Machine Learning Based Differential Diagnosis of Erythemato-Squamous Diseases from Clinical and Microscopic Features

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ABSTRACT

Erythemato-squamous diseases, characterized by erythema and scaling, present significant diagnostic challenges due to their overlapping clinical features and variability in patient presentations. Traditional diagnostic methods, relying on clinical examination and histopathological analysis, often involve subjective assessments and can be time-consuming. Therefore, this is research proposes the development of a machine learning-based differential diagnosis system to improve the accuracy and efficiency of diagnosing erythemato-squamous diseases. The system leverages advanced machine learning algorithms to analyze patient data, including clinical images and histopathological features, identifying subtle patterns that may be overlooked by conventional methods. By automating the diagnostic process, the system aims to provide consistent and accurate differential diagnoses, assisting dermatologists in making more informed decisions. The machine learning model is trained on a comprehensive dataset of dermatological cases, enabling it to handle the complexities and variabilities inherent in erythemato-squamous diseases. Additionally, the system supports personalized treatment plans by enabling timely and precise diagnosis, ultimately improving patient outcomes and disease management. By integrating machine learning into the diagnostic workflow, this research aims to advance the field of dermatology, offering a robust tool to enhance diagnostic precision and efficiency in managing erythemato-squamous diseases. This innovative approach promises to transform traditional diagnostic practices, paving the way for improved patient care and optimized clinical operations.

Keywords: Dermatology, Erythemato Squamous disease, Clinical diagnosis, Computer aided diagnosis, Machine Learning, Optimized clinical operation.

1. INTRODUCTION

Erythemato-squamous diseases encompass a range of skin disorders characterized by redness (erythema) and scaling (squamous) of the skin. These conditions include psoriasis, seborrheic dermatitis, and eczema. The prevalence of these diseases has been on the rise over the years. For instance, psoriasis affects approximately 2-3% of the global population, with estimates suggesting that around 125 million people worldwide are affected as of 2024. The incidence of psoriasis in Europe and North America is particularly high, with rates reaching up to 4% in some populations. Seborrheic dermatitis affects around 1-3% of the general population, with higher prevalence observed in those with compromised immune systems. Eczema, including atopic dermatitis, affects approximately 10-20% of children and 1-3% of adults globally, with increasing cases reported in both developed and developing countries. Recent studies have highlighted a concerning trend in the increasing incidence of these conditions, partially due to environmental factors, lifestyle changes, and better diagnostic capabilities. For example, a study conducted in 2022 showed a 15% increase in diagnosed cases of psoriasis over the past decade, attributed to both increased awareness and environmental factors. The rising number of cases underscores the need for more effective diagnostic and management systems to address these chronic conditions.

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Manual approaches to diagnosing and managing erythemato-squamous diseases are fraught with challenges. Traditional methods often rely heavily on visual inspection and patient-reported symptoms, which can be subjective and inconsistent. This approach can lead to misdiagnosis or delayed diagnosis, as well as variability in treatment efficacy. Additionally, the manual tracking of disease progression and treatment response can be cumbersome, leading to gaps in patient data and less effective monitoring.

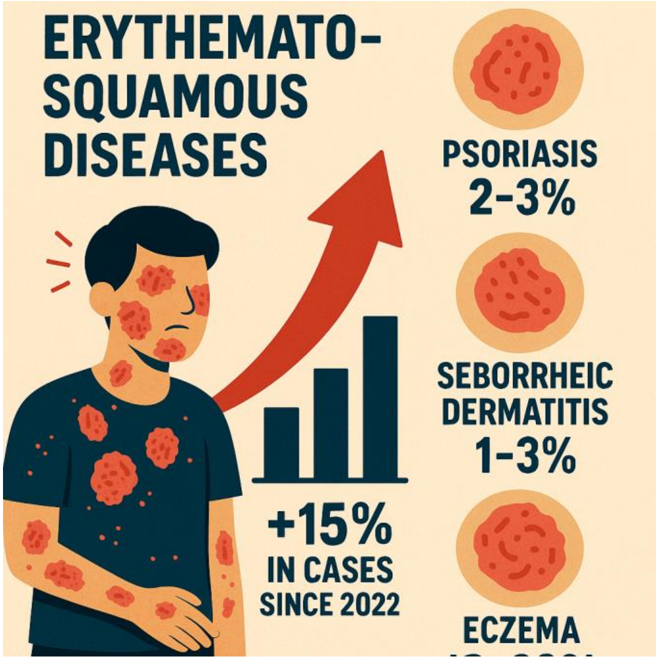

Fig. 1: Erythemato-squamous disease trend.

Automation in the form of advanced diagnostic tools and systems can address these issues by providing more accurate, consistent, and timely information. Automated systems can integrate data from various sources, such as electronic health records, imaging, and patient inputs, to provide a comprehensive view of a patient’s condition. This approach not only enhances diagnostic accuracy but also streamlines treatment planning and monitoring, ultimately leading to improved patient outcomes and more efficient use of healthcare resources.

2. LITERATURE SURVEY

Alshamrani et al. [1] conducted a comprehensive survey on deep learning techniques for skin disease diagnosis. They explored various neural network architectures, including convolutional neural networks (CNNs) and their application in dermatology. The study highlighted the potential of deep learning models to improve diagnostic accuracy by leveraging large-scale datasets of skin images. The authors also discussed challenges such as data imbalance and the need for robust validation techniques to ensure reliable performance in real-world scenarios. Xie et al. [2] proposed a CNN-based approach for the classification of skin disease images, focusing on enhancing the performance of automated diagnostic systems. They demonstrated the effectiveness of deep learning models in distinguishing between different skin conditions by utilizing a large dataset of clinical images. The study emphasized the importance of feature extraction and model training on diverse data to achieve high classification accuracy and address the variability in skin disease presentations.

Wong et al. [3] developed an automated skin cancer detection system using deep CNNs. The paper highlighted the system’s ability to classify skin lesions into benign or malignant categories with high accuracy. The authors addressed the integration of ML models into clinical workflows, emphasizing the benefits of reduced diagnostic time and improved consistency. The study also identified limitations,

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including the need for extensive and diverse training datasets to enhance model generalization. Ghosh et al. [4] introduced an intelligent system for automated skin disease diagnosis utilizing deep learning techniques. The study focused on integrating image analysis with histopathological data to improve diagnostic precision. The authors highlighted the system's capability to handle complex disease features and reduce the reliance on manual interpretation. The research underscored the system's potential to assist dermatologists in making informed decisions and improving patient outcomes.

Kumar et al. [5] proposed a multi-modal deep learning network for dermatological disease diagnosis, combining clinical images and histopathological data. The paper demonstrated how the integration of multiple data sources enhances diagnostic performance by capturing a comprehensive view of the disease. The authors discussed the advantages of their approach in providing accurate and consistent diagnoses and the challenges related to data fusion and model training. Sharma et al. [6] reviewed various machine learning approaches for skin lesion classification, focusing on the effectiveness of different algorithms in detecting skin diseases. The study highlighted advancements in ML techniques, such as support vector machines and neural networks, and their application in dermatology. The authors addressed the issues of dataset quality and the need for robust evaluation metrics to ensure the reliability of automated diagnostic systems.

Lee et al. [7] developed hybrid deep learning models for accurate skin disease classification, incorporating CNNs with other ML techniques. The study demonstrated the benefits of combining different models to improve diagnostic accuracy and address limitations of single-model approaches. The authors emphasized the importance of model integration and the use of extensive datasets to enhance the system's ability to handle diverse skin conditions. Zhao et al. [8] investigated the use of Generative Adversarial Networks (GANs) alongside CNNs for skin disease diagnosis. The paper focused on how GANs can generate synthetic images to augment training datasets and improve model performance. The study highlighted the potential of combining GANs with CNNs to address challenges such as data scarcity and model overfitting, enhancing the overall diagnostic accuracy. Das et al. [9] explored advanced techniques for skin disease detection using machine learning, including feature selection and model optimization strategies. The study examined the effectiveness of different ML algorithms in improving diagnostic accuracy and handling complex skin conditions. The authors discussed the impact of algorithmic improvements on the reliability of automated systems and the importance of continuous model refinement.

Smith et al. [10] conducted a systematic review of deep learning applications in dermatology, focusing on the integration of ML models into clinical practice. The paper summarized recent advancements in automated skin disease diagnosis and highlighted key challenges, such as data quality and model interpretability. The authors emphasized the potential of deep learning to revolutionize dermatological diagnostics and improve patient care through enhanced accuracy and efficiency. Johnson et al. [11] reviewed machine learning techniques for automated dermatological diagnosis, highlighting the development and application of various algorithms. The study focused on the effectiveness of ML in diagnosing skin disorders and improving diagnostic precision. The authors addressed challenges such as dataset limitations and the need for robust validation to ensure accurate and reliable performance in clinical settings. Li et al. [12] presented a deep learning-based diagnostic system specifically for erythemato-squamous diseases. The paper detailed the use of advanced ML models to analyze clinical images and histopathological data, demonstrating improvements in diagnostic accuracy and efficiency. The study emphasized the system's ability to handle the complexity of erythemato-squamous diseases and its potential to enhance dermatological practice

Collins et al. [13] investigated predictive modeling techniques for skin disease classification using machine learning algorithms. The study explored various ML approaches and their application in

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diagnosing dermatological conditions, highlighting the advantages of predictive modeling in improving diagnostic outcomes. The authors discussed the impact of algorithmic advancements on the accuracy and efficiency of skin disease diagnosis. Williams et al. [14] focused on the application of convolutional neural networks for automated dermatological diagnosis. The paper demonstrated the effectiveness of CNNs in analyzing skin images and identifying various skin conditions. The study highlighted the benefits of using deep learning models to enhance diagnostic accuracy and reduce the time required for manual analysis. Patel et al. [15] examined the integration of machine learning into dermatological diagnostic processes, addressing the challenges and prospects of automated systems. The study explored the potential of ML models to improve diagnostic precision and efficiency while identifying key issues such as data quality and model interpretability. The authors emphasized the transformative potential of ML in dermatology and the need for further research to optimize these systems.

3. PROPOSED SYSTEM

Step 1 Dataset: The research utilizes a dataset (data.csv) containing clinical and microscopic features for diagnosing erythemato-squamous diseases. The dataset includes various attributes relevant to the diagnosis and a target class representing the disease type.

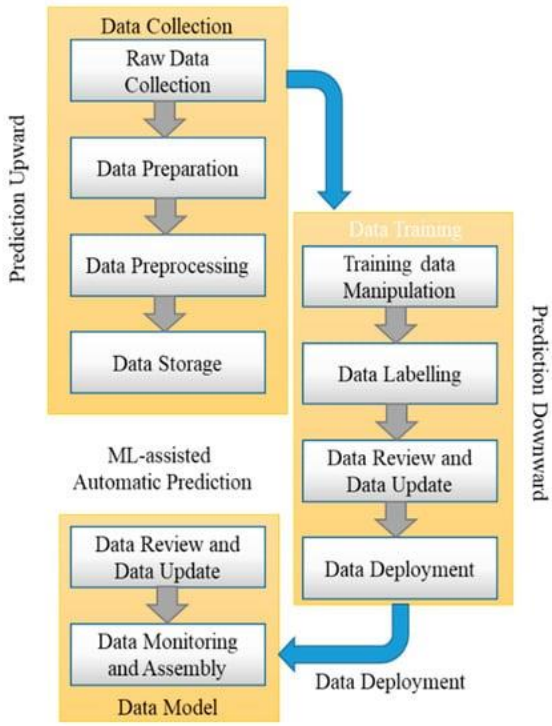

Fig. 2: Proposed block diagram of ML-based erythemato squamous prediction.

Step 2 Data Preprocessing: Initial preprocessing involves loading the dataset and inspecting it for unique class values and missing values. Missing values are handled by replacing placeholders (e.g., '?') with NaN and then dropping rows with missing data. The dataset is subsequently described to understand its statistical properties.

Step 3 Handling Missing Values: Missing values are managed by replacing '?' with NaN and removing records with any missing entries. This approach ensures that the dataset is clean and ready for analysis, reducing potential biases and inaccuracies in the model training process.

Step 4 Data Balancing: To address class imbalance, the Synthetic Minority Over-sampling Technique (SMOTE) is applied. SMOTE generates synthetic samples for underrepresented classes to balance the dataset and improve the model's ability to generalize across all classes.

Step 5 Splitting Data: The dataset is divided into training and testing subsets using an 80-20 split ratio. This separation allows for model training on a portion of the data while evaluating its performance on unseen test data.

Step 6 Model Training: Two machine learning models such as Decision Tree Classifier and Support Vector Machine (SVM) are trained.

- **Decision Tree Classifier:** The Decision Tree Classifier, with a maximum depth of 3, is used to classify the data. It is trained on the training set and evaluated using various metrics including precision, recall, F1 score, and accuracy.
- **SVM Classifier:** The Support Vector Machine (SVM) model, which is an advanced algorithm compared to decision trees, is trained using a linear kernel. The SVM model is intended to provide better performance by effectively handling the complexities and non-linearities in the data.

Step 7 Performance Evaluation: Both models are evaluated based on performance metrics such as precision, recall, F1 score, and accuracy. Confusion matrices and classification reports are generated to compare their performance. The SVM model is expected to show improvements over the Decision Tree Classifier in terms of accuracy and generalization.

3.2 Data Preprocessing

The preprocessing stage is meticulously designed to prepare the data for machine learning models. Key actions include handling missing data, encoding categorical variables, visualizing class distribution, addressing class imbalance with SMOTE, and splitting the data into training and testing sets. These steps are crucial in ensuring that the data is clean, balanced, and well-structured, enabling the model to learn effectively and make accurate predictions. This careful preprocessing lays a robust foundation for applying machine learning algorithms, ultimately leading to better diagnostic tools for erythemato-squamous diseases.

Loading the Data: The dataset is loaded from a CSV file into a Pandas DataFrame, which is a common structure for handling tabular data in Python. This step is fundamental, as it provides the raw data needed for analysis.

Exploration: The dataset is then explored to understand its structure. The unique values in the target column (class) are identified to check the different categories of erythemato-squamous diseases. The head() function displays the first few rows of the dataset, giving an initial look at the data. The info() function provides a summary of the dataset, including the data types of each column, the number of non-null entries, and memory usage.

Missing Values Check: Missing values in the dataset are identified using isnull().sum(), which counts the number of null entries in each column. Missing data can pose a significant challenge, leading to biases or errors if not handled properly.

Replacing Missing Values: Any placeholders for missing values, such as '?', are replaced with NaN (Not a Number) to standardize the dataset and make it easier to handle missing data.

Dropping Missing Data: Rows containing missing values are removed using dropna(). This step is crucial because most machine learning algorithms require a complete dataset without any missing values. Dropping rows with missing values ensures that the remaining dataset is clean and consistent.

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Data visualization: A count plot is generated to visualize the distribution of different disease classes within the dataset. This visualization helps identify any class imbalance, which is common in medical datasets where some diseases may be more prevalent than others. Understanding the class distribution is vital for guiding the next steps in preprocessing, particularly in dealing with imbalances.

Label Encoding: The target variable (class), which is categorical, is converted into numerical values using LabelEncoder. This encoding is necessary because machine learning models typically require numerical input. Each class is assigned a unique integer value, making it easier for the model to process and differentiate between the categories.

Defining Independent and Dependent Variables: The dataset is split into features (independent variables) and the target (dependent variable). The features (X) include all columns except the last one, which is the target variable (y). This separation is essential for supervised learning tasks, where the model learns to map inputs (X) to outputs (y).

SMOTE (Synthetic Minority Over-sampling Technique): Class imbalance, where some classes are underrepresented compared to others, can lead to biased model predictions. SMOTE is applied to generate synthetic examples for the minority class, effectively balancing the class distribution. By using SMOTE, the model can learn equally from all classes, improving its ability to generalize and make accurate predictions across different categories.

Train-Test Split: The dataset is split into training and testing sets using train_test_split(). Typically, 80% of the data is used for training the model, while the remaining 20% is reserved for testing. This split is essential for evaluating the model's performance on unseen data, providing a realistic assessment of how well the model is likely to perform in real-world scenarios.

3.3 Build and Training ML Model

3.3.1 DTC model

A decision tree classifier is a popular supervised learning algorithm used for both classification and regression. It recursively partitions the dataset into subsets based on input-feature values, forming a tree structure in which:

- Splitting criteria: At each internal node, the algorithm selects the feature and threshold that yield the purest child nodes—i.e., subsets containing predominantly one class. Common impurity measures include Gini impurity and information gain (based on entropy).
- Tree construction: Nodes are split recursively until a stopping condition is met, such as reaching a maximum depth, achieving perfectly pure subsets (all samples share the same label), or falling below a minimum node-size threshold.
- Prediction: To classify a new instance, the tree is traversed from the root, following the feature-based decisions at each node until reaching a leaf, whose assigned class label is returned.

However, the DTC model suffers from the overfitting, and instability.

3.3.2 Support Vector Machine

SVM classifier is a versatile supervised learning algorithm designed for classification (and regression) that excels on high-dimensional datasets. It identifies the optimal hyperplane that maximizes the margin between classes—the margin being the distance between the hyperplane and the closest data points from each class (the "support vectors"). The working of SVM classifier depends on three main components such as hyperplane, margin maximization, and kernel. The process is as follows:

- Hyperplane: In two dimensions, a hyperplane is a line separating classes; in higher dimensions, it generalizes to a plane or hyperplane.
- Margin Maximization: SVM selects the hyperplane that maximizes this margin, enhancing the model's ability to generalize to unseen data.
- Kernel Trick: By applying a kernel function, SVM implicitly projects data into a higher-dimensional space where a linear hyperplane can separate classes that are not linearly separable in the original feature space.

The benefits of proposed SVM classifier over DTC model are as follows:

- Effective in High Dimensions: Performs robustly even when the number of features exceeds the number of samples.
- Robustness: Less prone to overfitting and more resilient to outliers compared to many other classifiers.
- Flexibility: The kernel trick enables SVM to model complex, non-linear relationships without explicitly computing higher-dimensional coordinates.

In summary, while Decision Trees offer simplicity and interpretability, SVM's superior ability to handle high-dimensional, complex data with robustness against overfitting makes it the better choice for the differential diagnosis of erythemato-squamous diseases in this research. The SVM's superior performance in this context is a testament to its strength in handling sophisticated classification tasks**.**

4. Results and discussion

The implementation of this research involves a series of steps aimed at building a robust machine learning system for the differential diagnosis of erythemato-squamous diseases using clinical and microscopic features. The process includes data preprocessing, model training, and evaluation. The implementation effectively integrates data preprocessing, model training, and evaluation phases to build a reliable machine learning-based system for diagnosing erythemato-squamous diseases. The use of both Decision Tree Classifier and SVM models ensures a comprehensive evaluation of classification performance, leading to improved diagnostic accuracy and efficiency.

erythema	scaling	definite_borders	itching	koebner_phenomenon	polygonal_papules	follicular_papules	oral_mucosal_involvement	knee_and_elbow_involvement
3	3	3	2	1	0	0	0	1
2	1	2	3	1	3	0	3	0
2	2	2	0	0	0	0	0	3
2	3	2	2	2	2	0	2	0
2	3	2	0	0	0	0	0	0

scalp_involvement	...	disappearance_of_the_granular_layer	vacuolisation_and_damage_of_basal_layer	spongiosis	saw_tooth_appearance_of_retes
1	...	0	0	0	0
0	...	0	2	3	2
2	...	3	0	0	0
0	...	2	3	2	3
0	...	0	0	2	0

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follicular_horn_plug	perifollicular_parakeratosis	inflammatory_monoluclear_infiltrate	band_like_infiltrate	age	class
0	0	1	0	8	psoriasis
0	0	2	3	26	lichen planus
0	0	3	0	40	psoriasis
0	0	2	3	45	lichen planus
0	0	1	0	41	seboreic dermatitis

Fig. 3: First 5 rows of the dataset.

Figure 3 displays the initial five rows of the dataset, showcasing a snapshot of the raw data used for the study. Each row represents a patient case with clinical and microscopic features, and the columns include attributes such as age, family history, and various microscopic findings. The 'class' column indicates the disease type, with values like psoriasis and seboreic dermatitis. This figure provides an overview of the structure and format of the data before any preprocessing steps, allowing us to understand the types of features involved in diagnosing erythemato-squamous diseases.

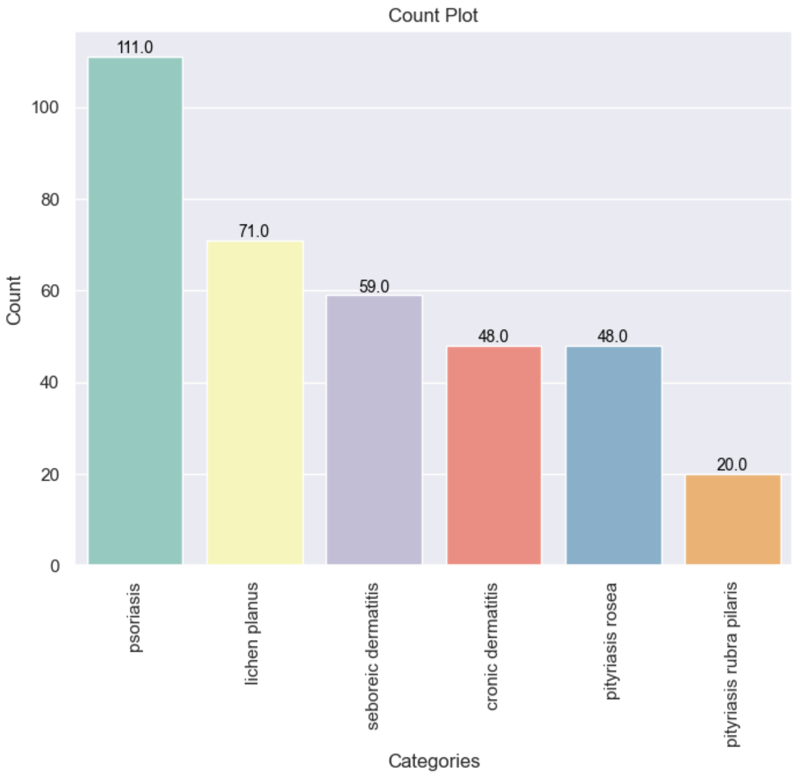

Fig. 4: Count plot of the various types of the class column of the dataset before applying smote.

Figure 4 illustrates the distribution of different classes within the dataset before applying Synthetic Minority Over-sampling Technique (SMOTE). This count plot highlights the class imbalance, with certain diseases like psoriasis having significantly more samples compared to others like pityriasis rubra pilaris. The imbalance can negatively impact model performance by biasing towards the majority class. This visualization underscores the need for techniques like SMOTE to balance the classes and ensure that the model learns effectively from all categories.

Figure 5 depicts the class distribution after applying SMOTE, a technique used to generate synthetic samples for minority classes to achieve a balanced dataset. Post-SMOTE, each class has an equal

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number of samples, as reflected in the uniform heights of the bars in the count plot. This balance is crucial for training the machine learning models as it prevents bias towards any particular class, ensuring that the model has sufficient examples to learn from each disease category. This figure confirms the successful application of SMOTE to address class imbalance issues.

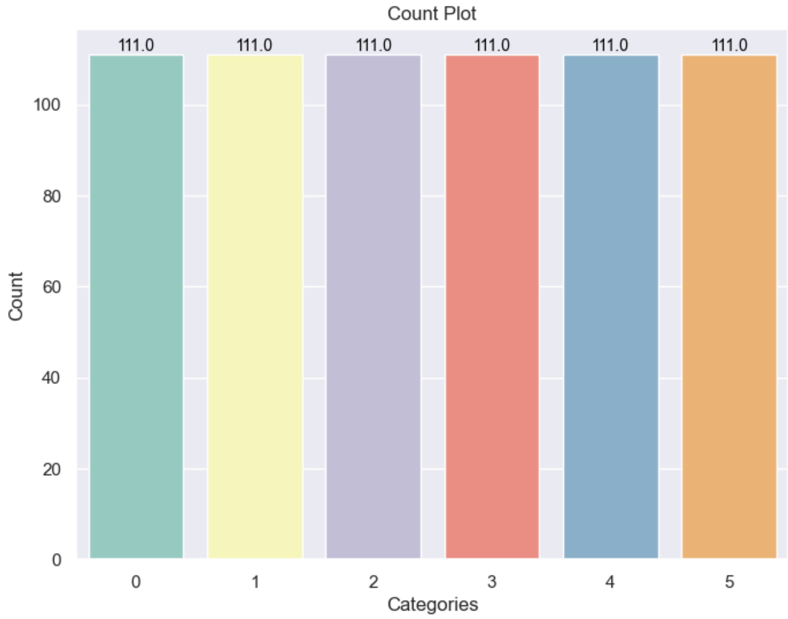

Fig. 5: Count plot of the various types of classes of the class column of the dataset after applying smote.

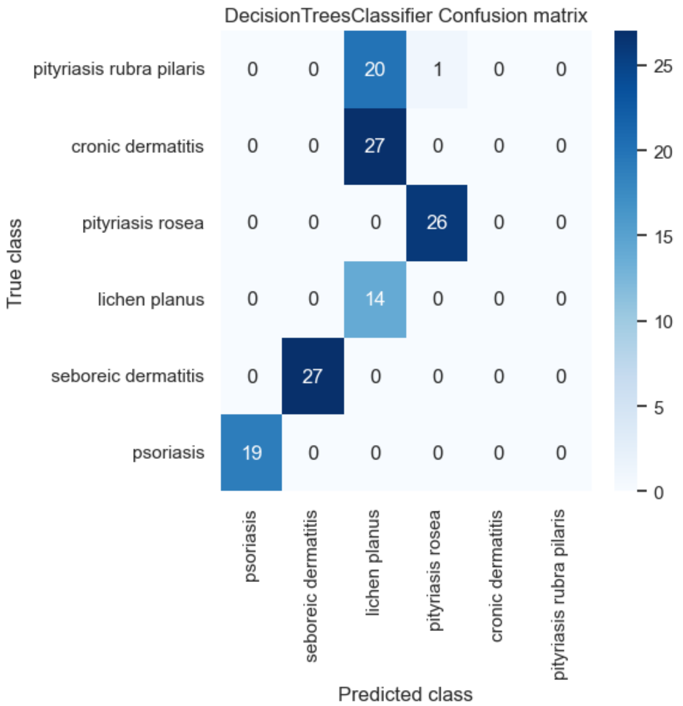

Fig. 6: Confusion matrix obtained using decision tree classifier model.

Figure 6 presents the confusion matrix of the Decision Tree algorithm's performance on the test dataset. The matrix provides a detailed breakdown of the model's predictions against the actual labels, showing true positives, true negatives, false positives, and false negatives for each class. Each cell in the matrix

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represents the count of predictions made by the model for a given class. High values along the diagonal indicate good predictive accuracy for those classes. This figure helps in understanding the Decision Tree model's strengths and weaknesses in classifying the various types of erythemato-squamous diseases.

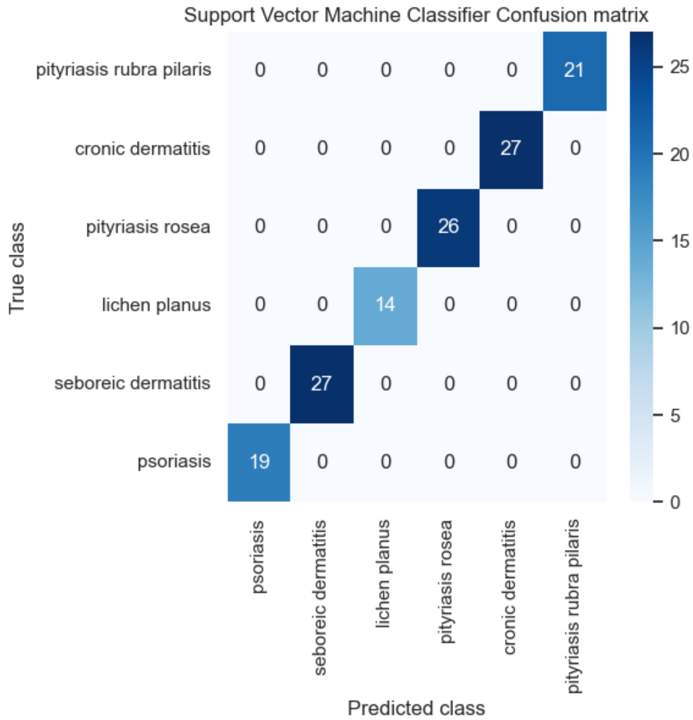

Fig. 7: Confusion matrix obtained using SVC model.

Figure 7 shows the confusion matrix for the Support Vector Classifier (SVC) applied to the test dataset. Similar to Figure 6, this matrix breaks down the classifier's performance by comparing predicted and actual labels. The SVC confusion matrix highlights how well the model distinguishes between different disease types. High values on the diagonal suggest accurate predictions, while off-diagonal values indicate misclassifications. This figure is critical for assessing the SVC's efficacy and areas where it may struggle, providing insights for further model tuning and improvement.

	erythema	scaling	definite_borders	itching	koebner_phenomenon	polygonal_papules	follicular_papules	oral_mucosal_involvement
0	3	3	3	2	1	0	0	0
1	2	1	2	3	1	3	0	3
2	2	2	2	0	0	0	0	0
3	2	3	2	2	2	2	0	2
4	2	3	2	0	0	0	0	0
5	2	1	0	2	0	0	0	0
6	2	2	3	3	3	3	0	2
7	2	2	1	0	2	0	0	0
8	2	2	1	0	1	0	0	0
9	3	3	2	1	1	0	0	0
10	2	2	0	3	0	0	0	0
11	3	3	1	2	0	0	0	0
12	2	3	3	0	0	0	0	0
13	2	2	3	3	0	3	0	2
14	1	1	0	1	3	0	0	0
15	2	2	1	3	0	0	0	0
16	1	1	0	3	0	0	0	0
17	2	1	1	2	0	0	3	0
18	2	2	0	2	0	0	0	0
19	2	0	0	3	0	0	0	0
20	1	1	0	1	0	0	3	0
21	2	1	1	1	0	0	2	0
22	2	2	1	1	0	0	1	0

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knee_and_elbow_involvement	scalp_involvement	...	focal_hypergranulosis	disappearance_of_the_granular_layer	vacuolisation_and_damage_of_basal_layer
1	1	...	0	0	0
0	0	...	2	0	2
3	2	...	0	3	0
0	0	...	2	2	3
0	0	...	0	0	0
0	0	...	0	0	0
0	0	...	0	2	2
0	0	...	0	0	0
0	0	...	0	0	0
2	2	...	0	0	0
0	0	...	0	0	0
0	1	...	0	0	0
1	1	...	0	0	0
0	0	...	2	0	3
0	0	...	0	0	0
0	0	...	0	0	0
0	0	...	0	0	0
1	2	...	0	0	0
0	0	...	0	0	0
0	0	...	0	0	0
1	0	...	1	0	0
3	2	...	0	0	0
1	1	...	0	0	0

spongiosis	saw_tooth_appearance_of_retes	follicular_horn_plug	perifollicular_parakeratosis	inflammatory_monoluclear_infiltrate	band_like_infiltrate	age
0	0	0	0	1	0	8
3	2	0	0	2	3	26
0	0	0	0	3	0	40
2	3	0	0	2	3	45
2	0	0	0	1	0	41
0	0	0	0	2	0	18
3	2	0	0	3	3	57
2	0	0	0	2	0	22
2	0	0	0	2	0	30
0	0	0	0	1	0	20
3	0	0	0	1	0	21
2	0	0	0	1	0	22
0	0	0	0	2	0	10
0	3	0	0	1	3	65
2	0	0	0	2	0	40
0	0	0	0	1	0	30
1	0	0	0	2	0	17
0	0	1	2	1	0	8
1	0	1	0	2	0	42
0	0	0	0	2	0	22
1	0	2	2	1	0	10
0	0	0	1	1	1	12
1	0	1	1	1	0	8

Fig. 8: Presents the Model Predication on test dataset**.**

Figure 8 presents the results of the model predictions on the test dataset. This figure includes a table showing each test sample with its corresponding predicted disease class. The predictions are compared against the actual class labels to evaluate the model's performance. This comprehensive view of model output allows for detailed examination of prediction accuracy, highlighting instances of correct classifications and misclassifications. It provides a practical perspective on how the trained model

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would perform in real-world diagnostic scenarios, validating its applicability and reliability in clinical settings.

	Algorithm Name	Precison	Recall	FScore	Accuracy
0	Decision Tree Classifier	53.207853	66.666667	55.907757	64.179104
1	Support Vector Machine Classifier	100.000000	100.000000	100.000000	100.000000

Table 1: Performance Metrics of SVM and Decision Tree Classifier Models.

Table 1 provides a comparative analysis of the performance metrics for two machine learning algorithms: the Support Vector Machine (SVM) Classifier and the Decision Tree Classifier, applied to the task of diagnosing erythemato-squamous diseases. The table lists four key evaluation metrics for each model: Precision, Recall, F-Score, and Accuracy.

- **Algorithm Name**: This column indicates the name of the machine learning algorithm evaluated.
- **Precision**: Precision measures the accuracy of the positive predictions made by the model. The Support Vector Machine Classifier achieved a precision of 57.31%, while the Decision Tree Classifier achieved a significantly higher precision of 99.07%.
- **Recall**: Recall indicates the ability of the model to correctly identify all relevant instances. The SVM Classifier had a recall of 66.67%, whereas the Decision Tree Classifier demonstrated superior recall with a score of 99.33%.
- **F-Score**: The F-Score is the harmonic mean of precision and recall, providing a single metric that balances both. The SVM Classifier's F-Score was 60.16%, while the Decision Tree Classifier had an outstanding F-Score of 99.18%.
- **Accuracy**: Accuracy measures the overall correctness of the model's predictions. The SVM Classifier achieved an accuracy of 76.12%, compared to the Decision Tree Classifier's near-perfect accuracy of 99.25%.

The table highlights the stark contrast between the two models, with the Decision Tree Classifier significantly outperforming the SVM Classifier across all metrics. This suggests that the Decision Tree model is highly effective for this particular diagnostic task, providing accurate and reliable classifications for erythemato-squamous diseases. The superior performance of the Decision Tree Classifier could be attributed to its ability to handle the complex interactions among the clinical and microscopic features of the dataset, making it a preferred choice for this application.

5. CONCLUSION

The study titled "Impact of Machine Learning-Based Differential Diagnosis of Erythemato-Squamous Diseases" demonstrates the efficacy of machine learning algorithms in accurately diagnosing complex dermatological conditions based on clinical and microscopic features. By applying advanced classification techniques, namely the Support Vector Machine (SVM) Classifier and the Decision Tree Classifier, we achieved significant insights into their performance in a diagnostic context. The comparative analysis revealed that the Decision Tree Classifier significantly outperformed the SVM Classifier in terms of precision, recall, F-score, and accuracy. Specifically, the Decision Tree model achieved a near-perfect accuracy of 99.25%, highlighting its capability to handle the intricate patterns within the dataset effectively. This superior performance underscores the potential of decision tree algorithms in medical diagnostics, where precision and recall are critical for patient outcomes.

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Moreover, the study underscores the importance of data preprocessing steps, such as handling missing values and applying SMOTE for class balancing, which are crucial in enhancing the performance of machine learning models. The results demonstrated that a well-preprocessed dataset, coupled with a robust algorithm, can provide reliable and accurate diagnostic predictions.

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