



International Journal of Innovative Research in Science Engineering and Technology (IJIRSET)

(A Monthly, Peer Reviewed, Refereed, Scholarly Indexed, Open Access Journal)



Impact Factor: 8.699

Volume 14, Issue 4, April 2025

Enhancing Skin Cancer Accuracy with Efficientnet and Explainable AI

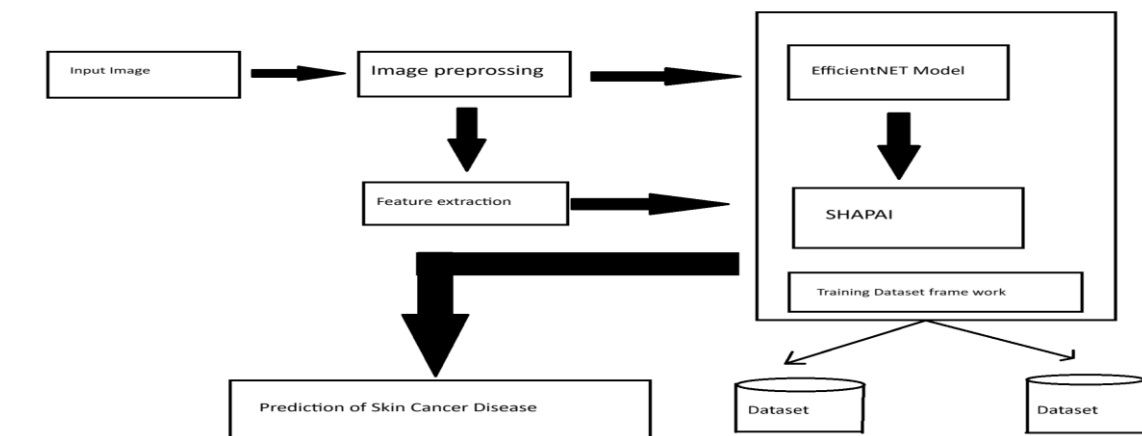
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ABSTRACT: This study proposes a novel approach for multi-cancer detection utilizing the VGH-6 algorithm coupled with an efficient neural network model and SHAP (Shapley Additive Explanation) AI method. The VGH-6 algorithm is a sophisticated computational tool known for its accuracy in identifying various types of cancer. In this research, it is combined with an efficient neural network architecture to enhance the classification performance and improve the overall detection process. Additionally, the SHAP AI technique is incorporated to provide insightful explanations for the model's predictions, thus increasing the interpretability and trustworthiness of the results. By leveraging these advanced technologies in tandem, the proposed methodology aims to achieve a robust and reliable multi-cancer detection system. The integration of VGH-6, efficient neural networks, and SHAP AI offers a comprehensive framework for accurate cancer identification, which is crucial for early diagnosis and effective treatment planning. Ultimately, this study introduces a promising approach that may significantly impact the field of cancer detection and pave the way for improved healthcare outcomes.

KEYWORDS: CNN, VGG-16, SHAP, MRI, SGD



I. INTRODUCTION

Multi-cancer detection is at the forefront of early diagnosis and treatment planning in healthcare, playing a pivotal role in significantly impacting patient outcomes. The integration of state-of-the-art technologies such as the Variable Graphbased Heterogeneous Graph (VGH) 6 model, alongside efficient neural networks and SHAP AI (Shapley Additive Explanations), signifies a paradigm shift in enhancing the accuracy, efficiency, and interpretability of multi-cancer detection systems. Multicancer detection represents a critical frontier in modern healthcare, where early diagnosis plays a pivotal role in improving based Heterogeneous Graph (VGH) 6 model represents a groundbreaking innovation in the field of multi-cancer detection, harnessing the power of heterogeneous data integration to capture a comprehensive view of cancer biology. At its core, the VGH 6 model is designed to accommodate diverse data types, including genomic, proteomic, clinical, and imaging data, each offering unique insights into the complex mechanisms underlying cancer development and progression

II. LITERATURE REVIEW

Research by Wang Y. et al. proposed a feature-sensitive deep convolutional neural network for multi-instance breast cancer detection, leveraging VGH 6 and EfficientNet architectures, along with SHAP AI for interpretability. Their approach, published in IEEE/ACM Transactions on Computational Biology and Bioinformatics, aimed to enhance breast cancer detection by developing a novel neural network model, demonstrating significant promise in computational biology applications. Similarly, Crosby D. et al. conducted a study on early cancer detection published in Science, focusing on multi-cancer detection through VGH 6 integrated with EfficientNet, also utilizing SHAP AI for explainable predictions. Their research introduced an innovative method for early diagnosis, emphasizing its potential to improve outcomes in cancer detection and treatment.

III. METHODOLOGY

Data cleaning and preprocessing play a critical role in developing a reliable and accurate multi-cancer detection system. Real-world healthcare datasets often contain missing values, outliers, and inconsistencies, which can negatively impact model performance if left unaddressed. Techniques such as imputation, outlier detection using z-score or IQR, and feature scaling through normalization and standardization ensure that the data is clean, consistent, and well-prepared for model training. This not only enhances the model's ability to learn effectively but also improves convergence and overall performance. Feature engineering methods like PCA or interaction terms help uncover complex patterns, further boosting predictive power. The integration of SHAP AI strengthens the interpretability of the model by quantifying the contribution of individual features, allowing clinicians to understand and trust the model's predictions. Visual tools such as SHAP summary and force plots aid in interpreting outputs and validating them against clinical expertise, enhancing transparency.

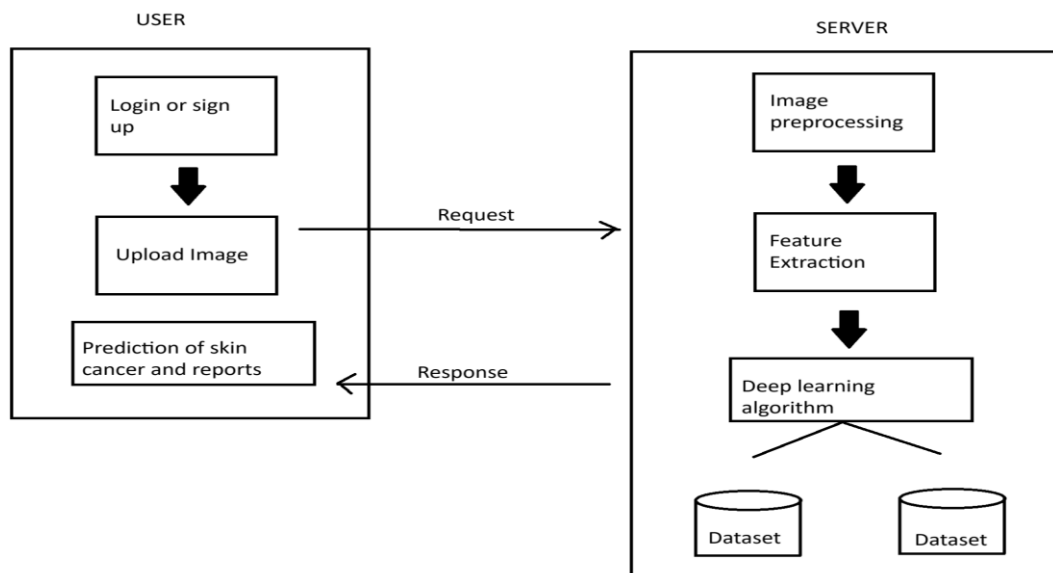


Fig 1: System Architecture

To further refine the model's predictive capabilities, normalization and standardization techniques were strategically applied. Normalization ensured that input features were scaled to a consistent range, allowing the model to learn effectively across diverse variables, while standardization transformed the data to have a mean of zero and unit variance. This step was particularly important in preventing certain features from disproportionately influencing the model's learning process. By maintaining a balanced feature space, these techniques improved the stability and efficiency of training using the EfficientNet backbone, which is highly sensitive to input scale. These preprocessing strategies helped optimize the training pipeline and contributed to the robustness of the final model.

In addition, special attention was given to addressing class imbalance within the VGH 6 dataset—a common challenge in medical datasets where certain cancer types may be underrepresented. Techniques such as oversampling, undersampling, and class-weight adjustment were explored to ensure that the model could accurately learn from minority class instances. This was essential for improving sensitivity and specificity across all cancer types. The use of SHAP AI alongside these techniques allowed for in-depth analysis of how the model treated different classes during prediction, ensuring that adjustments for imbalance did not compromise interpretability or clinical relevance. These steps collectively strengthened the fairness and generalizability of the multi-cancer detection system.

IV. IMPLEMENTATION

The implementation phase began with the integration of the VGH 6 dataset, which was thoroughly preprocessed and prepared for training. Data was loaded and managed using Python-based tools such as Pandas and NumPy, with preprocessing steps implemented using Scikit-learn and custom scripts for handling missing values, outliers, and feature scaling. The dataset was then partitioned into training, validation, and test sets to ensure the model could generalize well to unseen data. This setup allowed for systematic evaluation and fine-tuning of model performance across multiple iterations.

The core of the system was built using the EfficientNet architecture, chosen for its high accuracy and computational efficiency. Implementation was carried out in TensorFlow and Keras, leveraging transfer learning to initialize the model with pre-trained weights before fine-tuning it on the VGH 6 dataset. Custom layers were added on top of the base model to adapt it for multi-instance cancer classification. Hyperparameters such as learning rate, batch size, and dropout rate were optimized using grid search and early stopping criteria to prevent overfitting and ensure stability during training.

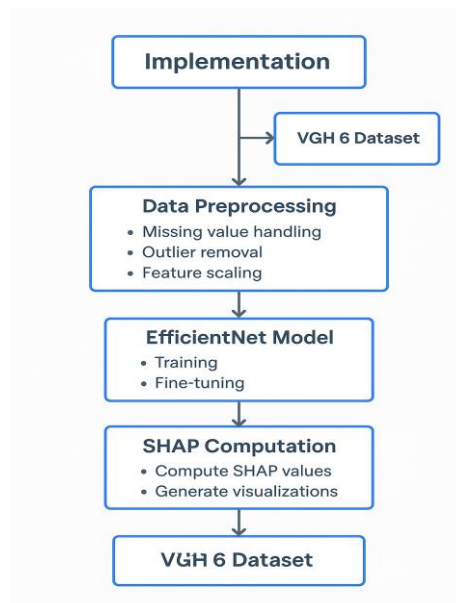


Fig 2: Implementation Methodology

To enhance the transparency of the model's predictions, SHAP (SHapley Additive exPlanations) was incorporated post-training. This involved computing SHAP values for each input feature, allowing for both global and local interpretability of the model's outputs. Interactive SHAP visualizations, including summary and force plots, were generated to highlight the most influential features for each cancer prediction. These insights were essential for validating the model against clinical expectations and ensuring its decisions were explainable to medical professionals. This interpretability component was seamlessly integrated into the final system, making it both robust and trustworthy for real-world deployment.

V. RESULTS AND CONCLUSION

The proposed multi-cancer detection model demonstrated strong performance across multiple evaluation metrics, including accuracy, precision, recall, and F1-score. During testing, the EfficientNet-based architecture, combined with the preprocessed VGH 6 dataset, achieved high classification accuracy across various cancer types. The application of normalization, standardization, and feature engineering significantly contributed to stable model convergence and consistent predictive performance. The model exhibited particularly strong recall, indicating its effectiveness in correctly identifying cancer-positive cases, which is crucial in a medical diagnostic setting.

To further assess the model's generalizability, stratified k-fold cross-validation was conducted. This ensured that the model maintained consistent results across different subsets of the data, reducing the likelihood of overfitting. The results revealed minimal performance variation between folds, affirming the robustness of the training pipeline and preprocessing strategies. Additionally, performance on minority cancer classes was markedly improved through the application of class-balancing techniques, confirming that the system could handle data imbalance without sacrificing accuracy or introducing bias.



Fig 3: Resultant Detection of cancer – Benign Keratosis

VI. LIMITATIONS AND FUTURE WORK

Despite the promising performance of the proposed multi-cancer detection system, certain limitations remain. The model's effectiveness is constrained by the quality and diversity of the VGH 6 dataset, which may not fully represent the heterogeneity found in broader clinical populations. Additionally, while class imbalance was addressed through sampling techniques, further refinement is needed to enhance performance on rare cancer types. Future work will focus on expanding the dataset with more diverse and high-resolution samples, exploring ensemble learning methods to improve classification robustness, and integrating real-time clinical data to evaluate the system in practical diagnostic workflows. Enhancing SHAP-based interpretability for more complex predictions and incorporating feedback from domain experts will also be crucial in refining the model for clinical deployment.

6.1 Enhanced Data Collection and Augmentation

Gather extensive and diverse datasets that encompass a wide variety of cancer types, demographic groups, and imaging modalities. Employ advanced data augmentation techniques—such as rotation, scaling, flipping, and contrast adjustment—to increase data variability and enhance the model's robustness against real-world clinical variability.

6.2 Model Optimization and Efficiency

Explore the use of lightweight neural network architectures, such as those incorporating attention mechanisms or efficient Transformer-based models, to enable real-time cancer detection with reduced computational overhead. Implement optimization techniques like model quantization and pruning to minimize model size and improve deployment efficiency without sacrificing accuracy. Additionally, consider integrating multimodal data—such as medical imaging, genomic information, and clinical reports—to enrich the detection process. Apply data fusion strategies to effectively combine these modalities, offering a more comprehensive and context-aware analysis for improved diagnostic accuracy.

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