

lung-cancer

May 21, 2025

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[1]: import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import cv2
import PIL as pl
import random
from sklearn.model_selection import train_test_split
import tensorflow as tf
from tensorflow.keras.utils import image_dataset_from_directory, img_to_array
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Conv2D, AvgPool2D, MaxPooling2D, Flatten,
↳Dense, Dropout

import os
for dirname, _, filenames in os.walk('/content/Lung Cancer'):
    for filename in filenames:
        print(os.path.join(dirname, filename))

import warnings
warnings.filterwarnings('ignore')
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/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (391).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (143).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (77).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (178).jpg

/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (248).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (193).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (67).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (170).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (91).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (264).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (151).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (118).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (280).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (281).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (191).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (292).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (190).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (94).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (12).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (302).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (356).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (156).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (42).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (309).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (129).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (186).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (288).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (402).jpg

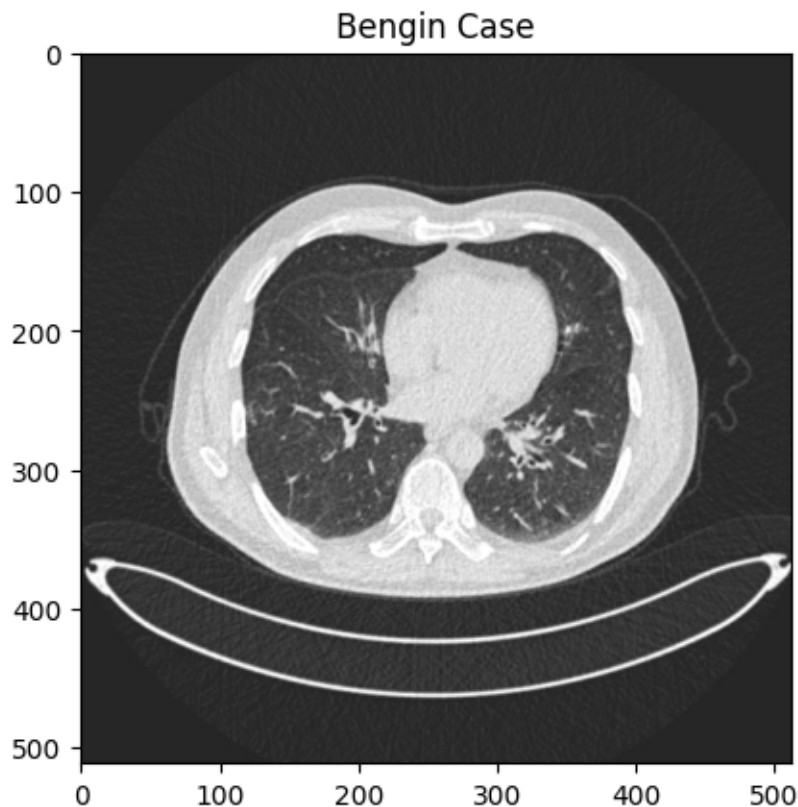
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(198).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(173).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(217).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(197).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(371).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(142).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(325).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(205).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(158).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(100).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(70).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(28).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal
Cases/Lung_cancer.jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(346).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(82).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(403).jpg
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(65).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(340).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(256).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(375).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(308).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(263).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(377).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(132).jpg

/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(102).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(318).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(407).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(175).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(117).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(287).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(368).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(55).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(282).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(75).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(227).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(184).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(389).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(104).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(59).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(330).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(408).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(182).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(120).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(396).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(98).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(80).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(335).jpg
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case
(58).jpg

```
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (298).jpg  
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (112).jpg  
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (247).jpg  
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (301).jpg  
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (76).jpg  
/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/Normal Cases/Normal case (266).jpg
```

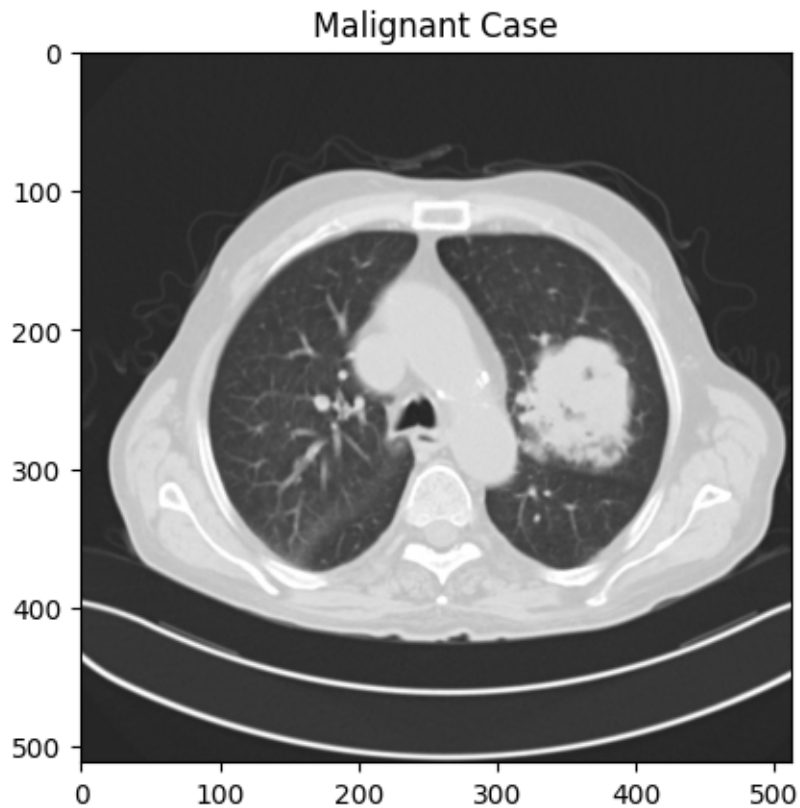
```
[5]: img = cv2.imread('/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/  
    ↪Bengin Cases/Bengin case (10).jpg')  
plt.title('Bengin Case')  
plt.imshow(img, label = 'Bengin Case')
```

```
[5]: <matplotlib.image.AxesImage at 0x7978de981e50>
```



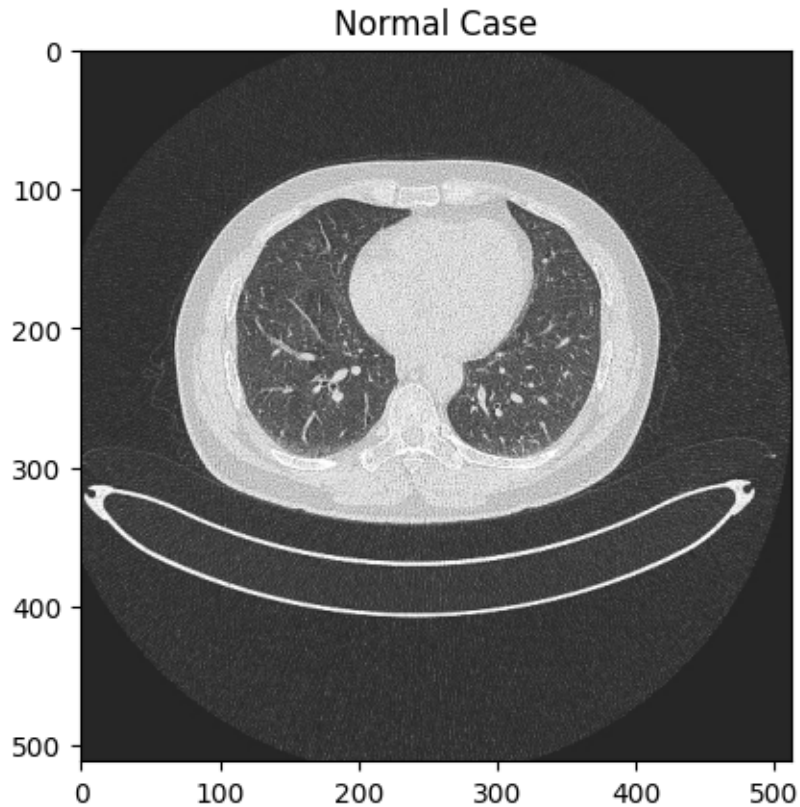
```
[7]: img = cv2.imread('/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/  
    ↪Malignant Cases/Malignant case (10).jpg')  
plt.title('Malignant Case')  
plt.imshow(img)
```

[7]: <matplotlib.image.AxesImage at 0x7978d9e72850>



```
[8]: img = cv2.imread('/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset/  
    ↪Normal Cases/Normal case (100).jpg')  
plt.title('Normal Case')  
plt.imshow(img)
```

[8]: <matplotlib.image.AxesImage at 0x7978d9eb1f90>



```
[9]: img.shape
```

```
[9]: (512, 512, 3)
```

```
[12]: dir = '/content/Lung Cancer/The IQ-OTHNCCD lung cancer dataset'
img_width = 256
img_height = 256
```

```
[14]: # Second section of the path
categories = ['Benign Cases', 'Malignant Cases', 'Normal Cases'] # Corrected_
↳directory names

# Now we get the images using complete path and store the images into img_data_
↳folder.
img_data = []
for cata in categories:
    folder = os.path.join(dir, cata)
    label = categories.index(cata)
    for img in os.listdir(folder):
        img_path = os.path.join(folder, img)
```

```

try:
    # Attempt to read and resize the image
    img_array = cv2.imread(img_path)
    img_array = cv2.resize(img_array, (img_height, img_width))

    # Check if the image array is not empty
    if img_array is not None and not img_array.size == 0:
        img_data.append([img_array, label])

except Exception as e:
    # It might be helpful to print the error and the file path here
    # to catch other potential issues like corrupt images.
    # print(f"Error processing {img_path}: {e}")
    continue

```

```

[15]: random.shuffle(img_data)
x=[]
y=[]
for features,labels in img_data:
    x.append(features)
    y.append(labels)

#Convert X and Y list into array
X=np.array(x, dtype = float)
Y=np.array(y, dtype = float)

```

```

[16]: print(X[19])

```

```

[[[38. 38. 38.]
  [38. 38. 38.]
  [38. 38. 38.]
  ...
  [38. 38. 38.]
  [38. 38. 38.]
  [38. 38. 38.]]

[[[38. 38. 38.]
  [38. 38. 38.]
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  ...
  [38. 38. 38.]
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  [38. 38. 38.]]

[[[38. 38. 38.]
  [38. 38. 38.]
  [38. 38. 38.]

```

```

...
[38. 38. 38.]
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...

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...
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[[38. 38. 38.]
 [38. 38. 38.]
 [38. 38. 38.]

...
 [38. 38. 38.]
 [38. 38. 38.]
 [38. 38. 38.]]]

```

```

[17]: for i in range(len(X)):
        X[i] = X[i]/255.0
X.shape

```

```

[17]: (1099, 256, 256, 3)

```

```

[18]: x, x_test, y, y_test = train_test_split(X, Y, test_size = 0.2)
x_train, x_val, y_train, y_val = train_test_split(x, y, test_size = 0.2)
model = Sequential()

```

```

[19]: from tensorflow.keras.preprocessing.image import ImageDataGenerator

# Define the ImageDataGenerator for data augmentation
datagen = ImageDataGenerator(
    rotation_range=15,      # Rotate the image by up to 15 degrees

```

```

width_shift_range=0.1, # Shift the image horizontally by up to 10% of the
↪width
height_shift_range=0.1, # Shift the image vertically by up to 10% of the
↪height
shear_range=0.1,      # Shear the image by up to 10 degrees
zoom_range=0.1,       # Zoom in or out by up to 10%
horizontal_flip=True,  # Flip the image horizontally
fill_mode='nearest'    # Fill in missing pixels with the nearest value
)

# Fit the ImageDataGenerator on your training data
datagen.fit(x_train)

# Define the number of augmented images to generate per original image
augmented_images_per_original = 6

```

```

[20]: model.add(Conv2D(128, (3, 3), padding = 'same', input_shape = X.shape[1: ],
↪activation = 'relu'))
model.add(AvgPool2D(2,2))
model.add(Conv2D(128, (3, 3), activation = 'relu', padding = 'same'))
model.add(Conv2D(128, (3, 3), activation = 'relu', padding = 'same'))
model.add(MaxPooling2D(2,2))
model.add(Conv2D(128, (3, 3), activation = 'relu', padding = 'same'))
model.add(Conv2D(128, (3, 3), activation = 'relu', padding = 'same'))

model.add(MaxPooling2D(2,2))
model.add(Conv2D(64, (3, 3), activation = 'relu', padding = 'same'))
model.add(Conv2D(64, (3, 3), activation = 'relu', padding = 'same'))

model.add(MaxPooling2D(2,2))
model.add(Flatten())
model.add(Dropout(0.2, seed = 12))
model.add(Dense(3000, activation = 'relu'))
model.add(Dense(1500, activation = 'relu'))
model.add(Dense(3, activation = 'softmax'))

```

```

[21]: # Save the model
model.save("lung_cancer_detection_model.h5")
from tensorflow.keras.models import load_model

# Load the saved model
loaded_model = load_model("lung_cancer_detection_model.h5")

```

WARNING:absl:You are saving your model as an HDF5 file via `model.save()` or `keras.saving.save_model(model)`. This file format is considered legacy. We recommend using instead the native Keras format, e.g. `model.save('my_model.keras')` or `keras.saving.save_model(model,

```
'my_model.keras')`.
```

WARNING:absl:No training configuration found in the save file, so the model was *not* compiled. Compile it manually.

```
[22]: model.compile(loss = 'sparse_categorical_crossentropy', optimizer = 'adam',  
      ↪ metrics = ['accuracy'])  
model.summary()
```

Model: "sequential"

Layer (type)	Output Shape	Param #
conv2d (Conv2D)	(None, 256, 256, 128)	3,584
average_pooling2d (AveragePooling2D)	(None, 128, 128, 128)	0
conv2d_1 (Conv2D)	(None, 128, 128, 128)	147,584
conv2d_2 (Conv2D)	(None, 128, 128, 128)	147,584
max_pooling2d (MaxPooling2D)	(None, 64, 64, 128)	0
conv2d_3 (Conv2D)	(None, 64, 64, 128)	147,584
conv2d_4 (Conv2D)	(None, 64, 64, 128)	147,584
max_pooling2d_1 (MaxPooling2D)	(None, 32, 32, 128)	0
conv2d_5 (Conv2D)	(None, 32, 32, 64)	73,792
conv2d_6 (Conv2D)	(None, 32, 32, 64)	36,928
max_pooling2d_2 (MaxPooling2D)	(None, 16, 16, 64)	0
flatten (Flatten)	(None, 16384)	0
dropout (Dropout)	(None, 16384)	0
dense (Dense)	(None, 3000)	49,155,000
dense_1 (Dense)	(None, 1500)	4,501,500
dense_2 (Dense)	(None, 3)	4,503

Total params: 54,365,643 (207.39 MB)

Trainable params: 54,365,643 (207.39 MB)

Non-trainable params: 0 (0.00 B)

```
[23]: # Import EarlyStopping callback
from tensorflow.keras.callbacks import EarlyStopping

# Define EarlyStopping callback
early_stopping = EarlyStopping(monitor='val_loss', patience=3,
    ↪restore_best_weights=True)
early_stopping = EarlyStopping(monitor='val_accuracy', patience=3,
    ↪restore_best_weights=True)
```

```
[24]: history = model.fit(x_train, y_train, validation_data = (x_val, y_val), epochs =
    ↪15)
```

```
Epoch 1/15
22/22          452s 20s/step -
accuracy: 0.4214 - loss: 1.1637 - val_accuracy: 0.5455 - val_loss: 0.8997
Epoch 2/15
22/22          456s 21s/step -
accuracy: 0.5077 - loss: 0.9337 - val_accuracy: 0.6307 - val_loss: 0.7950
Epoch 3/15
22/22          505s 21s/step -
accuracy: 0.5613 - loss: 0.8917 - val_accuracy: 0.5455 - val_loss: 0.8748
Epoch 4/15
22/22          502s 21s/step -
accuracy: 0.6137 - loss: 0.8134 - val_accuracy: 0.7500 - val_loss: 0.6595
Epoch 5/15
22/22          502s 21s/step -
accuracy: 0.7457 - loss: 0.6149 - val_accuracy: 0.8182 - val_loss: 0.4753
Epoch 6/15
22/22          489s 20s/step -
accuracy: 0.8187 - loss: 0.4122 - val_accuracy: 0.8466 - val_loss: 0.3643
Epoch 7/15
22/22          500s 20s/step -
accuracy: 0.9041 - loss: 0.2686 - val_accuracy: 0.9091 - val_loss: 0.3301
Epoch 8/15
22/22          452s 21s/step -
accuracy: 0.9029 - loss: 0.2420 - val_accuracy: 0.8693 - val_loss: 0.3528
Epoch 9/15
22/22          517s 21s/step -
accuracy: 0.9520 - loss: 0.1576 - val_accuracy: 0.9659 - val_loss: 0.1454
Epoch 10/15
```

```

22/22          500s 21s/step -
accuracy: 0.9697 - loss: 0.0853 - val_accuracy: 0.9545 - val_loss: 0.2041
Epoch 11/15
22/22          490s 21s/step -
accuracy: 0.9759 - loss: 0.0669 - val_accuracy: 0.9602 - val_loss: 0.1421
Epoch 12/15
22/22          514s 21s/step -
accuracy: 0.9869 - loss: 0.0443 - val_accuracy: 0.9659 - val_loss: 0.1305
Epoch 13/15
22/22          465s 21s/step -
accuracy: 0.9889 - loss: 0.0463 - val_accuracy: 0.9659 - val_loss: 0.1182
Epoch 14/15
22/22          499s 21s/step -
accuracy: 0.9973 - loss: 0.0183 - val_accuracy: 0.9659 - val_loss: 0.1595
Epoch 15/15
22/22          497s 21s/step -
accuracy: 0.9843 - loss: 0.0393 - val_accuracy: 0.9830 - val_loss: 0.0521

```

```
[25]: result = model.predict(x_test)
```

```

7/7          38s 5s/step

```

```
[26]: test_loss, test_accuracy = model.evaluate(x_test, y_test)
print("Test Loss:", test_loss)
print("Test Accuracy:", test_accuracy)
```

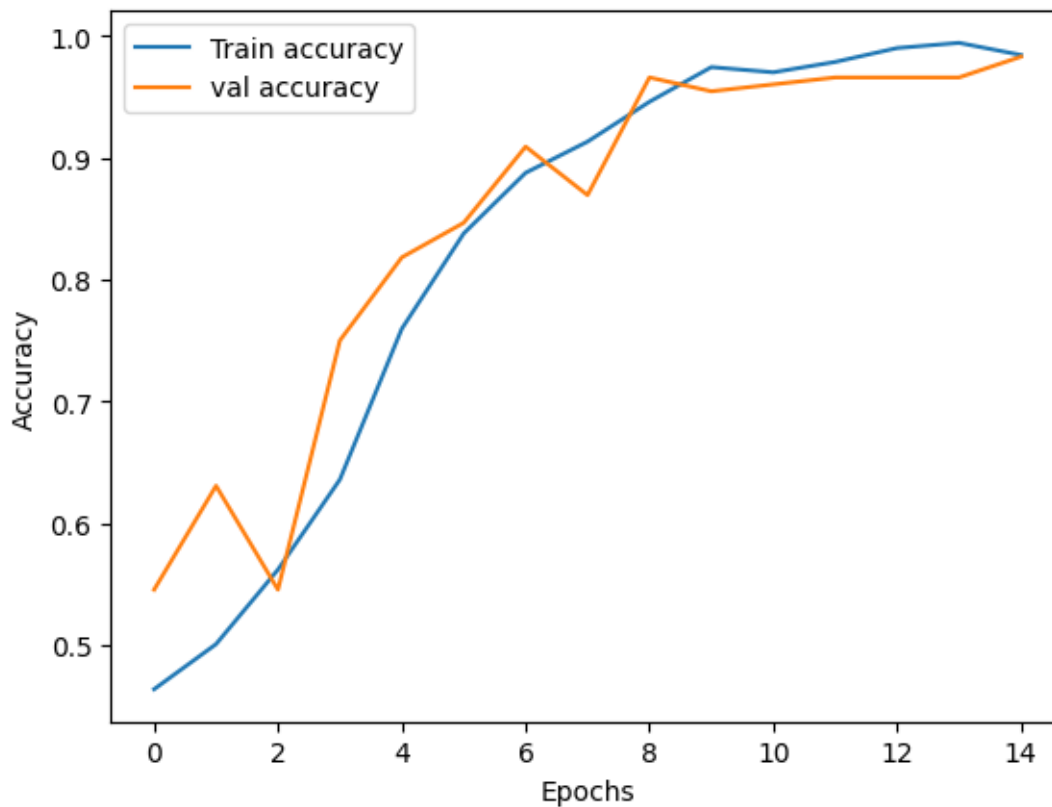
```

7/7          38s 5s/step -
accuracy: 0.9945 - loss: 0.0305
Test Loss: 0.05536875128746033
Test Accuracy: 0.9863636493682861

```

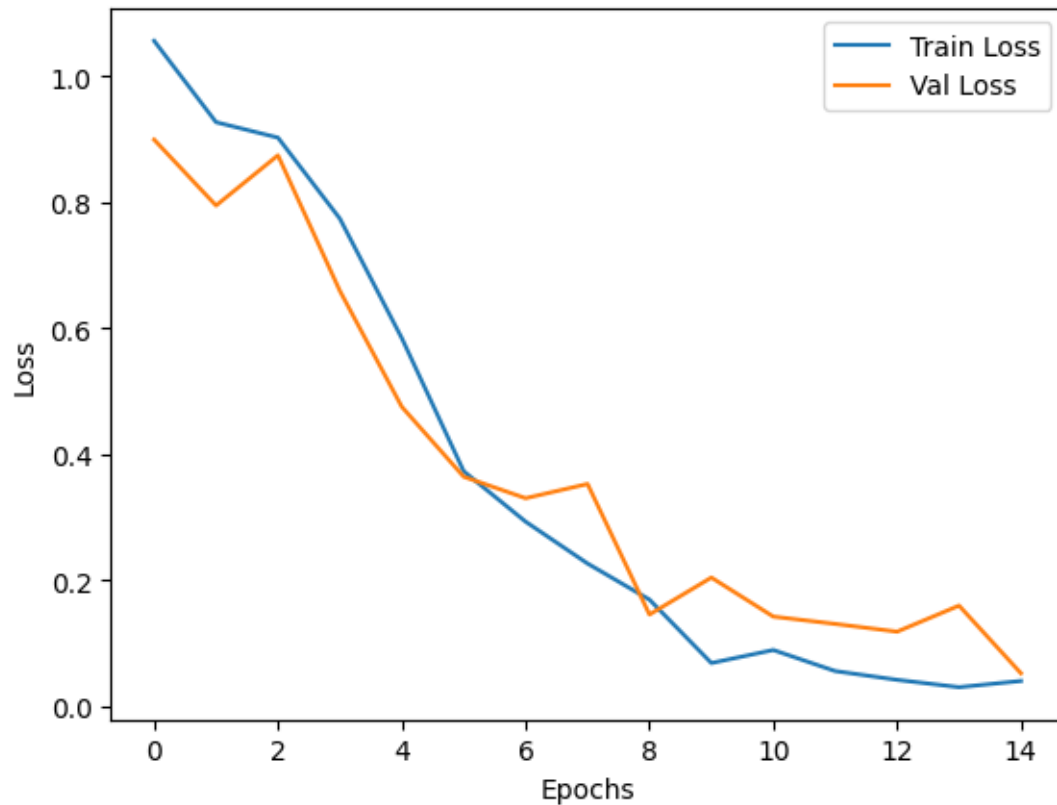
```
[27]: plt.plot(history.history['accuracy'], label = 'Train accuracy')
plt.plot(history.history['val_accuracy'], label = 'val accuracy')
plt.xlabel('Epochs')
plt.ylabel('Accuracy')
plt.legend(loc = 'best')
```

```
[27]: <matplotlib.legend.Legend at 0x7977a97132d0>
```



```
[28]: plt.plot(history.history['loss'], label = 'Train Loss')
plt.plot(history.history['val_loss'], label = 'Val Loss')
plt.xlabel('Epochs')
plt.ylabel('Loss')
plt.legend(loc = 'best')
```

```
[28]: <matplotlib.legend.Legend at 0x7977a96df550>
```



```
[30]: import cv2
import numpy as np
import matplotlib.pyplot as plt
import os # Import the os module

# Load the test image
image_path = '/content/Lung Cancer/LungcancerDataSet/Data/valid/BenginCases/
↳Bengin case (112).jpg'

# Check if the image file exists
if not os.path.exists(image_path):
    print(f"Error: Image file not found at {image_path}")
else:
    img = cv2.imread(image_path)

    # Check if the image was loaded successfully
    if img is None:
        print(f"Error: Could not load image from {image_path}")
    else:
        img = cv2.resize(img, (img_height, img_width))
```

```

# Expand dimensions to create a batch of size 1
img = np.expand_dims(img, axis=0)

# Make prediction
prediction = model.predict(img)

# Interpret prediction
class_label = np.argmax(prediction)
confidence = prediction[0][class_label]

print("Predicted Class Label:", class_label)
print("Confidence:", confidence)

# Mapping class labels to categories
class_labels_to_categories = {0: 'Benign', 1: 'Malignant', 2: 'Normal'}

# Display the predicted category
predicted_category = class_labels_to_categories[class_label]
print("Predicted Category:", predicted_category)

# Read the image again for displaying (since the 'img' variable was
↳ modified for prediction)
img_display = cv2.imread(image_path)
plt.imshow(cv2.cvtColor(img_display, cv2.COLOR_BGR2RGB))
plt.axis('off')
plt.title(predicted_category)
plt.show()

```

```

1/1          1s 930ms/step
Predicted Class Label: 0
Confidence: 1.0
Predicted Category: Benign

```

Bengin



```
[32]: import cv2
import numpy as np
import matplotlib.pyplot as plt
import os # Import the os module

# Load the test image
image_path = '/content/Lung Cancer/LungcancerDataSet/Data/valid/normal/Normal_
↳case (351).jpg'
img = cv2.imread(image_path)

# Check if the image was loaded successfully
if img is None:
    print(f"Error: Could not load image from {image_path}")
else:
    img = cv2.resize(img, (img_height, img_width))

    # Expand dimensions to create a batch of size 1
    img = np.expand_dims(img, axis=0)

    # Make prediction
    prediction = model.predict(img)
```

```

# Interpret prediction
class_label = np.argmax(prediction)
confidence = prediction[0][class_label]

print("Predicted Class Label:", class_label)
print("Confidence:", confidence)

# Mapping class labels to categories
class_labels_to_categories = {0: 'Benign', 1: 'Malignant', 2: 'Normal'}

# Display the predicted category
predicted_category = class_labels_to_categories[class_label]
print("Predicted Category:", predicted_category)

# Read the image again for displaying (since the 'img' variable was
↪modified for prediction)
img_display = cv2.imread(image_path)
plt.imshow(cv2.cvtColor(img_display, cv2.COLOR_BGR2RGB))
plt.axis('off')
plt.title(predicted_category)
plt.show()

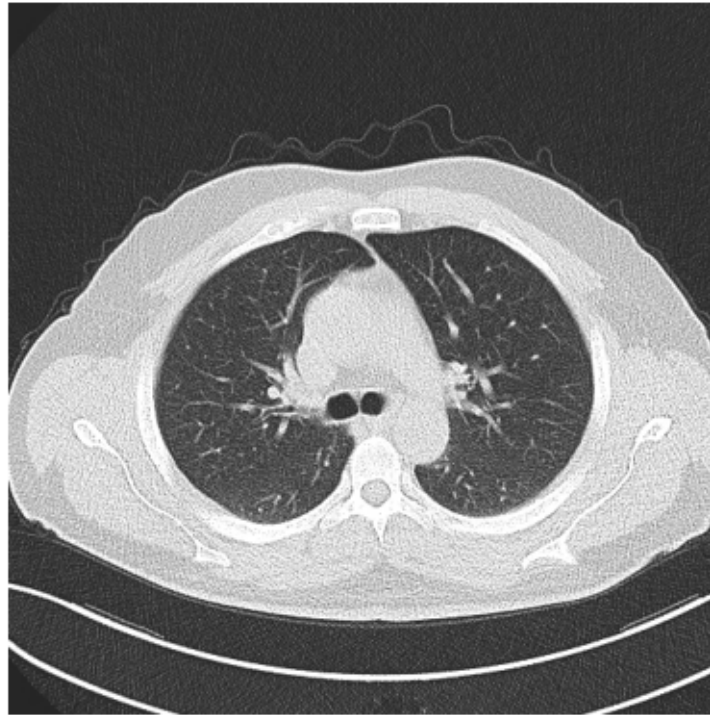
```

```

1/1          0s 495ms/step
Predicted Class Label: 2
Confidence: 1.0
Predicted Category: Normal

```

Normal

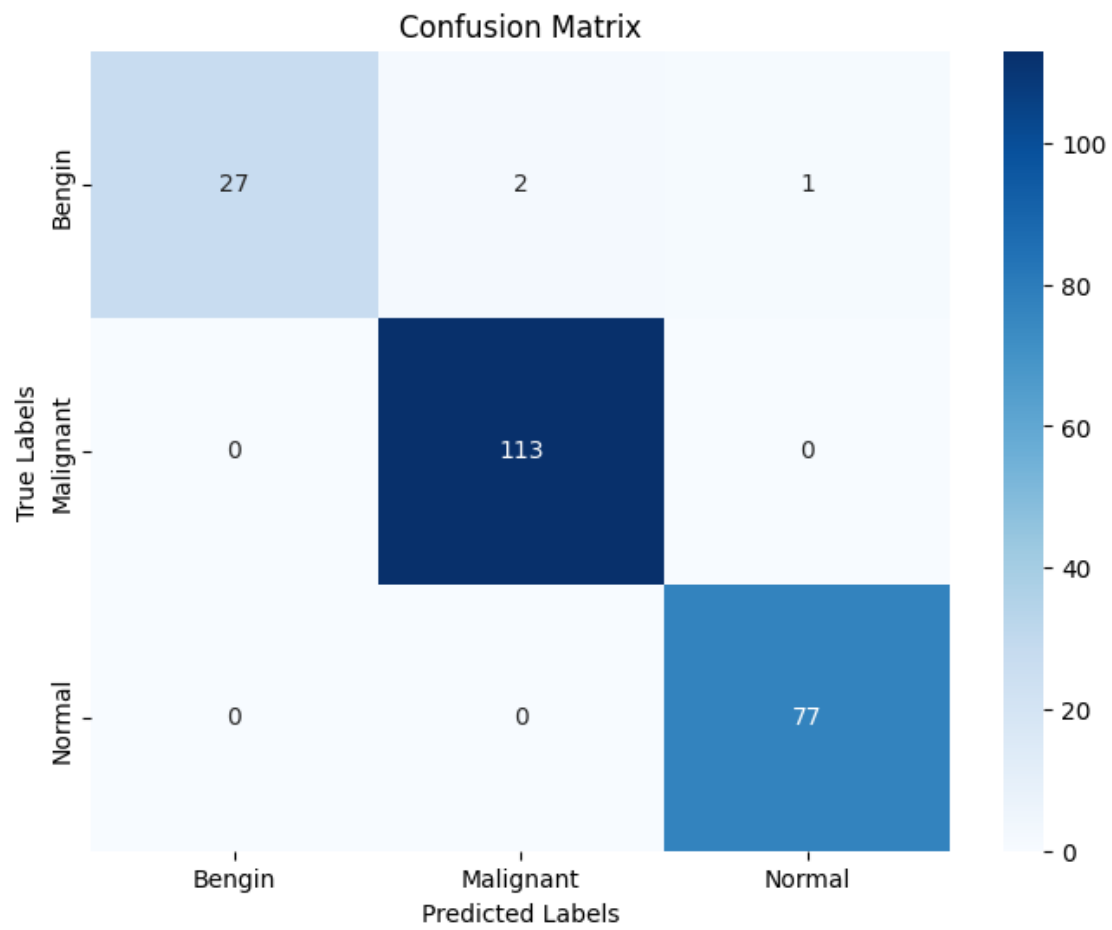


```
[33]: from sklearn.metrics import confusion_matrix
import seaborn as sns

# Define true labels and predicted labels
true_labels = y_test
predicted_labels = np.argmax(result, axis=1)

# Calculate confusion matrix
cm = confusion_matrix(true_labels, predicted_labels)

# Plot confusion matrix
plt.figure(figsize=(8, 6))
sns.heatmap(cm, annot=True, fmt='d', cmap='Blues',
            xticklabels=class_labels_to_categories.values(),
            yticklabels=class_labels_to_categories.values())
plt.xlabel('Predicted Labels')
plt.ylabel('True Labels')
plt.title('Confusion Matrix')
plt.show()
```

[]: