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FINAL GROUP PROJECT REPORT

SECTION: 01

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1.0 Introduction

Colorectal cancer, commonly known as colon cancer, remains a pressing global health concern, casting a significant shadow of morbidity and mortality across the world. This malady transcends borders, impacting diverse populations in distinct ways. The detection and diagnosis of colon cancer pose formidable challenges within the realm of healthcare on a global scale. In this dynamic landscape, the critical importance of detecting colon cancer at an early and treatable stage looms large. The timeliness of diagnosis is a matter of paramount concern, as it bears a direct and profound impact on patient outcomes and the allocation of precious healthcare resources.

As degree students deeply immersed in the field of healthcare, we recognize the pivotal role early detection plays in the prognosis of colon cancer patients globally. It can spell the difference between life and death, significantly influencing the quality of life and long-term survival prospects. Acknowledging the urgency of this issue, we embark on a comprehensive case study that delves into the specific nuances of colon cancer detection within the intricate tapestry of the global healthcare landscape.

Our mission is to identify the unique factors that exert their influence on early diagnosis and the subsequent effectiveness of medical interventions. By doing so, we aim not only to gain a deeper understanding of the challenges and opportunities within our healthcare system but also to contribute to the ongoing efforts to improve the response to this critical health concern in our country. Through rigorous research and analysis, we hope to shed light on the intricacies of colon cancer detection, ultimately forging a path toward better outcomes and enhanced patient care. In an era where healthcare is a cornerstone of societal well-being, we recognize the significance of our work in the broader context of global health and wellness.

1.1 Problem Background

Colorectal cancer on a global scale is a multifaceted health challenge influenced by various factors specific to each country. Several elements contribute to the difficulties in early detection of colon cancer worldwide:

1. Limited Awareness and Education: There is a lack of public awareness and understanding of colon cancer in many regions globally, leading to lower participation in screening programs and reduced knowledge about the disease.

2. Inadequate Screening Programs: Colon cancer screening, including colonoscopy and fecal occult blood tests, is not universally implemented or accessible to the extent necessary to ensure early detection in many countries.

3. Cultural and Language Diversity: Many countries have diverse populations with various ethnicities and languages, posing communication challenges that can affect healthcare access and awareness of colon cancer risks on a global scale.

4. Healthcare Disparities: Socioeconomic factors and regional disparities impact access to healthcare and resources globally, further complicating early detection efforts in various regions.

5. Diet and Lifestyle Choices: Dietary habits vary globally, and certain culinary traditions may contribute to the risk of colon cancer in different populations. Additionally, lifestyle factors such as physical inactivity can influence disease development on a global scale.

6. Resource Constraints: Globally, many healthcare systems face resource constraints, including shortages of medical personnel and equipment, which can hinder early detection and timely interventions for colon cancer. The allocation of resources for preventive measures, screening programs, and adequate medical infrastructure becomes a critical factor in determining the success of early detection efforts on a global scale.

In summary, the variable success rate in detecting colon cancer at an early stage is a pressing global issue, and understanding the underlying factors specific to each country is essential. This case study endeavours to explore these factors comprehensively, with the ultimate aim of proposing strategies and recommendations to enhance early detection rates and improve the chances of successful treatment for colon cancer worldwide. Addressing

challenges such as limited awareness, inadequate screening programs, cultural diversity, healthcare disparities, diet and lifestyle choices, and resource constraints on a global scale is crucial for developing effective, equitable, and sustainable approaches to mitigate the impact of colorectal cancer globally.

1.2 Problem Statement

The crux of the matter underpinning this global case study revolves around the uneven success rate of early colon cancer detection worldwide. Early diagnosis is a linchpin in the quest for improved patient outcomes, yet it's a variable that remains frustratingly inconsistent and suboptimal within the global healthcare framework. This inconsistency in timely detection is a concern of profound significance, with consequences that ripple throughout healthcare systems globally.

When colon cancer is diagnosed at a later stage on a global scale, it often necessitates more aggressive and complex treatments, and unfortunately, the odds of survival decrease significantly. These advanced-stage cases also result in a considerable upswing in healthcare costs, imposing additional burdens on both the global healthcare system and the affected individuals. As degree students in the healthcare field, we're acutely aware of the multifaceted challenges and ramifications associated with these delayed diagnoses on a global scale.

Therefore, uncovering the underlying reasons for this variability in early detection success is not merely an academic pursuit but a mission with tangible and far-reaching consequences globally. Our objective is clear: to gain comprehensive insights into the root causes of this inconsistency, thereby providing a foundation for targeted interventions aimed at enhancing patient outcomes and optimizing the allocation of healthcare resources on a global scale. The implications of our research are profound, and we are committed to making a meaningful contribution towards a more effective and equitable global healthcare system. In a healthcare landscape where time is often the difference between life and death, our work takes on heightened importance, underscoring the urgency of this investigation.

1.3 Aim & Objectives

The main objective of this study is to design and implement classification models that demonstrate high levels of accuracy in colon cancer diagnosis using advanced deep learning techniques. This goal is driven by the urgent need for more effective and efficient methods to identify colon cancer at an early stage, which is critical for improving patient outcomes and reducing the burden. common to this disease.

Early detection of colon cancer using deep learning:

- The first goal of this study is to focus on early detection. This involves developing deep learning models capable of identifying the presence of colon cancer at an early stage. By analysing diverse clinical and genetic data, these models aim to identify subtle patterns and markers associated with colon cancer before symptoms start to develop
- This aims to contribute to early intervention and rapid treatment of colon cancer, which can significantly increase a patient's chances of successful recovery.

Evaluate the efficiency of colon cancer classification based on deep learning architecture:

- This evaluation includes rigorous testing, cross-validation, and performance metrics to evaluate the effectiveness of the developed models.
- This goal is necessary to understand how the developed model are applied to the real-world and determine their potential to be use as clinical tools.

1.4 Research Scope

The study focuses on clinical and genetic data related to colon cancer. Deep learning methods are applied for colon cancer classification, with primary data sources including histopathological images. Advanced data analysis techniques, including the application of deep learning algorithms like EfficientNet from Convolutional Neural Networks (CNN), are employed.

The research utilizes a systematic process, encompassing data preprocessing, model development, cross-validation, and performance evaluation, to create, test, and validate deep learning models for colon cancer classification. The approach involves applying deep learning algorithms, particularly CNN, to analyze and classify the collected data. The goal is to create models capable of accurately identifying colon cancer cases

2.0 Data Collection & Preprocessing

The data that will be used are histopathological images data. All images' data set are collected from Kaggle. Nearly 5000 images are used in total with different label. The data will undergoes some of pre processing process before proceeding to model development.

2.1 Importing Dataset

With all datasets that have been collected, it is important for us to understand how the data worked and how to use it. Below are the lines of codes that were applied for importing our dataset. Since images are our data type, OpenCV are used to import the image into Python in Visual Studio Code.

```
import cv2
img = cv2.imread('D:/DEGREE/YEAR3SEM1/PROG BIOINFORMATICS/Project/Coding/colon_image_sets')
import numpy as np
import pandas as pd
import seaborn as sns
sns.set_style('darkgrid')
import matplotlib.pyplot as plt
from sklearn.model_selection import train_test_split
from sklearn.metrics import confusion_matrix, classification_report
```

After importing the data, we show the images. Below are the codes that read the data and store it in the data frame.

```
data_dir = 'D:/DEGREE/YEAR3SEM1/PROG BIOINFORMATICS/Project/Coding/colon_image_sets'
filepaths = []
labels = []

folds = os.listdir(data_dir)
for fold in folds:
    foldpath = os.path.join(data_dir, fold)
    filelist = os.listdir(foldpath)
    for file in filelist:
        fpath = os.path.join(foldpath, file)

        filepaths.append(fpath)
        labels.append(fold)

# Concatenate data paths with labels into one dataframe
Fseries = pd.Series(filepaths, name= 'filepaths')
Lseries = pd.Series(labels, name='labels')
```

```
modules loaded
                                                filepaths     labels
0     D:/DEGREE/YEAR3SEM1/PROG BIOINFORMATICS/Projec...  colon_aca
1     D:/DEGREE/YEAR3SEM1/PROG BIOINFORMATICS/Projec...  colon_aca
2     D:/DEGREE/YEAR3SEM1/PROG BIOINFORMATICS/Projec...  colon_aca
3     D:/DEGREE/YEAR3SEM1/PROG BIOINFORMATICS/Projec...  colon_aca
4     D:/DEGREE/YEAR3SEM1/PROG BIOINFORMATICS/Projec...  colon_aca
...                                                 ...        ...
9994  D:/DEGREE/YEAR3SEM1/PROG BIOINFORMATICS/Projec...    colon_n
9995  D:/DEGREE/YEAR3SEM1/PROG BIOINFORMATICS/Projec...    colon_n
9996  D:/DEGREE/YEAR3SEM1/PROG BIOINFORMATICS/Projec...    colon_n
9997  D:/DEGREE/YEAR3SEM1/PROG BIOINFORMATICS/Projec...    colon_n
9998  D:/DEGREE/YEAR3SEM1/PROG BIOINFORMATICS/Projec...    colon_n
```

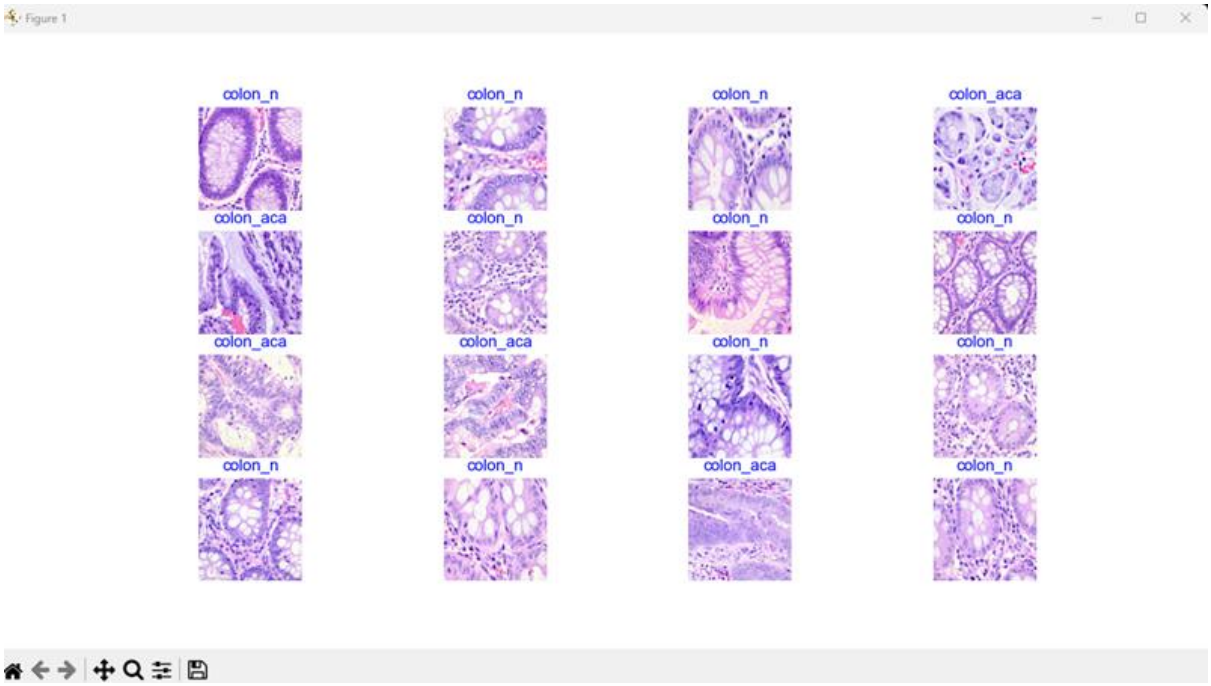
In the terminal, the output shows the directory of the file path where the images is located. Folder colon_aca referring to colon adenocarcinoma, while colon_n referring to colon benign tissue. The main packages that were used are Keras and Tensorflow which are essential for image processing.

2.2 Data Pre-Processing and Exploratory Data Analysis (EDA)

Data normalization is one of the steps taken as data preprocessing. This step is important for training deep learning models because it stabilizes the training process and improves convergence. In the code, normalization is applied as follows.

```
#Data Noramalization (Scaling)

for i in range(16):
    plt.subplot(4, 4, i + 1)
    image = images[i] / 255       # scales data to range (0 - 255)
    plt.imshow(image)
    index = np.argmax(labels[i])  # get image index
    class_name = classes[index]   # get class of image
    plt.title(class_name, color= 'blue', fontsize= 12)
    plt.axis('off')
plt.show()
```

Here, each image in the batch (image) is normalized by dividing by 255.This scales the pixel values from the original range of [0, 255] to the normalized range of [0,1]. Pixel value normalization is a common method in image processing and deep learning to ensure the model is insensitive to the absolute scale of pixel values.



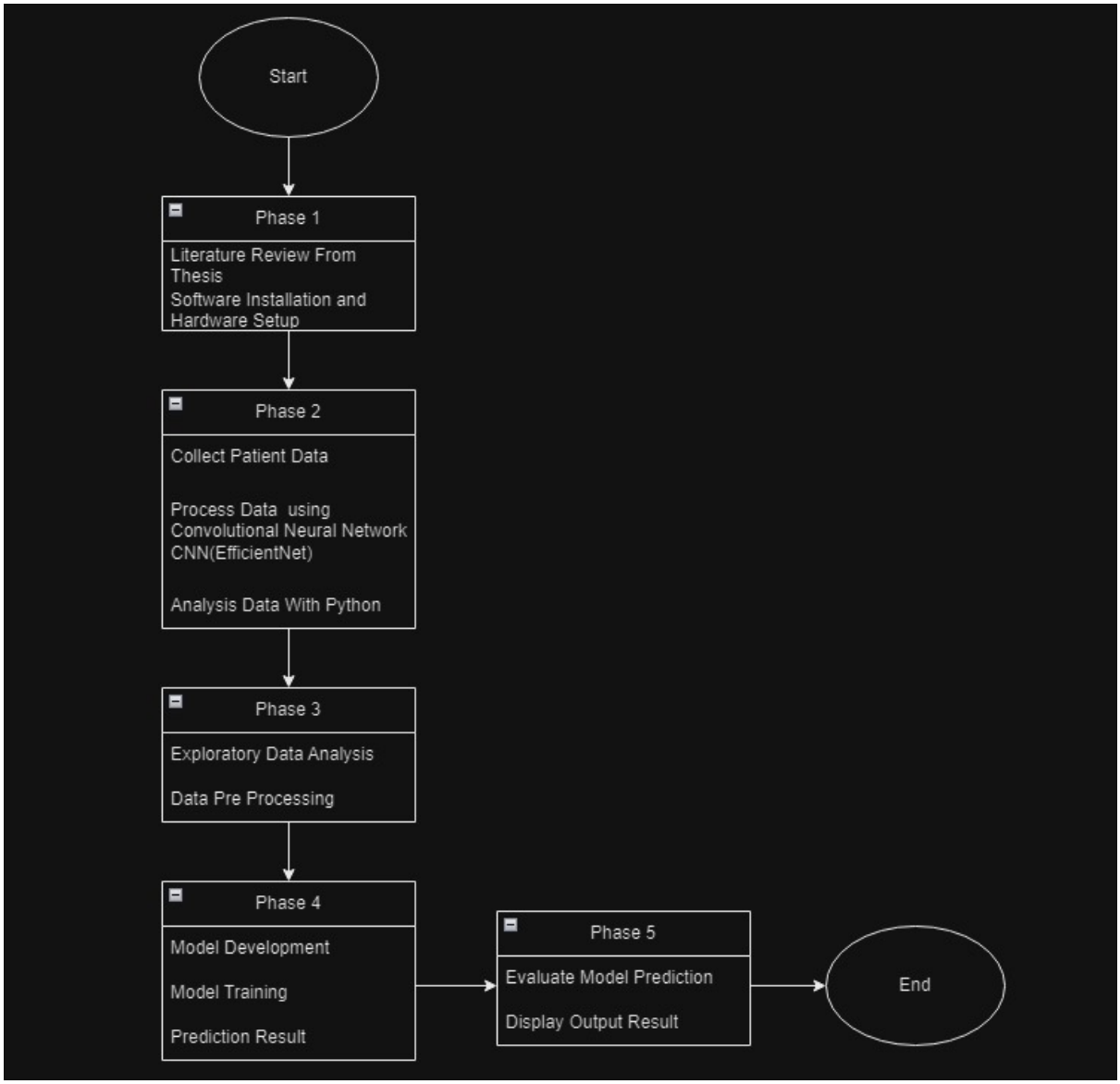
Output of normalize image

2.3 Hardware and Software requirements

The hardware that will be used in this research is matching the requirements needed and is important in order to ensure the process of designing and developing the K- Nearest Neighbours (KNN) for colon cancer classification. Hardware requirements for this research is a laptop with Intel Core i5 9th gen processor. The operating systems are Windows 11 with 8GB RAM memory.The software required is Microsoft Visual Studio as IDE which is easy to use. Python language were implement for the coding with multiple useful packages also installed. Besides that, Microsoft Word 2019 are used for documentation.

3.0 Flowchart

To develop the Convolutional Neural Network (CNN) for cancer image classification, several phases is taken to ensure the process conducted systematically. This included with literature review as first phase, data collection and pre processing at second phase. Next is model development and training and the final phases included model testing and result evaluation. Below is the flowchart to represent the flow of the project.



Flowchart

3.1 Model Development

This code is responsible for creating a convolutional neural network (CNN) model using the EfficientNetB3 architecture as a base model for image classification.

```
# Create Model Structure
img_size = (224, 224)
channels = 3
img_shape = (img_size[0], img_size[1], channels)
class_count = len(list(train_gen.class_indices.keys())) # to define number of classes in dense layer

# we will use efficientnetb3 from EfficientNet family.
base_model = tf.keras.applications.efficientnet.EfficientNetB3(include_top= False, weights= "imagenet", input_shape= img_shape, pooling= 'max')
# base_model.trainable = False

model = Sequential([
    base_model,
    BatchNormalization(axis= -1, momentum= 0.99, epsilon= 0.001),
    Dense(256, kernel_regularizer= regularizers.l2(l= 0.016), activity_regularizer= regularizers.l1(0.006),
    |   |   |   bias_regularizer= regularizers.l1(0.006), activation= 'relu'),
    Dropout(rate= 0.45, seed= 123),
    Dense(class_count, activation= 'softmax')
])

model.compile(Adamax(learning_rate= 0.001), loss= 'categorical_crossentropy', metrics= ['accuracy'])

model.summary()
```

```
Model: "sequential"
_________________________________________________________________
 Layer (type)                Output Shape              Param #
=================================================================
 efficientnetb3 (Functional  (None, 1536)              10783535
 )

 batch_normalization (Batch  (None, 1536)              6144
 Normalization)

 dense (Dense)               (None, 256)               393472

 dropout (Dropout)           (None, 256)               0

 dense_1 (Dense)             (None, 2)                 514

=================================================================
Total params: 11183665 (42.66 MB)
Trainable params: 11093290 (42.32 MB)
Non-trainable params: 90375 (353.03 KB)
_________________________________________________________________
```

Model build

3.2 Model Training

The below code is responsible for training the neural network model using the training data generated by the train_gen.10 epochs value is used for training the model This process took some time.

```
#Train the model

epochs = 10   # number of all epochs in training

history = model.fit(x= train_gen, epochs= epochs, verbose= 1, validation_data= valid_gen,
                    validation_steps= None, shuffle= False)
```

```
251/251 [==============================] - 108s 374ms/step - loss: 4.6541 - accuracy: 0.9685 - val_loss: 2.8599 - val_accuracy: 0.9967
Epoch 2/10
251/251 [==============================] - 93s 369ms/step - loss: 2.0271 - accuracy: 0.9928 - val_loss: 1.4008 - val_accuracy: 1.0000
Epoch 3/10
251/251 [==============================] - 92s 367ms/step - loss: 1.0571 - accuracy: 0.9938 - val_loss: 0.7415 - val_accuracy: 1.0000
Epoch 4/10
251/251 [==============================] - 92s 368ms/step - loss: 0.5714 - accuracy: 0.9980 - val_loss: 0.4093 - val_accuracy: 1.0000
Epoch 5/10
251/251 [==============================] - 93s 372ms/step - loss: 0.3386 - accuracy: 0.9980 - val_loss: 0.2457 - val_accuracy: 1.0000
Epoch 6/10
251/251 [==============================] - 92s 368ms/step - loss: 0.2155 - accuracy: 0.9988 - val_loss: 0.1578 - val_accuracy: 1.0000
Epoch 7/10
251/251 [==============================] - 92s 368ms/step - loss: 0.1499 - accuracy: 0.9998 - val_loss: 0.1178 - val_accuracy: 1.0000
Epoch 8/10
251/251 [==============================] - 93s 371ms/step - loss: 0.1145 - accuracy: 1.0000 - val_loss: 0.0901 - val_accuracy: 1.0000
Epoch 9/10
251/251 [==============================] - 93s 369ms/step - loss: 0.0997 - accuracy: 0.9998 - val_loss: 0.0830 - val_accuracy: 1.0000
Epoch 10/10
251/251 [==============================] - 94s 375ms/step - loss: 0.0917 - accuracy: 0.9990 - val_loss: 0.0858 - val_accuracy: 1.0000
250/401 [=================>............] - ETA: 12s - loss: 0.0849 - accuracy: 1.0000WARNING:tensorflow:Your input ran out of data; interrupt
```

Generate result of CNN model

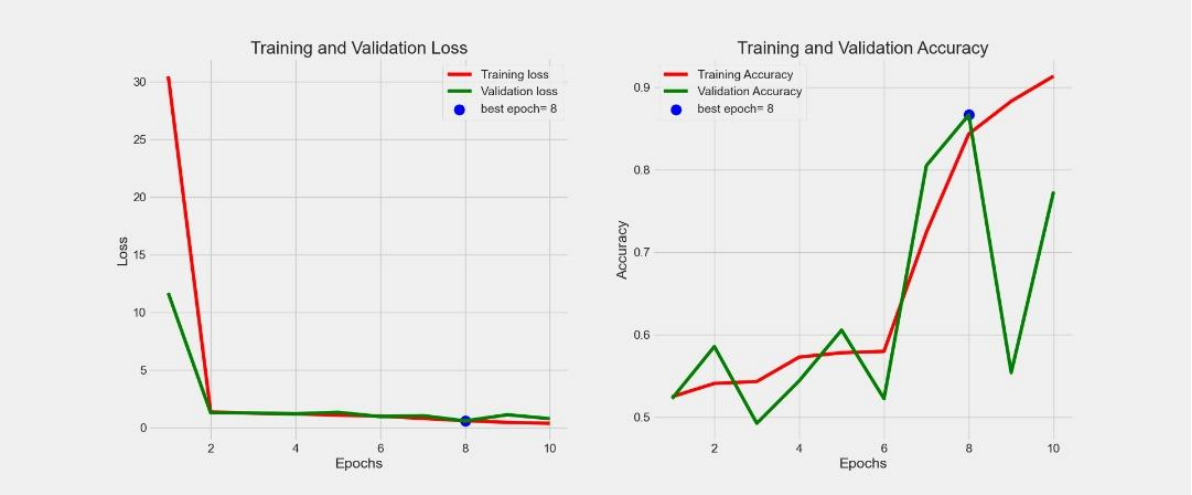
Display Model Performance

```
# Define needed variables
tr_acc = history.history['accuracy']
tr_loss = history.history['loss']
val_acc = history.history['val_accuracy']
val_loss = history.history['val_loss']
index_loss = np.argmin(val_loss)
val_lowest = val_loss[index_loss]
index_acc = np.argmax(val_acc)
acc_highest = val_acc[index_acc]
Epochs = [i+1 for i in range(len(tr_acc))]
loss_label = f'best epoch= {str(index_loss + 1)}'
acc_label = f'best epoch= {str(index_acc + 1)}'

# Plot training history
plt.figure(figsize= (20, 8))
plt.style.use('fivethirtyeight')

plt.subplot(1, 2, 1)
plt.plot(Epochs, tr_loss, 'r', label= 'Training loss')
plt.plot(Epochs, val_loss, 'g', label= 'Validation loss')
plt.scatter(index_loss + 1, val_lowest, s= 150, c= 'blue', label= loss_label)
plt.title('Training and Validation Loss')
plt.xlabel('Epochs')
plt.ylabel('Loss')
plt.legend()

plt.subplot(1, 2, 2)
plt.plot(Epochs, tr_acc, 'r', label= 'Training Accuracy')
plt.plot(Epochs, val_acc, 'g', label= 'Validation Accuracy')
plt.scatter(index_acc + 1 , acc_highest, s= 150, c= 'blue', label= acc_label)
plt.title('Training and Validation Accuracy')
plt.xlabel('Epochs')
plt.ylabel('Accuracy')
plt.legend()

plt.tight_layout
plt.show()
```

We decided to experiment with three distinct learning rates—0.01, 0.001, and 0.0001—while training our deep learning model. This exploration aims to assess the impact of learning rate variations on the model's convergence speed and final performance. By trying different values, WE hope to identify the learning rate that optimizes training efficiency and results in a well-generalized model.

Learning Rate: 0.1

Epoch	Val loss	Val accuracy
1	11.6766	0.5225
2	1.2853	0.5857
3	1.2613	0.4925
4	1.2030	0.5441
5	1.3266	0.6057
6	0.9561	0.5225
7	1.0367	0.8053
8	0.5829	0.8669
9	1.1137	0.5441
10	0.7755	0.7737



Model Performance

Learning Rate: 0.01

Epoch	Val loss	Val accuracy
1	129.8519	0.6855
2	0.7758	0.7537
3	4.5540	0.3727
4	1.2709	0.5092
5	1.2709	0.5092
6	9003.6963	0.5092
7	0.5978	0.8552
8	1.2828	0.8369
9	0.9641	0.8453
10	0.5169	0.8436

Model Performance

Learning Rate: 0.001

Epoch	Val loss	Val accuracy
1	0.5818	0.9850
2	0.1700	0.9950
3	0.1491	0.9950
4	0.1407	0.9983
5	0.1095	0.9967
6	0.1393	0.9983
7	1.9785	0.9950
8	0.5498	1.0000
9	0.2919	0.9584
10	2.3220	0.9983

Model Performance

After discussion, we concluded that learning rate with value 0.001 produced are really good training and validation accuracy with scoring average of 0.9961 for 10 epochs value. We decided to use this learning rate value for further model evaluation.

3.2 Model Evaluation

```
#Model Evaluation
ts_length = len(test_df)
test_batch_size = max(sorted([ts_length // n for n in range(1, ts_length + 1) if ts_length%n == 0 and ts_length/n <= 80]))
test_steps = ts_length // test_batch_size

train_score = model.evaluate(train_gen, steps= test_steps, verbose= 1)
valid_score = model.evaluate(valid_gen, steps= test_steps, verbose= 1)
test_score = model.evaluate(test_gen, steps= test_steps, verbose= 1)

print("Train Loss: ", train_score[0])
print("Train Accuracy: ", train_score[1])
print('-' * 20)
print("Validation Loss: ", valid_score[0])
print("Validation Accuracy: ", valid_score[1])
print('-' * 20)
print("Test Loss: ", test_score[0])
print("Test Accuracy: ", test_score[1])

preds = model.predict_generator(test_gen)
y_pred = np.argmax(preds, axis=1)

g_dict = test_gen.class_indices
classes = list(g_dict.keys())
```

```
Train Loss:  0.40593090653419495
Train Accuracy:  0.999251127243042
--------------------
Validation Loss:  0.4072151184082031
Validation Accuracy:  0.9983360767364502
--------------------
Test Loss:  0.40796664357185364
Test Accuracy:  0.9975062608718872
```

The evaluate method is used to obtain loss and precision scores for training, validation, and testing datasets. The steps parameter is set to test_steps to determine the number of batches to process. The output provides information about the performance of the trained model on the training, validation, and test datasets. Here's a breakdown of the output:

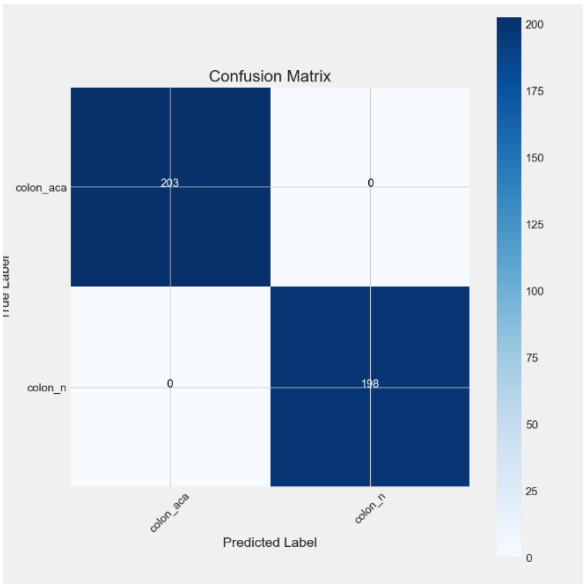
1. Training Results:
    - Train Loss: The loss (error) on the training set.
    - Train Accuracy: The accuracy achieved on the training set.
2. Validation Results:
    - Validation Loss: The loss on the validation set.
    - Validation Accuracy: The accuracy achieved on the validation set.
3. Test Results:
    - Test Loss: The loss on the test set.
    - Test Accuracy: The accuracy achieved on the test set.

In this case, the accuracy values from training, testing, and validation were scoring average of 0.99% (99%), meaning the model accuracy achieved are almost accurate on all three datasets.

4.0 Result, Testing and Validation

```
# Confusion matrix
cm = confusion_matrix(test_gen.classes, y_pred)

plt.figure(figsize= (10, 10))
plt.imshow(cm, interpolation= 'nearest', cmap= plt.cm.Blues)
plt.title('Confusion Matrix')
plt.colorbar()

tick_marks = np.arange(len(classes))
plt.xticks(tick_marks, classes, rotation= 45)
plt.yticks(tick_marks, classes)


thresh = cm.max() / 2.
for i, j in itertools.product(range(cm.shape[0]), range(cm.shape[1])):
    plt.text(j, i, cm[i, j], horizontalalignment= 'center', color= 'white' if cm[i, j] > thresh else 'black')

plt.tight_layout()
plt.ylabel('True Label')
plt.xlabel('Predicted Label')

plt.show()
```

The confusion_matrix function from the sklearn.metrics module is used to compute the confusion matrix.



Confusion Matrix

The confusion matrix provides the classification performance indices for:

- **True Positives (TP):** 203
- **True Negatives (TN):** 198
- **False Positives (FP):** 0
- **False Negatives (FN):** 0

This shows that our model has completed accurate predictions for all cases in the test set. More precisely: There were 293 cases that were actually positive (colon_aca) and were correctly predicted to be positive. There were 198 cases that were actually negative (colon_n) and were correctly predicted to be negative. No cases were incorrectly predicted as positive (false positive).

	precision	recall	f1-score	support
colon_aca	1.00	1.00	1.00	203
colon_n	1.00	1.00	1.00	198
accuracy			1.00	401
macro avg	1.00	1.00	1.00	401
weighted avg	1.00	1.00	1.00	401

Classification Report

The **classification_report** function computes and prints several metrics for each class and an overall summary. The metrics include:

Precision: The ratio of true positive predictions to the total number of positive predictions (true positives + false positives). It measures the accuracy of positive predictions.

Recall (Sensitivity or True Positive Rate): The ratio of true positive predictions to the total number of actual positive instances (true positives + false negatives). It measures the ability of the model to capture all positive instances.

F1-Score: The harmonic mean of precision and recall. It provides a balance between precision and recall. To calculate, use formula = 2 * (Precision * Recall) / (Precision + Recall)

Support: The number of actual instances of each class in the test set

In this case, we achieved the accuracy with value of 1.00 (100%) for all the metrics for each class. This indicates that our model is achieving perfect performance on the metrics for each class.

4.1 Client Feedback

The documents can be further improved by explaining in details of steps and algorithms involved in this study. Objectives need to be clearly written – this can be achieved by highlighting the problems that want to be solved and proposed algorithms used in this project, rather than mentioning vague and general statement.

Students able to perform coding following steps as per guided in the project guideline given. However, this project lacking in proper explanation and discussion in findings. Given good attitude and commitment shown in this project, both of students have potential to brush up their research skills further in PSM1.

5.0 Conclusions

In summary, the exploration of deep learning CNN for colon cancer classification using image data involves both model evaluation metrics and hyperparameter tuning. The ideal scenario is to achieve a model with precision, recall, and F1-Score all equal to 1, indicating perfect performance in identifying positive instances and capturing all actual positive instances. However, achieving such perfection in real-world scenarios may be rare, and considerations such as the complexity of the problem, data nature, and potential overfitting are crucial.

In the specific context of hyperparameter tuning, the investigation into different learning rates revealed that a learning rate of 0.001 resulted in excellent training and validation accuracy. The scoring average of 0.9961 over 10 epochs indicated robust performance. Consequently, the decision was made to adopt this learning rate value for further evaluation, emphasizing its effectiveness in training the deep learning model for colon cancer classification with image data. This underscores the importance of thoughtful hyperparameter selection and the impact it can have on the model's overall performance in medical image classification tasks.

6.0 Appendix

Link for Github:

Appendix A: Final Presentation with Clients Dr Noor Hidayah