Recall, and Matthews Correlation Coefficient (MCC) metrics. Table 1 is the results using Orange Data Mining:

Table 1

Result of Deep Learning

Model Deep Learning	Machine Learning	AUC	CA	F1	Precision	Recall	MCC
Inception V3	Neural Network	0.997	0.970	0.970	0.971	0.970	0.955
	SVM	0.999	0.980	0.980	0.980	0.980	0.970
	Logistic Regression	0.998	0.977	0.977	0.977	0.977	0.965
VGG-16	Logistic Regression	0.984	0.937	0.937	0.937	0.937	0.905
	SVM	0.988	0.930	0.930	0.930	0.930	0.895
	Neural Network	0.990	0.950	0.950	0.950	0.950	0.925
VGG-19	Logistic Regression	0.984	0.937	0.937	0.937	0.937	0.905
	SVM	0.988	0.930	0.930	0.930	0.930	0.895
	Neural Network	0.990	0.950	0.950	0.950	0.950	0.925

Source: Research Process

Inception V3 Performance Analysis

In this cross-validation comparison, Inception V3-SVM achieved the highest observed values (AUC = 0.999, CA = 0.980, MCC = 0.970). Its F1-score, Precision, and Recall were each 0.980, indicating balanced performance across the reported aggregate metrics. Because no statistical significance test was conducted, this result should be interpreted as the best observed model in this dataset rather than definitive superiority over every alternative.

Inception V3 with Logistic Regression also performed strongly (CA = 0.977; MCC = 0.965), while Inception V3 with Neural Network obtained CA = 0.970 and MCC = 0.955. The small differences suggest that the Inception V3 embedding provided a separable feature space for this dataset; the data do not establish that any classifier is universally optimal for dermatological images.

Figure 6 visualization results were obtained using the Multidimensional Scaling (MDS) and Silhouette Plot approaches.

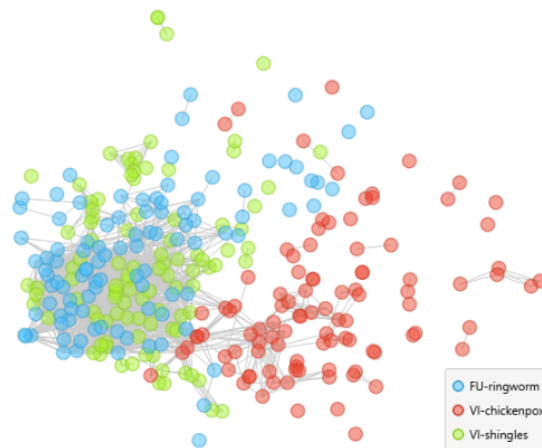


Figure 6. MDS Results using Inception V3 Approach

The MDS image for feature extraction using Inception V3 shows the mapping of high-dimensional data into two-dimensional space based on the distance between features. In this visualization, it can be seen that the ringworm, chickenpox, and shingles classes form relatively separated clusters. The ringworm cluster appears more compact and localized, while the chickenpox and shingles clusters show higher proximity, with some overlapping areas.

This pattern indicates that Inception V3 extracted features have good discriminative ability in distinguishing fungal and viral infection-based skin diseases. The overlap between chickenpox and shingles clusters can be explained by the similarity in visual characteristics of the two diseases, particularly in the patterns of lesion distribution and skin color. This finding is consistent with the Confusion Matrix results and classification metric values, where most classification errors occurred between these two classes.

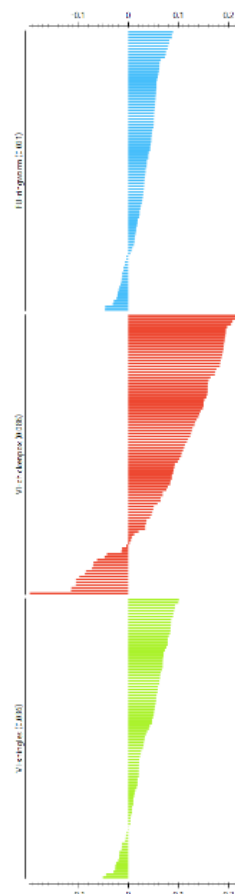


Figure 7. Silhouette Plot Results using Inception V3 Approach

The Silhouette Plot results for Inception V3 features show silhouette values that are mostly in the positive range, indicating that the majority of data has been well grouped into their respective clusters. The chickenpox class shows the highest average silhouette value, indicating that the features in this class have the best cluster separation compared to other classes.

Conversely, the ringworm and shingles classes show lower silhouette values, although they remain in the positive range. This indicates the proximity of features between certain classes, but not to the extent of causing significant cluster mixing. Overall, the Silhouette Plot results support the findings from the MDS visualization that feature extraction using Inception V3 produces sufficiently optimal feature representations for the skin disease classification process.

VGG-16 Performance Analysis

In feature extraction using VGG-16, classification performance generally decreased compared to Inception V3. Based on the table, the combination of VGG-16 and Neural Network produced the best results with CA of 0.950 and MCC of 0.925. This indicates that Neural Networks have better adaptive capability in capturing nonlinear relationships in features produced by VGG-16.

Conversely, Logistic Regression and SVM showed relatively lower performance, with CA of 0.937 and 0.930 respectively. This performance decline indicates that VGG-16 features have a more limited level of discrimination compared to Inception V3, so linear and margin-based classification algorithms do not work optimally on more complex features.

Figure 8 visualization results were obtained using the Multidimensional Scaling (MDS) and Silhouette Plot approaches.

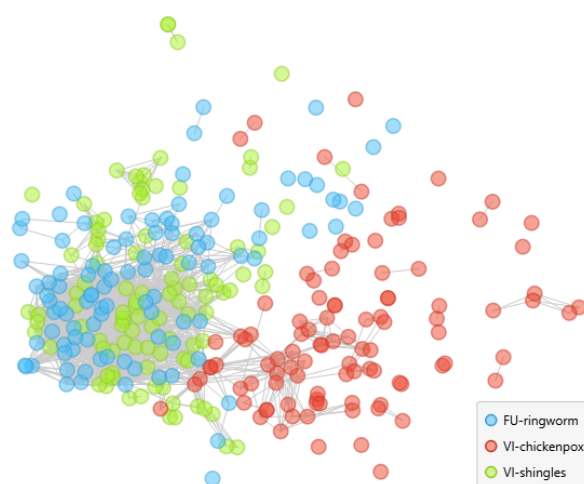


Figure 8. MDS Results using VGG-16 Approach

The MDS Distance visualization for feature extraction using VGG-16 shows the mapping of skin disease data into two-dimensional space based on the distance between features. In this image, it can be seen that the ringworm, chickenpox, and shingles clusters have not been clearly separated. The ringworm and shingles clusters tend to be close to each other and show considerable overlapping areas, while the chickenpox cluster is relatively more spread to the right side of the feature space.

This distribution pattern indicates that VGG-16 extracted features have a lower level of discrimination compared to Inception V3. The proximity between clusters, especially between ringworm and shingles, reflects the similarity in visual characteristics of the two diseases and VGG-16's limitations in capturing more subtle feature differences in skin disease images.

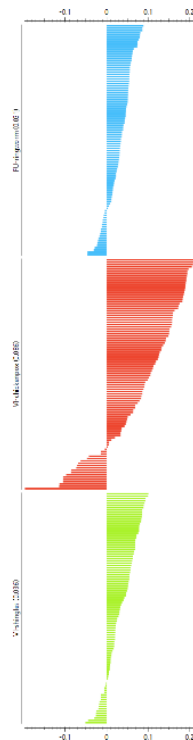


Figure 9. Silhouette Plot Results using VGG-16 Approach

The Silhouette Plot results for VGG-16 features show that the average silhouette value for each class is relatively low compared to the results from Inception V3. The chickenpox class has the highest silhouette value, indicating relatively better cluster separation. Conversely, the ringworm and shingles classes show smaller silhouette values approaching zero, indicating overlap between clusters.

These lower silhouette values indicate that some data are near cluster boundaries, thus potentially increasing classification errors. This finding is consistent with the numerical evaluation results, where the combination of VGG-16 with Logistic Regression and SVM produced lower accuracy values compared to Inception V3, while Neural Networks showed more adaptive performance to less separated feature conditions.

VGG-19 Performance Analysis

The experimental results on VGG-19 show a performance pattern identical to VGG-16. The combination of VGG-19 and Neural Network again produced the highest performance with CA of 0.950 and MCC of 0.925, while Logistic Regression and SVM each produced CA of 0.937 and 0.930.

The similarity of results between VGG-16 and VGG-19 indicates that increasing network depth at the feature extraction stage does not significantly improve classification performance in this research. This may be caused by the limited dataset size and the dominance of the classification algorithm's role compared to minor differences in feature representations produced by the two models.

Figure 10 visualization results were obtained using the Multidimensional Scaling (MDS) and Silhouette Plot approaches.

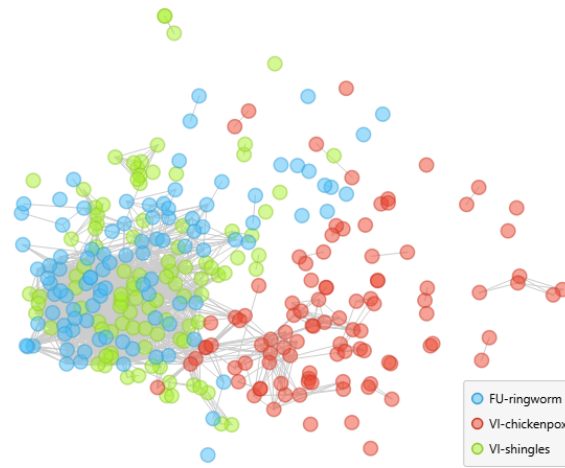


Figure 10. MDS Results using VGG-19 Approach

The MDS Distance visualization for feature extraction using VGG-19 shows a cluster distribution pattern very similar to the results obtained from VGG-16. The ringworm and shingles clusters appear close to each other and form a considerable overlapping area, while the chickenpox cluster tends to be more spread out and relatively separated to the right side of the feature space.

This condition indicates that increasing the model depth from VGG-16 to VGG-19 does not significantly improve cluster separation capability in the feature space. The proximity between clusters indicates that the features produced by VGG-19 have not been fully able to capture subtle visual differences between types of skin diseases, especially between ringworm and shingles which have similar visual characteristics.

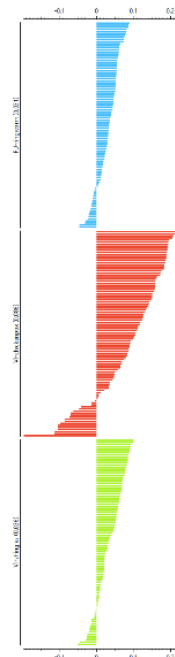


Figure 11. Silhouette Plot Results using VGG-19 Approach

The Silhouette Plot results for VGG-19 features show a silhouette value pattern almost identical to VGG-16. The chickenpox class has the highest average silhouette value, indicating relatively better cluster separation compared to other classes. Conversely, the ringworm and shingles classes show lower silhouette values approaching zero, indicating overlap between clusters.

These relatively low silhouette values indicate that most data are near cluster boundaries, thus increasing the potential for classification errors. This finding is consistent with the numerical

evaluation results, where VGG-19 performance was below Inception V3 and did not show significant improvement compared to VGG-16.

Discussion

Based on the experimental results and visualization analysis, there are quite clear differences in feature representation capability between Inception V3, VGG-16, and VGG-19 in the skin disease classification task. This comparison was conducted by examining numerical performance, cluster separation patterns in MDS visualization, and cluster quality based on Silhouette Plot.

Numerical Performance Comparison

Inception V3 showed the best performance among the three feature extraction models. The Inception V3-SVM combination produced the highest values in almost all evaluation metrics, with AUC = 0.999, CA = 0.980, and MCC = 0.970. Consistent F1, Precision, and Recall values at 0.980 indicate an excellent balance between sensitivity and classification precision.

Conversely, VGG-16 and VGG-19 showed relatively lower performance, with maximum accuracy values CA = 0.950 achieved by combination with Neural Networks. There was no significant performance improvement when network depth was increased from VGG-16 to VGG-19, indicating that additional complexity at the feature extraction stage does not provide real benefits on the dataset used.

MDS Visualization Comparison

The Multidimensional Scaling (MDS) results reinforced these numerical findings. In Inception V3, the ringworm, chickenpox, and shingles clusters appeared more separated, with the ringworm cluster relatively compact and clearer inter-cluster distances. Although there was still overlap between chickenpox and shingles, cluster separation was generally better compared to other models.

Conversely, MDS visualization on VGG-16 and VGG-19 showed almost identical patterns, with considerable cluster overlap, especially between ringworm and shingles. This pattern indicates that the features produced by both models have limited discrimination capability, making it difficult to separate skin disease classes that have similar visual characteristics.

Silhouette Plot Comparison

Silhouette Plot analysis provided additional confirmation of the MDS results. Inception V3 produced more dominantly positive silhouette values, indicating that most data were well grouped within their respective clusters. The chickenpox class consistently showed the highest silhouette values, indicating the best cluster separation.

On VGG-16 and VGG-19, average silhouette values were lower and approaching zero for the ringworm and shingles classes. These values indicate that much data is near cluster boundaries, thus increasing the potential for classification errors. This condition aligns with the decrease in accuracy and MCC values in both models compared to Inception V3.

Synthesis Discussion

The combined numerical and visual analyses suggest that feature-representation quality was more influential than network depth in this dataset. Inception V3 uses parallel multiscale convolutional branches, which can capture visual patterns at different receptive-field sizes; this architectural property offers a plausible explanation for its more separable embeddings relative to the sequential VGG representations (Simonyan & Zisserman, 2015, 2026; Szegedy et al., 2016).

VGG-16 and VGG-19 yielded less separated clusters, particularly for ringworm and shingles, and their best results were obtained with the Neural Network classifier. This pattern is consistent with the need for nonlinear decision boundaries when embeddings contain greater class overlap. However, the conclusions are limited by the small, public, three-class image set and the absence of external testing, patient-level separation checks, explainability analysis, and comparisons with fine-tuned end-to-end CNNs.

These findings provide an exploratory, reproducible baseline for selecting feature-

extractor/classifier combinations in low-code image-analysis workflows. They should not be used to support autonomous clinical diagnosis. Future work should use larger, clinically verified multi-site datasets, prevent any patient-level data leakage, report uncertainty and statistical comparisons, and compare fixed embeddings with fine-tuned and explainable end-to-end models.

CONCLUSION

This study provides a comparative baseline for classifying ringworm, chickenpox, and shingles from pretrained image embeddings using Orange Data Mining. Among the nine tested combinations, Inception V3-SVM produced the highest observed cross-validation performance, while the feature-space visualisations were consistent with improved separation under Inception V3. The contribution is not a new diagnostic system, but evidence that feature-extractor choice can materially affect a classical classifier's apparent performance in a small, balanced image benchmark.

The findings remain limited by the 300-image public dataset, three disease classes, and the absence of external clinical validation, statistical significance testing, and end-to-end fine-tuned CNN comparison. Future research should evaluate larger, clinically curated datasets; standardise acquisition and preprocessing; incorporate explainability and calibration analyses; and validate models across independent settings before considering practice-oriented deployment.

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AUTHOR CONTRIBUTION STATEMENT

Billy Hiskia Sigalingging contributed to the conceptualization of the study, data preparation, methodology development, implementation of image embedding and machine learning classification, data analysis, visualization, interpretation of results, and preparation of the manuscript. Imam Yuadi contributed to the supervision of the research, methodological review, interpretation and critical evaluation of the findings, and critical revision of the manuscript for important intellectual content. Both authors reviewed and approved the final version of the manuscript and agreed to be accountable for all aspects of the work, ensuring the integrity and accuracy of the research.

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