Automated Breast Cancer Diagnosis using Optimization Algorithm with Deep Learning on Histopathological Images

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Abstract: In the domain of medical diagnostics, the research for effectual and accurate breast cancer (BC) detection has stimulated the incorporation of cutting-edge technologies, mainly deep learning (DL). By leveraging complex patterns and features extracted by deep neural networks (DNNs), this technique aims to revolutionize the diagnostic setting, providing a highly accurate and early identification of BC. In the case of increasing patient outcomes, this research notes an important step towards the comprehension of advanced, technology-driven diagnostic tools in the realm of BC detection. This study designs a wide-ranging architecture for automated breast cancer diagnosis employing chimp optimization algorithm with deep learning (ABC-COADL) algorithm. EfficientNet, known for its higher performance in image classification functions has been utilized to remove important features from mammogram images. The LSTM-based classification algorithm (COA)could beutilized for hyperparameter tuning. Stimulated by the intelligent behavior of chimpanzees in problem-solving, COA modifies the dynamic nature of DL algorithms, proficiently navigating the huge search space for the best hyper parameters. The developed architecture is estimated on a wide-ranging database, representing its efficiency in automating BC diagnosis. Comparison analyses with existing approaches highlight the supremacy of the combined method with respect of distinct measures. The robustness of the model is further analysed through validation and cross-validation under diverse databases.

Keywords: Breast Cancer; Chimp Optimization Algorithm; Magnetic Resonance Imaging; EfficientNet; Deep Learning

1. Introduction

Breast Cancer (BC) is a different disease that comprises many entities with unique histological, biological, and medical features. This malignancy explodes from the development of irregular breast cells and may attack adjacent fine tissues [1]. Initially, its clinical screening was implemented by using radiology images, for instance Magnetic Resonance Imaging (MRI), ultrasound imaging and mammography. But, these non-invasive imaging technique not capable of defining cancerous regions proficiently [2]. To put end to this, biopsy method applied to analyse malignancy in BC tissues more widely. The procedure of biopsy contains assortment of tissue samples, rising them on microscopic glass slides, and stain these slides for enhanced visualization of cytoplasm and nuclei [4]. Then, an experienced pathologist can do microscopic study of these slides to decide diagnosis of BC. However, physical examination of difficult-natured histopathological images is a time-consuming task as well as tiresome procedure and might be lead to more errors [4]. Therefore, computer-aided diagnosis of histopathological images plays an important part in analysis of BC and its prediction [5]. However, the procedure of increasing tools for execution is inhibited by following tasks.

Primary, histopathological images of BC are fine-grained; highest resolution images portray rich regular structures and difficult textures [6]. The changeability in constancy and class among classes makes detection very difficult mainly when dealing with manifold classes [7]. The second task is restrictions of feature extraction models for histopathological images of BC. Customary feature extraction methodologies like gray-level co-occurrence matrix (GLCM) and scale-invariant feature transform (SIFT) rely on supervised data [8]. Besides, preceding knowledge of information is required to pick beneficial features, which makes feature extraction efficacy extremely low as well as computation weight very heavy. In the end, final removed features are low-level and unreliable features of histopathological images. Therefore, this leads to final method and provides poor classification outcomes [9]. DL models have high power to mechanically remove features, recover information, and learn innovative abstract data representations [10]. The techniques are capable of resolving problems of traditional feature extraction as well as effectively used in biomedical science, computer vision and so on.

This study designs a wide-ranging architecture for automated breast cancer diagnosis employing chimp optimization algorithm with deep learning (ABC-COADL) algorithm. EfficientNet, known for its higher performance in image classification functions has been utilized to remove important features from mammogram images. The LSTMbased classification method goal is to offer precise and reliable diagnoses. For optimizing the performance of the developed system, the Chimp optimization algorithm (COA) could be utilized for hyperparameter tuning. The developed architecture is estimated on a wide-ranging database, representing its efficiency in automating BC diagnosis. Comparison analyses with existing approaches highlight the supremacy of the combined method with respect of distinct measures.

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2. Literature Works

Salim and Sarath [11] devised an effectual mechanism for BC identification and classification employing HIs that exploit a DenseNet-related Chronological Circle Inspired Optimizer Algorithm (CCIOA). DL methods have been employed in the recommended BC classification method for accurately segmenting and recognizing the BC. The segmentation has been achieved ResuNet++, as well as effective optimizer method named Invasive Water Ebola Optimizer (IWEO) has been employed for fine-tuning the network's parameters of DL. Besides, DenseNet was implemented for BC identifying, whereas CCIOA was employed for training the DenseNet. In [12], an automated BC diagnosis approach including subsystem has been designed. The primary subsystem could be decreased noise. This method designed the primary subsystem dependent upon the models of stacked denoising-AE (SDAE)generative adversarial networks (GANs). The secondary subsystem was to categorize images; for remove higherlevel features from the images, DCNNs could be utilized. The final subsystem must be identified anomalies in the effectiveness of model.

Uppada et al. [13] designed an innovative Hybrid Segmentation technique that employs the energy feature coefficients achieved in Non-Subsampled Contourlet Transform for cell-nuclei segmentation of BC HIs. The method assessment has been accomplished through training database as well as for classification segmented features that could be removed through Multiclass-SVM (M-SVM), DT, MLP, and K-NN. In [14], an ensemble of a 2 CNN methods incorporated with Channel and Spatial attention has been developed. Features in the HIs could be parallelly removed by a 2 robustness custom deep frameworks like DAMCNN and CSAResnet techniques. Lastly, ensemble learning was utilized for additionally increasing the effectiveness. The analysis of the method must be performed employing BreakHis databases.

In [15], a 2 models have been designed to analyse BC at single and multi-magnification HIs. The primary developed method employs a pre-trained DenseNet201, CNN technique and fine-tuned through the openly accessible BreakHis database. The secondary method contains a 4 subsystems, all resultant to the magnifications as well as trained by relevant magnification images. Then, the outcomes achieved in such as 4 subsystems could be combined together for creating the ultimate decision. Yang et al. [16] projected an innovative multimodal DL technique incorporating whole slide H&E images (WSIs) and medical data. The DCNN has been implemented in such images for retrieving image features that must be integrated with the medical information. According to the integrated features, a new multimodal technique was made for forecasting the diagnosis of all patients.

3. The Proposed Model

In this study, we have proposed a comprehensive framework for ABC-COADL approach. It contains several processes in BC detection and classification. Fig. 1 demonstrates the workflow of proposed ABC-COADL approach.



Figure 1: Workflow of ABC-COADL approach

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3.1 EfficientNet model

For feature extraction, the ABC-COADL approach is utilized in EfficientNet model. In 2019 Mingxing Tan, et al. developed an innovative architecture scaling method that depends on a simple compound coefficient for scaling up the networks at a well- known manner [17]. In the majority of the approaches, scaling in the network dimensions could be achieved to resolution/ width/ depth, while, Efficient Net presents an identified set of scaling-coefficients. The scaling operation employed in this model has been also called as compound scaling. When $d = x^{\phi}$ represents the depth, $w = y^{\phi}$ denotes the width, $r = z^{\phi}$ has the resolution of an input channel, and lastly, ϕ represents the compound coefficient utilized for controlling the accessible resources for scaling the model next, the compound scaling is expressed as Eq. (1).

$$s \cdot r = x \cdot y^2 \cdot z^2 \approx 2, x \ge 1, y \ge 1, z \ge 1$$
(1)

In Eq. (1), *z* indicates any constants that support allocating the extra work to the width/ depth/ resolution network. Convolutional layers in a model have been processed as the optimum computationally expensivefunctions. Additionally, Floating-point functions per second (FLOPS) of a convolutional function are closely in proportion to d, w^2, r^2 . The relationship of FLOPS represents that twice the *d* outcomes to double the FLOPS, while, double the *w* or *r* leads to increase the FLOPS closely with four times. Consequently, to generate the over-all FLOPS below 2^{ϕ} , the limitations utilized such as $(x \cdot y^2 \cdot z^2) \approx 2$.

For AD classification employing brain images, we are deliberated the framework of EfficientNetBO, and EfficientNetB7. Initially, we will consider the frameworkas well as performances of BO architecture. Meanwhile, the models have been difficult, we can be subdivided the model. Although Efficient Netcan be eight variants, we have attempted multiple variant, B7. The modifications at EfficientNetB7 framework.

3.2 LSTM based classification

At this stage, the LSTM-based classification system aims to provide accurate and reliable diagnoses. LSTM is one of the types of recurrent neural networks (RNNs) that planned to perfect sequential data by taking longer term dependencies and modifying vanishing gradient problem which affects customary RNNs [18]. A LSTM cell is the main structure block of an LSTM system and prepared by several gates in order to manage flow of information.

The LSTM preserves a cell state (CS) that goes al'ong whole sequence and permits it to seizure longer-term dependencies. The upgrade to CS directed by 3 gates namely forget (f), input (i), and an output (o). A forget gate defines what data from CS (C_t) must be rejected or kept. The input gate regulates novel data that must be kept in CS. The candidate cell state (\tilde{C}_t) is novel data to be further to CS. The new CS is a mixture of what was preserved by forget gate as well as what was included by input gate as well as candidate cell state.

$$f_{t} = \sigma (W_{f} \cdot [h_{t-1}, x_{t}] + b_{f}), (2)$$

$$i_{t} = \sigma (W_{i} \cdot [h_{t-1}, x_{t}] + b_{i}), (3)$$

$$\tilde{C}_{t} = \tanh(W_{C} \cdot [h_{t-1}, x_{t}] + b_{C}), (4)$$

$$C_{t} = f_{t} \odot C_{t-1} + i_{t} \odot \tilde{C}_{t}, (5)$$

Whereas W is weight matrix and b denotes bias term, h_{t-1} denotes hidden state at preceding time step, x_t signifies input at current time step, σ represents logistic function, and \odot denotes element-wise multiplication operation. The output gate defines what next hidden state must be, depends on CS.

$$o_t = \sigma(W_o \cdot [h_{t-1}, x_t] + b_o), (6)$$

$$h_t = o_t \odot \tanh(C_t). (7)$$

The device conveyed in above equations permits LSTM to take as well as absorb dependencies in successive data. Also, makes appropriate for many challenges like speech detection, natural language processer, and time-series study.

3.3 Hyperparameter tuning

To optimize the efficiency of the proposed method, the COA is employed for hyperparameter tuning.In COA, there are four distinct phases of hunting namely Pushing, chasing, blocking, and assaulting [19]. Initially, chimpanzees are randomly generated to begin the COA and later divided into the four classes, with mathematical modelling for all the grouping as follows:

$$p_{chimp}^{t+1} = p_{prey}^{t} - \kappa \cdot \left| J \cdot p_{prey}^{t} - \zeta \cdot p_{chimp}^{t} \right| (8)$$

$$\kappa = 2 \cdot \beta \cdot r_{1} - \beta (9)$$

$$J = 2 \cdot (r_{2}) (10)$$

$$\zeta = according to chaotic mappings (11)$$

Where *t* indicates the iteration number, κ , *J*, and ζ represent the coefficient vector, *prey* denotes the fittest solution attained, and *P*_{chimp} is the optimum location of the chimp. ζ is the chaotic mapping vector. As well, β represents the non-linearly dropped coefficient range from 2.5 to 0, *r*₁ and *r*₂ are random integers within [0,1].

The most effective and primary method to statistically duplicate chimpanzee behaviors is by using prey, given the limited understanding of the first location of prey. The COA is liable for housing four of the highest-level chimpanzees. Consequently, other individuals are compelled to reposition based on the selected position, as follows: $p^{t+1} = \frac{1}{4} \times (p_1 + p_2 + p_3 + p_4) (12)$

Where

$$p_1 = p_A - a_1 \cdot |c_1 p_A - m_1 x| p_2 = p_B - a_2 \cdot |c_2 p_B - m_2 x| p_3 = p_C - a_3 \cdot |c_3 p_C - m_3 p|$$

$$p_4 = p_D - a_4 \cdot |c_4 p_D - m_4 p| (13)$$

The chaotic value mimics social behavior in classical COA, as follows:

$$p^{t+1} = \begin{cases} \zeta \ \eta_m \ge \frac{1}{2} \\ Eq. (5) \ \eta_m < \frac{1}{2} \end{cases}$$
(14)

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In Eq. (14), η_m refers to random integer ranges from zero to one. This simplified view of learning may result in moderate or premature convergence.

The fitness selection is the significant factor that impacts the performance of the COA method. The hyperparameter selection algorithm includes the solution encoding technique for determining the efficiency of the candidate solutions. In this study, the COA approachdeliberates accuracy as the main criterion for designing the FF that could be expressed in the mathematical form as follows.

$$itness = \max(P) (15)$$
$$P = \frac{TP}{TP + FP} (16)$$

From the mathematical form, FP means the false positive value and TP refers the true positive.

F



Figure 2: 100x dataset (a-b) Confusion matrices and (c-d) PR and ROC curves

Fig. 2 displays the classifier analysis of the ABC-COADL systemon 100x dataset. Figs. 2a-2b represents the confusion matrix attained by the ABC-COADL method at 70:30 of TRPH/TSPH. The figure indicated that the ABC-COADL technique can be correctly recognized and categorized with two classes. Moreover, Fig. 2c displays the PR analysis of the ABC-COADL system. The figure described that the

ABC-COADLalgorithmobtains greater PR analysiswith each class. Also, Fig. 2d shows the ROC analysis of the ABC-COADL technique. The figure revealed that the ABC-COADL methodolgoy leads to improved outcomes with higher ROC values on diverse classes.

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4. Performance validation

The performance outcomes of the ABC-COADLsystem can be examined on the BreakHis dataset. It contains 100x dataset including 2081 samples under a 2 classes as described in Table 1.

Table 1: Details of dataset

Class	Magnification : 100X				
Benign	644				
Malignant	1437				
Total	2081				

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In Table 2 and Fig. 3, a BC detection analysis of ABC-COADL algorithm with 70:30 of TRPH/TSPH. The obtained outcome shows that the ABC-COADLsystemcan beeffectual and properly recognizes benign and malignant samples. According to 70% of TRPH, the ABC-COADL approach gives average $accu_v$ of 87.50%, $prec_n$ of 86.46%,

 $reca_l$ of 84.17%, $spec_y$ of 84.17%, F_{score} of 85.16%, and MCC of 70.60%. Besides, on 30% of TSPH, the ABC-COADL methodology gains average $accu_y$ of 89.12%, $prec_n$ of 86.99%, $reca_l$ of 86.24%, $spec_y$ of 86.24%, F_{score} of 86.60%, and MCC of 73.23% respectively.

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Class	Accuracy	Precision	Kecan	specificity	r-score	MUU	
TRPH(70%)							
Benign	87.50	84.06	75.00	93.35	79.27	70.60	
Malignant	87.50	88.87	93.35	75.00	91.05	70.60	
Average	87.50	86.46	84.17	84.17	85.16	70.60	
TSPH(30%)							
Benign	89.12	82.18	79.44	93.03	80.79	73.23	
Malignant	89.12	91.80	93.03	79.44	92.41	73.23	
Average	89.12	86.99	86.24	86.24	86.60	73.23	



Figure 3: Avergae of ABC-COADL algorithm on 70:30 of TRPH/TSPH

Table 3 and Fig. 4 displays the comparison analysis of ABC-COADLsystem with recent approaches on 100X dataset. The achieved outcomes shows that the ABC-COADL algorithm can be exceed better outcomes compared to other models. According to $accu_{v}$, the ABC-COADL methodology gets greater $accu_v$ of 89.12% whereas the PFTAS-QDA, InceptionV3, ResNet-50, Inception ResNetV2, and Xception techniques acquires reduced $accu_{v}$ of 82.64%, 76.96%, 71.26%, 70.45%, and 81.85% individually. Additionally, with $prec_n$, the ABC-COADL model get improved $prec_n$ of 86.99% but, the PFTAS-QDA, InceptionV3, ResNet-50, Inception ResNetV2, and Xception approaches obtain slower $prec_n$ of 82.64%, 92.03%, 72.97%, 91.31%, and 89.07% correspondingly. Lastly, on $reca_l$, the ABC-COADL algorithm gets greater $reca_l$ of 86.24% however, the PFTAS-QDA, InceptionV3, ResNet-50, InceptionResNetV2, and Xception systems achieved minimum $reca_l$ of 82.51%, 69.25%, 88.12%, 63.14%, and 84.87% respectively.

Table 3: Comparisonanalysis of ABC-COADL algorithm
with recent methods on 100X dataset

with recent methods on room dataset							
Magnification : 100X							
Methods	Accuracy	Precision	Recall	F-Score			
ABC-COADL	89.12	86.99	86.24	86.60			
PFTAS-QDA	82.64	82.64	82.51	81.58			
InceptionV3	76.96	92.03	69.25	80.51			
ResNet-50	71.26	72.97	88.12	81.57			
InceptionResNetV2	70.45	91.31	63.14	74.45			
Xception	81.85	89.07	84.87	86.91			

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Magnification : 100X

Figure 4: Comparative outcome of ABC-COADL algorithm with 100X database

5. Conclusion

In this study, wedesigns a wide-ranging architecture for ABC-COADL algorithm. TheABC-COADL algorithm comprises EfficientNet, known for its higher performance in image classification functions has been utilized to remove important features from mammogram images. The LSTM-based classification method goal is to offer precise and reliable diagnoses. For optimizing the performance of the developed system, the COA could be utilized for hyperparameter tuning. The developed architecture is estimated on a wide-ranging database, representing its efficiency in automating BC diagnosis. Comparison analyses with existing approaches highlight the supremacy of the combined method with respect of distinct measures. The robustness of the model is further analysed through validation and cross-validation under diverse databases.

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