

ARTIFICIAL INTELLIGENCE-BASED SUPERVISED LEARNING APPROACHES FOR DERMATOPHYTOSIS PREDICTION

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Abstract

Artificial Intelligence (AI) has emerged as an important technology in modern healthcare, particularly in disease prediction and medical diagnosis. Dermatomycoses are common fungal skin infections that are increasing globally due to environmental factors such as rising temperature and humidity. Early and accurate diagnosis of these infections is essential for effective treatment and prevention of complications. This study investigates the application of supervised machine learning techniques for dermatomycoses prediction using clinical dermatology data. The research utilizes the publicly available Dermatology Dataset obtained from the UCI Machine Learning Repository. Several preprocessing techniques, including handling missing values, normalization, and feature selection, were applied to improve data quality and model performance. Two supervised learning algorithms, Support Vector Machine (SVM) and K-Nearest Neighbors (KNN), were implemented and evaluated for disease classification. The dataset was divided into training and testing subsets using an 80:20 ratio. The performance of both models was evaluated using standard classification metrics such as accuracy, precision, recall, F1-score, and confusion matrix analysis. Experimental results demonstrated that the SVM model outperformed the KNN model in predicting dermatological disease patterns. The SVM classifier achieved an accuracy of approximately 91%, while KNN achieved an accuracy of approximately 85%. In addition, SVM produced fewer false predictions and showed better generalization capability compared to KNN. The findings of this study highlight the effectiveness of supervised learning approaches in supporting dermatological disease prediction and healthcare decision-making. The results suggest that Support Vector Machine (SVM) is a more reliable and accurate model for dermatomycoses prediction. This research also demonstrates the potential of Artificial Intelligence in improving early diagnosis and enhancing healthcare services in dermatology.

1. INTRODUCTION

Artificial Intelligence (AI) has become an important technology in modern healthcare

because of its ability to analyze large amounts of medical data and support clinical decision-making. Machine learning, a major branch of AI, enables

computer systems to identify hidden patterns, classify diseases, and make predictions with high accuracy. In recent years, AI-based diagnostic systems have been increasingly applied in various medical fields, including radiology, cardiology, oncology, and dermatology. These systems assist healthcare professionals by improving diagnostic accuracy, reducing human error, and enabling early disease detection. [1]

Dermatophytoses are among the most common fungal skin infections affecting millions of people worldwide. These infections are caused by dermatophyte fungi that grow in warm and humid environments and commonly affect the skin, hair, and nails. The prevalence of dermatophytoses has increased significantly due to environmental changes such as rising global temperatures and humidity levels. This issue is particularly common in South Asian countries, where climatic conditions support fungal growth and transmission. If left untreated, these infections may spread rapidly and lead to discomfort, secondary infections, and long-term skin complications. Therefore, early and accurate diagnosis is essential for effective treatment and disease control. [2][3]

Traditional diagnostic approaches for dermatophytoses mainly depend on clinical examination and laboratory testing. Although these methods are widely used, they may require considerable time, specialized expertise, and laboratory resources. In some cases, delayed or inaccurate diagnosis can result in inappropriate treatment and worsening of the infection. Consequently, there is a growing need for intelligent and automated systems that can support healthcare professionals in predicting and diagnosing skin diseases more efficiently. [4]

Machine learning techniques provide a promising solution for medical disease classification and prediction. Supervised learning algorithms are particularly effective because they learn patterns from labeled datasets and use those patterns to classify new data. Among the widely used supervised learning algorithms, Support Vector Machine (SVM) and K-Nearest Neighbors (KNN) have shown strong performance in medical classification tasks. SVM is known for its ability to

handle complex and high-dimensional datasets with high accuracy, while KNN is valued for its simplicity and ease of implementation. These algorithms have been successfully applied in several healthcare applications, including skin disease classification and medical diagnosis. [5]

This study aims to evaluate and compare the performance of SVM and KNN models for predicting dermatophytoses using a dermatology dataset obtained from the UCI Machine Learning Repository. The study follows a systematic machine learning workflow that includes data preprocessing, feature selection, model training, testing, and performance evaluation. The models are assessed using standard evaluation metrics such as accuracy, precision, recall, and F1-score. The main objective of this research is to determine the most effective supervised learning model for dermatophytoses prediction and to highlight the potential role of AI-based systems in improving dermatological diagnosis and healthcare decision-making.

2. Literature Review

The recent studies have suggested the emerging role of Machine Learning in Dermatology. Artificial Intelligence has been created and in this instance, the machine learning algorithms work to help identify and diagnose skin conditions. This enables the processing of vast amounts of information to detect patterns and in turn patterns for diagnosis. AI then plays a significant part in the progress of dermatology practices and research. [10]

Different algorithms, such as Support Vector Machine (SVM), K-Nearest Neighbors (KNN), and deep learning, have been used for skin disease classification. The SVM classification has been highlighted among these. The studies show that SVM is appropriate for classification problems since it is able to handle high dimensional data and to provide an optimal margin for classification. This can be useful where data needs to be processed through a number of features, as is the case with medical data. SVMs have been used with great success in medical diagnosis, including the detection of skin diseases, such as melanoma. KNN is another widely-used algorithm

due to its simplicity and efficiency. This algorithm is done using the distance and proximity measurement. It determines the data points that are closest to a data point and uses the most frequently occurring data point class among the closest data points to the data point to assign the class to the data point. KNN is easy to implement, but there are a few disadvantages. It may not be appropriate for large data sets because it can take a longer period of time to make predictions. Moreover, it can be affected by outliers and irrelevant data, which can affect its accuracy. [13] According to recent research on machine learning models, SVM is better than KNN in medical classification. This is because SVM has the capability of modelling more complicated data relationships and enhanced generalization. [14] It has been found that SVM is more precise compared to KNN. A single study, e.g., indicates that the accuracy of SVM is 91 percent, and that of KNN is 85 percent. This result demonstrates that SVM predicts disease more accurately. Moreover, the current literature indicates that AI should be used in the initial diagnosis and the improvement of healthcare. [15] AI systems will help physicians with a fast and accurate diagnosis, reducing human error. This has been noted to be quite useful in resource-constrained environments. To conclude, previous studies justify the application of machine learning algorithms, especially SVM and KNN, in the classification of skin diseases, where SVM works better in most applications. [16]

3. Methodology:

This study follows a supervised machine learning approach to predict dermatophytoses using clinical dermatology data [17]. The methodology consists of several stages, including dataset collection, data preprocessing, feature extraction, model selection, training and testing, and performance evaluation. Two supervised learning algorithms, namely Support Vector Machine (SVM) and K-Nearest Neighbors (KNN), were implemented and compared to determine the most effective model for disease prediction.

3.1 Proposed Method / Workflow

The proposed framework follows a systematic workflow for dermatophytoses prediction. Initially, the dermatology dataset was collected and preprocessed to remove inconsistencies and prepare the data for machine learning analysis. Relevant clinical features were then selected and normalized before being used for model training. The processed data was divided into training and testing sets. Finally, both SVM and KNN models were evaluated using standard performance metrics such as accuracy, precision, recall, and F1-score. The overall workflow of the study consists of the following steps; Dataset Collection, Data Preprocessing, Feature Selection and Extraction, Model Training using SVM and KNN, Testing and Prediction, Performance Evaluation and Comparison shown in figure 1:

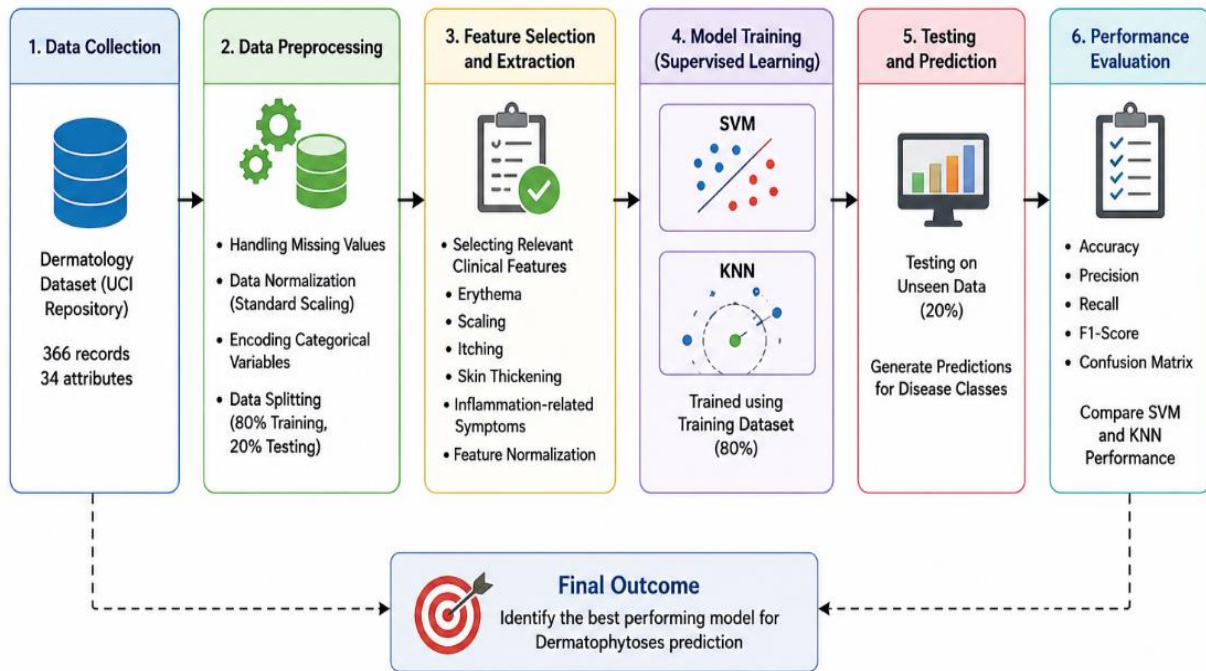


Figure 1: Proposed Workflow Diagram

3.2 Dataset Description

The study utilized the Dermatology Dataset obtained from the UCI Machine Learning Repository, which is a publicly available dataset commonly used for skin disease classification research. The dataset contains 366 patient records and 34 attributes representing clinical and histopathological features associated with dermatological conditions.

The attributes include several important clinical symptoms such as; Erythema, Scaling, Itching, Skin thickening, Inflammation, Family history, Age of patients.

Although the dataset was originally designed for general dermatological disease classification, it provides useful clinical characteristics that are relevant for studying dermatophytoses and related skin infections. The dataset contains numerical and categorical variables that require preprocessing before machine learning implementation.

3.3 Data Preprocessing

Data preprocessing is one of the most important stages in machine learning because raw medical datasets frequently contain incomplete information, inconsistent formatting, irrelevant variables, and features with different numerical ranges. These issues can negatively affect the performance and reliability of machine learning algorithms. Therefore, preprocessing is necessary to clean, organize, and transform the data into a suitable format before model training. Proper preprocessing improves prediction accuracy, reduces computational complexity, and increases the overall efficiency of the classification models. In this study, several preprocessing techniques were applied to the Dermatology Dataset before implementing the supervised learning algorithms. The preprocessing stage included handling missing values, normalizing numerical features, encoding categorical variables, and splitting the dataset into training and testing subsets [20].

3.4 Feature Extraction

The idea of feature extraction is to choose significant variables within the data set to enhance the performance of a model. In the research, clinical characteristics like erythema, scaling, and itching are directly entered as input variables. No image-based algorithms, such as CNN, are used because the dataset is in the form of a table. All the features are normalized so that the SVM and KNN models would perform better [21]. Feature selection is a crucial process in machine learning that identifies the most relevant variables contributing to prediction accuracy. In medical diagnosis systems, selecting meaningful clinical features improves model efficiency, reduces unnecessary complexity, and enhances disease classification performance. In this study, important clinical symptoms associated with skin diseases were selected as input variables for the supervised learning models. The selected features represented significant dermatological indicators commonly observed in fungal and inflammatory skin conditions. The selected features included; Erythema, Scaling, Itching, Skin thickening, Inflammation-related symptoms, Family history and Age-related information. These clinical variables were chosen because they provide valuable information regarding skin disease characteristics and assist machine learning algorithms in distinguishing between disease classes. Feature extraction was performed directly on the tabular dataset. Since the dataset did not contain medical images, image-processing techniques and deep learning approaches such as Convolutional Neural Networks (CNNs) were not required in this study. Instead, structured clinical features were used for classification purposes. Additionally, all selected features were normalized before training to ensure improved model stability and balanced feature contribution. Effective feature selection reduced computational overhead and improved the predictive capability of both SVM and KNN models.

3.5 Model Selection

Medical datasets often contain missing or incomplete records because of human error, unavailable patient information, or

inconsistencies during data collection. Missing values can reduce model accuracy and may lead to incorrect predictions if not handled properly. Therefore, identifying and managing missing data is a critical preprocessing step. In the Dermatology Dataset, some attributes contained incomplete values, particularly in patient-related information such as age. To address this issue, missing records were carefully examined and processed using appropriate imputation techniques. Numerical missing values were replaced using statistical methods such as mean or median substitution, while some inconsistent entries were removed where necessary to maintain data quality and consistency. Handling missing values ensured that the dataset remained complete and suitable for machine learning analysis. This step also minimized the possibility of biased predictions and improved the reliability of both SVM and KNN models [22].

3.5 Machine Learning Models

This study utilized two supervised learning algorithms for dermatophytoses prediction: Support Vector Machine (SVM) and K-Nearest Neighbors (KNN). These algorithms were selected because of their effectiveness in classification tasks and their widespread use in healthcare and medical diagnosis systems.

Both models were trained using preprocessed clinical data and evaluated to determine which algorithm provided better prediction performance for dermatological disease classification.

3.5.1 Support Vector Machine (SVM)

Support Vector Machine (SVM) is a powerful supervised machine learning algorithm commonly used for classification and pattern recognition tasks. The main objective of SVM is to identify an optimal hyperplane that separates data points belonging to different classes while maximizing the margin between them.

SVM is particularly effective for:

- High-dimensional datasets
- Complex classification problems
- Non-linear data relationships
- Medical diagnosis applications

In this study, the SVM classifier was trained using normalized clinical features extracted from the Dermatology Dataset. The algorithm learned the underlying patterns associated with dermatological conditions and generated predictions for the testing dataset.

The SVM classification concept can be represented as:

$$y = w^T x + b$$

Where:

- w represents the weight vector
- x represents input features
- b represents the bias term

SVM was selected because of its strong generalization ability and high classification accuracy in medical datasets. The algorithm is capable of minimizing classification errors and handling complex relationships among clinical variables.

Furthermore, SVM performs efficiently even when the dataset contains many features, making it suitable for dermatological disease prediction.

3.5.2 K-Nearest Neighbors (KNN)

K-Nearest Neighbors (KNN) is a simple and instance-based supervised learning algorithm widely used for classification tasks. Unlike SVM, KNN does not build an explicit training model; instead, it classifies new data points based on similarity and proximity to neighboring samples.

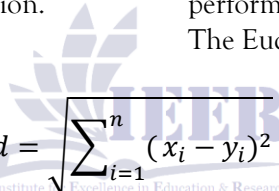
The KNN algorithm works through the following steps:

1. Calculate the distance between data points.
2. Identify the nearest neighboring samples.
3. Select the majority class among the nearest neighbors.
4. Assign the predicted class label to the new data sample.

In this study:

- Euclidean distance was used as the similarity measurement metric.
- The value of K was selected experimentally to achieve optimal prediction performance.

The Euclidean distance formula is represented as:



$$d = \sqrt{\sum_{i=1}^n (x_i - y_i)^2}$$

Where:

- x_i and y_i represent feature values of two data points
- n represents the total number of features

KNN was selected because of its simplicity, ease of implementation, and effectiveness in pattern recognition problems. However, the algorithm may become computationally expensive for large datasets because predictions require distance calculations for all neighboring samples.

Despite this limitation, KNN remains an effective baseline classifier for medical prediction systems and provides useful comparative analysis against more advanced algorithms such as SVM.

3.6 Model Training and Testing

After completing data preprocessing and feature selection, the dataset was used for training and testing the supervised learning models. The purpose of this stage was to allow the machine learning algorithms to learn patterns from the

dataset and evaluate their ability to predict dermatological diseases accurately on unseen data. The processed dataset was divided into two subsets 80% training dataset and 20% testing dataset

The training dataset was used to train the machine learning models by providing clinical features and their corresponding disease classifications. During the training phase, the algorithms learned the relationship between input features such as erythema, scaling, itching, and inflammation-related symptoms and the target disease classes.

The Support Vector Machine (SVM) model was trained to identify an optimal decision boundary that could effectively separate different disease classes. The model attempted to maximize the margin between classes while minimizing classification errors. The K-Nearest Neighbors (KNN) model stored the training samples and classified new data points based on the similarity and distance between neighboring instances.

The training process enabled both algorithms to recognize hidden patterns and relationships within the dermatology dataset. Proper training is essential because it directly influences the predictive capability and generalization performance of machine learning models.

After the completion of training, both models were evaluated using the testing dataset. The testing dataset contained unseen records that were not used during model training. This step was important to determine how effectively the models could generalize to new patient data rather than simply memorizing the training samples [23].

During testing, the trained models generated predictions for the unseen data samples, and the predicted outputs were compared with the actual class labels. The prediction results were then analyzed using performance evaluation metrics such as accuracy, precision, recall, and F1-score [24].

The training and testing process was implemented using the Python programming language with the help of machine learning libraries such as Scikit-learn. The implementation environment included Jupyter Notebook for data analysis, preprocessing, model development, and evaluation.

The experimental results demonstrated that the Support Vector Machine (SVM) model achieved higher prediction accuracy and better generalization performance compared to the K-Nearest Neighbors (KNN) model. SVM produced fewer misclassifications and showed greater stability in handling complex clinical data, making it a more effective approach for dermatophytoses prediction.

4. Results

The performance of the supervised learning models was evaluated using standard classification metrics, including accuracy, precision, recall, and F1-score. The experimental results demonstrated that both Support Vector Machine (SVM) and K-Nearest Neighbors (KNN) were capable of classifying dermatological disease data; however, SVM achieved better overall performance compared to KNN. After training and testing the models on the Dermatology Dataset, the SVM classifier produced higher prediction accuracy and more reliable classification results. The SVM model achieved an overall accuracy of approximately 91%, whereas the KNN model achieved an accuracy of approximately 85%. The higher accuracy of SVM indicates its stronger capability to classify dermatological conditions correctly and generalize effectively to unseen data samples. Figure 3 illustrates the comparison of classification accuracy between the SVM and KNN models. The results clearly show that SVM outperformed KNN in terms of predictive performance and classification efficiency. In addition to accuracy, precision and recall values were also analyzed to evaluate the quality of model predictions. The SVM model achieved higher precision values, indicating that it generated fewer false-positive predictions compared to KNN. Similarly, the recall value of SVM was higher, demonstrating its improved ability to correctly identify positive disease cases. The F1-score analysis further confirmed the superior performance of SVM. Since the F1-score combines both precision and recall into a single metric, the higher F1-score obtained by SVM reflects a better balance between identifying positive cases and minimizing incorrect predictions.

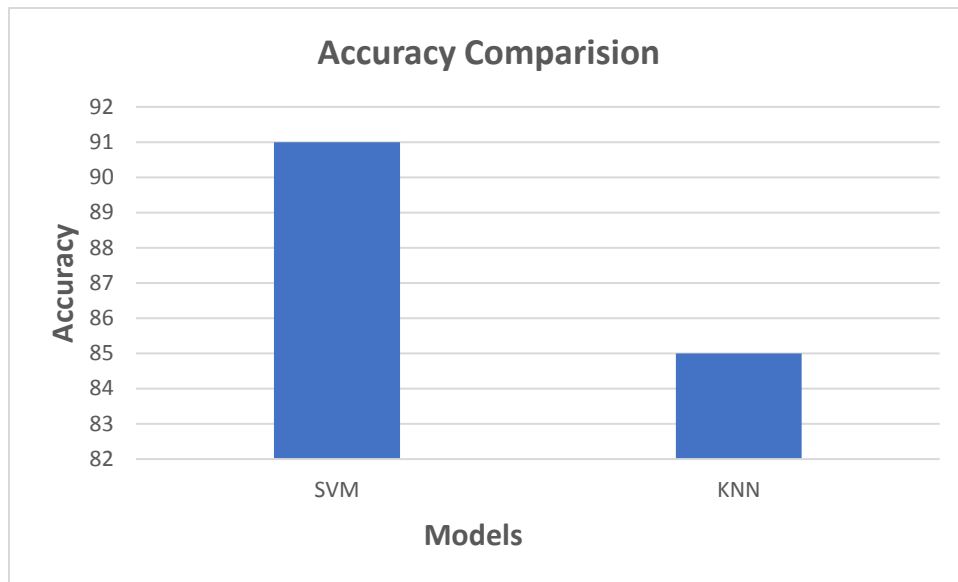


Figure 3: Comparison of Accuracy between SVM and KNN Models

Figure 4 presents the comparative analysis of precision and recall for both machine learning models. The graph indicates that SVM consistently achieved better classification performance across all evaluation metrics.

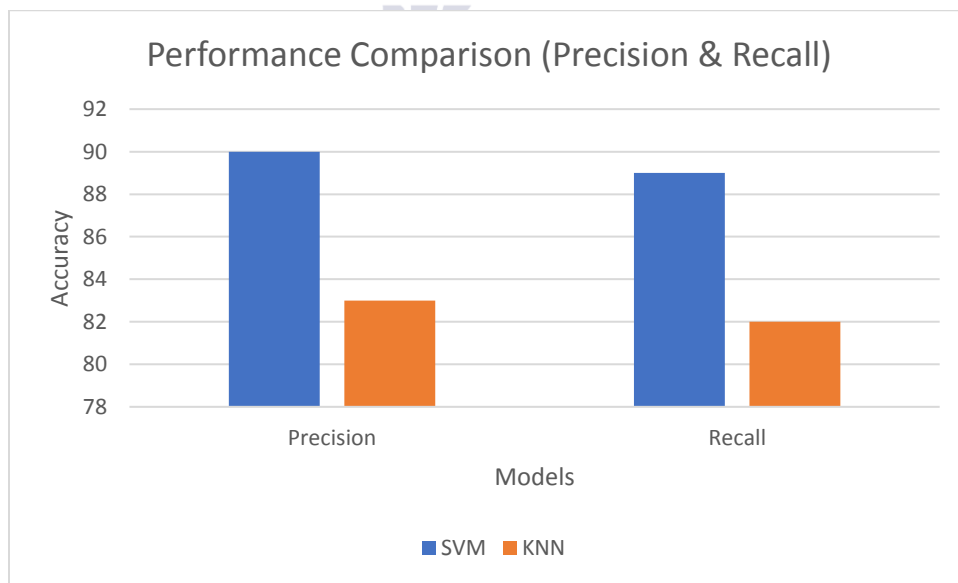


Figure 4: Precision and Recall Comparison of SVM and KNN Models

Table 1 presents the confusion matrix of the Support Vector Machine (SVM) model used for dermatophytoses prediction. The results show that the SVM model correctly classified 50 positive cases as True Positives and 41 negative cases as True Negatives. However, the model incorrectly

predicted 5 positive cases as negative (False Negatives) and 4 negative cases as positive (False Positives). The lower number of misclassifications demonstrates the strong predictive capability of the SVM model and its effectiveness in classifying dermatological disease data accurately. Table 2

illustrates the confusion matrix of the K-Nearest Neighbors (KNN) model. The KNN classifier correctly identified 45 positive cases and 37 negative cases. However, the model produced 10 False Negative predictions and 8 False Positive predictions. Compared to the SVM model, KNN generated a higher number of incorrect classifications, which reduced its overall prediction accuracy and reliability in detecting dermatophytoses. Table 3 presents the comparative performance analysis of the SVM and

KNN models using evaluation metrics such as accuracy, True Positives, True Negatives, False Positives, and False Negatives. The results indicate that the SVM model achieved higher classification accuracy (91%) compared to the KNN model (85%). Furthermore, SVM produced fewer false predictions, demonstrating better generalization performance and classification stability. These findings suggest that SVM is more effective and reliable than KNN for dermatophytoses prediction using the dermatology dataset.

Table 1: Confusion Matrix for Support Vector Machine (SVM)

Actual Class	Predicted Yes	Predicted No
Actual Yes	50 (True Positive)	5 (False Negative)
Actual No	4 (False Positive)	41 (True Negative)

Table 2: Confusion Matrix for K-Nearest Neighbors (KNN)

Actual Class	Predicted Yes	Predicted No
Actual Yes	45 (True Positive)	10 (False Negative)
Actual No	8 (False Positive)	37 (True Negative)

Table 3: Performance Comparison of SVM and KNN Models

Evaluation Metric	SVM	KNN
Accuracy	91%	85%
True Positives (TP)	50	45
True Negatives (TN)	41	37
False Positives (FP)	4	8
False Negatives (FN)	5	10

The confusion matrices shown in Figure 5 provide a detailed overview of model predictions. The confusion matrix of the SVM model demonstrated that the algorithm correctly classified most of the testing samples while producing fewer misclassifications. The confusion matrix analysis indicates that SVM generated fewer false

predictions than KNN, which contributed to its higher accuracy and reliability. The lower number of false negatives in SVM is particularly important in medical diagnosis because missed disease cases can delay treatment and increase health complications.

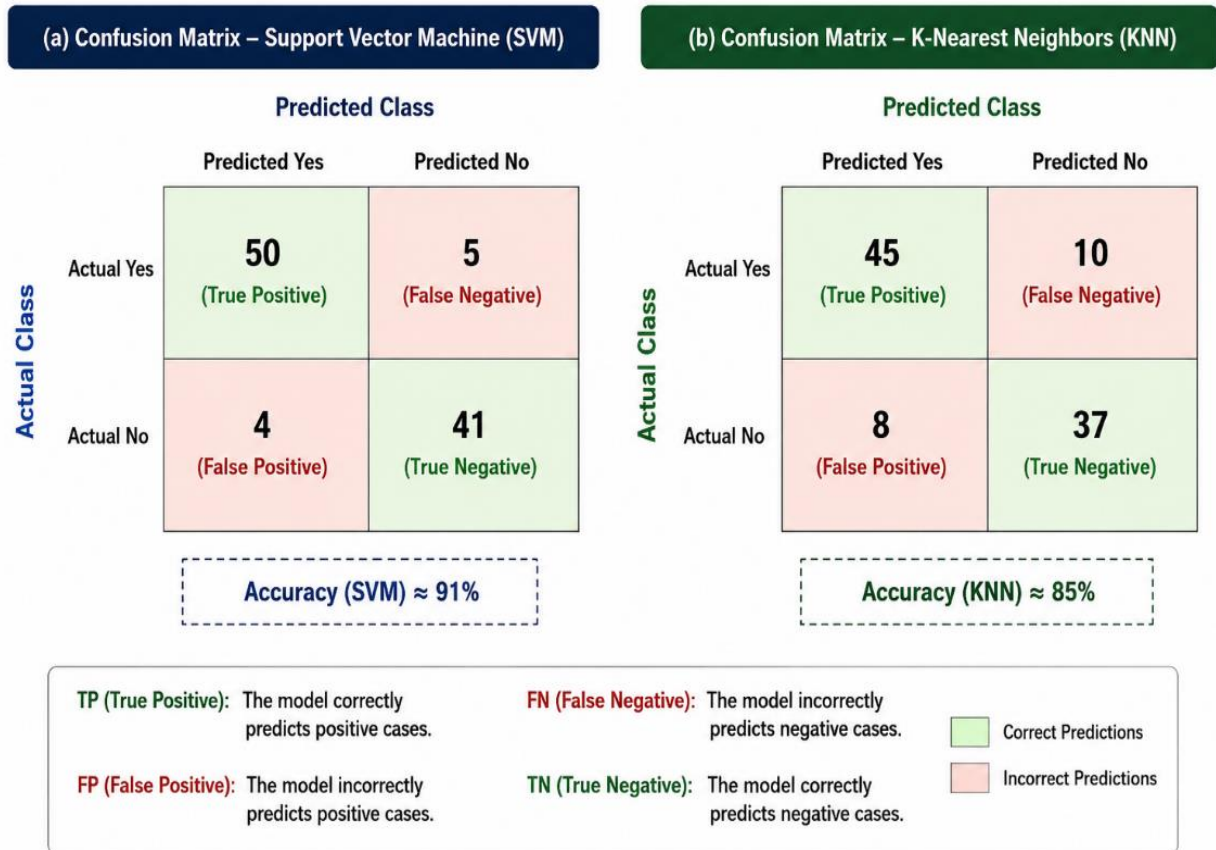


Figure 5: Confusion matrix for SVM and KNN Models

The improved performance of SVM can be attributed to its ability to handle high-dimensional data and create an optimal decision boundary between disease classes. In contrast, KNN relies heavily on distance calculations and neighboring samples, making it more sensitive to noise, irrelevant features, and data distribution variations.

Overall, the experimental findings demonstrate that both supervised learning models are useful for dermatological disease prediction; however, SVM proved to be the more effective and stable model for dermatophytoses prediction. The results also highlight the potential of Artificial Intelligence and machine learning techniques in supporting early disease detection and improving healthcare decision-making systems.

5. Conclusion

This study investigated the application of supervised machine learning approaches for the prediction of dermatophytoses using the Dermatology Dataset obtained from the UCI Machine Learning Repository. Two widely used supervised learning algorithms, Support Vector Machine (SVM) and K-Nearest Neighbors (KNN), were implemented and evaluated to determine their effectiveness in dermatological disease classification.

The research followed a systematic machine learning methodology that included data preprocessing, feature selection, model training, testing, and performance evaluation. Important clinical features such as erythema, scaling, itching, and inflammation-related symptoms were utilized as input variables for prediction. The models were evaluated using standard classification metrics

including accuracy, precision, recall, F1-score, and confusion matrix analysis.

The experimental findings demonstrated that both machine learning models were capable of predicting dermatological disease patterns; however, the Support Vector Machine (SVM) model achieved superior performance compared to the K-Nearest Neighbors (KNN) model. The SVM classifier produced higher accuracy, fewer false predictions, and better generalization capability. In contrast, KNN showed comparatively lower performance due to its sensitivity to neighboring data points and data distribution variations.

The confusion matrix analysis further confirmed the effectiveness of the SVM model in correctly classifying positive and negative disease cases with fewer misclassifications. These results indicate that SVM is a more reliable and efficient algorithm for dermatophytoses prediction and medical classification tasks.

The study also highlights the growing importance of Artificial Intelligence and machine learning techniques in healthcare and dermatology. AI-based diagnostic systems can support healthcare professionals by improving early disease detection, reducing diagnostic errors, and assisting in clinical decision-making processes. Such intelligent systems can be particularly beneficial in regions with limited medical resources and high prevalence of skin infections.

Despite the promising results, the study has certain limitations. The dataset used in this research was relatively small and not specifically designed for dermatophytoses classification. Additionally, the study utilized only tabular clinical data and did not include image-based analysis or deep learning techniques. Therefore, future research can focus on using larger and more specialized dermatological datasets, incorporating medical image analysis, and applying advanced deep learning models such as Convolutional Neural Networks (CNNs) to further improve prediction accuracy and diagnostic performance.

In conclusion, the findings of this study demonstrate that supervised learning algorithms, particularly Support Vector Machine (SVM), provide an effective and reliable approach for

dermatophytoses prediction. The integration of Artificial Intelligence into dermatological diagnosis has significant potential to enhance healthcare services and contribute to more accurate and timely disease detection.

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