Deep Transfer Learning Methods for Classification Colorectal Cancer Based on Histology Images

Ahmed Sami Alhanaf
Faculty of Electrical and Electronics
Computer Engineering
Yildiz Technical University
Istanbul, Turkey
Ahmed.alhanaf@std.yildiz.edu.tr
eng.ahmedsamik@gmail.com

Saif Al-jumaili
Electrical and Computer Engineering
Altinbas University
Istanbul, Turkey
saif.aljumaili@ogr.altinbas.edu.tr
saifabdalrhman@gmail.com

Gokhan Bilgin
Faculty of Electrical and Electronics
Computer Engineering
Yildiz Technical University
Istanbul, Turkey
gbilginmail@gmail.co

Adil Deniz Duru
Neuroscience and Psychology Research in Sports Lab
Marmara University
Istanbul, Turkey
deniz.duru@marmara.edu.tr

Salam Alyassri
Electrical and Computer Engineering
Altinbas University
Istanbul, Turkey
salamyassir@gmail.com

Hasan Hüseyin Balik
Faculty of Electrical and Electronics
Computer Engineering
Yildiz Technical University
Istanbul, Turkey
balik@@yildiz.edu.tr

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***Abstract*— Deep transfer learning is one of the common techniques used to classify different types of cancer. The goal of this research is to focus on and adopt a fast, accurate, suitable, and reliable for classification of colorectal cancer. Digital histology images are adjustable to the application of convolutional neural networks (CNNs) for analysis and classification, due to the sheer size of pixel data present in them. Which can provide a lot of information about colorectal cancer. We used ten different types of pr-trained models with two type method of classification techniques namely (normal classification and k-fold crosse validation) to classify the tumor tissue, we used two different kinds of datasets were these datasets consisting of three classes (normal, low tumors, and high tumors). Among all these eight models of deep transfer learning, the highest accuracy achieved was 96.6% with Darknet53 for 5-Fold and for normal classification the highest results obtained was 98.7% for ResNet50. Moreover, we compared our result with many other papers in stat-of-the-art, the results obtained show clearly the proposed method was outperformed the other papers.**

Keywords*— *Deep Learning, CNN, Colorectal Cancer, Classification, Transfer learning

I. INTRODUCTION

In the past, modern technology was not available, so detecting diseases was a cumbersome and difficult issue. With the advancement of science and modern technologies that have begun to spread in abundance [1], one has been able to employ these techniques to serve the health sector, where diagnosing the disease of the human body is not easy and still challenging to pathology due to the need for a lot of information and accurate diagnosis.

There are many diseases that are not known and are spreading widely [2]. From that, science has developed to include the medical field, in particular through radiographic images, that may help the pathology in the health sector. The use of modern technologies such as Deep Learning is a great deal in the field of analysis and diagnosis since it has proven high efficiency and great accuracy in analyzing several types of radiographic diseases such as Covid19 [2,3,4], Alzheimer's [5, 6], Brain tumors [7]... etc.

The use of the tissue image gives greater efficiency, as it has been tested in recent scientific research [8], because theories and algorithms have the ability to analyze images and indicate the differences between healthy cells from the patient and classify them accurately.

Colon cancer is considered one of the fatal illnesses in humans because of the major deaths it causes, so it is considered one of the most prominent diseases that cause death [9]. Hence, pre-trained models are used to classify colorectal cancer [5] in this paper, the dataset is separated with a ratio (70:30) for training and tasing. This criterion is used with all eight models. We used different ways to evaluate the performance of other algorithms and find out which one can classify colon cancer efficiently as well as to check whether the model can classify the picture or not[10].

Our major contributions to this article are as follows:

- We used a pre-trained model and reuse them to classify the given dataset from large high-resolution input images.
- We explore different pre-trained models for learning and training strategies to examine the framework's ability to evaluate the performance of models
- We report the results of comprehensive examination experiments in the whole tested models and comparisons to compare between them.

II. MODELING OF THE PRE-TRAINED METHOD

Convolutional neural networks (CNNs) have been widely used to achieve different histology image analysis tasks such as nuclei detection and classification. To retrain the Pre-Trained Model, we used two different ways to reach the final results (The normal Classification method and the K-Fold Cross Validation method), this model has many types to classify the dataset, where the results are presented in the section.

Normal Classification Method (NCM) can be explained as the dataset will be divided into two parts and these two parts are called training data and validation data. So, we choose 70% of the data for training and 30% for validation. Therefore, it obtained high performance of this model since it will be trained on the greatest number of the data which can lead to providing a neural network with a strong capability of classifying colon cancer.

K-Fold Cross Validation Method [7] (KFCVM) can be considered one of the best ways of the pre-trained methods

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which should have the ability to define the data and classify it with high accuracy if it will be used in the right way and avoid any mistakes that can be caused by different external or internal factors such as the overfitting, underfitting, not enough dataset, etc. Therefore, we use KFCVM due to it can prevent consideration that factors of anything that can involve misleading the results of classification.

III. DATA SETS

The proposed framework is evaluated on two colorectal Datasets in order to demonstrate its capabilities. The first colorectal cancer (CRC) dataset for exactly the same task of colorectal grading [11, 12]. The dataset consists of 139 visual fields with an average size of 4548 × 7520 pixels obtained at 20× magnification. These visual fields are classified into three different classes (normal, low grade, and high grade) based on the organization of glands in the visual fields by the expert pathologist. We extend this dataset with more visual fields extracted from another 68 Hematoxylin and Eosin (H&E) stained Whole Slide Images (WSIs) using the same criteria. Our extended colorectal cancer (Extended CRC) [13] dataset consists of 247 visual fields with an average size of 5000×7300 pixels [14]. So, the total image for three classes as shown In Table 1 below, where GRADE-1 is represents normal tissue, GRADE-2 is a low-tumor and GRADE-3 is high-tumor cancer.

Table 1 Models used description

Data source	Grade-1	Grade-2	Grade-3	Total
CRC	71	33	35	139
Extended	106	88	53	247
	177	121	88	386

In order for the models to be suitable for classification, we changed the last three layers in all ten models, and we also changed the dimensions of the images because the images did not match the input and dimensions needed by the models used. Table 2 shows the models that were used with the required image dimensions for each of them, as well as the depth (layers used for their design) for each one.

Table 2 different pretrained models

Network	Depth	Image Input Size
GoogleNet	22	224x224
Inceptionv3	48	299x299
Densenet201	201	224x224
Resnet18	18	224x224
Resnet50	50	224x224
Resnet101	101	224x224
Xception	71	299x299
NasnetMobile	*	224x224
Darknet53	53	256x256
VGG16	16	224x224

Figure 1 shows a sample of the images that were used to classify colon cancer that consist of three different types namely GRADE-1 is representing normal-tissue, GRADE-2 is a low-tumour and GRADE-3 is high-tumour cancer.

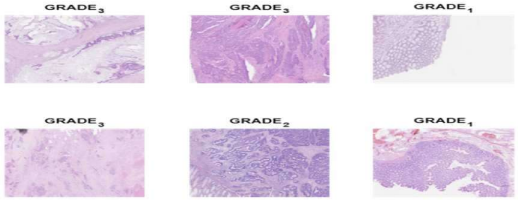

Fig. 1 Six visual field regions of colorectal tissue

IV. RESULTS

There were 386 pictures that have been used as an input to the models to classify them into three classes, so we trained the dataset by dividing the data into the two parts as shown in Figure 2.

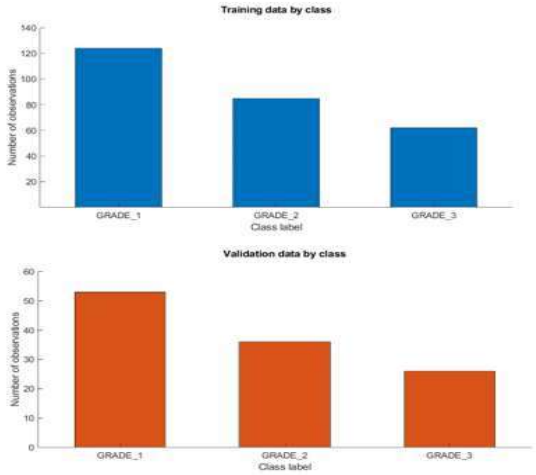

Fig. 2 Training and validation distribution

After that, we applied cross-fold validation and trained our mode, we get the result as shown in Table 3. Cross Validation isa an extremely significant method that is widely applied by data researchers. The difficulty with deep learning models is that you will not be able to know how well the model is performing until you test its performance on an independent data set (the independent data set that the model has not previously trained on). We explored and evaluated the performance of model by measuring the values such as precision, sensitivity, f-measure, g-mean, and AUC (Area Under The curve). There are many techniques used for validation and this is where cross-validation comes in to help us estimate how well your model is performing. One type of cross-validation is K-Fold validation. It is one of the most common types of deep learning. The following steps are used to perform K-fold cross-validation and are as follows:

- split the whole dataset for training in to the number of k which mean subset of dataset,each k named a fold, where we named as f1, f2, f3....fk.
- Where i = 1 to i = k, keep each only one fi as validation where the remine of the data will be used for training. Train our machine learning model using the cross-validation training set and calculate the accuracy of your model by validating the predicted results against the validation set.
- The average is the result for machine learning by calculate all K- fold results.

The k-fold cross validation approach uses all of the items in the original training data set for both training and validation. In addition, each submission is validated only once. Generally, the value of k is assumed to be 5, however this is not a hard and fast rule, and k can take any number. We take 5-Fold to check the performance of such models that showed in Table 3, we get an accuracy in each fold and then we take the average of accuracy

Table 3 Performance and Results by Using Two Types Of Classification Techniques, whereas KFCVM refers to the K-Fold Cross Validation Method and NC refers to Normal Classification.

Models	Sensitivity	Specificity	Precision	AUC	F-Measure	G-Mean	Accuracy (KFCVM)%	Accuracy (NC)%
Resnet 50	1	0.88517	0.8806	0.9997	0.93651	0.94083	93. 8	98.7
Densnet201	0.99435	0.92344	0.91667	0.9998	0.95393	0.95824	95.6	93.5
Xception	0.8571	0.47368	0.61672	0.9820	0.76293	0.68825	71.5	83.4
Vgg16	1	0.8756	0.87192	0.9982	0.93158	0.93573	93.3	98.2
Resnet 18	0.9661	0.79907	0.7943	0.9857	0.87472	0.8760	93.8	91.3
Darknet 53	1	0.93245	0.9215	0.9999	0.97375	0.96321	96.6	91.3
GoogleNet	0.9845	0.8743	0.86180	0.9827	0.93158	0.93573	93.0	92.5
NasnetMobile	0.88701	0.62679	0.66809	0.9051	0.76214	0.74563	74.6	83.4
Resnet 101	0.9524	0.8154	0.85124	0.9878	0.92157	0.92425	90.9	94.8

To ensure the accuracy of the selected model, we used the folding technique in order to prevent data bias and thus increase the accuracy and not improve the measurement results. Which thus generally affects the latest results in CNN models, we conclude that it is the best one for your problem.

We compared the obtained results with the most recent papers published in the literature. Based on the comparison, the results obtained by the method used are remarkable compared to the results of previous papers. Table 4 shows the comparison in more detail.

Table 4 Comparison with recent papers

Ref.	Year	Modality	Dataset Availability	Accuracy
[15]	2020	Colonoscopy	Private	0.867
[16]	2020	Histopathology	Public	0.9452
[17]	2020	Colonoscopy	Private	0.83
[18]	2020	Histopathology	Private	0.953
[19]	2020	Wireless Capsule Endoscopy	Private	0.9319
[20]	2019	Colonoscopy	Private	0.90
[21]	2019	MRI	Private	0.94
[22]	2019	Histopathology	Private	0.945
[23]	2019	Endoscopy	Private	0.90
[24]	2018	Histopathology	Private	0.9348
[25]	2018	Histopathology	Public	0.96
[26]	2018	Laser Microscopy Images (LMI)	Private	0.908
Our Resutls		**Histopathology**	**Public**	**0. 987**

V. CONCLUSION

We used deep transfer learning by adopting k-fold with different types of models to classify the histology images under three types of cancer for colorectal cancer. Different datasets are used to achieve accurate results and build a system that can carry out all possible types of colorectal cancer. The selected networks were well-suited for the colorectal cancer grading task, which relies on recognizing abnormalities in glandular structures. These clinically significant structures vary in size and shape that cannot be captured efficiently with standard classifiers due to computational and memory constraints. We also tested 5-fold cross-validation on the same data, and we obtained a higher accuracy for a few models like GoogleNet, DenseNet, and DarkNet53. This indicates that the method we proposed can achieve high results. We also compared our results with other papers that were recently published that also used CNN in order to classify colorectal cancer. Our results outperformed compared to the other papers.

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