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Ensemble Residual Network with Iterative Randomized Hyperparameter Optimization for Colorectal Cancer Classification

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Abstract: - The analysis of WSI images is widely acknowledged as a method, for identifying stages of cancer and evaluating the spread of cancer cells in tissues. In histopathology image analysis deep learning models are gaining increasing importance. To enhance the effectiveness of these models it is crucial to train and fine-tune Convolutional Neural Network algorithms by adjusting hyperparameters like batch size, convolution depth, and learning rate (LR). However, determining the hyperparameters can be challenging as they significantly impact model performance. This study examines how hyperparameters influence cancer classification, in histopathology images using the CNN architecture. A method called iterative randomized hyperparameter optimization is proposed, which gradually reduces variations over time by adjusting parameters after each network layer. The combination of hyperparameters is applied to version 1 of ResNet18, ResNet50, and ResNet101 models and version 2 of ResNet50, ResNet101, and ResNet151. The results are then combined using the Adaptive Boosting algorithm. The results are quite promising on ensemble version 1 residual networks, achieving an accuracy of 98.7% when tested on nine tissue classes.

Keywords: Adaptive boosting, Deep learning, Ensemble, Hyperparameters, Optimization, Residual network.

I. INTRODUCTION

Colorectal Carcinoma is a prevalent form of cancer, its composition undergoes significant changes as the disease progresses [1]. It is therefore crucial to identify the various tissues that exist with tumor cells during a pathological colonoscopy examination. In this work, multiresolution techniques using deep learning are employed on Whole-Slide Images (WSI) of CRC tissue. Histological images, also known as Whole-Slide Images (WSI), provide microscopic views of tissue structures. Pathologists typically examine stained samples on slides using a microscope. Hematoxylin-eosin staining is commonly employed to enhance the visualization of specific tissue components. Once the tissue is converted into a digital image, a Whole Slide Image is generated. With advancements in computing capability as well as the modern image processing models, deep learning models for image processing have rapidly progressed [2]. The usage of digital image histopathology, enabled by modern slide scanners, has become increasingly relevant in tumor diagnosis. Li et al. in [3] recently provided an overview related to diagnosis options for histopathological image classification, using deep learning models. Deep learning has significantly impacted the diagnosis as well as the treatment of histopathological classification. Colorectal cancer, in particular, has witnessed a surge in scientific publications due to the adoption of algorithms based on deep learning. However, despite its potential to yield drastic changes in results, the adjusting of hyperparameters in Deep Learning has received limited attention, as evident from [3]. Batch size, learning rate, and convolution depth are crucial hyperparameters in training deep neural networks, and govern the extent of model adjustments with each update of model weights in response to estimated errors. Selecting an appropriate batch size, learning rate, convolution depth, etc. is challenging since a too-small value can prolong the training process or lead to stagnation, while a too-high value can result in suboptimal weight sets learned too quickly. Although there have been various contributions to hyperparameter optimization, this still remains an open research problem that heavily depends on the nature of the data and the problem being addressed in [4-6]. In most classification systems studies related to histopathological images for diagnosing colorectal cancer highlighted in [7-8], deep learning models are typically employed with default parameters, without conducting a detailed analysis of hyperparameter influence on system behavior.

This paper introduces a framework, for optimizing hyperparameters as well as ensemble the residual network in the Whole Slide Image (WSI) image classification system specifically focusing on the network. The research emphasizes the importance of selecting hyperparameters to improve accuracy. By conducting experiments, the paper compares the performance of Residual Networks version 1 and 2 using optimized hyperparameter combinations for

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classifying colorectal cancer (CRC) images. As learning techniques for WSI analysis continue to evolve the Residual Network was chosen due to its ability to deliver results compared to other deep neural networks while also enabling easier training. The main objective of this research is to enhance tumor type identification accuracy in images by leveraging the power of the Residual Network. The study aims to achieve goals; a) Identifying optimized hyperparameter combinations for versions of ResNet models; b) Determining the best-performing ResNet models; c) comparing these results with existing techniques, in the field.

This paper has been organized as follows: Section 2 will review previous studies on deep learning, while Section 3 will describe the methodology employed for deep learning models. Section 4 will provide comprehensive details of the experiment conducted, and finally, Section 5 will conclude the paper by suggesting potential avenues for future research in this domain.

II. RELATED WORKS

Numerous research studies have investigated methods to identify, categorize, and segment colorectal cancer (CRC) by analysing Whole Slide Images (WSI). In one study [9] a unique dataset was created, comprising 5000 images of cancer in humans. The dataset included eight types of tissues. To build this dataset ten slides containing CRC tissue were carefully. Divided into overlapping tiles measuring 150 × 150 pixels. The analysis focused on tissue types such, as cells, background, adipose tissue, normal mucosal glands, stroma, tumor epithelium and debris. These images formed a collection of 625 × 8 images that were used for training and testing the image classification task. The researchers employed four classification methods (linear SVM, Decision Trees function SVM, neighbour and radial basis). Found that the RBF SVM (Radial Basis Function Support Vector Machine) achieved the highest performance with an accuracy of 87.4% in separating tissues. Here the highest classification accuracy itself is less than 90%. Also, the method says that "average staining intensity is considerably varied between the tissue samples." Staining variability is a common challenge in histopathological image analysis, and the proposed method explicitly addresses how it handles or mitigates the impact of staining variations on classification accuracy. In another study [10], a system was proposed for classifying CRC tissues using nets (ConvNets). This study utilized data, from two sources. The first source consisted of a group of full slide images depicting cancer from 74 patients. The researchers used a dataset of cancer images, which consisted of 5000 patches measuring 150×150 pixels. They explored the importance of staining normalization in classifying CRC tissue from H&E stained images. The dataset was subjected to staining normalization resulting in an accuracy of only 79.7%. The scalability of the proposed methodology is not explicitly discussed. Whether the model's performance scales well with an increasing amount of data or if there are limitations in scalability is an important consideration.

[11] use the Epistroma dataset which addresses the importance of hyperparameters, especially the learning rate, but the sensitivity of the proposed model to changes in other hyperparameters is not extensively discussed. Deep learning models, especially complex ones like VGG19, often lack interpretability. Understanding the rationale behind the model's decisions, especially in a critical domain like medical diagnostics, is crucial. The paper could discuss efforts or methods employed to enhance model interpretability.

In [12], Alinsaif et al. Employed deep learning algorithms like DenseNet, SqueezeNet, ResNet and MobileNet to present two approaches. The first approach involved extracting features using trained models without fine-tuning while the second approach focused on fine-tuning pre-trained CNN models. The latter approach proved effective. Showed better classification results. To reduce the feature space while maintaining accuracy, ILFS (Infinite Latent Feature Selection) was utilized when training a support vector machine with deep learning features. The paper focuses primarily on deep learning techniques and doesn't extensively compare the proposed approach with traditional image analysis or machine learning methods commonly used in histopathological image classification. The researchers evaluated the results on datasets including [9]. The Epistroma dataset was mentioned earlier in [11]. By implementing SVM classification they achieved outcomes with a training accuracy of 95.4% and an AUC of 0.906, for Kathers proposed problem. ResNet [13] uses an architecture called learning, which allows it to handle the challenges of vanishing gradients by incorporating ultra-deep networks. It's interesting to note that increasing the depth of the Residual Network initially improves accuracy but beyond a point, it can lead to training errors. By adding more layers, a more effective approach is to optimize hyperparameters, for enhanced accuracy. However, existing research on AI-based computer-aided systems often relies on parameter configuration for feature extraction, which can impact the results [14-17]. In [14] the number of epochs used was 500 to 2000 and there was no special graphic processing unit used. In [15] the number of epochs used was 30 and the learning rate selected was 0.0001

which produces good accuracy with high computational time. In [16] the number of epochs used was 200. [18] has the limitation of time-consuming processes as well as less accuracy. [19] and [20] shows the importance of fine-tuning and selecting hyperparameters. Based on the above literature shows the necessity of hyperparameter optimization as well as the novelty of the model proposed.

III. PROPOSED METHOD

The proposed approach aims to enhance the accuracy of cancer classification by optimizing and combining versions of the ResNet models. We specifically differentiate between Version 1 and Version 2 of the ResNet architecture. To ensure diagnosis we tune the model by optimizing its hyperparameters. We systematically explore combinations of hyperparameters using a randomized search method. Additionally, we apply the Ensemble Adaptive Boost (EAB) technique to combine the ResNet18, ResNet50, and ResNet101 models while optimizing their weights. This practical solution significantly improves image classification accuracy and generalization resulting in performance, in classifying colorectal cancer and achieving higher F1 scores. Overall general block diagram has been shown in figure 1.

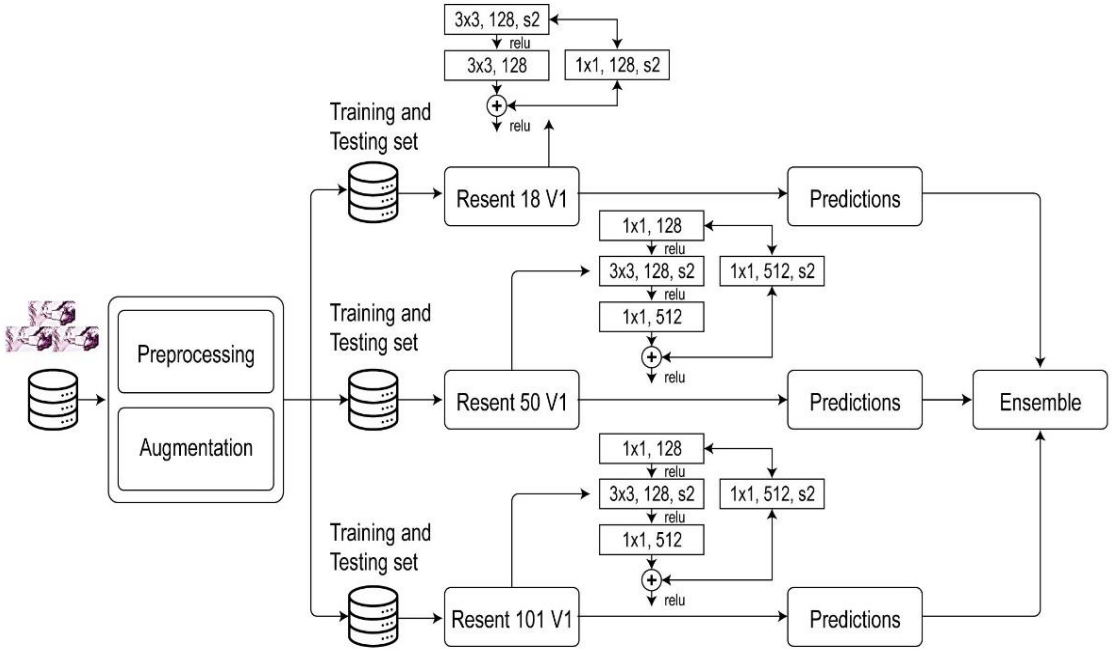
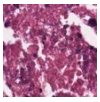
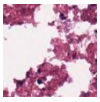
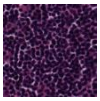
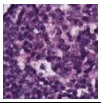
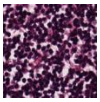
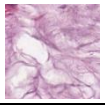
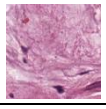
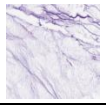
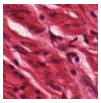
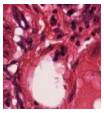
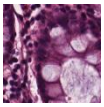
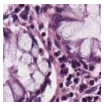
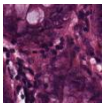
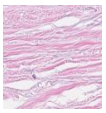
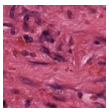
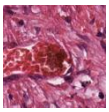
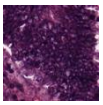
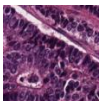
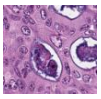


Figure 1 Proposed Method

3.1 Kather-Crc-Data Set

The dataset contains 100,000 different image patches that display tissue and colorectal cancer (CRC), in humans. These images are stained with hematoxylin and eosin (H&E), have a size of 224x224 pixels. Each patch has a resolution of 0.5 microns, per pixel (MPP). To compile this dataset various tissue types were carefully selected from a database, including detritus, background, adipose tissue, normal mucosal glands, mucus, stroma, tumor epithelium, lymphocytes and muscle. Table 1 of the NCT CRC HE 100K database provides samples representing each CRC tissue type. Kather et al. Evaluated texturing approaches using tenfold cross validation as described in [21] (http;//dx.doi.org/10.5281/ zenodo.1214456). Table 1 showcases the composition of images, in both the NCT CRC HE 100K (100K Dataset) and CRC VAL HE 7K (7K Dataset) databases.

Table 1 Dataset Structure and Samples

Class	Number of Images	Sample 1	Sample 2	Sample 3
Adipose(ADI)	10,407			
background (BACK)	10,566			
Debris(DEB)	10,512			
Lymphocytes (LYM)	11,557			
Mucus(MUC)	8,896			
Muscle(MUS)	13,536			
normal mucosa(NORM)	8,763			
Stroma(STR)	10,446			
tumor epithelium(TUM)	14,317			

3.2 Residual Network

Residual blocks play a role in the architecture of ResNet. Unlike designs that stack layers with batch normalization and activation layers ResNet takes a different approach. In the past models were limited to using a few layers but subsequent research revealed that increasing the layer count could significantly improve the performance of CNNs. Residual Networks consist of arrangements of convolutional, pooling and connected layers. There are ResNet architectures such, as ResNet 18 (with two layers) and ResNet 50,101,152 (with three layers). This paper introduces a novel methodology to ensemble and optimize the behavior of residual network models, specifically concentrating on the classification of WSI images with nine tissue variants.

ResNet Version 1 and ResNet Version 2 are the two most common versions. The ResNet design, which makes use of a stacked residual network model, wasn't taken into account in this situation. In ResNet V1, a second non-linearity is applied after the addition operation between the input, indicated as x, and the residual mapping F(x). More specifically, batch normalization, ReLU activation, and convolution operation are completed in that order. Before being sent to the following block as the new input, the result of the addition operation in ResNet V1 is subjected to ReLU activation. The result of the addition operation between the identity mapping and the residual mapping is the main focus of ResNet V2. Because there is no ultimate non-linearity in ResNet V2, an identity connection may be

used as a straight route from the input to the output. ResNet V2 adds batch normalization and ReLU activation to the input before multiplying by the weight. ResNet V1 and ResNet V2 can be distinguished from one another by how the addition operation is handled and non-linearity is applied

3.3 Residual Network Hyperparameter Optimization

The first step involves resizing the images to dimensions of 128×128×3 and augmenting them with rotated and shifted versions along, with the images using a batch size of 32. To assess the accuracy of the selected dataset we tested models, including ResNet18, ResNet50 ResNet101, ResNet50V2 ResNet101V2, and ResNet152V2. Afterward, we trained the model to optimize the following parameters:

- The "batch size" refers to how many images are processed simultaneously in each training iteration. If the batch size is too small it can slow down the convergence of the model. On the other hand, if it's too large it may impact training speed.
- "Conv3_depth" represents the Convolutional layer.
- "Conv4_depth" represents the fourth Convolutional layer.
- "Pooling" determines which type of aggregation function is used for pooling (e.g., average or max pooling).
- The "learning rate" determines how quickly a model learns weights during training.

The "optimizer" is a method used to adjust parameters (weights and biases) in a network during training. In this paper three optimizers were analysed as shown in Table 2.

The Residual Network (ResNet) model was fine-tuned by adjusting hyperparameters using a randomized optimization method. This process aimed to find the hyperparameters for accurately diagnosing Colorectal Cancer. Table 2 shows the range of hyperparameters that were trained for ResNet. In our approach we employed a randomized optimization technique to thoroughly search for the combination of hyperparameters, within the ResNet architecture. This technique systematically explores all combinations to identify the set.

Table 2 Range of hyperparameters trained for Resnet

Hyperparameter (v)	**Symbol**	**Range (m)**
ResNet_Version	V	['version1', 'version2']
Batch_Size	B_s	[32, 64]
conv3_depth	C_{d3}	[4, 8, 12]
conv4_depth	C_{d4}	[6, 23, 36]
Pooling	P	['avg', 'max']
Learning rate	L_r	[0.1, 0.01, 0.001]
Optimizer	O	['adam', 'sgdm' 'rmsprop']

Once the hyperparameters were optimized we proceeded to extract features from the dataset using these optimized values. These extracted features were then inputted into a connected layer to compute classification scores.

3.4 Iterative Randomized Hyperparameter Optimization

Let ν denote the nuisance parameters, where we aim to maximize the m values as shown in equation (1) and table 2. Here v represents

$$v \in (V, B_s, C_{d3}, C_{d4}, P, L_r, O) \qquad (1)$$

One straightforward approach to setting up an iterative randomized search is by defining a vector of lower bounds v_l as shown in equation 2 and a vector of upper bounds v_u as shown in equation 3 for each component of 'ν'.

$$v_l \in (V, B_s, C_{d3}, C_{d4}, P, L_r, O)_l \qquad (2)$$

$$v_u \in (V, B_s, C_{d3}, C_{d4}, P, L_r, O)_u \qquad (3)$$

Iterative randomized search process entails selecting equidistant points of n within each interval in the form [v_{li}, v_{ui}] including v_{li} and v_{ui}. This creates a total of n^m possible combinations to check. Where m is the number of nuisance parameters. The maximum value is then chosen after the values for each pair of points have been calculated.

3.5 Ensemble method

By leveraging the Ensemble Adaptive Boost (EAB) method we can merge the outcomes of the ResNet V1 and ResNet V2 models to create a solution, for scene recognition or classification. This approach involves assigning weights, to the predictions made by each model and combining them into a precise forecast. By applying AdaBoost, a recognized technique that combines the predictions of weak learners, our objective is to enhance classification accuracy. In this study, we employ network models to form these learners by merging predictions and adjusting sample weights. Ensemble Adaptive Boost (EAB) is an advanced ensemble technique that mathematically combines the predictive power of ResNet-18, ResNet-50, and ResNet-101 models, offering a robust framework for improved image classification. EAB assigns weight coefficients to each ResNet architecture, denoted asα_{18},α_{50}, and α_{101}, respectively, and formulates the ensemble prediction as:

The final prediction $F(X)$ for RESNET Version 1 can be expressed in equation (4):

$$F(X) = \Sigma\ (\alpha_k\ x\ \mathrm{M}_k(X)) \qquad (4)$$

where *k* is {18, 50, 101}.

Similarly, for RESNET Version 2,

$$F(X) = \Sigma\ (\alpha_k\ x\ \mathrm{M}_k(X)) \qquad (5)$$

where *k* is {50, 101, 151}.

In equation (4), F(X) represents the final prediction for input data X. α_k is the weight assigned to the k-th weak learner, and $\mathrm{M}_k(X)$ is the prediction of the k-th weak learner for input X. Notably, these weights are dynamically adapted during the training process to optimize the ensemble's performance, following the principle of minimizing the exponential loss for RESNET Version 1 as shown in equation 6:

$$L(\alpha_{18}, \alpha_{50}, \alpha_{101}) = \Sigma\ exp(-Y\ x\ F(X)) \qquad (6)$$

Similarly, for RESNET Version 2,

$$L(\alpha_{50}, \alpha_{101}, \alpha_{151}) = \Sigma\ exp(-Y\ x\ F(X)) \qquad (7)$$

This loss function aims to incentivize a focus, on models that exhibit accuracy when applied to the specific dataset. The adaptability of EAB enhances the ensembles capacity to harness the strengths of each ResNet architecture resulting in a combined model that excels in classification tasks. Through the Adaptive Boost technique, we combine the feature learning capabilities of ResNet 18, ResNet 50, and ResNet 101 with adaptive weight optimization. The outcome is a mathematically grounded solution, for image classification leading to improved accuracy and generalization.

IV. RESULTS AND DISCUSSIONS

The main hardware elements, in the setup consist of an NVIDIA RTX Desktop GPU (RTX 6000), with a compute capability of 8.9 an Intel Core i7 processor and a RAM capacity of 16 GB. For programming, we utilized Matlab

R2022a within a Windows 10 operating system environment. To assess the effectiveness of the search approach we conducted experiments using two datasets; one, with 100,000 image patches and another with 7,180 patches. We chose these datasets for testing purposes. In each dataset, 40% of the images were used for training 20% for validation and the remaining 40%, for testing. We utilized a randomized search optimization technique to find the combination of hyperparameters, for a Residual Network. Among the 647 hyperparameter combinations, our method identified the one, which is presented in Table 3 and suited for our chosen database. The resulting Residual Network achieved a training accuracy of 99% and a validation accuracy of 98% as demonstrated in Table 4. In Table 4 and Table 5, you can find a summary of the performance of ResNet versions v1 and v2. These versions were trained for 15 epochs using the 'sgdm' optimizer, max pooling and specific configurations for the layers. We also compared their performance, with our proposed ResNet model, which had its hyperparameters fine-tuned using the randomized search optimization method on both the 7K and 100K datasets.

Table 3 The optimum hyperparameters

Hyperparameter	Symbol	Range
Version	V	[version1]
Batch Size	B_s	[32]
conv3_depth	C_{d3}	[4]
conv4_depth	C_{d4}	[23]
Pooling	P	[avg]
Learning rate	L_r	[0.01]
Optimizer	O	[‘sgdm’]

Table 4 Accuracy results of CRC-VAL-HE-7K Database

	Proposed iterative optimization method		
Resnet Version	Model	Training Accuracy (%)	Validation Accuracy (%)
V1	Resnet18	96.90	96.80
	Resnet50	97.6	97.63
	Resnet101	97	97.42
V2	Resnet50	96.7	95
	Resnet101	96	94.4
	Resnet152	96.57	96

Table 5 Accuracy results of NCT-CRC-HE-100K DATABASE

	Proposed iterative optimization method		
Resnet Version	Model	Training Accuracy (%)	Validation Accuracy (%)
V1	Resnet18	98	97.68
	Resnet50	98.68	98.19
	Resnet101	98	98.3
V2	Resnet50	96	96
	Resnet101	95.8	97
	Resnet152	96.5	96.79

In this research paper, we fine-tuned the hyperparameters of the ResNet model using a randomized search optimization technique. After tuning we tested the model on a dataset. Found that it outperformed models, like ResNet18, ResNet50 ResNet50V2 ResNet101, ResNet101V2, and ResNet152V2 when applied to the same dataset. Among the versions of ResNet models Version 1 showed performance compared to Version 2. Fig. 2 and Fig. 3 display the batch loss and validation loss for two databases; NCT-CRC-HE-100K and CRC-VAL-HE-7K. It is clear from these figures that ResNet50 Version 1 achieved batch loss and validation loss compared to other models. The confusion matrices presented in Fig. 4 for CRC-VAL-HE-7K and NCT-CRC-HE-100K databases respectively indicate that the proposed optimized Resnet 101 achieved image accuracy with a rate of 98%. When we combined instances of Version 1 in an approach there was further improvement in accuracy despite variations in dataset sizes. Table 6 provides a comparison of our accuracy results with works. In [14], they employed ResNet 18. Resnet 50, on the Warwick QE dataset, achieving accuracies of 85% and 88% respectively. [15] used ResNet 18, ResNet 50, and Resnet 101 models on the CRC-VAL-HE-7K dataset. They achieved accuracy rates of 94.81%, 96.94%, and 95.35% respectively. When applied to the NCT-CRC-HE-100K dataset these models achieved accuracy rates of 98.61%, 99.68%, and 99.31%. Their proposed method called "Ensemble Iterative Randomized Hyperparameter Optimization" achieved an accuracy of 98.53% on the CRC-VAL-HE-7K dataset using ResNet V1 models, which slightly increased to 98.65% on the NCT-CRC-HE-100K dataset with the network configuration. Table 7 presents the F1 scores for this proposed approach with ResNet V1 models on both datasets; The precision was found to be at a rate of 91.3% for the CRC-VAL-HE-7K dataset with a recall rate of 93.9% and an F1 score of 94.09%. On the other hand, for the NCT-CRC-HE-100K dataset this ensemble method demonstrated a precision rate of 93% a recall rate of 94.8% and a high F1 score of 95.89%. Overall this proposed ensemble method utilizing iterative randomized hyperparameter optimization consistently outperforms ResNet models in terms of accuracy and F1 scores on both datasets showcasing its effectiveness in classifying cancer cases effectively. This indicates that combining types of ResNet models while optimizing their hyperparameters provides an approach, in colorectal cancer classification.

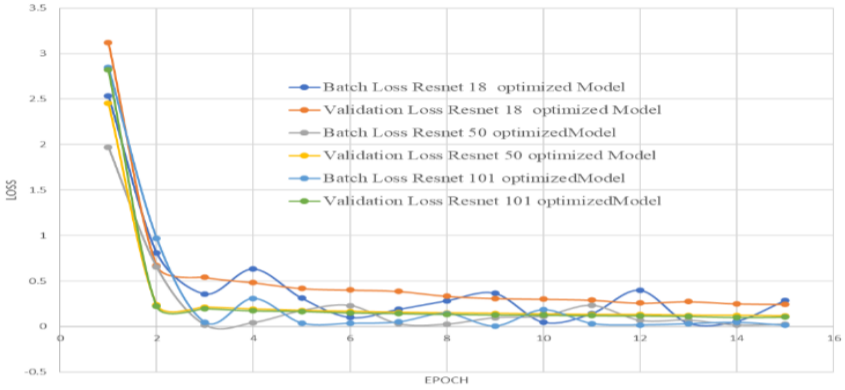


Figure. 2 Batch loss and validation Loss on NCT-CRC-HE-100K database

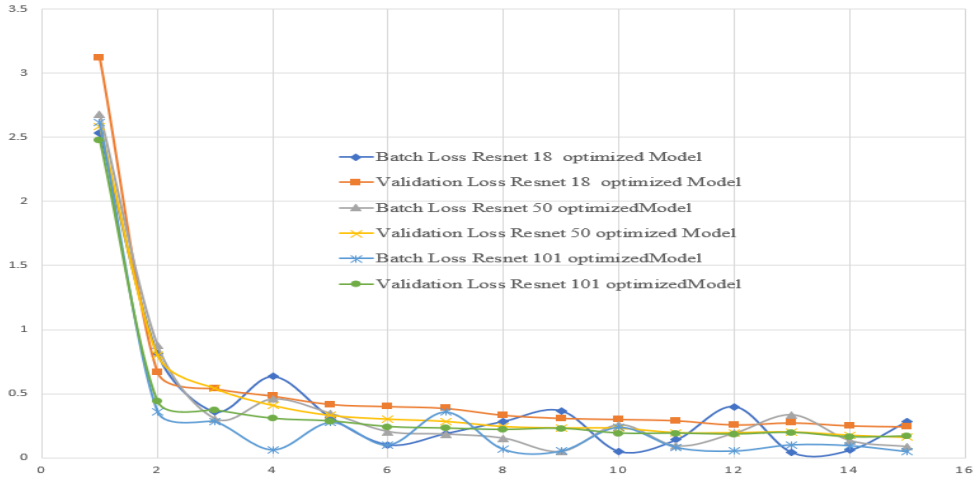


Figure. 3 Batch loss and validation Loss on CRC-VAL-HE-7K database

Figure. 4 (a) Confusion Matrix of proposed optimized Resnet 101 for CRC-VAL-HE-7K database

Figure. 4 (b) Confusion Matrix of proposed optimized Resnet 101 for NCT-CRC-HE-100K database

Table 6 Comparison of the obtained results with other related methods

Reference	Dataset	Network	Acc %
Khazaee Fadafen, et al.,2023	Warwick- QU	ResNet18	85
		ResNet-50	88
Kumar et al., 2023	CRC-VAL-HE-7K	ResNet18	94.81
		ResNet50	96.94
		ResNet101	95.35
Kumar et al., 2023	NCT-CRC-HE-100K	ResNet18	98.61
		ResNet50	99.68
		ResNet101	99.31
	CRC-VAL-HE-7K	ResNet18 V1	96.90
		ResNet50 V1	97.6
		ResNet101 V1	97
Proposed Ensemble Iterative Randomized Hyperparameter optimization	CRC-VAL-HE-7K	Ensemble ResNet V1	98.53
Proposed Ensemble Iterative Randomized Hyperparameter optimization	NCT-CRC-HE-100K	Ensemble ResNet V1	98.65

Table 7 Comparing the F1 Score of various residual network (Proposed Iterative Randomized Hyperparameter optimization)

Dataset	Network	Precision	Recall	F1 score
CRC-VAL-HE-7K	Ensemble ResNet V1	91.3	93.90	94.09
NCT-CRC-HE-100K	Ensemble ResNet V1	93	94.8	95.89

V. CONCLUSION

In our research, we have introduced a method to enhance the performance of ResNet models, for classifying colorectal cancer. Our focus was on the Kather CRC dataset, which contains 100,000 image patches stained with hematoxylin and eosin (H&E). Our study was to tune the hyperparameters of ResNet models. Utilize iterative randomized hyperparameter optimization. The results clearly demonstrate enhancements in accuracy when compared to ResNet models like ResNet18, ResNet50 ResNet50V2 ResNet101, ResNet101V2 and ResNet152V2. Interestingly we consistently observed that Version 1 of ResNet outperformed Version 2. Moreover, by adopting our Ensemble Adaptive Boost (EAB) technique as part of a combined approach using ResNet models together we achieved accuracy rates that exceeded those of individual models alone. On the CRC-VAL-HE-7K dataset, we obtained an accuracy rate of 98.53% while on the NCT-CRC-HE-100K dataset, the accuracy increased to 98.65%. Additionally assessing F1 scores further confirmed the effectiveness of our method with Version 1 models for both datasets; reaching values high as 94.09% and 95.89% respectively. Based on these findings we conclude that this ensemble approach coupled with hyperparameter optimization holds promise for colorectal cancer classification and showcases its potential, for practical clinical applications.

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