Import the Libraries

In [1]:
```
# Import the libraries
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import tensorflow as tf
from tensorflow.keras import layers
from tensorflow.keras.callbacks import EarlyStopping
# Remove Warnings
import warnings
warnings.filterwarnings('ignore')
```

```
2024-02-03 19:30:20.688567: E external/local_xla/xla/stream_executor/cuda/cuda_dnn.cc:9261] Unable to register cuDNN factory: Attempting to register factory for plugin cuDNN when one has already been registered
2024-02-03 19:30:20.688681: E external/local_xla/xla/stream_executor/cuda/cuda_fft.cc:607] Unable to register cuFFT factory: Attempting to register factory for plugin cuFFT when one has already been registered
2024-02-03 19:30:20.964375: E external/local_xla/xla/stream_executor/cuda/cuda_blas.cc:1515] Unable to register cuBLAS factory: Attempting to register factory for plugin cuBLAS when one has already been registered
```

In [2]:
```
# load the dataset
df = pd.read_csv('/kaggle/input/paddy-disease-classification/train.csv')
```

Sneak Preview of Data

Achieve a rapid glimpse of your dataset with just one line of code! This convenient approach allows you to swiftly review the initial rows of your data, providing you with an instant grasp of the dataset's content without the need to scroll through the entire file.

In [3]:
```
df.head()
```

Out[3]:

	image_id	label	variety	age
0	100330.jpg	bacterial_leaf_blight	ADT45	45
1	100365.jpg	bacterial_leaf_blight	ADT45	45
2	100382.jpg	bacterial_leaf_blight	ADT45	45
3	100632.jpg	bacterial_leaf_blight	ADT45	45
4	101918.jpg	bacterial_leaf_blight	ADT45	45

In [4]:
```
#Check the shape of data
print(f'The Training Dataset has {df.shape[0]} rows and {df.shape[1]} columns.')
```

```
The Training Dataset has 10407 rows and 4 columns.
```

Let's Check Number of Unique "labels" in our Training Data

In [5]:
```
df['label'].unique().tolist()
```

Out[5]:
```
['bacterial_leaf_blight',
 'bacterial_leaf_streak',
 'bacterial_panicle_blight',
 'blast',
 'brown_spot',
 'dead_heart',
 'downy_mildew',
 'hispa',
 'normal',
 'tungro']
```

Let's Check Number of Unique "Varieties" in our Training Data

In [6]:
```
df['variety'].unique().tolist()
```

Out[6]:
```
['ADT45',
 'IR20',
 'KarnatakaPonni',
 'Onthanel',
 'Ponni',
 'Surya',
 'Zonal',
 'AndraPonni',
 'AtchayaPonni',
 'RR']
```

Observation:

1. We have 10407 images in our training data
2. We have 10 unique disease
3. We also have 10 unique varieties of rice

Summary of Data Characteristics

Descriptive statistics are employed to succinctly summarize and gain insight into the fundamental characteristics of the dataset.

In [7]:
```
df.describe()
```

Out[7]:

	age
count	10407.000000
mean	64.043624
std	8.958830
min	45.000000
25%	60.000000
50%	67.000000
75%	70.000000
max	82.000000

Observation:

- We find only one numeric column **age** when we describe it:
    1. The range of age is from 45 to 82

Let's Check the values of "Age" and "Variety" by Grouping

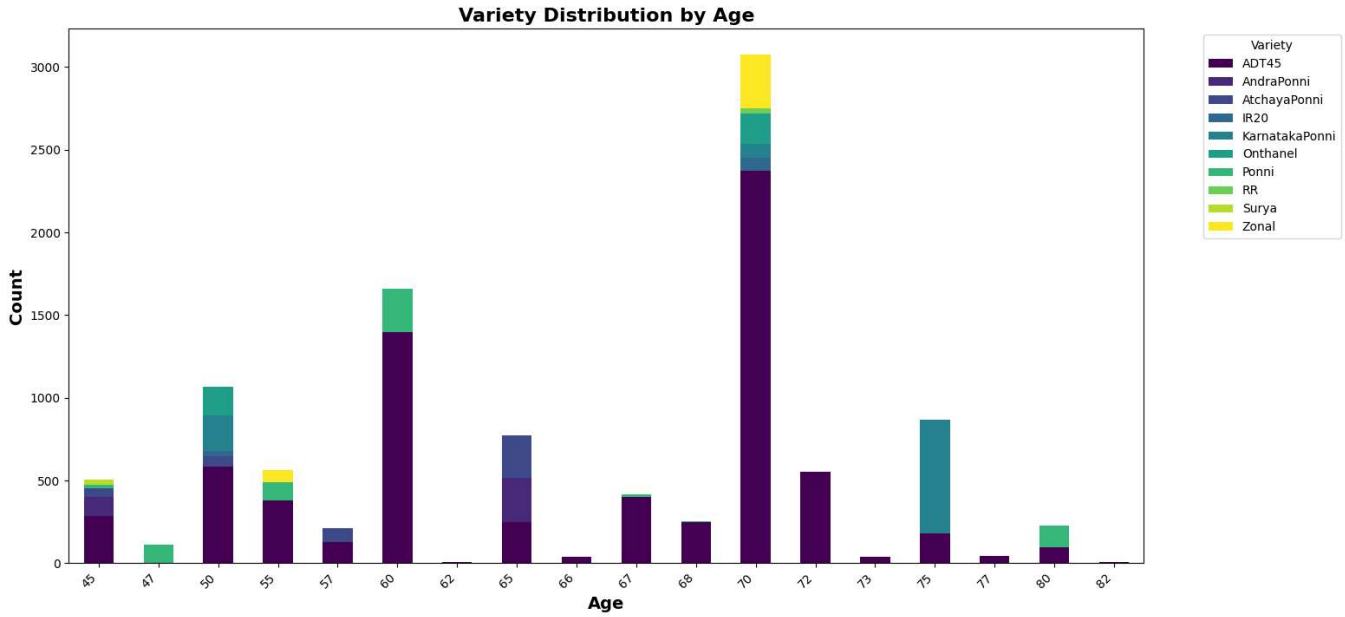
In [8]:
```
df.groupby("age")["variety"].value_counts()
```

Out[8]:

age	variety	
45	ADT45	286
	AndraPonni	112
	AtchayaPonni	55
	Surya	32
	Ponni	20
47	Ponni	112
50	ADT45	584
	KarnatakaPonni	218
	Onthanel	172
	AtchayaPonni	60
	IR20	32
55	ADT45	379
	Ponni	110
	Zonal	74
57	ADT45	126
	AtchayaPonni	87
60	ADT45	1394
	Ponni	266
62	ADT45	5
65	AndraPonni	265
	AtchayaPonni	259
	ADT45	250
66	ADT45	36
67	ADT45	401
	Ponni	14
68	ADT45	247
	Ponni	6
70	ADT45	2371
	Zonal	325
	Onthanel	179
	KarnatakaPonni	84
	IR20	82
	RR	36
72	ADT45	552
73	ADT45	38
75	KarnatakaPonni	686
	ADT45	180
77	ADT45	42
80	Ponni	129
	ADT45	96
82	ADT45	5

Name: count, dtype: int64

In [9]:
```
# Group by age and variety, then get the counts
grouped_counts = df.groupby("age")["variety"].value_counts().unstack().fillna
(0)

# Plot the grouped counts using a bar plot
fig, axes = plt.subplots(figsize=(16, 8))
grouped_counts.plot(kind='bar', stacked=True, ax=axes, cmap='viridis')

# Customize the plot
plt.title("Variety Distribution by Age", fontsize=16, fontweight='bold')
plt.xlabel("Age", fontsize=14, fontweight='bold')
plt.ylabel("Count", fontsize=14, fontweight='bold')
plt.xticks(rotation=45, ha='right')

# Add a legend
plt.legend(title='Variety', bbox_to_anchor=(1.05, 1), loc='upper left')

plt.show()
```



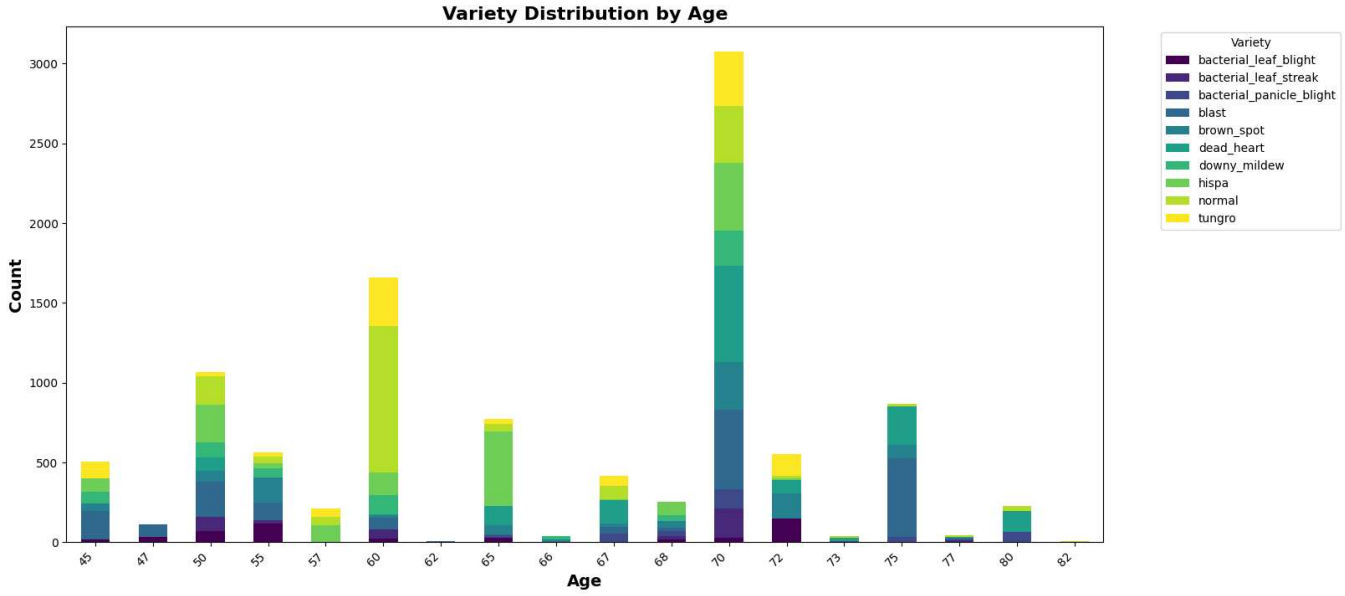
Let's Check the values of "Age" and "Label" by Grouping

In [10]:
```
df.groupby("age")["label"].value_counts()
```

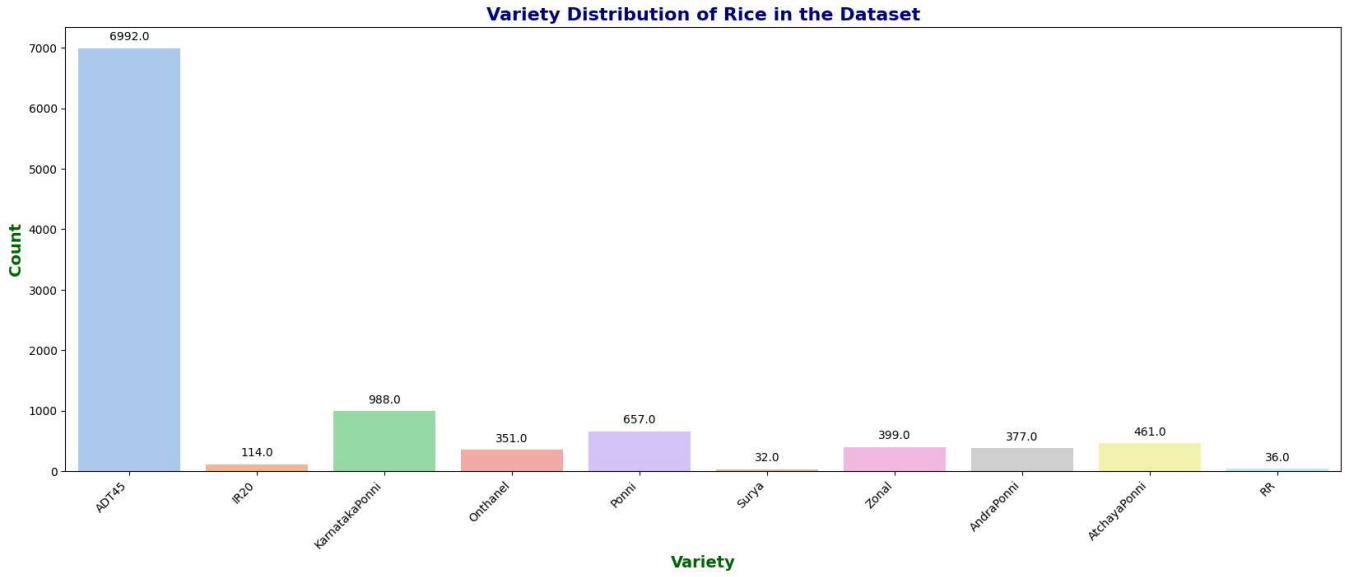
Out[10]:
```
age  label
45   blast                          179
     tungro                         104
     hispa                           83
     downy_mildew                    75
     brown_spot                      48
                                   ...
77   dead_heart                       4
80   dead_heart                     129
     bacterial_panicle_blight        66
     normal                          30
82   normal                           5
Name: count, Length: 95, dtype: int64
```

In [11]:

```
# Group by age and variety, then get the counts
grouped_counts = df.groupby("age")["label"].value_counts().unstack().fillna(0)

# Plot the grouped counts using a bar plot
fig, axes = plt.subplots(figsize=(16, 8))
grouped_counts.plot(kind='bar', stacked=True, ax=axes, cmap='viridis')

# Customize the plot
plt.title("Variety Distribution by Age", fontsize=16, fontweight='bold')
plt.xlabel("Age", fontsize=14, fontweight='bold')
plt.ylabel("Count", fontsize=14, fontweight='bold')
plt.xticks(rotation=45, ha='right')

# Add a legend
plt.legend(title='Variety', bbox_to_anchor=(1.05, 1), loc='upper left')

plt.show()
```

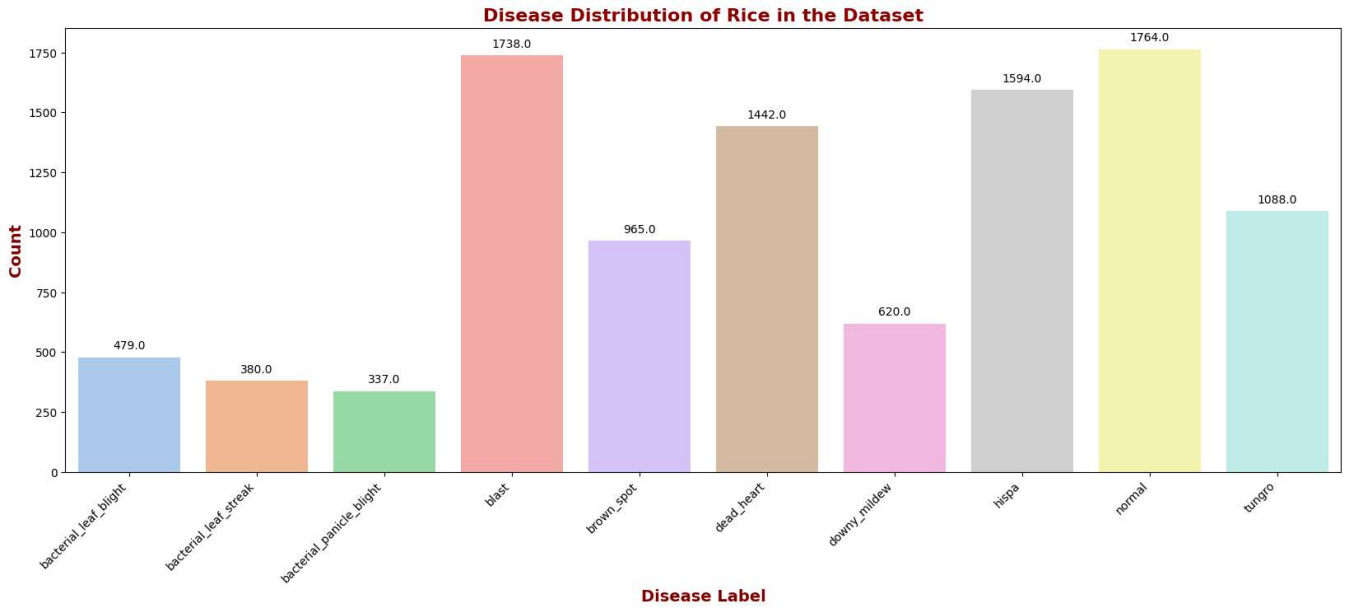


In [12]:
```
# Set a custom color palette
custom_palette = sns.color_palette("pastel")

# Plot the data count based on the variety name using countplot
fig, axes = plt.subplots(1, 1, figsize=(20, 7))
sns.countplot(x='variety', data=df, palette=custom_palette, ax=axes)

# Customize the plot
plt.title("Variety Distribution of Rice in the Dataset", fontsize=16, fontweigh
t='bold', color='navy')
plt.xlabel("Variety", fontsize=14, fontweight='bold', color='darkgreen')
plt.ylabel("Count", fontsize=14, fontweight='bold', color='darkgreen')
plt.xticks(rotation=45, ha='right')  # Rotate x-axis labels for better visibili
ty

# Add annotations (counts) on top of each bar
for p in axes.patches:
    axes.annotate(f'{p.get_height()}', (p.get_x() + p.get_width() / 2., p.get_h
eight()),
                  ha='center', va='center', xytext=(0, 10), textcoords='offset
points', fontsize=10, color='black')

plt.show()
```



- ADT45 is the most common variety inside the training data

In [13]:
```
# Set a custom color palette
custom_palette = sns.color_palette("pastel")

# Plot the data count based on the label using countplot
fig, axes = plt.subplots(1, 1, figsize=(20, 7))
sns.countplot(x='label', data=df, palette=custom_palette, ax=axes)

# Customize the plot
plt.title("Disease Distribution of Rice in the Dataset", fontsize=16, fontweigh
t='bold', color='darkred')
plt.xlabel("Disease Label", fontsize=14, fontweight='bold', color='maroon')
plt.ylabel("Count", fontsize=14, fontweight='bold', color='maroon')
plt.xticks(rotation=45, ha='right')  # Rotate x-axis labels for better visibili
ty

# Add annotations (counts) on top of each bar
for p in axes.patches:
    axes.annotate(f'{p.get_height()}', (p.get_x() + p.get_width() / 2., p.get_h
eight()),
                  ha='center', va='center', xytext=(0, 10), textcoords='offset
points', fontsize=10, color='black')

plt.show()
```



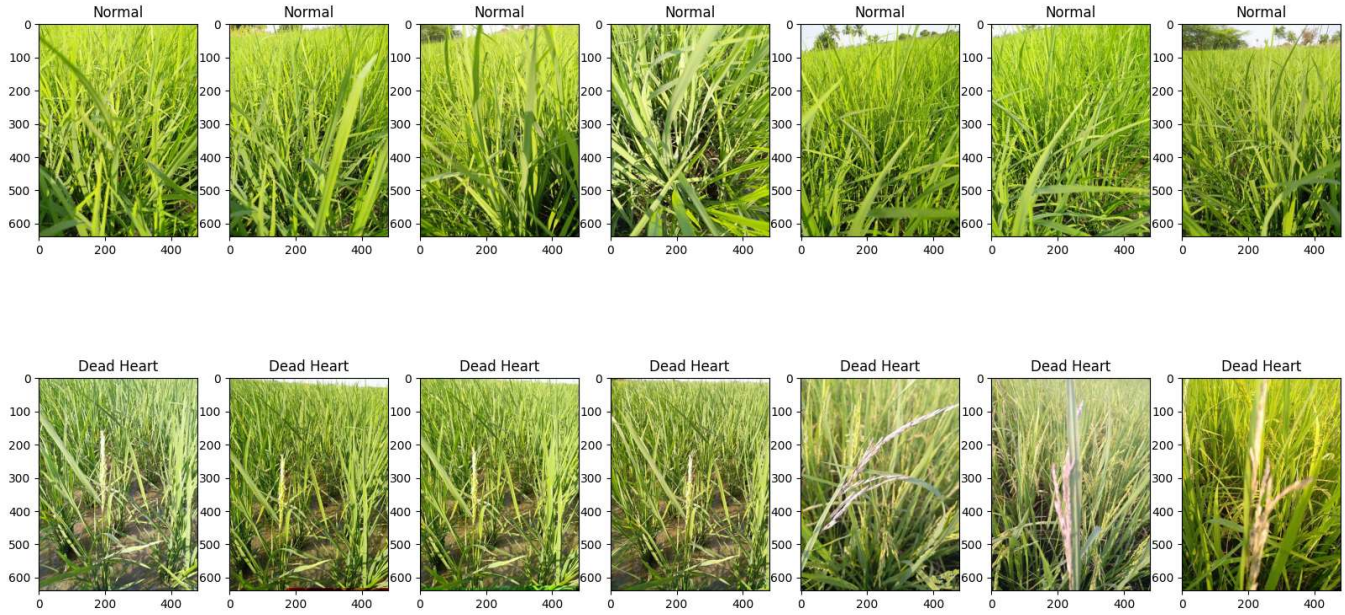
In [14]:
```
normal = df[df['label']=='normal']
normal = normal[normal['variety']=='ADT45']
normal_items = normal.image_id[:7].values
normal_items.tolist()
```

Out[14]:
```
['100007.jpg',
 '100025.jpg',
 '100135.jpg',
 '100165.jpg',
 '100171.jpg',
 '100186.jpg',
 '100188.jpg']
```

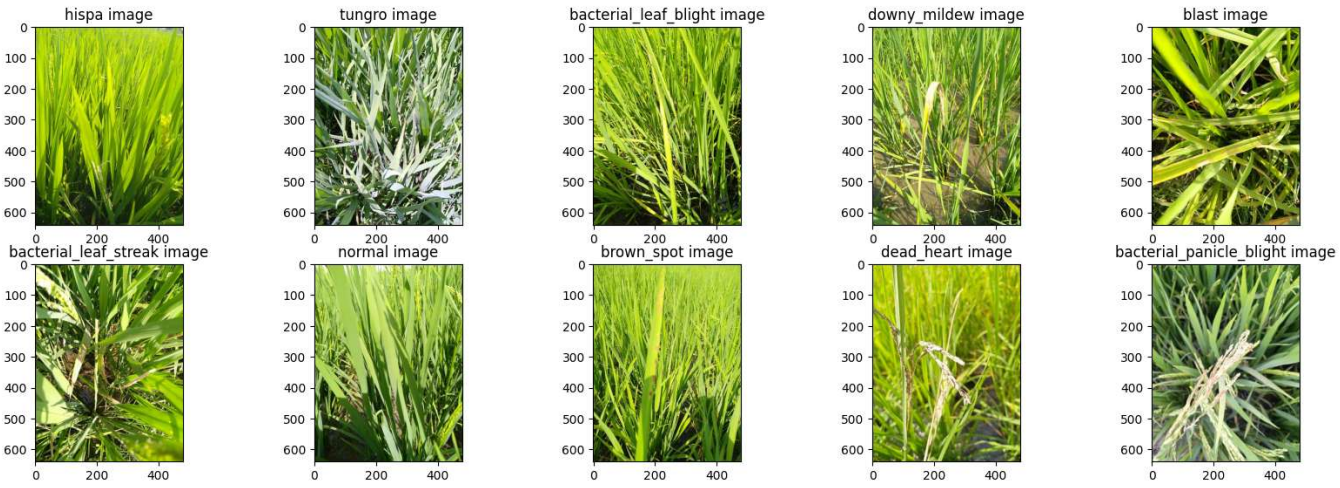
In [15]:
```
dead = df[df['label']=='dead_heart']
dead = dead[dead['variety']=='ADT45']
dead_items = dead.image_id[:7].values
dead_items.tolist()
```

Out[15]:
```
['101165.jpg',
 '102750.jpg',
 '108367.jpg',
 '109900.jpg',
 '100222.jpg',
 '100670.jpg',
 '100715.jpg']
```

In [16]:
```
plt.figure(figsize=(20, 10))
columns = 7
path = '/kaggle/input/paddy-disease-classification/train_images/'

for i, image_loc in enumerate(np.concatenate((normal_items, dead_items))):
    plt.subplot(10//columns + 1, columns, i+1)
    if i < 7:
        image = plt.imread(path+"normal/"+image_loc)
        plt.title('Normal')
    else:
        image = plt.imread(path+"dead_heart/"+image_loc)
        plt.title('Dead Heart')
    plt.imshow(image)
```



In [17]:
```
images = [
    '/kaggle/input/paddy-disease-classification/train_images/hispa/106590.jpg',
    '/kaggle/input/paddy-disease-classification/train_images/tungro/109629.jpg',
    '/kaggle/input/paddy-disease-classification/train_images/bacterial_leaf_blight/109372.jpg',
    '/kaggle/input/paddy-disease-classification/train_images/downy_mildew/102350.jpg',
    '/kaggle/input/paddy-disease-classification/train_images/blast/110243.jpg',
    '/kaggle/input/paddy-disease-classification/train_images/bacterial_leaf_streak/101104.jpg',
    '/kaggle/input/paddy-disease-classification/train_images/normal/109760.jpg',
    '/kaggle/input/paddy-disease-classification/train_images/brown_spot/104675.jpg',
    '/kaggle/input/paddy-disease-classification/train_images/dead_heart/105159.jpg',
    '/kaggle/input/paddy-disease-classification/train_images/bacterial_panicle_blight/101351.jpg'
]

diseases = ['hispa' , 'tungro', 'bacterial_leaf_blight', 'downy_mildew', 'blast',
            "bacterial_leaf_streak" , 'normal' , 'brown_spot' , 'dead_heart' , 'bacterial_panicle_blight' ]

diseases = [disease + ' image' for disease in diseases]
plt.figure(figsize=(20,10))
columns = 5
for i, image_loc in enumerate(images):
    plt.subplot(len(images)//columns+1,columns,i+1)
    image = plt.imread(image_loc)
    plt.title(diseases[i])
    plt.imshow(image)
```



In [18]:
```
from sklearn.preprocessing import LabelEncoder
encoder = LabelEncoder()

df['label'] = encoder.fit_transform(df['label'])
df['variety'] = encoder.fit_transform(df['variety'])
```

In [19]:
```
df.head()
```

Out[19]:

	image_id	label	variety	age
0	100330.jpg	0	0	45
1	100365.jpg	0	0	45
2	100382.jpg	0	0	45
3	100632.jpg	0	0	45
4	101918.jpg	0	0	45

In [20]:
```
batch_size=32
image_width=224
image_height=224
```

In [21]:
```
train_ds = tf.keras.utils.image_dataset_from_directory(
    directory=path,
    validation_split = 0.3,
    subset = "training",
    seed = 123,
    image_size = (image_height, image_width),
    batch_size = batch_size
)
```

```
Found 10407 files belonging to 10 classes.
Using 7285 files for training.
```

In [22]:
```
val_ds = tf.keras.utils.image_dataset_from_directory(
    directory=path,
    validation_split=0.2,
    subset="validation",
    seed=123,
    image_size=(image_height, image_height),
    batch_size=batch_size
)
```

```
Found 10407 files belonging to 10 classes.
Using 2081 files for validation.
```

In [23]:
```
class_names = train_ds.class_names
print(class_names)
```

```
['bacterial_leaf_blight', 'bacterial_leaf_streak', 'bacterial_panicle_blight',
'blast', 'brown_spot', 'dead_heart', 'downy_mildew', 'hispa', 'normal', 'tungr
o']
```

In [24]:
```
for image_batch , label_batch in train_ds:
    print(image_batch.shape)
    print(label_batch.shape)
    break
```

```
(32, 224, 224, 3)
(32,)
```

In [25]:
```
normalization_layer = tf.keras.layers.Rescaling(1./255)
```

In [26]:
```
normalized_ds = train_ds.map(lambda x,y: (normalization_layer(x),y))
image_batch , label_batch = next(iter(normalized_ds))
first_image = image_batch[0]
# Notice the pixel values are now in `[0,1]`
print(np.min(first_image),np.max(first_image))
```

```
0.0 1.0
```

In [27]:
```
num_classes = len(class_names)

model = tf.keras.Sequential([
    tf.keras.layers.Rescaling(1./255),
    tf.keras.layers.Conv2D(32, 3, activation='relu'),
    tf.keras.layers.MaxPooling2D(),
    tf.keras.layers.Conv2D(64, 3, activation='relu'),
    tf.keras.layers.MaxPooling2D(),
    tf.keras.layers.Conv2D(128, 3, activation='relu'),
    tf.keras.layers.MaxPooling2D(),
    tf.keras.layers.Conv2D(256, 3, activation='relu'),
    tf.keras.layers.MaxPooling2D(),
    tf.keras.layers.Flatten(),
    tf.keras.layers.Dense(512, activation='relu'),
    tf.keras.layers.Dense(64, activation='relu'),
    tf.keras.layers.Dropout(0.15),
    tf.keras.layers.Dense(num_classes, activation='softmax')
])
```

In [28]:
```
model.compile(
    optimizer='adam',
    loss=tf.keras.losses.SparseCategoricalCrossentropy(from_logits=True),
    metrics=['accuracy']
)
```

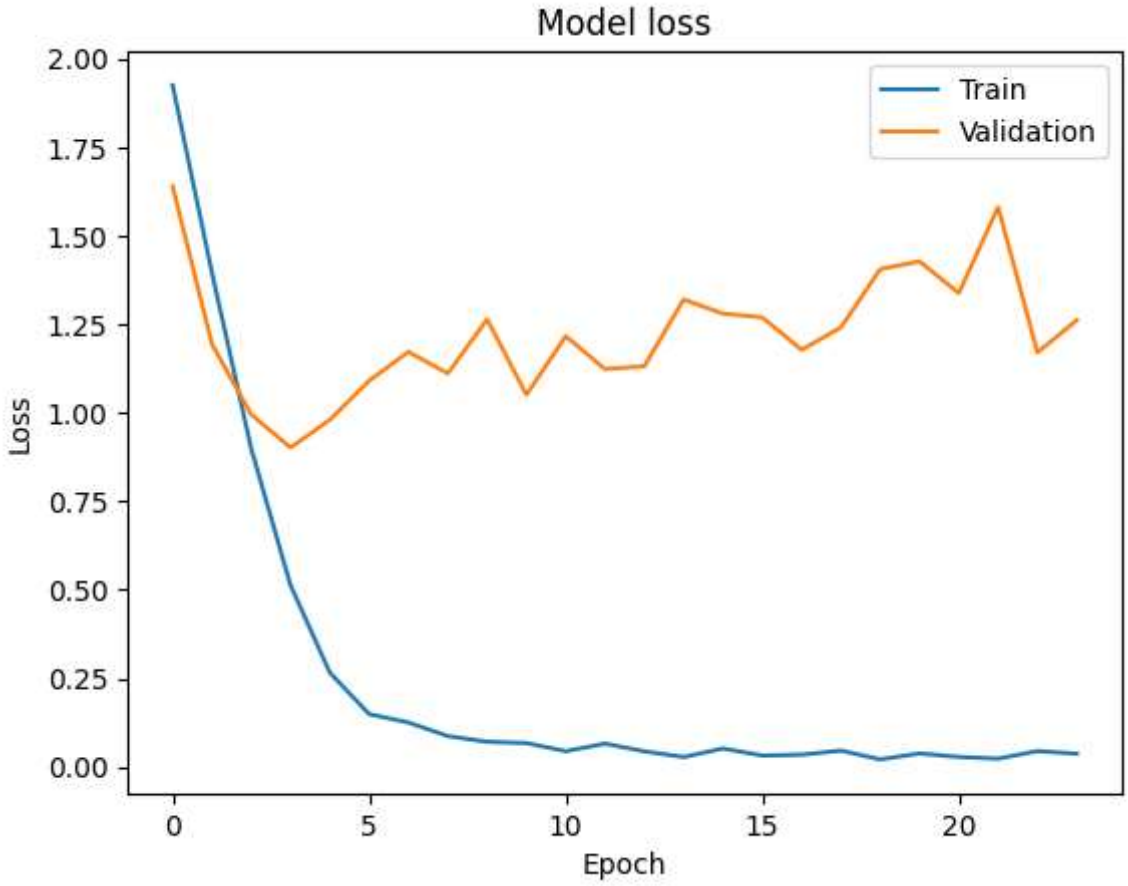
In [29]:

```
%%time
# Define the callback function
early_stopping = EarlyStopping(patience=20)

history = model.fit(train_ds,
          validation_data = val_ds,
          epochs=100,
          callbacks=[early_stopping])

# Evaluate the model
loss = model.evaluate(val_ds)

# Plotting the training and testing loss
plt.plot(history.history['loss'])
plt.plot(history.history['val_loss'])
plt.title('Model loss')
plt.ylabel('Loss')
plt.xlabel('Epoch')
plt.legend(['Train', 'Validation'], loc='upper right')
plt.show()

# Plotting the training and testing accuracy
plt.plot(history.history['accuracy'])
plt.plot(history.history['val_accuracy'])
plt.title('Model accuracy')
plt.ylabel('Accuracy')
plt.xlabel('Epoch')
plt.legend(['Train', 'Validation'], loc='lower left')
```

```
Epoch 1/100

WARNING: All log messages before absl::InitializeLog() is called are written to
STDERR
I0000 00:00:1706988665.162202      81 device_compiler.h:186] Compiled cluster us
ing XLA!  This line is logged at most once for the lifetime of the process.
```

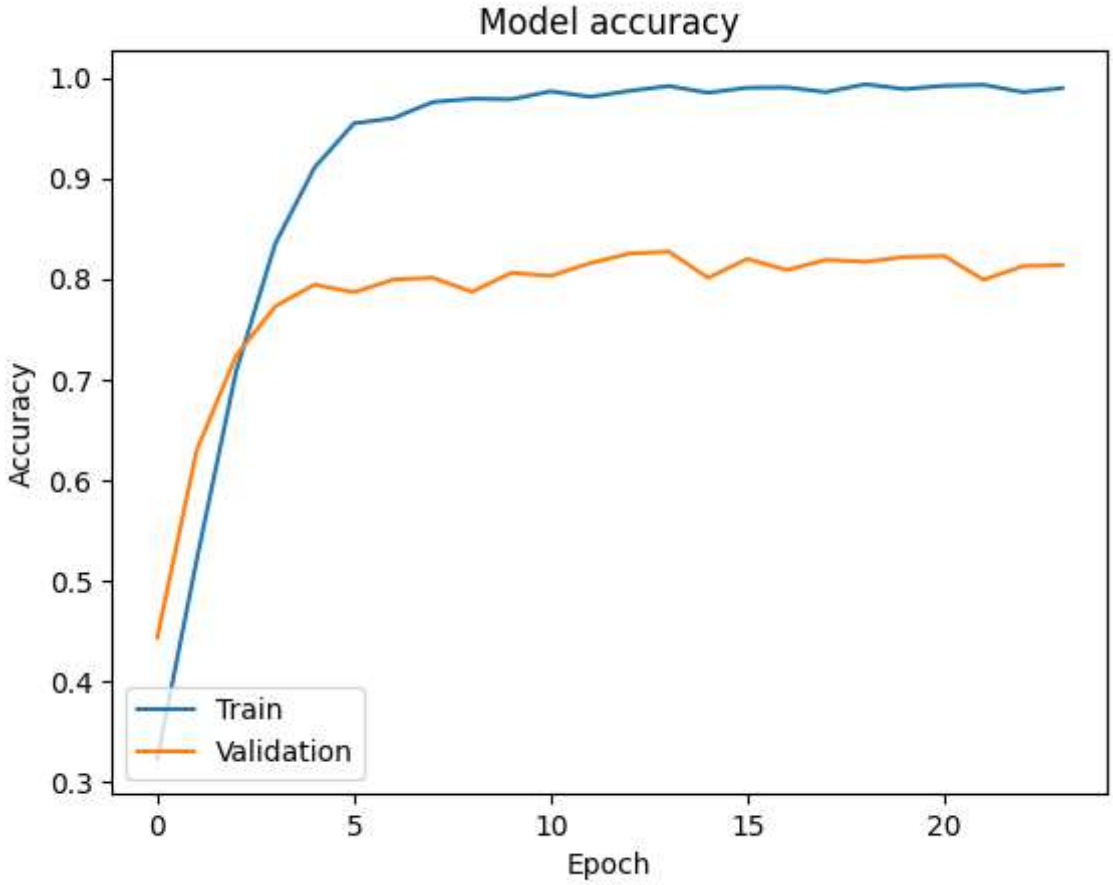
```
228/228 [==============================] - 34s 110ms/step - loss: 1.9249 - accur
acy: 0.3224 - val_loss: 1.6389 - val_accuracy: 0.4435
Epoch 2/100
228/228 [==============================] - 15s 65ms/step - loss: 1.3959 - accura
cy: 0.5198 - val_loss: 1.1937 - val_accuracy: 0.6290
Epoch 3/100
228/228 [==============================] - 16s 67ms/step - loss: 0.8987 - accura
cy: 0.7072 - val_loss: 0.9953 - val_accuracy: 0.7232
Epoch 4/100
228/228 [==============================] - 15s 65ms/step - loss: 0.5132 - accura
cy: 0.8350 - val_loss: 0.9019 - val_accuracy: 0.7727
Epoch 5/100
228/228 [==============================] - 16s 67ms/step - loss: 0.2664 - accura
cy: 0.9108 - val_loss: 0.9803 - val_accuracy: 0.7943
Epoch 6/100
228/228 [==============================] - 15s 65ms/step - loss: 0.1495 - accura
cy: 0.9546 - val_loss: 1.0909 - val_accuracy: 0.7866
Epoch 7/100
228/228 [==============================] - 15s 66ms/step - loss: 0.1258 - accura
cy: 0.9596 - val_loss: 1.1720 - val_accuracy: 0.7991
Epoch 8/100
228/228 [==============================] - 15s 66ms/step - loss: 0.0876 - accura
cy: 0.9757 - val_loss: 1.1111 - val_accuracy: 0.8011
Epoch 9/100
228/228 [==============================] - 16s 66ms/step - loss: 0.0714 - accura
cy: 0.9790 - val_loss: 1.2641 - val_accuracy: 0.7871
Epoch 10/100
228/228 [==============================] - 16s 66ms/step - loss: 0.0678 - accura
cy: 0.9784 - val_loss: 1.0509 - val_accuracy: 0.8059
Epoch 11/100
228/228 [==============================] - 16s 67ms/step - loss: 0.0449 - accura
cy: 0.9864 - val_loss: 1.2164 - val_accuracy: 0.8030
Epoch 12/100
228/228 [==============================] - 15s 66ms/step - loss: 0.0662 - accura
cy: 0.9809 - val_loss: 1.1235 - val_accuracy: 0.8155
Epoch 13/100
228/228 [==============================] - 16s 67ms/step - loss: 0.0445 - accura
cy: 0.9868 - val_loss: 1.1316 - val_accuracy: 0.8251
Epoch 14/100
228/228 [==============================] - 15s 66ms/step - loss: 0.0283 - accura
cy: 0.9916 - val_loss: 1.3199 - val_accuracy: 0.8270
Epoch 15/100
228/228 [==============================] - 16s 68ms/step - loss: 0.0525 - accura
cy: 0.9850 - val_loss: 1.2800 - val_accuracy: 0.8011
Epoch 16/100
228/228 [==============================] - 15s 66ms/step - loss: 0.0326 - accura
cy: 0.9900 - val_loss: 1.2694 - val_accuracy: 0.8198
Epoch 17/100
228/228 [==============================] - 16s 68ms/step - loss: 0.0350 - accura
cy: 0.9903 - val_loss: 1.1777 - val_accuracy: 0.8087
Epoch 18/100
228/228 [==============================] - 15s 66ms/step - loss: 0.0465 - accura
cy: 0.9857 - val_loss: 1.2410 - val_accuracy: 0.8188
Epoch 19/100
228/228 [==============================] - 16s 67ms/step - loss: 0.0218 - accura
cy: 0.9934 - val_loss: 1.4057 - val_accuracy: 0.8169
Epoch 20/100
228/228 [==============================] - 15s 66ms/step - loss: 0.0384 - accura
cy: 0.9886 - val_loss: 1.4273 - val_accuracy: 0.8217
Epoch 21/100
228/228 [==============================] - 16s 68ms/step - loss: 0.0287 - accura
```

```
cy: 0.9919 - val_loss: 1.3381 - val_accuracy: 0.8227
Epoch 22/100
228/228 [==============================] - 15s 66ms/step - loss: 0.0237 - accura
cy: 0.9929 - val_loss: 1.5807 - val_accuracy: 0.7991
Epoch 23/100
228/228 [==============================] - 16s 67ms/step - loss: 0.0452 - accura
cy: 0.9856 - val_loss: 1.1707 - val_accuracy: 0.8126
Epoch 24/100
228/228 [==============================] - 15s 65ms/step - loss: 0.0377 - accura
cy: 0.9896 - val_loss: 1.2614 - val_accuracy: 0.8136
66/66 [==============================] - 3s 40ms/step - loss: 1.2614 - accuracy:
0.8136
```




```
CPU times: user 17min, sys: 50.8 s, total: 17min 51s
Wall time: 6min 39s
```

Out[29]: `<matplotlib.legend.Legend at 0x7cb6d44a69b0>`


Model accuracy
Accuracy
Epoch
Train
Validation
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0
5
10
15
20

In [30]:
```
model.summary()
```

```
Model: "sequential"
_________________________________________________________________
 Layer (type)                Output Shape              Param #
=================================================================
 rescaling_1 (Rescaling)     (None, 224, 224, 3)       0

 conv2d (Conv2D)             (None, 222, 222, 32)      896

 max_pooling2d (MaxPooling2  (None, 111, 111, 32)      0
 D)

 conv2d_1 (Conv2D)           (None, 109, 109, 64)      18496

 max_pooling2d_1 (MaxPoolin  (None, 54, 54, 64)        0
 g2D)

 conv2d_2 (Conv2D)           (None, 52, 52, 128)       73856

 max_pooling2d_2 (MaxPoolin  (None, 26, 26, 128)       0
 g2D)

 conv2d_3 (Conv2D)           (None, 24, 24, 256)       295168

 max_pooling2d_3 (MaxPoolin  (None, 12, 12, 256)       0
 g2D)

 flatten (Flatten)           (None, 36864)             0

 dense (Dense)               (None, 512)               18874880

 dense_1 (Dense)             (None, 64)                32832

 dropout (Dropout)           (None, 64)                0

 dense_2 (Dense)             (None, 10)                650

=================================================================
Total params: 19296778 (73.61 MB)
Trainable params: 19296778 (73.61 MB)
Non-trainable params: 0 (0.00 Byte)
_________________________________________________________________
```

In [31]:
```
loss , accu = model.evaluate(val_ds)
print(f"the Testing loss is {loss:.2f}")
print(f"The testing accuracy is {accu*100:.2f}%")
```

```
66/66 [==============================] - 3s 41ms/step - loss: 1.2614 - accuracy:
0.8136
the Testing loss is 1.26
The testing accuracy is 81.36%
```

In [32]:
```
test_ds = tf.keras.utils.image_dataset_from_directory(
    '/kaggle/input/paddy-disease-classification/test_images/',
    image_size=(image_height, image_width),
    batch_size=batch_size,
    label_mode=None,
    shuffle=False)
```

```
Found 3469 files belonging to 1 classes.
```

In [33]:
```
y_pred =  model.predict(test_ds, batch_size = batch_size, verbose = 1)
y_pred.shape
```

```
109/109 [==============================] - 9s 79ms/step
```

Out[33]:
```
(3469, 10)
```

In [34]:
```
y_pred_classes = y_pred.argmax(axis = 1)
y_pred_classes.shape
```

Out[34]:
```
(3469,)
```

In [35]:
```
y_classes_names = [class_names[x] for x in y_pred_classes]
```

In [36]:
```
predictions = pd.read_csv('/kaggle/input/paddy-disease-classification/sample_submission.csv')
predictions['label'] = y_classes_names
predictions.to_csv('submission.csv', index = False)
```

In [ ]:
```

```