```
!kaggle datasets download -d andrewmvd/lung-and-colon-cancer-histopathological-images
```

```
Dataset URL: https://www.kaggle.com/datasets/andrewmvd/lung-and-colon-cancer-histopathological-images
License(s): CC-BY-SA-4.0
Downloading lung-and-colon-cancer-histopathological-images.zip to /content
100% 1.76G/1.76G [00:55<00:00, 35.4MB/s]
100% 1.76G/1.76G [00:55<00:00, 34.1MB/s]
```

```
import zipfile

with zipfile.ZipFile('lung-and-colon-cancer-histopathological-images.zip', 'r') as zip_ref:
    zip_ref.extractall('lung-and-colon-cancer-histopathological-images')
```

```
!ls lung-and-colon-cancer-histopathological-images
```

```
lung_colon_image_set
```

```
# import system libs
import os
import time
import shutil
import pathlib
import itertools
from PIL import Image

# import data handling tools
import cv2
```

```
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

# import Deep learning Libraries
import tensorflow as tf
from tensorflow import keras
from tensorflow.keras.models import Sequential
from tensorflow.keras.optimizers import Adam, Adamax
from tensorflow.keras.preprocessing.image import ImageDataGenerator
from tensorflow.keras.layers import Conv2D, MaxPooling2D, Flatten, Dense, Activation, Dropout, BatchNormalization
from tensorflow.keras import regularizers

# Ignore Warnings
import warnings
warnings.filterwarnings("ignore")

print ('modules loaded')
```

```
modules loaded
```

```
# Generate data paths with labels
data_dir = '/content/lung-and-colon-cancer-histopathological-images/lung_colon_image_set'
filepaths = []
labels = []

folds = os.listdir(data_dir)
```

```
for fold in folds:
    foldpath = os.path.join(data_dir, fold)
    flist = os.listdir(foldpath)

    for f in flist:
        f_path = os.path.join(foldpath, f)
        filelist = os.listdir(f_path)

        for file in filelist:
            fpath = os.path.join(f_path, file)
            filepaths.append(fpath)

            if f == 'colon_aca':
                labels.append('Colon Adenocarcinoma')

            elif f == 'colon_n':
                labels.append('Colon Benign Tissue')

            elif f == 'lung_aca':
                labels.append('Lung Adenocarcinoma')

            elif f == 'lung_n':
                labels.append('Lung Benign Tissue')

            elif f == 'lung_scc':
                labels.append('Lung Squamous Cell Carcinoma')

# Concatenate data paths with labels into one dataframe
Fseries = pd.Series(filepaths, name= 'filepaths')
Lseries = pd.Series(labels, name='labels')
df = pd.concat([Fseries, Lseries], axis= 1)
```

```
df
```

	filepaths	labels
0	/content/lung-and-colon-cancer-histopathologic...	Lung Adenocarcinoma
1	/content/lung-and-colon-cancer-histopathologic...	Lung Adenocarcinoma
2	/content/lung-and-colon-cancer-histopathologic...	Lung Adenocarcinoma
3	/content/lung-and-colon-cancer-histopathologic...	Lung Adenocarcinoma
4	/content/lung-and-colon-cancer-histopathologic...	Lung Adenocarcinoma
...	...	...
24995	/content/lung-and-colon-cancer-histopathologic...	Colon Benign Tissue
24996	/content/lung-and-colon-cancer-histopathologic...	Colon Benign Tissue
24997	/content/lung-and-colon-cancer-histopathologic...	Colon Benign Tissue
24998	/content/lung-and-colon-cancer-histopathologic...	Colon Benign Tissue
24999	/content/lung-and-colon-cancer-histopathologic...	Colon Benign Tissue

25000 rows × 2 columns

```
strat = df['labels']
train_df, dummy_df = train_test_split(df,  train_size= 0.8, shuffle= True, random_state= 123, stratify= strat)

# valid and test dataframe
strat = dummy_df['labels']
valid_df, test_df = train_test_split(dummy_df,  train_size= 0.5, shuffle= True, random_state= 123, stratify= strat)
```

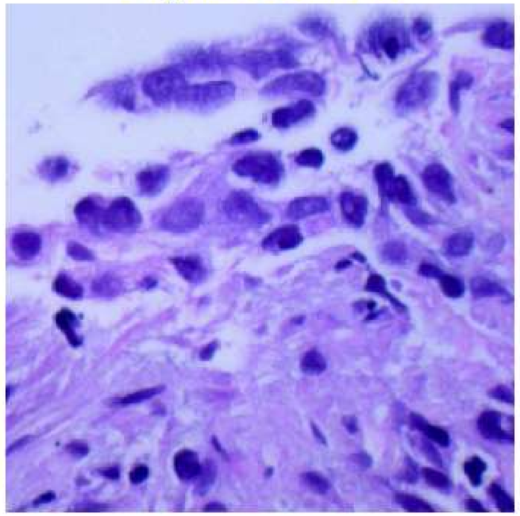
```
# crobed image size
batch_size = 64
img_size = (224, 224)
channels = 3
img_shape = (img_size[0], img_size[1], channels)

tr_gen = ImageDataGenerator()
ts_gen = ImageDataGenerator()

train_gen = tr_gen.flow_from_dataframe( train_df, x_col= 'filepaths', y_col= 'labels', target_size= img_size, class_mode= 'categorical
                                    color_mode= 'rgb', shuffle= True, batch_size= batch_size)

valid_gen = ts_gen.flow_from_dataframe( valid_df, x_col= 'filepaths', y_col= 'labels', target_size= img_size, class_mode= 'categorical
                                        color_mode= 'rgb', shuffle= True, batch_size= batch_size)

test_gen = ts_gen.flow_from_dataframe( test_df, x_col= 'filepaths', y_col= 'labels', target_size= img_size, class_mode= 'categorical',
                                    color_mode= 'rgb', shuffle= False, batch_size= batch_size)
```

```
Found 20000 validated image filenames belonging to 5 classes.
Found 2500 validated image filenames belonging to 5 classes.
Found 2500 validated image filenames belonging to 5 classes.
```

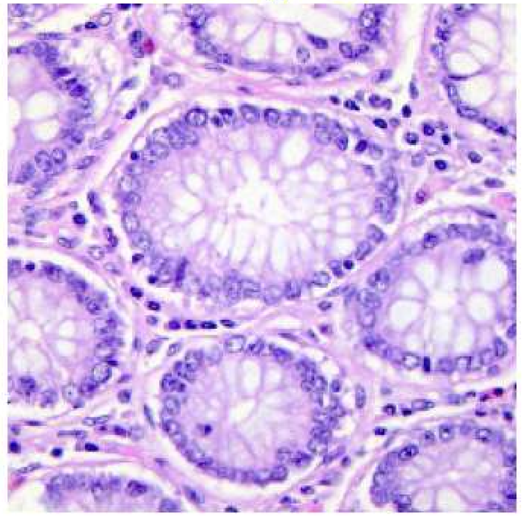
```
g_dict = train_gen.class_indices
classes = list(g_dict.keys())
images, labels = next(train_gen)

plt.figure(figsize= (20, 20))

for i in range(16):
    plt.subplot(4, 4, i + 1)
    image = images[i] / 255
```

```
    plt.imshow(image)
    index = np.argmax(labels[i])
    class_name = classes[index]
    plt.title(class_name, color= 'blue', fontsize= 12)
    plt.axis('off')
plt.show()
```

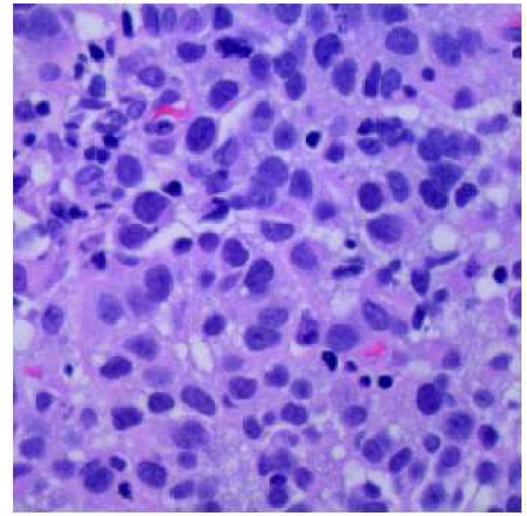
Lung Adenocarcinoma



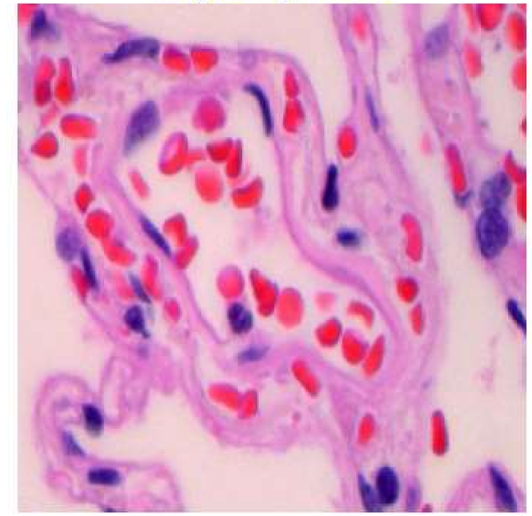
Colon Benign Tissue



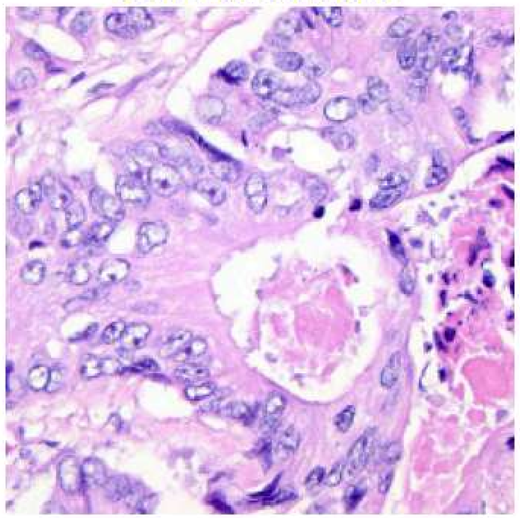
Lung Squamous Cell Carcinoma



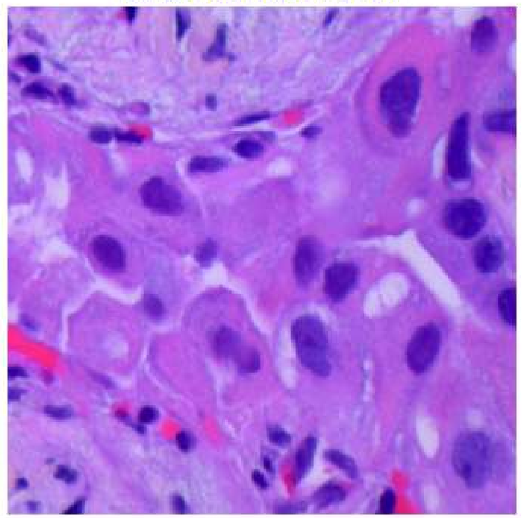
Lung Benign Tissue



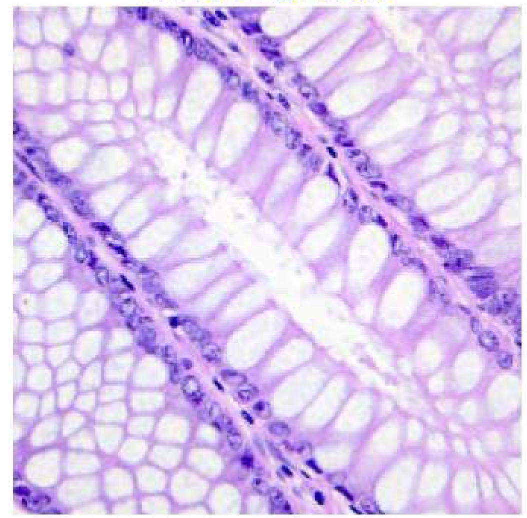
Colon Adenocarcinoma



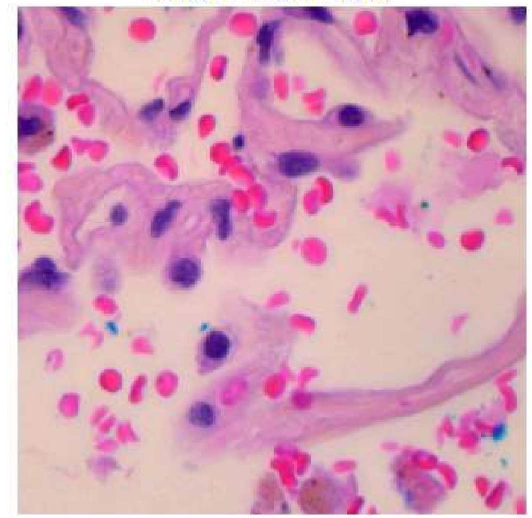
Lung Adenocarcinoma



Colon Benign Tissue

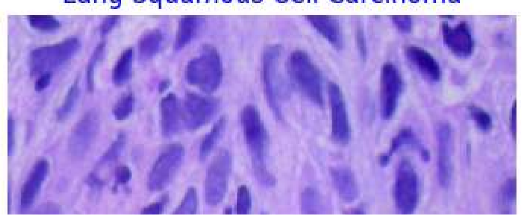


Lung Benign Tissue

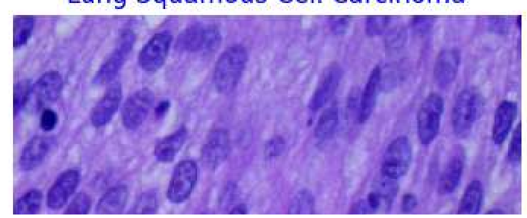


Lung Benign Tissue

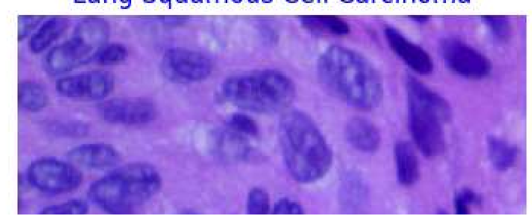
Lung Squamous Cell Carcinoma

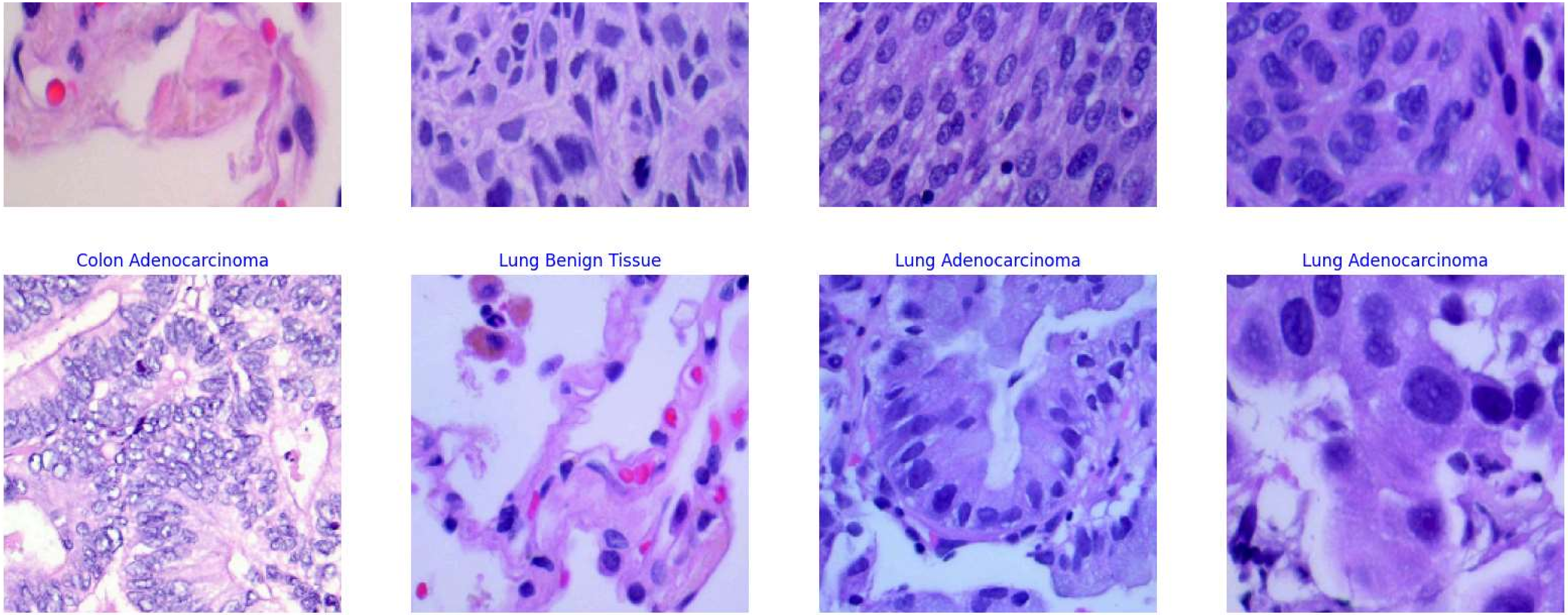


Lung Squamous Cell Carcinoma



Lung Squamous Cell Carcinoma




Colon Adenocarcinoma
Lung Benign Tissue
Lung Adenocarcinoma
Lung Adenocarcinoma

```
import tensorflow as tf
from tensorflow.keras.layers import Layer, GlobalAveragePooling2D, Dense, Multiply, Reshape, Conv2D, MaxPooling2D, Flatten, Dropout
from tensorflow.keras.models import Sequential
from tensorflow.keras.optimizers import Adam

# Global Context Attention Layer
class GlobalContextAttention(Layer):
    def __init__(self, channels, **kwargs):
        super(GlobalContextAttention, self).__init__(**kwargs)
        self.channels = channels
        self.dense1 = Dense(channels // 16, activation='relu')  # Reduction
        self.dense2 = Dense(channels, activation='sigmoid')  # Scaling

    def call(self, inputs):
        x = GlobalAveragePooling2D()(inputs)
        x = Reshape((1, 1, self.channels))(x)
        x = self.dense1(x)
        x = self.dense2(x)
        return Multiply()([inputs, x])

    def get_config(self):
        config = super().get_config()
        config.update({"channels": self.channels})
        return config

# This is CNN Model with Global Context Attention
model = Sequential([
    # Early Layers (No GC Attention)
    Conv2D(64, (3,3), padding="same", activation="relu", input_shape=img_shape),
    Conv2D(64, (3,3), padding="same", activation="relu"),
    MaxPooling2D((2, 2)),
```

```
    Conv2D(128, (3,3), padding="same", activation="relu"),
    Conv2D(128, (3,3), padding="same", activation="relu"),
    MaxPooling2D((2, 2)),

    # GC Attention only in deeper layers
    Conv2D(256, (3,3), padding="same", activation="relu"),
    Conv2D(256, (3,3), padding="same", activation="relu"),
    GlobalContextAttention(256),  # GC applied here
    MaxPooling2D((2, 2)),

    Conv2D(512, (3,3), padding="same", activation="relu"),
    Conv2D(512, (3,3), padding="same", activation="relu"),
    GlobalContextAttention(512),  # GC applied here
    MaxPooling2D((2, 2)),

    Conv2D(512, (3,3), padding="same", activation="relu"),
    Conv2D(512, (3,3), padding="same", activation="relu"),
    GlobalContextAttention(512),  # GC applied here
    MaxPooling2D((2, 2)),

    Flatten(),
    Dense(256, activation="relu"),
    Dropout(0.4),  #dropout for regularization
    Dense(64, activation="relu"),
    Dense(5, activation="softmax")
])

model.compile(optimizer=Adam(learning_rate=0.0005), loss='categorical_crossentropy', metrics=['accuracy'])

#  model summary
model.summary()
```

```
Model: "sequential"
```

Layer (type)	Output Shape	Param #
conv2d_6 (Conv2D)	(None, 224, 224, 64)	1,792
conv2d_7 (Conv2D)	(None, 224, 224, 64)	36,928
max_pooling2d_2 (MaxPooling2D)	(None, 112, 112, 64)	0
conv2d_8 (Conv2D)	(None, 112, 112, 128)	73,856
conv2d_9 (Conv2D)	(None, 112, 112, 128)	147,584
max_pooling2d_3 (MaxPooling2D)	(None, 56, 56, 128)	0
conv2d_10 (Conv2D)	(None, 56, 56, 256)	295,168
conv2d_11 (Conv2D)	(None, 56, 56, 256)	590,080
global_context_attention (GlobalContextAttention)	(None, 56, 56, 256)	8,464
max_pooling2d_4 (MaxPooling2D)	(None, 28, 28, 256)	0
conv2d_12 (Conv2D)	(None, 28, 28, 512)	1,180,160
conv2d_13 (Conv2D)	(None, 28, 28, 512)	2,359,808
global_context_attention_1 (GlobalContextAttention)	(None, 28, 28, 512)	33,312
max_pooling2d_5 (MaxPooling2D)	(None, 14, 14, 512)	0
conv2d_14 (Conv2D)	(None, 14, 14, 512)	2,359,808

conv2d_15 (Conv2D)	(None, 14, 14, 512)	2,359,808
global_context_attention_2 (GlobalContextAttention)	(None, 14, 14, 512)	33,312
max_pooling2d_6 (MaxPooling2D)	(None, 7, 7, 512)	0
flatten (Flatten)	(None, 25088)	0
dense_6 (Dense)	(None, 256)	6,422,784
dropout (Dropout)	(None, 256)	0
dense_7 (Dense)	(None, 64)	16,448
dense_8 (Dense)	(None, 5)	325

Total params: 15,919,637 (60.73 MB)
Trainable params: 15,919,637 (60.73 MB)
Non-trainable params: 0 (0.00 B)

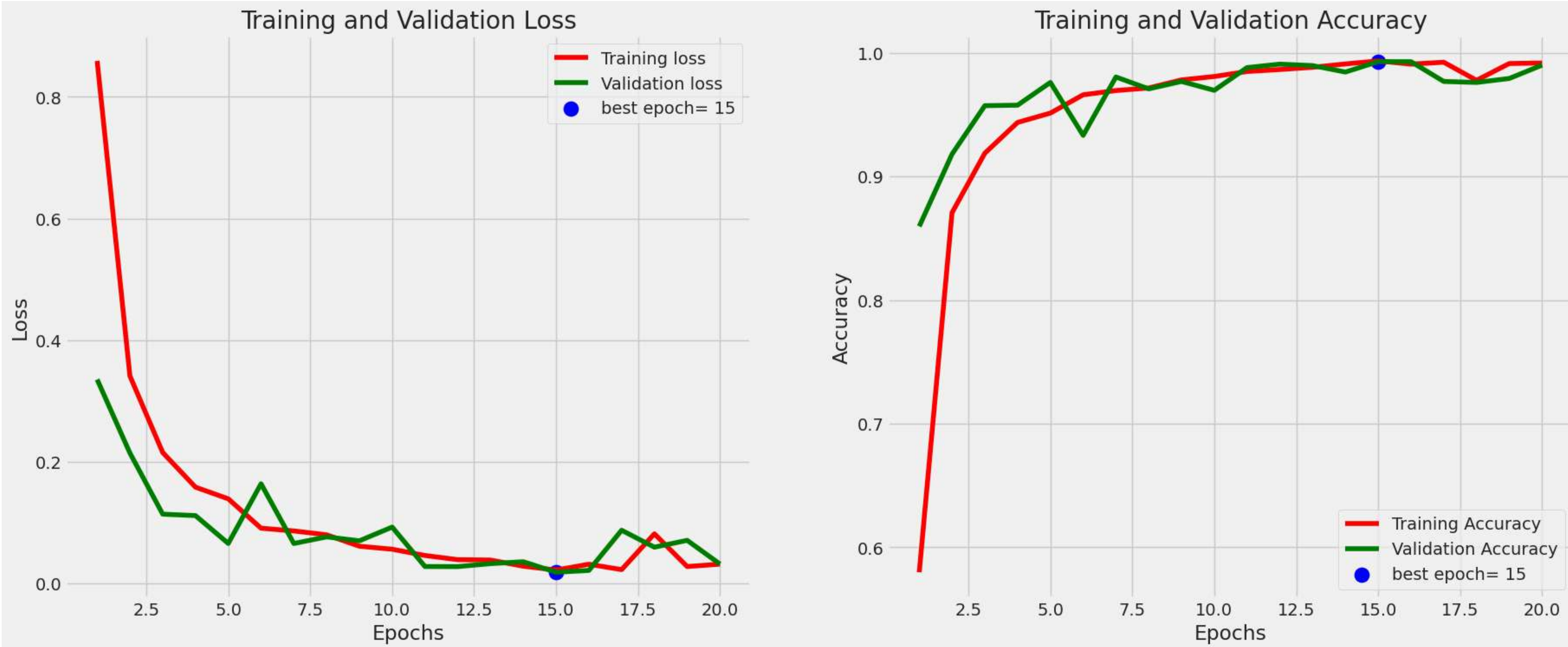
```
epochs = 20   # number of all epochs in training

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

```
Epoch 1/20
313/313 ━━━━━━━━━━━━━━━━━━━━ 362s 941ms/step - accuracy: 0.4007 - loss: 1.2143 - val_accuracy: 0.8596 - val_loss: 0.3352
Epoch 2/20
313/313 ━━━━━━━━━━━━━━━━━━━━ 231s 736ms/step - accuracy: 0.8581 - loss: 0.3753 - val_accuracy: 0.9180 - val_loss: 0.2142
Epoch 3/20
313/313 ━━━━━━━━━━━━━━━━━━━━ 230s 736ms/step - accuracy: 0.9079 - loss: 0.2398 - val_accuracy: 0.9572 - val_loss: 0.1137
Epoch 4/20
313/313 ━━━━━━━━━━━━━━━━━━━━ 230s 734ms/step - accuracy: 0.9409 - loss: 0.1649 - val_accuracy: 0.9576 - val_loss: 0.1113
Epoch 5/20
313/313 ━━━━━━━━━━━━━━━━━━━━ 231s 736ms/step - accuracy: 0.9514 - loss: 0.1412 - val_accuracy: 0.9760 - val_loss: 0.0656
Epoch 6/20
313/313 ━━━━━━━━━━━━━━━━━━━━ 262s 736ms/step - accuracy: 0.9650 - loss: 0.0930 - val_accuracy: 0.9332 - val_loss: 0.1636
Epoch 7/20
313/313 ━━━━━━━━━━━━━━━━━━━━ 230s 735ms/step - accuracy: 0.9678 - loss: 0.0876 - val_accuracy: 0.9804 - val_loss: 0.0655
Epoch 8/20
313/313 ━━━━━━━━━━━━━━━━━━━━ 230s 734ms/step - accuracy: 0.9749 - loss: 0.0725 - val_accuracy: 0.9708 - val_loss: 0.0764
Epoch 9/20
313/313 ━━━━━━━━━━━━━━━━━━━━ 263s 736ms/step - accuracy: 0.9788 - loss: 0.0599 - val_accuracy: 0.9768 - val_loss: 0.0699
Epoch 10/20
313/313 ━━━━━━━━━━━━━━━━━━━━ 229s 731ms/step - accuracy: 0.9838 - loss: 0.0457 - val_accuracy: 0.9696 - val_loss: 0.0925
Epoch 11/20
313/313 ━━━━━━━━━━━━━━━━━━━━ 229s 732ms/step - accuracy: 0.9862 - loss: 0.0411 - val_accuracy: 0.9880 - val_loss: 0.0276
Epoch 12/20
313/313 ━━━━━━━━━━━━━━━━━━━━ 230s 733ms/step - accuracy: 0.9828 - loss: 0.0512 - val_accuracy: 0.9908 - val_loss: 0.0275
Epoch 13/20
313/313 ━━━━━━━━━━━━━━━━━━━━ 230s 733ms/step - accuracy: 0.9894 - loss: 0.0339 - val_accuracy: 0.9896 - val_loss: 0.0324
Epoch 14/20
```

```
313/313 ━━━━━━━━━━━━━━━━━━━━ 229s 730ms/step - accuracy: 0.9919 - loss: 0.0230 - val_accuracy: 0.9844 - val_loss: 0.0355
Epoch 15/20
313/313 ━━━━━━━━━━━━━━━━━━━━ 229s 732ms/step - accuracy: 0.9943 - loss: 0.0212 - val_accuracy: 0.9928 - val_loss: 0.0182
Epoch 16/20
313/313 ━━━━━━━━━━━━━━━━━━━━ 229s 729ms/step - accuracy: 0.9938 - loss: 0.0216 - val_accuracy: 0.9928 - val_loss: 0.0212
Epoch 17/20
313/313 ━━━━━━━━━━━━━━━━━━━━ 229s 731ms/step - accuracy: 0.9948 - loss: 0.0151 - val_accuracy: 0.9768 - val_loss: 0.0873
Epoch 18/20
313/313 ━━━━━━━━━━━━━━━━━━━━ 262s 732ms/step - accuracy: 0.9882 - loss: 0.0418 - val_accuracy: 0.9760 - val_loss: 0.0594
Epoch 19/20
313/313 ━━━━━━━━━━━━━━━━━━━━ 229s 732ms/step - accuracy: 0.9904 - loss: 0.0318 - val_accuracy: 0.9792 - val_loss: 0.0707
Epoch 20/20
313/313 ━━━━━━━━━━━━━━━━━━━━ 262s 734ms/step - accuracy: 0.9916 - loss: 0.0307 - val_accuracy: 0.9900 - val_loss: 0.0316
```

```python
# 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()
```




```
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("Valid Loss: ", valid_score[0])
print("Valid Accuracy: ", valid_score[1])
print('-' * 20)
print("Test Loss: ", test_score[0])
print("Test Accuracy: ", test_score[1])
```

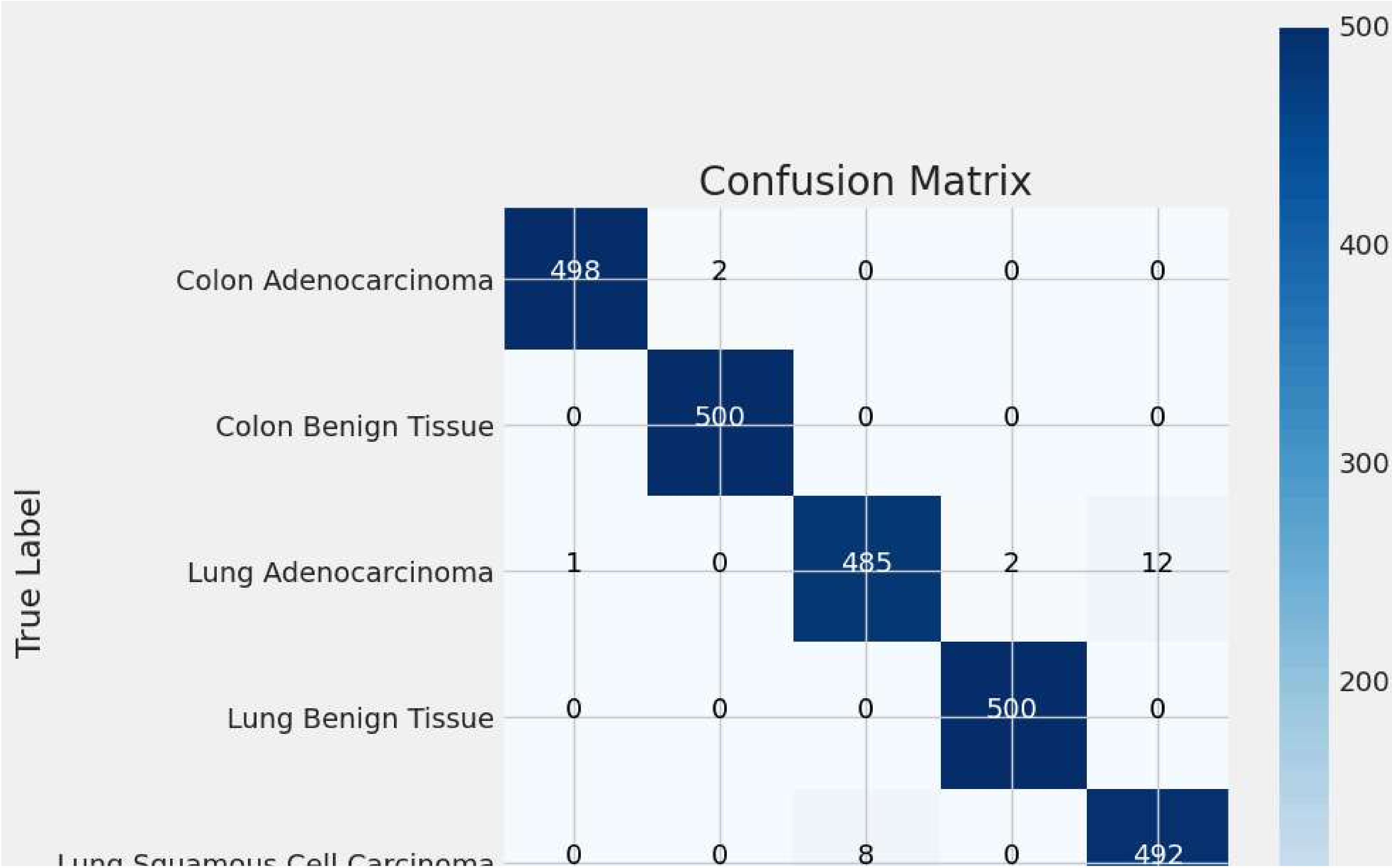
```
50/50 ━━━━━━━━━━━━━━━━━━━━ 18s 365ms/step - accuracy: 0.9958 - loss: 0.0149
50/50 ━━━━━━━━━━━━━━━━━━━━ 14s 279ms/step - accuracy: 0.9870 - loss: 0.0580
50/50 ━━━━━━━━━━━━━━━━━━━━ 13s 265ms/step - accuracy: 0.9876 - loss: 0.0371
Train Loss:  0.010479768738150597
Train Accuracy:  0.9965624809265137
--------------------
Valid Loss:  0.043072182685136795
Valid Accuracy:  0.9900000095367432
--------------------
Test Loss:  0.031637050211429596
Test Accuracy:  0.9900000095367432
```

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

```
40/40 ━━━━━━━━━━━━━━━━━━━━ 15s 355ms/step
```

```
g_dict = test_gen.class_indices
```

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

# 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()
```


Confusion Matrix
True Label
Colon Adenocarcinoma
Colon Benign Tissue
Lung Adenocarcinoma
Lung Benign Tissue
498 2 0 0 0
0 500 0 0 0
1 0 485 2 12
0 0 0 500 0
0 0 8 0 492
500
400
300
200


Lung Squamous Cell Carcinoma
100
Adenocarcinoma
n Benign Tissue
Adenocarcinoma
g Benign Tissue
Cell Carcin