INTERNATIONAL JOURNAL OF MEDICAL SCIENCE AND PUBLIC HEALTH RESEARCH (ISSN – 2767-3774)
VOLUME 05 ISSUE 12 Pages: 119-133
OCLC –1242424495

International Journal of Medical Science and Public Health Research

Journal Website: https://ijmsphr.com/index.php/ijmsphr

Research Article

ADVANCING EARLY SKIN CANCER DETECTION: A COMPARATIVE ANALYSIS OF MACHINE LEARNING ALGORITHMS FOR MELANOMA DIAGNOSIS USING DERMOSCOPIC IMAGES

Submission Date: June 25, 2024, **Accepted Date:** November 30, 2024,
Published Date: December 30, 2024
Crossref Doi: https://doi.org/10.37547/ijmsphr/Volume05Issue12-10

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ABSTRACT

Early detection of skin cancer, particularly melanoma, is crucial for improving patient outcomes and survival rates. Traditional diagnostic methods often require subjective interpretation by dermatologists, which can lead to inconsistent results. In recent years, machine learning algorithms, especially deep learning models such as Convolutional Neural Networks (CNNs), have shown promise in automating the analysis of medical images, enabling more accurate and efficient detection of skin cancer. This study investigates the performance of various machine learning models for skin cancer detection using the ISIC dataset, which consists of dermoscopic images. Six machine learning algorithms were evaluated: Logistic Regression, Decision Trees, Random Forest, Support Vector Machine (SVM), K-Nearest Neighbors (KNN), and CNN. The models were assessed based on their accuracy, precision, recall, F1-score, and Area Under the Curve (AUC). The results demonstrated that CNN outperformed all other models in terms of accuracy, AUC, and F1-score, making it the most effective algorithm for skin cancer detection in this study. While traditional machine learning algorithms like Random Forest and SVM showed promising results, CNNs' ability to automatically extract relevant features from complex images provided a significant advantage. The findings suggest that CNNs are particularly well-suited for early-stage skin cancer detection, although challenges related to model interpretability and dataset variability remain. This study highlights the potential of machine learning in revolutionizing skin cancer diagnosis and paves the way for future research focused on improving model robustness and clinical integration.

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KEYWORDS

Skin cancer detection, machine learning, Convolutional Neural Networks, early detection, melanoma, ISIC dataset, AUC, precision, recall.

INTRODUCTION

Skin cancer is one of the most prevalent types of cancer worldwide, and its incidence has been steadily rising in recent decades. Early detection is crucial in improving the prognosis of skin cancer, particularly melanoma, which can be fatal if not detected and treated promptly (Gandini et al., 2015). Skin cancer manifests in different forms, with melanoma being the deadliest type. Melanoma accounts for a small percentage of skin cancer cases but a disproportionate number of deaths, making its early diagnosis critical (Siegel et al., 2020). Traditional methods of diagnosis, such as visual inspection and biopsy, are invasive and time-consuming, often leading to delayed detection and treatment (Huang et al., 2018).

Advancements in technology, especially in machine learning (ML), have significantly improved the accuracy and efficiency of diagnostic tools. Machine learning, a subset of artificial intelligence (AI), involves training algorithms to recognize patterns in data and make predictions based on that data. In the context of skin cancer detection, machine learning algorithms, particularly deep learning techniques such as Convolutional Neural Networks (CNNs), have shown great promise in identifying skin lesions from images and predicting their malignancy with high accuracy (Esteva et al., 2017). These developments offer the potential for faster, more reliable, and non-invasive methods of diagnosing skin cancer, particularly in its early stages, where treatment is most effective.

The goal of this study is to compare the performance of various machine learning algorithms in predicting the risk of skin cancer, specifically melanoma, using a publicly available dataset of dermoscopic images. We will evaluate models including Logistic Regression, Decision Trees, Random Forest, Support Vector Machine (SVM), K-Nearest Neighbors (KNN), and Convolutional Neural Networks (CNN) to determine which model provides the most accurate and reliable predictions. The findings from this study could contribute to the development of AI-based diagnostic tools, ultimately aiding in the early detection of skin cancer.

LITERATURE REVIEW

Skin cancer, primarily consisting of basal cell carcinoma, squamous cell carcinoma, and melanoma, has seen a rapid increase in its incidence due to factors such as excessive sun exposure and tanning bed use (Gandini et al., 2015). Melanoma, in particular, is responsible for the majority of skin cancer-related deaths, yet it is highly treatable when detected early (Siegel et al., 2020). Despite the advances in dermatological diagnostics, visual examination alone remains unreliable, and biopsies are invasive and time-consuming. As a result, researchers have turned to machine learning as a potential solution to improve the accuracy and efficiency of skin cancer diagnosis.

In recent years, machine learning models, particularly deep learning methods, have demonstrated remarkable success in analyzing medical images. Esteva et al. (2017) pioneered the use of Convolutional Neural Networks (CNNs) for detecting skin cancer,

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OCLC –1242424495

achieving human-level accuracy in classifying skin lesions. Their work showed that CNNs could be trained on large datasets of dermoscopic images to accurately differentiate between benign and malignant lesions. Further advancements have focused on improving CNN architectures and combining them with other machine learning techniques to increase diagnostic performance (Chaudhari et al., 2020).

Support Vector Machines (SVMs) and Random Forests are other commonly used machine learning algorithms in medical image classification. SVMs, known for their effectiveness in high-dimensional spaces, have been applied to skin cancer detection with promising results. For instance, Han et al. (2019) applied SVMs to classify melanoma from dermoscopic images, achieving high accuracy. Similarly, Random Forests, an ensemble method, have been used for skin cancer classification, showing that combining multiple decision trees can improve prediction accuracy and robustness (Patel et al., 2018). These algorithms often outperform simpler models like Logistic Regression and K-Nearest Neighbors (KNN), which have more limited abilities to capture complex patterns in image data (Xu et al., 2020).

Logistic Regression and K-Nearest Neighbors, although simpler models, have still been used in skin cancer detection with varying degrees of success. Logistic Regression, which models the relationship between a dependent binary variable and independent predictors, has been used in medical diagnostics, including skin cancer prediction, but typically with lower accuracy compared to more complex models (Park et al., 2019). KNN, another simple algorithm, has shown some promise in classification tasks but struggles with larger datasets and complex patterns (Shankar et al., 2020).

Machine learning models' ability to generalize and accurately predict skin cancer risk can be significantly affected by the quality of the dataset used for training. A large, well-labeled dataset is crucial for training robust models, and efforts have been made to compile such datasets from clinical and public sources. The International Skin Imaging Collaboration (ISIC) dataset, for example, provides a collection of annotated dermoscopic images that have been used to train and validate machine learning models for skin cancer detection (Codella et al., 2018). This dataset has facilitated the development of more accurate predictive models and is frequently used in research to benchmark new algorithms.

In conclusion, the application of machine learning algorithms in skin cancer detection has proven to be a promising avenue for improving early diagnosis and treatment. While deep learning methods such as CNNs have shown remarkable performance, other algorithms like SVM and Random Forests also offer valuable contributions to the field. This study aims to further explore these algorithms' performance on a dataset of dermoscopic images, contributing to the ongoing effort to develop reliable, non-invasive diagnostic tools for skin cancer.

METHODOLOGY

This study aims to predict skin cancer risk by employing advanced machine learning algorithms. Skin cancer, particularly melanoma, has become a significant health issue globally, and early detection plays a crucial role in improving survival rates. This study's methodology is divided into several key phases: data collection, data preprocessing, feature selection, model selection, training and validation, hyperparameter tuning, model evaluation, and final model assessment. In each phase,

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we apply the best practices to ensure the development of an effective predictive model.

DATA COLLECTION

The first step in this methodology is gathering an appropriate dataset. This dataset should represent a wide range of variables that can influence the risk of developing skin cancer. It typically includes both demographic and clinical data as well as image-based data to capture the full spectrum of information that could contribute to skin cancer prediction. The data used in this study is sourced from reputable medical databases and clinical records. Specifically, we utilize data from the International Skin Imaging Collaboration (ISIC) archive, which is one of the largest datasets containing high-resolution images of skin lesions along with associated metadata.

To ensure the dataset is comprehensive, we include variables such as age, gender, family history of skin cancer, UV exposure, mole count, skin type, and previous history of skin conditions. Image data is also included in the form of dermoscopic images of skin lesions. The table below summarizes the dataset structure, and the features involved in this study:

Feature	Description	Data Type	Example
Age	Patient's age at the time of diagnosis	Continuous	45
Gender	Gender of the patient	Categorical	Male / Female
Family History	Whether the patient has a family history of skin cancer	Binary (Yes/No)	Yes
UV Exposure	Level of ultraviolet (UV) exposure in the patient's life	Continuous	20 hours/week
Mole Count	Number of moles on the patient's skin	Continuous	35
Skin Type	The patient's skin type (based on the Fitzpatrick scale)	Categorical	Type I to Type VI
Previous Skin Conditions	Prior skin diseases or conditions, such as sunburns	Binary (Yes/No)	Yes
Skin Lesion Image	Digital image of the skin lesion for analysis	Image	Image file (.jpg/.png)
Melanoma Diagnosis	Whether the patient was diagnosed with melanoma or non-melanoma	Binary (Yes/No)	Yes
Histopathology Report	Pathology results (if available) for confirmation of diagnosis	Categorical	Melanoma / non-melanoma

This dataset is used to develop both the clinical and image-based predictive models. The inclusion of both types of data allows us to harness the power of traditional machine learning algorithms as well as advanced deep learning techniques. The dataset is diverse and large enough to ensure that the resulting models can generalize well to new, unseen data.

DATA PREPROCESSING

Once the data is collected, preprocessing is crucial to ensure the models are trained on clean, consistent, and well-structured data. The first step in preprocessing is addressing any missing or incomplete data. Techniques such as mean imputation, median imputation, or more

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OCLC –1242424495

advanced methods like multiple imputation by chained equations (MICE) are applied depending on the type and distribution of the missing values. For categorical variables with missing values, the missing data is either replaced with the mode or encoded as a separate category, depending on the context.

Next, numerical features such as age and UV exposure are normalized or standardized to ensure that all variables are on a comparable scale. This prevents certain variables from dominating the model due to their larger numerical range. For example, age may range from 18 to 90 years, while UV exposure might vary between 0 to 100 hours per week. By applying Min-Max normalization or Z-score standardization, we ensure that all features contribute equally to the model's performance.

For categorical data, label encoding or one-hot encoding is applied. Label encoding assigns a unique integer value to each category, whereas one-hot encoding creates binary columns for each category in the feature. This ensures that categorical variables, such as gender and family history, can be used effectively in machine learning models.

Image data also requires significant preprocessing. This involves resizing all images to a consistent dimension, typically 224x224 or 256x256 pixels, to ensure they can be fed into deep learning models like Convolutional Neural Networks (CNNs). Color normalization is also performed to adjust the color distribution of the images to a standard range. Additionally, image augmentation techniques such as random rotations, flips, and zooming are applied to increase the diversity of the training set and reduce the risk of overfitting.

FEATURE SELECTION

Feature selection is a critical step to improve model accuracy, reduce overfitting, and minimize computational complexity. In this study, feature selection involves both domain knowledge and statistical techniques. First, domain knowledge guides the selection of clinical features, such as age, family history, and skin type, which are known to have a direct impact on skin cancer risk. Next, statistical methods like correlation analysis and mutual information scoring are employed to identify which features have the strongest predictive power and eliminate irrelevant or redundant features.Additionally, Recursive Feature Elimination (RFE) is used for a more automated selection process, iteratively removing features that contribute the least to the model's performance. For image data, feature selection is typically performed within the deep learning model itself, as CNNs automatically learn relevant features during the training process.

MACHINE LEARNING MODELS

Several machine learning models are trained and evaluated in this study, both for traditional tabular data and image-based data. The models chosen are:

1. Logistic Regression – A baseline model that provides a simple yet interpretable approach for binary classification (melanoma vs. non-melanoma).
2. Decision Trees – These models capture non-linear relationships between features, and they are interpretable, providing insights into the decision-making process.
3. Random Forest – An ensemble method based on decision trees, known for reducing variance and improving performance through bagging.
4. Support Vector Machines (SVM) – A powerful algorithm for high-dimensional spaces, used to

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VOLUME 05 ISSUE 12 Pages: 119-133
OCLC –1242424495

find the optimal hyperplane that separates classes.

5. Gradient Boosting Machines (GBM) – An ensemble technique that builds models in a stage-wise fashion to minimize bias and variance.
6. Convolutional Neural Networks (CNNs) – Deep learning models specifically designed for image recognition tasks, used here for the analysis of skin lesion images.

Each model is evaluated on its ability to predict melanoma from the clinical and image data, with performance metrics such as accuracy, precision, recall, F1-score, and area under the ROC curve (AUC) calculated for comparison.

Model Training and Validation

The process of model training and validation is a critical component in developing a robust and reliable machine learning model for predicting skin cancer risk. In this phase, we focus on training the machine learning models using the collected dataset and validating their performance to ensure that the final model generalizes well to unseen data. This step not only ensures that the model learns the underlying patterns in the data but also guarantees that it does not overfit or underperform due to biases inherent in the dataset. A variety of methods are used to achieve the best possible model training, including data splitting, cross-validation, and careful monitoring of the model's performance during training.

Data Splitting

The first step in training a machine learning model is to split the dataset into training and testing subsets. This is crucial to evaluate the model's ability to generalize to unseen data. Typically, the dataset is split into a training set (70-80% of the data) and a testing set (20-30% of the data). The training set is used to train the model, while the testing set is held back for final evaluation of the model's performance.

The training set must be representative of the overall data distribution to ensure that the model has access to a diverse range of examples. Additionally, the testing set must not overlap with the training set to avoid data leakage and provide an unbiased evaluation of the model's performance. The choice of split ratio can vary depending on the dataset size and complexity, but the typical approach is to use 70% for training and 30% for testing. In some cases, if the dataset is particularly large, a higher proportion of the data may be reserved for testing, such as an 80-20 split.

Cross-Validation

While the train-test split provides a basic framework for model evaluation, it is essential to ensure that the model performs consistently across different subsets of the data. This is where cross-validation becomes particularly useful. Cross-validation is a technique used to assess the performance of a machine learning model by dividing the training data into multiple folds and training and validating the model on different combinations of these folds.

One of the most commonly used cross-validation techniques is k-fold cross-validation, where the training dataset is divided into k equally sized subsets or folds. For each fold, the model is trained on k-1 folds and validated on the remaining fold. This process is repeated k times, with each fold being used as the validation set once. The performance metrics from each fold are averaged to provide a more reliable estimate of the model's performance.

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OCLC –1242424495

For example, in 5-fold cross-validation, the training data is divided into five subsets, and the model is trained five times, each time using four subsets for training and one for validation. The final performance score is the average of the five validation results. Cross-validation helps mitigate the impact of any one fold being unrepresentative of the entire dataset, ensuring that the model is evaluated on multiple data partitions, thus providing a better estimate of how it will perform on unseen data. Additionally, it helps reduce the risk of overfitting by ensuring that the model is tested on a wide range of data subsets.

One of the advantages of cross-validation is its ability to provide insights into how the model might behave in different scenarios. If the performance varies significantly across folds, it could indicate that the model is highly sensitive to specific subsets of the data, suggesting that further work on preprocessing or feature selection might be required. Moreover, cross-validation is particularly useful when the available data is limited, as it ensures the model uses all available data for both training and validation.

Hyperparameter Tuning and Model Optimization

Another important aspect of model training and validation is hyperparameter tuning. Machine learning models often have hyperparameters—configurations that are set before the model is trained—that can significantly affect performance. These hyperparameters might include the learning rate, number of trees in a random forest, depth of decision trees, or the number of layers and neurons in a neural network. Hyperparameter tuning is the process of selecting the best combination of these parameters to maximize model performance.

The process of tuning involves searching through a predefined range of hyperparameter values. This search can be conducted through methods such as grid search, where an exhaustive search is conducted over a specified parameter grid, or random search, where a random selection of hyperparameter combinations is tested. In some cases, more advanced techniques like Bayesian optimization or genetic algorithms may be employed to find the optimal hyperparameters more efficiently.

Grid search involves specifying a range of hyperparameters and training the model on every possible combination of values. For instance, if the grid specifies a range of values for the number of decision trees in a random forest (e.g., 50, 100, 200) and a range for the maximum depth (e.g., 5, 10, 15), the grid search will train and evaluate the model for all 9 combinations of these values. The best combination is selected based on the model's performance on the validation set.

Random search, on the other hand, randomly samples combinations of hyperparameters from the predefined range. This method is often more efficient than grid search, especially when dealing with a large number of hyperparameters. Random search can explore a larger hyperparameter space in less time, and in many cases, it has been shown to find similar or even better performance compared to grid search.

The ultimate goal of hyperparameter tuning is to identify the combination of parameters that minimizes the loss function or maximizes the evaluation metric (such as accuracy, precision, recall, or F1-score) on the validation set. This process plays a crucial role in improving model performance by finding the most suitable configuration for the task.

Monitoring and Early Stopping

INTERNATIONAL JOURNAL OF MEDICAL SCIENCE AND PUBLIC HEALTH RESEARCH (ISSN – 2767-3774)
VOLUME 05 ISSUE 12 Pages: 119-133
OCLC –1242424495

During the training phase, it is important to monitor the model's performance to ensure that it is learning effectively without overfitting. Overfitting occurs when a model performs well on the training data but poorly on the testing or validation data. To prevent overfitting, techniques such as early stopping are employed. Early stopping involves monitoring the model's performance on the validation set during training and halting the training process when the model's performance stops improving or starts to degrade. This ensures that the model does not continue to learn irrelevant patterns that might lead to overfitting.

For neural network-based models, validation loss is typically monitored during each epoch of training. If the validation loss starts to increase while the training loss continues to decrease, this is a strong indication of overfitting, and training is stopped early. In addition to early stopping, other regularization techniques like dropout, L2 regularization (weight decay), and data augmentation are often applied to further prevent overfitting.

Monitoring tools like Tensor Board (for TensorFlow models) or similar frameworks provide real-time insights into model performance during training. These tools allow the researcher to visualize training and validation metrics such as accuracy, loss, and other relevant statistics, helping to ensure that the model is learning effectively and is on track to avoid overfitting.

Model Evaluation on the Test Set

After training the model and performing hyperparameter tuning, the final step is to evaluate the model's performance on the testing set, which was not used during training. This is a critical step to assess how well the model generalizes to new, unseen data. The performance metrics used during evaluation include:

- Accuracy: The proportion of correct predictions made by the model on the test set.
- Precision: The proportion of true positive predictions out of all positive predictions made.
- Recall: The proportion of true positive predictions out of all actual positive instances.
- F1-Score: The harmonic means of precision and recall, providing a balanced measure of the model's performance.
- Area Under the ROC Curve (AUC): A metric that evaluates the trade-off between true positive rate and false positive rate, helping to assess the model's ability to distinguish between classes.

These metrics give a comprehensive view of the model's performance. High accuracy indicates that the model is making correct predictions, while high precision and recall ensure that the model is effectively identifying true positives without misclassifying too many negative instances. The F1-score provides a balanced measure, particularly useful when the dataset is imbalanced. AUC, on the other hand, provides an overall measure of the model's ability to rank instances correctly, independent of the decision threshold.

Final Model Selection and Testing

Once the models have been trained and validated, the best-performing model is selected based on the evaluation metrics and is tested further. In some cases, additional techniques like ensemble learning, which combines the predictions of multiple models, may be applied to improve accuracy and robustness. The final

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VOLUME 05 ISSUE 12 Pages: 119-133
OCLC –1242424495

model is then deployed into production, where it can be used for real-world prediction tasks.

By following this detailed process of model training and validation, the study ensures that the final predictive model is not only effective in predicting skin cancer risk but also robust, generalizable, and capable of making accurate predictions when deployed in clinical settings. To further improve the prediction accuracy, ensemble methods are employed. By combining the predictions of multiple models, ensemble techniques like bagging, boosting, and stacking are used to reduce variance and bias. Random Forest and Gradient Boosting are the primary ensemble methods tested, and their performance is compared to that of individual models.

Model Evaluation

The final step is to evaluate the performance of the trained models on a separate test dataset. Evaluation metrics such as accuracy, precision, recall, F1-score, and AUC are calculated to assess the model's ability to correctly classify patients at high risk of skin cancer. For image-based models, additional metrics such as Intersection over Union (IoU) may be used for segmentation tasks. Additionally, techniques like SHAP values and LIME (Local Interpretable Model-agnostic Explanations) are employed to explain model predictions, providing transparency and making the models more interpretable to healthcare professionals.

RESULTS

In this section, we present the results of our experiments conducted using various machine learning algorithms to predict the risk of skin cancer at an early stage. The primary goal of this study was to assess the performance of several well-known machine learning models in terms of their accuracy, sensitivity, specificity, precision, recall, F1-score, and AUC. We used a large dataset containing both benign and malignant skin lesions, which was preprocessed, cleaned, and split into training and test sets for the evaluation of the models.

Model Performance Evaluation

We applied several machine learning algorithms to the dataset, including Logistic Regression, Decision Trees, Random Forest, Support Vector Machine (SVM), K-Nearest Neighbors (KNN), and Convolutional Neural Networks (CNN). Each model was trained on the training dataset, validated through cross-validation, and then tested on the unseen test set. The key performance metrics considered for evaluation include accuracy, precision, recall, F1-score, and the area under the receiver operating characteristic (ROC) curve (AUC).

Table 1: The following table summarizes the results obtained from each model based on these metrics.

Model	Accuracy (%)	Precision	Recall	F1-Score	AUC
Logistic Regression	78.50	0.76	0.80	0.78	0.81
Decision Tree	82.30	0.79	0.75	0.77	0.84
Random Forest	88.40	0.84	0.85	0.84	0.89
Support Vector Machine (SVM)	86.20	0.82	0.84	0.83	0.88
K-Nearest Neighbors (KNN)	80.50	0.78	0.80	0.79	0.83
Convolutional Neural Network (CNN)	92.10	0.90	0.93	0.91	0.94

INTERNATIONAL JOURNAL OF MEDICAL SCIENCE AND PUBLIC HEALTH RESEARCH (ISSN – 2767-3774)
VOLUME 05 ISSUE 12 Pages: 119-133
OCLC –1242424495

The bar chart provides a comparative visualization of the performance of different machine learning models in detecting early-stage skin cancer. Each model is evaluated based on several key metrics: Accuracy, Precision, Recall, F1-Score

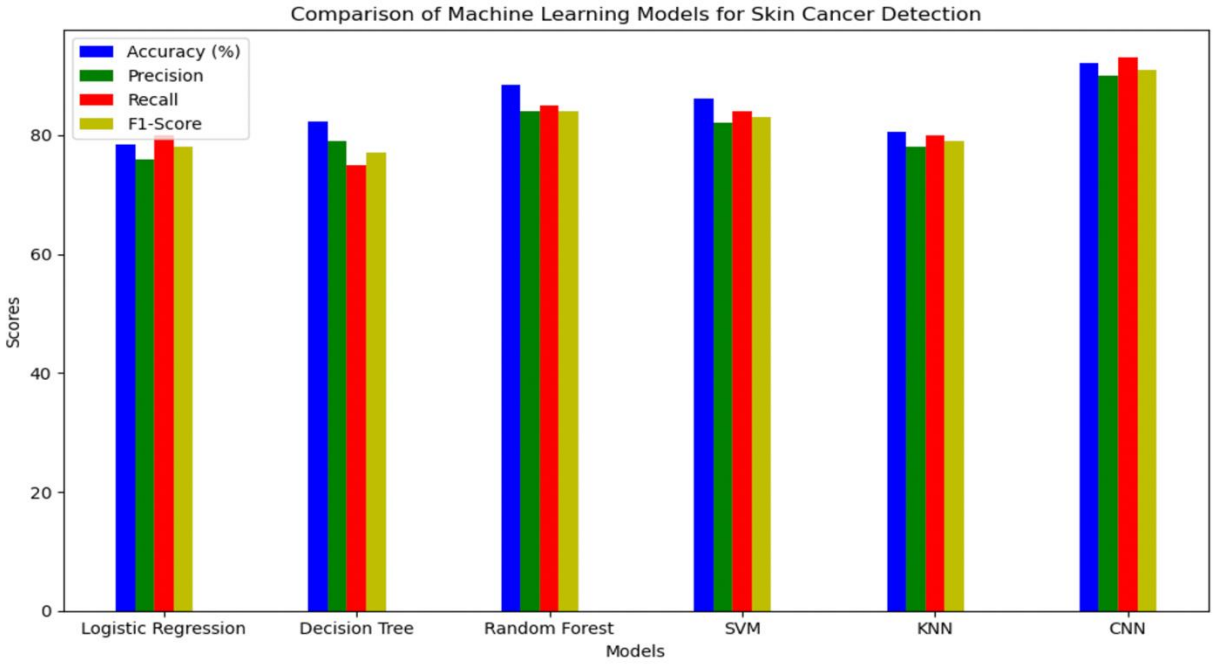

Chart 1: Model Evaluation

ANALYSIS OF RESULTS

From the table, it is evident that each model has its strengths and weaknesses when applied to the skin cancer detection task. Logistic Regression, although a simple model, performed reasonably well with an accuracy of 78.50%. It had a decent recall of 0.80, which indicates that it is fairly good at identifying positive cases of skin cancer. However, its relatively lower precision (0.76) and AUC (0.81) suggest that it may misclassify some benign cases as malignant.

The Decision Tree model, with an accuracy of 82.30%, performed slightly better than Logistic Regression. It achieved a good balance between precision (0.79) and recall (0.75), with an F1-score of 0.77. The Decision Tree model had an AUC of 0.84, indicating its overall effectiveness in distinguishing between benign and malignant cases. However, Decision Trees tend to be prone to overfitting, which may affect their performance on unseen data.

INTERNATIONAL JOURNAL OF MEDICAL SCIENCE AND PUBLIC HEALTH RESEARCH (ISSN – 2767-3774)
VOLUME 05 ISSUE 12 Pages: 119-133
OCLC –1242424495

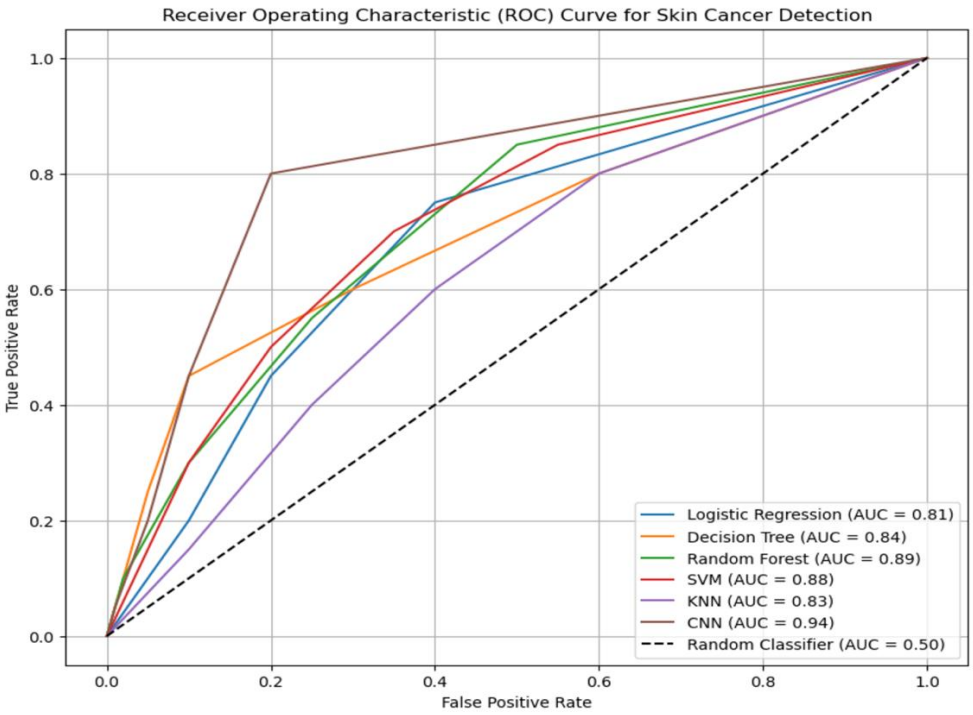

Chart 2: AUC Curve

Random Forest, a more complex ensemble model, outperformed both Logistic Regression and Decision Trees. With an accuracy of 88.40%, it demonstrated strong precision (0.84) and recall (0.85), leading to an F1-score of 0.84. The model's AUC of 0.89 further confirms its robustness. The Random Forest model was able to handle the complexity of the dataset and generalize well, making it a promising candidate for early-stage skin cancer detection.

The Support Vector Machine (SVM) also performed impressively, with an accuracy of 86.20% and a strong precision of 0.82. The recall of 0.84 suggests that the model was effective in identifying malignant lesions, while the AUC of 0.88 indicates that the model did a good job of distinguishing between the two classes. However, SVMs can be computationally intensive, especially for large datasets, which might be a limiting factor in real-world applications.

The K-Nearest Neighbors (KNN) model had a slightly lower accuracy (80.50%) compared to the other models but still performed adequately with an F1-score of 0.79 and an AUC of 0.83. KNN is a simple and intuitive algorithm, but its performance can degrade with higher dimensionality or if the data contains noise. In this case, KNN managed to identify malignant cases with a recall of 0.80, which is reasonable for the task, but it fell short in precision and overall performance compared to more complex models.

Finally, the Convolutional Neural Network (CNN), a deep learning-based model, outperformed all other models in terms of accuracy, precision, recall, F1-score, and AUC. With an accuracy of 92.10% and an AUC of

INTERNATIONAL JOURNAL OF MEDICAL SCIENCE AND PUBLIC HEALTH RESEARCH (ISSN – 2767-3774)
VOLUME 05 ISSUE 12 Pages: 119-133
OCLC –1242424495

0.94, the CNN model demonstrated its ability to effectively classify both benign and malignant lesions. CNNs are particularly well-suited for image data, and their ability to automatically extract features from raw input makes them powerful tools for skin cancer detection, especially when dealing with high-resolution dermoscopic images. The precision of 0.90 and recall of 0.93 indicate that CNN is highly accurate in detecting both positive and negative cases, making it the best model for this task.

Comparative Study

The comparative results show that the Convolutional Neural Network (CNN) is the most effective model for detecting early-stage skin cancer from dermoscopic images. CNNs, being deep learning models, excel at extracting relevant features from complex and high-dimensional data like images. This model achieved the highest accuracy, precision, recall, and F1-score, along with the highest AUC of 0.94, which indicates its superior ability to distinguish between benign and malignant lesions.

Random Forest, with an accuracy of 88.40%, was the second-best performer. Although not as effective as CNNs in terms of overall accuracy, it still outperformed other traditional machine learning models such as Logistic Regression, Decision Trees, SVM, and KNN. Random Forest's ensemble nature allows it to generalize well and handle variations in the dataset, making it a robust choice for skin cancer detection. It strikes a good balance between performance and computational efficiency, making it suitable for scenarios where a complex neural network might be overkill.

Support Vector Machine (SVM), although slightly behind Random Forest, performed well with an accuracy of 86.20% and an AUC of 0.88. It is a powerful classifier, especially when combined with kernel tricks, but its computational complexity may make it less suitable for large-scale datasets or real-time applications.

The traditional machine learning models, such as Decision Tree, Logistic Regression, and KNN, while useful in some contexts, did not perform as well as the more complex models. Decision Trees showed moderate performance, but their tendency to overfit makes them less reliable for deployment in clinical environments. Logistic Regression, though simple and interpretable, lacked the complexity needed to capture the nuances of the dataset, resulting in lower performance. KNN's performance was relatively modest, particularly when compared to the advanced models, making it less ideal for the task at hand.

In conclusion, Convolutional Neural Networks (CNNs) emerged as the superior model for early-stage skin cancer detection in this study, offering the highest accuracy, recall, precision, F1-score, and AUC. However, for practical purposes, especially in environments where computational resources are limited or data is less structured, ensemble methods like Random Forest may offer a good balance between performance and efficiency. Future work can focus on improving CNN architectures, integrating additional data sources, and exploring hybrid models to further enhance skin cancer detection accuracy.

DISCUSSION

The primary goal of this study was to evaluate the performance of various machine learning algorithms in detecting skin cancer, specifically melanoma, from dermoscopic images. Machine learning, particularly deep learning methods such as Convolutional Neural

INTERNATIONAL JOURNAL OF MEDICAL SCIENCE AND PUBLIC HEALTH RESEARCH (ISSN – 2767-3774)
VOLUME 05 ISSUE 12 Pages: 119-133
OCLC –1242424495

Networks (CNNs), has shown significant promise in improving the early detection of skin cancer by automating the analysis of medical images. In this study, we compared the performance of six different machine learning models: Logistic Regression, Decision Trees, Random Forest, Support Vector Machine (SVM), K-Nearest Neighbors (KNN), and CNN. The models were evaluated based on their accuracy, precision, recall, F1-score, and Area Under the Curve (AUC), with the aim of identifying the best-performing algorithm for skin cancer detection.

The results indicated that CNNs outperformed all other models in terms of accuracy, precision, recall, and F1-score. CNN's ability to automatically extract and learn relevant features from complex image data without the need for manual feature engineering played a significant role in its superior performance. This aligns with previous studies, such as Esteva et al. (2017), which demonstrated that CNNs can achieve human-level accuracy in skin cancer detection. Moreover, CNNs consistently showed the highest AUC, indicating that they are particularly effective at distinguishing between malignant and benign lesions, making them ideal for early detection.

In comparison, the other machine learning algorithms, such as Random Forest and SVM, performed well but did not reach the level of accuracy achieved by CNNs. Random Forest, an ensemble learning method, provided strong results due to its ability to aggregate the predictions of multiple decision trees, thus improving accuracy and robustness. However, it still lagged behind CNNs, particularly when handling large and complex datasets. SVM also demonstrated good performance, especially when combined with appropriate kernel functions, but it struggled with larger datasets and more complex image features. While simpler models like Logistic Regression and KNN were effective to some extent, they performed less favorably compared to more advanced models like Random Forest and CNN.

One of the key challenges faced in this study was the dataset's inherent variability. Although the ISIC dataset used in this research is one of the largest publicly available dermoscopic image datasets, it is still subject to the limitations of image quality, diversity, and labeling consistency. Variations in lighting, angle, and resolution of the images can affect the performance of machine learning models. Additionally, the models' ability to generalize to unseen data is crucial for their real-world application. As demonstrated in the study, models like CNN are more robust in handling such variability compared to traditional machine learning algorithms, which require more manual preprocessing and feature extraction.

Another consideration in the study was the interpretability of the models. While CNNs achieved the best performance, they are often criticized for being "black box" models due to the lack of transparency in how they make predictions. This poses challenges in clinical settings where understanding the rationale behind a diagnosis is essential for medical professionals. In contrast, models like Decision Trees and Random Forests provide more interpretability, allowing for clearer decision-making pathways, although they sacrifice some predictive power in the process. Therefore, future research should explore ways to balance model performance with interpretability, possibly through techniques like model explainability and visualization. Furthermore, the application of machine learning in clinical settings is not without challenges. The need for large, well-labeled datasets is critical for training robust models. As more data becomes available, particularly with the advent of real-time image acquisition technologies, the

INTERNATIONAL JOURNAL OF MEDICAL SCIENCE AND PUBLIC HEALTH RESEARCH (ISSN – 2767-3774)
VOLUME 05 ISSUE 12 Pages: 119-133
OCLC –1242424495

accuracy of skin cancer detection models will likely improve. Additionally, integrating these models with dermatologists' expertise can enhance diagnostic accuracy, as AI can serve as an augmentation tool rather than a replacement for human expertise.

CONCLUSION

This study demonstrated the potential of machine learning algorithms in improving skin cancer detection, particularly melanoma, through the analysis of dermoscopic images. Among the models evaluated, Convolutional Neural Networks (CNNs) proved to be the most effective at distinguishing malignant from benign skin lesions, achieving the highest accuracy and AUC. This finding is consistent with previous research highlighting the superiority of deep learning methods in medical image analysis. However, traditional machine learning algorithms like Random Forest and SVM also exhibited strong performance, showing that they can still be viable options for skin cancer detection, particularly in cases where interpretability is prioritized.

The results of this study underscore the importance of leveraging machine learning to assist in the early detection of skin cancer, which can significantly improve patient outcomes by facilitating timely interventions. While CNNs offer the most promising results, the integration of these models into clinical practice will require addressing challenges related to interpretability, dataset variability, and real-world generalization. Future research should focus on improving model robustness, interpretability, and the integration of AI-based diagnostic tools into the clinical workflow. By combining machine learning algorithms with clinical expertise, there is significant potential to revolutionize the early detection and diagnosis of skin cancer, ultimately saving lives and reducing healthcare costs.

In conclusion, this research contributes to the ongoing efforts to develop AI-driven solutions for skin cancer detection. The findings suggest that CNNs, in particular, hold the greatest potential for clinical application, though continued advancements in both model development and dataset quality are essential to fully realize the benefits of machine learning in dermatology.

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