In [1]:

```
from tensorflow.keras.preprocessing.image import ImageDataGenerator
from tensorflow.keras.layers import Dense, Flatten, Dropout
from tensorflow.keras import Sequential
from tensorflow.keras.optimizers import RMSprop
from tensorflow.keras.callbacks import ModelCheckpoint
import seaborn as sns
import matplotlib.pyplot as plt
import tensorflow as tf
import os
import cv2
import matplotlib.image as mpimg
import pandas as pd
import wandb
import random
import numpy as np
from wandb.keras import WandbCallback
```

In [2]:

```
import visualkeras
```

In [3]:

```
BASE_DIR = 'teethdecay/teeth_dataset' #teethdecay
train_folder = os.path.join(BASE_DIR,'train')
test_folder = os.path.join(BASE_DIR,'test')

df_train = pd.DataFrame()
df_image = []
df_label = []

label_num = 0

for i_label in os.listdir(train_folder):
    for j_image in sorted(os.listdir(os.path.join(train_folder,i_label))): #return full
        df_image.append(os.path.join('train',i_label,j_image)) # return path_image
        df_label.append(label_num)
    label_num += 1
df_train['images'] = df_image
df_train['target'] = df_label
#caries = 0, no-caries = 1
df_train.to_csv('./train.csv')

# TEST TO CSV
df_test = pd.DataFrame()
df_image = []
df_label = []

label_num = 0

for i_label in os.listdir(test_folder):
    for j_image in sorted(os.listdir(os.path.join(test_folder,i_label))): #return full i
        df_image.append(os.path.join('test',i_label,j_image))
        df_label.append(label_num)
    label_num += 1
df_test['images'] = df_image
df_test['target'] = df_label
#caries = 1, no-caries = 0
df_test.to_csv('./test.csv')
```

In [4]:

```
df_train.tail(5),df_test.tail(5)
```

Out[4]:

```
(                        images  target
 1255  train\no-caries\nc8_5.jpg       1
 1256  train\no-caries\nc8_6.jpg       1
 1257  train\no-caries\nc8_7.jpg       1
 1258  train\no-caries\nc8_8.jpg       1
 1259  train\no-caries\nc8_9.jpg       1,
                       images  target
 289  test\no-caries\nc9_5.jpg       1
 290  test\no-caries\nc9_6.jpg       1
 291  test\no-caries\nc9_7.jpg       1
 292  test\no-caries\nc9_8.jpg       1
 293  test\no-caries\nc9_9.jpg       1)
```

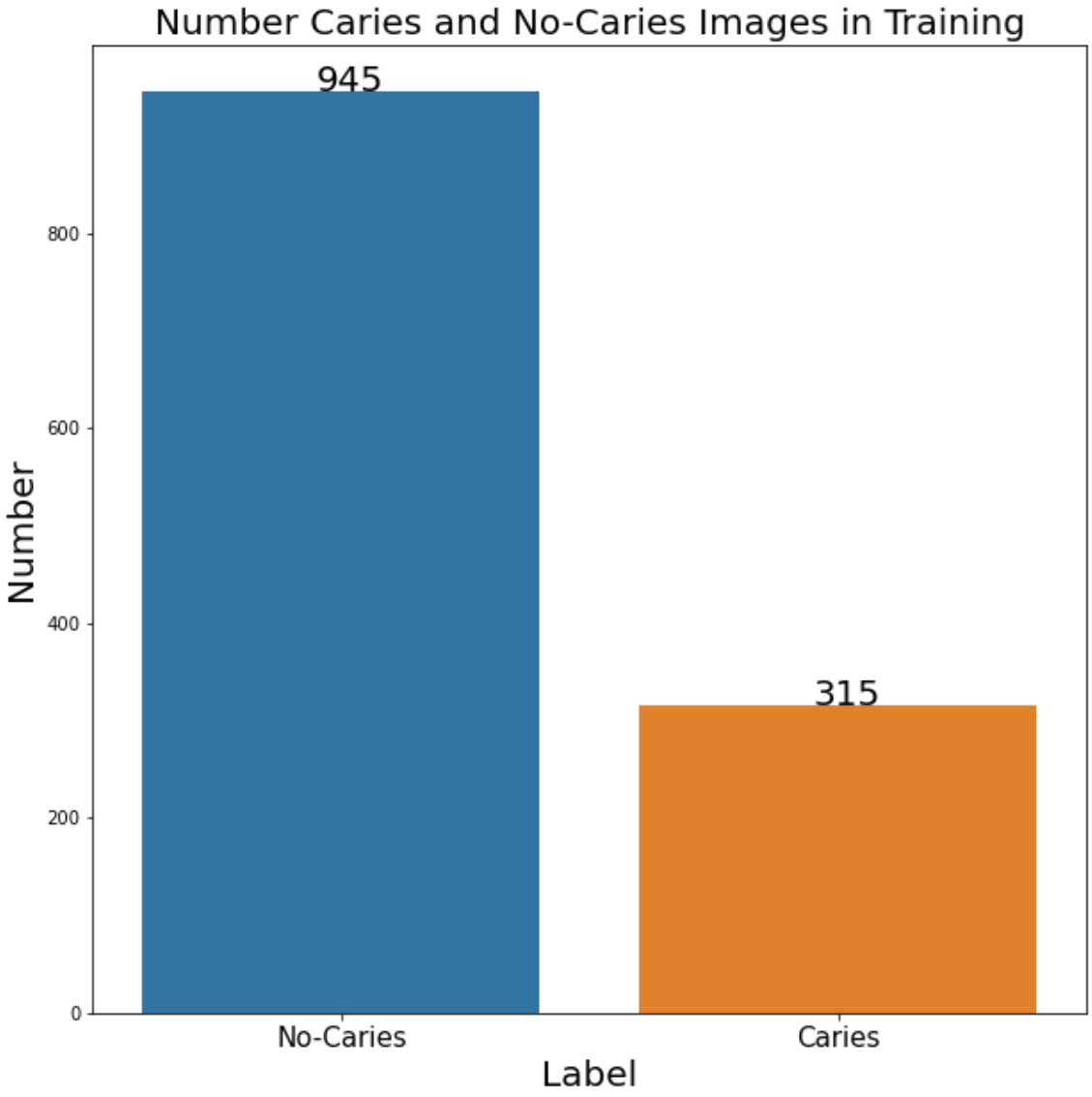
In [5]:

```
print('Number of train images:',len(df_train))
print('Number of test images:',len(df_test))
```

```
Number of train images: 1260
Number of test images: 294
```

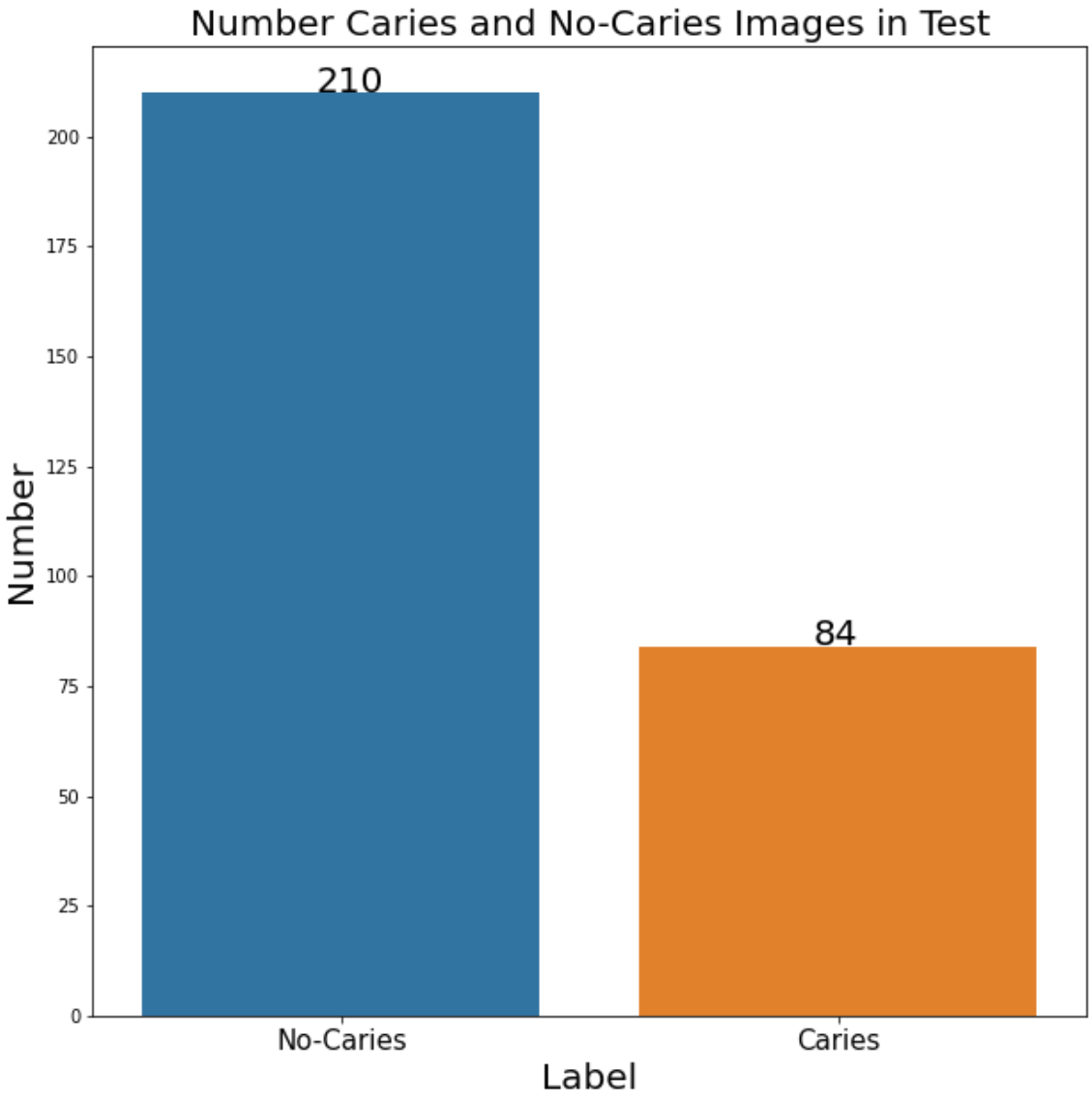
In [6]:

```
plt.figure(figsize=(10,10))
ax = sns.countplot(x = 'target', data = df_train)
ax.set_title('Number Caries and No-Caries Images in Training', size=20)
ax.set_xlabel("Label",fontsize=20)
ax.set_ylabel("Number",fontsize=20)
ax.set_xticklabels(['No-Caries', 'Caries'],fontsize=15)
for p in ax.patches:
    ax.annotate('{:.0f}'.format(p.get_height()), (p.get_x()+0.35, p.get_height()+0.2),fo
```



In [7]:

```
plt.figure(figsize=(10,10))
ax = sns.countplot(x = 'target', data = df_test)
ax.set_title('Number Caries and No-Caries Images in Test', size=20)
ax.set_xlabel("Label",fontsize=20)
ax.set_ylabel("Number",fontsize=20)
ax.set_xticklabels(['No-Caries', 'Caries'],fontsize=15)
for p in ax.patches:
    ax.annotate('{:.0f}'.format(p.get_height()), (p.get_x()+0.35, p.get_height()+0.2),fo
```

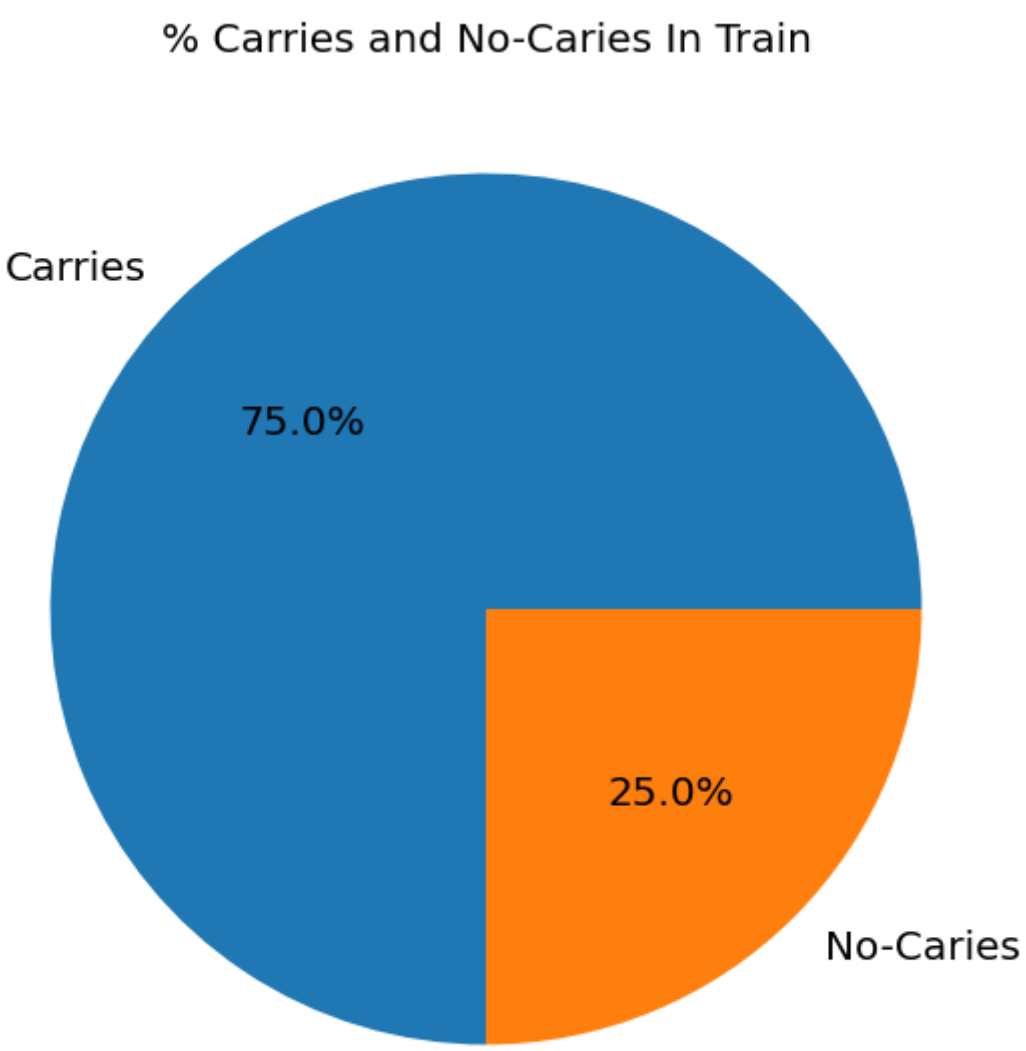


In [8]:

```
bar, ax = plt.subplots(figsize = (10,10))
bar.patch.set_facecolor('white')
plt.pie(df_train['target'].value_counts(),
        labels = ['Carries','No-Caries'],
        autopct="%.1f%%",textprops={'fontsize':20})
plt.title('% Carries and No-Caries In Train', size=20)
```

Out[8]:

```
Text(0.5, 1.0, '% Carries and No-Caries In Train')
```

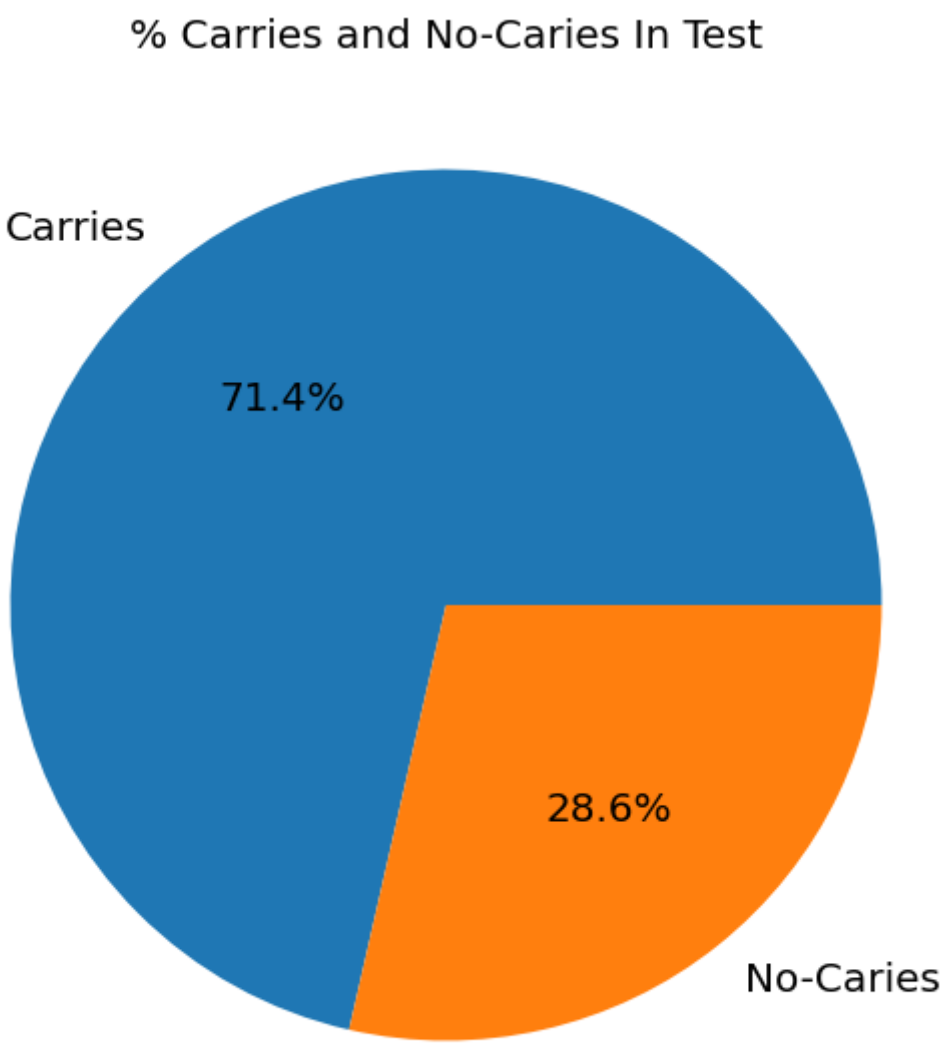


In [9]:

```
bar, ax = plt.subplots(figsize = (10,10))
bar.patch.set_facecolor('white')
plt.pie(df_test['target'].value_counts(),
        labels = ['Carries','No-Caries'],
        autopct="%.1f%%",textprops={'fontsize':20})
plt.title('% Carries and No-Caries In Test', size=20)
```

Out[9]:

```
Text(0.5, 1.0, '% Carries and No-Caries In Test')
```



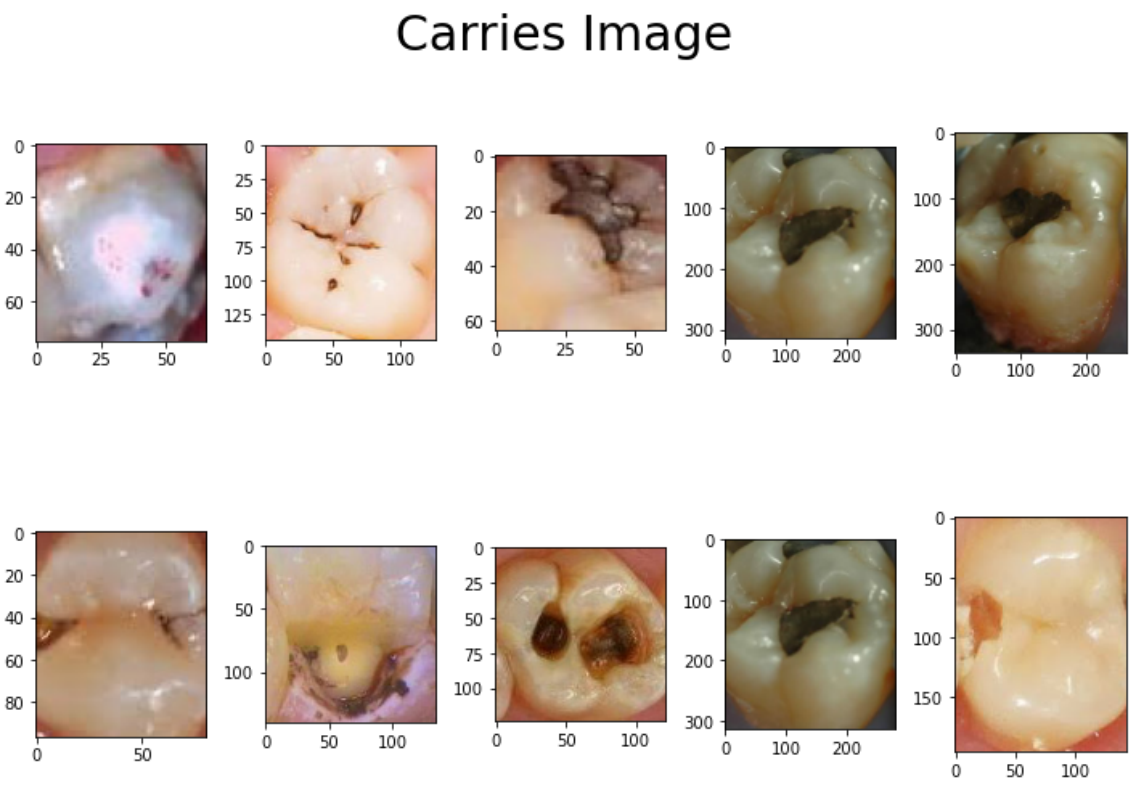
In [10]:

```
print('Choose 224x224 rescale is best choice')
```

```
Choose 224x224 rescale is best choice
```

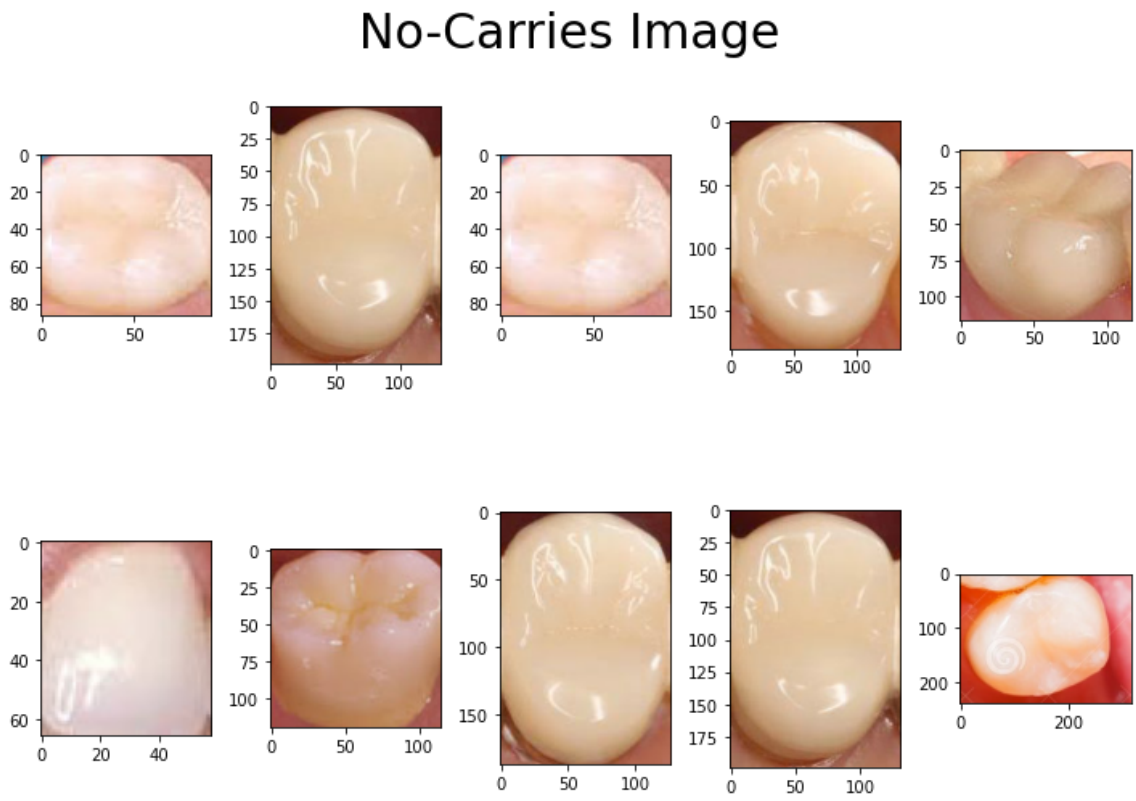
In [11]:

```
f , ax = plt.subplots(2,5)
f.set_size_inches(10, 10)
f.suptitle('Carries Image',x=0.5,y=0.8,fontsize=30,verticalalignment='bottom')
k = 0
for i in range(2):
    for j in range(5):
        img = cv2.imread(os.path.join('toothdecay/teeth_dataset','train','caries',random
        # im_resized = cv2.resize(img, (224, 224), interpolation=cv2.INTER_LINEAR)
        ax[i,j].imshow(cv2.cvtColor(img, cv2.COLOR_BGR2RGB))
        k = k + 1
    plt.tight_layout()
```



In [12]:

```
f , ax = plt.subplots(2,5)
f.set_size_inches(10, 10)
f.suptitle('No-Carries Image',x=0.5,y=0.8,fontsize=30,verticalalignment='bottom')
k = 0
for i in range(2):
    for j in range(5):
        img = cv2.imread(os.path.join('toothdecay/teeth_dataset','train','no-caries',ran
        # im_resized = cv2.resize(img, (224, 224), interpolation=cv2.INTER_LINEAR)
        ax[i,j].imshow(cv2.cvtColor(img, cv2.COLOR_BGR2RGB))
        k = k + 1
    plt.tight_layout()
```



In [13]:

```
train_generator = ImageDataGenerator(
    rescale = 1.0/255.,
    rotation_range=30,
    width_shift_range=0.1,
    height_shift_range=0.1,
    shear_range=0.1,
    zoom_range=0.1,
    horizontal_flip=True,
    vertical_flip=True,
    fill_mode='nearest',
    brightness_range=(0.5, 1.5),
)
val_generator = ImageDataGenerator(rescale=1./255.)
```

In [14]:

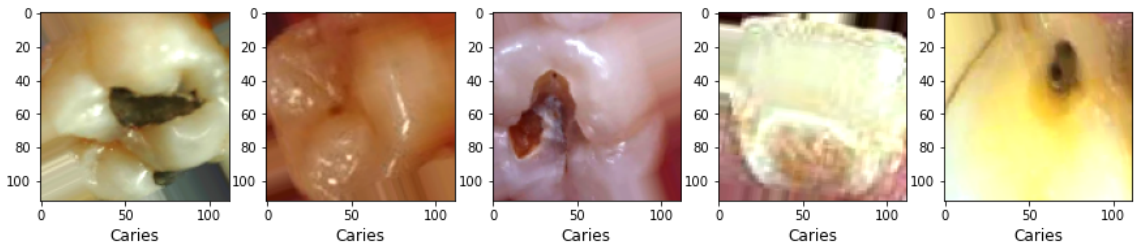
```
train_datagen = train_generator.flow_from_directory(
    train_folder,
    batch_size=10,
    target_size=(224, 224)
)
val_datagen = val_generator.flow_from_directory(
    test_folder,
    batch_size=round(len(df_test)/2), # 14/2 = 7
    target_size=(224, 224)
)
```

```
Found 1260 images belonging to 2 classes.
Found 294 images belonging to 2 classes.
```

In [18]:

```
pic = train_generator.flow_from_directory(
    'toothdecay/teeth_dataset/train',
    batch_size=1,
    target_size=(112, 112))
f,ax = plt.subplots(1,5)
f.set_figheight(15)
f.set_figwidth(15)
for i in range(5):
    img, label = pic.next()
    ax[i].imshow(img[0])
    ax[i].set_xlabel('Caries' if np.argmax(label) == 0 else 'No-Caries',fontsize=12)
```

```
Found 60 images belonging to 2 classes.
```



In [20]:

```
base_model = tf.keras.applications.EfficientNetB2(input_shape=(224, 224, 3),weights=None
```

In [19]:

```
model = Sequential()
model.add(base_model)
model.add(Flatten())
model.add(Dense(512, activation="relu"))
model.add(Dropout(0.3))
model.add(Dense(256, activation="relu"))
model.add(Dropout(0.6))
model.add(Dense(2, activation="softmax"))
model.summary()
```

```
---------------------------------------------------------------------------
-
NameError                                 Traceback (most recent call las
t)
~\AppData\Local\Temp/ipykernel_17332/3945132583.py in <module>
      1 model = Sequential()
----> 2 model.add(base_model)
      3 model.add(Flatten())
      4 model.add(Dense(512, activation="relu"))
      5 model.add(Dropout(0.3))

NameError: name 'base_model' is not defined
```

In [32]:

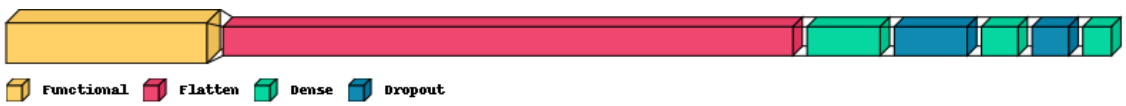
```
tf.keras.utils.plot_model(model, show_shapes = True, show_dtype = True, show_layer_names
```

```
('You must install pydot (`pip install pydot`) and install graphviz (see i
nstructions at https://graphviz.gitlab.io/download/) (https://graphviz.git
lab.io/download/)) ', 'for plot_model/model_to_dot to work.')
```

In [33]:

```
from PIL import ImageFont
font = ImageFont.load_default()
visualkeras.layered_view(model, legend=True, font=font,to_file='output.png')
```

Out[33]:



In [34]:

```
model.compile(
    optimizer=tf.keras.optimizers.RMSprop(learning_rate=0.0001),
    loss="categorical_crossentropy",
    metrics=['accuracy']
)
```

In [35]:

```
path_checkpoint = 'tmp/efficienetb0_checkpoint'
os.makedirs(path_checkpoint,exist_ok=True)

# https://keras.io/api/callbacks/model_checkpoint/
# https://www.tensorflow.org/tensorboard/scalars_and_keras
Checkpoint = tf.keras.callbacks.ModelCheckpoint(filepath='best_model.h5',
                                                monitor='val_acc',
                                               mode='max',
                                                verbose=1)
callback = [Checkpoint,
            tf.keras.callbacks.EarlyStopping(patience = 5, monitor= "val_acc",verbose=1
            tf.keras.callbacks.TensorBoard(log_dir = "logs/{}".format('Toothdecay'))]
```

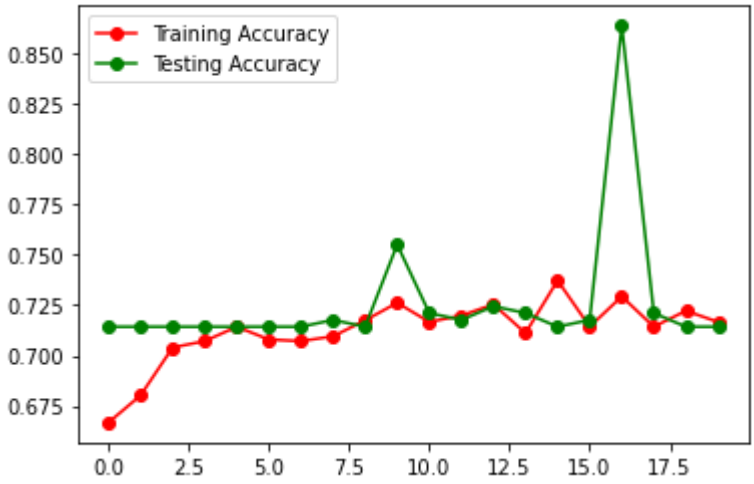
In [36]:

```
history = model.fit(
    train_datagen,
    validation_data=val_datagen,
    epochs=20,
    callbacks=[
        callback
    ])
```

```
C:\Users\vamsh\anaconda3\lib\site-packages\keras\utils\generic_utils.p
y:494: CustomMaskWarning: Custom mask layers require a config and must
override get_config. When loading, the custom mask layer must be passed
to the custom_objects argument.
  warnings.warn('Custom mask layers require a config and must override
'

Epoch 1/20
126/126 [==============================] - 489s 4s/step - loss: 1.4012
- accuracy: 0.6667 - val_loss: 0.6165 - val_accuracy: 0.7143

Epoch 00001: saving model to best_model.h5
WARNING:tensorflow:Early stopping conditioned on metric `val_acc` which
is not available. Available metrics are: loss,accuracy,val_loss,val_acc
uracy
Epoch 2/20
126/126 [==============================] - 471s 4s/step - loss: 1.0797
- accuracy: 0.6802 - val_loss: 0.5987 - val_accuracy: 0.7143

Epoch 00002: saving model to best_model.h5
```

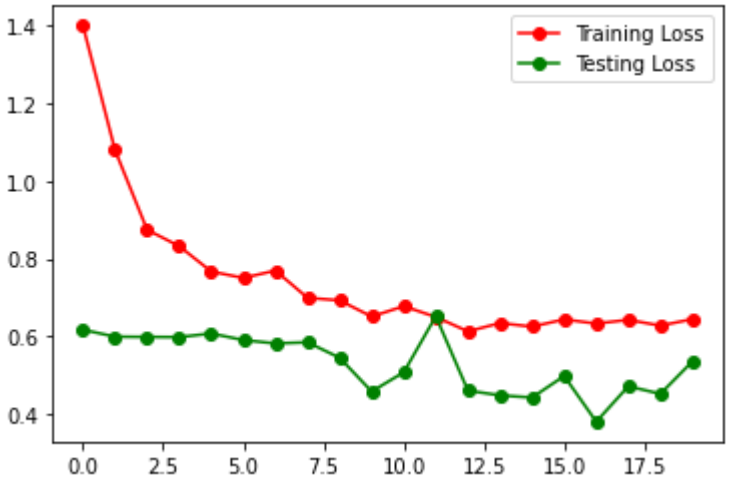
In [37]:

```
plt.plot(history.history["accuracy"] , 'ro-' , label = "Training Accuracy")
plt.plot(history.history["val_accuracy"] , 'go-' , label = "Testing Accuracy")
plt.legend()
plt.show()
```



In [38]:

```
plt.plot(history.history["loss"] , 'ro-' , label = "Training Loss")
plt.plot(history.history["val_loss"] , 'go-' , label = "Testing Loss")
plt.legend()
plt.show()
```



In [39]:

```
val_generator = ImageDataGenerator(rescale=1./255.)
val_datagen = val_generator.flow_from_directory(
    test_folder,
    batch_size=round(len(df_test)/2), # 14/2 = 7
    target_size=(224, 224),
    shuffle=False
)
```

```
Found 294 images belonging to 2 classes.
```

In [40]:

```
Y_true = val_datagen.classes
Y_true
```

Out[40]:

```
array([0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1])
```

In [41]:

```
Y_pred  = model.predict(val_datagen).round()
Y_pred[0:5]
```

Out[41]:

```
array([[1., 0.],
       [1., 0.],
       [1., 0.],
       [1., 0.],
       [1., 0.]], dtype=float32)
```

In [42]:

```
Y_true_onehot = tf.keras.utils.to_categorical(Y_true)
Y_true_onehot[0:5]
```

Out[42]:

```
array([[1., 0.],
       [1., 0.],
       [1., 0.],
       [1., 0.],
       [1., 0.]], dtype=float32)
```

In [43]:

```
from sklearn.metrics import confusion_matrix , classification_report
target_names = ['caries','no-caries']
print(classification_report(Y_true_onehot , Y_pred, target_names = target_names))
```

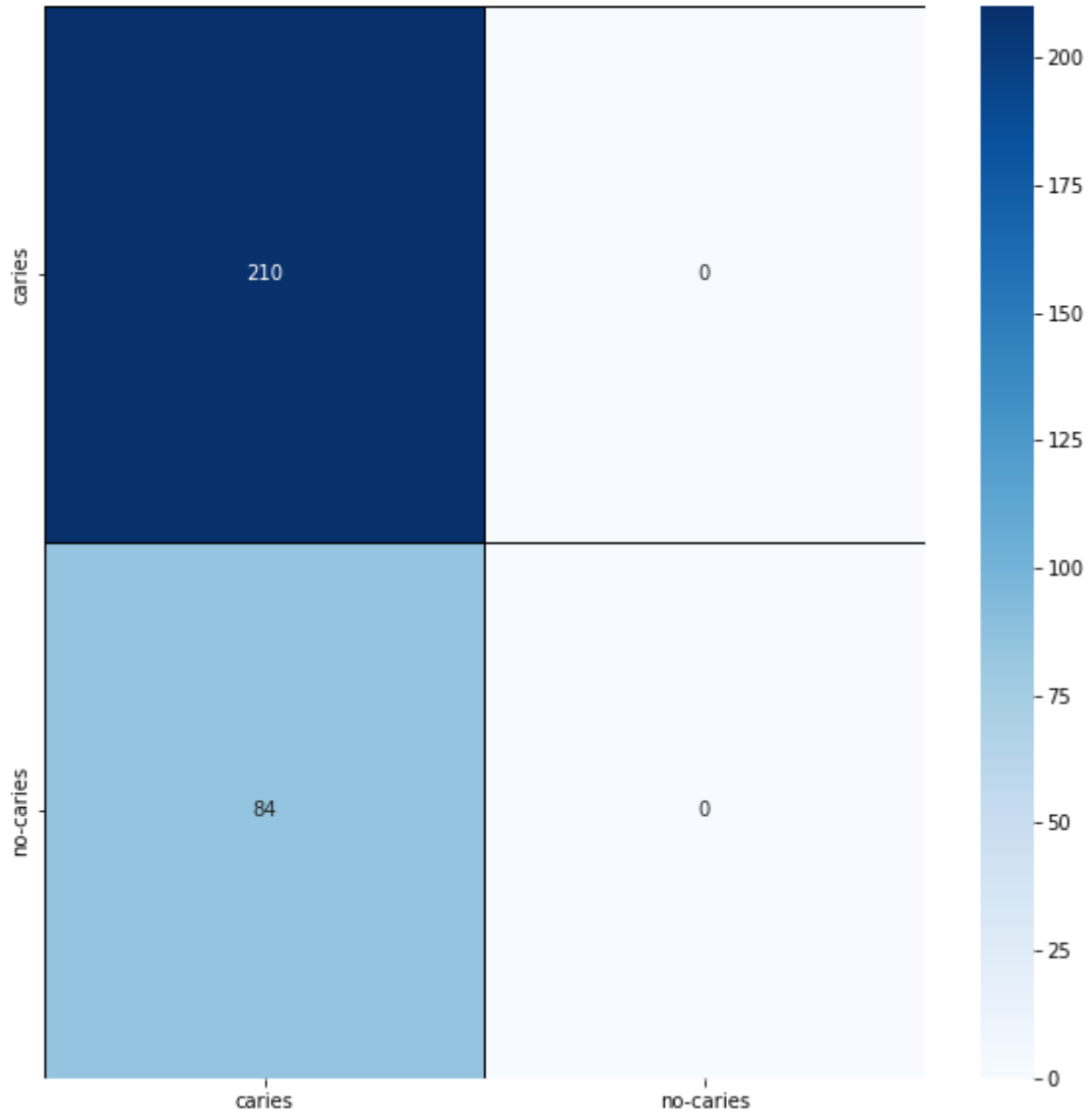
```
              precision    recall  f1-score   support

      caries       0.71      1.00      0.83       210
   no-caries       0.00      0.00      0.00        84

   micro avg       0.71      0.71      0.71       294
   macro avg       0.36      0.50      0.42       294
weighted avg       0.51      0.71      0.60       294
 samples avg       0.71      0.71      0.71       294


C:\Users\vamsh\anaconda3\lib\site-packages\sklearn\metrics\_classificatio
n.py:1248: UndefinedMetricWarning: Precision and F-score are ill-defined a
nd being set to 0.0 in labels with no predicted samples. Use `zero_divisio
n` parameter to control this behavior.
  _warn_prf(average, modifier, msg_start, len(result))
```

In [44]:

```
cm = confusion_matrix(Y_true_onehot.argmax(axis = 1) , Y_pred.argmax(axis = 1))
cm = pd.DataFrame(cm , index = ['caries','no-caries'] , columns = ['caries','no-caries']
plt.figure(figsize = (10,10))
sns.heatmap(cm,cmap= "Blues", linecolor = 'black' , linewidth = 1 , annot = True, fmt=''
```

Out[44]:

<AxesSubplot:>



In [45]:

```
from sklearn.metrics import roc_auc_score,precision_score,recall_score,f1_score,roc_curv
print("roc_auc_score:",roc_auc_score(Y_true_onehot,Y_pred))
```

roc_auc_score: 0.5

In [46]:

```
precision_score(Y_true_onehot,Y_pred,average=None)
```

```
C:\Users\vamsh\anaconda3\lib\site-packages\sklearn\metrics\_classificatio
n.py:1248: UndefinedMetricWarning: Precision is ill-defined and being set
to 0.0 in labels with no predicted samples. Use `zero_division` parameter
to control this behavior.
  _warn_prf(average, modifier, msg_start, len(result))
```

Out[46]:

```
array([0.71428571, 0.        ])
```

In [47]:

```
recall_score(Y_true_onehot,Y_pred,average=None)
```

Out[47]:

```
array([1., 0.])
```

In [48]:

```
f1_score(Y_true_onehot,Y_pred,average=None)
```

Out[48]:

```
array([0.83333333, 0.        ])
```

In [49]:

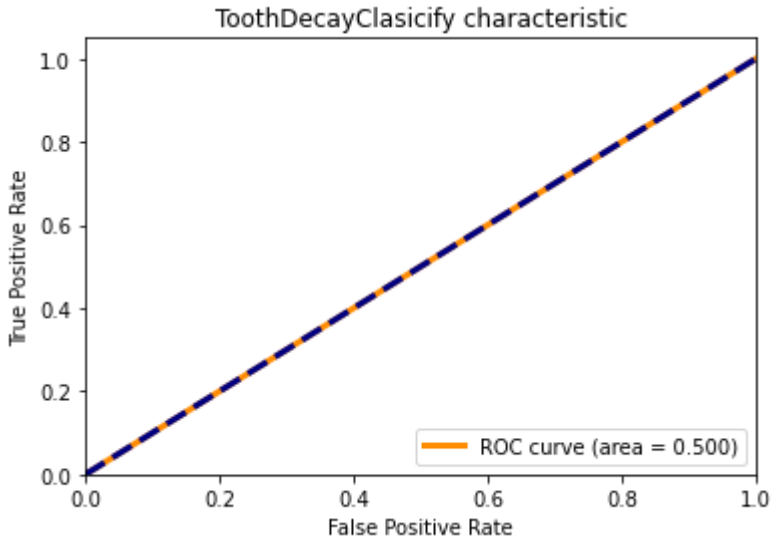
```
fpr = dict()
tpr = dict()
roc_auc = dict()
for i in range(2):
    fpr[i], tpr[i], _ = roc_curve(Y_true_onehot[:, i], Y_pred[:, i])
    roc_auc[i] = auc(fpr[i], tpr[i])
```

In [50]:

```
fpr["micro"], tpr["micro"], _ = roc_curve(Y_true_onehot.ravel(), Y_pred.ravel())
roc_auc["micro"] = auc(fpr["micro"], tpr["micro"])
```

In [51]:

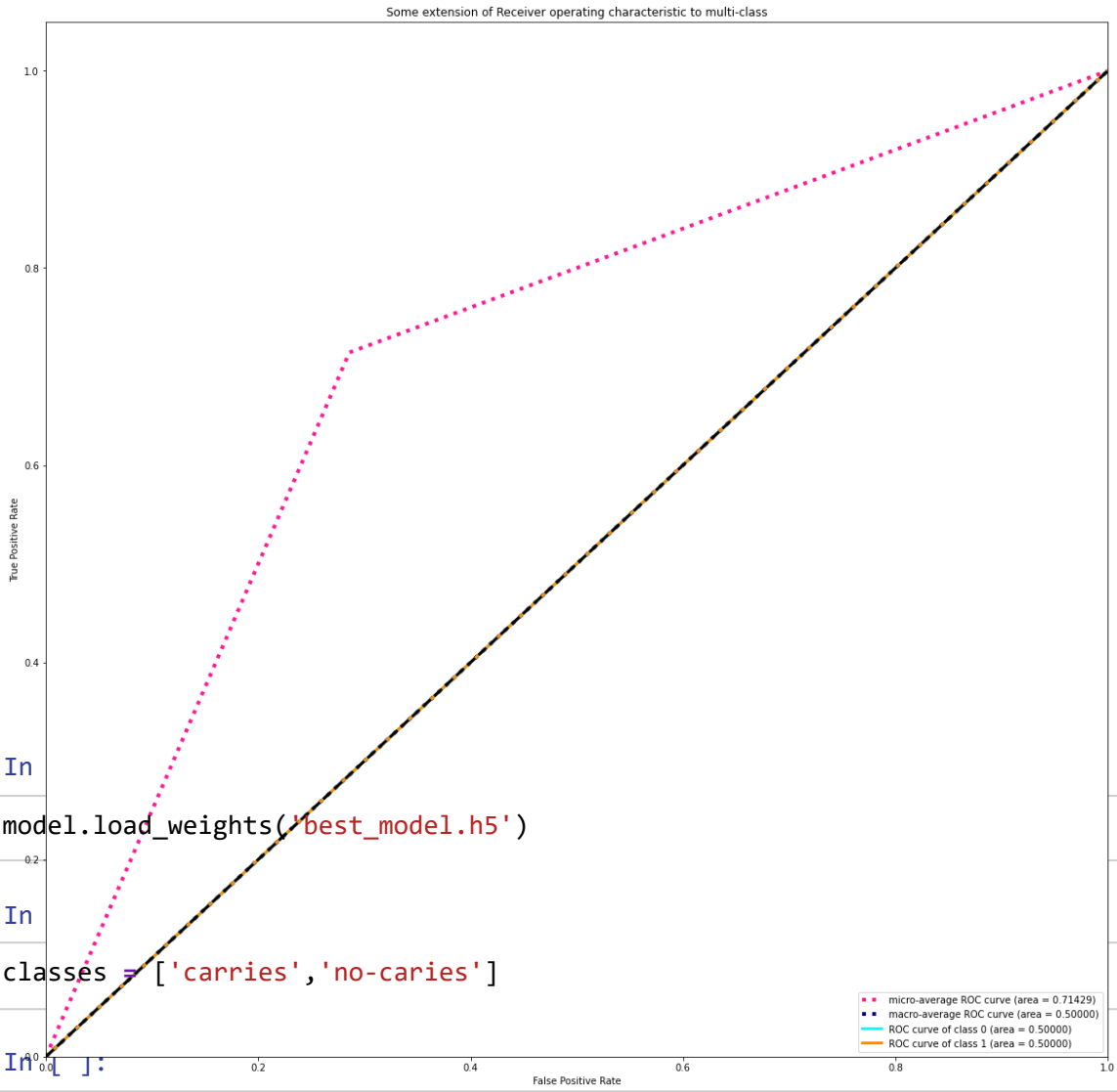
```
plt.figure()
lw = 3
plt.plot(fpr[1], tpr[1], color='darkorange',
         lw=lw, label='ROC curve (area = %0.3f)' % roc_auc[1])
plt.plot([0, 1], [0, 1], color='navy', lw=lw, linestyle='--')
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('ToothDecayClasicify characteristic')
plt.legend(loc="lower right")
plt.show()
```



In [52]:

```
from scipy import interp
from itertools import cycle
# First aggregate all false positive rates
all_fpr = np.unique(np.concatenate([fpr[i] for i in range(2)]))

# Then interpolate all ROC curves at this points
mean_tpr = np.zeros_like(all_fpr)
for i in range(2):
    mean_tpr += interp(all_fpr, fpr[i], tpr[i])

# Finally average it and compute AUC
mean_tpr /= 2

fpr["macro"] = all_fpr
tpr["macro"] = mean_tpr
roc_auc["macro"] = auc(fpr["macro"], tpr["macro"])

# Plot all ROC curves
plt.figure(figsize = (20,20))
plt.plot(fpr["micro"], tpr["micro"],
         label='micro-average ROC curve (area = {0:0.5f})'
               ''.format(roc_auc["micro"]),
         color='deeppink', linestyle=':', linewidth=4)

plt.plot(fpr["macro"], tpr["macro"],
         label='macro-average ROC curve (area = {0:0.5f})'
               ''.format(roc_auc["macro"]),
         color='navy', linestyle=':', linewidth=4)

colors = cycle(['aqua', 'darkorange', 'cornflowerblue'])
for i, color in zip(range(2), colors):
    plt.plot(fpr[i], tpr[i], color=color, lw=lw,
             label='ROC curve of class {0} (area = {1:0.5f})'
             ''.format(i, roc_auc[i]))
plt.plot([0, 1], [0, 1], 'k--', lw=lw)
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Some extension of Receiver operating characteristic to multi-class')
plt.legend(loc="lower right")
plt.show()
```

```
C:\Users\vamsh\AppData\Local\Temp/ipykernel_14852/2925625859.py:9: Depreca
tionWarning: scipy.interp is deprecated and will be removed in SciPy 2.0.
0, use numpy.interp instead
  mean_tpr += interp(all_fpr, fpr[i], tpr[i])
```



In

```
model.load_weights('best_model.h5')
```

In

```
classes = ['carries','no-caries']
```

In [ ]:

```
import cv2
```

In [ ]:

```
srcdir = 'toothdecay/teeth_dataset/test/caries'
count=0

for temp in os.listdir(srcdir):
    img = cv2.imread(os.path.join(srcdir, temp))
    cv2.imwrite(temp, img)
    cv2.imshow('caries', img)
    cv2.waitKey(0)
    img = cv2.resize(img, (112, 112))
    result = model.predict(img.reshape(1, 112, 112, 3))
    max_prob = max(result[0])
    class_ind = list(result[0]).index(max_prob)
    class_name = classes[class_ind]
    print(class_name)
    count+=1
    if count>3:
        break
```

In [ ]:

```
```