image-captioning-for-smart-farming

July 4, 2024

[1]:
```
from google.colab import files
files.upload()
```

```
<IPython.core.display.HTML object>
```

```
Saving kaggle.json to kaggle.json
```

[1]:
```
{'kaggle.json':
b'{"username":"aloksingh077","key":"8d905146f1b8f911e33ecbb0a93e9869"}'}
```

[2]:
```
import os

# Set the KAGGLE_CONFIG_DIR environment variable to point to the /content␣
 ↪directory.
# This tells the Kaggle API where to find the kaggle.json configuration file,␣
 ↪which contains your Kaggle credentials.
# The /content directory is commonly used in Google Colab for storing files.
os.environ['KAGGLE_CONFIG_DIR'] = '/content'
```

[3]:
```
!kaggle competitions download -c plant-pathology-2020-fgvc7
```

```
Warning: Your Kaggle API key is readable by other users on this system! To fix
this, you can run 'chmod 600 /content/kaggle.json'
Downloading plant-pathology-2020-fgvc7.zip to /content
 99% 775M/779M [00:09<00:00, 129MB/s]
100% 779M/779M [00:09<00:00, 86.0MB/s]
```

[4]:
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!unzip plant-pathology-2020-fgvc7.zip -d plant_pathology
```

```
Archive:  plant-pathology-2020-fgvc7.zip
  inflating: plant_pathology/images/Test_0.jpg
  inflating: plant_pathology/images/Test_1.jpg
  inflating: plant_pathology/images/Test_10.jpg
  inflating: plant_pathology/images/Test_100.jpg
  inflating: plant_pathology/images/Test_1000.jpg
  inflating: plant_pathology/images/Test_1001.jpg
  inflating: plant_pathology/images/Test_1002.jpg
  inflating: plant_pathology/images/Test_1003.jpg
  inflating: plant_pathology/images/Test_1004.jpg
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[5]:
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# Install the EfficientNet package quietly.
# EfficientNet is a family of neural networks that are highly efficient and␣
 ↪accurate for image classification tasks.
!pip install -q efficientnet
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[6]:
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# Importing essential libraries for data manipulation, visualization, and␣
 ↪building machine learning models.

import os  # For interacting with the operating system.
import gc  # For garbage collection to free up memory.
import re  # For regular expression operations.
import cv2  # For image processing.
import math  # For mathematical operations.
import numpy as np  # For numerical operations on large arrays and matrices.
import scipy as sp  # For scientific and technical computing.
import pandas as pd  # For data manipulation and analysis.

import tensorflow as tf  # For building and training machine learning models.
from IPython.display import SVG  # For displaying SVG images in Jupyter␣
 ↪notebooks.
import efficientnet.tfkeras as efn  # For using EfficientNet models.
from keras.utils import plot_model  # For visualizing Keras models.
import tensorflow.keras.layers as L  # For defining layers in Keras models.
from keras.utils import model_to_dot  # For converting models to DOT format.
import tensorflow.keras.backend as K  # For Keras backend operations.
from tensorflow.keras.models import Model  # For creating Keras models.
from tensorflow.keras.applications import DenseNet121  # For using DenseNet121␣
 ↪model.

import seaborn as sns  # For data visualization.
from tqdm import tqdm  # For progress bars.
import matplotlib.cm as cm  # For colormap support.
from sklearn import metrics  # For evaluating machine learning models.
import matplotlib.pyplot as plt  # For plotting data.
from sklearn.utils import shuffle  # For shuffling datasets.
from sklearn.model_selection import train_test_split  # For splitting datasets␣
 ↪into train and test sets.

tqdm.pandas()  # For progress bars in pandas operations.
import plotly.express as px  # For interactive visualizations.
import plotly.graph_objects as go  # For creating visualizations.
import plotly.figure_factory as ff  # For creating special visualizations.
from plotly.subplots import make_subplots  # For creating subplot␣
 ↪visualizations.

np.random.seed(0)  # For reproducibility.
tf.random.set_seed(0)  # For reproducibility.

import warnings
warnings.filterwarnings("ignore")  # To ignore warnings.
```

[7]:
```
EPOCHS = 20
SAMPLE_LEN = 100
IMAGE_PATH = "/content/plant_pathology/images"
TEST_PATH = "/content/plant_pathology/test.csv"
TRAIN_PATH = "/content/plant_pathology/train.csv"
SUB_PATH = "/content/plant_pathology/sample_submission.csv"

sub = pd.read_csv(SUB_PATH)
test_data = pd.read_csv(TEST_PATH)
train_data = pd.read_csv(TRAIN_PATH)
```

[8]:
```
train_data.head()
```

[8]:

	image_id	healthy	multiple_diseases	rust	scab
0	Train_0	0	0	0	1
1	Train_1	0	1	0	0
2	Train_2	1	0	0	0
3	Train_3	0	0	1	0
4	Train_4	1	0	0	0

[9]:
```
from tqdm import tqdm  # Import tqdm for progress bars
tqdm.pandas()  # Add progress bars to pandas operations

IMAGE_PATH = "/content/plant_pathology/images/"  # Correct image path
SAMPLE_LEN = 100  # Example value, adjust as needed

def load_image(image_id):
    file_path = image_id + ".jpg"  # Construct file path for the image
    image = cv2.imread(IMAGE_PATH + file_path)  # Read the image from the␣
 ↪specified path

    if image is None:
        print(f"Error loading image: {file_path}")  # Print error message if␣
 ↪image is not found
        return None  # Handle error appropriately by returning None

    return cv2.cvtColor(image, cv2.COLOR_BGR2RGB)  # Convert image to RGB color␣
 ↪space

# Load images with error handling
train_images = train_data["image_id"][:SAMPLE_LEN].progress_apply(load_image) ␣
 ↪# Apply load_image function to each image_id

# Remove any None values from the list of images
train_images = train_images.dropna().tolist()  # Drop None values and convert␣
 ↪to a list
```

```
# Explanation:
# - tqdm.pandas(): Adds progress bars to pandas operations.
# - IMAGE_PATH: Specifies the path to the directory containing the images.
# - SAMPLE_LEN: Number of images to load, can be adjusted.
# - load_image: Function to load and convert images to RGB, with error handling␣
 ↪for missing images.
# - train_images: Loads images from the dataset, applies load_image function,␣
 ↪and removes any None values.
```

```
100%|      | 100/100 [00:05<00:00, 19.19it/s]
```

[10]:
```
fig = px.imshow(cv2.resize(train_images[0], (205, 136)))  # Create an␣
 ↪interactive plot to display a resized image
fig.show()  # Show the plot in the notebook
```

[11]:
```
# Calculate mean pixel values for each color channel and overall for all images␣
 ↪in train_images
red_values = [np.mean(train_images[idx][:, :, 0]) for idx in␣
 ↪range(len(train_images))]  # Mean red channel values
green_values = [np.mean(train_images[idx][:, :, 1]) for idx in␣
 ↪range(len(train_images))]  # Mean green channel values
blue_values = [np.mean(train_images[idx][:, :, 2]) for idx in␣
 ↪range(len(train_images))]  # Mean blue channel values
values = [np.mean(train_images[idx]) for idx in range(len(train_images))]  #␣
 ↪Mean values across all channels (RGB)
```

[12]:
```
fig = ff.create_distplot([values], group_labels=["Channels"],␣
 ↪colors=["purple"])  # Create a distribution plot for pixel values across all␣
 ↪channels
fig.update_layout(showlegend=False, template="simple_white",␣
 ↪title_text="Distribution of channel values")  # Customize plot layout and␣
 ↪add title
fig.data[0].marker.line.color = 'rgb(0, 0, 0)'  # Set marker line color to␣
 ↪black for better visibility
fig.data[0].marker.line.width = 0.5  # Set marker line width for better␣
 ↪appearance
fig
```

[13]:
```
fig = ff.create_distplot([red_values], group_labels=["R"], colors=["red"])  #␣
 ↪Create a distribution plot for red channel pixel values
fig.update_layout(showlegend=False, template="simple_white",␣
 ↪title_text="Distribution of red channel values")  # Customize plot layout␣
 ↪and add title
fig.data[0].marker.line.color = 'rgb(0, 0, 0)'  # Set marker line color to␣
 ↪black for better visibility
```

```
fig.data[0].marker.line.width = 0.5  # Set marker line width for better␣
 ↪appearance
fig
```

[14]:
```
fig = ff.create_distplot([green_values], group_labels=["G"], colors=["green"]) ␣
 ↪# Create a distribution plot for green channel pixel values
fig.update_layout(showlegend=False, template="simple_white",␣
 ↪title_text="Distribution of green channel values")  # Customize plot layout␣
 ↪and add title
fig.data[0].marker.line.color = 'rgb(0, 0, 0)'  # Set marker line color to␣
 ↪black for better visibility
fig.data[0].marker.line.width = 0.5  # Set marker line width for better␣
 ↪appearance
fig
```

[15]:
```
fig = ff.create_distplot([blue_values], group_labels=["B"], colors=["blue"])  #␣
 ↪Create a distribution plot for blue channel pixel values
fig.update_layout(showlegend=False, template="simple_white",␣
 ↪title_text="Distribution of blue channel values")  # Customize plot layout␣
 ↪and add title
fig.data[0].marker.line.color = 'rgb(0, 0, 0)'  # Set marker line color to␣
 ↪black for better visibility
fig.data[0].marker.line.width = 0.5  # Set marker line width for better␣
 ↪appearance
fig
```

[16]:
```
import plotly.graph_objects as go

fig = go.Figure()

# Assuming you have lists red_values, green_values, blue_values defined␣
 ↪somewhere

for idx, values in enumerate([red_values, green_values, blue_values]):
    if idx == 0:
        color = "Red"
    elif idx == 1:
        color = "Green"
    elif idx == 2:
        color = "Blue"

    # Add a box trace for each color channel
    fig.add_trace(go.Box(x=[color]*len(values), y=values, name=color,␣
 ↪marker=dict(color=color.lower())))

fig.update_layout(
```

```
    yaxis_title="Mean value",
    xaxis_title="Color channel",
    title="Mean value vs. Color channel",
    template="plotly_white"
)
```

[17]:
```
fig = ff.create_distplot([red_values, green_values, blue_values],
                         group_labels=["R", "G", "B"],
                         colors=["red", "green", "blue"])  # Create a␣
 ↪distribution plot for red, green, and blue channel pixel values
fig.update_layout(title_text="Distribution of red channel values",␣
 ↪template="simple_white")  # Customize plot layout and add title
fig.data[0].marker.line.color = 'rgb(0, 0, 0)'  # Set marker line color for red␣
 ↪channel to black for better visibility
fig.data[0].marker.line.width = 0.5  # Set marker line width for red channel
fig.data[1].marker.line.color = 'rgb(0, 0, 0)'  # Set marker line color for␣
 ↪green channel to black for better visibility
fig.data[1].marker.line.width = 0.5  # Set marker line width for green channel
fig.data[2].marker.line.color = 'rgb(0, 0, 0)'  # Set marker line color for␣
 ↪blue channel to black for better visibility
fig.data[2].marker.line.width = 0.5  # Set marker line width for blue channel
fig
```

[18]:
```
def visualize_leaves(cond=[0, 0, 0, 0], cond_cols=["healthy"], is_cond=True):
    if not is_cond:
        cols, rows = 3, min([3, len(train_images) // 3])
        fig, ax = plt.subplots(nrows=rows, ncols=cols, figsize=(30, rows * 20 /␣
 ↪3))
        for col in range(cols):
            for row in range(rows):
                ax[row, col].imshow(train_images[-row * 3 - col - 1])  # Access␣
 ↪images directly from the list
        plt.show()
        return None

    cond_0 = "healthy == {}".format(cond[0])
    cond_1 = "scab == {}".format(cond[1])
    cond_2 = "rust == {}".format(cond[2])
    cond_3 = "multiple_diseases == {}".format(cond[3])

    cond_list = []
    for col in cond_cols:
        if col == "healthy":
            cond_list.append(cond_0)
        if col == "scab":
            cond_list.append(cond_1)
```

```
        if col == "rust":
            cond_list.append(cond_2)
        if col == "multiple_diseases":
            cond_list.append(cond_3)

    # Subset of data, adjust as needed
    data = train_data.loc[:100]
    for cond in cond_list:
        data = data.query(cond)

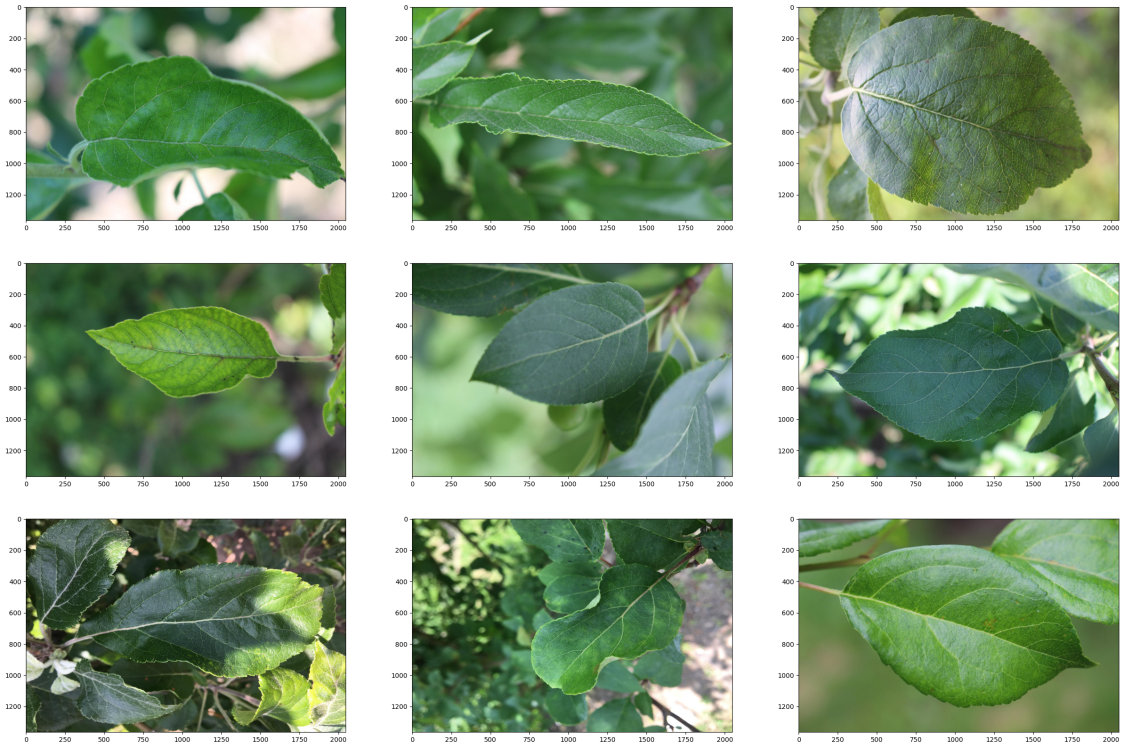
    # Get indices from the filtered data
    indices = data.index.tolist()

    # Access images from the list using these indices if within range
    images = [train_images[i] for i in indices if i < len(train_images)]

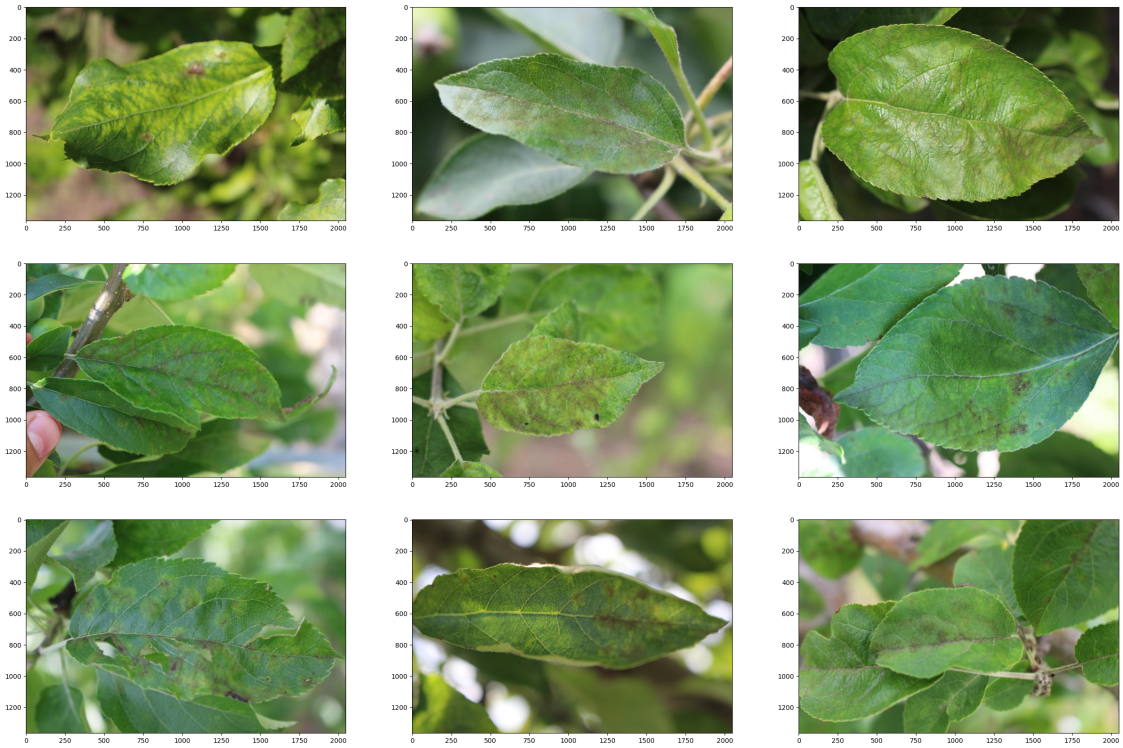
    cols, rows = 3, min([3, len(images) // 3])

    fig, ax = plt.subplots(nrows=rows, ncols=cols, figsize=(30, rows * 20 / 3))
    for col in range(cols):
        for row in range(rows):
            idx = row * 3 + col
            if idx < len(images):  # Check if index is within the range of␣
 ↪images list
                ax[row, col].imshow(images[idx])  # Access images by simple␣
 ↪indexing
    plt.show()

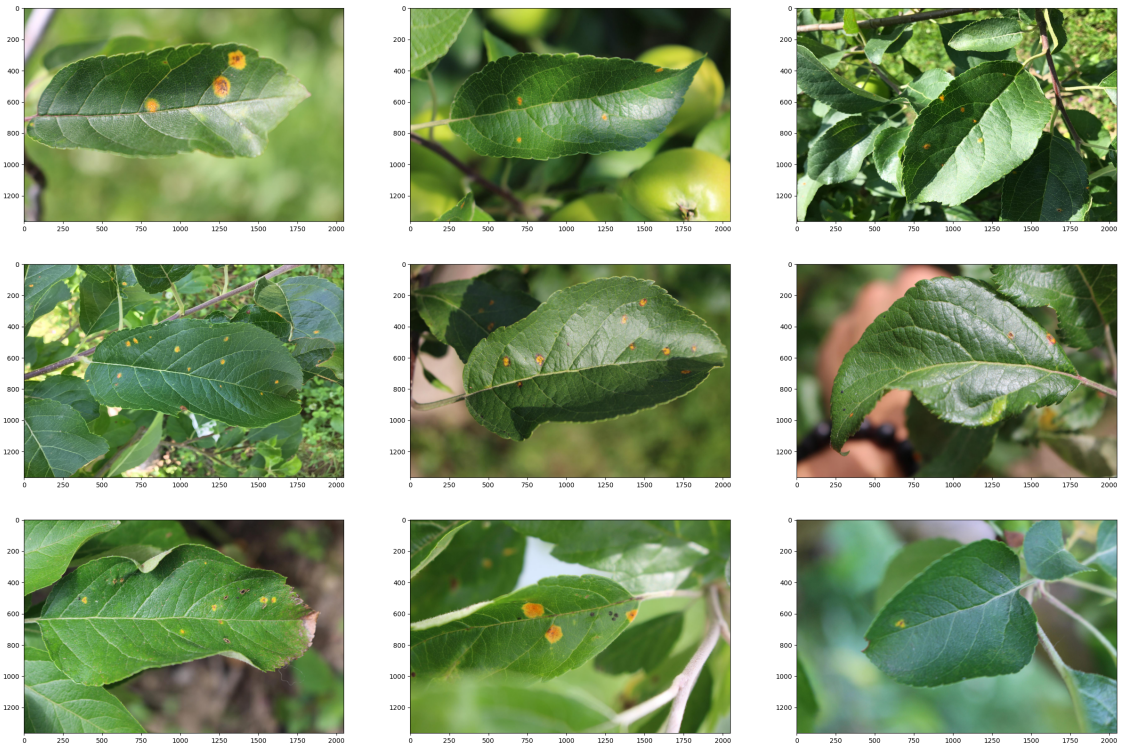
# Example usage:
visualize_leaves(cond=[1, 0, 0, 0], cond_cols=["healthy"])
```



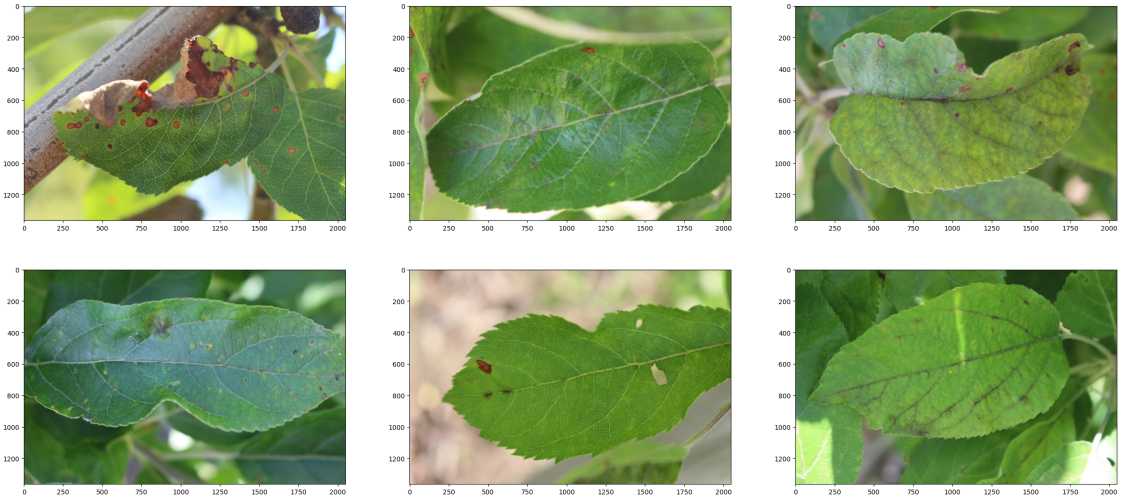
[19]:
```
visualize_leaves(cond=[0, 1, 0, 0], cond_cols=["scab"])
```



[20]:
```
visualize_leaves(cond=[0, 0, 1, 0], cond_cols=["rust"])
```



[21]:
```
visualize_leaves(cond=[0, 0, 0, 1], cond_cols=["multiple_diseases"])
```



[22]:
```
fig = go.Figure([go.Pie(labels=train_data.columns[1:],
           values=train_data.iloc[:, 1:].sum().values)])  # Create a pie chart␣
 ↪showing the distribution of target labels
fig.update_layout(title_text="Pie chart of targets", template="simple_white") ␣
 ↪# Customize plot layout and add title
fig.data[0].marker.line.color = 'rgb(0, 0, 0)'  # Set marker line color to␣
 ↪black for better visibility
fig.data[0].marker.line.width = 0.5  # Set marker line width for better␣
 ↪visibility
fig.show()  # Display the pie chart
```

[23]:
```
def edge_and_cut(img):
    emb_img = img.copy()
    edges = cv2.Canny(img, 100, 200)  # Detect edges using Canny edge detection
    edge_coors = []
    for i in range(edges.shape[0]):
        for j in range(edges.shape[1]):
            if edges[i][j] != 0:
                edge_coors.append((i, j))  # Collect coordinates of edge points

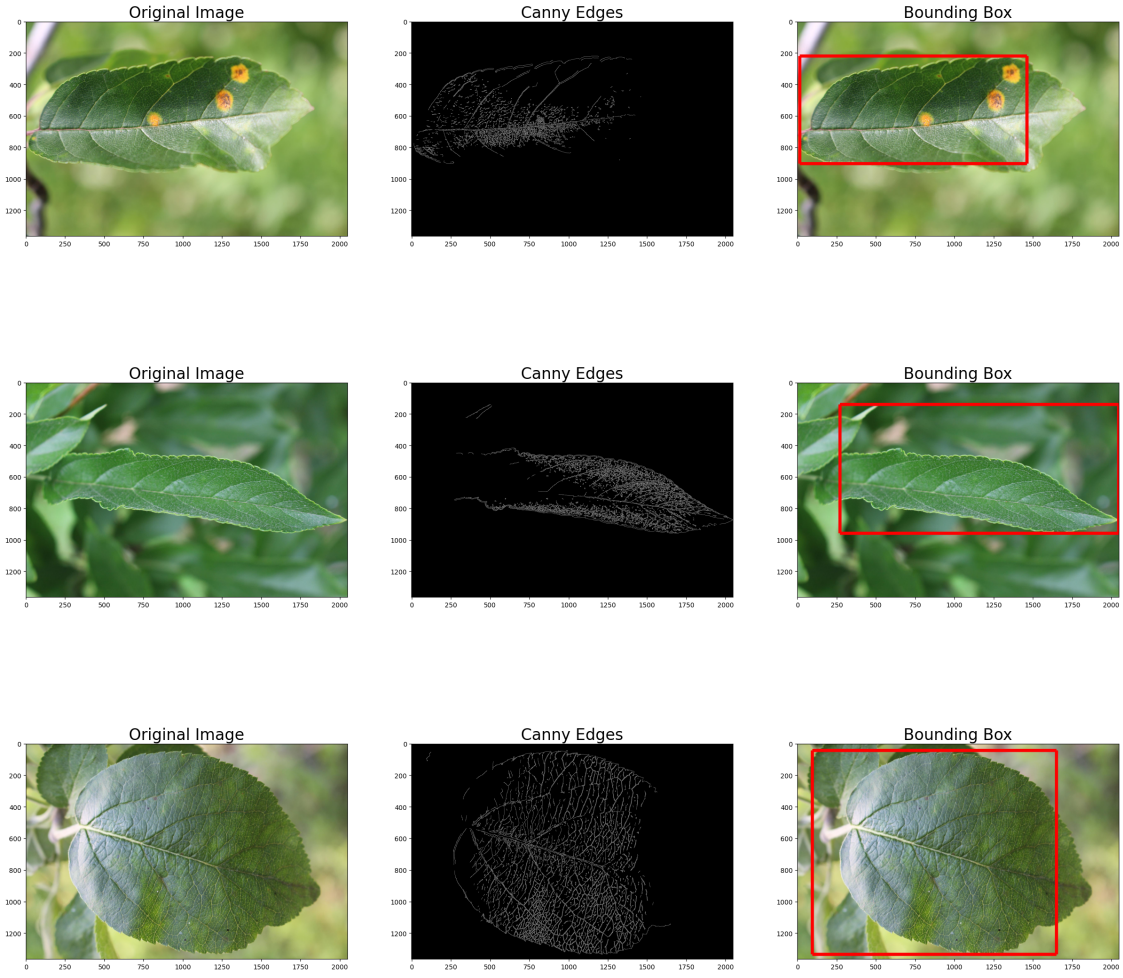
    # Determine bounding box coordinates based on edge points
    row_min = edge_coors[np.argsort([coor[0] for coor in edge_coors])[0]][0]
    row_max = edge_coors[np.argsort([coor[0] for coor in edge_coors])[-1]][0]
    col_min = edge_coors[np.argsort([coor[1] for coor in edge_coors])[0]][1]
    col_max = edge_coors[np.argsort([coor[1] for coor in edge_coors])[-1]][1]
    new_img = img[row_min:row_max, col_min:col_max]  # Crop the image based on␣
 ↪bounding box

    # Highlight bounding box in the original image
    emb_img[row_min-10:row_min+10, col_min:col_max] = [255, 0, 0]
    emb_img[row_max-10:row_max+10, col_min:col_max] = [255, 0, 0]
    emb_img[row_min:row_max, col_min-10:col_min+10] = [255, 0, 0]
    emb_img[row_min:row_max, col_max-10:col_max+10] = [255, 0, 0]

    # Plot the original image, edges, and image with bounding box
    fig, ax = plt.subplots(nrows=1, ncols=3, figsize=(30, 20))
    ax[0].imshow(img, cmap='gray')
    ax[0].set_title('Original Image', fontsize=24)
    ax[1].imshow(edges, cmap='gray')
    ax[1].set_title('Canny Edges', fontsize=24)
    ax[2].imshow(emb_img, cmap='gray')
    ax[2].set_title('Bounding Box', fontsize=24)
    plt.show()
```

[24]:
```
# Apply the edge_and_cut function to specific images from the train_images list
edge_and_cut(train_images[3])  # Apply to the 4th image in the list
edge_and_cut(train_images[4])  # Apply to the 5th image in the list
```

```
edge_and_cut(train_images[5])  # Apply to the 6th image in the list
```



[25]:
```
def invert(img):
    fig, ax = plt.subplots(nrows=1, ncols=3, figsize=(30, 20))

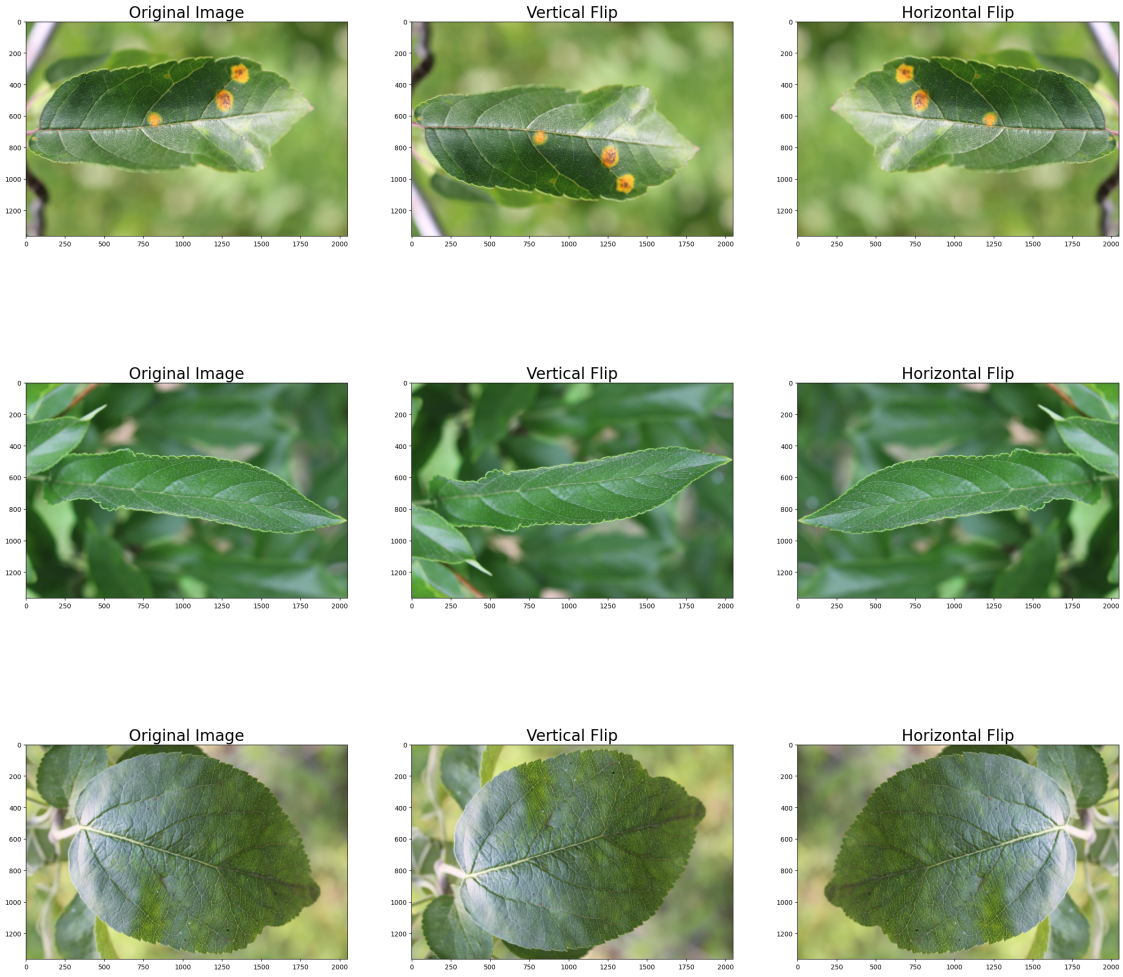
    # Display the original image
    ax[0].imshow(img)
    ax[0].set_title('Original Image', fontsize=24)

    # Display the vertically flipped image
    ax[1].imshow(cv2.flip(img, 0))
    ax[1].set_title('Vertical Flip', fontsize=24)

    # Display the horizontally flipped image
    ax[2].imshow(cv2.flip(img, 1))
    ax[2].set_title('Horizontal Flip', fontsize=24)
```

```
    plt.show()
```

[26]:
```
invert(train_images[3])
invert(train_images[4])
invert(train_images[5])
```



[27]:
```
def conv(img):
    fig, ax = plt.subplots(nrows=1, ncols=2, figsize=(20, 20))

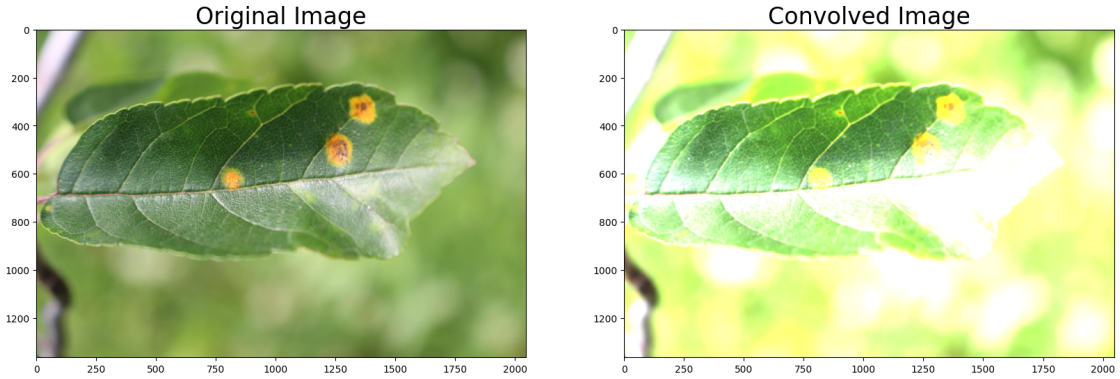
    # Define a kernel for the convolution operation
    kernel = np.ones((7, 7), np.float32) / 25
    # Apply the convolution operation
    conv = cv2.filter2D(img, -1, kernel)

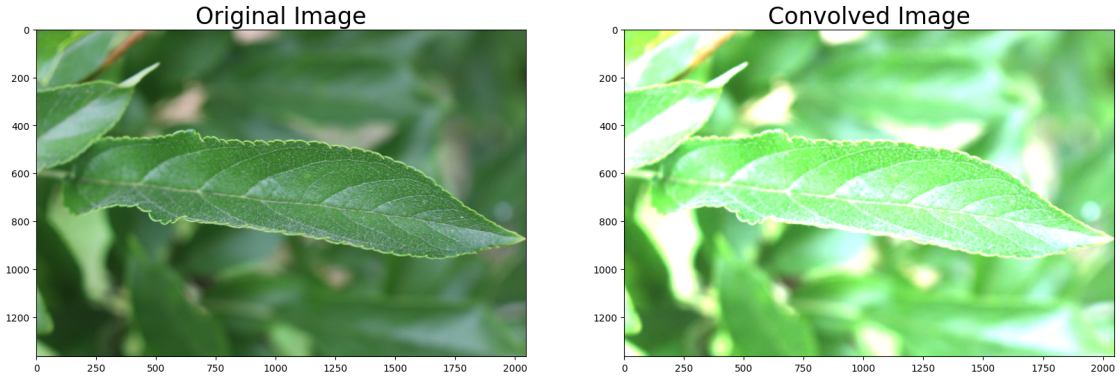
    # Display the original image
    ax[0].imshow(img)
    ax[0].set_title('Original Image', fontsize=24)
```

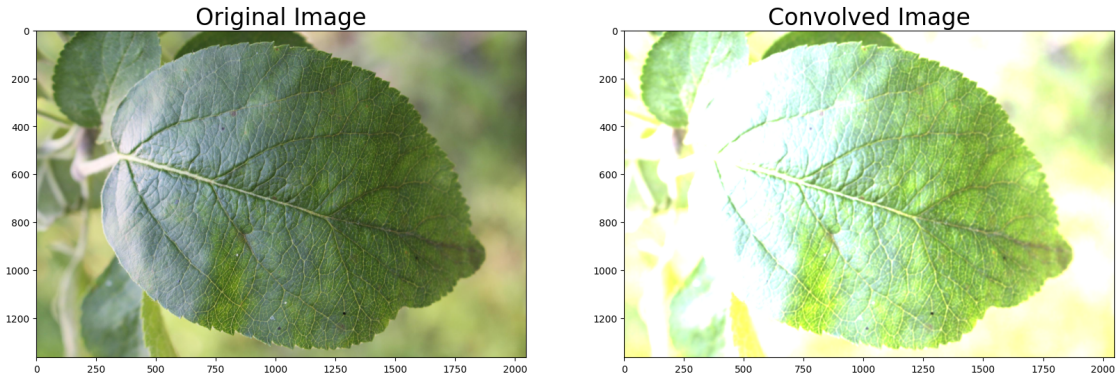
```
    # Display the convolved image
    ax[1].imshow(conv)
    ax[1].set_title('Convolved Image', fontsize=24)

    plt.show()
```

[28]:
```
conv(train_images[3])
conv(train_images[4])
conv(train_images[5])
```







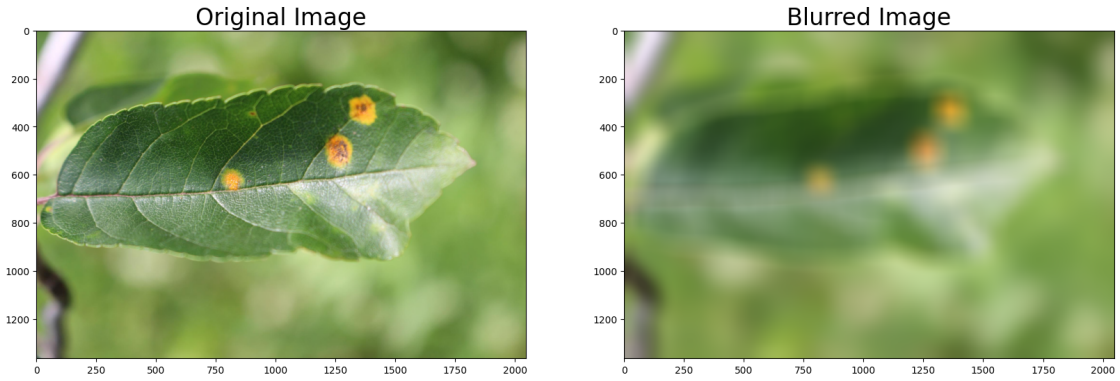
[29]:
```
def blur(img):
    fig, ax = plt.subplots(nrows=1, ncols=2, figsize=(20, 20))

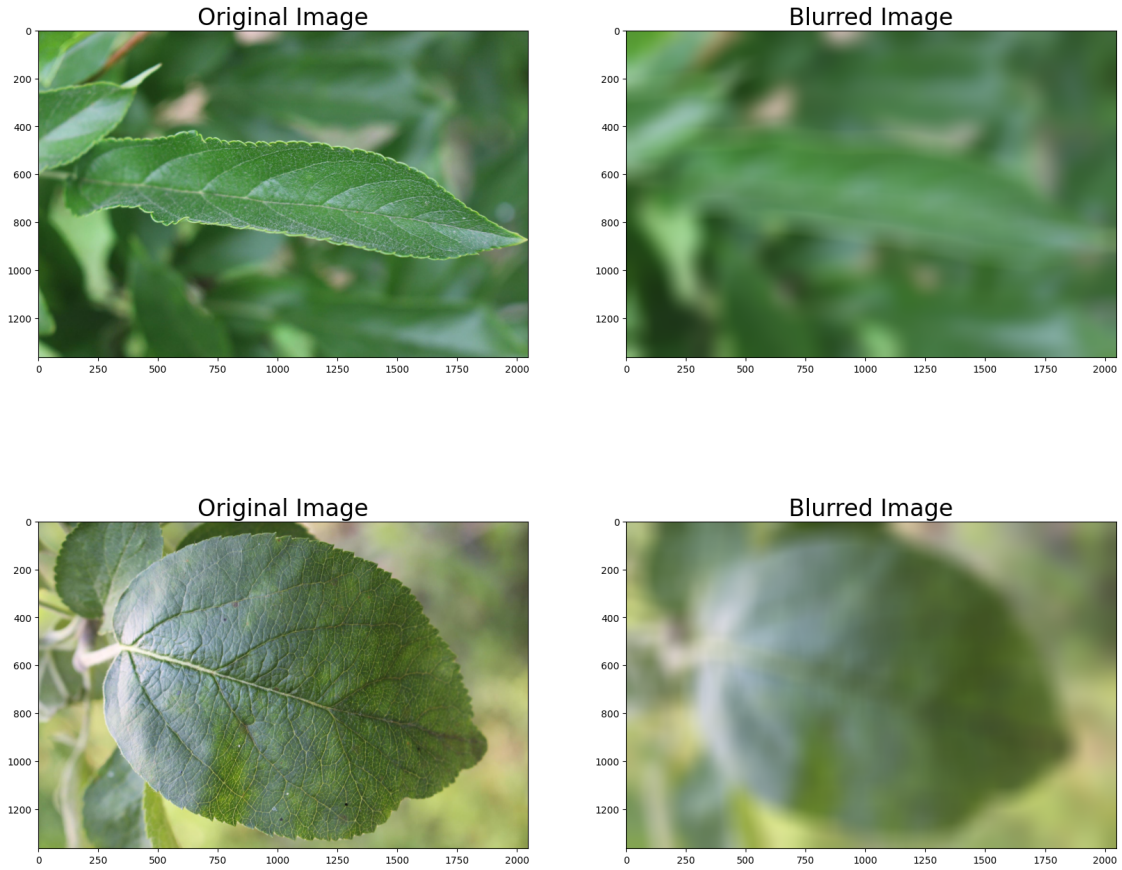
    # Display the original image
    ax[0].imshow(img)
    ax[0].set_title('Original Image', fontsize=24)

    # Apply a blurring operation with a 100x100 kernel size
    ax[1].imshow(cv2.blur(img, (100, 100)))
    ax[1].set_title('Blurred Image', fontsize=24)

    plt.show()
```

[30]:
```
blur(train_images[3])
blur(train_images[4])
blur(train_images[5])
```





[31]:
```
import tensorflow as tf
from sklearn.model_selection import train_test_split

# Use AUTOTUNE to automatically tune the number of threads
AUTO = tf.data.experimental.AUTOTUNE

# Since you are running on a CPU, no need to set up TPU
# Determine the batch size (you can adjust this based on your system's memory)
BATCH_SIZE = 16

# Manually set the path to your dataset
GCS_DS_PATH = '/content/plant_pathology'  # Replace with the actual path to␣
 ↪your dataset

# Function to format image paths based on GCS_DS_PATH
def format_path(st):
    return GCS_DS_PATH + '/images/' + st + '.jpg'

# Assuming you have already loaded train_data and test_data DataFrames
test_paths = test_data.image_id.apply(format_path).values
```

```
train_paths = train_data.image_id.apply(format_path).values

train_labels = np.float32(train_data.loc[:, 'healthy':'scab'].values)
train_paths, valid_paths, train_labels, valid_labels = \
    train_test_split(train_paths, train_labels, test_size=0.15,␣
 ↪random_state=2020)

# Verify that the paths are correctly generated
print(train_paths[:5])
print(test_paths[:5])
```

```
['/content/plant_pathology/images/Train_602.jpg'
 '/content/plant_pathology/images/Train_1514.jpg'
 '/content/plant_pathology/images/Train_1571.jpg'
 '/content/plant_pathology/images/Train_607.jpg'
 '/content/plant_pathology/images/Train_58.jpg']
['/content/plant_pathology/images/Test_0.jpg'
 '/content/plant_pathology/images/Test_1.jpg'
 '/content/plant_pathology/images/Test_2.jpg'
 '/content/plant_pathology/images/Test_3.jpg'
 '/content/plant_pathology/images/Test_4.jpg']
```

[32]:
```
def decode_image(filename, label=None, image_size=(512, 512)):
    """
    Decodes an image from a file, normalizes it, and resizes it.

    Args:
        filename (str): Path to the image file.
        label (optional): Label associated with the image. Default is None.
        image_size (tuple): Target size to resize the image. Default is (512,␣
 ↪512).

    Returns:
        If label is provided: (image, label) tuple.
        Otherwise: image.
    """
    # Read the image file
    bits = tf.io.read_file(filename)

    # Decode the image file as a JPEG image, expecting 3 color channels (RGB)
    image = tf.image.decode_jpeg(bits, channels=3)

    # Normalize the image to the range [0, 1]
    image = tf.cast(image, tf.float32) / 255.0

    # Resize the image to the target size
    image = tf.image.resize(image, image_size)
```

```
    # Return the image and label (if provided), otherwise just the image
    if label is None:
        return image
    else:
        return image, label

def data_augment(image, label=None):
    """
    Applies random augmentations to the image for data augmentation.

    Args:
        image (Tensor): Input image tensor.
        label (optional): Label associated with the image. Default is None.

    Returns:
        If label is provided: (augmented image, label) tuple.
        Otherwise: augmented image.
    """
    # Apply random horizontal flip
    image = tf.image.random_flip_left_right(image)

    # Apply random vertical flip
    image = tf.image.random_flip_up_down(image)

    # Return the augmented image and label (if provided), otherwise just the␣
 ↪image
    if label is None:
        return image
    else:
        return image, label
```

[33]:
```
# Create the training dataset
train_dataset = (
    tf.data.Dataset
    .from_tensor_slices((train_paths, train_labels))  # Create a dataset from␣
 ↪the training paths and labels
    .map(decode_image, num_parallel_calls=AUTO)       # Decode and preprocess␣
 ↪the images in parallel
    .map(data_augment, num_parallel_calls=AUTO)       # Apply data augmentation␣
 ↪in parallel
    .repeat()                                         # Repeat the dataset␣
 ↪indefinitely (useful for training)
    .shuffle(512)                                     # Shuffle the dataset␣
 ↪with a buffer size of 512
    .batch(BATCH_SIZE)                                # Batch the data
```

```
    .prefetch(AUTO)                                          # Prefetch the data for␣
 ↪better performance
)

# Create the validation dataset
valid_dataset = (
    tf.data.Dataset
    .from_tensor_slices((valid_paths, valid_labels))  # Create a dataset from␣
 ↪the validation paths and labels
    .map(decode_image, num_parallel_calls=AUTO)       # Decode and preprocess␣
 ↪the images in parallel
    .batch(BATCH_SIZE)                                       # Batch the data
    .cache()                                                 # Cache the data for␣
 ↪better performance
    .prefetch(AUTO)                                          # Prefetch the data for␣
 ↪better performance
)

# Create the test dataset
test_dataset = (
    tf.data.Dataset
    .from_tensor_slices(test_paths)                          # Create a dataset from␣
 ↪the test paths
    .map(decode_image, num_parallel_calls=AUTO)       # Decode and preprocess␣
 ↪the images in parallel
    .batch(BATCH_SIZE)                                       # Batch the data
)
```

[34]:
```
# Define a function to build the learning rate schedule function
def build_lrfn(lr_start=0.00001, lr_max=0.00005,
               lr_min=0.00001, lr_rampup_epochs=5,
               lr_sustain_epochs=0, lr_exp_decay=.8):
    # Adjust the maximum learning rate based on the number of replicas in sync
    lr_max = lr_max * strategy.num_replicas_in_sync

    # Define the learning rate schedule function
    def lrfn(epoch):
        # Ramp up phase: gradually increase the learning rate
        if epoch < lr_rampup_epochs:
            lr = (lr_max - lr_start) / lr_rampup_epochs * epoch + lr_start
        # Sustain phase: maintain the learning rate at the maximum value
        elif epoch < lr_rampup_epochs + lr_sustain_epochs:
            lr = lr_max
        # Exponential decay phase: gradually decrease the learning rate
        else:
            lr = (lr_max - lr_min) *\
```

```
                lr_exp_decay**(epoch - lr_rampup_epochs\
                               - lr_sustain_epochs) + lr_min
        return lr

    return lrfn  # Return the learning rate schedule function
```

[35]:
```
# Define the learning rate function without TPU strategy
def build_lrfn(lr_start=0.00001, lr_max=0.00005,
               lr_min=0.00001, lr_rampup_epochs=5,
               lr_sustain_epochs=0, lr_exp_decay=.8):
    def lrfn(epoch):
        if epoch < lr_rampup_epochs:
            lr = (lr_max - lr_start) / lr_rampup_epochs * epoch + lr_start
        elif epoch < lr_rampup_epochs + lr_sustain_epochs:
            lr = lr_max
        else:
            lr = (lr_max - lr_min) *\
                 lr_exp_decay**(epoch - lr_rampup_epochs\
                                - lr_sustain_epochs) + lr_min
        return lr
    return lrfn

# Use the learning rate function
lrfn = build_lrfn()

# Calculate the number of steps per epoch based on the batch size and the size␣
 ↪of the training dataset
STEPS_PER_EPOCH = train_labels.shape[0] // BATCH_SIZE

# Create a learning rate scheduler callback using the learning rate function␣
 ↪(lrfn)
lr_schedule = tf.keras.callbacks.LearningRateScheduler(lrfn, verbose=1)

# Now print out to verify
print(f"STEPS_PER_EPOCH: {STEPS_PER_EPOCH}")
print(f"Learning rate schedule for the first few epochs:")
for epoch in range(10):
    print(f"Epoch {epoch + 1}: {lrfn(epoch)}")
```

```
STEPS_PER_EPOCH: 96
Learning rate schedule for the first few epochs:
Epoch 1: 1e-05
Epoch 2: 1.8000000000000004e-05
Epoch 3: 2.6000000000000002e-05
Epoch 4: 3.4000000000000007e-05
Epoch 5: 4.2000000000000004e-05
Epoch 6: 5e-05
```

```
Epoch 7: 4.2000000000000004e-05
Epoch 8: 3.5600000000000005e-05
Epoch 9: 3.0480000000000006e-05
Epoch 10: 2.6384000000000004e-05
```

[36]:
```python
# Define and compile the model
model = tf.keras.Sequential([
    tf.keras.applications.DenseNet121(input_shape=(512, 512, 3),
                                      weights='imagenet',
                                      include_top=False),
    tf.keras.layers.GlobalAveragePooling2D(),
    tf.keras.layers.Dense(train_labels.shape[1], activation='softmax')
])

model.compile(optimizer='adam',
              loss='categorical_crossentropy',
              metrics=['categorical_accuracy'])

model.summary()
```

```
Downloading data from https://storage.googleapis.com/tensorflow/keras-
applications/densenet/densenet121_weights_tf_dim_ordering_tf_kernels_notop.h5
29084464/29084464 [==============================] - 0s 0us/step
Model: "sequential"
_________________________________________________________________
 Layer (type)                Output Shape              Param #
=================================================================
 densenet121 (Functional)    (None, 16, 16, 1024)      7037504

 global_average_pooling2d (  (None, 1024)              0
 GlobalAveragePooling2D)

 dense (Dense)               (None, 4)                 4100

=================================================================
Total params: 7041604 (26.86 MB)
Trainable params: 6957956 (26.54 MB)
Non-trainable params: 83648 (326.75 KB)
_________________________________________________________________
```

[ ]:
```python
# Train the model using the train_dataset for the specified number of epochs
history = model.fit(
    train_dataset,
    epochs=EPOCHS,              # Number of epochs to train the model
    callbacks=[lr_schedule],    # List of callbacks to apply during training,␣
 ↪in this case, a learning rate scheduler
```

```
    steps_per_epoch=STEPS_PER_EPOCH,  # Number of steps (batches) per epoch, calculated based on the training data size and batch size
    validation_data=valid_dataset  # Dataset for validation at the end of each epoch
)
```

[ ]:
```
display_training_curves(
    history.history['categorical_accuracy'],
    history.history['val_categorical_accuracy'],
    'accuracy')
```

[ ]:
```
import plotly.graph_objects as go
import plotly.express as px
import cv2

# Function to process an image for model input
def process(img):
    return cv2.resize(img / 255.0, (512, 512)).reshape(-1, 512, 512, 3)

# Function to make predictions using the model
def predict(img):
    return model.predict(process(img))[0]

# Initialize Plotly figure with subplots
fig = make_subplots(rows=4, cols=2)

# Function to visualize predictions for each image
def visualize_image_predictions(image, index):
    preds = predict(image)
    class_names = ["Healthy", "Multiple diseases", "Rust", "Scab"]
    pred_class = class_names[np.argmax(preds)]

    # Color coding for predicted class
    colors = {name: px.colors.qualitative.Plotly[0] for name in class_names}
    colors[pred_class] = px.colors.qualitative.Plotly[1]
    colors[pred_class] = "seagreen"
    bar_colors = [colors[name] for name in class_names]

    # Add image to subplot
    fig.add_trace(go.Image(z=cv2.resize(image, (205, 136))), row=index+1, col=1)

    # Add bar chart with predictions to subplot
    fig.add_trace(go.Bar(x=class_names, y=preds, marker=dict(color=bar_colors)), row=index+1, col=2)

# Visualize each image with predictions
for i, image in enumerate(train_images[:4]):
```

```
    visualize_image_predictions(image, i)

# Update layout and display the plot
fig.update_layout(height=1200, width=800, title_text="DenseNet Predictions",␣
 ↪showlegend=False, template="plotly_white")
fig.show()
```

[ ]:
```
probs_dnn = model.predict(test_dataset, verbose=1)
sub.loc[:, 'healthy':] = probs_dnn
sub.to_csv('submission_dnn.csv', index=False)
sub.head()
```

[ ]:
```
with strategy.scope():
    model = tf.keras.Sequential([
        efn.EfficientNetB7(input_shape=(512, 512, 3),  # Define input shape for␣
 ↪EfficientNetB7 model
                           weights='imagenet',         # Initialize with␣
 ↪pretrained ImageNet weights
                           include_top=False),         # Exclude the top␣
 ↪classification layer

        L.GlobalAveragePooling2D(),                    # Reduce spatial␣
 ↪dimensions using Global Average Pooling
        L.Dense(train_labels.shape[1],                 # Output layer with␣
 ↪softmax activation for multiclass
                activation='softmax')
    ])

    model.compile(optimizer='adam',                    # Use Adam optimizer for␣
 ↪training
                  loss='categorical_crossentropy',     # Categorical␣
 ↪crossentropy loss for multiclass classification
                  metrics=['categorical_accuracy'])    # Track categorical␣
 ↪accuracy during training

    model.summary()  # Print a summary of the model architecture
```

[ ]:
```
SVG(tf.keras.utils.model_to_dot(Model(model.layers[0].input, model.layers[0].
 ↪layers[11].output), dpi=70).create(prog='dot', format='svg'))
```

[ ]:
```
SVG(tf.keras.utils.model_to_dot(model, dpi=70).create(prog='dot', format='svg'))
```

[ ]:
```
history = model.fit(train_dataset,
                    epochs=EPOCHS,
                    callbacks=[lr_schedule],
                    steps_per_epoch=STEPS_PER_EPOCH,
```

```
                    validation_data=valid_dataset)
```

[ ]:
```
display_training_curves(
    history.history['categorical_accuracy'],
    history.history['val_categorical_accuracy'],
    'accuracy')
```

[ ]:
```
fig = make_subplots(rows=4, cols=2)
```

[ ]:
```
# Example for train_images[2]
preds = predict(train_images[2])
colors = {
    "Healthy": px.colors.qualitative.Plotly[0],
    "Scab": px.colors.qualitative.Plotly[0],
    "Rust": px.colors.qualitative.Plotly[0],
    "Multiple diseases": px.colors.qualitative.Plotly[0]
}

# Determine the predicted class
if list.index(preds.tolist(), max(preds)) == 0:
    pred = "Healthy"
elif list.index(preds.tolist(), max(preds)) == 1:
    pred = "Scab"
elif list.index(preds.tolist(), max(preds)) == 2:
    pred = "Rust"
elif list.index(preds.tolist(), max(preds)) == 3:
    pred = "Multiple diseases"

# Set color for the predicted class
colors[pred] = px.colors.qualitative.Plotly[1]
colors["Healthy"] = "seagreen"

# Add image and bar chart to subplot
fig.add_trace(go.Image(z=cv2.resize(train_images[2], (205, 136))), row=1, col=1)
fig.add_trace(go.Bar(x=["Healthy", "Multiple diseases", "Rust", "Scab"],␣
 ↪y=preds, marker=dict(color=colors)), row=1, col=2)

# Repeat the above for other train_images[n] (0, 1, 3)

# Update layout and display
fig.update_layout(height=1200, width=800, title_text="EfficientNet␣
 ↪Predictions", showlegend=False)
fig.update_layout(template="plotly_white")
```

[ ]:
```
probs_efn = model.predict(test_dataset, verbose=1)
sub.loc[:, 'healthy':] = probs_efn
sub.to_csv('submission_efn.csv', index=False)
```

```
sub.head()
```

[ ]:
```
#Considering these factors, EfficientNet might be slightly better
#if you value efficiency and scalability alongside accuracy.
#EfficientNet is known for achieving comparable or better performance
#with fewer parameters and lower computational cost.
#If the choice is purely based on the provided accuracy and epochs,
#both models are very similar, but EfficientNet's design for efficiency gives␣
↪it a slight edge.
```