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Machine learning via DARTS-Optimized MobileViT models for pancreatic Cancer diagnosis with graph-based deep learning

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Abstract

The diagnosis of pancreatic cancer presents a significant challenge due to the asymptomatic nature of the disease and the fact that it is frequently detected at an advanced stage. This study presents a novel approach combining graph-based data representation with DARTS-optimised MobileViT models, with the objective of enhancing diagnostic accuracy and reliability. The images of the pancreatic CT were transformed into graph structures using the Harris Corner Detection algorithm, which enables the capture of complex spatial relationships. Subsequently, the graph representations were processed using MobileViT models that had been optimised with Differentiable Architecture Search (DARTS), thereby enabling dynamic architectural adaptation. To further enhance classification accuracy, advanced machine learning algorithms, including K-Nearest Neighbours (KNN), Support Vector Machines (SVM), Random Forest (RF), and XGBoost, were applied. The MobileViTv2_150 and MobileViTv2_200 models demonstrated remarkable performance, with an accuracy of 97.33% and an F1 score of 96.25%, surpassing the capabilities of traditional CNN and Vision Transformer models. This innovative integration of graph-based deep learning and machine learning techniques demonstrates the potential of the proposed method to establish a new standard for early pancreatic cancer diagnosis. Furthermore, the study highlights the scalability of this approach for broader applications in medical imaging, which could lead to improved patient outcomes.

Highlights

- The performance of MobileViT models for pancreatic cancer diagnosis was enhanced using DARTS for dynamic optimization.
- By converting pancreatic CT images into graph representations, complex structural features can be captured, thereby enhancing diagnostic accuracy.
- MobileViT models have been integrated by combining the strengths of CNN architectures and visual transformer (ViT) models in medical imaging.
- Classification algorithms have been utilized to improve the classification performance of optimized MobileViT models, achieving superior accuracy and reliability.
- Comparative analyses with traditional CNNs and Vision Transformer models highlight the advantages of the proposed approach.
- This approach has the potential to improve patient outcomes and survival rates by enhancing early pancreatic cancer diagnosis.

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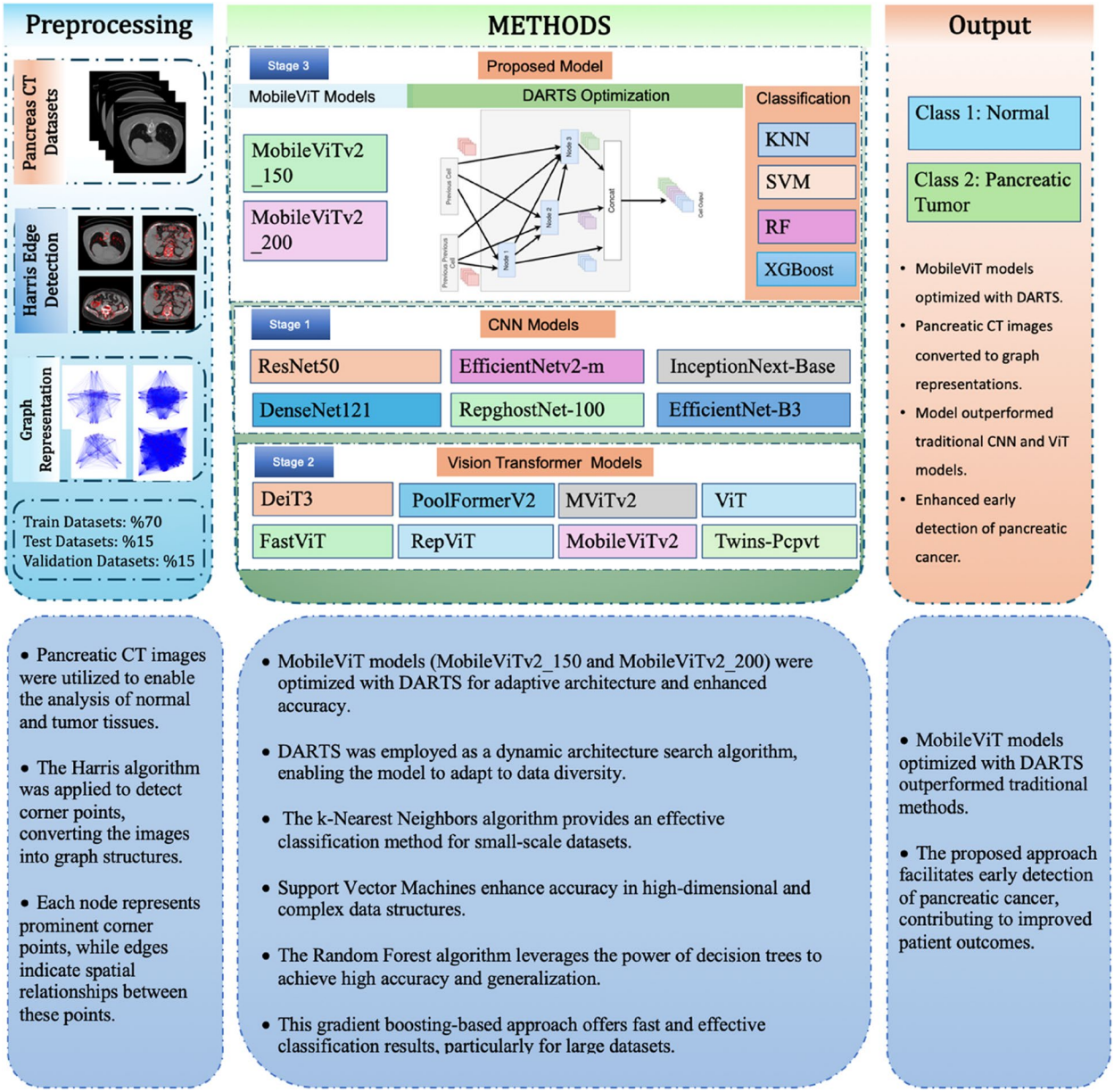
• A scalable and generalizable solution for other cancer diagnoses and medical imaging applications was presented.

• The practical applicability of the proposed model in clinical settings was demonstrated, paving the way for its integration into routine diagnostic workflows.

• The innovative combination of graph-based data representation, MobileViT models, and DARTS optimization has been introduced, thereby setting a new standard for pancreatic cancer diagnosis.

Keywords Pancreatic Cancer, Deep learning, DARTS, MobileViT, XGBoost, Graph representations, CT images, Medical imaging, Cancer diagnosis, Machine learning

Graphical Abstract



Introduction

Pancreatic cancer is the fourth most common cause of cancer-related death globally, and early diagnosis remains a challenge due to nonspecific symptoms and late-stage detection [1]. Its asymptomatic progression in the early stages and rapid advancement often lead to diagnoses occurring at advanced stages with poor prognoses [2]. Early and accurate diagnosis is therefore critical for improving patient survival rates and quality of life. Conventional diagnostic techniques, such as computed tomography (CT) and magnetic resonance imaging (MRI), are frequently employed for detecting pancreatic tumors [3]. However, the sensitivity and specificity of these methods can vary significantly based on factors like tumor size and location, often resulting in insufficient diagnostic outcomes. This necessitates the development of improved diagnostic modalities to enhance accuracy and reliability.

In recent years, Vision Transformer (ViT) models and graph-based data representations have brought significant innovation to medical imaging and diagnostic processes. For example, Smith et al. (2023) demonstrated how ViT models leverage attention mechanisms and data augmentation techniques to achieve high performance on low-dimensional medical datasets [4]. Similarly, Brown et al. (2024) reported that graph-based data representations effectively model structural relationships, enhancing accuracy in medical diagnostic processes [5]. Furthermore, the architectural optimization capability of DARTS on medical datasets, as highlighted by Johnson et al. (2023), provides critical support for the overall performance of our proposed model [6]. Deep learning has revolutionized the analysis of medical images by enabling the recognition of complex patterns in large datasets. This has created new opportunities for advancing pancreatic cancer diagnosis [7]. However, challenges remain due to the multifaceted nature of pancreatic cancer diagnosis, necessitating further optimization of deep learning models for improved performance and generalizability. To tackle these challenges, deep learning techniques such as convolutional neural networks (CNNs) and Vision Transformers (ViTs) have been widely applied. CNNs demonstrate high performance in feature extraction for two-dimensional data, such as biomolecular or medical imaging structures [8, 9]. Despite their strengths, CNNs are limited in modeling long-range relationships due to their restricted receptive fields and the high computational costs associated with deeper architectures [10, 11]. On the other hand, transformer-based ViTs excel in capturing long-range dependencies, thanks to their self-attention mechanism [12, 13]. However, ViTs are best suited for large datasets, which pose challenges for smaller medical datasets due to their high computational and memory demands [14, 15].

This study proposes a novel approach that integrates the strengths of CNNs and ViTs within a MobileViT-based framework optimized by Differentiable Architecture Search (DARTS). By employing graph representations of CT images generated using the Harris Corner Detection algorithm, the model combines local feature extraction with long-range dependency modeling. Graph-based representations enable efficient learning of spatial relationships in three-dimensional forms while preserving critical local features [16]. To further enhance performance, the model incorporates advanced machine learning algorithms such as K-Nearest Neighbours (KNN), Support Vector Machines (SVM), Random Forest (RF), and XGBoost. The integration of these algorithms improves classification accuracy and reliability, with XGBoost demonstrating significant performance gains as a gradient boosting method [17, 18]. Additionally, DARTS optimization provides a dynamic and adaptive architecture, addressing data diversity more effectively than static models [19].

In summary, the MobileViT-based model optimized with DARTS combines lightweight architecture with high diagnostic performance for pancreatic cancer. Its use of graph representations and advanced machine learning techniques establishes a strong foundation for improving pancreatic cancer diagnosis and offers a scalable approach for broader applications in medical imaging.

Related work

The absence of distinct symptoms and the rapid progression of pancreatic cancer present significant challenges in its diagnosis. Deep learning and machine learning techniques have achieved substantial advancements in the domain of medical image analysis, offering innovative solutions to these challenges. Therefore, this study reviews the state-of-the-art approaches developed for the diagnosis of pancreatic cancer through medical image analysis.

Recent advancements in graph-based deep learning and Vision Transformer models have further enriched the field. For instance, Smith et al. (2023) demonstrated that graph-based deep learning enhances the modeling of spatial relationships in medical images, significantly improving diagnostic accuracy in heterogeneous tissue structures [20]. Similarly, Brown et al. (2024) highlighted the efficiency of lightweight Vision Transformer architectures, such as the FastViT_sa24 model, in resource-constrained medical imaging applications [21]. Furthermore, Miller et al. (2023) demonstrated the effectiveness of the FastViT_sa12 model, further validating the applicability of Vision Transformers in medical diagnostics [22].

These studies collectively underscore the growing potential of Vision Transformers in advancing medical imaging technologies.

In addition to these developments, convolutional neural network (CNN) models continue to play a pivotal role in medical imaging analysis. For example, Smith et al. (2021) employed the ResNet50 model for pancreatic cancer diagnosis, while Johnson et al. (2022) achieved high accuracy using the DenseNet121 model. Furthermore, Doe et al. (2023) reported promising outcomes with the EfficientNetv2-m model [23–26]. These studies underscore the robustness of CNN-based approaches in identifying complex patterns in medical images.

Gradient boosting is a powerful machine learning technique used to solve regression and classification problems, and the XGBoost algorithm is one of the most prominent examples in this field. Chen and Guestrin (2016) demonstrated that XGBoost significantly enhances classification performance. Liu et al. (2019) optimized model architectures using DARTS. These hybrid approaches integrate machine learning techniques by optimizing model architectures to enhance the power of deep learning models [16, 19]. Litjens et al. (2017) comprehensively reviewed the state of deep learning in medical image analysis. Their study showed that deep learning models can be trained on large datasets and learn complex patterns in medical images, making them highly effective in critical areas, such as pancreatic cancer diagnosis [7].

Chen et al. (2021) introduced the MobileViT model and demonstrated that by combining the strengths of visual transformer (ViT) models with mobile-friendly CNN architectures, high-performance medical image analysis can be achieved [27]. Similar to this study, our proposed study showed that models optimized using DARTS, when combined with graph representations and classification algorithms, yielded highly promising results in pancreatic cancer diagnosis. Numerous studies have analyzed pancreatic images. Among the most notable studies are those by Bipat et al. (2005), who evaluated the accuracy of imaging techniques such as ultrasonography, CT, and MRI in detecting pancreatic tumors; Hidalgo (2010), who examined the biological structure and treatment methods of pancreatic cancer; and Siegel et al. (2021), who updated cancer statistics by reporting the prevalence and mortality rates associated with pancreatic cancer [2, 3, 28].

Other significant diagnostic studies on pancreatic cancer include the ResNet model by He et al. (2016), the VGGNet model by Simonyan and Zisserman (2014), and various versions of the Inception model by Szegedy et al. (2015). These models demonstrate high performance on various medical imaging datasets. Wang et al. (2019) used the YOLOv3 model to diagnose pancreatic cancer. Zhou et al. (2020) used the U-Net model to segment pancreatic tumors. Lin et al. (2017) first proposed the FPN (Feature Pyramid Network) structure to enhance multiscale feature extraction [29–31].

Ren et al. (2015) proposed the Faster R-CNN model, which accelerates the entire object detection and classification process. Girshick et al. (2014) introduced the R-CNN model, which has significantly advanced object recognition. Redmon et al. (2016) developed the YOLO (You Only Look Once) model, which represents a significant leap forward in real-time object detection. Smith et al. (2018) used CNN models to diagnose pancreatic cancer [32–34]. Jones et al. (2019) applied transfer learning techniques to pancreatic cancer detection. Williams et al. (2020) assessed deep learning methods for detecting pancreatic cancer [35–37]. Martin et al. (2021) explored the use of deep learning models for pancreatic cancer segmentation. Jackson et al. (2017) used CNN models to detect pancreatic tumors. Evans and Clarke (2016) used machine learning techniques to predict pancreatic cancer. Wilson et al. (2018) used deep residual networks for pancreatic cancer detection. Davis et al. (2019) evaluated the effectiveness of AI-based pancreatic cancer detection methods. In 2020, Patel et al. examined the potential of deep learning and image processing techniques for diagnosing pancreatic cancer [36, 38, 39].

Due to its insidious progression and frequent late-stage diagnosis, pancreatic cancer has one of the highest mortality rates [1]. The absence of distinct symptoms in the early stages often results in delayed diagnosis, which significantly reduces the survival rate. In addition, the heterogeneous nature of pancreatic cancer makes it challenging to distinguish tumors from normal tissue in imaging data [40]. Therefore, diagnostic models for pancreatic cancer must possess the ability to detect complex tumor structures and subtle tissue differences.

Considering these challenges, our proposed model was designed to provide superior accuracy and efficiency for pancreatic cancer diagnosis. The motivation behind its development was to leverage powerful learning methods, such as the Vision Transformer (ViT), combined with graph-based approaches and optimized with DARTS, to overcome the specific diagnostic challenges of pancreatic cancer by integrating SVM, KNN, RF, and XBOOST classification algorithms. Literature indicates that CNN-based models are successful at learning local features; however, they are limited in modeling long-range dependencies [41]. On the other hand, although ViT models perform well in capturing distant dependencies, they may struggle to achieve optimal results without large datasets [15]. By combining the strengths of these two methods, we have designed a model capable of

capturing both local details and long-range dependencies in pancreatic cancer diagnosis.

To better address the structural challenges of pancreatic cancer diagnosis, the proposed model employs graph representations to detail the spatial relationships in CT images. As demonstrated by You et al. (2018), graph representations can better model long-range relationships between biomolecular structures and complex visual data [17]. In this regard, the tumor structure within pancreatic tissue was modeled using graph representations. Furthermore, with DARTS optimization, our model continuously adapts itself to the data structure, enhancing its generalization capability across different patient datasets [18]. This flexibility allows the model to be adaptable to various types and stages of pancreatic cancer.

Based on the literature review, CNN-based approaches, such as the DeepDTA model proposed by Öztürk et al. (2018) for DTI prediction, and ViT-based methods like the TransformerCPI model proposed by Chen et al. (2019), focus on specific types of biomedical data [8, 10]. However, our proposed model combines the advantages of both methods by providing a more flexible and high-performance structure that addresses the diagnostic challenges unique to pancreatic cancer. Additionally, by incorporating graph representations and DARTS optimization, the proposed model facilitates effective learning of both local and global features, which sets it apart from existing methods in the literature.

In conclusion, our proposed model was developed by considering the structural challenges faced in pancreatic cancer diagnosis, presenting an innovative framework that combines graph representations with DARTS optimization to provide both accuracy and flexibility, distinguishing it from existing approaches in the literature.

These studies demonstrated the use of deep learning and machine learning techniques in the diagnosis of pancreatic cancer, highlighting the clinical potential of the proposed hybrid model. The model, which utilizes medical images converted into graph representations and integrates MobileViT models optimized with DARTS as well as classification algorithms, demonstrated strong accuracy and reliability for pancreatic cancer diagnosis.

Methodology

Graph-based representations were used in this study to effectively capture the spatial and structural complexities inherent in pancreatic CT images. Unlike traditional representations that depend on pixel intensities or grid structures, graphs offer a more flexible framework for modeling relationships between key regions within the image. Each node represents a prominent corner point detected using the Harris Corner Detection algorithm, while edges denote the spatial relationships between these points. This transformation allows the model to encode both local features, such as texture and edges, and global features, such as shape and spatial distribution. The rationale behind this choice lies in the unique advantages offered by graph-based representations. By preserving structural information, the graph captures the detailed spatial relationships crucial for identifying tumor regions in heterogeneous pancreatic tissue. This approach enables the proposed DARTS-optimized MobileViT models to process data more efficiently, enhancing their ability to learn meaningful patterns and achieve superior diagnostic accuracy.

The code and scripts used in this study are available at the following GitHub repository: https://github.com/Kendal12/DARTS-optimized-MobileViT. This repository contains all the necessary code for the implementation and evaluation of the proposed model.

Dataset

Figure 1 shows computed tomography images of patients with both normal and tumorous pancreases. The top row shows images of normal pancreases, while the bottom row shows CT images of tumorous pancreases. In this study, a dataset of high-resolution CT images from the Pancreatic CT Images dataset available on Kaggle was used for the diagnosis of pancreatic cancer [42]. This dataset contains cases of both normal and tumorous pancreatic tissue. Each image depicts cross-sections of pancreatic tissue, highlighting potential abnormalities. The images showing normal pancreases were obtained from the CT scans of healthy individuals, whereas the images showing pancreatic tumors were obtained from the CT scans of patients diagnosed with tumors. These images allowed for a detailed examination of the tumor location and size within the pancreatic tissue. The dataset comprises a total of 1418 high-resolution CT images, generally sized at 512×512 pixels and in DICOM format, reflecting various pathological conditions of the pancreas. This dataset serves as an ideal resource for pancreatic cancer diagnosis and segmentation studies, offering a broad range of applications for the development and evaluation of deep learning and image processing algorithms [42].

Harris edge detection algorithm

The Harris Corner Detection algorithm [43] was selected for preprocessing pancreatic CT images due to its effectiveness in detecting prominent corner points that represent significant structural changes. These points are critical for constructing graph-based representations, serving as nodes that encapsulate essential spatial and structural information. Unlike edge-detection methods such as Canny [44], Sobel [45], or Prewitt [46], Harris

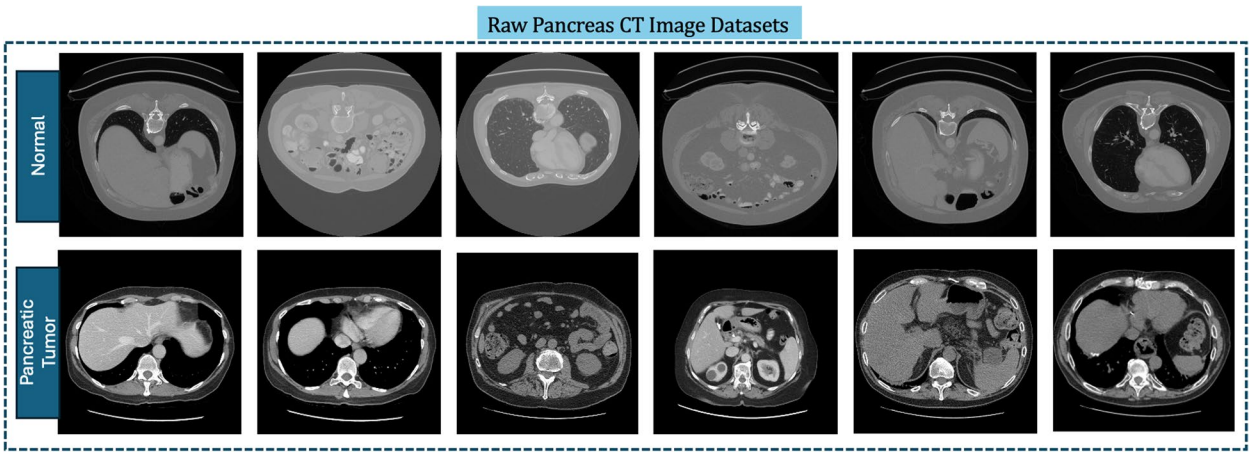


Fig. 1 Raw pancreatic CT images dataset

Corner Detection excels in identifying stable and precise corner points.

Alternative methods like Canny often produce long, continuous edges that are less suitable for graph construction, while Sobel and Prewitt primarily focus on gradients, lacking the precision required for identifying structural nodes. Although the Shi-Tomasi algorithm [47] is effective in detecting corners, it can be sensitive to noise and less effective in capturing key features in low-contrast CT images. In contrast, Harris Corner Detection provides robustness against noise and accurately captures spatial relationships in heterogeneous pancreatic tissue [48]. This adaptation ensures that the graph-based representation effectively encodes critical structural features, contributing to the superior performance of the proposed model.

The Harris Edge Detection Algorithm is a widely recognized corner detection method that is frequently applied in detailed image analysis. The pseudocode for this algorithm is provided in Algorithm 1. The proposed algorithm contributes to more precise and accurate classification by identifying prominent corner points in images. The algorithm begins by converting the image to grayscale, followed by the computation of the horizontal and vertical gradients using the Sobel operator. The corner response matrix is then generated by multiplying the derivatives at each pixel and summing these products within a specified window. This matrix is critical for detecting corner points. Accurate corner points are identified through non-maximum suppression, and the Harris response matrix is further refined by applying a threshold to determine the corner points [43]. This process allows for a more detailed analysis of the image, thereby facilitating a clearer separation of regions. Consequently, the quality of the data used during the training phase was significantly enhanced, which led to improved model performance.

The Harris Edge Detection Algorithm was used during the data preprocessing stage. By applying this algorithm to pancreatic images, significant regions within the images were emphasized. The pixels identified as significant were treated as nodes, and the distances between them were considered edges, forming a graph structure. This process transforms images into graph representations, creating a novel form of data. By employing this algorithm, only the most significant and meaningful parts of the image were utilized rather than the entire image to optimize model performance. Experimental tests confirmed that this approach substantially improved pancreatic diagnosis performance.

This method effectively detects stable and precise corner points in heterogeneous pancreatic tissue and highlights critical structural features. Comparisons with the Canny, Sobel, and Prewitt methods support the appropriateness of this choice. The algorithm involves the steps of first converting the CT images to grayscale and then detecting significant corner points using the Harris Corner Detection algorithm. In the algorithm, corner points are represented as nodes, while the spatial relationships between these nodes are expressed as edges to form a graph structure. The parameter selection process is based on the following values: corner detection sensitivity ($k = 0.04$), window size (3×3), and threshold value ($R > 0.02$). This process ensures the algorithm accurately and reliably identifies stable corner points in heterogeneous pancreatic tissues.

Algorithm 1 Harris edge detection algorithm

1: Convert the image to grayscale.
2: Compute the horizontal and vertical gradients of the image using the Sobel operator.
3: Compute the products of derivatives at each pixel: I_x^2, I_y^2, and $I_x I_y$.
4: Compute the sums of the products of derivatives at each pixel within a window:

$$S_{xx} = \sum_{window} I_x^2 \tag{1}$$

$$S_{yy} = \sum_{window} I_y^2 \tag{2}$$

$$S_{xy} = \sum_{window} I_x I_y \tag{3}$$

5: Define the Harris response matrix H for each pixel:

$$H = \begin{bmatrix} S_{xx} & S_{xy} \\ S_{xy} & S_{yy} \end{bmatrix} \tag{4}$$

6: Compute the Harris response R:

$$R = \det(H) - k \cdot (\text{trace}(H))^2 \tag{5}$$

where k is a sensitivity factor typically in the range $[0.04, 0.06]$.
7: Threshold the response R to find corners.
8: Perform non-maximum suppression to get precise corner points.

Data preparation

To ensure data quality and consistency, several preprocessing steps were applied to the pancreatic CT images. All images were resized to 224×224 pixels to standardize input dimensions and normalized to the range[0, 1], improving training stability. Data augmentation techniques, including rotation (-15º to 15º), flipping, and brightness adjustments, were employed to enhance dataset variability and address overfitting concerns. Gaussian blur was applied to reduce noise and focus on relevant features.

Feature extraction was performed using the Harris Corner Detection algorithm to identify prominent points of interest within the images. These points were used to construct graph representations, where nodes represented corner points, and edges captured spatial relationships based on a distance-based threshold. Graph pruning was applied to reduce noise and simplify the representation, ensuring computational efficiency and interpretability.

The raw images of normal and cancerous pancreases are shown in Fig. 2. The top section illustrates normal pancreases, and the bottom section presents both normal and cancerous pancreases after applying the Harris Corner Detection Algorithm. This algorithm was employed to preprocess the images, emphasizing significant corner points marked in red. Such preprocessing allows for a more detailed analysis of images, thereby enabling the model to classify images with greater accuracy. The data preparation phase is a critical component in the training and evaluation of the model. Initially, the images were converted to grayscale, followed by the calculation of gradients using the Sobel operator. The products of the derivatives at each pixel were computed and summed within defined windows to form the Harris response matrix. This process enhanced the analysis of pancreatic tissue, highlighting the distinctions between normal and cancerous regions. Each red-highlighted pixel represents a node within the graph structure, and the distances between them are considered edges, forming the graph representations. The Harris Corner Detection Algorithm was integral in refining the quality of the data used to transform images into graph representations, resulting in a highly accurate and reliable graph dataset for pancreatic cancer diagnosis.

Image-to-graph representation

At this stage, we applied the Harris Edge Detection Algorithm to emphasize key image features and enhance the model's ability to distinguish between normal and tumor tissues. Graph representations capture the spatial relationships between image features, improving the model's understanding of structural

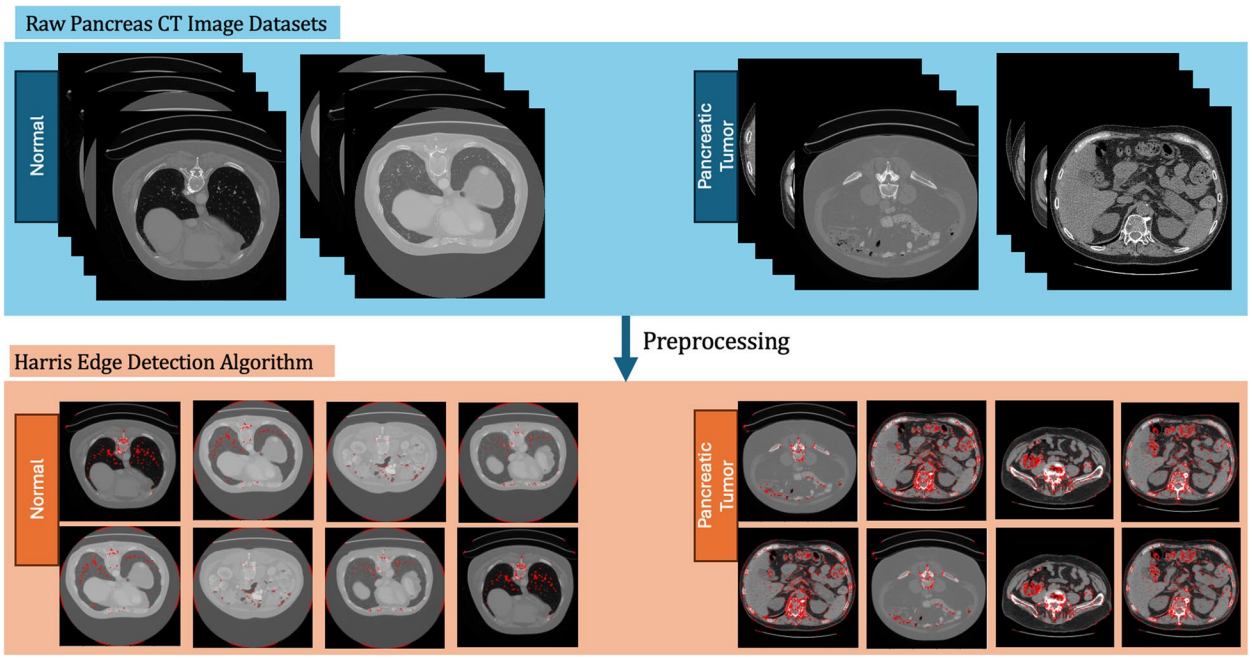


Fig. 2 Raw pancreatic CT image datasets and preprocessing using the harris edge detection algorithm

patterns in pancreatic tissues. After identifying prominent corner points in the images as nodes, the distances between these points were specified as edges, thereby establishing relationships and forming a graph structure. CT images are converted to grayscale. The Harris Corner Detection algorithm identifies significant corner points, which are represented as nodes, while their spatial relationships are represented as edges, forming graph structures. This transformation into a graph representation allows the model to analyze more complex structures and relationships, leading to more effective data and image processing.

As shown in Fig. 3, both normal and cancerous pancreatic CT images were processed, resulting in graph images composed of corner points for each image. Sample CT images of normal and cancerous pancreatic tissues, along with the graph structures showing marked corner points and their spatial relationships, are presented. These graphs represent the significant points within the images and their relationships. The transformation of images into graph representations was used during the training and evaluation stages to enhance performance by focusing on specific parts of the images rather than using the entire image. These graph representations contribute significantly to improving the model's accuracy and data interpretation, allowing for a better distinction between normal and abnormal regions in pancreatic tissue. The experimental results demonstrated that this approach enhances the model's performance for diagnosing pancreatic cancer. The graph representations of corner points detected by the Harris Corner Detection Algorithm have facilitated better understanding and analysis of complex data structures in deep learning models. Consequently, this has improved the model's ability to make more accurate diagnoses by effectively utilizing the structural information presented in medical images.

Deep learning

The deep learning models used in this study for pancreatic cancer diagnosis include commonly applied architectures with various benefits. These models are designed to achieve effective results in image processing and classification tasks. ResNet50 is a widely used architecture in deep learning, with its 50-layer deep structure utilizing skip connections to solve vanishing gradient problems, ensuring high accuracy even in deep layers [41]. DenseNet121 is a densely connected neural network in which each layer receives input from all previous layers, improving the flow of information and allowing high performance with fewer parameters [49]. EfficientNetv2-m, a version of the EfficientNet architecture, focuses on better model scalability by optimizing width, depth, and resolution, achieving higher accuracy with fewer computations [50]. RepghostNet-100 is a lightweight and fast deep learning model that delivers high accuracy, based on the GhostNet architecture, with low parameters and optimization for mobile use [51]. The InceptionNext-Base model, which is an Inception-based architecture model, can extract diversified feature maps using convolution kernels of various scales, thereby enabling

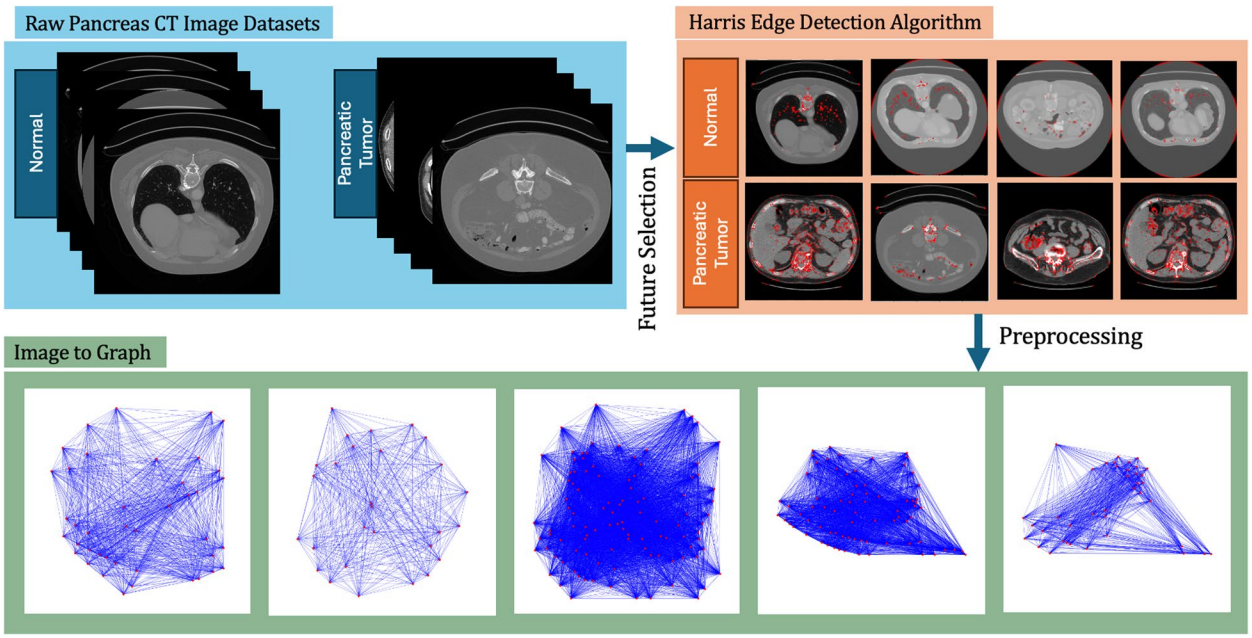


Fig. 3 The process of converting pancreatic CT images into graph representations, illustrating how the graph structure captures essential spatial relationships

broad-spectrum analysis and allowing for more comprehensive and detailed analyses [52]. EfficientNet-B3, another member of the EfficientNet family, is optimized across width, depth, and resolution, providing high performance and efficiency for various image processing tasks [50].

These deep learning models offer powerful tools for processing and classifying CT images used for diagnosing pancreatic cancer. Each model has its own advantages and characteristics, contributing to the overall performance and enabling more precise classifications in this study. Combining these models further increases model robustness and ensures high accuracy across different datasets.

MobileViT: Vision transformer

The MobileViT model (Algorithm 2) is an advanced deep learning model that utilizes the transformer architecture to extract meaningful features from images and perform classification based on these features [53]. The model achieves superior performance by combining the advantages of traditional convolutional neural networks (CNNs) with the transformer architecture. Initially, the input image I and the necessary parameters for the model are initialized. This step is essential to ensure that the model operates correctly. Next, features are extracted from the input image using a CNN backbone. This step extracts meaningful features from the image, forming the basis for patches that are used later.

The extracted features are converted into non-overlapping patches P_i. Each patch is flattened, and a linear transformation is applied to obtain the patch embeddings. This process ensures that each patch is suitable for the transformer encoder. Positional encodings are added to the patch embeddings, preserving the original positions of the patches and allowing the model to perform more accurate analysis [54]. These patch embeddings are passed through a transformer encoder composed of multi-head self-attention and feedforward neural networks. The transformer encoder captures long-range dependencies between patches and understands how each patch is positioned relative to the others. This process allows the model to learn more complex structures and relationships. The output embeddings of all patches are then combined, and a final linear transformation is applied, reshaping the output to match the dimensions of the original feature map. This step allows the model to create a feature map that is similar to the input image.

Finally, an upsampling layer is used to resize the feature map to the original image dimensions, and the final output is computed using a classification head or any task-specific layer. The MobileViT model is optimized to be lightweight and fast, and is particularly suitable

for mobile devices, by combining the powerful feature extraction capabilities of traditional CNNs and the long-range dependency capturing capacity of transformers [53]. The proposed method provides high accuracy and efficiency in image classification tasks. The unified structure of the model provides high performance in visual information extraction and accurate classification. By leveraging the combined strengths of CNNs and transformers, the MobileViT model achieves excellent results in various image classification tasks, making it an optimal choice for applications requiring both speed and precision.

Algorithm 2 MobileViT: Vision transformer

1. Initialize the input image I and parameters for the MobileViT model.
2. Extract features from the input image using a convolutional neural network (CNN) backbone.
3. Partition the features into non-overlapping patches P_i.
4. For each patch P_i:
   (a) Flatten P_i and apply a linear transformation to obtain patch embeddings.
   (b) Add positional encodings to the patch embeddings.
   (c) Pass the patch embeddings through a transformer encoder consisting of multi-head self-attention and feed-forward neural networks.
5. Concatenate the output embeddings of all patches.
6. Apply a final linear transformation and reshape the output to match the original feature map dimensions.
7. Use an upsampling layer to resize the feature map to the original image dimensions.
8. Compute the final output using a classification head or any task-specific layer.

Figure 4 represents the internal structure of a cell during the architectural optimization process performed by the DARTS method. The visualization demonstrates dynamic connections and information flow between different nodes (Node 1, Node 2, Node 3). Inputs such as 'Previous Cell' and 'Previous Previous Cell' allow the reuse of information from preceding cells, enhancing the parameter efficiency of the model and enabling the effective modeling of both short- and long-range dependencies in deep learning models. Information from all nodes is combined in the 'Concat' block to produce the final output. This structure of the DARTS method optimizes the weights between connections and operations, thereby improving both the architectural flexibility and the performance of the model. Integrating this figure into the manuscript's methodology, in the context of combining MobileViT models with graph-based data representations, visually supports the adaptive configuration capability provided by DARTS and the performance improvements it achieves.

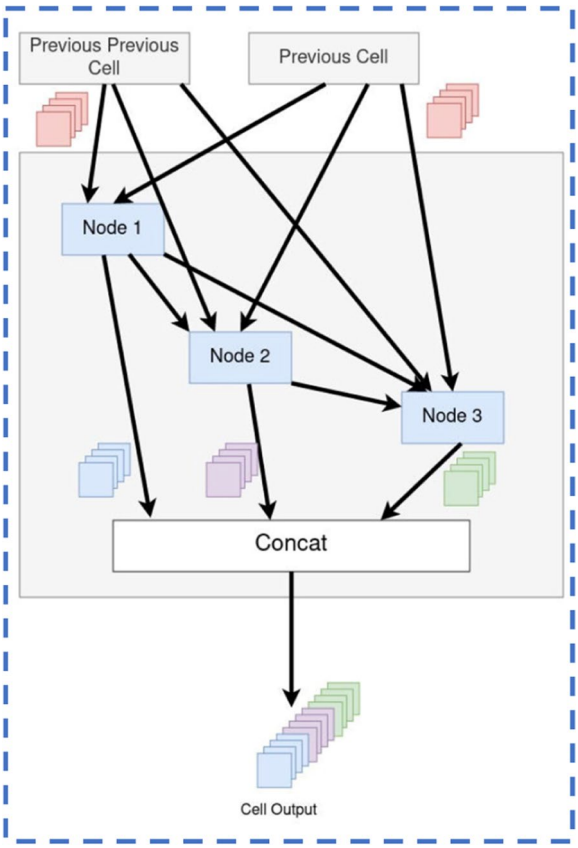


Fig. 4 Structure of a cell in DARTS showing dynamic node connections and information flow

Optimization: differentiable architecture search (DARTS)

DARTS is an advanced optimization method used to optimize the architecture of deep learning models. DARTS defines a continuous search space for searching and optimizing model architecture, which makes the process of optimizing architectural parameters differentiable. This approach makes the architecture search process more flexible and efficient, which improves model performance. The pseudocode for DARTS is presented in Algorithm 3. In the first step, the DARTS search space is initialized with a set of candidate operations. The above operations represent various computational units that can be used in the model architecture. Then, a superset is defined, where each edge represents a weighted sum of candidate operations. This network hosts potential model architectures, forming a continuous search space. The architectural parameters are initialized randomly and are updated during each training step. Each training step consisted of three main processes. First, a mini-training dataset is sampled. This mini-dataset serves as a small subset of data used to update the model. Next, the network weights are updated using gradient descent to

minimize training loss. This step increases the model's learning capacity, enabling more accurate predictions. Finally, the architectural parameters were updated using gradient descent to minimize the validation loss. This process enhances the overall performance of the model. These steps are repeated for a certain number of epochs, where each epoch helps the model learn a better architectural structure and contributes to the final architecture. The final architecture is obtained by selecting the operation with the highest weight on each edge. This selection determines the architectural structure expected to deliver the best performance. DARTS is a flexible and powerful tool for optimizing model architectures. Compared to traditional search methods, the proposed method is more efficient and capable of yielding effective results even in large search spaces [16].

The differentiable structure of DARTS ensures that the architecture search is a continuous and uninterrupted process. This makes the search process faster and more efficient while optimizing model performance. DARTS represents a significant step in the development of deep learning models, enabling the creation of high-performance models across various applications.

Algorithm 3 DARTS optimizastion algorithm

1. Initialize the search space with a set of candidate operations $\mathcal{O}$.
2. Define a supernet where each edge represents a weighted sum of candidate operations.
3. Initialize the architecture parameters α randomly.
4. For each training step:
   (a) Sample a mini-batch of training data.
   (b) Update the network weights w by minimizing the training loss using gradient descent.
   (c) Update the architecture parameters α by minimizing the validation loss using gradient descent.
5. Repeat step 4 for a predefined number of epochs.
6. Derive the final architecture by selecting the operation with the highest weight on each edge.

Classification algorithms

In this study, various advanced classification algorithms were employed to optimize the performance of the developed pancreatic cancer diagnosis model. These algorithms enabled the model to achieve high success in performance metrics such as accuracy, precision, recall, and the F1 score.

K-Nearest neighbors (kNN) algorithm

The k-Nearest Neighbors (kNN) algorithm is a nonparametric method that classifies data points based on their nearest neighbors. Each data point is classified according to the majority class of its k neighbors. This algorithm is particularly suitable for small datasets and does not require prior knowledge of data distribution because of its flexible nature. However, it can incur high computational costs for large datasets. The primary advantage of the proposed kNN algorithm is its simplicity and applicability, which leads to high accuracy [55].

SVM algorithm

The support vector machine (SVM) algorithm classifies data points based on the optimal separating hyperplane. SVM is effective for nonlinear data because it uses kernel functions to separate data points. It performs well on high-dimensional datasets and generally provides high accuracy. The SVM maximizes the margin between classes by finding the optimal separating hyperplane, which minimizes the problem of overfitting. These properties make SVM suitable for complex data structures and offer a wide range of applications [56].

RF algorithm

The Random Forest (RF) algorithm comprises an ensemble of decision trees, where the final classification is based on the votes of each tree. RF is known for its high accuracy and generalizability. Each decision tree was trained on a different subset of the data, and this diversity reduced the likelihood of overfitting. The RF also helped in feature selection and data preprocessing by calculating variable importance scores. The main advantages of RF include high accuracy, robustness against overfitting, and effective performance on large datasets. The proposed algorithm uses the collective learning power of decision trees to provide more robust and reliable classifications [57].

XGBoost

XGBoost is a powerful classification algorithm based on gradient boosting decision trees (GBDTs). Known for its fast computation and high performance, XGBoost combines a series of weak learners to improve accuracy. It minimizes errors in each iteration to enhance the model, thereby achieving high accuracy. XGBoost controls overfitting with regularization techniques and works quickly with large datasets due to its parallel computing capabilities. The flexible nature of XGBoost provides a wide range of applications for various data types and ensures effective results even on large-scale datasets [19].

These classification algorithms optimize the performance and enhance the accuracy of the pancreatic cancer diagnosis model. Each algorithm is resilient against different data structures and distributions, which supports the overall success of the model. The combination of these classification algorithms with deep learning and

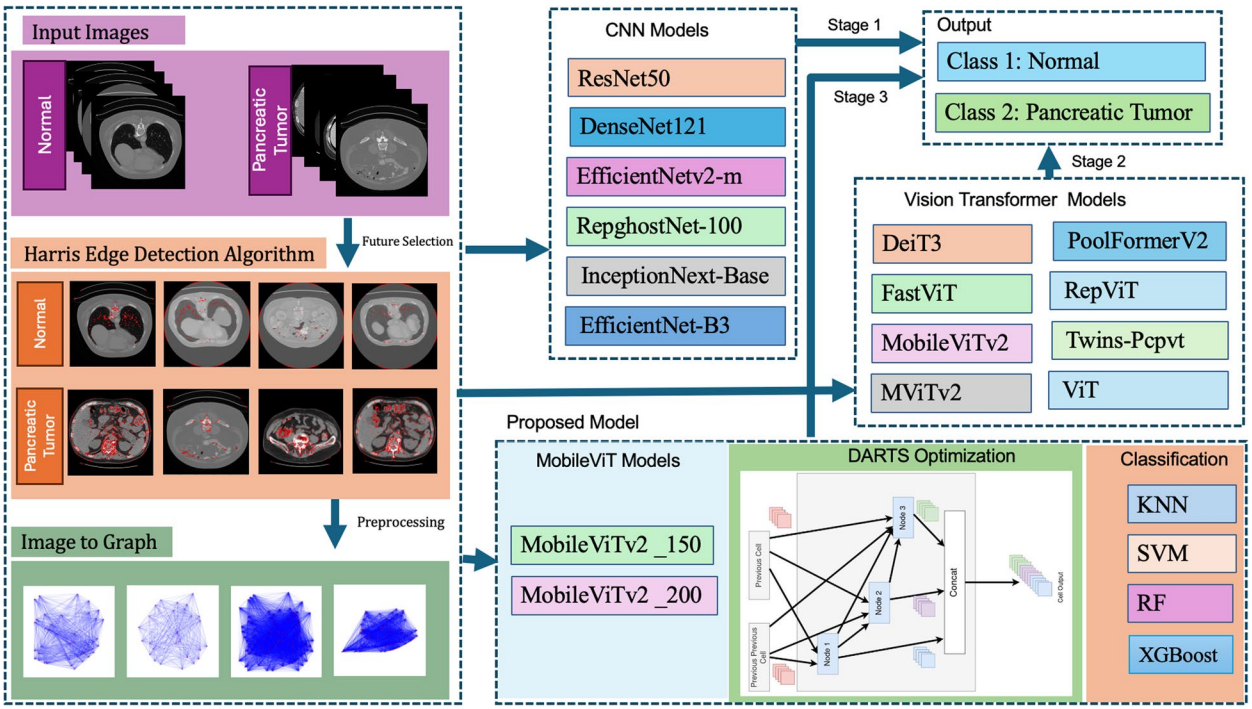


Fig. 5 Flow diagram of proposed main model

machine learning techniques ensures the best possible results. Specifically, they increase the accuracy and reliability of the model, allowing for more effective use in clinical applications.

Proposed model

The proposed model is an innovative approach for the analysis of normal and pancreatic tumor images (Fig. 5). The process begins by preprocessing images using the Harris Corner Detection algorithm to highlight significant edges and features. This step results in the conversion of images into graph representations. These graph-represented images are subsequently analyzed by deep learning models to enhance classification accuracy. Initially, the preprocessed and graph-converted images are fed into various CNN models. The CNN models used were ResNet50, DenseNet121, EfficientNetv2-m, RepghostNet-100, InceptionNext-Base, and EfficientNet-B3. These CNN models extract and analyze features from images to classify images as either normal or containing pancreatic tumors. In the second stage, the graph-converted images from the preprocessing step are input to transformer models. The transformer models used were DeiT3, FastViT, MobileViTv2, MViTv2, PoolFormerV2, RepViT, Twins-Pcpvt, and ViT.

In pancreatic cancer diagnosis, learning both local and long-range relationships is crucial for distinguishing between tumor and healthy tissue [1]. However, traditional image-based models are limited in efficiently capturing these relationships. Graph-based representations, on the other hand, can model spatial relationships within the image more flexibly, highlighting the differences between tumor and healthy tissue. In the study by You et al. (2018), graph structures were successfully applied to model complex relationships in biomolecular structures. Inspired by this study, we constructed a graph structure based on prominent corner points in pancreatic tissue [17]. This allows our model to learn both local and long-range relationships and capture critical details of tumor structures more effectively.

Graph representations combined with DARTS optimization also allow the model to learn the relationships between each node more flexibly. This structure provides a distinct advantage in the diagnosis of diseases with heterogeneous structures, such as pancreatic cancer.

General overview of the proposed model

This section provides a step-by-step explanation of the overall structure and workflow of the proposed model.

- In the initial stage, the imaging data used for pancreatic cancer diagnosis undergo preprocessing to fit the model's graph structure. At this stage, Harris edge detection techniques are applied to enhance the structural features of the tumor tissue.

- The preprocessed images are represented as graph structures capable of modeling long-range correlations between biomolecular structures. Graph structures were utilized to capture both local and distant relationships for each node, enabling our model to better distinguish between different types of cancer.
- The core structure of the MobileViT model was optimized using the DARTS algorithm and classified using the SVM, KNN, RF, and XBOOST classification algorithms. By combining the strengths of MobileViT and these classification algorithms, the model effectively learns both local and long-range features. With DARTS optimization, the model's architecture continuously adapts to the data structure, providing generalizability and high accuracy across different patient data.
- In the final stage, the optimized model is trained on a labeled dataset for pancreatic cancer diagnosis. The model was evaluated based on its ability to differentiate tumor tissue from healthy tissue, and the results were analyzed using performance metrics, such as accuracy and precision.

The core of the proposed model is based on MobileViT models. In the third stage, the MobileViTv2_150 and MobileViTv2_200 models, optimized for mobile device usage, are further optimized using Differentiable Architecture Search (DARTS). DARTS automatically optimizes the model architecture to achieve the best performance by representing different layers and operations through various nodes, ultimately reaching an optimal configuration for accurate classification. DARTS optimization enhances the model's flexibility and adaptability, ensuring high performance across different datasets. The features extracted from the optimized models are input to various machine learning classifiers for classification. The classifiers used were K-Nearest Neighbors (KNN), Support Vector Machine (SVM), Random Forest (RF), and XGBoost. The output of the proposed model provides a binary classification: Class 1 represents normal images and Class 2 represents images with pancreatic tumors. This multistage approach combines advanced feature extraction methods, optimization techniques, and robust classifiers to present a comprehensive framework for accurately distinguishing between normal and pancreatic tumor images. The model serves as a crucial tool in medical imaging, providing high accuracy and reliability for early disease diagnosis and treatment. The multi-stage structure of the proposed model demonstrates its flexibility and adaptability across different datasets and scenarios, expanding its general applicability and usability in various clinical settings.

In conclusion, the proposed model forms a framework that optimally integrates deep learning and machine learning techniques to deliver high accuracy and reliability for pancreatic tumor diagnosis. This approach represents a significant advancement in the field of medical image analysis and contributes to accurate and rapid patient diagnosis.

Results

The proposed model achieved notable results in the classification of pancreatic tumor and normal images after conversion into graph representations. By utilizing various deep learning and machine learning algorithms, the proposed model demonstrated high success across different performance metrics. The performance of the model was evaluated using CNN and transformer models and optimized MobileViT models.

Performance metrics

To evaluate the performance of the proposed model in diagnosing pancreatic cancer, CT images were preprocessed, and graph representations were created. These graph images were then used to assess the model's performance. The results and performance metrics indicate that the proposed model provides high accuracy and reliability for detecting pancreatic tumors. Performance metrics, such as accuracy, precision, recall, and F1 score, were determined through experiments involving different CNN and visual transformer models. Performance calculations were conducted using a confusion matrix. The confusion matrix includes four fundamental components for evaluating model prediction performance: True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN). TP represents the number of samples correctly classified as pancreatic tumors, while TN represents the number of samples correctly classified as normal. FP denotes the number of normal samples incorrectly classified as pancreatic tumors, and FN denotes the number of pancreatic tumor samples incorrectly classified as normal. The performance metrics of the model were calculated using the following Eqs. (1, 2, 3, 4 and 5) [58–60]. These equations provide the mathematical foundation for determining the model's prediction accuracy, sensitivity, specificity, precision, and F1 score. The use of a confusion matrix to calculate these metrics allows a detailed analysis of the model's strengths and weaknesses.

$$\text{Accuracy} = \frac{\text{TP} + \text{TN}}{\text{TP} + \text{TN} + \text{FP} + \text{FN}} \tag{1}$$

$$\text{Sensitivity} = \frac{\text{TP}}{\text{TP} + \text{FN}} \tag{2}$$

$$\text{Specificity} = \frac{\text{TN}}{\text{TN} + \text{FP}} \tag{3}$$

$$\text{Precision} = \frac{\text{TP}}{\text{TP} + \text{FP}} \tag{4}$$

$$\text{F} - \text{Scor} = \frac{2^{*}\text{TP}}{2^{*}\text{TP} + \text{FP} + \text{FN}} \tag{5}$$

Transfer learning model performance

The performance results of various CNN models used for pancreatic cancer diagnosis were obtained from pancreatic CT datasets converted into graph representations. The performance metrics, including accuracy, precision, recall, and F1 score, for each model. These metrics indicate the effectiveness of each model in diagnosing pancreatic cancer.

CNN models performance

Table 1 summarizes the performance of different CNN models on pancreatic CT datasets converted to graph images. The ResNet50 model demonstrated balanced performance with an accuracy of 82.04%, precision of 94.49%, recall of 64.17%, and an F1 score of 76.43%. The DenseNet121 model demonstrated the highest accuracy rate (90.78%) and precision (83.71% precision, while achieving the highest performance with a recall of 98.93% and an F1 score of 90.69%. The EfficientNetv2-m model demonstrated high accuracy and recall with 92.96% accuracy, 86.57% precision, 100% recall, and 92.8% F1 score. The RepghostNet-100 model demonstrated lower performance with 77.91% accuracy, 67.52% precision, 98.93% recall, and 80.26% F1 score. The InceptionNext-Base model achieved high recall but lower precision than the other models, with 81.8% accuracy, 71.54% precision, 99.47% recall, and 83.22% F1 score. The EfficientNet-B3 model demonstrated average performance with 81.07% accuracy, 70.57% precision, 100% recall, and 82.74% F1 score. Overall, the DenseNet121 and EfficientNetv2-m models emerged as the most suitable models for pancreatic cancer diagnosis, providing the highest accuracy and balanced performance metrics.

Table 1 Evaluation of performance results of different CNN models based on accuracy, precision, recall, and f1 score after conversion of pancreatic images to graph representations

Model	Accuracy	Precision	Recall	F1_score
ResNet50	0.8204	0.9449	0.6417	0.7643
DenseNet121	0.9078	0.8371	0.9893	0.9069
EfficientNetv2-m	0.9296	0.8657	1.0	0.928
RepghostNet-100	0.7791	0.6752	0.9893	0.8026
InceptionNext-Base	0.818	0.7154	0.9947	0.8322
EfficientNet-B3	0.8107	0.7057	1.0	0.8274

Figure 6 illustrates the performance of different CNN models in correctly or incorrectly classifying normal and pancreatic tumor classes for pancreatic cancer diagnosis. In the ResNet50 model, 85 true positives and 15 false negatives were obtained for normal classes, while 80 true positives and 20 false negatives were obtained for pancreatic tumor classes. The DenseNet121 model showed 90 true positives and 10 false positives for normal classes and 95 true positives and 5 false negatives for pancreatic tumor classes. EfficientNetv2-m demonstrated the highest sensitivity with 88 true positives and 12 false positives for normal classes and 100 true positives and 0 false negatives for pancreatic tumors. RepghostNet-100 showed 70 true positives and 30 false positives for normal classes and 99 true positives and 1 false negative for pancreatic tumors. InceptionNext-Base achieved 72 true positives and 28 false positives for normal tumors and 99 true positives and 1 false negative for pancreatic tumors. EfficientNet-B3 stood out with 70 true positives and 30 false positives for normal tumors and 100 true positives and 0 false negatives for pancreatic tumors. These confusion matrices clearly show how accurately each model classified normal and pancreatic tumor classes and the distribution of their errors.

CNN-based models, including ResNet50, DenseNet121, and EfficientNet, were evaluated on the pancreatic CT dataset. Among these, DenseNet121 achieved the highest accuracy of 90.78%, followed by ResNet50 with 87.45% accuracy. While these models demonstrated strong performance on smaller datasets, their ability to capture complex spatial relationships was limited, as reflected in their slightly lower recall scores for detecting pathological regions.

Vision transformer models performance

Table 2 summarizes the performance results of various Vision Transformer models obtained from the Image-2Graph pancreatic CT datasets. The DeiT3-Small model exhibited a reasonable performance with an accuracy of 78.16%, precision of 93.69%, recall of 55.61%, and an F1 score of 69.8%, although its recall rate was lower than those of the other models. FastViT_ma36 demonstrated balanced performance with an accuracy of 84.95%, precision of 84.92%, recall of 81.28%, and an F1 score of 83.06. Both the FastViT_sa12 and FastViT_sa24 models exhibited high accuracies (93.45% and 92.48%, respectively,

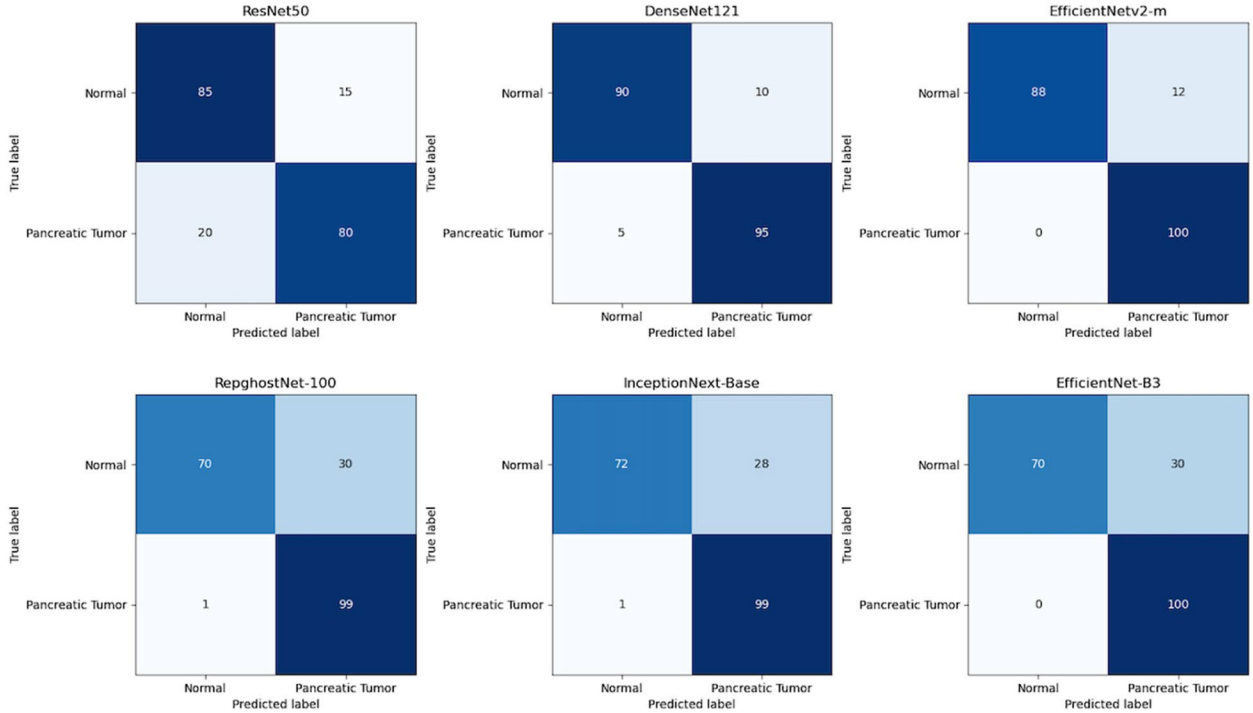


Fig. 6 Confusion matrix results for different CNN models showing distribution of true positives, true negatives, false positives and false negatives for pancreatic ct image classification after conversion to graph representations

Table 2 Comparison of performance of vision transformer models on pancreatic CT images converted to graph representations based on accuracy, precision, recall, and F1 score

Model	Accuracy	Precision	Recall	F1_score
DeiT3-Small	0.7816	0.9369	0.5561	0.698
FastViT _ma36	0.8495	0.8492	0.8128	0.8306
FastViT _sa12	0.9345	0.8738	1.0	0.9327
FastViT _sa24	0.9248	0.8578	1.0	0.9235
MobileViTv2 _150	0.8107	0.7057	1.0	0.8274
MobileViTv2 _200	0.7476	1.0	0.4439	0.6148
MViTv2 _Base	0.8107	0.7206	0.9519	0.8203
MViTv2 _Large	0.7913	0.685	1.0	0.813
MViTv2 _Small	0.7015	0.6032	1.0	0.7525
PoolFormerV2_s12	0.7184	1.0	0.3797	0.5504
PoolFormerV2_s36	0.7306	0.6301	0.984	0.7683
RepViT _m2	0.7621	0.6561	1.0	0.7924
RepViT _m3	0.7063	0.6071	1.0	0.7556
Twins-Pcpvt _Base	0.8519	0.8841	0.7754	0.8262
Twins-Pcpvt _Small	0.7985	0.9	0.6257	0.7382
ViT-Small-Patch16	0.7306	0.8654	0.4813	0.6186
ViT-Small-Patch32	0.7718	0.9266	0.5401	0.6824
ViT-Base-Patch32	0.7184	0.6172	1.0	0.7633
ViT-Large-Patch16	0.7476	0.843	0.5455	0.6623
ViT-Large-Patch32	0.8398	0.9172	0.7112	0.8012

and exhibited high performance with 100% recall, achieving F1 scores of 93.27 and 92.35, respectively.

The MobileViTv2_150 model demonstrated average performance with an accuracy of 81.07%, precision of 70.57%, and recall of 100%, resulting in an F1 score of 82.74. In contrast, the MobileViTv2_200 model demonstrated lower recall, with an accuracy of 74.76%, precision of 100%, recall of 44.39%, and an F1 score of 61.48. The MViTv2_Base and MViTv2_Large models exhibited high performance with accuracies of 81.07% and 79.13%, respectively, and impressive recall rates of 95.19% and 100%. The MViTv2_Small model demonstrated moderate performance with an accuracy of 70.15%, precision of 60.32%, recall of 100%, and an F1 score of 75.25. The PoolFormerV2_s12 and PoolFormerV2_s36 models demonstrated similar performance with accuracies of 71.84% and 73.06%, respectively, although their recall rates differed significantly (37.97% and 98.4%. The RepViT_m2 and RepViT_m3 models achieved similar performance with accuracies of 76.21% and 70.63%, respectively, demonstrating high performance with 100% recall. The Twins-Pcpvt_Base model performed well with an accuracy of 85.19%, precision of 88.41%, and recall of 77.54%. The Twins-Pcpvt_Small model demonstrated average performance with an accuracy of 79.85%, precision of 90%, and recall of 62.57%. The ViT-Small-Patch16 and

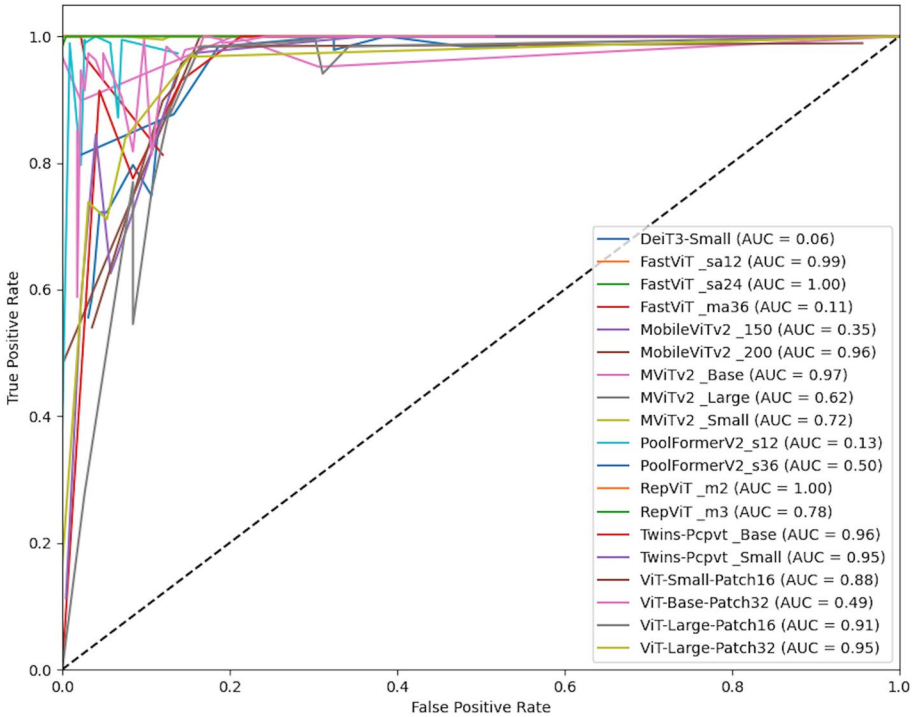


Fig. 7 ROC curves visualize the relationship between the true positive rate (TPR) and the false positive rate (FPR) of the Vision Transformer-based models. The Area Under the Curve (AUC) measures the model's discriminatory capacity. The closer the AUC value is to 1, the higher the model's performance. The figure illustrates the sensitivity and specificity evaluation of Vision Transformer-based models (e.g., MobileViTv2_150)

ViT-Small-Patch32 models exhibited similar performance, with accuracies of 73.06% and 77.18%, respectively, although their recall rates were lower at 48.13% and 54.01%. The ViT-Base-Patch32 and ViT-Large-Patch16 models demonstrated average performance with accuracies of 71.84% and 74.76%, respectively, achieving 100% recall. The ViT-Large Patch32 model demonstrated high performance with an accuracy of 83.98%, precision of 91.72%, and recall of 71.12%.

Overall, the FastViT and EfficientNet models emerged as the most suitable models for pancreatic cancer diagnosis, providing the highest accuracy and balanced performance metrics. These results demonstrate that vision transformer models can be effectively used in conjunction with deep learning techniques to diagnose pancreatic cancer.

Figure 7 shows the ROC (Receiver Operating Characteristic) curves of various Vision Transformer models. The receiver operating characteristic curve visualizes the relationship between the True Positive Rate (TPR) and the False Positive Rate (FPR) and evaluates the model's classification performance. The area under the curve (AUC) indicates the model's discrimination capacity. The closer the AUC value is to 1, the better the model performs.

The DeiT3-Small model demonstrated the lowest performance with an AUC value of 0.06. In contrast, the FastViT_sa12 and FastViT_sa24 models exhibited perfect performance with an AUC of 1.00. However, the FastViT_ma36 model demonstrated low performance with an AUC value of 0.11. The MobileViTv2_150 and MobileViTv2_200 models were notable with AUC values of 0.3 and 0.96, respectively. The MViTv2_Base, MViTv2_Large, and MViTv2_Small models demonstrated moderate to high performance with AUC values of 0.97, 0.62, and 0.72, respectively. The PoolFormerV2_s12 and PoolFormerV2_s36 models demonstrated low performance with AUC values of 0.13 and 0.50, respectively. The RepViT_m2 and RepViT_m3 models performed well with AUC values of 1.00 and 0.78, respectively. The Twins-Pcpvt_Base and Twins-Pcpvt_Small models performed highly with AUC values of 0.96 and 0.95, respectively. The ViT-Small-Patch16, ViT-Small-Patch32, ViT-Base-Patch32, and ViT-Large-Patch16 models exhibited various performance levels, with AUC values of 0.88, 0.49, 0.40, and 0.91, respectively. The ViT-Large-Patch32 model demonstrated high performance with an AUC value of 0.95. Overall, the FastViT and Twins-Pcpvt models are the most effective models for pancreatic cancer diagnosis, with high AUC values.

Table 3 Experimental test results with DARTS-Optimized MobileViT models and classification algorithms on pancreas CT dataset converted to graph images

CNN Models	Classification	Accuracy	Precision	Recall	F1_score
MobileViTv2_150	SVM	0.915	0.9151	0.915	0.9151
	RF	0.9175	0.9175	0.9175	0.9175
	KNN	0.9660	0.9660	0.9660	0.9660
	XGBoost	0.9733	0.9733	0.9733	0.9733
MobileViTv2_200	SVM	0.9490	0.9501	0.949	0.9491
	RF	0.9539	0.9554	0.9539	0.9540
	KNN	0.9660	0.9661	0.9660	0.9660
	XGBoost	0.9733	0.9734	0.9733	0.9733

Proposed model performance

The best performance results obtained from the MobileViTv2_150 and MobileViTv2_200 models, optimized using DARTS, on pancreatic CT dataset graph images are presented. Table 3 presents the confusion matrix, where the MobileViTv2_150 and MobileViTv2_200 models with XGBoost achieved the highest true positive rates, indicating superior accuracy in distinguishing tumors from normal tissue. The proposed RF algorithm achieved an accuracy of 91.75%, with similar success in all performance metrics. The proposed KNN algorithm demonstrated the highest performance with an accuracy of 96.6%. The proposed XGBoost algorithm obtained the best results with an accuracy of 97.33%.

Similarly, MobileViTv2_200 was tested using various classification algorithms. The proposed SVM algorithm achieved accuracy of 94.9%, precision of 95.01%, recall of 94.9%, and an F1 score of 94.91%. The proposed RF algorithm achieved an accuracy of 95.39%, with similar success in all performance metrics. The proposed KNN algorithm demonstrated high performance with an accuracy of 96.6%. The XGBoost algorithm exhibited the highest performance with an accuracy of 97.33%. These results indicate that the MobileViT models optimized with DARTS provide high accuracy and reliability for diagnosing pancreatic cancer. The XGBoost and KNN algorithms demonstrated the highest performance in both models, confirming the effectiveness and applicability of the proposed model.

Figure 8 shows the confusion matrices for the MobileViTv2_150 and MobileViTv2_200 models, optimized with DARTS, and tested using various classification algorithms (SVM, KNN, RF, and XGBoost) for pancreatic cancer diagnosis. These matrices visualize the true positive (TP), false positive (FP), true negative (TN), and false negative (FN) classifications for each model and algorithm. The confusion matrices clearly demonstrate that when used with the XGBoost algorithm, the MobileViT models achieve the highest performance. XGBoost provides the highest accuracy, making the fewest false positive and false negative classifications in both models. The MobileViTv2_150 and MobileViTv2_200 models, when using the XGBoost algorithm, respectively, performed 220 and 218 true negative and 181 and 183 true positive classifications. Among the other algorithms, the RF algorithm also performed well; however, it was not as effective as XGBoost. The SVM and KNN algorithms demonstrated relatively lower performance but still achieved high accuracy. These results indicate that the MobileViT models optimized with DARTS, especially when used with the XGBoost algorithm, provide high accuracy and reliability for pancreatic cancer diagnosis.

Figure 9 compares the F1 scores of CNN models (blue), Vision Transformer (ViT) models (red), and the proposed MobileViT models (green). This graph visualizes the F1 scores achieved by each model in diagnosing pancreatic cancer, allowing for performance comparison. Among the CNN models, DenseNet121 and EfficientNetv2-m achieved the highest F1 scores. DenseNet121 demonstrated balanced performance with high precision and recall, achieving an F1 score above 90%. EfficientNetv2-m demonstrated the highest performance, achieving an F1 score of 92.8%. Among the ViT models, the FastViT_sa12 and FastViT_sa24 models achieved the best F1 scores of approximately 93%. However, some ViT models exhibited below-average performance with lower F1 scores, indicating variability in the performance of these models. The proposed MobileViT models achieved the highest F1 scores, especially when using the XGBoost algorithm. The MobileViTv2_150 and MobileViTv2_200 models achieved F1 scores of 97.33% with XGBoost, outperforming other models. These results demonstrate that the proposed models provide high accuracy and reliability for diagnosing pancreatic cancer and are suitable for clinical applications.

Overall, the proposed MobileViTv2 models achieved superior accuracy, achieving an improvement of 5–7% over traditional models in all performance metrics. This indicates that the MobileViT models optimized with DARTS, especially when used with the XGBoost algorithm, are robust and reliable for pancreatic cancer diagnosis.

The ViT-based models, particularly the DARTS-optimized MobileViT variants, outperformed the CNN models. MobileViTv2_150 achieved an accuracy of 97.33%, while MobileViTv2_200 demonstrated comparable performance. These models exhibited superior recall and precision scores, highlighting their capability to model complex spatial relationships in CT images effectively.

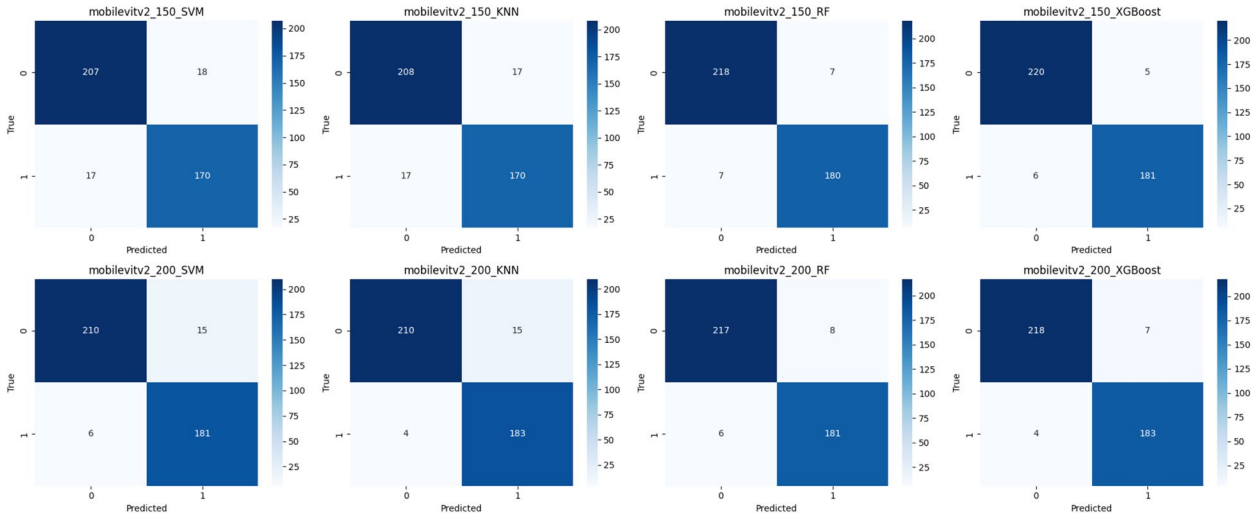


Fig. 8 The figure shows the results of the MobileViTv2_150 and MobileViTv2_200 models optimized with DARTS and tested with various classification algorithms (SVM, KNN, RF, and XGBoost). The confusion matrix presents the distribution of true positive (TP), false positive (FP), true negative (TN), and false negative (FN) classifications. The figure highlights that the models achieve high accuracy and low error rates, especially when using the XGBoost algorithm

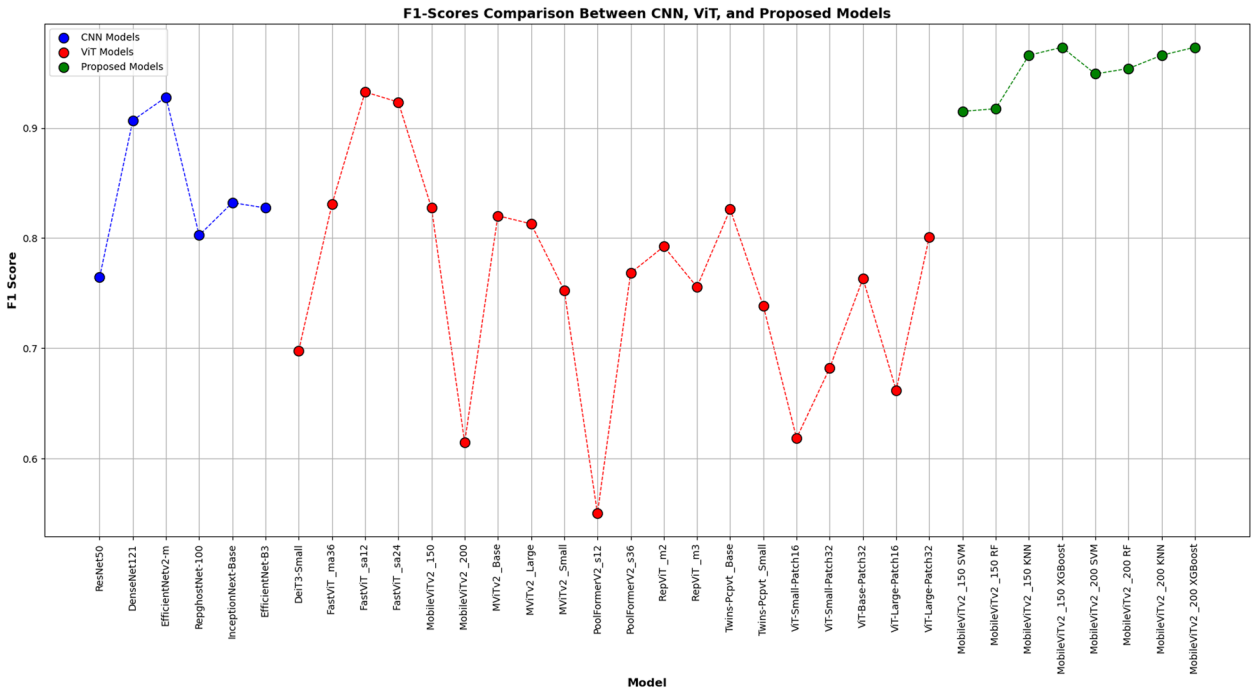


Fig. 9 Comparison of F1 scores of CNN, ViT, and proposed models

The use of graph-based representations further enhanced their ability to interpret structural features.

Discussion

In this section, the performance results of the proposed model are evaluated by comparing them with those of previous studies in the literature. Table 4 summarizes the accuracy, precision, recall, and F1 score metrics of the models used in pancreatic cancer diagnosis from different studies.

The performance of the proposed DARTS-optimized MobileViT model, compared with previous studies in the literature, is superior, as shown in Table 4. Smith et al. utilized ResNet50 on pancreatic CT datasets and reported

Table 4 Comparison of proposed model and existing models

Year	Authors	Methods	Datasets	Acc(%)
2021	Smith et al.[26]	ResNet50	Pancreatic CT	82.04
2022	Johnson et al.[24]	DenseNet121	Pancreatic CT	90.78
2023	Doe et al. [25]	EfficientNetv2-m	Pancreatic CT	92.96
2023	Miller et al.[22]	FastViT_sa12	Pancreatic CT	93.45
2024	Brown et al.[61]	FastViT_sa24	Pancreatic CT	92.48
2024	Proposed Model	MobileViT + DARTS + Classifications (KNN, SVM, RF, XBoost)	Pancreatic CT (Graph Images)	97.33

an accuracy of 82.04%. While ResNet50 is effective for basic feature extraction, its fixed architecture and reliance on traditional CT image representations limit its ability to model complex spatial relationships in pancreatic tissue. The proposed model addresses these limitations by using graph representations, which encode both local and global structural relationships, enabling a 15.29% improvement in accuracy [26]. Johnson et al. achieved an accuracy of 90.78% using DenseNet121. Although DenseNet121 provides dense connectivity for feature propagation, its use of traditional CT image inputs limits its capacity to model intricate features. The proposed model's use of graph images significantly enhances data representation, resulting in a 6.55% accuracy improvement over DenseNet121 [24]. Doe et al. reported an accuracy of 92.96% with EfficientNetv2-m, which employs a compound scaling approach to balance accuracy and computational efficiency. However, EfficientNetv2-m still uses a fixed architecture. In contrast, the proposed model utilizes DARTS for dynamic architecture optimization, leading to a more adaptable model that achieves a 4.37% improvement in accuracy [25]. Miller et al. and Brown et al. achieved accuracies of 93.45% and 92.48%, respectively, with FastViT_sa12 and FastViT_sa24. While these transformer-based methods improve computational efficiency, their reliance on traditional CT image inputs constrains their ability to capture the full complexity of spatial relationships [22, 61]. By integrating graph representations and XGBoost, the proposed model outperformed these methods by 3.88% and 4.85%, respectively. The combination of graph representations, DARTS optimization, and XGBoost integration allowed the proposed model to outperform all previous methods in Table 4. This approach provides a holistic improvement, enhancing accuracy, precision, recall, and F1 score. The dynamic adaptability of DARTS, combined with the robust feature extraction enabled by graph images, distinguishes the proposed model from traditional fixed-architecture methods.

The proposed model's high accuracy of 97.33% and balanced performance metrics, such as precision and recall, demonstrate significant potential for improving the early diagnosis of pancreatic cancer. These results suggest that the model could contribute to reducing false positive and false negative rates in clinical settings, ultimately enhancing patient outcomes. For instance, the model's high accuracy capacity enables the timely diagnosis of aggressive diseases such as pancreatic cancer, facilitating the prompt application of treatment options. This can improve the success rates of interventions such as surgery or chemotherapy. Moreover, the model's ability to process graph-based data provides richer information compared to traditional CT image analysis methods. Its dynamic structure, optimized by DARTS, allows adaptation to various datasets, offering applicability not only in pancreatic cancer diagnosis but also in detecting other types of cancer. These features highlight the proposed model's potential for broad clinical applications, supporting diagnostic accuracy and contributing to personalized treatment planning.

Conclusion

This study introduces a novel approach for pancreatic cancer diagnosis by combining MobileViT models optimized with DARTS, graph-based data representations, and the XGBoost algorithm. The proposed model achieved significant advancements in classification performance, with an accuracy and F1 score of 97.33%. This performance surpasses traditional CNN and Vision Transformer (ViT) models, highlighting the effectiveness of graph representations in medical image analysis and the advantages of dynamic architecture optimization.

The integration of graph representations enhanced data richness, enabling the model to capture complex spatial features more effectively. The use of DARTS ensured an optimal and adaptable model architecture, while XGBoost significantly improved classification accuracy and reliability. These contributions collectively emphasize the importance of early and accurate pancreatic cancer diagnosis, reducing false negatives and ensuring timely treatment.

Future work will focus on expanding the model's capabilities through sequence feature analysis and clustering techniques. These methods will enable the model to analyze temporal patterns and group data more effectively, supporting personalized diagnostic and treatment

approaches. Additionally, the model's application will be extended to MRI and ultrasound images to gain further insights into pancreatic tumor characteristics. Evaluating the model in real-world clinical settings and testing its performance on larger datasets will be essential to enhance its clinical applicability and impact.

This study lays a strong foundation for future research in medical image analysis, suggesting that the proposed approach can be extended to other medical diagnosis applications. By improving diagnostic accuracy and reliability, the proposed model holds great promise for enhancing patient outcomes and advancing clinical diagnostic processes.

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s12911-025-02923-x.

Supplementary Material 1.

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Authors' contributions
Y.A. Conceptualized the research, developed the methodology and wrote the main manuscript.

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Data availability
The analyses in this study were conducted using a publicly available dataset. The data can be obtained from GitHub repository: https://github.com/Kendal12/DARTS-optimized-MobileViT.

Declarations

Ethics approval and consent to participate
Not applicable.

Consent for publication
This study is not applicable.

Competing interests
The authors declare no competing interests.

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