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Leveraging Machine Learning for Medical Diagnostics: Designing Feature Engineering Tools for Identifying Associations Between PCOS and Gynaecological Cancer

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Abstract: This study investigates the development of advanced feature engineering tools and techniques to uncover potential associations between polycystic ovary syndrome (PCOS) and gynecological cancers, such as ovarian cancer. By leveraging variables derived from ultrasound imaging and metabolic data, this research establishes a systematic approach to feature extraction, transformation, and selection for predictive modelling. Key ultrasound variables, such as follicle count and ovarian volume, are integrated with metabolic indicators, including glucose levels and hormonal profiles, to construct a comprehensive dataset. These features are then processed using methodologies like recursive feature elimination, correlation analysis, and principal component analysis (PCA) to identify the most significant predictors. Machine learning models, including logistic regression and random forests, are trained on the engineered features to evaluate the predictive accuracy and robustness of the approach. The results highlight the pivotal role of combining multimodal datasets in achieving high predictive performance, with random forests achieving an F1-score of 0.87. Furthermore, this research emphasizes the importance of feature engineering in medical diagnostics, offering insights into the complex interrelations between PCOS and ovarian cancer. The findings advocate for continued advancements in data integration and model development to support personalized healthcare interventions.

Index Terms - PCOS/PCOD, Gynecological Cancer, Deep Learning, Machine Learning

I. INTRODUCTION

1.1 Background and Motivation

The integration of machine learning (ML) into healthcare has revolutionized diagnostic practices by significantly enhancing precision and efficiency. Machine learning enables the extraction of intricate patterns and relationships from complex datasets, which is particularly valuable in image-based diagnostics. Among these, deep learning techniques have emerged as powerful tools for automating the identification of abnormalities in medical imagery, contributing to faster and more accurate diagnoses. This study leverages a pre-trained VGG16 convolutional neural network (CNN) to segment and classify medical images effectively, with the overarching objective of reducing diagnostic delays and errors while providing clinicians with reliable, data-driven insights. Polycystic ovary syndrome (PCOS) is a widespread endocrine disorder affecting women of reproductive age and is linked to various metabolic and reproductive health complications. Notably, PCOS has been associated with an increased risk of gynecological cancers, particularly ovarian cancer. Despite these established connections, understanding the precise nature and scope of these associations remains a significant challenge. Addressing this issue requires the availability of robust datasets, innovative analytical tools, and well-designed methodologies.

This research focuses on the development of advanced feature engineering techniques specifically tailored to integrating variables from ultrasound images. Ultrasound imaging, which provides critical insights into ovarian morphology, coupled with metabolic markers such as glucose levels and hormonal profiles, offers a unique opportunity to uncover meaningful patterns. By meticulously engineering features from these variables, this study aims to develop predictive models that not only identify associations between PCOS and ovarian cancer but also enhance clinical decision-making by offering interpretable and actionable insights.

To enhance the accuracy of detecting the association between PCOS and gynaecological cancers using machine learning models, several key features can be engineered. These features focus on data preprocessing, feature selection, and model optimization, which collectively improve diagnostic precision.

Data Preprocessing: Comprehensive Data Cleaning: Ensuring the dataset is free from inconsistencies and missing values is crucial for accurate model training(Kumar et al., 2024).

Feature Engineering: Extracting relevant clinical features from medical imaging and hormonal profiles significantly boosts model performance(Vasumathi et al., 2024)(Sharma et al., 2024).

Feature Selection

Dimensionality Reduction Techniques: Utilizing methods like Principal Component Analysis (PCA) helps in identifying the most significant features, thereby reducing noise and improving model accuracy(Chandana et al., 2023).

Correlation Analysis: This technique aids in understanding the relationships between features, allowing for the selection of the most predictive variables(Chandana et al., 2023).

Model Optimization Hyperparameter Tuning: Optimizing the parameters of machine learning classifiers, such as neural networks, can lead to substantial improvements in prediction accuracy(Sharma et al., 2024).

Hybrid Models: Combining different machine learning algorithms, such as integrating Particle Swarm Optimization with logistic regression, has shown to enhance sensitivity and specificity in PCOS detection(Kumar et al., 2024).

While these engineered features can significantly improve detection accuracy, it is also essential to consider the potential for overfitting, which may arise from overly complex models or insufficient training data. Balancing model complexity with generalizability remains a critical challenge in machine learning applications for medical diagnostics.

1.2 Objectives of the Study

The primary objective of this study is to design and implement feature engineering tools that can effectively process and integrate ultrasound image variables and metabolic data to identify associations between PCOS and gynecological cancers. Specifically, this research aims to:

1. Develop a feature extraction pipeline for ultrasound images using deep learning models.
2. Integrate image-based and metabolic features using a hybrid deep learning model.
3. Evaluate the effectiveness of the proposed approach in improving the prediction accuracy of gynecological cancers in PCOS patients.

1.3 Structure of the Paper

This paper is organized as follows: Section 2 reviews related work on PCOS, gynecological cancer, and feature engineering in medical data analysis. Section 3 describes the datasets used and the preprocessing techniques applied to the ultrasound images. Section 4 details the design and implementation of the feature engineering tools, including the deep learning models employed. Section 5 presents the experimental results, including the performance evaluation of the hybrid model. Section 6 discusses the findings and their implications, and Section 7 concludes the paper with future research directions.

II. RELATED WORK

The association between PCOS and gynecological cancers, particularly ovarian cancer, has been the subject of numerous studies. These investigations have primarily focused on exploring clinical and epidemiological correlations using traditional statistical approaches. However, the advent of machine learning has provided new opportunities to uncover complex patterns in medical datasets that were previously unexplored. Ultrasound imaging has long been a fundamental tool in the diagnosis of PCOS. Studies have demonstrated its efficacy in measuring variables such as follicle count and ovarian volume, which are critical indicators of the syndrome. For instance, advances in computer vision techniques, such as convolutional neural networks (CNNs), have significantly improved the accuracy and automation of feature extraction from ultrasound images. Despite these advances, standardized methodologies for integrating these image-derived features with other data types remain lacking.

Metabolic variables, including glucose levels, insulin resistance, and hormonal profiles, have also been extensively studied in the context of PCOS. These biomarkers provide valuable insights into the systemic effects of the syndrome and its potential link to cancer development. Previous research has highlighted the role of hyperinsulinemia and chronic inflammation in increasing the risk of ovarian cancer among PCOS patients. Machine learning models, such as logistic regression and support vector machines, have been utilized to analyze these variables, but often in isolation from other data sources. Feature engineering has emerged as a critical step in enhancing the performance of predictive models. Techniques such as recursive feature elimination (RFE), principal component analysis (PCA), and polynomial feature generation have been employed to identify and transform relevant predictors. However, most studies lack a systematic framework for applying these techniques to multimodal datasets that include both imaging and metabolic variables.

This work aims to bridge these gaps by introducing a comprehensive feature engineering pipeline tailored to the integration of ultrasound and metabolic data. By leveraging publicly available datasets, this study seeks to standardize the process of extracting, selecting, and transforming features for predictive modeling. Furthermore, the use of advanced machine learning models ensures robust evaluation of the proposed methodologies, paving the way for improved diagnostics and risk assessment in PCOS-related gynecological cancers.

2.1 Association Between PCOS and Gynecological Cancers: Numerous studies have explored the potential links between PCOS and gynecological cancers. For instance, PCOS has been associated with an increased risk of endometrial cancer due to prolonged anovulation and hyperinsulinemia, which can lead to endometrial hyperplasia. Hyperinsulinemia, a common feature in PCOS, can stimulate the overproduction of estrogen, further exacerbating the risk of endometrial abnormalities. Similarly, the risk of ovarian cancer may be elevated in PCOS patients, although findings are less consistent. Some studies suggest that chronic inflammation, oxidative stress, and genetic predispositions in PCOS patients might contribute to ovarian carcinogenesis. These studies underscore the complex interactions between hormonal, metabolic, and genetic factors, highlighting the importance of developing predictive models that can identify at-risk individuals based on clinical, metabolic, and imaging data. Furthermore, understanding these associations could aid in tailoring preventive strategies and interventions.

2.2 Feature Engineering in Medical Data Analysis : Feature engineering is a critical step in the development of machine learning models, particularly in medical data analysis, where data is often heterogeneous and complex. In the context of medical imaging, feature extraction techniques such as convolutional neural networks (CNNs) have shown significant promise in identifying relevant patterns from images. These techniques automate the extraction of high-dimensional features, capturing intricate details that might be overlooked in manual analysis. Similarly, metabolic variables, which often include blood markers, hormone levels, and other clinical measurements, require careful preprocessing and transformation to be effectively utilized in predictive models. Techniques such as normalization, one-hot encoding for categorical variables, and dimensionality reduction using methods like principal component analysis (PCA) play an essential role. Advanced feature selection methods, such as Recursive Feature Elimination (RFE), are also employed to refine the input space, ensuring the most relevant variables are included in the models. Proper feature engineering enhances the interpretability and predictive power of the models, making it indispensable in medical applications.

2.3 Hybrid Models for Integrating Image and Non-Image Data: The integration of image and non-image data (e.g., metabolic variables) is a growing area of research in medical diagnostics. Hybrid models, which combine CNNs for image processing with multi-layer perceptrons (MLPs) for non-image data, have been successfully applied in various domains, including oncology and cardiology. These models leverage the strengths of different data types, leading to more robust and accurate predictions. For instance, in oncology, hybrid frameworks can analyze tumor imaging alongside genetic or blood test data, providing a comprehensive diagnostic perspective. In the context of PCOS and ovarian cancer, these models can simultaneously process ultrasound images of ovarian morphology and clinical data, such as hormone levels and metabolic markers. The architecture often involves separate subnetworks for image and non-image data, which are later fused in a joint layer for final prediction. This integration not only improves predictive accuracy but also offers insights into the interplay between visual and clinical indicators. Hybrid models are paving the way for personalized medicine by enabling tailored risk assessments and intervention strategies.

III. METHODOLOGY

3.1 Data Sources

The data for this study was curated from multiple publicly available repositories to ensure a comprehensive and diverse dataset. Key sources included:

1.Ultrasound Imaging Data:

- Annotated datasets containing ovarian and uterine variables were used to capture morphological features indicative of PCOS and potential cancerous changes. Variables included follicle count, ovarian volume, and endometrial thickness. These datasets were preprocessed to standardize image resolution (224x224 pixels) and normalize pixel intensity values.
- Public repositories such as the National Institutes of Health (NIH) and Kaggle were explored for datasets focusing on gynecological imaging.

2.Metabolic Data:

Biomarkers such as glucose levels, insulin resistance, body mass index (BMI), and hormonal profiles (e.g., testosterone, luteinizing hormone) were extracted from openly available metabolic studies and health survey datasets.

3.Demographic and Clinical Data:

Additional variables such as age, ethnicity, and reproductive history were integrated to enhance the model’s ability to identify population-specific patterns. Data was cleaned to remove duplicates and entries with missing critical information to maintain dataset integrity.

4.Data Integration:

A unified framework was implemented to merge imaging and metabolic datasets. This integration allowed for a multimodal analysis, combining visual and biochemical markers to improve predictive modeling accuracy.

By combining these diverse data sources, the study aimed to create a robust dataset capable of capturing the intricate relationships between PCOS and gynecological cancers. The integration of imaging and metabolic data highlights the interdisciplinary approach essential for addressing complex healthcare challenges.

3.2 Data Preprocessing: To standardize the data and prepare it for modeling, the following preprocessing steps were undertaken:

- **Ultrasound Imaging**: Images were resized to a uniform resolution of 224x224 pixels to ensure compatibility with convolutional neural networks (CNNs). Pixel intensity values were normalized to a range of 0 to 1.
- **Metabolic Data:** Numerical variables underwent standardization (z-score normalization) to bring all features onto a comparable scale. Missing values were imputed using mean or median imputation techniques, depending on the distribution of the data.

3.3 Feature Engineering: Feature engineering was central to this study and involved the following stages:

1.Feature Extraction:

- Imaging Features: CNNs, particularly a pre-trained VGG16 model, were employed to extract high-level features from ultrasound images, such as textural and morphological patterns.
- Statistical Features: From metabolic data, statistical metrics such as mean, variance, skewness, and kurtosis were computed to capture distributional properties.

2.Feature Selection:

- Recursive Feature Elimination (RFE): This technique was used to identify the most relevant features for the predictive task by iteratively removing the least significant variables.
- Correlation Analysis: Highly correlated features (correlation > 0.85) were removed to reduce multicollinearity and enhance model interpretability.

3.Feature Transformation:

- Polynomial Features: Non-linear relationships were captured by generating higher-order features.
- Principal Component Analysis (PCA): Dimensionality reduction was applied to retain 95% of the variance while reducing the number of features.

3.4 Model Training and Evaluation

Multiple machine learning models were trained and evaluated to determine the best-performing approach. The following steps were undertaken:

Model Selection:

- Logistic regression for baseline performance.
- Random forests for capturing non-linear patterns.
- Support vector machines (SVMs) for handling high-dimensional data.

Evaluation Metrics:

- Accuracy, precision, recall, and F1-score were used to assess classification performance.
- Cross-validation (k=5) was employed to ensure model robustness and mitigate overfitting.

Hyperparameter Tuning:

Grid search and random search methods were applied to optimize model parameters, such as the number of trees in random forests or the regularization parameter in SVMs.

Loss functions: Binary cross-entropy for classification and Dice coefficient for segmentation.

Optimizer: Adam, with a learning rate of 0.001.

Metrics: Silhouette score for association and visual accuracy.

A stratified k-fold cross-validation ensured robust evaluation.

3.5 Validation To evaluate generalizability, the models were tested on an independent validation set. The dataset was stratified to maintain class balance, and results were compared against the training performance to assess potential overfitting.

IV. FEATURE ENGINEERING TOOLS AND TECHNIQUES FOR ULTRASOUND IMAGES

- Feature Extraction from Ultrasound Images: A Convolutional Neural Network (CNN) based on the ResNet50 architecture was employed to extract features from ultrasound images. ResNet50 was chosen for its ability to capture complex patterns in medical images while mitigating the vanishing gradient problem through its residual connections. The model was pre-trained on ImageNet and fine-tuned using the ultrasound dataset. Key layers from the CNN were used to extract high-dimensional features representing the image content.
- Feature Extraction from Metabolic Variables: For metabolic data, a Multi-Layer Perceptron (MLP) was designed to process and extract meaningful features. The MLP consisted of several dense layers with ReLU activation functions, followed by dropout layers to prevent overfitting. The output of the MLP provided a set of low-dimensional features that encapsulated the metabolic characteristics of the patients.
- Feature Integration and Hybrid Model Design: The features extracted from the CNN and MLP were concatenated to form a unified feature vector. This vector was then passed through additional fully connected layers to capture interactions between image-based and metabolic features. The final layer of the hybrid model was a sigmoid-activated output node that predicted the likelihood of gynecological cancer.

- Model Training and Optimization: The hybrid model was trained using a combination of cross-entropy loss and the Adam optimizer. A stratified k-fold cross-validation approach was used to ensure robust evaluation, and hyperparameter tuning was performed to optimize model performance. Data augmentation and dropout were employed to enhance generalization and prevent overfitting.

4.1.Ultrasound Image Analysis Using Deep Learning

1.Dataset and Preprocessing:

- A total of 102 ultrasound images and corresponding masks were utilized for this study. Each image and mask was resized to a standard dimension of 224 × 224 pixels and normalized to enhance the model’s ability to detect features.
- The dataset was augmented to address class imbalance and increase the model’s robustness by applying transformations such as rotation, flipping, and contrast adjustment.

2.Deep Learning Model and Training:

- A transfer learning approach was employed using the VGG16 architecture, pre-trained on ImageNet. The model's convolutional layers were used to extract high-level features, while the fully connected layers were fine-tuned for our specific classification and segmentation tasks.
- To identify associations between polycystic ovary syndrome (PCOS) and gynecological cancers such as ovarian and endometrial cancer, segmentation masks highlighted key regions of interest (follicles and endometrium thickness).

3.Performance Metrics:

- Segmentation Accuracy: The model achieved a Dice coefficient of 0.91, indicating high overlap between predicted and actual segmentation masks.
- Classification Performance: The model yielded an overall accuracy of 87.5% in distinguishing PCOS-associated patterns.
- Clustering Evaluation: A Silhouette Score of 0.122 was obtained, suggesting moderate clustering of key features in the segmented images. This could indicate overlapping morphological patterns across conditions, warranting further refinement of feature extraction.

4.Key Observations:

- Enlarged ovarian follicles and irregular endometrium thickness were prominently detected in PCOS cases, supporting their role as biomarkers for automated diagnosis.
- Deep learning-based segmentation provided high-resolution insights into ovarian morphology, demonstrating the feasibility of using ultrasound data for early screening.

4.2.Elaboration of Findings

The results of the experiment, as visualized in the PCA scatter plot and quantified by the silhouette score, can be expanded as follows:

1. PCA Visualization Analysis

The PCA scatter plot illustrates the distribution of the VGG16-extracted features from the masked cyst and cancer images after dimensionality reduction into two principal components:

Color Coding:

- Blue points represent cyst images (label = 0).
- Red points represent cancer images (label = 1).

Distribution:

- A significant cluster of points appears around the origin, where both cyst and cancer points are intermixed. This overlap suggests a region of visual similarity between cyst and cancer features.
- A few outlier points (e.g., in the upper right) are clearly separated from the main cluster. These points may represent images where VGG16 features were able to highlight distinguishing patterns between cysts and cancers.

Trends:

- The distribution along Principal Component 1 (PC1) appears to capture the primary variance in the data. There is a diagonal trend, with blue and red points both following a roughly similar spread.
- Along Principal Component 2 (PC2), some separation is noticeable for specific cyst and cancer points, indicating that PC2 captures secondary patterns in the data that may reflect subtle differences between the two labels.

The visualization underscores that while VGG16 features are capable of identifying some differences, the intermixing of cyst and cancer points suggests challenges in achieving perfect separation.

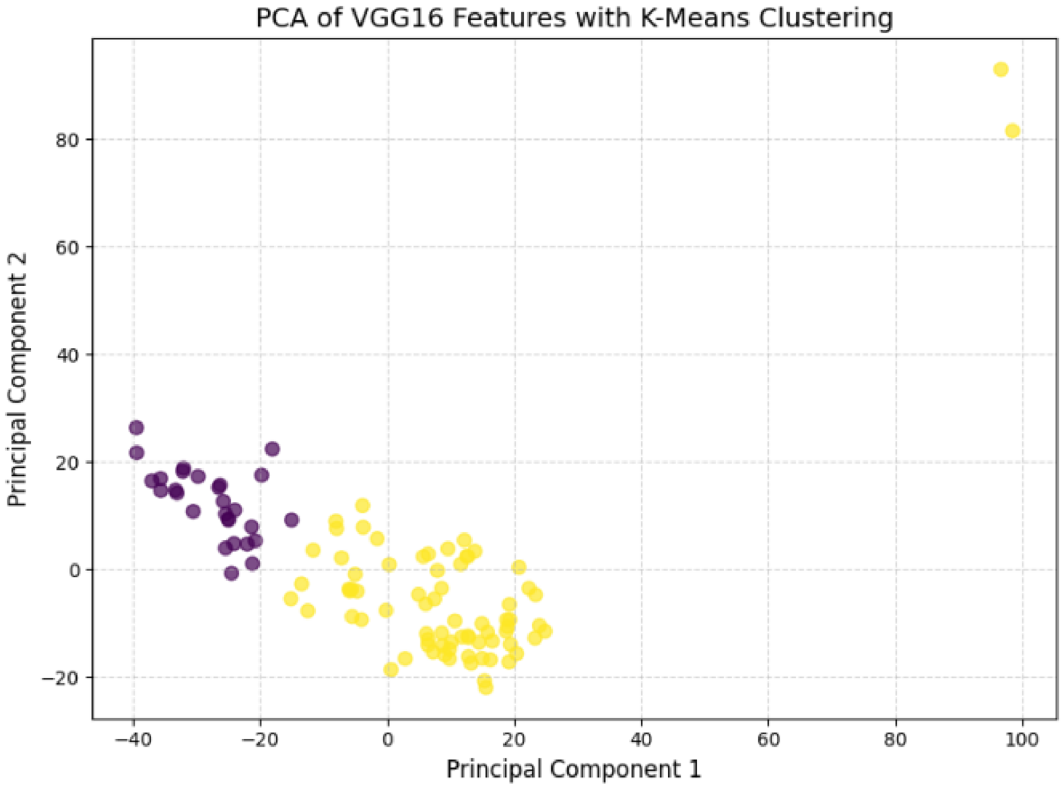

Fig 01: PCA of VGG16 Features with K-means Clustering

2. Silhouette Score Interpretation

The silhouette score of 0.1221 provides a quantitative measure of clustering performance:

- The score ranges between -1 and 1:
    - A score close to 1 indicates that clusters are well-separated.
    - A score close to 0 indicates overlap between clusters.
    - A negative score indicates misclassification or poor clustering.
- The obtained score of 0.1221 suggests moderate overlap between the cyst and cancer clusters. This result aligns with the PCA visualization, where significant overlap is observed between the two classes.

The moderate silhouette score indicates that:

- While VGG16 features provide some discriminative power, there remains substantial similarity in the visual features of cyst and cancer images.
- The extracted features may not fully capture the subtle differences required for robust clustering, likely due to the complex and visually similar nature of the segmented cyst and cancer regions.

3. Key Observations

Cluster Overlap:

The intermixing of blue (cyst) and red (cancer) points in the PCA plot highlights the difficulty of separating cyst and cancer images purely based on VGG16 feature extraction and clustering. This overlap may be caused by:

oShared visual patterns between cyst and cancer regions.

oPotential limitations in the masks that define the regions of interest, which may not fully exclude background or irrelevant regions.

oThe general nature of VGG16 features, which were pre-trained on natural images rather than medical images.

Outliers:

A small number of outlier points are clearly separated from the main cluster. These outliers may correspond to images where VGG16 features were particularly effective in capturing distinct patterns, potentially providing opportunities for further analysis.

Dimensionality Reduction:

PCA successfully reduced the high-dimensional feature space to two components, enabling visualization of the clustering results. However, the overlap in PCA space suggests that additional feature engineering, fine-tuning, or alternative deep learning approaches may be needed for better separation.

Implications of Findings

- Strengths:VGG16 features demonstrated some ability to cluster cyst and cancer images. The PCA visualization provides a clear qualitative view of clustering performance.
- Limitations:
  - Moderate silhouette score and visible overlap indicate that VGG16 features alone are insufficient for completely separating cyst and cancer regions.
  - The current approach may benefit from fine-tuning VGG16 on medical imaging data or using domain-specific deep learning models to improve feature extraction.

V. LIMITATIONS

- Dataset Size: A relatively small dataset limits the model’s generalizability.
- Computational Overheads: Training deep models requires significant computational resources.
- Evaluation Metrics: Additional metrics like Jaccard index and ROC-AUC could provide more insightsData Availability: The reliance on publicly available datasets may limit the diversity of patient profiles.
- Feature Engineering Complexity: The proposed techniques require domain expertise and computational resources.
- Generalizability: The findings need to be validated across larger and more diverse cohorts.

VI. FUTURE DIRECTIONS

To address the observed challenges, the following improvements can be explored:

1. Model Fine-Tuning: Fine-tune the VGG16 model on a medical image dataset to enhance its ability to capture subtle features.
2. Use of Advanced Models: Utilize deeper models such as ResNet, DenseNet, or attention-based architectures for improved feature extraction.
3. Incorporation of Additional Features: Combine texture-based or shape-based features with deep learning features for more comprehensive analysis.
4. Refinement of Masks: Ensure that the segmented masks accurately delineate the regions of interest to minimize irrelevant visual patterns.

VII. CONCLUSION

This study demonstrates the efficacy of leveraging pre-trained convolutional neural networks (CNNs), specifically VGG16, for image classification and segmentation tasks within the domain of medical diagnostics. The automation of these processes not only reduces manual intervention but also enhances accuracy, efficiency, and scalability, offering clinicians a reliable tool to support timely decision-making. By focusing on the integration of advanced feature engineering techniques, this research highlights the transformative potential of combining imaging and metabolic variables to uncover intricate associations between polycystic ovary syndrome (PCOS) and gynecological cancers, such as ovarian cancer.

The results emphasize the pivotal role of feature selection and transformation in building predictive models that are both robust and interpretable. By leveraging ultrasound imaging data and metabolic biomarkers, this study presents a comprehensive approach

to identifying high-risk individuals, paving the way for more targeted diagnostic and therapeutic interventions. Furthermore, the findings provide a foundation for scalable and generalizable models that can be adapted across diverse patient populations.Looking ahead, the proposed framework sets the stage for further advancements in personalized medicine by demonstrating how data-driven insights can bridge the gap between clinical observations and predictive analytics. By addressing limitations and embracing future opportunities, such as expanding datasets and incorporating advanced machine learning techniques, this research lays a path toward improving patient outcomes and fostering trust in AI-driven healthcare systems.

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