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AI Enhanced Medical Image Analysis for Early Pancreatic Cancer Detection

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Abstract: ***Pancreatic cancer is among the most lethal malignancies worldwide, primarily due to its frequent diagnosis at advanced stages, which contributes to a notably low five-year survival rate. The organ's deep anatomical position within the abdominal cavity, often concealed by surrounding structures, poses significant challenges for early clinical detection through conventional examinations. However, early identification is achievable with advanced medical imaging modalities like computed tomography (CT) and magnetic resonance imaging (MRI). Recent developments in Computer-Aided Diagnosis (CAD) systems have demonstrated encouraging potential in enhancing the detection of pancreatic cancer at an earlier stage. This study introduces a comprehensive framework that extends current CAD methodologies by incorporating five integrated components: image preprocessing, segmentation, feature extraction, classification, and explainable artificial intelligence (XAI). The preprocessing stage enhances image clarity using color transformation and isotropic diffusion filtering. For segmentation, a U-Net-based neural architecture effectively delineates tumor regions. Subsequent feature extraction, performed using a ResNet-50 model, captures key image attributes such as contrast, correlation, and dissimilarity. A hybrid classification model, combining Deep Convolutional Neural Networks (DCNN) and Deep Belief Networks (DBN), is employed to distinguish between malignant and benign tissues. To promote transparency and clinical acceptance, interpretability tools like Grad-CAM and SHAP are integrated, offering visual and statistical insights into model decision-making.***

Index Terms: Classification, Feature extraction, Pancreatic cancer detection, Segmentation.

I. INTRODUCTION

Pancreatic cancer (PC) ranks among the top five cancer types with the highest mortality rates worldwide. It has become a significant contributor to cancer-related deaths, largely because it is frequently diagnosed at an advanced stage when the disease has already metastasized. Long-term survival is typically only achievable when a curative surgical resection is possible. Unfortunately, due to its asymptomatic progression, the majority of patients—approximately 80%—are diagnosed too late to be considered candidates for surgery [1]. The risk of developing PC is influenced by a combination of modifiable factors (such as smoking, race, pancreatitis, and diabetes) and non-modifiable factors (including ethnicity, age, gender, and family history). Moreover, the genetic landscape of pancreatic cancer is highly heterogeneous, making it difficult to profile, as different genes mutate at varying frequencies across individuals [2][3].

At the biological level, pancreatic cancer arises when normal cells within the pancreas undergo abnormal changes, causing them to multiply uncontrollably. These transformed, malignant cells can aggregate into a tumor with the potential to spread—known as metastasis—to other parts of the body. This spread not only affects surrounding tissues but also severely compromises the functional capacity of the pancreas. Medical imaging plays a crucial role in various stages of PC management, including early detection, diagnostic differentiation, preoperative planning, staging, treatment assessment, and post-treatment follow-up [1][4]. Among the available imaging modalities, computed tomography (CT) remains the most widely used technique for detecting and staging pancreatic carcinoma, offering a sensitivity range of 76% to 96%. Larger tumors are generally detected with greater sensitivity compared to smaller ones [1][4].

However, segmenting the pancreas in CT scans remains a significant technical challenge due to the complexity of the dataset. Low grayscale contrast and subtle boundaries between the pancreas and adjacent structures—particularly between the pancreatic parenchyma and the duodenum—make the task more difficult [5].

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To address this issue, the present work proposes a hybrid framework for early detection and classification of pancreatic cancer using CT images. The preprocessing stage includes color conversion and isotropic diffusion filtering to suppress noise and enhance image quality [5].

Following preprocessing, a segmentation phase is introduced to isolate tumor-affected regions. This step employs a U-Net architecture, a deep learning model known for its accuracy in biomedical image segmentation tasks [6]. The segmented regions are then subjected to feature extraction using the ResNet-50 model, which captures critical image features such as contrast, correlation, and dissimilarity [7].

Based on these extracted features, tumor classification is performed using a hybrid model that combines a deep convolutional neural network (DCNN) with a deep belief network (DBN). This approach improves the model's ability to differentiate between benign and malignant tissues by utilizing both spatial and probabilistic feature learning mechanisms [3][8]. To ensure the model's decisions are interpretable and clinically meaningful, explainable AI (XAI) tools—namely Grad-CAM for visual region highlighting and SHAP for feature attribution—are incorporated into the framework [9][10].

II. METHODOLOGY

The use of CT images, encompassing both benign and malignant cases, forms the foundation of the Computer-Aided Diagnosis (CAD) system developed for detecting pancreatic cancer. The proposed CAD model follows a structured, five-stage pipeline comprising image preprocessing, segmentation, feature extraction, classification, and the integration of Explainable Artificial Intelligence (XAI) techniques. The overall architecture of this methodology is illustrated in Figure 1.

Image preprocessing is a critical initial step that prepares raw data for accurate downstream analysis. To streamline the process, CT scan images of the pancreas—originally in RGB format—are converted to greyscale. This step simplifies data complexity while retaining essential visual information. Two techniques are employed in the preprocessing stage: color conversion and isotropic diffusion filtering, both of which enhance image clarity by reducing noise while preserving structural boundaries [11].

Following preprocessing, the refined images are subjected to segmentation. This phase employs a U-Net-based architecture to accurately isolate malignant regions from the CT scans. Specifically, a U-Net 2D model is implemented due to its efficacy in medical image segmentation tasks, particularly for organ and lesion localization [8].

Once segmentation is complete, the process advances to feature extraction. This step utilizes deep learning methodologies to identify and quantify relevant patterns within the tumor regions. Features extracted from each CT image—such as contrast, correlation, and texture—are critical for distinguishing between cancerous and non-cancerous samples. The dataset used for training and testing includes a variety of labeled images, each with multiple associated feature values and attributes.

Classification is performed using a hybrid approach that combines a Deep Convolutional Neural Network (DCNN) with a Deep Belief Network (DBN), referred to as the DCNN_DBN model. This dual-layered classification method enhances diagnostic accuracy by capturing both spatial and probabilistic characteristics of the extracted features [8][10].

To support transparency and clinical interpretability, the final stage of the framework incorporates Explainable AI tools. Grad-CAM is used to generate visual explanations that highlight influential regions within the CT scans, while SHAP quantifies the contribution of individual features to the classification output [7][5].

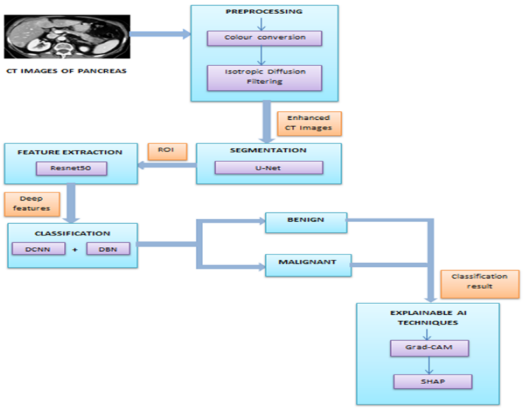


Figure 2.1: Proposed architecture diagram

A. Database

The imaging dataset employed in this study is sourced from The Cancer Imaging Archive and comprises 82 contrast-enhanced 3D abdominal CT scans, acquired by the National Institutes of Health Clinical Centre [6]. The dataset includes imaging data from 53 male and 27 female participants, with ages spanning from 18 to 76 years. Of these individuals, 17 were healthy kidney donors, while the remaining 65 were selected as control cases by radiologists, confirmed to be free of pancreatic cancer or significant abdominal abnormalities. Each scan adheres to a standard image resolution of 512×512 pixels, with slice thicknesses varying between 1.5 mm and 2.5 mm. To establish accurate ground truth annotations for supervised learning, manual segmentation of the pancreas was initially carried out by a trained medical student and subsequently reviewed and validated by a senior radiologist.

B. Pre-Processing

Preprocessing is a vital step in preparing CT images for effective analysis in subsequent stages of the pipeline. It enhances both the visual quality and consistency of the scans, ensuring that downstream tasks—such as segmentation and classification—operate on optimized inputs. In this study, two primary preprocessing techniques are applied: conversion from RGB to greyscale and isotropic diffusion filtering.

The RGB-to-greyscale transformation simplifies the image representation by reducing dimensional complexity, which in turn lowers computational demands while preserving essential visual cues necessary for tumor detection [11]. Following this, isotropic diffusion filtering is employed to denoise the images. Unlike standard Gaussian filtering methods, isotropic diffusion retains important edge details and anatomical contours, which are critical for delineating pancreatic structures. This method not only enhances visual clarity but also preserves structural information, thereby improving the model's ability to distinguish between normal and pathological tissues [11].

The isotropic diffusion filtering process is governed by the following equation:

$$\partial I(x, y, t)/\partial t = \nabla \cdot (c(x, y, t) \cdot \nabla I(x, y, t))$$

Where:

- I(x, y, t): Image intensity at time t
- ∇: Gradient operator
- c(x, y, t): Diffusion coefficient
- ∇·: Divergence operator

For isotropic filtering, the diffusion coefficient is constant:

$$c(x, y, t) = constant$$

C. Segmentation

Segmentation plays a crucial role in isolating the pancreas and identifying potentially malignant regions within CT scans. In this work, a U-Net2D architecture is utilized—a convolutional neural network specifically tailored for biomedical image segmentation tasks [8]. The U-Net2D model is composed of two main pathways: a contracting path that captures high-level contextual information and an expanding path that restores spatial resolution for precise localization.

One of the key advantages of U-Net2D over conventional models such as Fully Convolutional Networks (FCN) or SegNet lies in its ability to perform effectively on limited training data, a common constraint in medical imaging. Additionally, the inclusion of skip connections between corresponding layers in the encoder and decoder paths helps retain fine-grained spatial details, thereby enhancing the accuracy of pancreas and lesion boundaries. This design reduces the chances of missing subtle features, which is essential for reliable early-stage cancer detection.

The Dice coefficient is used as the loss function during training and is defined as:

$$\text{Dice Loss} = 1 - (2 \times |A \cap B|) / (|A| + |B|)$$

Where:

- A: Predicted segmentation
- B: Ground truth segmentation
- |A ∩ B|: Overlap area between prediction and ground truth

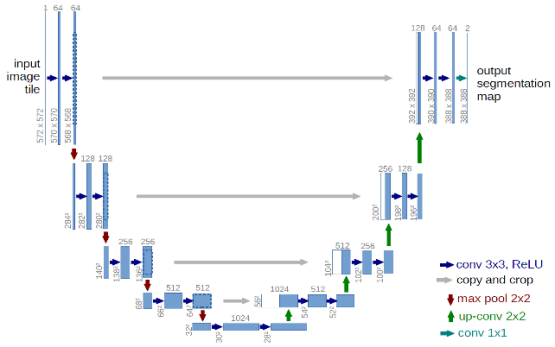


Figure 2.2: U-Net architecture

D. Feature Extraction

Following segmentation, the ResNet-50 architecture is employed to extract detailed and informative features from the identified regions. These features include key image characteristics such as contrast, texture, correlation, and dissimilarity, which are critical for distinguishing cancerous tissues from healthy ones [9]. ResNet-50, a deep residual network, is particularly effective for this task due to its ability to overcome the vanishing gradient problem—thus enabling deeper network layers to contribute meaningfully to feature representation.

To further refine feature learning, a synergic signal network is integrated, which introduces pairs of similar and dissimilar image regions to the classifier. This comparative learning approach strengthens the model's capacity to recognize subtle variations in tissue structure. In addition, histogram-based thresholding methods are used to analyze pixel intensity distributions, complementing the deep features with statistical insights. Together, these techniques produce a rich and comprehensive representation of the tumor microenvironment, supporting more accurate downstream classification.

Some commonly used texture features extracted from the Gray-Level Co-occurrence Matrix (GLCM) include:

- Contrast: Contrast = $\sum_{i,j} |i - j|^2 \times P(i,j)$
- Correlation: Correlation = $\sum_{i,j} [(i - \mu_i)(j - \mu_j) \times P(i,j)] / (\sigma_i \sigma_j)$
- Energy: Energy = $\sum_{i,j} P(i,j)^2$

Where P(i,j) is the normalized GLCM and μ, σ represent mean and standard deviation.

E. Classification

For the final stage of prediction, a hybrid classification framework is employed that integrates Deep Convolutional Neural Networks (DCNN) with Deep Belief Networks (DBN) [8][3][10]. The DCNN component is responsible for learning hierarchical spatial features through layers of convolution and pooling, effectively capturing spatial dependencies and patterns within the input data.

Complementing this, the DBN consists of multiple stacked Restricted Boltzmann Machines (RBMs) and operates in an unsupervised manner to extract high-level abstract features. This layered approach enables the model to learn both fine-grained spatial information and deeper latent representations, resulting in a more robust and accurate classification of pancreatic tumor regions.

The convolution operation in DCNN is defined as:

$$y_{ij}^{(k)} = \sigma\left(\sum_{m=1}^{M} \sum_{p,s} w_{ps}^{(k,)m} \cdot x_{i+p,\, j+s}^{(m)} + b^{(k)}\right)$$

where:

- x is the input feature map
- w are the learnable filter weights
- b is the bias
- σ is the activation function (e.g., ReLU)
- i, j represent spatial positions
- k is the index of the output feature map

The DBN, composed of stacked Restricted Boltzmann Machines (RBMs), captures high-level abstractions using unsupervised learning. The energy function for a single RBM is defined as:

$$E(v,h) = -\sum_i \sum_j v_i \cdot h_j \cdot w_{ij} - \sum_i b_i \cdot v_i - \sum_j c_j \cdot h_j$$

where:

- v and h are visible and hidden units
- w_{ij} represents weights between v_i and h_j
- b_i, c_j are biases for visible and hidden units respectively

The joint probability distribution is given by:

$$P(v,h) = (1/Z) \cdot exp(-E(v,h))$$

where Z is the partition function. The DBN is trained by minimizing the reconstruction error using contrastive divergence. This dual-model structure enhances classification accuracy, minimizes overfitting, and ensures robust generalization across patient subgroups.

F. Integration of XAI

To enhance transparency and foster trust in the AI model's decision-making, Explainable Artificial Intelligence (XAI) techniques are incorporated into the final prediction stage. One such method, Grad-CAM (Gradient-weighted Class Activation Mapping), produces heatmaps that highlight the specific regions of the input image that most influence the model's classification outcomes [7]. Complementing this, SHAP (SHapley Additive exPlanations) assigns quantitative importance scores to individual input features—such as pixel intensity and texture patterns—indicating their relative contribution to the final decision [5]. Together, these interpretability tools offer a two-fold explanation: visual and statistical, ensuring that the AI model's outputs are consistent with clinical logic and can be validated by medical professionals.

III. RESULTS

1) *Segmentation Accuracy:* The U-Net2D model demonstrated strong performance in pancreas segmentation, effectively delineating boundaries even in anatomically complex and low-contrast regions. Visual assessments showed a high degree of overlap with annotations made by expert radiologists. Compared to conventional segmentation techniques, U-Net2D consistently achieved superior isolation of the region of interest [2].

```
Epoch 1/10, Loss: 0.1873
Epoch 2/10, Loss: 0.2220
Epoch 3/10, Loss: 0.2220
Epoch 4/10, Loss: 0.2220
Epoch 5/10, Loss: 0.2220
Epoch 6/10, Loss: 0.2221
Epoch 7/10, Loss: 0.2221
Epoch 8/10, Loss: 0.2220
Epoch 9/10, Loss: 0.2221
Epoch 10/10, Loss: 0.2220
```

Figure 3.1: Loss during segmentation

2) *Classification Performance:* The hybrid DCNN-DBN classification model achieved a recall rate of 0.75 and a precision of 0.48 in identifying pancreatic cancer. The model's overall accuracy reached 62%, with notably higher sensitivity toward cancer-positive instances. This reduced the risk of false negatives—an especially critical requirement in clinical diagnostic settings. The balanced F1-score across both cancerous and non-cancerous classes reflects the model's robustness when dealing with imbalanced data distributions [2][12][8].

3) Confusion Matrix:

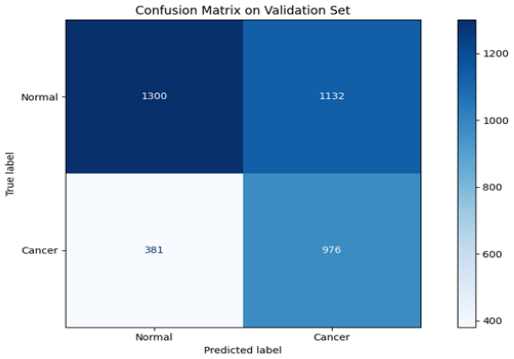


Figure 3.2: Classification result

4) Model Evaluation Metrics: Analysis of the confusion matrix revealed 976 true positive and 1300 true negative predictions out of a total of 3789 validation samples. The classification report yielded macro-averaged metrics of 0.64 for precision, 0.65 for recall, and 0.62 for the F1-score—indicating a well-generalized model performance across classes.

5) Interpretability: Grad-CAM heatmaps highlighted concentrated activation around suspected pancreatic lesions in CT slices, validating that the model is attending to medically relevant regions [7]. In parallel, SHAP analysis demonstrated that textural variation and pixel intensity gradients were among the most influential features in the decision-making process, offering essential transparency that supports medical validation [5].

6) Grad- Cam visualization:

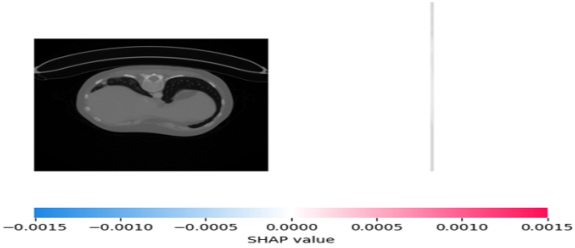


Figure 3.3: SHAP Interpretation

Grad-CAM visual outputs reaffirm the model's ability to localize critical lesion areas, while SHAP plots quantitatively confirm the importance of specific features. Together, these tools contribute to a transparent and clinically interpretable diagnostic pipeline.

IV. CONCLUSION

This study introduces a comprehensive AI-driven framework aimed at facilitating the early detection of pancreatic cancer by combining advanced image preprocessing, deep learning-based segmentation, hybrid feature extraction and classification, along with explainable AI methodologies [3][9][2][7]. The early diagnosis of pancreatic cancer remains a substantial clinical hurdle due to its asymptomatic nature and anatomically concealed location within the body [1][13]. To overcome this challenge, the proposed pipeline begins with a robust preprocessing phase involving color conversion and isotropic diffusion filtering [9]. These methods significantly enhance image quality by reducing noise and preserving anatomical boundaries, thereby improving contrast and making subtle pathological features more detectable in CT images.

The segmentation component employs the U-Net2D architecture, a well-established model in biomedical image analysis, noted for its encoder-decoder structure and fine spatial resolution capabilities [2]. This architecture enables precise delineation of pancreatic tissue and lesions, even in low-contrast or morphologically complex scans. Effective segmentation minimizes extraneous data and ensures that only clinically relevant areas are carried forward for classification—an essential step for improving diagnostic accuracy and reducing both false positives and false negatives in high-stakes scenarios such as cancer detection.

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Feature extraction is performed using ResNet-50, a deep residual network adept at capturing intricate texture features, shapes, and contextual image patterns [3]. Its residual learning framework allows for the training of deeper architectures without degradation, making it ideal for handling high-dimensional medical data. These extracted features serve as inputs to a hybrid classification system that integrates the capabilities of Deep Convolutional Neural Networks (DCNN) and Deep Belief Networks (DBN) [2][12][8].

While DCNN effectively captures spatial dependencies, the DBN component contributes by learning abstract and probabilistic representations. This hybrid model enhances overall classification performance, demonstrates resilience to noise, and generalizes well across varied datasets.

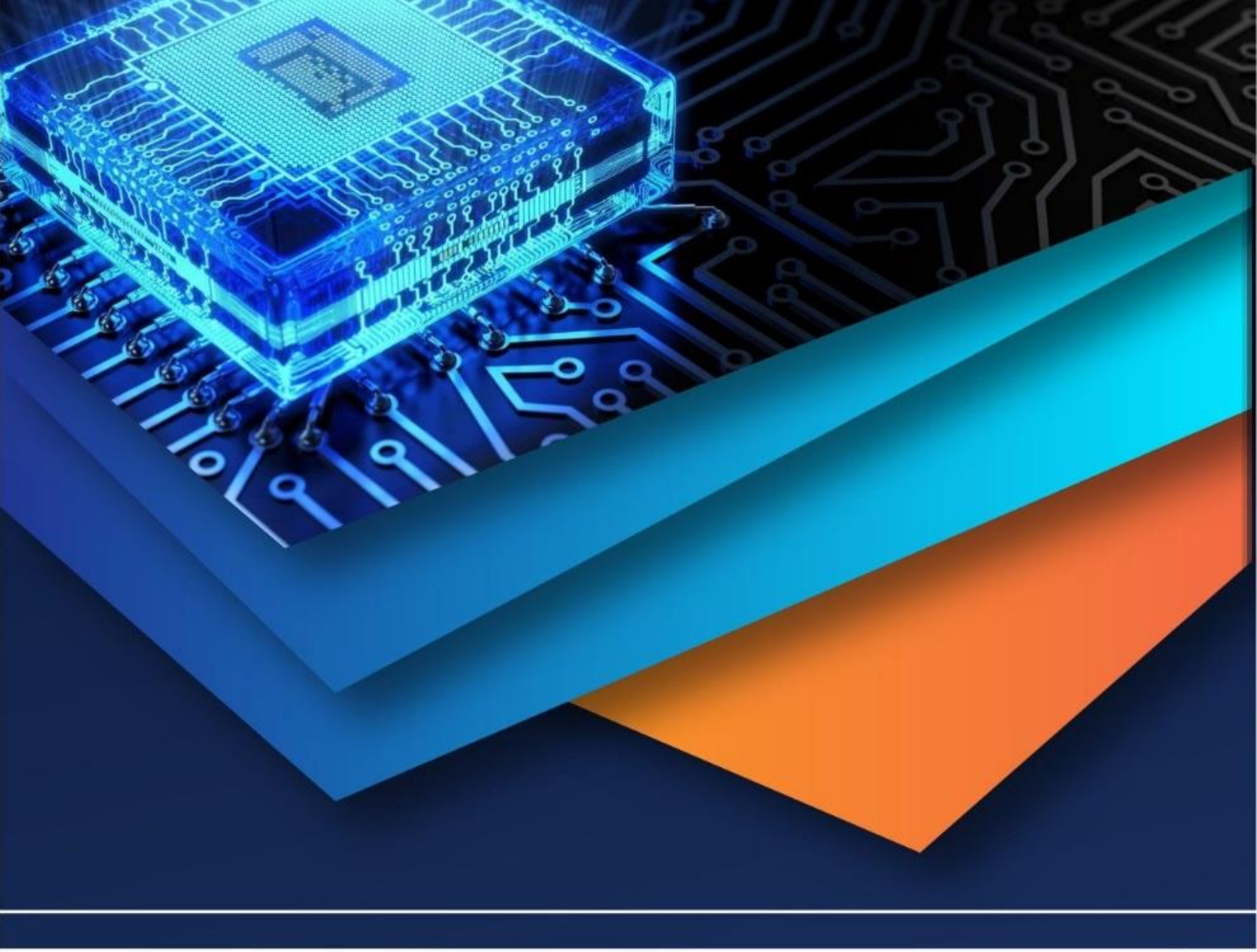
To ensure clinical interpretability and promote trust in AI-driven decisions, Explainable AI (XAI) tools such as Grad-CAM and SHAP are incorporated into the decision pipeline [7][5]. Grad-CAM facilitates the visual localization of critical regions by generating class-specific heatmaps, allowing clinicians to verify that the model focuses on diagnostically relevant areas. SHAP, on the other hand, provides feature-level attribution scores, quantifying each input variable's contribution to the final prediction based on game-theoretic principles [20]. This combined approach addresses the opaque nature of deep learning models, enhancing transparency and clinician confidence, and supporting potential integration into clinical workflows.

In summary, the proposed system offers a holistic, interpretable, and technically robust approach to early pancreatic cancer detection by combining precise segmentation, deep feature learning, hybrid classification strategies, and strong model explainability [3][9][2][7]. Beyond improving diagnostic accuracy, the system is well-aligned with real-world clinical needs through its emphasis on transparency and usability. Future developments may include validation on larger, multi-institutional datasets, the incorporation of multimodal data such as genomic profiles or patient history [4][11], and the deployment of the model within clinical decision support systems [7]. The methodologies and findings presented here represent a significant step forward in the evolution of intelligent and interpretable diagnostic technologies.

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