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import numpy as np
import tensorflow as tf
import matplotlib.pyplot as plt

validation_set = tf.keras.utils.image_dataset_from_directory(
    'valid',
    labels="inferred",
    label_mode="categorical",
    class_names=None,
    color_mode="rgb",
    batch_size=32,
    image_size=(128, 128),
    shuffle=True,
    seed=None,
    validation_split=None,
    subset=None,
    interpolation="bilinear",
    follow_links=False,
    crop_to_aspect_ratio=False
)
class_name = validation_set.class_names
print(class_name)

Found 17572 files belonging to 38 classes.
['Apple__Apple_scab', 'Apple__Black_rot',
'Apple__Cedar_apple_rust', 'Apple__healthy', 'Blueberry__healthy',
'Cherry_(including_sour)__Powdery_mildew',
'Cherry_(including_sour)__healthy',
'Corn_(maize)__Cercospora_leaf_spot Gray_leaf_spot',
'Corn_(maize)__Common_rust_', 'Corn_(maize)__Northern_Leaf_Blight',
'Corn_(maize)__healthy', 'Grape__Black_rot',
'Grape__Esca_(Black_Measles)',
'Grape__Leaf_blight_(Isariopsis_Leaf_Spot)', 'Grape__healthy',
'Orange__Haunglongbing_(Citrus_greening)', 'Peach__Bacterial_spot',
'Peach__healthy', 'Pepper_bell__Bacterial_spot',
'Pepper_bell__healthy', 'Potato__Early_blight',
'Potato__Late_blight', 'Potato__healthy', 'Raspberry__healthy',
'Soybean__healthy', 'Squash__Powdery_mildew',
'Strawberry__Leaf_scorch', 'Strawberry__healthy',
'Tomato__Bacterial_spot', 'Tomato__Early_blight',
'Tomato__Late_blight', 'Tomato__Leaf_Mold',
'Tomato__Septoria_leaf_spot', 'Tomato__Spider_mites Two-
spotted_spider_mite', 'Tomato__Target_Spot',
'Tomato__Tomato_Yellow_Leaf_Curl_Virus',
'Tomato__Tomato_mosaic_virus', 'Tomato__healthy']

cnn = tf.keras.models.load_model('trained_plant_disease_model.keras')

#Test Image Visualization
import cv2

```

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image_path = 'test/test/CornCommonRust2.JPG'
# Reading an image in default mode
img = cv2.imread(image_path)
img = cv2.cvtColor(img,cv2.COLOR_BGR2RGB) #Converting BGR to RGB
# Displaying the image
plt.imshow(img)
plt.title('Test Image')
plt.xticks([])
plt.yticks([])
plt.show()

```



## Testing Model

```

image =
tf.keras.preprocessing.image.load_img(image_path,target_size=(128,128)
)
input_arr = tf.keras.preprocessing.image.img_to_array(image)
input_arr = np.array([input_arr]) # Convert single image to a batch.
predictions = cnn.predict(input_arr)

1/1 _____ 0s 312ms/step

print(predictions)

[[2.48401288e-20 9.04236435e-28 2.88789419e-23 1.28832551e-27
 6.01825061e-29 7.61019816e-27 4.08602100e-27 1.74400430e-21

```

```
1.00000000e+00 1.71647058e-26 6.90304185e-28 1.40465183e-32
3.50232848e-33 3.72740419e-30 3.00502277e-29 1.32949716e-24
8.17121520e-28 2.34655410e-29 2.35893755e-23 3.62711239e-23
1.76477638e-22 0.00000000e+00 1.11176116e-23 9.57925922e-33
3.38716346e-32 3.04961885e-31 2.16357116e-28 2.12268611e-29
3.29158651e-35 6.45825484e-25 2.29523579e-26 1.60172217e-33
7.19117565e-30 0.00000000e+00 1.85613166e-33 0.00000000e+00
3.14494029e-36 9.52453890e-31]]
```

```
result_index = np.argmax(predictions) #Return index of max element
print(result_index)
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# Displaying the disease prediction
model_prediction = class_name[result_index]
plt.imshow(img)
plt.title(f"Disease Name: {model_prediction}")
plt.xticks([])
plt.yticks([])
plt.show()
```

Disease Name: Corn\_(maize)\_\_Common\_rust\_

