

DA 1

BINARY CLASSIFICATION OF BREAST CANCER

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https://github.com/Amlan131/DA_1

CODE

This code imports essential libraries for image-based machine learning tasks:

```
import numpy as np
import tensorflow as tf
from keras.preprocessing.image import ImageDataGenerator
import matplotlib.pyplot as plt
```

This code configures TensorFlow to optimize GPU usage:

```
gpus = tf.config.experimental.list_physical_devices('GPU')
for gpu in gpus:
    tf.config.experimental.set_memory_growth(gpu, True)
```

This code preprocesses the training images for use in a deep learning model:

Loads and preprocesses images from the specified directory (train) for training.

Automatically assigns labels based on folder names and converts them to a one-hot encoded format.

Resized to 128x128 pixels

Batched in groups of 4

Shuffled for randomness in training

```
training_set = tf.keras.utils.image_dataset_from_directory(
    r"D:\01 STUDY MATERIAL\ai project\Breast-Splitted\train",
    labels="inferred",
    label_mode="categorical",
    class_names=None,
    color_mode="rgb",
    batch_size=4,
    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 = training_set.class_names
print(class_name)
Found 4745 files belonging to 2 classes.
```

```
['benign', 'malignant']
```

```
validation_set = tf.keras.utils.image_dataset_from_directory(
    r"D:\01 STUDY MATERIAL\ai project\Breast-Splitted\val",
    labels="inferred",
    label_mode="categorical",
    class_names=None,
    color_mode="rgb",
    batch_size=4,
    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 1581 files belonging to 2 classes.
['benign', 'malignant']
```

This code defines and compiles a Convolutional Neural Network (CNN) for binary image classification:

```
cnn = tf.keras.models.Sequential()
cnn.add(tf.keras.layers.Conv2D(filters=32,kernel_size=3,padding='same',activation='relu',input_shape=[128,128,3]))
cnn.add(tf.keras.layers.Conv2D(filters=32,kernel_size=3,activation='relu'))
cnn.add(tf.keras.layers.MaxPool2D(pool_size=2,strides=2))
cnn.add(tf.keras.layers.Conv2D(filters=64,kernel_size=3,padding='same',activation='relu'))
cnn.add(tf.keras.layers.Conv2D(filters=64,kernel_size=3,activation='relu'))
cnn.add(tf.keras.layers.MaxPool2D(pool_size=2,strides=2))
cnn.add(tf.keras.layers.Conv2D(filters=128,kernel_size=3,padding='same',activation='relu'))
cnn.add(tf.keras.layers.Conv2D(filters=128,kernel_size=3,activation='relu'))
cnn.add(tf.keras.layers.MaxPool2D(pool_size=2,strides=2))
cnn.add(tf.keras.layers.Conv2D(filters=256,kernel_size=3,padding='same',activation='relu'))
cnn.add(tf.keras.layers.Conv2D(filters=256,kernel_size=3,activation='relu'))
cnn.add(tf.keras.layers.MaxPool2D(pool_size=2,strides=2))
cnn.add(tf.keras.layers.Dropout(0.25))
cnn.add(tf.keras.layers.Dense(units=1500,activation='relu'))
cnn.add(tf.keras.layers.Dropout(0.4))
cnn.add(tf.keras.layers.Dense(units=2,activation='sigmoid'))
cnn.compile(optimizer=tf.keras.optimizers.legacy.Adam(
    learning_rate=0.0001),loss='binary_crossentropy',metrics=['accuracy'])
cnn.summary()
Model: "sequential"
```

Layer (type)	Output Shape	Param #
=====		

conv2d (Conv2D)	(None, 128, 128, 32)	896
conv2d_1 (Conv2D)	(None, 126, 126, 32)	9248
max_pooling2d (MaxPooling2D (None, 63, 63, 32))		0
conv2d_2 (Conv2D)	(None, 63, 63, 64)	18496
conv2d_3 (Conv2D)	(None, 61, 61, 64)	36928
max_pooling2d_1 (MaxPooling (None, 30, 30, 64) 2D)		0
conv2d_4 (Conv2D)	(None, 30, 30, 128)	73856
conv2d_5 (Conv2D)	(None, 28, 28, 128)	147584
max_pooling2d_2 (MaxPooling (None, 14, 14, 128) 2D)		0
conv2d_6 (Conv2D)	(None, 14, 14, 256)	295168
conv2d_7 (Conv2D)	(None, 12, 12, 256)	590080
max_pooling2d_3 (MaxPooling (None, 6, 6, 256) 2D)		0
dropout (Dropout)	(None, 6, 6, 256)	0
flatten (Flatten)	(None, 9216)	0
dense (Dense)	(None, 1500)	13825500
dropout_1 (Dropout)	(None, 1500)	0
dense_1 (Dense)	(None, 2)	3002

```

=====
Total params: 15,000,758
Trainable params: 15,000,758
Non-trainable params: 0

```

Trains the CNN model for 10 epochs using the training and validation datasets, storing the training history.

```

training_history = cnn.fit(x=training_set,validation_data=validation_set,epochs=10)
Epoch 1/10
1187/1187 [=====] - 23s 14ms/step - loss: 0.5513 - accuracy: 0.7583 -
val_loss: 0.5055 - val_accuracy: 0.8027
Epoch 2/10

```

```

1187/1187 [=====] - 16s 14ms/step - loss: 0.4748 - accuracy: 0.8063 -
val_loss: 0.4729 - val_accuracy: 0.8109
Epoch 3/10
1187/1187 [=====] - 16s 14ms/step - loss: 0.4420 - accuracy: 0.8333 -
val_loss: 0.4960 - val_accuracy: 0.8242
Epoch 4/10
1187/1187 [=====] - 16s 14ms/step - loss: 0.3989 - accuracy: 0.8548 -
val_loss: 0.3815 - val_accuracy: 0.8564
Epoch 5/10
1187/1187 [=====] - 16s 14ms/step - loss: 0.3885 - accuracy: 0.8626 -
val_loss: 0.3614 - val_accuracy: 0.8703
Epoch 6/10
1187/1187 [=====] - 16s 14ms/step - loss: 0.3794 - accuracy: 0.8660 -
val_loss: 0.3514 - val_accuracy: 0.8722
Epoch 7/10
1187/1187 [=====] - 16s 14ms/step - loss: 0.3492 - accuracy: 0.8717 -
val_loss: 0.4022 - val_accuracy: 0.8665
Epoch 8/10
1187/1187 [=====] - 16s 14ms/step - loss: 0.3353 - accuracy: 0.8717 -
val_loss: 0.3446 - val_accuracy: 0.8760
Epoch 9/10
1187/1187 [=====] - 16s 14ms/step - loss: 0.3131 - accuracy: 0.8843 -
val_loss: 0.3404 - val_accuracy: 0.8697
Epoch 10/10
1187/1187 [=====] - 16s 14ms/step - loss: 0.2955 - accuracy: 0.8839 -
val_loss: 0.3230 - val_accuracy: 0.8748

```

Evaluates the CNN on the training set and prints the training accuracy.

```

train_loss, train_acc = cnn.evaluate(training_set)
print('Training accuracy:', train_acc)
1187/1187 [=====] - 6s 5ms/step - loss: 0.2486 - accuracy: 0.9041
Training accuracy: 0.9041095972061157

```

Evaluates the CNN on the validation set and prints the validation accuracy.

```

val_loss, val_acc = cnn.evaluate(validation_set)
print('Validation accuracy:', val_acc)
396/396 [=====] - 2s 5ms/step - loss: 0.3230 - accuracy: 0.8748
Validation accuracy: 0.8747628331184387

```

Saves the trained CNN model to a file named trnew_cancer_modelv1.o.keras.

```

cnn.save('trnew_cancer_modelv1.o.keras')
training_history.history
{'loss': [0.5512648820877075,
0.4747887849807739,
0.4420156478881836,
0.39887040853500366,

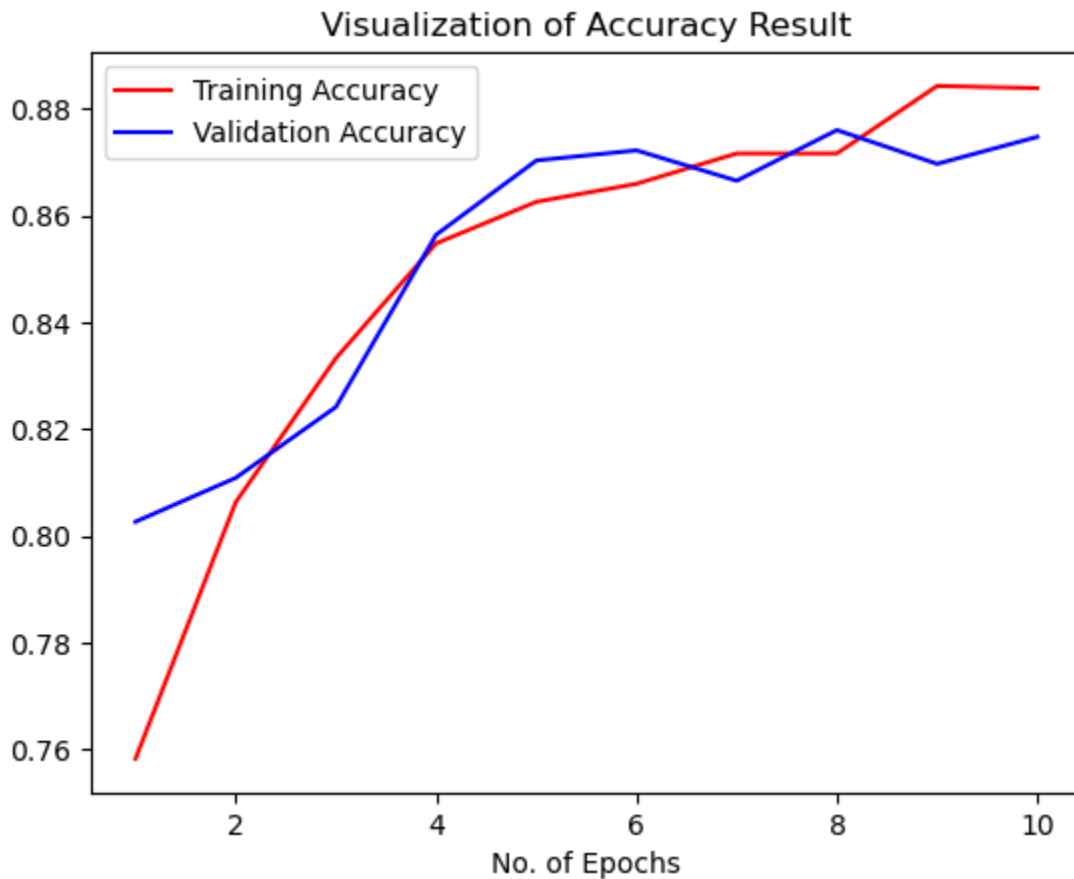
```

```

0.388454407453537,
0.3794495761394501,
0.3492189943790436,
0.33529233932495117,
0.3130831718444824,
0.29554569721221924],
'accuracy': [0.7582718729972839,
0.806322455406189,
0.8332982063293457,
0.8547945022583008,
0.8625922203063965,
0.8659641742706299,
0.8716543912887573,
0.8716543912887573,
0.8842992782592773,
0.8838777542114258],
'val_loss': [0.5055041909217834,
0.47289153933525085,
0.49602824449539185,
0.3814983665943146,
0.3614308536052704,
0.35138577222824097,
0.4021930992603302,
0.344621866941452,
0.3404453694820404,
0.3230063319206238],
'val_accuracy': [0.8026565313339233,
0.8108791708946228,
0.824161946773529,
0.8564199805259705,
0.8703352212905884,
0.8722327351570129,
0.8665401935577393,
0.8760278224945068,
0.8697026968002319,
0.8747628331184387]]
import json
with open('training_hist_cancer.json','w') as f:
    json.dump(training_history.history,f)
print(training_history.history.keys())
dict_keys(['loss', 'accuracy', 'val_loss', 'val_accuracy'])

epochs = [i for i in range(1,11)]
plt.plot(epochs,training_history.history['accuracy'],color='red',label='Training Accuracy')
plt.plot(epochs,training_history.history['val_accuracy'],color='blue',label='Validation Accuracy')
plt.xlabel('No. of Epochs')
plt.title('Visualization of Accuracy Result')
plt.legend()
plt.show()

```



```

class_name = validation_set.class_names
test_set = tf.keras.utils.image_dataset_from_directory(
    r"D:\oi STUDY MATERIAL\ai project\Breast-Splitted\test",
    labels="inferred",
    label_mode="categorical",
    class_names=None,
    color_mode="rgb",
    batch_size=1,
    image_size=(128, 128),
    shuffle=False,
    seed=None,
    validation_split=None,
    subset=None,
    interpolation="bilinear",
    follow_links=False,
    crop_to_aspect_ratio=False
)

```

Found 1583 files belonging to 2 classes.

```

y_pred = cnn.predict(test_set)
predicted_categories = tf.argmax(y_pred, axis=1)
1583/1583 [=====] - 5s 3ms/step

```

```
true_categories = tf.concat([y for x, y in test_set], axis=0)
Y_true = tf.argmax(true_categories, axis=1)
Y_true
<tf.Tensor: shape=(1583,), dtype=int64, numpy=array([0, 0, 0, ..., 1, 1, 1], dtype=int64)>
```

```
from sklearn.metrics import confusion_matrix, classification_report
cm = confusion_matrix(Y_true, predicted_categories)
sklearn.metrics.roc_auc_score(y_true, y_score, *, average='macro', sample_weight=None,
max_fpr=None, multi_class='raise', labels=None)
Cell In[35], line 1
    sklearn.metrics.roc_auc_score(y_true, y_score, *, average='macro', sample_weight=None,
max_fpr=None, multi_class='raise', labels=None)
                ^
```

SyntaxError: iterable argument unpacking follows keyword argument unpacking

Prints the precision, recall, and F1-score for each class using the true labels (Y_true) and predicted categories (predicted_categories).

```
print(classification_report(Y_true, predicted_categories, target_names=class_name))
precision recall f1-score support
```

```
benign      0.78    0.79    0.78    496
malignant   0.90    0.90    0.90   1087

accuracy                0.86   1583
macro avg      0.84    0.84    0.84   1583
weighted avg   0.86    0.86    0.86   1583
```

```
import seaborn as sns
plt.figure(figsize=(40, 40))
sns.heatmap(cm, annot=True, annot_kws={"size": 10})
plt.xlabel('Predicted Class', fontsize = 20)
plt.ylabel('Actual Class', fontsize = 20)
plt.title('Plant Disease Prediction Confusion Matrix', fontsize = 25)
plt.show()
```

NameError Traceback (most recent call last)

```
Cell In[1], line 2
    1 import seaborn as sns
----> 2 plt.figure(figsize=(40, 40))
      3 sns.heatmap(cm, annot=True, annot_kws={"size": 10})
      5 plt.xlabel('Predicted Class', fontsize = 20)
```

NameError: name 'plt' is not defined

TESTING

```
import numpy as np
import tensorflow as tf
from keras.preprocessing.image import ImageDataGenerator
import matplotlib.pyplot as plt
cnn = tf.keras.models.load_model('trnew_cancer_model.keras')
```



```

import cv2
import tensorflow as tf
import numpy as np
import matplotlib.pyplot as plt
import os
import random

# Define paths for benign and malignant folders
benign_path = r"D:\01 STUDY MATERIAL\ai project\Breast-Splitted\test\benign"
malignant_path = r"D:\01 STUDY MATERIAL\ai project\Breast-Splitted\test\malignant"

# Get all image file paths from both folders
benign_images = [os.path.join(benign_path, img) for img in os.listdir(benign_path) if
img.endswith(('.png', '.jpg', '.jpeg'))]
malignant_images = [os.path.join(malignant_path, img) for img in os.listdir(malignant_path) if
img.endswith(('.png', '.jpg', '.jpeg'))]

# Randomly select 9 images (combined from both classes)
selected_images = random.sample(benign_images, 4) + random.sample(malignant_images, 5)
random.shuffle(selected_images) # Shuffle to mix benign and malignant images

# Predefined class names
class_name = ['Benign', 'Malignant']

# Load and process each image
plt.figure(figsize=(12, 12))
for idx, image_path in enumerate(selected_images):
    # Read and preprocess the image
    img = cv2.imread(image_path)
    img_rgb = cv2.cvtColor(img, cv2.COLOR_BGR2RGB) # Convert BGR to RGB for visualization

    # Determine the actual classification based on the folder name
    actual_label = 'Benign' if 'benign' in image_path.lower() else 'Malignant'

    # Resize and prepare for model prediction
    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.expand_dims(input_arr, axis=0) # Convert single image to a batch

    # Make predictions
    predictions = cnn.predict(input_arr)
    result_index = np.argmax(predictions) # Get the predicted class index
    predicted_label = class_name[result_index] # Map index to class name

    # Plot the image with actual and predicted labels
    plt.subplot(3, 3, idx + 1)
    plt.imshow(img_rgb)
    plt.title(f'Actual: {actual_label}\nPredicted: {predicted_label}', color='green' if actual_label ==
predicted_label else 'red')
    plt.axis('off')

```

```
plt.tight_layout()
plt.show()
```

1/1 [=====] - 6s 6s/step

1/1 [=====] - os 14ms/step

1/1 [=====] - os 25ms/step

1/1 [=====] - os 12ms/step

1/1 [=====] - os 20ms/step

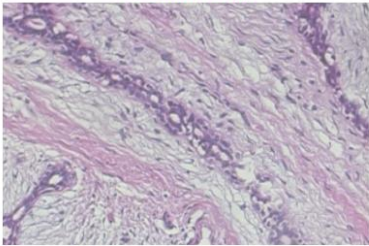
1/1 [=====] - os 15ms/step

1/1 [=====] - os 10ms/step

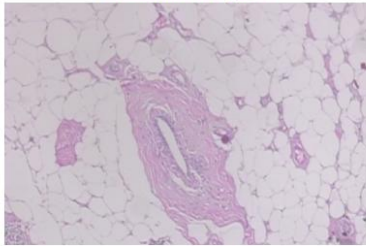
1/1 [=====] - os 10ms/step

1/1 [=====] - os 20ms/step

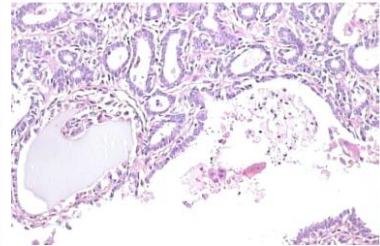
Actual: Benign
Predicted: Benign



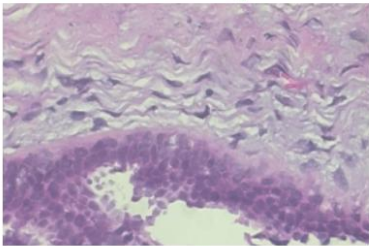
Actual: Malignant
Predicted: Malignant



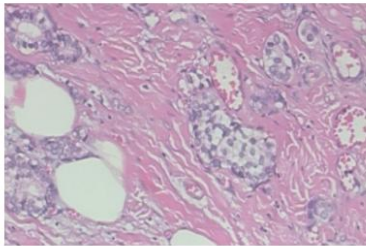
Actual: Malignant
Predicted: Malignant



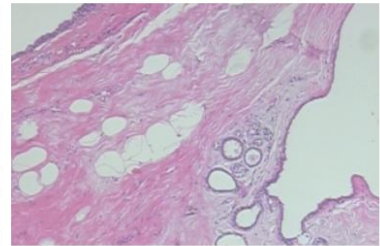
Actual: Benign
Predicted: Benign



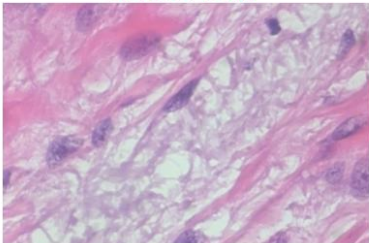
Actual: Malignant
Predicted: Benign



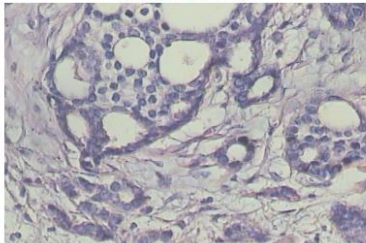
Actual: Benign
Predicted: Benign



Actual: Malignant
Predicted: Benign



Actual: Benign
Predicted: Benign



Actual: Malignant
Predicted: Malignant

