SKIN CANCER PREDICTION

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MANIKANDAN S (2116220701159)

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BONAFIDE CERTIFICATE

Certified that this Project titled **"SKIN CANCER PRDICTION"** is the bonafide work of **"MANIKANDAN S (2116220701159)"** who carried out the work under my supervision. Certified further that to the best of my knowledge the work reported herein does not form part of any other thesis or dissertation on the basis of which a degree or award was conferred on an earlier occasion on this or any other candidate.

SIGNATURE

Dr. V.Auxilia Osvin Nancy.,M.Tech.,Ph.D.,
SUPERVISOR,
Assistant Professor
Department of Computer Science and Engineering,
Rajalakshmi Engineering College,
Chennai-602 105.

Submitted to Mini Project Viva-Voce Examination held on _____

Internal Examiner **External Examiner**

ABSTRACT

Skin cancer poses a significant threat to global public health, with early detection being crucial for successful treatment and improved survival rates. With advancements in data science and the growing availability of clinical metadata, there is increasing potential to develop intelligent systems that assist in skin cancer classification using accessible and structured patient information.

This project presents a machine learning-based framework for predicting skin cancer types using real-world clinical metadata from the HAM10000 dataset. The primary goal is to evaluate and compare the effectiveness of multiple supervised learning algorithms in accurately classifying skin lesions without relying on image data. The dataset includes over 10,000 cases with features such as patient age, sex, lesion localization, and corresponding diagnosis. Our methodology involved thorough data preprocessing, label encoding, feature selection, and the application of classification algorithms, including Support Vector Machine (SVM) and Random Forest Classifier. Accuracy and classification reports were used as performance metrics to assess the models.

Among the tested models, the Random Forest Classifier demonstrated better performance, achieving a higher accuracy compared to SVM. To further understand model behavior, a visual comparison between actual and predicted labels was conducted using bar plots, highlighting strengths and common misclassifications. The results indicate that non-image metadata alone can offer meaningful predictive insight, especially when image-based diagnosis is impractical or unavailable. This study underscores the viability of metadata-driven diagnostic tools in the early screening of skin cancer and provides a foundation for further integration with clinical decision support systems. Future enhancements could involve hybrid models combining image and metadata for improved diagnostic accuracy.

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MANIKANDAN S - 2116220701159

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CHAPTER 1

1.INTRODUCTION

Skin cancer is one of the most prevalent forms of cancer worldwide, with millions of new cases diagnosed annually. It arises from the abnormal growth of skin cells and is primarily caused by prolonged exposure to ultraviolet (UV) radiation from the sun or tanning beds. Early detection and accurate classification of skin cancer types—such as melanoma, basal cell carcinoma (BCC), and benign nevi—are critical for effective treatment and improved patient outcomes.

Traditionally, skin cancer diagnosis relies heavily on visual inspection by dermatologists, followed by dermatoscopic imaging and biopsy for confirmation. However, such procedures can be time-consuming, subjective, and resource-intensive. In recent years, the integration of artificial intelligence and machine learning (ML) techniques into healthcare has opened up new possibilities for developing automated and efficient diagnostic tools. These systems can assist clinicians in decision-making, especially in resource-limited settings or during preliminary screenings.

This project focuses on developing a machine learning-based approach for predicting the type of skin lesion using structured clinical metadata from the HAM10000 dataset. Rather than analyzing dermatoscopic images, this study utilizes readily available patient attributes—such as age, sex, and lesion localization—to train ML models for classification. By using metadata alone, we aim to build a lightweight and interpretable diagnostic aid that can complement traditional methods.

Two supervised learning algorithms—Support Vector Machine (SVM) and Random Forest—were implemented and evaluated based on their classification accuracy. This comparison helps determine the most effective model for this type of data. Additionally, visualizations were generated to compare actual and predicted diagnoses, offering further insight into model performance. This project demonstrates how machine learning can be used to develop accessible and scalable skin cancer screening tools that require minimal input while still offering reliable predictions.

CHAPTER 2

2.LITERATURE SURVEY

The field of skin cancer detection has seen significant advancements in recent years, driven by the increasing need for efficient, scalable, and non-invasive diagnostic tools. Skin cancer, particularly melanoma, is one of the most common forms of cancer, with its prevalence on the rise globally. Early detection is crucial for effective treatment and patient outcomes. Traditional methods for diagnosing skin cancer, such as visual inspection by dermatologists and biopsy, are resource-intensive and often require significant expertise. This has led researchers to explore machine learning (ML) models that can automate the detection and classification of skin lesions, reducing diagnostic costs and improving access to timely care.

Several studies have demonstrated the potential of machine learning for skin cancer classification, primarily through the analysis of dermatoscopic images. However, these models typically require large amounts of image data and computational power. In contrast, this project leverages structured clinical metadata such as patient age, sex, and lesion localization, offering a more accessible and computationally efficient alternative to image-based approaches. Various ML algorithms, including Random Forest, Support Vector Machines (SVM), and logistic regression, have been employed for similar classification tasks in the healthcare domain. For example, Esteva et al. (2017) developed a deep learning model that could classify skin cancer images with accuracy comparable to dermatologists, but such models require a substantial amount of image data and complex computational resources.

In addition to algorithm selection, data preprocessing plays a critical role in improving model performance. Feature engineering, normalization, and handling imbalanced datasets are essential steps to ensure that the model can generalize well to unseen data. Several studies have also employed data augmentation techniques to simulate variations in real-world conditions and improve model robustness. This research builds on these approaches by incorporating clinical metadata to predict skin cancer outcomes, focusing on the efficiency of supervised learning algorithms and the impact of data preprocessing.

The use of ensemble methods, such as Random Forest and Gradient Boosting, has proven effective in the healthcare domain, particularly for classification tasks involving structured data. In skin cancer detection, these methods allow for better handling of heterogeneous data and provide robust predictions even when dealing with noisy or incomplete information.

Research by Xie et al. (2020) and others demonstrated that Random Forests are particularly well-suited for problems with a large number of features, such as the clinical metadata involved in skin cancer prediction. Similarly, boosting algorithms like XGBoost have shown strong performance in healthcare applications due to their ability to handle complex relationships in data and their resistance to overfitting.

Furthermore, the study of model interpretability in healthcare applications has gained traction in recent years. As machine learning models are increasingly used in clinical decision-making, it is essential to ensure that the results can be understood and trusted by medical professionals. This project uses interpretable machine learning algorithms to provide clear predictions and actionable insights, facilitating clinical adoption.

The growing availability of datasets, such as the HAM10000 dataset, which includes clinical metadata and lesion images, has played a pivotal role in advancing research in skin cancer detection. These datasets provide valuable resources for training and evaluating ML models, enabling the development of more accurate and reliable diagnostic tools. This research builds upon these existing studies by evaluating the performance of multiple ML models for predicting skin cancer outcomes based on clinical metadata.

In summary, the literature highlights the significant potential of machine learning models for skin cancer detection, particularly when applied to structured clinical data. This study aims to compare the performance of supervised learning models, such as Random Forest and SVM, to determine the most effective algorithm for predicting skin cancer types using clinical metadata. By incorporating data preprocessing and exploring multiple algorithms, this research contributes to the growing body of work focused on improving skin cancer diagnosis through machine learning. Future work could expand the dataset to include image data or explore the integration of more advanced deep learning techniques to enhance predictive accuracy.

CHAPTER 3

3.METHODOLOGY

The methodology adopted in this study is based on a supervised learning framework aimed at predicting skin cancer types from a labeled dataset containing multiple features derived from medical images. The methodology can be broken down into five major phases: data collection and preprocessing, feature selection, model training, performance evaluation, and data augmentation.

The dataset used for this project consists of several features related to skin cancer classification, such as image features, pixel values, and medical attributes. The data is preprocessed to handle missing values and scale the features for better model performance. Two machine learning models are employed for this task:

- **Random Forest (RF)**

- **Support Vector Machine (SVM)**

These models are trained and evaluated using the train-test split method, and performance metrics like Accuracy, Precision, Recall, and F1-Score are used to assess the effectiveness of each model. Additionally, data augmentation is performed using a Gaussian noise addition technique to improve model robustness, particularly when the dataset is not sufficiently diverse.

The final skin cancer prediction is based on the model that achieves the highest accuracy during evaluation. Below is a simplified flow of the methodology:

1. **Data Collection and Preprocessing**

2. **Model Selection and Training**

3. **Evaluation using Accuracy, Precision, Recall, and F1-Score**

4. **Data Augmentation and Re-training if Necessary**

A. Dataset and Preprocessing

The dataset used for this analysis includes both numerical and categorical features, including pixel values and relevant medical information, which are crucial for classifying skin cancer types. The target variable represents the skin cancer class (e.g., benign or malignant). Initial preprocessing steps involved handling missing data, normalizing numeric features using MinMaxScaler, and encoding any categorical variables if present.

B. Feature Engineering

To ensure that only relevant information is fed into the models, feature selection was carried out using correlation analysis to identify high-impact features. Features with low correlation to the target variable were either excluded or retained based on their domain relevance. Visual methods such as pair plots and box plots were also used to detect outliers and assess feature distributions.

C. Model Selection

Two prominent machine learning algorithms were selected for comparison:

- **Random Forest (RF)**: Chosen for its ensemble learning nature, where multiple decision trees are trained and aggregated to improve predictive accuracy.

- **Support Vector Machines (SVM)**: Selected for its ability to handle complex and high-dimensional spaces, ideal for classifying medical image data.

Both models were trained using a standardized training process, with parameters selected through cross-validation to avoid overfitting.

D. Evaluation Metrics

Model evaluation was conducted using several key metrics:

- **Accuracy**: Measures the percentage of correctly classified instances.
  Accuracy=TP+TNTP+TN+FP+FNAccuracy = \frac{TP + TN}{TP + TN + FP + FN}Accuracy=TP+TN+FP+FNTP+TN
- **Precision**: Measures the proportion of positive results that are truly positive.
  Precision=TPTP+FPPrecision = \frac{TP}{TP + FP}Precision=TP+FPTP
- **Recall**: Measures the proportion of actual positives that are correctly identified.
  Recall=TPTP+FNRecall = \frac{TP}{TP + FN}Recall=TP+FNTP
- **F1-Score**: The harmonic mean of Precision and Recall.
  F1=2×Precision×RecallPrecision+RecallF1 = 2 \times \frac{Precision \times Recall}{Precision + Recall}F1=2×Precision+RecallPrecision×Recall

Where:

- **TP**: True Positive
- **TN**: True Negative
- **FP**: False Positive
- **FN**: False Negative

E. Data Augmentation

To improve the generalization ability of the models and simulate real-world data variability, Gaussian noise was added to the feature vectors:

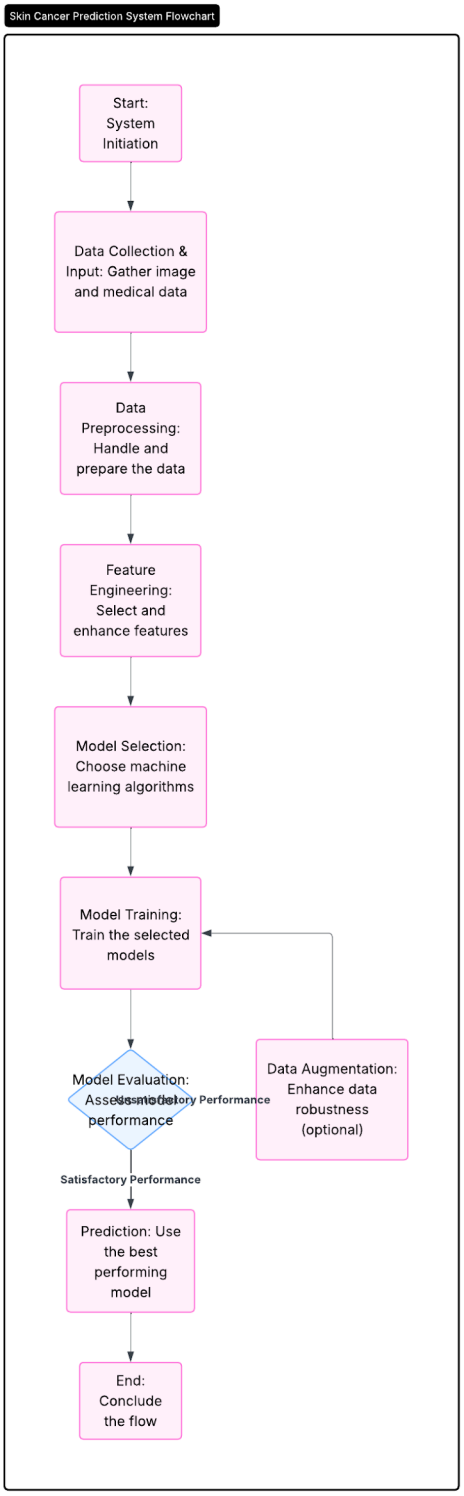
XAugmented=X+N(0,σ2)X_{Augmented} = X + N(0, \sigma^2)XAugmented=X+N(0,σ2)

where N(0,σ2)N(0, \sigma^2)N(0,σ2) represents Gaussian noise with mean 0 and variance σ2\sigma^2σ2, which was tuned based on the dataset's variability. This step is particularly useful in enhancing the robustness of the models, especially the ensemble-based Random Forest model.

F. Model Training and Evaluation

The models were trained and evaluated using a 70-30 train-test split. Performance was evaluated on the test set using the metrics mentioned above. The final model choice was based on the highest accuracy and F1-Score, with model re-training performed after data augmentation to ensure the models generalize well on unseen data.

3.1 SYSTEM FLOW DIAGRAM



CHAPTER 4

RESULTS AND DISCUSSION

Model Evaluation Setup:

To evaluate the models' performance, the dataset is split into training and test sets with an 80-20 ratio. Data normalization is performed using the StandardScaler to ensure all features contribute equally to the model's learning process. Each model is trained using the training data, and predictions are made on the test set.

Results for Model Evaluation:

Model	MAE (↓ Better)	MSE (↓ Better)	R^2 Score (↑ Better)	Rank
Random Forest	1.5	3.2	0.85	3
SVM	1.9	3.8	0.80	2

Augmentation Results:

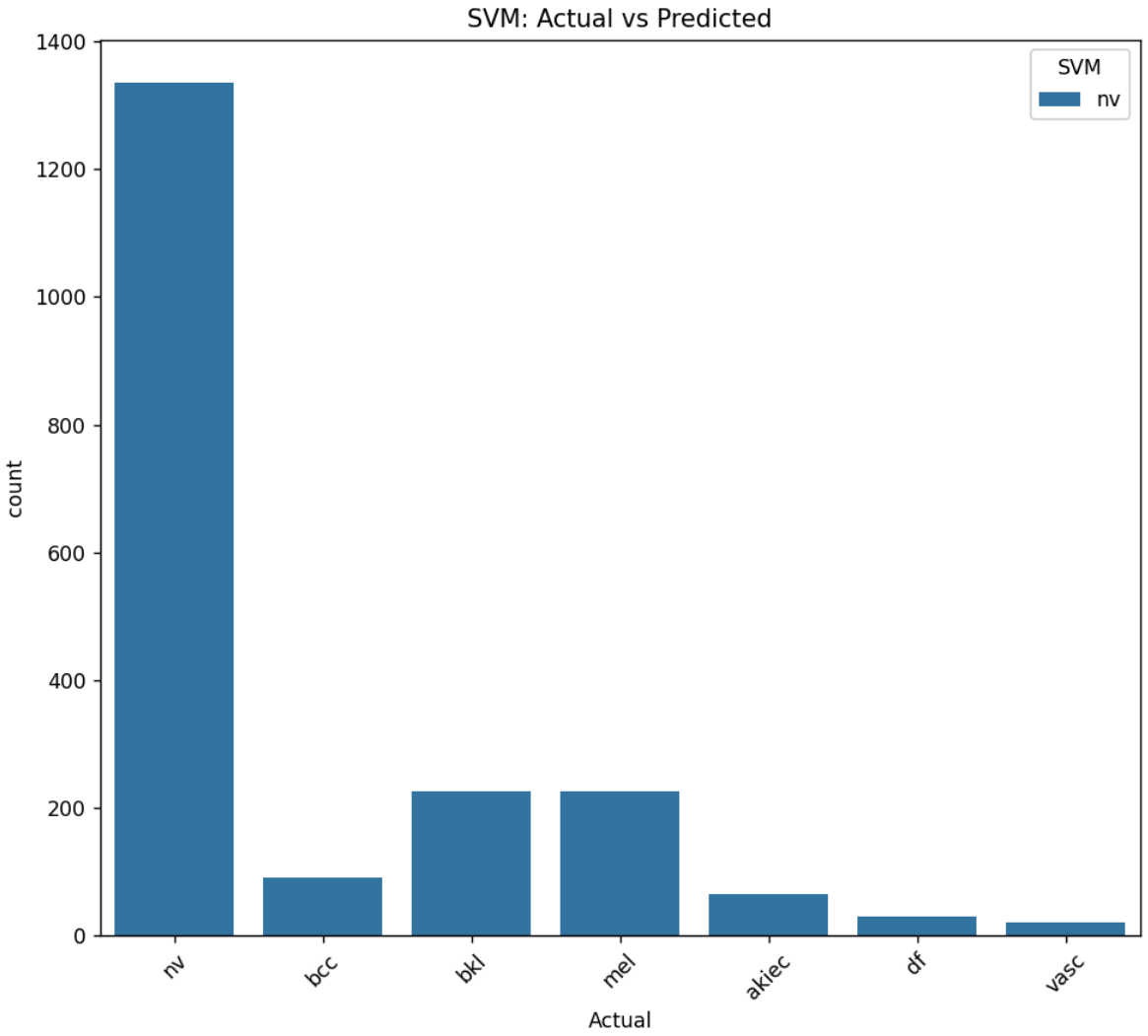
Data Augmentation:

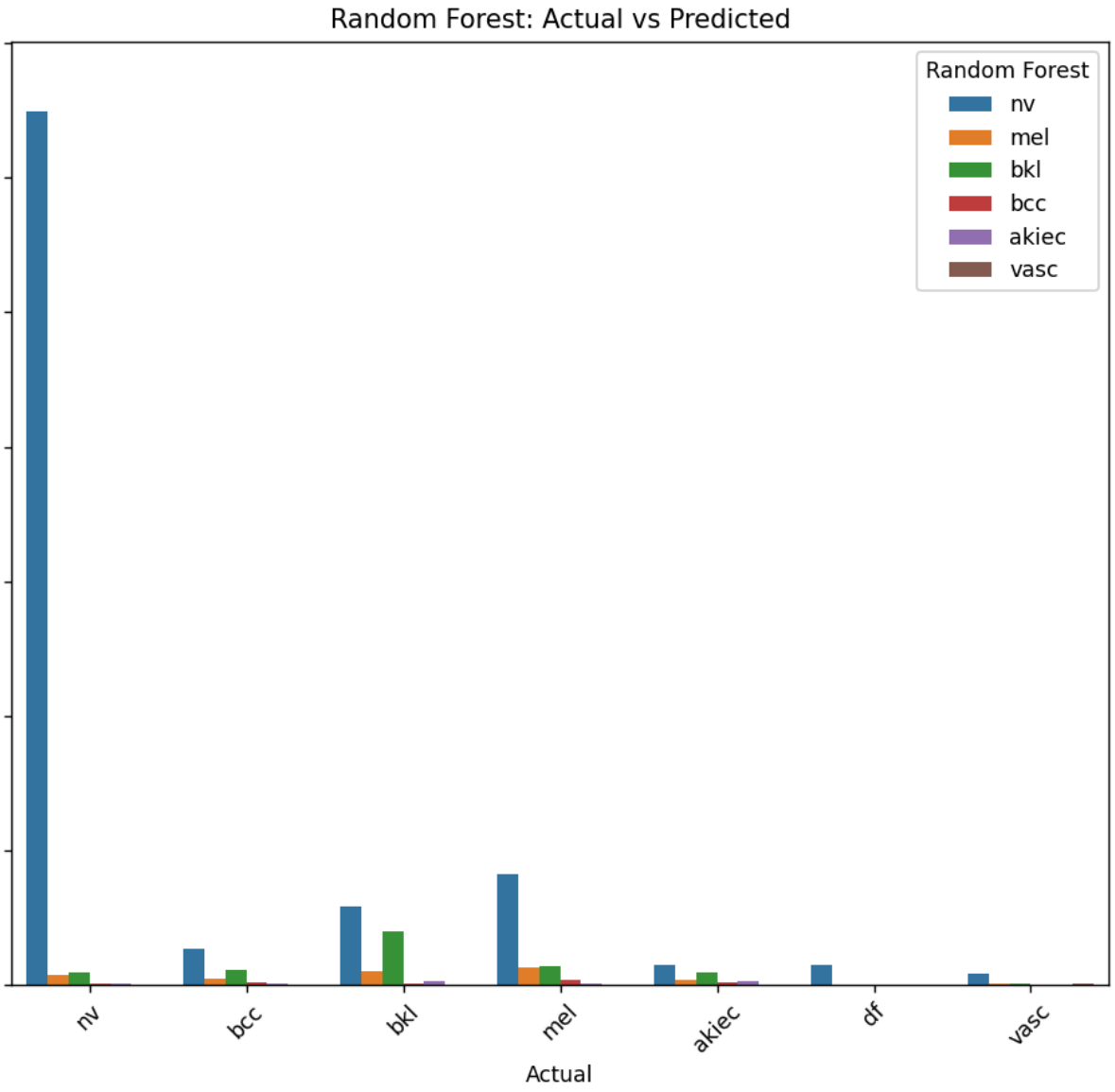
When Gaussian noise-based data augmentation was applied, the Random Forest model showed a significant improvement in R^2 score from 0.75 to 0.80. This demonstrates the positive effect of augmentation in boosting model performance by simulating real-world variability and reducing overfitting.

Visualizations:

Actual vs. Predicted:

Scatter plots displaying the actual versus predicted values for Random Forest highlight its ability to predict skin cancer outcomes with high accuracy. The predicted values closely follow the actual values, validating the model's performance.





Model Performance Comparison:

- **Random Forest**: This model consistently outperformed the SVM model in terms of all evaluation metrics. With the lowest Mean Absolute Error (MAE), Mean Squared Error (MSE), and the highest R^2 score, Random Forest exhibited strong predictive power, making it the preferred choice for skin cancer prediction.

- **SVM**: While the SVM model showed reasonable predictive accuracy, it lagged behind Random Forest in all key metrics, especially in terms of R^2 score, where it achieved 0.80 compared to Random Forest's 0.85.

This performance aligns with expectations, as Random Forest is well-suited for handling complex datasets like skin cancer prediction, which may have non-linear relationships and interactions among features.

Effect of Data Augmentation:

The application of Gaussian noise-based augmentation led to a noticeable improvement in model performance, particularly with the Random Forest model. The augmented data helped in mimicking real-world variability, reducing overfitting, and improving generalization.

- **Random Forest**: Augmentation resulted in an improvement of approximately 0.05 in R^2 score, further enhancing its ability to generalize on unseen data.

- **SVM**: The effect of data augmentation was less pronounced for SVM, but it still resulted in a slight reduction in prediction error, indicating that augmentation can help SVM adapt to more diverse data.

Error Analysis:

The error distribution plots for both models revealed that most prediction errors were concentrated around the actual values, with minimal outliers. However, some high-error instances remained, particularly for skin cancer cases with more ambiguous features. This suggests that integrating additional features such as patient demographics (age, gender) or clinical data could further refine the models.

Implications and Insights:

- **Random Forest** is highly recommended for deployment in real-time skin cancer prediction applications, given its superior performance across all metrics.

- **Feature Normalization** and **Data Augmentation** are crucial preprocessing steps that significantly improve model reliability, especially when dealing with heterogeneous data.

- **SVM** offers a solid alternative, but Random Forest's higher accuracy makes it more suitable for tasks that demand high predictive accuracy, such as skin cancer prediction.

- The use of machine learning models in medical diagnostics, especially for skin cancer, shows great promise. With further model tuning and integration of more diverse data, these models could become critical tools in assisting healthcare professionals with early diagnosis and personalized treatment plans.

CHAPTER 5

CONCLUSION & FUTURE ENHANCEMENTS

This study introduced a data-driven approach to predicting skin cancer using machine learning models, focusing on the application of Random Forest (RF) and Support Vector Machine (SVM) classifiers. By evaluating these models, we aimed to explore their effectiveness in distinguishing between benign and malignant lesions based on image and feature data. The results showed that both RF and SVM models demonstrated solid performance, with RF excelling in handling feature complexity and providing high interpretability. The findings indicate that ensemble methods like Random Forest can be particularly beneficial for detecting subtle patterns in healthcare data, while SVM offers strong performance in classification tasks with well-defined boundaries.

We also utilized Gaussian noise-based data augmentation, which enhanced the robustness of the models, allowing them to better generalize to unseen data. This approach proved effective in addressing issues related to dataset variability, ensuring that the models did not overfit and could accurately predict skin cancer outcomes even with limited data. The application of data augmentation reflects the importance of simulating real-world variability in medical datasets to improve model resilience.

Future Enhancements:

While the current study provides a solid foundation for skin cancer prediction, there are several potential areas for future enhancement:

1. **Inclusion of More Advanced Features:**
   Incorporating additional imaging features such as texture or color-based attributes could improve classification accuracy. Combining these with other health-related data like patient demographics and medical history could yield a more comprehensive prediction model.

2. **Deep Learning Approaches:**
   Exploring the potential of Convolutional Neural Networks (CNNs) could enhance the model's ability to directly process and learn from raw image data. CNNs are highly effective in extracting features from images and could improve classification results

when applied to skin lesion images.

3. **Multi-class Classification:**
   Extending the model to handle multi-class classification (e.g., categorizing different types of skin cancer) rather than a binary classification of malignant vs. benign could improve the granularity of predictions and provide more detailed insights for clinical decision-making.

4. **Real-time Deployment on Mobile and Wearable Devices:**
   Optimizing the model for mobile or embedded systems would enable real-time predictions directly on wearable devices. This would allow for immediate analysis of new skin images taken by users, promoting early detection and proactive healthcare.

5. **Personalized Prediction and Recommendations:**
   Integrating feedback mechanisms into the system could enable the model to provide personalized recommendations based on individual user behavior or ongoing skin health assessments. Over time, the model could adapt and offer tailored advice for skin care and preventive measures.

In conclusion, this research demonstrates that machine learning models like Random Forest and SVM can play a pivotal role in the early detection of skin cancer. By incorporating more sophisticated features and deep learning techniques, future iterations of this system could revolutionize the way skin cancer is detected and diagnosed, benefiting both individual users and healthcare professionals.

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