

Original Article

A Lightweight Attention based Deep Learning Framework for Pancreatic Cancer Detection in CT Images

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Abstract - Pancreatic Cancer is one of the deadliest cancers, with a five-year survival rate of about 11% because it is often diagnosed late. Current deep learning methods for detecting Pancreatic Cancer from Computed Tomography (CT) images frequently struggle with overfitting, high computational demands, and poor multi-scale feature representation. This paper presents a Lightweight Convolutional Neural Network (LWCNN) framework based on the Electrophorus Chain Hunt Algorithm (ECHA) for automated PDAC detection. In this study, firstly, an efficient segmentation of the pancreas and multi-level feature extraction from the image using a BAM-based U-Net architecture are performed. Subsequently, Modified Local Ternary Pattern (MLTP), Statistical Texture Pattern (STP), and LayerCAM features are integrated to construct a comprehensive feature representation. The fused features are classified by a light-weight CNN with the help of ECHA. The proposed framework is evaluated on the publicly available Medical Segmentation Decathlon (MSD) dataset, which comprises 420 three-dimensional CT volumes. The experimental results showed 95.80% accuracy, 96.39% sensitivity, and 95.20% specificity. Additionally, 10-fold cross-validation resulted in an accuracy of 94.05%, demonstrating solid robustness and generalization. Comparative and ablation studies confirm that integrating BAM-based segmentation, hybrid feature fusion, and ECHA optimization improves pancreatic cancer detection performance while keeping computational efficiency.

Keywords - Deep learning, Pancreatic cancer, Attention module, and Convolutional Neural Network.

1. Introduction

With an 11% five-year survival rate, pancreatic cancer ranks third among US cancer-related deaths. The poor prognosis, invasiveness, quick advancement, and significant medication resistance associated with pancreatic cancer all lead to unfavorable outcomes [1-3]. Chemotherapy, surgery, and radiation therapy are common methods used in treating cancer in patients at early stages of diagnosis. In this regard, the identification of risk factors in addition to early detection can make a substantial difference in reducing mortality and improving survival rates. Despite pancreatic cancer being relatively uncommon when compared with some other cancer types like colorectal, lung, and breast cancer, late diagnosis of this type of cancer still represents a significant medical problem. The conventional way to identify the risk of developing pancreatic cancer includes biomarkers, lifestyle-related factors, genetic factors, family history, and clinical features. In the case of high-risk individuals with a history of pancreatic cystic lesions, family history of pancreatic cancer, and rare pathogenic mutations, current practice involves imaging of the pancreas [4, 5]. Nevertheless, due to the lack of specific signs in the early stages of the development of the

disease, the diagnosis of pancreatic cancer becomes problematic [6]. As a result, in many cases, patients discover that they have pancreatic cancer at an advanced stage of its development, thus making the treatment process using chemotherapy and radiotherapy less effective [1, 2, 7]. At the moment, there is no established method of screening for pancreatic cancer. The diagnosis is made by means of imaging methods, namely EUS, CT, MRI, and PET scans. Manual diagnosis requires extensive clinical knowledge as CT image quality varies between scanners and operators, and abnormal textural features can be difficult to discern. Further more research is needed to develop a reliable algorithm for detecting pancreatic tumors with accuracy [3].

In recent years, increasing research efforts have focused on developing and applying diverse techniques for the early detection of pancreatic cancer [8, 9]. Numerous characteristics, such as disease codes, biochemical data, and patient reports, have been integrated into the models. Nevertheless, the wider clinical use of these models outside of their initial developmental contexts is hampered by the dependence on characteristics that represent patients'



subjective experiences, like pain, or the actions of healthcare providers, like the application of diagnostic codes [8-11]. A selection of suitable machine learning techniques, especially deep learning approaches that operate on huge and noisy sequential datasets, is necessary for the creation of realistic risk prediction models [9, 12]. AI-based approaches have increasingly been employed to solve various clinical decision-support problems [13]. These problems include the determination of the optimal moment of intervention in intensive care [14], the evaluation of cancer risk, and the estimation of the likely progression of acute diseases from longitudinal EHRs [15]. In the field of pancreatic cancer research, several ML approaches were employed to predict the individual risk on the basis of patient-specific data. These ML approaches have used a variety of data types, including health survey data, primary-care data, hospital data, and EHR systems [8, 12]. Even though these studies showcase the usefulness of health data for cancer risk assessment, the earlier approaches mostly focused on the presence or absence of the codes corresponding to certain diseases. Thus, they could not completely consider the temporal order of the events [9, 16]. AI may be able to help radiologists identify PDAC early on by utilizing a large volume of imaging data. DL models are a subclass of AI methods, in particular, CNNs are especially best for analysis of image and showed great result in the diagnosis of various types of cancer [17] which is based on image. CNNs use the scan as the input and use a series of successive convolution and pooling processes to automatically extract pertinent features for the diagnostic purpose [18]. There have been great achievements for Convolutional Neural Network techniques in the field of medical imaging and diagnoses of diseases including different types of cancers with high success rates. In comparison to the application of Convolutional Neural Network for other cancer diagnoses, its application for the detection and early diagnosis of pancreatic cancer is still rare [5, 19]. Computer-aided diagnostic systems that are clinically useful should be able to identify whether cancer is present and, if so, locate the lesion in the input image with little to no assistance from the user. The use of DL models for automated PDAC diagnosis has recently come under investigation. However, the majority of studies do not simultaneously localize lesions; instead, they just perform a binary categorization of the input image as malignant or not. Moreover, the bulk of articles do not address tiny, early-stage lesions; only one research [18, 19] information shows the effectiveness of model on small tumors. The task of diagnosing pancreatic cancer is not an easy one even for very skilled radiologists since pancreatic masses on CT scans tend to have irregular morphology and vague borders [5]. This research develops an effective DL model for effective pancreas cancer prediction by addressing the challenges with current methods.

- BAM-enabled U-Net segmentation utilizing channel-based and spatial attention to achieve efficient and effective lesion identification.

- MLTP, STP, and LayerCAM multi-modal feature fusion, creating discriminative features.
- ECHA, a new bio-inspired meta-heuristic algorithm that combines social coot chain movements with cooperative electric eel foraging strategies, for optimizing LWCNN hyperparameters.
- The proposed model evaluation methodology employs 5-fold cross-validation, 10-fold cross-validation, training logs analysis, ablation study, and memory usage analysis to prove the efficacy and robustness of the proposed framework.

The rest of this study is structured in the following manner: Section 2 discusses existing methods for detecting pancreatic cancer, including the strengths and weaknesses of these techniques. Section 3 discusses the proposed ECHA-LWCNN method in detail. Section 4 discusses the experimental results and gives an elaborate analysis of the findings. Section 5 concludes the study and proposes future work directions.

2. Literature Review

The following review of related literature discusses various approaches to PDAC detection, considering methodological strengths, statistical soundness, and knowledge gaps that have driven the development of the novel ECHA-LWCNN.

2.1. Traditional Machine Learning

In early detection methods of PDAC, hand-crafted features combined with machine learning were used with clinical characteristics. In a systematic review of clinical prediction models, Santos et al. [8] found that classic ML techniques like SVM and Logistic Regression (LR) showed acceptable levels of predictive capability but had poor generalizability. Keyl et al. [20] proposed the development of a model based on Random Survival Forest (RSF) which included both radiomic and clinical features for predicting survival. This study was constrained by having a relatively small number of samples and excluding patients with no visible tumour. Cichosz et al. [11] presented machine learning models that used routine biochemical parameters for pancreatic cancer prediction but did not perform well because of the heterogeneous image acquisition protocols. Chen et al. [21] used an RSF model for pancreatic cancer risk prediction among people with chronic pancreatitis but pointed out that imaging protocols played an important role in predicting.

2.2. CNN-based Detection Frameworks

The deep convolutional neural network models have greatly contributed to improved diagnostics for pancreatic cancer because they can extract imaging features. For instance, Tong et al. [22] came up with a radiomic framework involving ResNet-50 that successfully distinguished between PDAC and chronic pancreatitis, albeit with the external test

set still relatively small. On the other hand, Liu et al. [4] came up with an artificial intelligence model based on the Faster R-CNN which can detect pancreatic cancer, which proved very effective in lesion detection although it required many computational resources. The study conducted by Hong et al. [10] was on the development of a CNN model for the identification of cancer cells through three-dimensional optical diffraction tomography but did not prove very applicable to clinical CT imaging. A hybrid model by researchers [5] which includes both Sparrow Search Algorithm and stacked deep learning architecture was suggested for the early diagnosis of pancreatic cancer and better accuracy in diagnostics; however, there was no statistical evaluation using metrics such as ROC-AUC or cross-validation.

2.3. Segmentation-based Approaches

Pancreatic tumor segmentation is still essential for automatic detection of PDAC. Alves et al. [17] proposed framework using nnU-Net for simultaneous segmentation and detection of pancreatic tumors, contributing to interpretability by providing lesion localization. Yet, the method suffered from low generalizability on unseen data and was demanding on human annotations. Liang et al. [23] combined the advantages of radiomics and deep learning in their pancreatic cyst classification study; however, the need for two distinct steps for segmentation and classification was highlighted.

2.4. Attention Mechanisms for Biomedical Imaging

Attention mechanism-based methods can enhance feature learning through highlighting important anatomical locations and suppressing background elements. For instance, The Bottleneck Attention Module was proposed by Park et al. [24], which can implement channel and spatial attention without additional computational burden. Multi-attention approaches have also been integrated in U-Net for detecting brain tumours by Al Abboodi et al. [25], proving the usefulness of attention in feature enhancement for biomedical images. Moreover, an attention mechanism was used in a hard hierarchical decision structure by Agarwal et al. [3] to achieve better classification in early diagnosis of PDAC with increased computation cost. Lastly, Park et al. [26] designed a group neural network using longitudinal electronic health records in early prediction of pancreatic cancer, demonstrating superior temporal modeling but not investigating imaging-based methods for diagnosis of PDAC.

2.5. Optimization via Bio-Inspired Approaches in Deep Learning

Gradient-based approaches face the issue of local minima during deep learning of deep neural networks with complex datasets in the medical image domain [12]. The Coot Optimisation Algorithm (COA) by Naruei and Keynia [27] emulates the social behaviour of coots' birds to solve optimization problems more efficiently. Maged et al. [28] suggested an EEFO algorithm, where the foraging behaviour

of electric eels helped solve the optimization problem better. Moreover, Ramesh et al. [5] have shown that bio-inspired optimization techniques can detect pancreatic cancer using the sparrow search algorithm. Nonetheless, the issue of hybrid optimization approaches for optimizing pancreatic cancer detection is under researched.

2.6. Recent Developments

In recent times, there have been developments in the areas of intelligent medical image analysis and lightweight deep learning. According to Ju and Cai [29], the use of YOLOv8 ensures fast detection of medical images in real-time, thereby allowing the development of lightweight structures. Siegel et al. [1] presented recent epidemiological statistics underscoring the increase in the prevalence of pancreatic cancer worldwide and need for its early detection. Furthermore, Monowar et al. [30] suggested a lightweight CNN structure for classification of medical images. This shows that high accuracy does not always come at a cost of high computational requirements.

2.7. Research Gaps

From the above literature review, it can be seen that there are a number of research gaps in the current literature that lead to the introduction of the ECHA-LWCNN framework.

- Current PDAC detection systems generally emphasize specific components such as segmentation, feature extraction, attention models, and optimization without considering the integration of these systems into an end-to-end framework.
- Traditional performance parameters including accuracy, sensitivity, and specificity with the Area Under the ROC curve (AUC) scores have been extensively used in the literature, whereas statistical tests, confidence intervals, and errors analyses in relation to the use of cross-validation are less investigated.
- Deep learning models have computationally complex structures and architectures making them not suitable to be used in resource-constrained medical environments.
- Current literature mostly uses handcrafted and deep learning features for feature extraction, but there is less use of combination methods to integrate both handcrafted, statistical, and activation features into a single detection system.
- Bio-inspired optimization has been shown to work well with medical image analysis problems including pancreatic cancer detection; however, there is no literature on the use of hybrid bio-inspiration for light CNN hyperparameter optimization.

This research gap leads to the proposal of the novel ECHA-LWCNN method.

2.8. Problem Statement

Due to the insufficiency of early diagnosis techniques, pancreatic cancer can lead to a high mortality rate. Therefore,

the detection of the early pancreatic cancer is essential and more researchers have introduced automated pancreatic cancer detection systems in recent years using machine and DL approaches. However, these researches often suffer from major drawbacks like inaccurate detection, the need for more computational resources, and ineffective detection in large datasets. In order to overcome these challenges and to obtain efficient detection of pancreatic cancer, the LW-CNN takes as the input feature, and the convolutional layer is presented as,

$$h = q(\omega v + \beta) \quad (1)$$

Where ω and β is the weight and bias of the CNN respectively, Leaky ReLU activation function is represented as,

$$L_R(v) = \begin{cases} vv \geq 0 \\ 0.01vv < 0 \end{cases} \quad (2)$$

The weight and bias of the CNN are tuned using the ECHA optimization and the LW-CNN is trained to minimize the reconstruction errors, which is presented as a loss function, represented in the Equation (3), here N represents data points, v_p represents observed value, and $\hat{v}_p$ represents predicted value. Thus the ECHA-LWCNN model reduces the loss function effectively using the ECHA algorithm.

$$f_1 = \frac{1}{N} \sum_{p=1}^N (v_p - \hat{v}_p)^2 \quad (3)$$

3. Proposed Model

Pancreatic carcinoma has a unfavourable clinical outcomes and is usually fatal. Patients who do not have a tumor just need to be monitored more closely, but if a pancreatic tumor is diagnosed, immediate treatment and a clear surgical strategy are necessary. Accurate detection of pancreatic tumors is essential for successful surgical therapy because postponing treatment raises the risk of aggravation and mortality. Artificial intelligence not only improves the precision of medical images analysis but also increases accessibility to such diagnostic skills. In this case, the process begins with acquiring a CT scan of the patient, where the scanner captures a few slices of the abdomen along with the pancreas. After acquiring the CT scan, the image screening process takes place by locating the accurate position of the pancreas and identifying the abnormalities, tumors, cysts, or other irregularities in the pancreas. This led to finding the potential areas of concern in the pancreas. Following this, the pancreas segmentation is performed, which identifies the boundaries of the pancreas and distinguishes it from the surrounding tissues. This segmentation can be achieved by automated algorithms. After segmenting the images, the diagnosis of the tumor is carried out by using AI-based methods including ML and DL approaches with efficient tumor detection. Along with predicting risk and survival, these methods were also used to assess the response to treatment, differentiate pancreatic cancer masses from other surrounding healthy tissues, and measure cancer mass differentiation. The system model of the pancreatic cancer detection is illustrated in Figure 1.

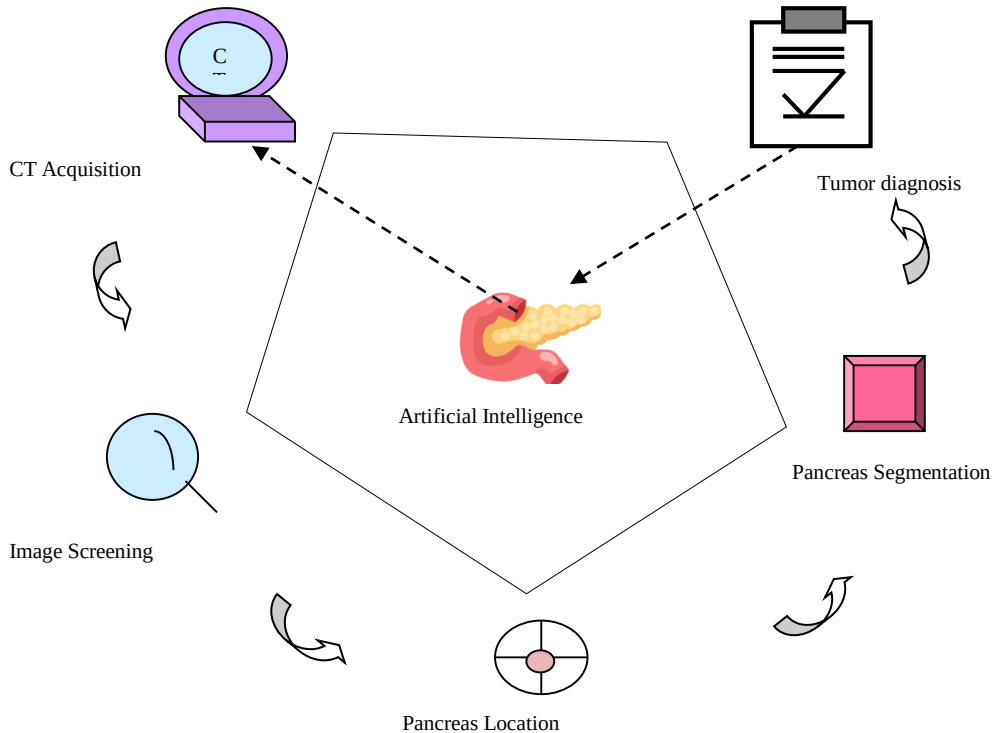


Fig. 1 System model of pancreatic cancer detection

3.1. Pancreatic Cancer Detection with the Proposed Electrophorous-Chain Hunt algorithm based Lightweight Convolutional Neural Network Model

The research develops a DL-based model for efficient pancreatic cancer detection. Initially, the input CT images are gathered from the Medical Decathlon [31] Dataset, which consists of pancreatic tumor and lesion images, and the images are preprocessed using an add weighted function, which improves the quality of the image by enhancing its intensity and contrast.

The preprocessed images are then fed for segmentation, which is performed by the Bottle neck Attention Module (BAM) based UNET approach and segments the targeted regions, where the BAM reduces the computational overhead and the UNet segments the complex images effectively.

Following the segmentation, relevant integrated texture and layer features such as modified local ternary pattern, statistical texture pattern, and layer CAM features are extracted for effective detection. These features are concatenated and passed to the proposed ECHA-LWCNN model for the detection of cancer-positive and cancer-negative cases. Here, the lightweight CNN decreases the quantity of parameters and extracts the high-level features for pancreas CT images, which aids in efficient detection. Furthermore, the lightweight CNN is optimized using the Electrophorous-Chain Hunt Algorithm (ECHA), which is the hybridization of chain movement characteristics and hunting characteristics of COOT [27] and Electrical Eel [28] respectively, which enhances the detection performance of the model by tuning the CNN parameters. The systematic representation of the developed ECHA-LWCNN model is depicted in Figure 2.

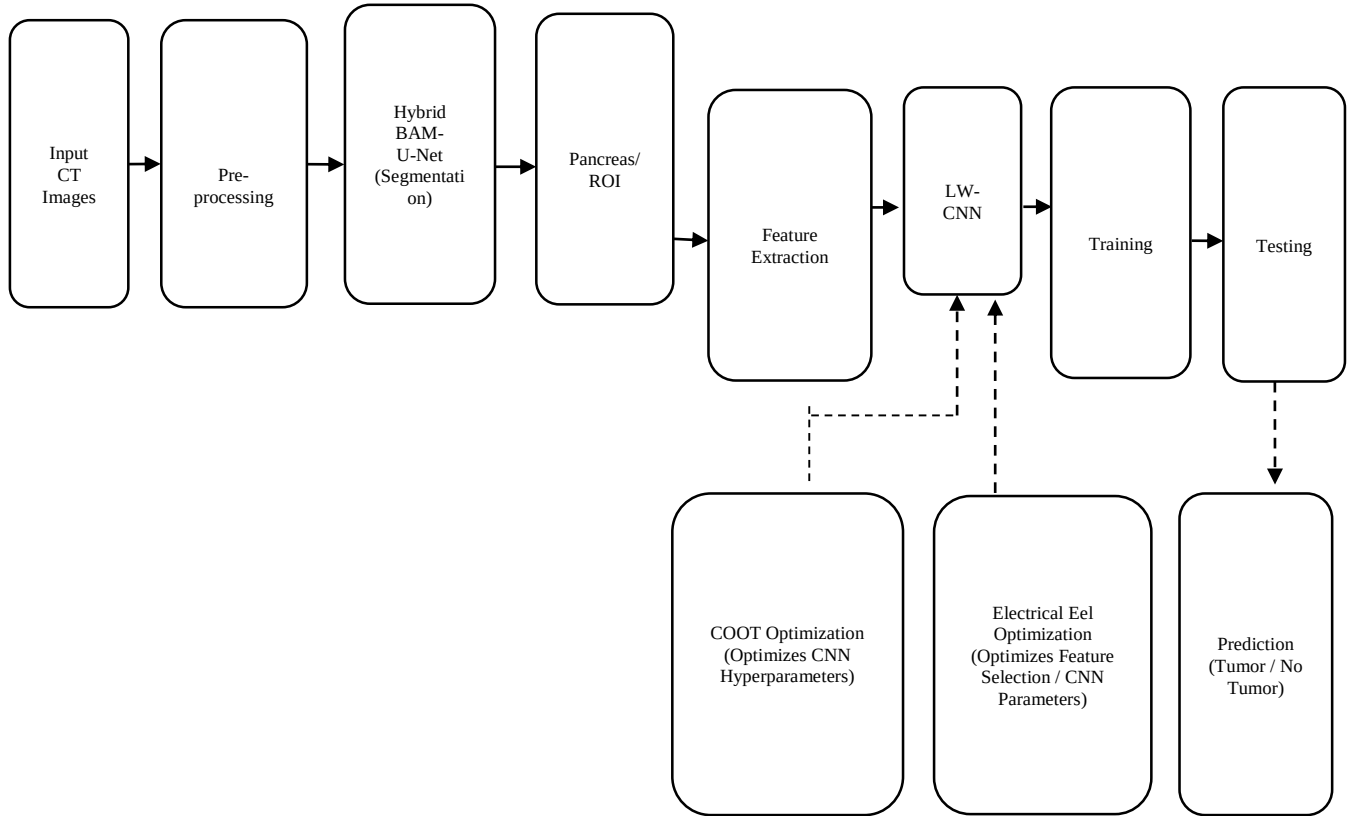


Fig. 2 Systematic diagram of ECHA-LWCNN model

3.2. Input from Medical Decathlon Dataset

The input data of Commuted Tomography-scans was acquired from the MSD dataset [31], which consists of pancreatic tumor images with size of and these input images are represented as,

$$J = \{J_1(l, r), J_2(l, r), \dots, J_k(l, r)\} \quad (4)$$

Where J indicates the dataset and the input image ranges from 1 to k , and

$\{J_1(l, r), J_2(l, r), \dots, J_k(l, r)\}$ are the pixel intensities.

3.3. Preprocessing using Addweighted function

The poor image quality degrades the model's performance; therefore, preprocessing is required to improve the quality of an image. Here, an addweighted function [29] is used to improve the clarity of the images by appropriately modifying contrast and brightness at size, which aids in

improved accuracy. The preprocessing image is represented as,

$$P(J) = Aw\{J_1(l,r), J_2(l,r), \dots, J_k(l,r)\} \quad (5)$$

Where $P(J)$, is the preprocessed image.

3.4. Segmentation using BAM based UNET

Following preprocessing, the CT images of size are segmented using BAM-U-Net, where the preprocessed image is divided into regions with similar properties as a group of pixels called image segments. The segmentation is performed in 2D images and the information from the background image is used to create masks, which then sub-divide the certain image.

The U-Net architecture is hybridized with the BAM to attain efficient segmentation performance, where the U-net can segment complex medical images and can capture both fine and coarse features and the BAM reduces the computational overhead and facilitates the gradient flow. Figure 3 presents the structural design of the U-Net incorporating the BAM module.

The UNet network is make up an encoder and decoder and the encoder consists of four down-sampling modules [30], which extract the image features. Each down sampling module consists of two Convolutional layers and a max-pooling layer.

Up sampling is done four times successively in the decoder part for gradual restoration of the spatial dimensions of the feature maps that have been created using the encoder part. In the process, the decoder parts undergo concatenation with the feature maps from the encoder part.

This is done using skip connections. Spatial information, which can get lost due to down sampling, gets preserved. Through this recovery of finer pixel-level information during decoding, the method helps with image segmentation accuracy.

Here, pooling layers are utilized to achieve down sampling and minimize the size of parameter matrices, whereas Convolutional layers are largely used for feature extraction.

Furthermore, a BAM attention module [31] is incorporated after the down-sampling of the UNet to improve the segmentation performance and also focus on local features.

The BAM incorporates a 2D attention map $Q(f) \in V^{c \times h \times w}$ for the input feature representation generated by the

U-Net convolutional layer and refined feature representation expressed as,

$$f' = f + f \otimes Q(f) \quad (6)$$

Where the element-wise multiplication is signified as $\otimes$, and the attention mechanism with the gradient flow facilitates the gradient flow. At first, both channel $Q_c(f) \in V^c$ and spatial $Q_s(f) \in V^{h \times w}$ attention maps are computed and the outputs of these branches are adjusted to.

In the channel attention branch, an average pooling is used to combine the feature map and a MULTI-LAYER PERCEPTRON (MLP) estimates the attention across channels along with the Batch Normalization (BN), which is added after MLP adjusts the scale with spatial output. Then the channel attention layer is computed as,

$$Q_c(f) = BN \left(MLP(AvgPool(f)) \right) \quad (7)$$

Similarly, the spatial attention branch emphasizes the features in different spatial locations and the convolutional layer reduces the feature to $V^{1 \times h \times w}$ and is computed as,

$$Q_s(f) = BN \left(x_3^{1 \times 1} \left(x_2^{3 \times 3} \left(x_1^{3 \times 3} \left(x_0^{1 \times 1}(f) \right) \right) \right) \right) \quad (8)$$

In this, x represents convolution operation and superscripts signify filter sizes of the convolutions. After obtaining the channel and spatial attention from the two branches, the attentions are combined and produce a final 2D attention map $Q(f)$, which is computed as,

$$Q(f) = 1 + \sigma(Q_c(f) + Q_s(f)) \quad (9)$$

Where σ is the sigmoid function. The refined feature map f' is then served as an input after downsampling in UNet segmentation. The network uses up-sampling 2D layers to up-sample the refined feature maps following multiple convolution and max pooling.

Lastly, it uses associated layers to concatenate the comparable refined feature maps from the down-sampled portion.

A thorough feature map with both high and low features is produced by this distinctive arrangement. Until the original resolution of the input is reached, upsampling is done again.

The map for the fourth class of segmentation is created by final convolution layer. Softmax activation applied which assigns a possibility distribution to each pixel across the four classes and segments the preprocessed image as (R^*) of size $[512 \times 512 \times 1]$.

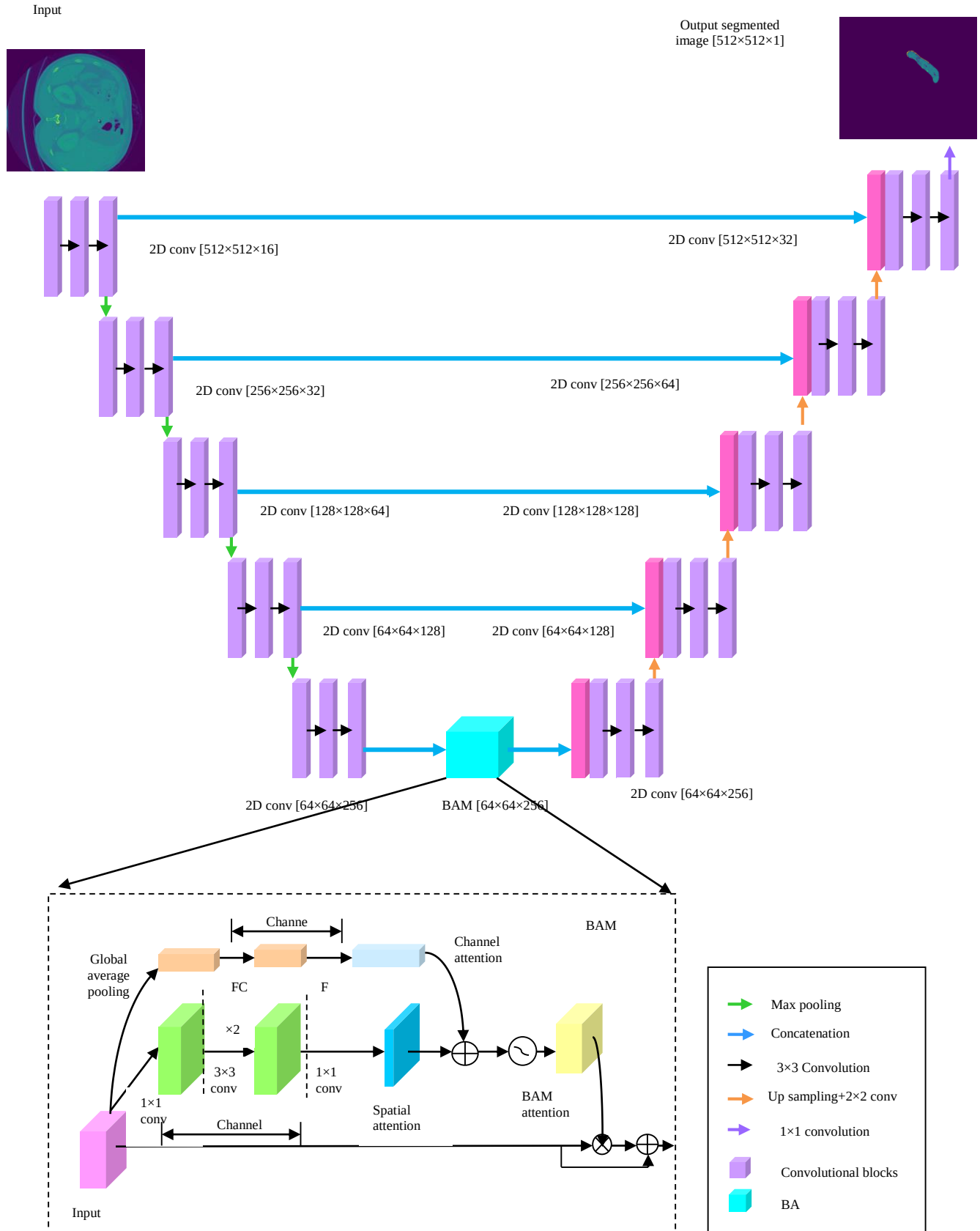


Fig. 3 Architecture of BAM-based U-Net

3.5. Multi-Modal Feature Extraction and Fusion

In pancreatic cancer detection, extraction of feature has importance, where the relevant features from the segmented images are extracted and can be used as input for the ECHA-LWCNN model. The efficacy and accuracy of the detection of pancreatic cancer can be strongly impacted by the features selected. In this research, the modified local ternary pattern, statistical texture pattern, and layer CAM features are extracted from segmented image (R^*). Modified Local Ternary Pattern (MLTP) is a modified version of LTP and the threshold values are set to zero [33]. The MLTP is applied to image size $[512 \times 512]$ to obtain efficient features. By comparing the center pixel intensity with the neighbor pixel intensity, the three shades of binary values are attained and are expressed as (10), where, the neighbor pixel's binary values are $a_i(m_y, n_y)$, O_p and O_z signify the value of central and neighbor pixel intensity respectively. The Left Side Pattern (LSP) and Right-Side Pattern (RSP) are the two segments that make up the binary $a_i(m_y, n_y)$. In LSP, the positive binary values of the matrix 3×3 are regarded as zeros, whereas the negative binary values are regarded as positive values.

$$a_i(m_y, n_y) \begin{cases} -1, & O_z < O_p \\ 0, & O_z = O_p \\ 1, & O_z > O_p \end{cases} \quad (10)$$

In the case of RSP, the individual elements in the 3×3 neighbourhood are coded using bits where 1 indicates a positive response and 0 indicates a negative response. The bit codes generated using LSP as well as RSP are then translated to decimal form, which are then allocated to the center pixel of 3×3 and MLTP is represented with an image size of $[224 \times 224]$ as,

$$MLTP(R^*) = \sum_{i=0}^7 a_i(m_y, n_y) 2^i \quad (11)$$

Mean and median are the two statistical texture features [20], which are extracted from the segmented image. The proportion of the cumulative pixel intensity relative to the total pixel values is the mean of the pixel intensities. The mean can be expressed as,

$$mean = \frac{1}{GN} \sum_{m,n \in FG} R^*(m, n) \quad (12)$$

When there is an odd count, the total pixel median in the segmented image can be found using the following formula:

$$Median = R^*(m, n) \text{ of } \frac{GN+1^{th}}{2} \text{ pixel} \quad (13)$$

The statistical texture pattern is the average of both mean and median and is expressed as,

$$STP(R^*) = \frac{Mean + Median}{2} \quad (14)$$

LayerCAM helps create trustworthy class activation maps based on layers of a deep neural network [34]. Indeed, class-based gradients that are extracted during backpropagation are used to provide different weights for spatial locations of each feature representation, making the model recognize regions responsible for predicting a particular class. The LayerCAM computes the class activation map of a particular layer based on the importance weights of the activations in every spatial position in the following way:

$$\hat{B}_{uv}^g = w_{uv}^{ge} \cdot B_{uv}^g \quad (15)$$

CAM is obtained through a weighted linear combination of the results along the channel dimension. It is expressed as follows:

$$L_{cam}(R^*) = ReLU(\sum_g \hat{B}^g) \quad (16)$$

The extracted features such as MLTP, STP, and layer CAM features of size $[224 \times 224]$ are concatenated to form a feature vector, which is resized to $[255 \times 255 \times 3]$ and expressed as,

$$F_{vec} = [MLTP(R^*) || STP(R^*) || L_{cam}(R^*)] \quad (17)$$

3.6. Electrophorus-Chain Hunt Algorithm based Lightweight Convolutional Neural Network for Pancreatic Cancer Detection

The ECHA-LWCNN is developed for efficient pancreatic cancer detection with the combination of lightweight CNN and ECHA. Traditional CNN often suffered from overfitting issues, incorrect detection, computational overhead, and complexities. In order to overcome these issues, this research introduced a lightweight CNN that reduces the number of parameters in the CNN and extracts high-level features. The reduced parameters resolve the risk of overfitting with reduced complexity and computation overhead as well as the extraction of high-level features improves the detection accuracy with reduced error. Initially, the extracted features are concatenated as feature vector (F_{vec}) and fed to the lightweight CNN model with a size of $[255 \times 255 \times 3]$. Three Convolutional layers, three max-pooling layers, four Leaky ReLU layers, one flattens layer, two Fully Connected (FC) layers, one dropout layer, and one softmax layer are included in the architecture. Six filters and a kernel size $[128 \times 128 \times 6]$ are present in the conv-1 layer. Every pooling layer employed $[2 \times 2]$ filters, and every activation function used Leaky ReLU. There are sixteen filters and a kernel size of

$$x' = q'(\omega'h' + \beta') \quad (18)$$

Where x' are the updated weights from the model after effective tuning using the ECHA optimization. The optimized model is trained and attained minimized loss function. Figure 4 depicts the structure of the developed ECHA-LWCNN model.

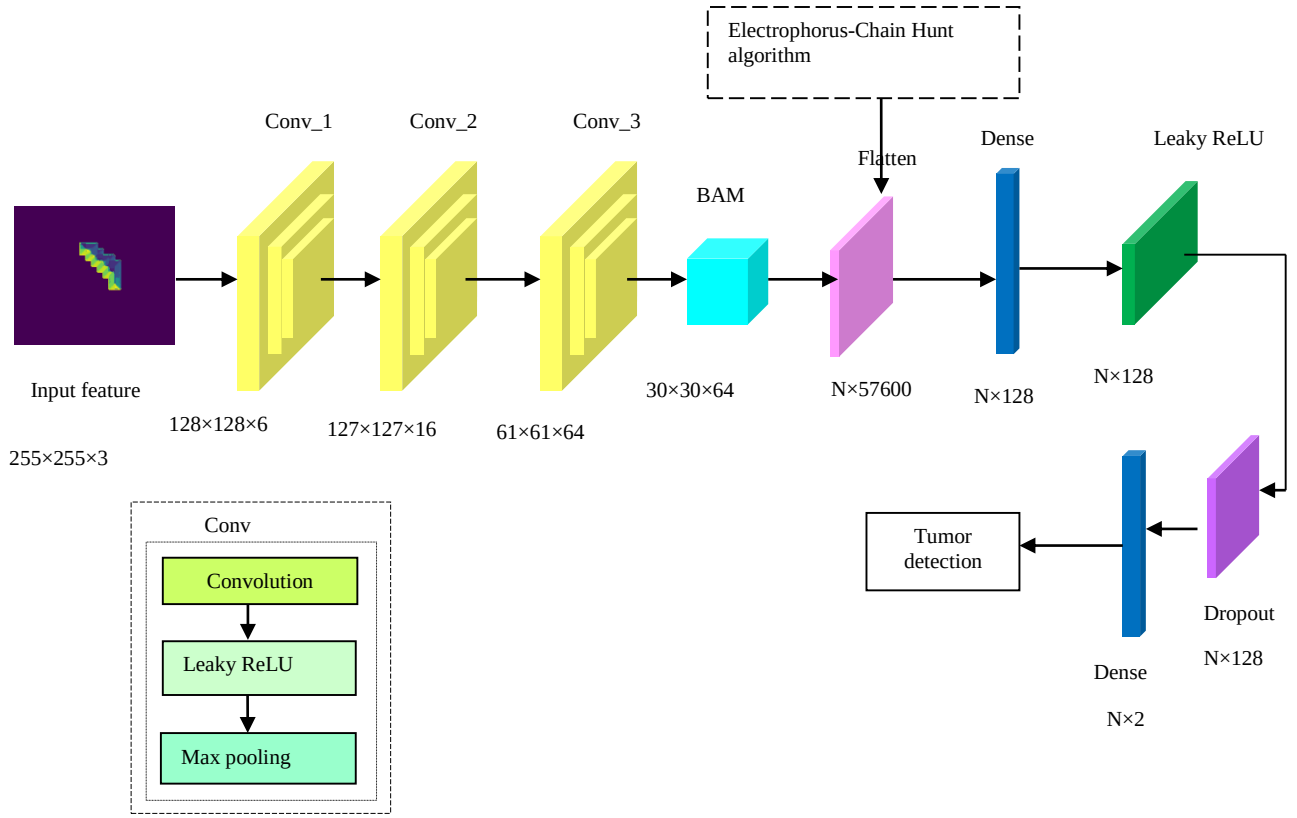


Fig. 4 Structure of ECHA-LWCNN model

3.6.1. Electrophorus-Chain Hunt Algorithm (ECHA)

The ECHA is created by swarm characteristics of coots [27] like leadership and chain movement with the foraging behavior of electric eels [28] like interaction, hunting, resting, and migration to train the pancreatic cancer detection model by fine-tuning the weight and bias of the classifier. This leads to the improvement of accuracy in pancreatic cancer detection. The incorporation of the eel's foraging behavior with the swarm characteristics of a coot provides enhanced exploration abilities and prevents premature convergence.

Inspiration

The swarm behavior of coot is modeled after the Rallidae rail family. Coot movements and behaviors on the water are varied. Out of which, the coots use leadership and chain movements here. Each coot follows its front coot as they form a chain on the water's surface. A few coots in front of the group, who are group leaders, guide the entire group toward the destination. The foraging behavior of eels involved is inspired by the Electric eels, from the family Gymnotidae native to South America, and integrates the integrated various activity characteristics of electric eels. A cooperative approach is employed where each electric eel acts as a possible solution. In each step, the most optimized solution becomes a potential solution. The optimal candidate solution acts as the desired prey in each stage. This phase of interaction is akin to global exploration, in which individual eels cooperate with one another according to their relative positions. While typical

optimizations focus on improving results, the combination of swarm characteristics and foraging behavior helps achieve the global optimum, which is necessary for accurate pancreatic cancer detection. So, In the ECHA algorithm, while coots' leadership and chain movements ensure focused and directed search, they may lead to premature convergence. Eel's hunting and migrating behaviors provide enhanced exploration capabilities preventing the solution from stuck in local optima and ensuring a thorough search in search space while avoiding premature convergence. Additionally, the interactive behavior introduces flexibility and resilience, allowing the solution to quickly adapt and improve the convergence rates. The phases involved in the ECHA are detailed below.

(i) Initialization

The solutions are initialized as a random population and are evaluated using the target function. The place of the random solution in the population is randomly generated in the search space by the below equation and is represented as,

$$Z_j^\tau = rand(1, d) \cdot (X - Y) + Y \quad (19)$$

Where, Z_j^τ is the j^{th} solution's position at iteration τ , X is UB, and Y is LB. Also d represents the problem dimensions.

(ii) Fitness Evaluation

The optimal solution is determined as the fitness and the solution with high accuracy is determined as the best fitness

in this case. The fitness is evaluated using the Equation (20) as,

$$f^t(Z_j^t) = \max(\text{accuracy}(Z_j^t)) \quad (20)$$

(iii) Solution Update

The solutions are updated using various phases after finding the fitness function and are detailed below,

(iv) Cooperative Randomness Phase

Case (i) If the current iteration is less than the quarter of the maximum iterations as $\tau < \frac{1}{4}\tau_{max}$.

$$Z_j^{\tau+1} = \begin{cases} 0.5[Z_j^t + D \cdot rn_1(Z_{rand} - Z_j^t)] + 0.5[Z_k^t + M(Z_{rand} - Z_j^t)] & \text{if } f^t(Z_j^t) < f^t(Z_k^t) \\ 0.5[Z_j^t + D \cdot rn_1(Z_{rand} - Z_j^t)] + 0.5[Z_j^t + M(Z_{rand} - Z_k^t)] & \text{else} \end{cases} \quad (21)$$

$$Z_j^{\tau+1} = 0.5[Z_{new} + \eta((Z_{new}) - \text{round}(rn_2(Z_j^t)))] + 0.5[0.5(Z_{j-1}^t + Z_j^t)] \quad (22)$$

Where, $D = [1 - (\frac{\tau}{\tau_{max}})]$ is the iteration-based change of position factor, rn_1 a randomly generated value within the specified interval $[0,1]$, $M = N_1 \times U$, is the churn factor N_1 , is a value in total population N , Z_k^t is the k^{th} solution at iteration τ , and $f^t()$ is the fitness factor.

(v) Circular Motion-based Chining Phase

Case (ii) If the current iteration lies between a quarter and two by a fourth of the maximum iterations $\frac{1}{4}(t_{max}) \leq \tau < \frac{2}{4}(t_{max})$. Here, the chain movement is implemented using the average position of the two solutions. The chain movement of the solution helps to avoid the earlier attacks from the attackers. In order to make it as simple and effective in harsh environments, the solutions enhance the positions by improving the weak and worst solutions in the group, which improves the overall positions of all the solutions. This exhibits cooperative behavior by forming a large circular arrangement and linked with each other to stay in constant communication and collaboration with position updates governed by the Equation (21) as Equation (22), Where, Z_{new} is the new position with respect to the chain movement, η is the curling factor, rn_2 is the random circular arrangement factor, round is the roundoff factor.

$$Z_j^{\tau+1} = 0.5[rn_3(H) - rn_4T_s - Lv(H - Z_j^t)] + 0.5[Z_{lead}^K + 2T_s' \cos(2T_s\pi) \times Z_{lead}(K) - Z_j^t] \quad (24)$$

Where, $\cos$ is the cosine factor, H is the random position within the search space with respect to the optimum position, T_s is the transition factor, Z_{lead}^K is the K^{th} index based on the leader's position, Lv indicates the levy flight function, and T_s' is the pseudo-random factor.

Where, $rn_3 = \tau e^{\frac{\tau-1}{\tau_{max}}}$ and $rn_4 = \tau e^{\frac{\tau}{\tau_{max}}}$, rn_3 and rn_4 are the leader solution factors based on the displacement of the solutions.

The solution is considered that be random movement with to and fro in the search space and this movement explores different regions in the search space. If the algorithms get stuck in local optima, this movement helps to escape from local optima. Nevertheless, in order to effectively escape from local optima, the solution employs a cooperative approach, which extends its searching area with a global exploration stage. The interactive behavior also adds more power to the solution to escape the local optima and improve random movement in the population and the solution's new position is updated as Equation (21),

(vi) Transition based Leading Phase

Case (iii) If the current iteration lies between two by fourth and the total of the maximum iterations as $\frac{2}{4}(t_{max}) \leq \tau < t_{max}$. The solutions in the search space are led by the leading one in the whole population and adjust their position based on the leading solutions. If there is more than one leading solution, there is a chance of occurring a convergence problem. So, the leader selection is done by a certain mechanism, which is as follows,

$$K = 1 + (j \text{MOD} l_n) \quad (23)$$

Where j is the modulus factor, MOD the index number of the current solution, l_n represents leader solutions numbers, also represents the index value of the leader. In order to find the leading solution from all other solutions, the solutions need a transition from all solutions to one solution (leading) based on its capability on migratory behavior.

The migratory behavior enabled a transition and gave the solution as well as improved leader selection in the time-constrained problems. Thus, based on the k^{th} index leader with increased transition-based selection, the solution's position is mathematically modulated as Equation (24),

(vii) Declaration of Best Solution

The fitness values for the newly modified solutions are then re-evaluated to identify the optimal solution.

(viii) Termination

The optimization process continues until the maximum number of iterations is achieved, while fitness evaluation is performed again and again to get the best solution possible. If condition is satisfied, process is completed. If not, it keeps re-evaluating fitness. The flowchart of the ECHA optimization is depicted in Figure 5.

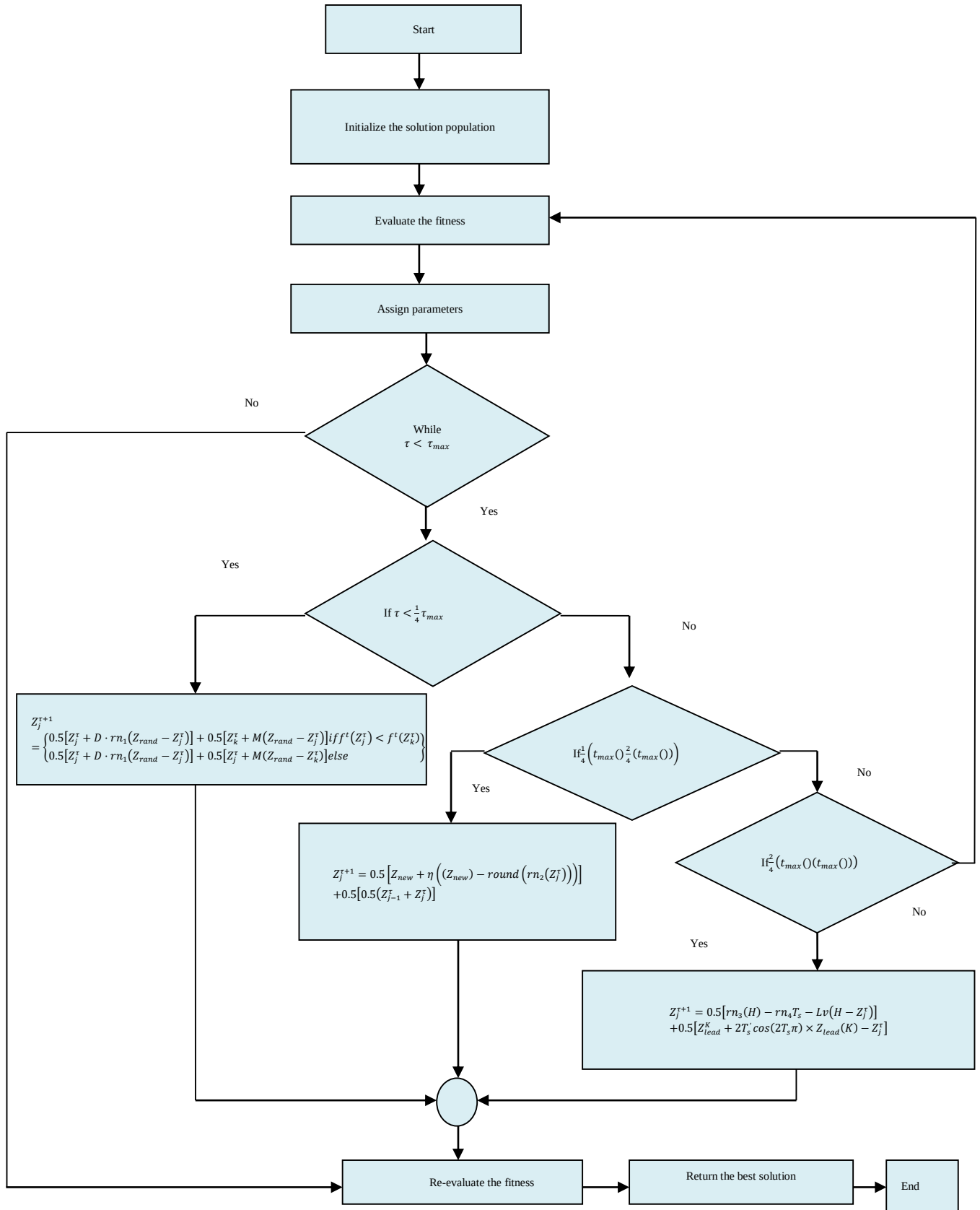


Fig. 5 Flowchart of ECHA

4. Result and Discussion

Experimental outcomes as well as effectiveness of ECHA-LWCNN model is discussed here. The effectiveness of the proposed method is assessed using varying training percentages and in terms of accuracy, sensitivity, and specificity, which are compared with the other existing approaches to show the efficiency of the developed model.

4.1. Experimental Setup

PYTHON software is used to build up the experimental configuration, and Windows 11 OS with 16GB RAM is used for implementation. With 128GB of internal memory, the machine can process data quickly enough to finish the trials. Table 1 represents the hyperparameter details of the proposed model.

Table 1. Hyperparameter details of ECHA-LWCNN

Batch size	32
Epochs	500
Rate of Learning	0.001
Optimizer	ECHA
Filters nos. of Conv_1	6
Filters nos. of Conv_2	16
Filters nos. of Conv_2	64
Pooling	Max Pooling (2×2)
Activation	Leaky ReLU ($\alpha = 0.01$)
Dropout	0.5
Dense layers	2
Output activation	Softmax
Hardware	Windows 11, 16 GB RAM

4.2. Dataset Description

Medical Segmentation Decathlon dataset (MSD) [31]: The ECHA-LWCNN model makes use of the MSD dataset, which is made up of 420 3D volumes of CT scan images with three labels (0, 1, 2): 0 denotes the background, 1 the pancreas, and 2 the tumor. Memorial Sloan Kettering Cancer Center is the source of the images.

4.3. Experimental Outcomes

The experimental outcomes of the pancreas cancer detection model along with the corresponding input images, preprocessed, segmented, and masked images of the ECHA-LWCNN model is illustrated in Figure 6.

4.3.1. Analysis of the Experimental Results

The intermediate and ultimate outputs of the designed ECHA-LWCNN model on three CT images have been shown in Figure 6 below. It can be seen from the diagram that the entire process has been illustrated from the input CT image to the final classification output, which includes input CT image, pre-processing, segmentation of pancreas, MLTP feature extraction, STP feature extraction, localization of features using LayerCAM, concatenated representation of features, and ultimately classification. For Sample 1, the input CT image consists of several structures in the abdomen area

having different levels of intensity with anatomical information surrounding them. Post-preprocessing, the anatomical structures are clearly visible, which shows that the preprocessing stage retains relevant information and provides an appropriate image for analysis. The output segment of the image only shows the pancreas with a significant reduction of the irrelevant information present in the surrounding abdominal structures. The MLTP and STP feature representations show local texture patterns in the segmented part of the pancreas. The high-response areas suggest that the local intensity and statistical texture features are captured effectively. The LayerCAM feature representation shows that the attention is focused on relevant regions only instead of the whole abdomen image. This makes for a discriminative feature representation

In the case of Sample 2, the pancreas has a distinct anatomy and spatial position than that in Sample 1. Even with the differences in shape, the segmentation process still succeeds in identifying the pancreas. In terms of the MLTP and STP maps, there is localized information in terms of structure and texture from the segmented area. As for the LayerCAM map, it creates a localized activation from the relevant region. This shows that the use of hand-crafted texture features and activation-based deep features complements each other, despite differences in pancreatic shape. For Sample 3, the segmented pancreas region is relatively smaller in the presented slice. However, the MLTP and STP visualization still has localized activations in the segmented region, indicating that the process of feature extraction still works for relatively smaller portions of the CT slice as an anatomical region. The LayerCAM visualization also yields localized activation in the respective region. This is especially significant since some of the small or less noticeable regions might be challenging to identify from the surrounding tissue with the help of only global image information. There are multiple conclusions that may be drawn from the intermediate representations in all three datasets. First, the proposed U-Net architecture based on BAM significantly decreases the effect of non-relevant abdominal regions through separating the pancreas prior to classification. Second, there are two different complementary ways to describe textures using MLTP and STP, where the former method focuses on intensity transitions in the neighbourhood while the latter characterizes statistical features of the segmented region. Third, LayerCAM provides localization of spatial cues for deep network discriminative response focused on the correct anatomical area. Fourth, the proposed concatenation of the descriptors provides a more informative representation. This is especially important due to the presence of different pancreatic morphology and sizes in Samples 1-3. Thus, it is possible to say that the proposed approach is able to extract meaningful information regardless of changes in the appearance of the image. This confirms the quantitative results of the study conducted for the ECHA-LWCNN framework.

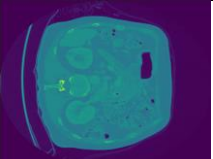
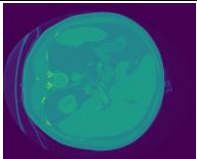
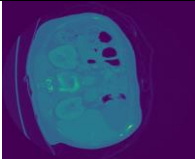
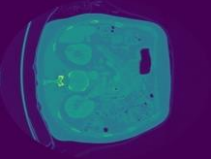
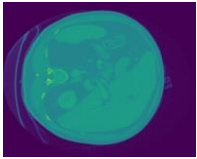
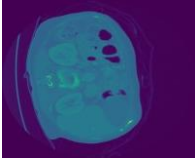
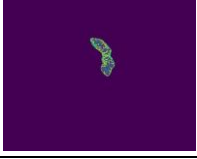
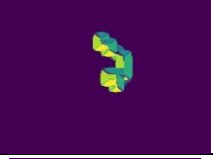
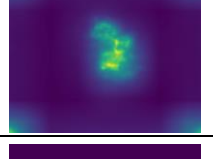
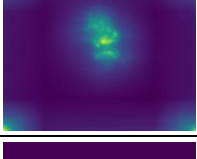
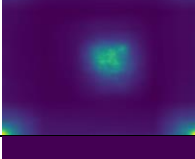
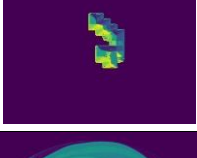
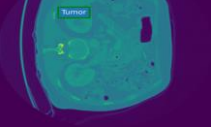
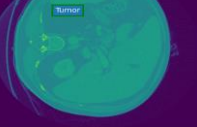
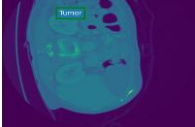
	Sample 1	Sample 2	Sample 3
Input			
Pre-processed			
Segmented			
MLTP			
STP			
Layer CAM			
Concatenated feature			
Output			

Fig. 6 Experimental outcomes of the developed ECHA-LWCNN model

4.4. Performance Metrics

The effectiveness of the proposed ECHA-LWCNN model is evaluated using key performance measures, including accuracy, sensitivity, and specificity.

i) Accuracy: It represents the percentage of predictions that are correctly classified out of the total predictions generated by the model. This is assessed as

$$accuracy = \frac{P_{TP} + P_{TN}}{P_{TP} + P_{TN} + P_{FP} + P_{FN}} \quad (25)$$

ii) Sensitivity: The ability to accurately recognize true positive cases is defined as sensitivity. It is expressed as

$$sensitivity = \frac{P_{TP}}{P_{TP} + P_{FN}} \quad (26)$$

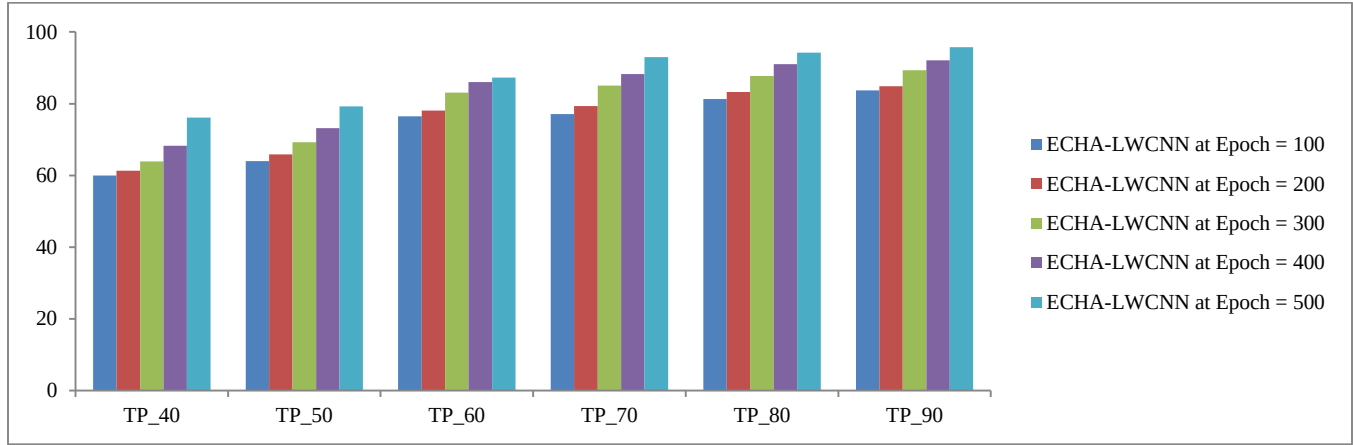
iii) Specificity: The ability to accurately differentiate negative instances is defined as specificity and is determined mathematically as

$$specificity = \frac{P_{TN}}{P_{TN} + P_{FP}} \quad (27)$$

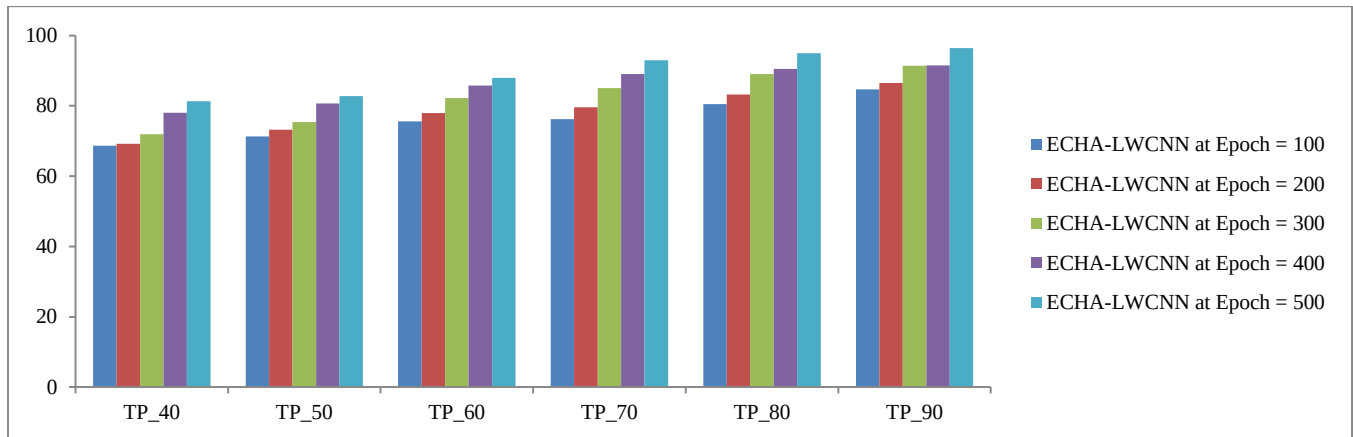
4.5. Performance Evaluation based on Training Percentage (TP)

The performance evaluation of the developed ECHA-LWCNN model using various epochs such as 100, 200, 300, 400, and 500 based on various TP like 40, 50, 60, 70, 80, and 90 is presented in Figure 7. The ECHA-LWCNN's accuracy is depicted in Figure 7 (a), where the model attains accuracies

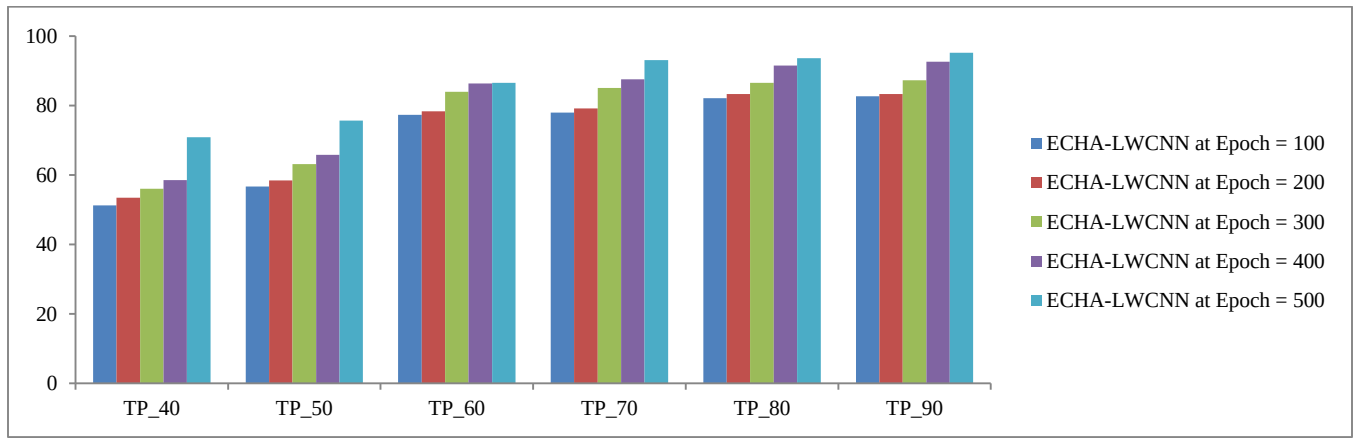
of 83.67%, 84.88%, 89.32%, 92.06%, and 95.80% for respective epochs at TP 90. Similarly, the model achieves sensitivities of 84.71%, 86.45%, 91.38%, 91.53%, and 96.39% for respective epochs at TP 90 and as depicted in Figure 7(b). For the respective epochs, the model attains specificities of 82.63%, 83.30%, 87.27%, 92.58%, and 95.20% at TP 90 as depicted in Figure 7(c).



(a) Accuracy



(b) Sensitivity



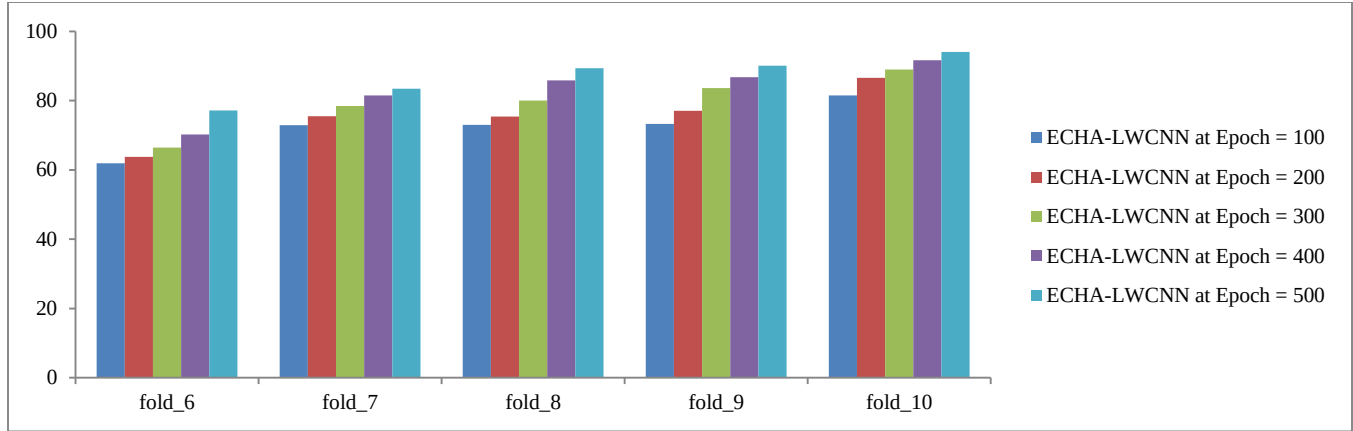
(c) Specificity

Fig. 7 Performance evaluation of the ECHA-LWCNN model with TP

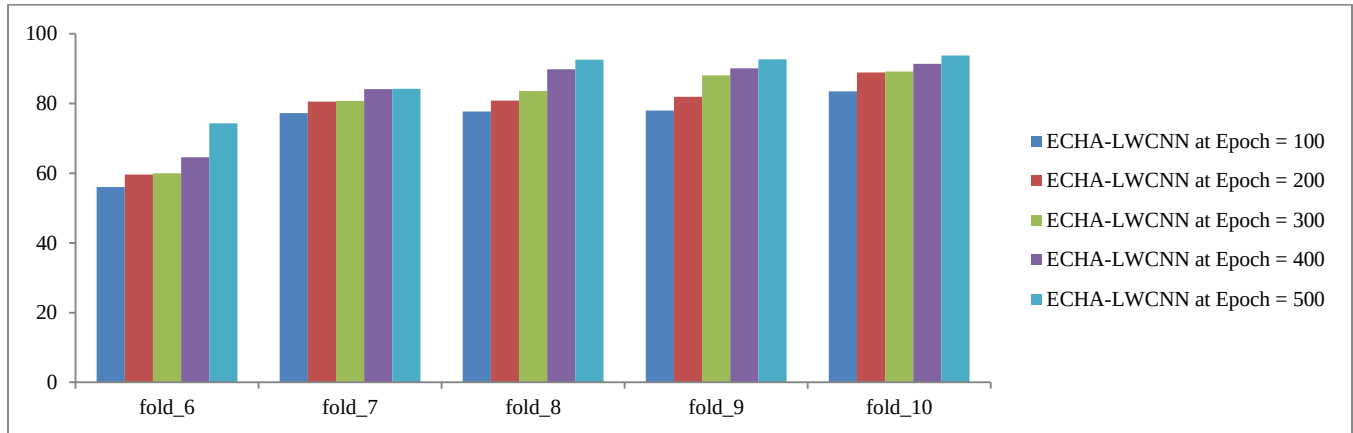
4.6. Performance Evaluation (K-Fold)

Effectiveness of proposed ECHA-LWCNN model using various epochs such as 100, 200, 300, 400, and 500 based on various k-fold values like 6, 7, 8, 9, and 10 is presented in Figure 8. The ECHA-LWCNN accuracy is shown in Figure 8(a). For the corresponding epochs at K-fold 10, the model achieves accuracies of 81.46%, 86.52%, 88.96%, 91.62%, and

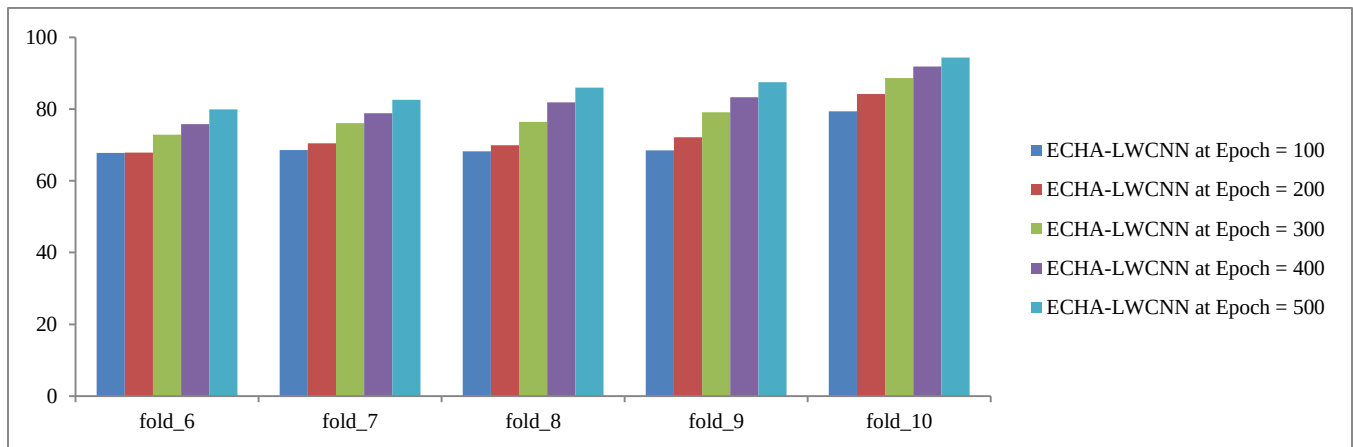
94.05%. Similarly, the model's sensitivity is shown in Figure 8(b) and achieves sensitivities of 83.54%, 88.89%, 89.23%, 91.37%, and 93.75% for respective epochs at K-fold 10. The model achieves specificities of 79.39%, 84.16%, 88.68%, 91.86%, and 94.36% at K-fold 10 for the respective epochs as shown in Figure 8(c).



(a) Accuracy



(b) Sensitivity



(c) Specificity

Fig. 8 Performance evaluation of the ECHA-LWCNN model with KF

4.7. Comparative Methods

Existing techniques such as DLR [20], RSF [21], HDS [3], MMRF-ResNet [23], and GrpNN [24] are compared with the developed ECHA-LWCNN to prove its effectiveness in the detection of pancreatic cancer.

4.7.1. Comparative Evaluation for TP

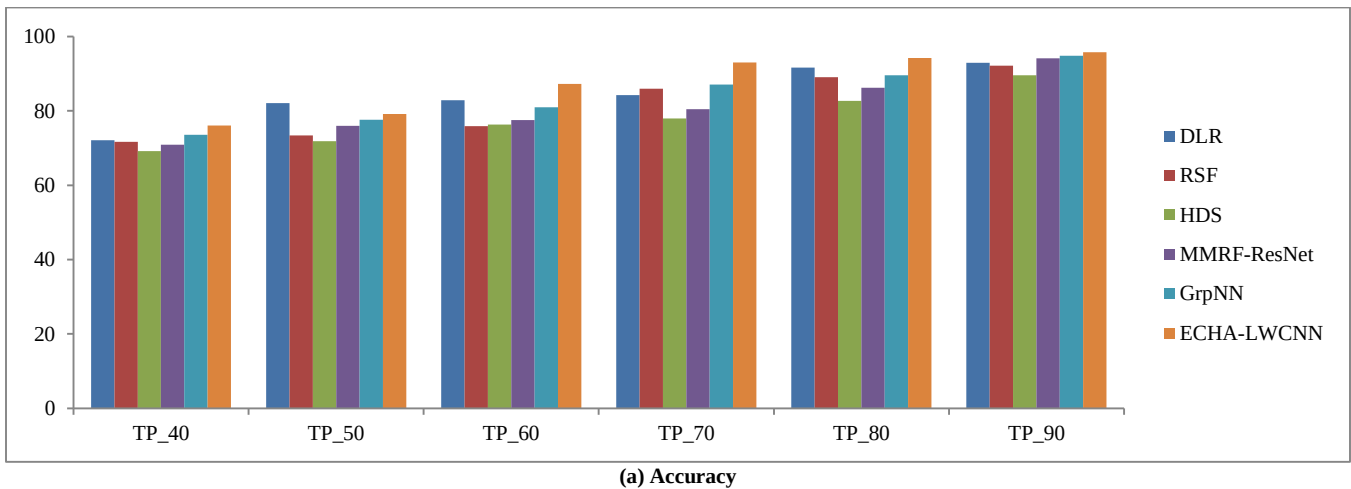
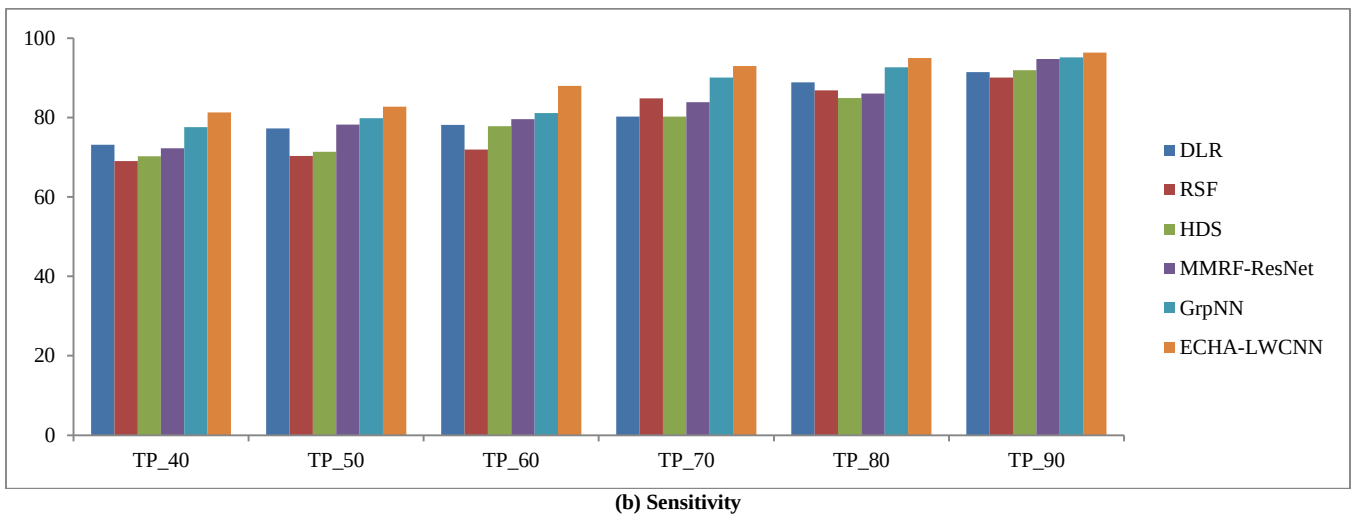
The comparative evaluation of the developed ECHA-LWCNN model based on TP is presented in Figure 9, where the ECHA-LWCNN model attains accuracy of 95.80% showing improvements of 2.95%, 3.80%, 6.48%, 1.69% and 1.00% over DLR, RSF, HDS, MMRF-ResNet, and GrpNN respectively at TP 90 and is depicted in Figure 9(a). Likewise, the ECHA-LWCNN model attains a sensitivity of 96.39% indicating improvements over the mentioned methods as 6.15%, 6.55%, 4.63%, 1.7%, and 1.25% respectively for TP 90, which is presented in Figure 9 (b).

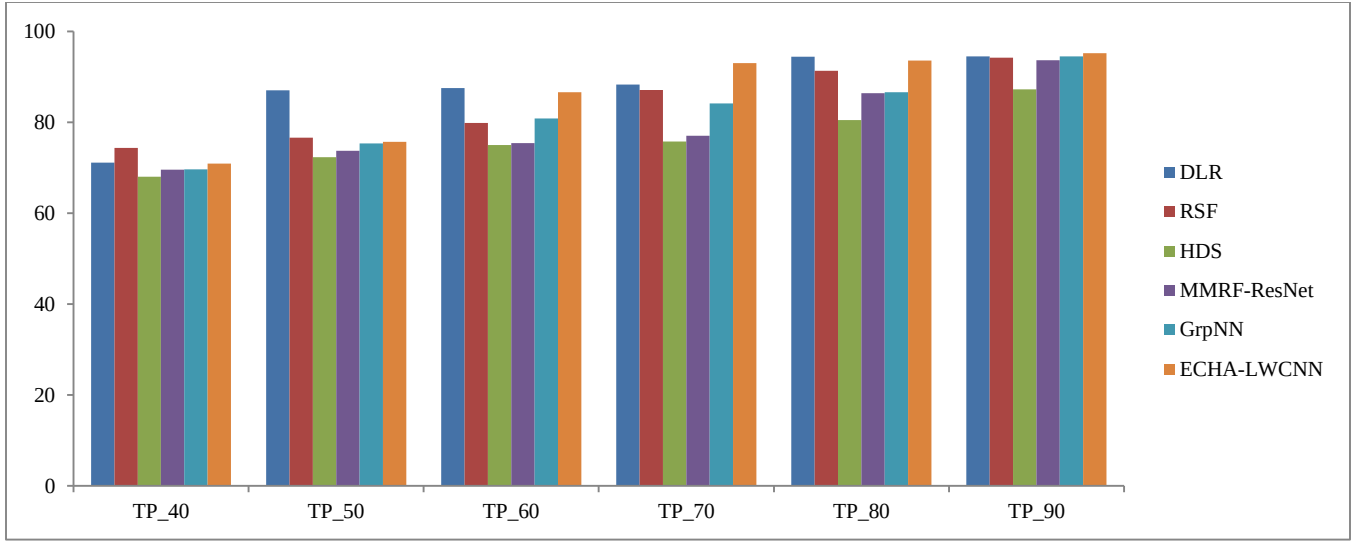
The specificity of the ECHA-LWCNN model is 95.20%, showing improvements of 0.73%, 1.02%, 9.12%, 1.66%, and 0.75% over the respective existing techniques at TP 90 and is

depicted in Figure 9 (c). The improvements in these results indicate the effectiveness of the developed model than other existing methods.

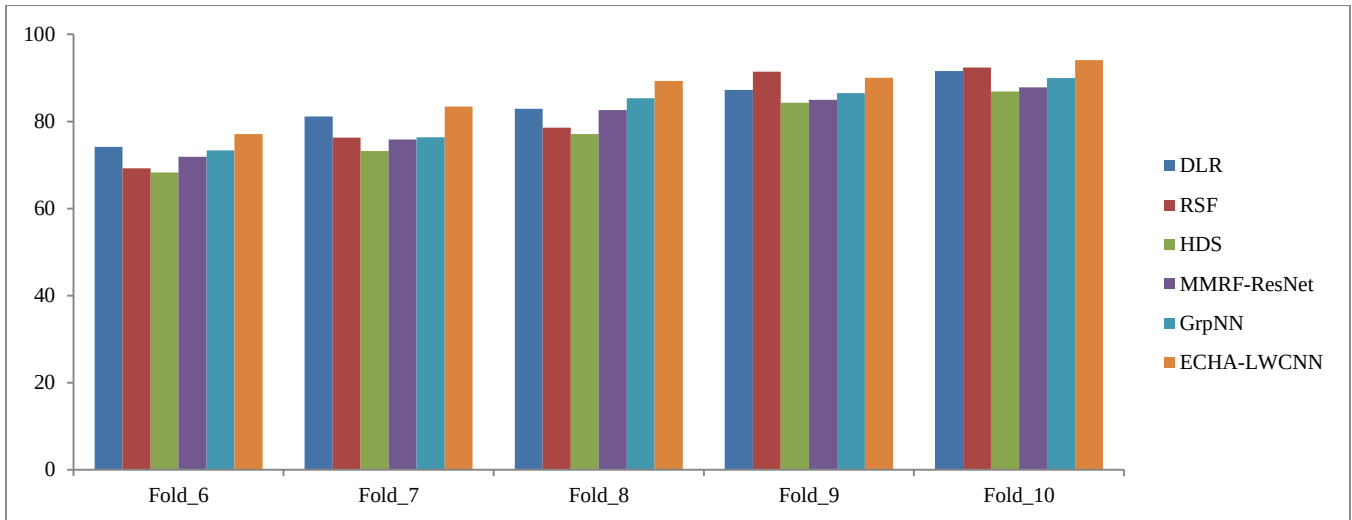
4.7.2. Comparative Evaluation for K-Fold

Figure 10 presents a comparative analysis of the ECHA-LWCNN model across different k-fold configurations. The model achieves an accuracy of 94.05% for k-fold 10, with improvements of 2.62%, 1.76%, 7.59%, 6.59%, and 4.35% over DLR, RSF, HDS, MMRF-ResNet, and GrpNN, respectively. Figure 10(a) illustrates this comparison based on accuracy. Similarly, the ECHA-LWCNN model attain a sensitivity of 93.75% at k-fold 10, which showing an enhancement over the previously mentioned approaches as 0.57%, 2.62%, 6.94%, 5.91%, and 2.15%, respectively (Figure 10(b)). The ECHA-LWCNN model's specificity is 94.36%, as shown in Figure 10(c), with improvements of 4.66%, 0.90%, 8.25%, 7.26%, and 6.53% over corresponding approaches at k-fold 10. The improvements in these outcomes show how much more efficient the created approach is than other approaches.

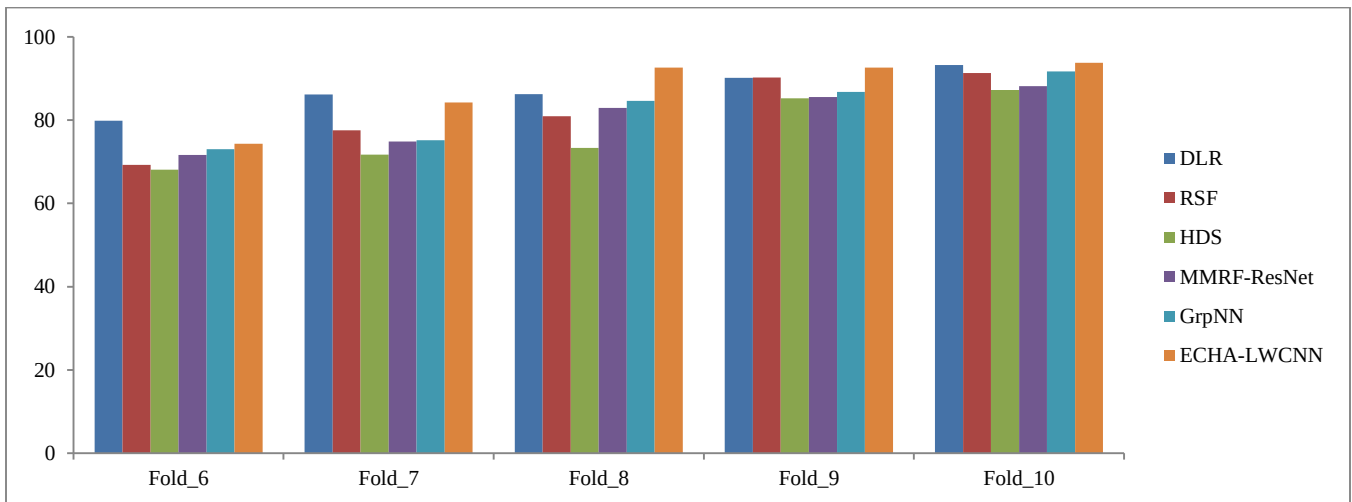




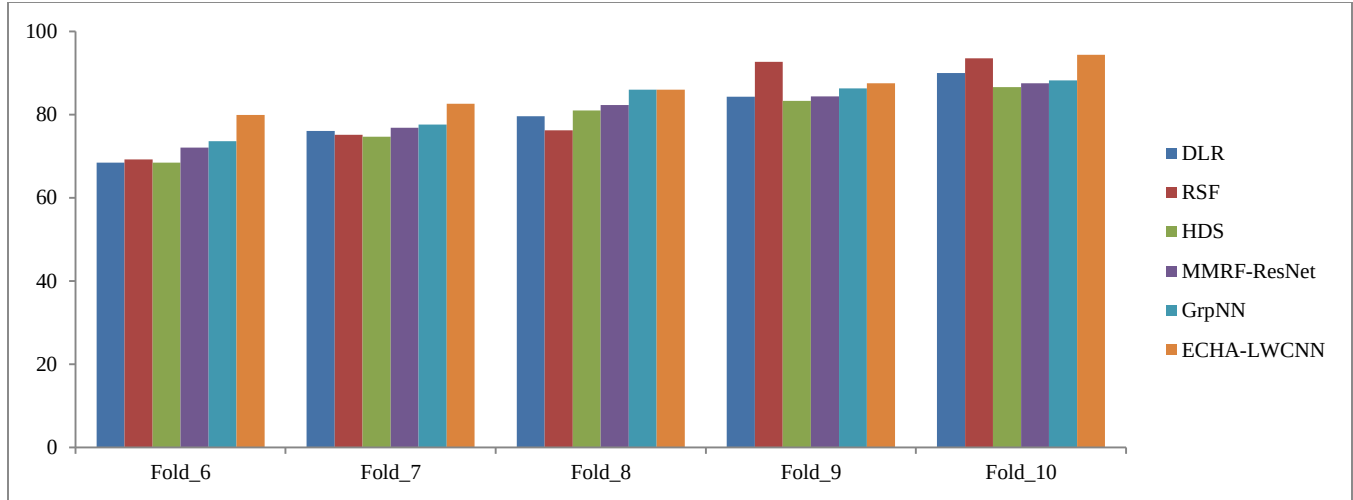
(c) Specificity
Fig. 9 Comparative evaluation of the ECHA-LWCNN model with TP



(a) Accuracy



(b) Sensitivity



(c) Specificity

Fig. 10 Comparative evaluation of the ECHA-LWCNN model with KF

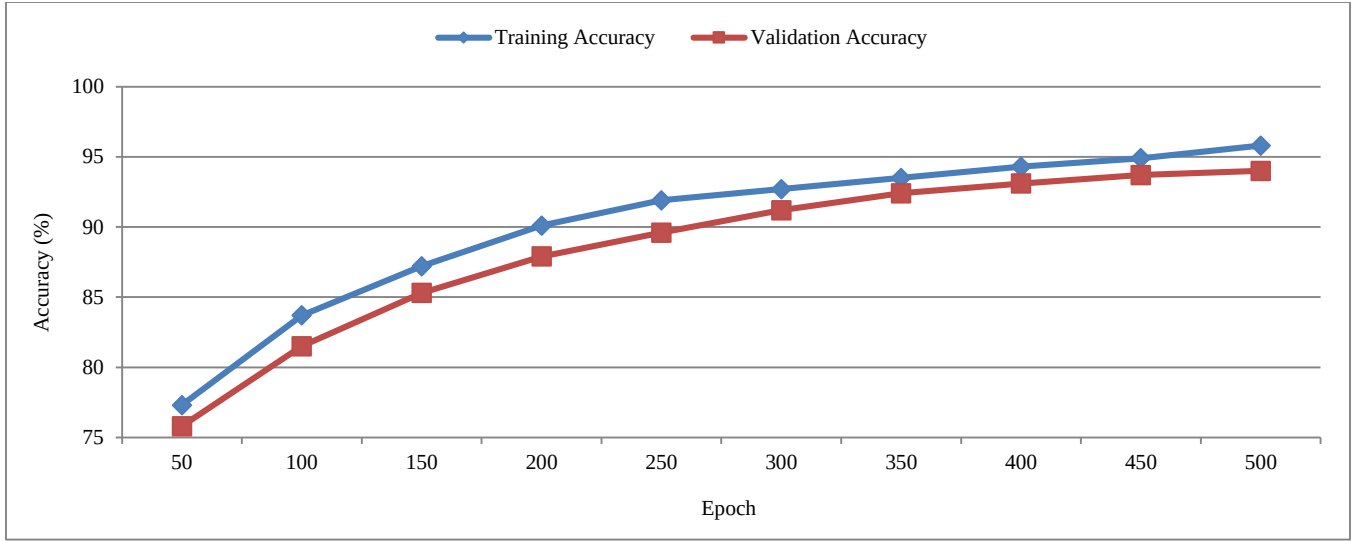
4.8. Convergence Behaviour of the Proposed ECHA-LWCNN

The convergence behaviour of the suggested ECHA-LWCNN model shows that the model converged consistently in the entire process of optimization. Training loss as well as validation loss showed consistent reduction from 0.4812 and 0.5103 after 50 epochs to 0.1067 and 0.1388 after 500 epochs, respectively. Meanwhile, accuracy for training and validation increased from 77.34% and 75.82% to 95.80% and 94.05%. Learning rate of the model was gradually reduced from 0.001 to 6.3×10^{-5} , making the model converge consistently and minimize oscillations in later phases of training. Minimal

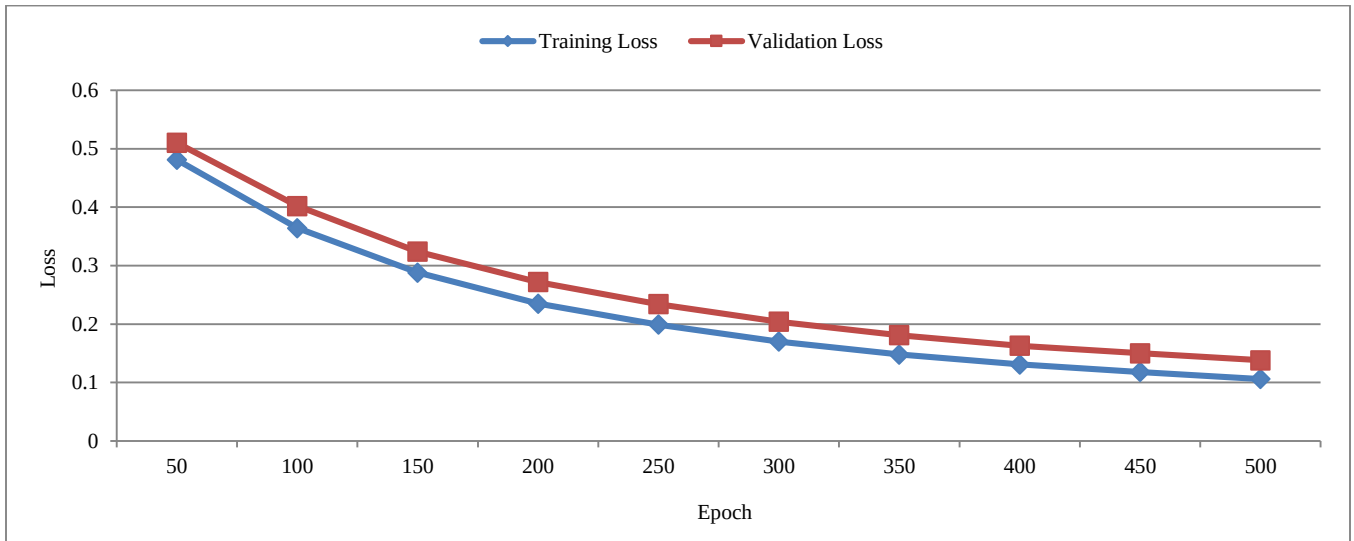
difference (1.75%) between the training and validation accuracy indicates minimal overfitting of the suggested method. Table 2 represents training history for ECHA-LWCNN over 500 training epochs. ECHA-LWCNN exhibits steady convergence, achieving 95.80% accuracy during training and 94.05% accuracy during validation, indicating good generalization with minimal overfitting. Both losses decrease consistently throughout training, demonstrating stable convergence and effective optimization. Accuracy curves are shown in Figure 11(a) whereas loss curves are shown in Figure 11(b).

Table 2. Training setup and learning results of ECHA-LWCNN

Epoch	Loss (Training)	Loss (Validation)	% Accuracy (Training)	% Accuracy (Validation)	LR
50	0.4812	0.5103	77.34	75.82	0.001
100	0.3641	0.4017	83.67	81.45	0.001
150	0.2873	0.3244	87.21	85.37	0.0005
200	0.2344	0.2718	90.14	87.92	0.0005
250	0.1987	0.2341	91.88	89.64	0.00025
300	0.1701	0.2042	92.73	91.18	0.00025
350	0.1482	0.1814	93.52	92.34	0.000125
400	0.1312	0.1631	94.29	93.07	0.000125
450	0.1178	0.1499	94.88	93.71	0.000063
500	0.1067	0.1388	95.80	94.05	0.000063



(a)



(b)

Fig. 11(a) Accuracy curves, and (b) Loss curves.

4.9. Analysis of Ablation

The analysis of ablation was conducted to evaluate the individual impact and effectiveness of each module incorporated into ECHA-LWCNN framework. The purpose of the analysis of ablation is to evaluate the effects of individual module within the proposed ECHA-LWCNN method. The combination of BAM-based U-Net, hybrid feature fusion, LWCNN, and ECHA optimization has shown the best result. The exclusion of the BAM-based U-Net negatively impacts

the multi-scale feature extraction ability; omission of the hybrid feature fusion negatively impacts distinguishing capability of learned features. In turn, the substitution of the ECHA optimizer by the standard approach of weight optimization negatively impacts the classification results, thus proving the efficiency of the ECHA optimizer in improving convergence. Table 3 shows the ablation results obtained by evaluating the effect of individual module.

Table 3. Analysis of ablation of ECHA-LWCNN framework

Configuration	Model Description	Accuracy (%)
C1	Standard U-Net + Standard CNN (Baseline)	84.31
C2	Standard U-Net + Lightweight CNN (LWCNN)	88.15
C3	BAM U-Net + LWCNN	90.27
C4	BAM U-Net + LWCNN + MLTP + STP + LayerCAM	93.38
C5	Proposed ECHA-LWCNN (BAM U-Net + MLTP + STP + LayerCAM + ECHA)	95.80

5. Comparative Discussion

When comparing the proposed ECHA-LWCNN model with the current approaches, the developed model offered high efficiency in pancreatic cancer detection. Although the existing approaches show considerable performance, they still suffer from various shortcomings, which hinder their performance. The DLR [20] model tested on a very small number of data mainly for the validation cohort, which leads to generalization issues. The RSF [21] model suffered from

the risk of overfitting and the HDS [7] required more computational time. In MMRF-ResNet [23], the ResNet is prone to overfitting and has interpretability issues, and the GrpNN model [24] is tested on a limited sample size, which leads to generalization issues. The above-mentioned limitations are resolved by the developed ECHA-LWCNN model, where the LWCNN decreases potential for overfitting, also ECHA minimizes the time complexity. Table 4 presents a comparison of the proposed model with existing approaches.

Table 4. Comparative discussion of ECHA-LWCNN

Methods	TP=90			KF=10		
	Accuracy (%)	Sensitivity (%)	Specificity (%)	Accuracy (%)	Sensitivity (%)	Specificity (%)
DLR	92.97	91.43	94.51	91.59	93.22	89.97
RSF	92.16	90.08	94.24	92.40	91.29	93.51
HDS	89.59	91.93	87.25	86.91	87.24	86.58
MMRF-ResNet	94.18	94.72	93.64	87.86	88.20	87.51
GrpNN	94.84	95.19	94.49	89.97	91.73	88.20
Proposed ECHA-LWCNN	95.80	96.39	95.20	94.05	93.75	94.36

5.1. ROC Analysis

A model with better overall performance is one whose ROC curve is located closer toward the top-left portion of the plot. The positioning indicating that model attains an extremely low FPR, while having a very high TPR, demonstrating the effectiveness of the model in differentiating cancerous and non-cancerous cases. Developed technique's

Receiver Operating Characteristic curve analysis is explained below. Figure 12 displays the ROC analysis's results. The developed ECHA-LWCNN outperformed the traditional methods such as DLR, RSF, HDS, MMRF-ResNet, and GrpNN, by attaining a TPR score of 0.938, 0.942, 0.948, 0.953, 0.961, and 0.9622 for FPR of 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, and 0.9.

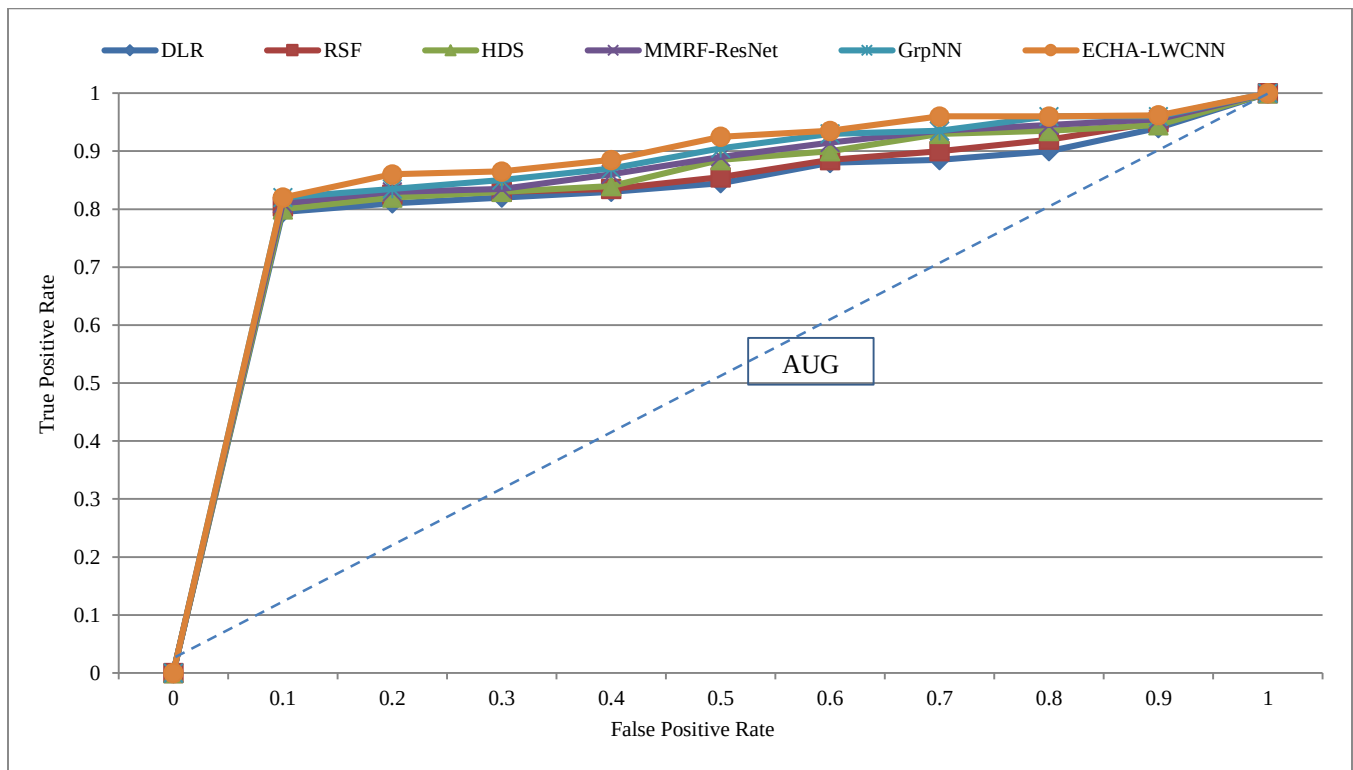


Fig. 12 ROC analysis curve

5.2. ECHA Convergence Analysis

The convergence behaviour of the suggested ECHA algorithm against GA, PSO, COA, and EEFO is demonstrated in Figure 13. In all the optimization methods, it is observed that there is a steady decrease in the objective function value with an increase in iterations. Nevertheless, the ECHA converges faster within the first few iterations and also obtains

a lower fitness value than the other competitors. The better convergence behaviour is possible due to the combination of cooperative chain and adaptive searching methods which coordinate exploratory and exploitative search behaviors. Thus, the ECHA algorithm produces optimal parameters for the lightweight CNN.

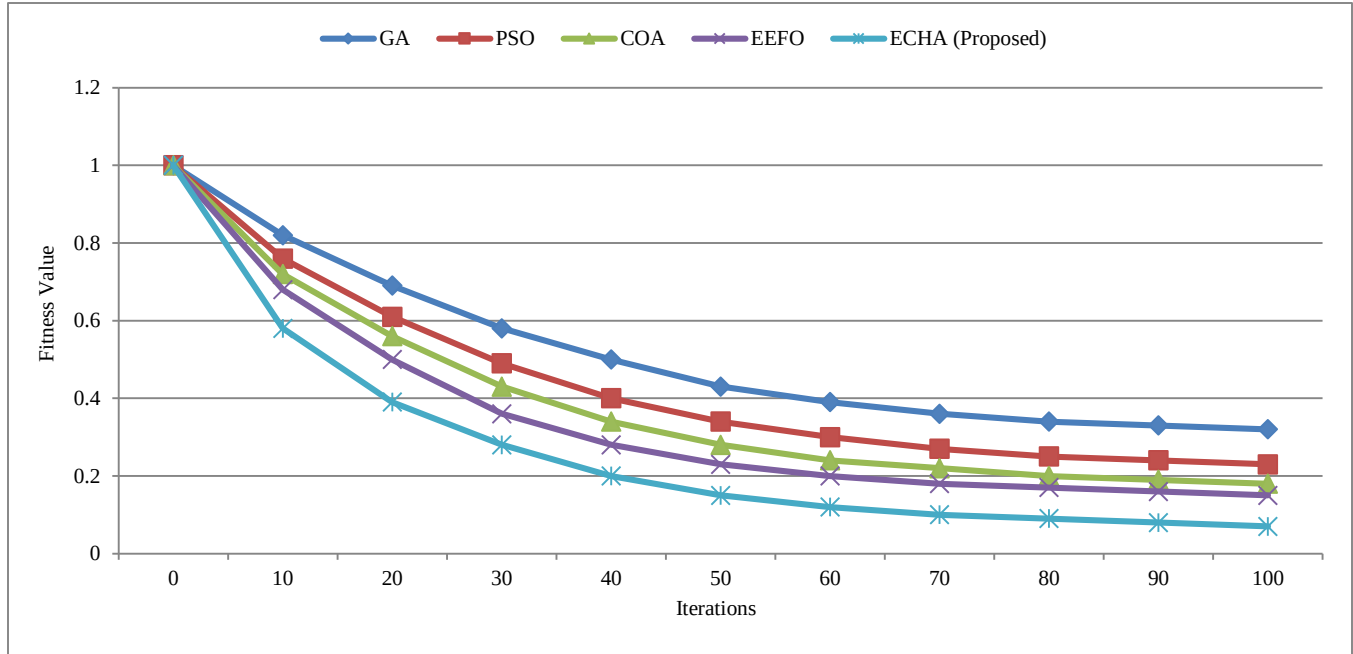


Fig. 13 Convergence analysis of ECHA and baseline optimization algorithms

5.3. Comparative Memory Usage Analysis

The memory consumption analysis was done to compare the computational efficiency of the suggested ECHA-LWCNN model with that of some of the pancreatic cancer detection models. From the memory consumption analysis shown in Figure 14, it is clear that the ECHA-LWCNN model consumes only 497 KB of memory, indicating a low memory requirement when compared with DLR (623 KB), RSF (613 KB), HDS (543 KB), and MMRF-ResNet (631 KB), although being comparable with GrpNN. This is because of the lightweight architecture of the CNN model and efficient optimization of parameters through the proposed Electrophorus Chain Hunt Algorithm (ECHA). The memory consumption analysis for different pancreatic cancer diagnosis techniques is illustrated through Figure 14.

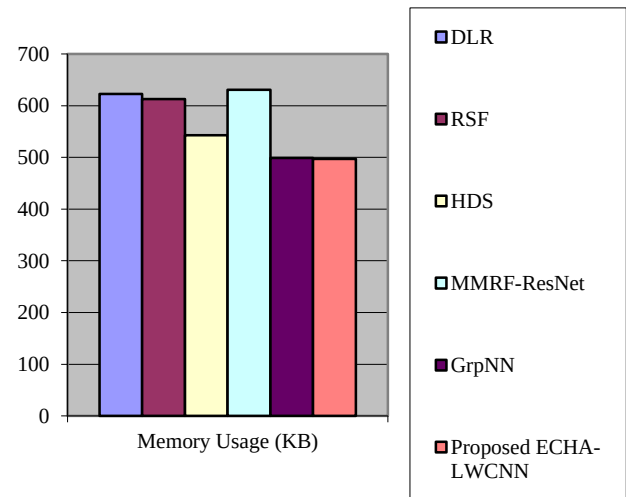


Fig. 14 Comparative memory usage analysis

5.4. Performance Evaluation against Existing Approaches

Enhanced efficiency of ECHA-LWCNN framework is due to the mutual contribution of the different modules of the framework. CT images of the pancreas have several challenges due to the differences in the shape, size, surroundings, and lesions of the pancreas. These challenges have been tackled by the proposed framework in a sequential manner using segmentation, hybrid features, classification, and optimization.

In the case of BAM-U-Net, localization of the pancreas is carried out and elimination of unwanted background noise occurs first before any further operations. Attention mechanisms play an important role in representing the spatial and channel features better by focusing on the clinically important area. MLTP, STP, and LayerCAM features complement each other in their own ways. While MLTP and

STP take into account the local and statistical texture features, LayerCAM represents spatial activation features. LWCNN makes the architecture less complex through the selection of the relevant features, thus avoiding overfitting, also reducing the computations of the network. Additionally, the ECHA algorithm looks for an optimal structure of the lightweight classifier, thereby optimizing the usage of the combined feature representation.

This model attained a performance of 95.80% accuracy, 96.39% sensitivity, and 95.20% specificity, and the Ten_fold CV technique provided an accuracy of 94.05%. The small standard deviation is indicative of a consistent performance of the algorithm across all validation folds. In comparison to previously published results for deep learning algorithms, the proposed framework exhibits a competitive performance while retaining a light-weight design.

Furthermore, the qualitative analysis presented in Figure 6 confirms these results. First, pancreas segmentation is performed based on BAM, next MLTP and STP produce local responses of texture features, and finally LayerCAM points out meaningful regions. The concatenation of these features is used before classification. In conclusion, the achieved boost

in performance is due to (i) attention-driven pancreas localization, (ii) complementary hybrid feature extraction, (iii) efficient classification, and (iv) ECHA optimization.

6. Summary and Conclusion

The proposed model of ECHA-LWCNN was designed for accurate detection of PDAC. The segmentation process of the CT scans was performed using a BAM-based U-Net to minimize computational complexity of the entire framework. Various features from the images are effectively extracted, which reduces the dimensionality and aids in the improved performance of pancreatic cancer detection. Additionally, the employment of the LWCNN minimizes the risk of overfitting and through the tuning of weight and bias of the LWCNN classifier; the ECHA facilitates effective pancreatic cancer detection. With results of 95.80%, 96.39%, and 95.20% in, accuracy, sensitivity and specificity respectively, the experimental results showed that the created model performs better than the current methods. The approach can serve as an efficient tool for pancreatic cancer detection. In the future, the plan is to explore improved ensemble techniques for detecting pancreatic cancer and test the model on different medical datasets to better understand and enhance its overall performance and reliability.

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