Screening Breast Cancer from Mammograms Using Machine Learning Methods

Introduction

Breast cancer is a prevalent threat and is the second leading cause of death among women globally. Mammography is one of the most common methods of breast cancer screening. It works based on the differences in the X-ray absorption between various components of the breast such as fat, tumor tissue, and calcifications (Raman et. al, 2011). However, mammography is associated with high risk of false positives and negatives, with an average screening sensitivity of mammography in the U.S. of 86.9% and average specificity of 88.9% (Lehman et al, 2016). As early diagnosis can greatly improve outcomes for patients, it is imperative to develop Computer Aided Detection (CAD) techniques for detecting the disease. However, detecting abnormalities with mammography can be a difficult task as the tumors only occupy a small portion of the entire image.

Using machine learning tools can significantly increase the accuracy of screening. Previous studies have shown that deep-learning techniques have performed better than radiologists in classifying tumors (Shen et al., 2019). In this project, we focused on the transfer learning process and used the VGG-16 network that has been pre-trained on the ImageNet database with additional layers and fine-tuned parameters to evaluate its performance in classifying normal mammograms, mammograms with benign tumors, and mammograms with malignant tumors. To optimize performance, we also applied various image augmentation techniques.

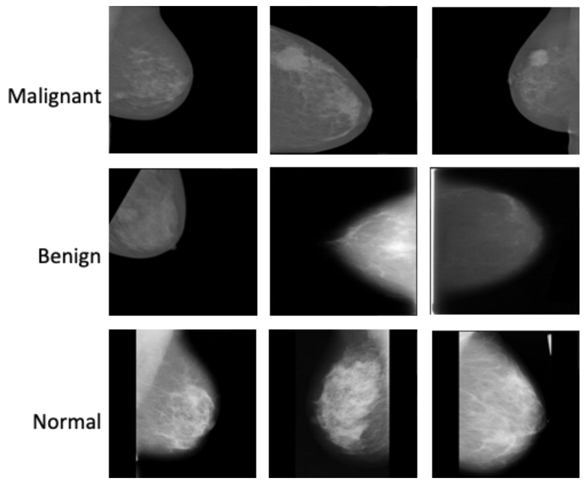

Figure 1. Example images from each classification class.

Datasets

For the baseline methods, we used the MIAS (Mammographic Image Analysis Society) dataset, which contains 322 total mammogram images (207 normal, 63 benign, 52 malignant) along with a text file with labels for each image. To compensate for the small number of images and to balance the classes, we augmented the images using random shearing, random rotation, horizontal flip, and the addition of random noise.

However, even after augmentation, the MIAS dataset proved too small to provide good testing and validation accuracies to the model. Therefore, images from two other datasets — INbreast and DDSM — were also added to the input mammogram dataset. The characteristics of each dataset are shown in Table 1. The resultant combined dataset had 207 normal, 1093 benign and 1316 malignant mammogram images, and the individual contributions of each dataset can be visualized in Figure 2. This combined dataset was again augmented using random shearing, random rotation, horizontal flipping and addition of random noise in order to balance the three classes. The final augmented dataset included 3948 images.

	MIAS	INbreast	DDSM
Total Images	322	106	2188
Normal Images	207	0	0
Benign Images	63	35	995
Malignant Images	52	71	1193
Lesion Type	All kinds	All kinds	All kinds
Ground Truth	Center and radius of a circle around area of interest	Pixels of region of interest	Pixel level boundary of the findings
Image File Type	PGM	DICOM	LJPEG

Table 1. Characteristics of the 3 mammogram image databases used in the project.

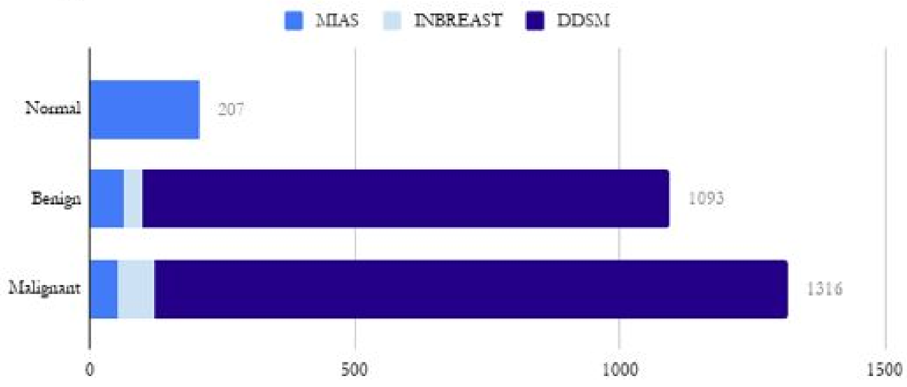

Figure 2. Bar graph showing contribution of each individual dataset to the final combined one.

Baseline Exploration

Standard Classifiers

Our baseline methods were done using standard classifiers. As mentioned previously, we started with only the MIAS dataset, and chose to use the text features from the dataset (such as the character of background tissue or class of abnormality present) instead of using the raw images in order to reduce dimensionality. We used LabelEncoder to transform non-numerical labels to numerical labels. Afterward, we split the training and test data with 80% in the training dataset and 20% in the test dataset.

For k-NN, hyperparameters chosen after tuning using GridSearchCV, were: leaf_size = 1, Chebyshev distance formula, p=1 (Manhattan distance), weights = distance, and k = 1. The accuracy of our model on the test data for this code was 0.833.

The MIAS dataset contains a disproportionate number of normal images. Therefore, despite the high accuracy score, it is important to note that the amount of normal mammography scans in the dataset is skewing the results, as seen in Figure 3. The ROC curve for the normal class is also very good as seen in Figure 4. On the other hand, the k-NN algorithm seems to have some issues differentiating between benign and malignant.

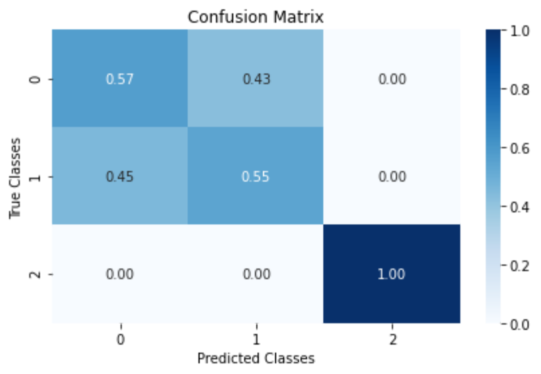

Figure 3 : Confusion matrix for k-NN Classifier.
[0: Benign, 1: Malignant, 2: Normal]

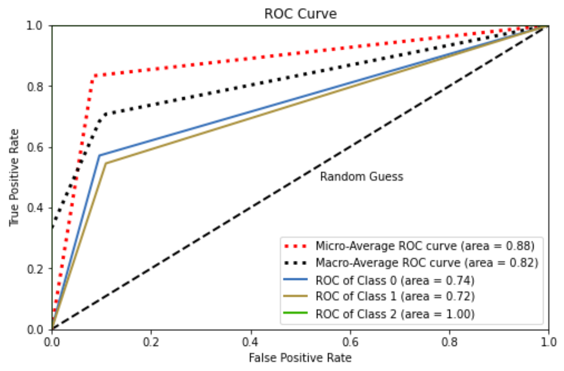

Figure 4 : ROC for k-NN Classifier.
[0: Benign, 1: Malignant, 2: Normal]

We used the same extracted features to implement a support vector classification, logistic regression, and random forest methods. Using a linear kernel for the support vector machine attempt yielded an accuracy of 0.803. A random forest classifier was also attempted using 10 trees, and the accuracy was found to be 0.803. Overall, we discovered that our baseline methods performed poorly when classifying malignant versus benign tumours.

Transfer Learning

To test more complex architectures, we used transfer learning with the pre-trained VGG-16 model. The VGG network consisted of a 13-layered convolutional neural network using 3x3 filters and 2x2 max-pooling layers (Simonyan & Zisserman, 2015). Multiple smaller-sized kernels, as opposed to a single large kernel, increases the depth of the network and can allow it to learn more complex features. We choose VGG-16 because of its depth, as it has good feature learning ability and can adapt to a variety of data sets including tumor images.

We used the MIAS dataset, and cropped the images to the region of the tumors in the case of an abnormality, and to the center for normal images. This was so that the model would only concentrate on the region of interest and disregard edges and unnecessary pixels. After processing the images, we split the images with a 60-20-20 training-validation-test split.

For the model, we used a learning rate of 1e-5 and only trained the last fully connected layers by freezing all the other layers. We set the epoch and batch size to 20, and added multiple new dense layers following the pre-trained VGG-16. The training loss consistently decreased and the training accuracy increased over the epochs (Figure 5). However the model seems to have some issues with overfitting as the validation loss was higher than the training loss.

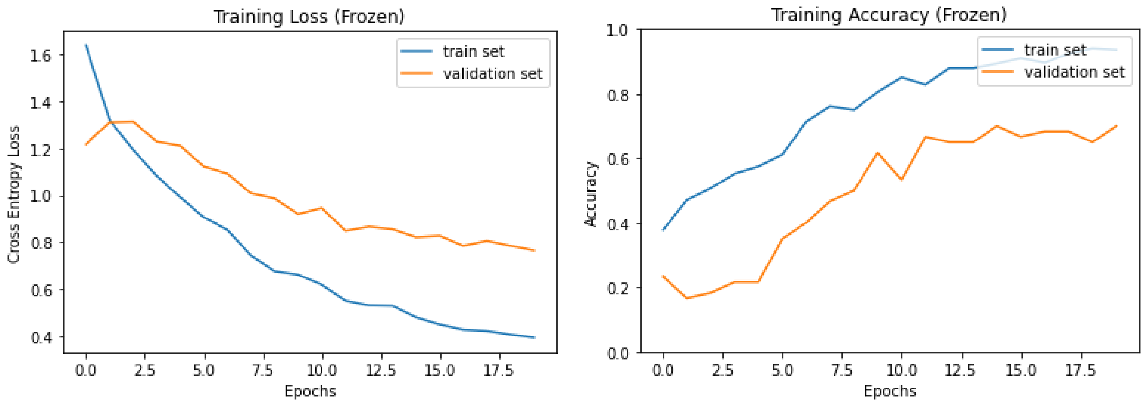

Figure 5: Training loss (left) and accuracy (right) for baseline transfer learning model.

The validation and testing accuracies were approximately 0.59 and 0.47, respectively. As seen in the confusion matrices below, this model had a similar issue as the k-NN baseline, where the normal images skewed the results. The ROC curve is shown in Figure 7, where the normal class had an area of 0.82 and the malignant and benign classes had areas of 0.54 and 0.65, respectively.

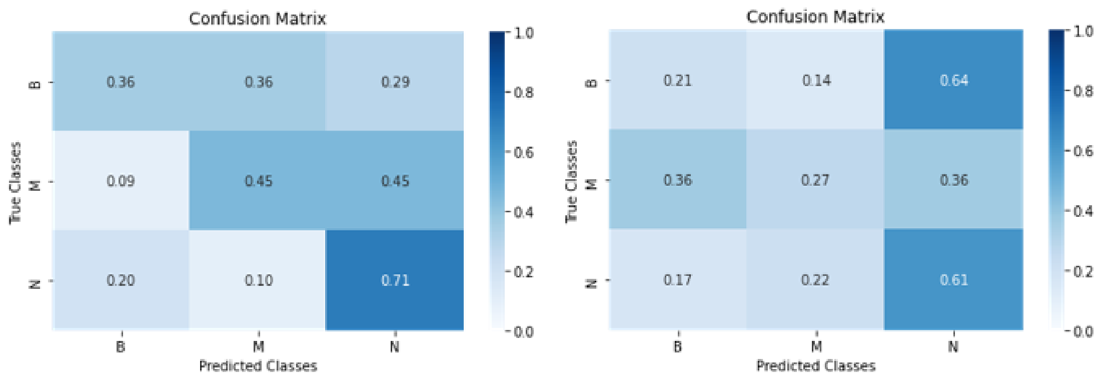

Figure 6: Validation (left) and testing (right) Confusion Matrices for baseline transfer learning model.

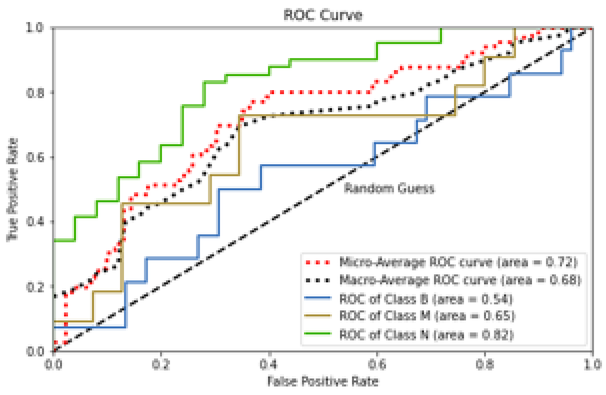

Figure 7: ROC curves for baseline transfer learning model.

Improved Model

For our improved model, we combined three separate datasets and augmented the images for even distribution of images for each class. We no longer cropped the images to a region of interest as done previously. This is because of two reasons: firstly, we felt that this was unnecessary with a larger number of images, and secondly, not all of the datasets provided us with the location of the region of interest.

Below is a table of a list of notable experiments along with a graph that compares the accuracies from validation and testing for the experiments using the compiled dataset. It is clear that having the large compiled dataset greatly increased the accuracy of our model from 67% and 44% to 96% for both validation and testing, as seen in experiments A and B.

List of Notable Experiments with Variables and Accuracy Results

Experiment	Dataset	Number of Dense Layers	Regularizer	Input Regularizer Parameter	Output Layer Activation Function	Number of Epochs	Validation Accuracy	Testing Accuracy
A	MIAS	2	Dropout	0.2	Softmax	20	66.67%	43.94%
B	Compiled	2	Dropout	0.2	Softmax	20	96.38%	96.25%
C	Compiled	1	Dropout	0.2	Softmax	20	95.86%	97.41%
D	Compiled	1	Dropout	0.2	Sigmoid	20	97.54%	94.83%
E	Compiled	1	L1	0.001	Sigmoid	20	95.34%	95.73%
F	Compiled	1	L2	0.001	Sigmoid	20	96.77%	96.51%
G	Compiled	1	L2	0.001	Sigmoid	100	95.47%	96.38%
H	Compiled	1	L1L2	0.001	Sigmoid	100	96.90%	95.47%
I	Compiled	1	L1L2	0.001	Sigmoid	20	96.12%	96.64%
J	Compiled	1	L1L2	0.01	Sigmoid	20	97.02%	95.60%
K	Compiled	1	L1L2	0.1	Sigmoid	20	96.12%	96.64%
L	Compiled	2	L1L2	0.001	Sigmoid	20	97.02%	95.59%

Table 2. Notable experiments and results (Final model is highlighted in yellow).

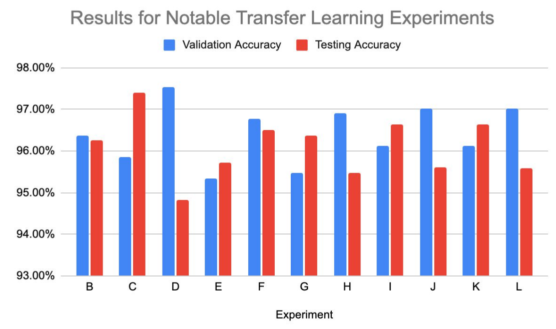

Figure 7. Graph of validation and testing accuracies from notable experiments.

Before progressing further, we decided to research how previous studies had tackled a similar problem. A breast cancer classification study conducted by Guan and Loew found that a model that uses a fully connected layer with Rectified Linear Unit (ReLU) for its activation function and dropout set to .5, as well as an output layer with sigmoid as the activation function has successful results (Guan & Loew, 2017).

From the model mentioned in the paper, we simplified the model by removing one of the dense layers so it would only have one dense layer with an activation function of ReLU. Our results (experiments B to C) showed that there was a slight improvement in performance with a single layer. For our output layer, we used the sigmoid function, as we found a miniscule difference in performance between sigmoid and softmax.

While testing, we discovered issues of overfitting as shown in Figure 8, which occurs when the validation loss is higher than the training loss. We tried to regularize as we already tried using dropout, which modifies the network in order to combat overfitting. Regularization techniques that modify the cost function are useful since they try to minimize the error as it introduces a shrinkage factor.

We tested three types of regularizers: lasso regression (L1), ridge regression (L2), and a combination of the two (L1L2). L1 simply penalizes the high coefficients, and in doing so, some features can be removed since the coefficients of the less important features can be shrunk to 0. L2 shrinks the coefficients of the predictors of least importance, however, never making them 0. L1L2 is the sum of the absolute (L1) and the squared weight (L2).

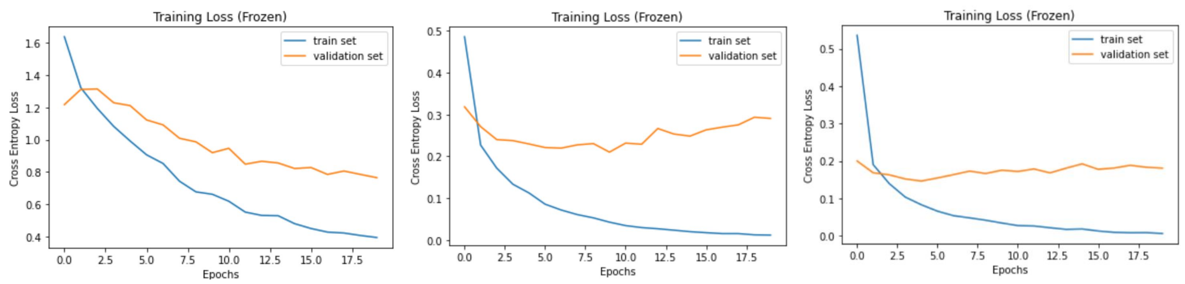

Figure 8: Example of model overfitting for experiments B (left), C (middle), and D (right).

We observed that L2 performed better than L1 and Dropout in minimizing overfitting. After trying L1L2 regularization on our model, we saw even better results because of how it is able to take the combination of lasso and ridge regression (experiments E, F, I). Below are the training loss and accuracies of our final model, which uses L1L2 (Figure 9).

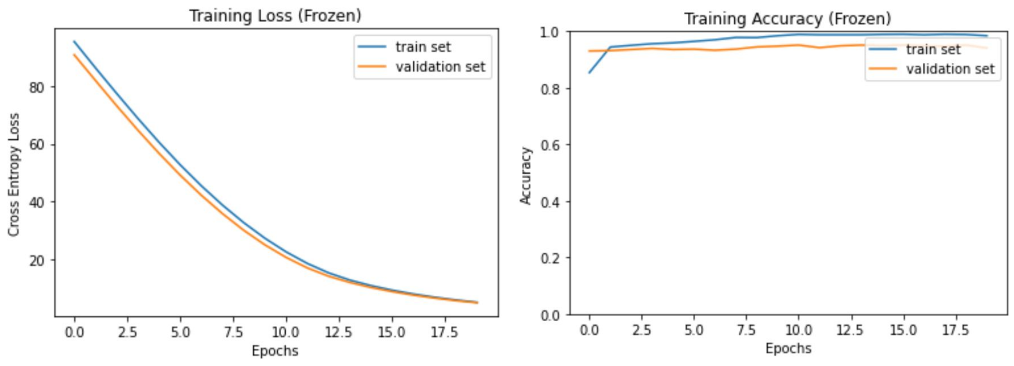

Figure 9: Training loss and accuracy for final transfer learning model.

After determining that the best results were obtained using L1L2 regularization, we varied the input value trying .1, .01, and .001. We found that .01 performed best (experiments I, J, and K). Lastly, we changed the number of epochs for both L2 and L1L2 from 20 to 100 (experiments F, G, H, and I). Despite our initial intuition that more epochs would lead to superior results, we saw that the best accuracy was obtained for training and validation at 20 epochs. In terms of batch size, we decided to use 20 for all our tests.

Our final transfer learning model had remarkably improved performance in regards to classifying between malignant and benign mammograms. The model showed overall improvement with accuracies consistently around 0.96. This is seen in both the validation and testing confusion matrices as the vast majority of predicted classes matched the true classes (Figure 10). In addition the ROC curves for all three classes had an area of 0.99 (Figure 11).

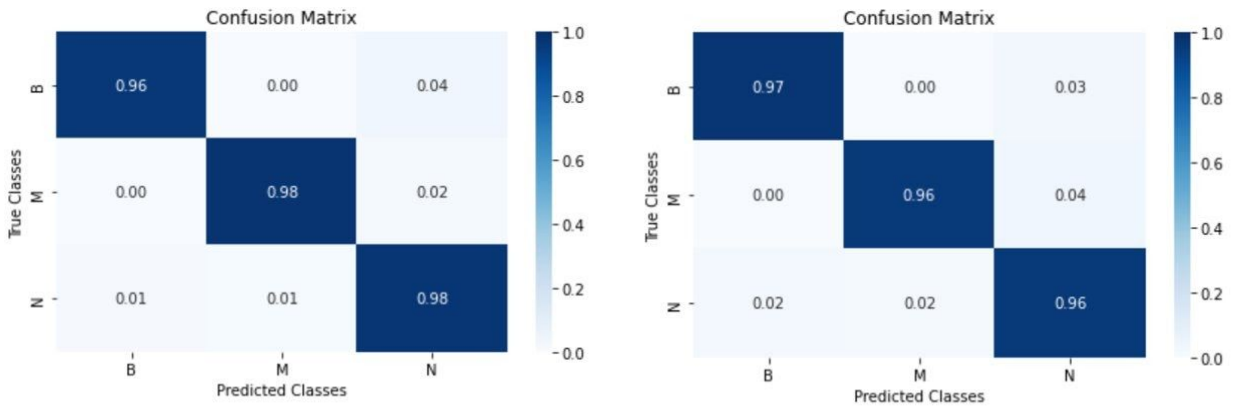

Figure 10: Testing (left) and validation (right) confusion matrices for final transfer learning model.

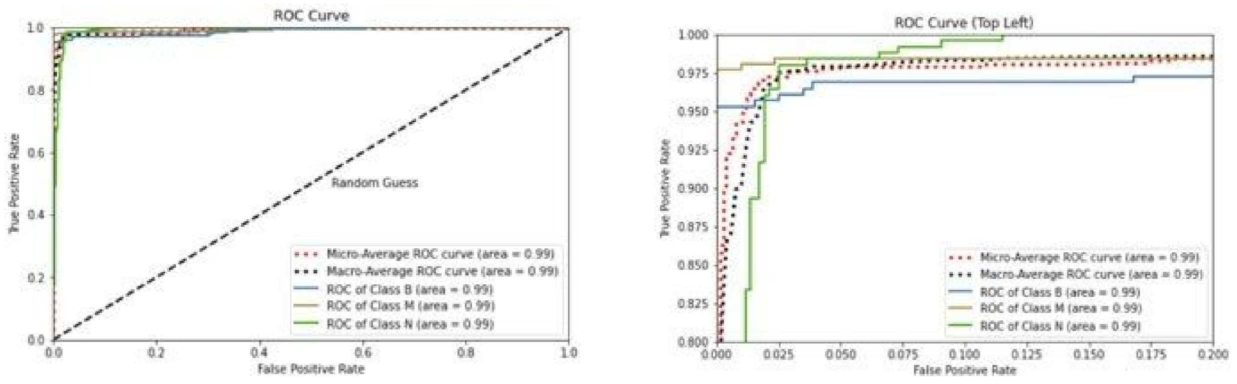

Figure 11: ROC for final transfer learning model.

Discussion

For the final project, we propose a method for the classification of breast cancer using transfer learning concepts. We also demonstrate a method of data augmentation to increase the size of the dataset to improve generalization and classification of the model. By using the VGG-16 model and improving upon existing baseline by fine-tuning, we achieved successful results, with our final model obtaining 96.64% testing accuracy. Further work can be done to improve our existing model to detect the different classes of abnormalities present in the tumors. Additionally, taking advantage of imaging techniques other than mammography could help build a more robust and flexible model.

Acknowledgements

We thank Professor Sabuncu and the ECE 5970/BME 5130 teaching assistants for guiding us in the right direction and providing meaningful feedback throughout the course of the project.

References

Guan, S., & Loew, M. (2017). Breast Cancer Detection Using Transfer Learning in Convolutional Neural Networks. *2017 IEEE Applied Imagery Pattern Recognition Workshop (AIPR)*, 1–8. https://doi.org/10.1109/AIPR.2017.8457948

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Shen, L., Margolies, L. R., Rothstein, J. H., Fluder, E., McBride, R., & Sieh, W. (2019). Deep Learning to Improve Breast Cancer Detection on Screening Mammography. *Scientific Reports*, *9*(1), 12495. https://doi.org/10.1038/s41598-019-48995-4

Simonyan, K., & Zisserman, A. (2015). Very Deep Convolutional Networks for Large-Scale Image Recognition. *ArXiv:1409.1556 [Cs]*. http://arxiv.org/abs/1409.1556

In [1]:

```
from google.colab import drive

drive.mount('/content/gdrive')
```

```
Mounted at /content/gdrive
```

In [2]:

```
%cd /content/gdrive/My Drive/Cornell/2020-2021/Biomedical ML Final Project - Melted Paper/
```

```
/content/gdrive/.shortcut-targets-by-id/13OShW0589KdYJRWaN9GrhtF2vtwdrUUW/Biomedical ML Final
Project - Melted Paper
```

Augment Dataset

Perform random number of image transformations to balance the classes

In [3]:

```
import os, time, cv2, random
import numpy as np
import pandas as pd
from sklearn.preprocessing import LabelEncoder
from tensorflow.keras.utils import to_categorical
import skimage as sk
import skimage.transform
```

In [4]:

```
augment_path = os.path.join('Datasets', 'final-dataset-augment')
normal_images_path = os.path.join('Datasets', 'final-dataset', 'N')
benign_images_path = os.path.join('Datasets', 'final-dataset', 'B')
malignant_images_path = os.path.join('Datasets', 'final-dataset', 'M')
```

In [5]:

```
normal_images = os.listdir(normal_images_path)
benign_images = os.listdir(benign_images_path)
malignant_images = os.listdir(malignant_images_path)
```

In [6]:

```
images, labels = [], []
```

In [7]:

```
for img in normal_images:
  labels.append('N')
  image = cv2.imread(os.path.join(normal_images_path, img), cv2.IMREAD_GRAYSCALE)
  image = image.reshape((image.shape[0], image.shape[1], 1))
  images.append(image)
```

In [8]:

```
for img in benign_images:
  labels.append('B')
  image = cv2.imread(os.path.join(benign_images_path, img), cv2.IMREAD_GRAYSCALE)
  image = image.reshape((image.shape[0], image.shape[1], 1))
  images.append(image)
```

In [9]:

```
for img in malignant_images:
  labels.append('M')
  image = cv2.imread(os.path.join(malignant_images_path, img), cv2.IMREAD_GRAYSCALE)
  image = image.reshape((image.shape[0], image.shape[1], 1))
  images.append(image)
```

In [10]:

```
le = LabelEncoder()
le_labels = to_categorical(le.fit_transform(labels))
```

In [11]:

```
def get_class_count(labels):
  '''
  Get the number of images in each class.
  '''
  num_classes = len(labels[0])
  counts = np.zeros(num_classes)
  for label in labels:
    for i in range(num_classes):
      counts[i] += label[i]
  return counts.tolist()
```

In [12]:

```
def random_shearing(img):
  tf = sk.transform.AffineTransform(shear=random.uniform(-0.3, 0.3))
  return sk.transform.warp(img, tf, order=1, preserve_range=True, mode='wrap')

def random_noise(img):
  return sk.util.random_noise(img)

def random_rotation(img):
  return sk.transform.rotate(img, random.uniform(-30, 30))

def horizontal_flip(img):
  return img[:, ::-1]
```

In [13]:

```
transformation_functions = {
  'shear': random_shearing,
  'rotate': random_rotation,
  'noise': random_noise,
  'horizontal_flip': horizontal_flip,
}
```

In [14]:

```
def transform_images(img, transforms: dict):
  '''
  Perform a random number of image transformations.
  '''
  num_transformations = random.randint(0, len(transforms))
  transformed_image = img
  for i in range(num_transformations):
    key = random.choice(list(transforms))
    transformed_image = transforms[key](img)

  return transformed_image
```

In [15]:

```
def generate_more_images(images, labels, transformation_functions):
  '''
  Determine the number of images needed in each class for balance,
  then transform images to augment.
  '''
  more_images = images
  more_labels = labels

  class_balance = get_class_count(labels)
  img_to_add = [max(class_balance) - i for i in class_balance]

  for i in range(len(img_to_add)):
    if int(img_to_add[i]) == 0:
      continue
    label = np.zeros(len(img_to_add))
    label[i] = 1
    class_label_indices = [i for i, x in enumerate(labels) if np.array_equal(x, label)]
    class_images = [images[i] for i in class_label_indices]

    for k in range(int(img_to_add[i])):
      transformed_image = transform_images(class_images[k % len(class_images)],
transformation_functions)
      transformed_image = transformed_image.reshape(1, transformed_image.shape[0], transformed_imag
e.shape[1], 1)

      more_images = np.append(more_images, transformed_image, axis=0)
      more_labels = np.append(more_labels, label.reshape(1, len(label)), axis=0)
  return more_images, more_labels
```

In [16]:

```
augmented_images, augmented_labels = generate_more_images(images, le_labels,
transformation_functions)
```

In [17]:

```
print('Original number of images: {}'.format(len(augmented_images)))
print('Augmented number of images: {}'.format(len(images)))
```

```
Original number of images: 3948
Augmented number of images: 2616
```

In [ ]:

```
for i in range(len(augmented_images)):
  path = os.path.join(augment_path, augmented_labels[i], 'image' + str(i) + '.jpg')
  cv2.imwrite(path, augmented_images[i])
```

In [4]:

```
from google.colab import drive

drive.mount('/content/gdrive')
```

```
Mounted at /content/gdrive
```

In [5]:

```
%cd /content/gdrive/My Drive/Cornell/2020-2021/Biomedical ML Final Project - Melted Paper/
```

```
/content/gdrive/.shortcut-targets-by-id/13OShW0589KdYJRWaN9GrhtF2vtwdrUUW/Biomedical ML Final
Project - Melted Paper
```

Compile Dataset

Combine images from MIAS, INbreast, DDSM

In [6]:

```
import os, time, cv2, random
import numpy as np
import pandas as pd
```

In [7]:

```
all_mias_path = os.path.join('Datasets', 'archive', 'sam', 'all-mias')
ddsm_path = os.path.join('Datasets', 'archive', 'full-dataset', 'DDSM Dataset')
inbreast_path = os.path.join('Datasets', 'archive', 'full-dataset', 'INbreast Dataset')
final_path = os.path.join('Datasets', 'final-dataset')
```

In [9]:

```
df = pd.read_table(os.path.join(all_mias_path, 'Info.txt'), delimiter=' ')
df.SEVERITY = df.SEVERITY.fillna('N')
lookUp = df[['REFNUM', 'SEVERITY']].set_index('REFNUM').T.to_dict()
df.head()
```

```
/usr/local/lib/python3.6/dist-packages/ipykernel_launcher.py:3: UserWarning: DataFrame columns are
not unique, some columns will be omitted.
  This is separate from the ipykernel package so we can avoid doing imports until
```

Out[9]:

	REFNUM	BG	CLASS	SEVERITY	X	Y	RADIUS	Unnamed: 7
0	mdb001	G	CIRC	B	535.0	425.0	197.0	NaN
1	mdb002	G	CIRC	B	522.0	280.0	69.0	NaN
2	mdb003	D	NORM	N	NaN	NaN	NaN	NaN
3	mdb004	D	NORM	N	NaN	NaN	NaN	NaN
4	mdb005	F	CIRC	B	477.0	133.0	30.0	NaN

In [10]:

```
all_mias = [img for img in os.listdir(all_mias_path) if img.endswith('.jpg')]
ddsm_benign = [img for img in os.listdir(os.path.join(ddsm_path, 'Benign Masses')) if img.endswith(
'.png') and ' ' not in img]
ddsm_malignant = [img for img in os.listdir(os.path.join(ddsm_path, 'Malignant Masses')) if img.end
swith('.png') and ' ' not in img]
inbreast_benign = [img for img in os.listdir(os.path.join(inbreast_path, 'Benign Masses')) if img.e
ndswith('.png') and ' ' not in img]
```

```
inbreast_malignant = [img for img in os.listdir(os.path.join(inbreast_path, 'Malignant Masses')) if
img.endswith('.png') and ' ' not in img]
```

In [14]:

```
print('MIAS Dataset \n --------------')
print('Number of normal images: {}'.format(sum(x['SEVERITY'] == 'N' for x in lookUp.values())))
print('Number of benign images: {}'.format(sum(x['SEVERITY'] == 'B' for x in lookUp.values())))
print('Number of malignant images: {}'.format(sum(x['SEVERITY'] == 'M' for x in lookUp.values())))
print('\nINbreast Dataset \n --------------')
print('Number of benign images: {}'.format(len(inbreast_benign)))
print('Number of malignant images: {}'.format(len(inbreast_malignant)))
print('\nDDSM Dataset \n --------------')
print('Number of benign images: {}'.format(len(ddsm_benign)))
print('Number of malignant images: {}'.format(len(ddsm_malignant)))
```

```
MIAS Dataset
 --------------
Number of normal images: 207
Number of benign images: 63
Number of malignant images: 52

INbreast Dataset
 --------------
Number of benign images: 35
Number of malignant images: 71

DDSM Dataset
 --------------
Number of benign images: 995
Number of malignant images: 1193
```

In [15]:

```
target_size = (224, 224)
```

In [16]:

```
for img in all_mias:
  img_original = cv2.imread(os.path.join(all_mias_path, img))
  img_original = cv2.resize(img_original, target_size)
  label = lookUp[img.split('.')[0]]['SEVERITY']
  cv2.imwrite(os.path.join(final_path, label, img), img_original)
```

In [17]:

```
for img in ddsm_benign:
  img_original = cv2.imread(os.path.join(ddsm_path, 'Benign Masses', img))
  img_original = cv2.resize(img_original, target_size)
  cv2.imwrite(os.path.join(final_path, 'B', img), img_original)
```

In [18]:

```
for img in ddsm_malignant:
  img_original = cv2.imread(os.path.join(ddsm_path, 'Malignant Masses', img))
  img_original = cv2.resize(img_original, target_size)
  cv2.imwrite(os.path.join(final_path, 'M', img), img_original)
```

In [19]:

```
for img in inbreast_benign:
  img_original = cv2.imread(os.path.join(inbreast_path, 'Benign Masses', img))
  img_original = cv2.resize(img_original, target_size)
  cv2.imwrite(os.path.join(final_path, 'B', img), img_original)
```

In [20]:

```
for img in inbreast_malignant:
  img_original = cv2.imread(os.path.join(inbreast_path, 'Malignant Masses', img))
```

```
    img_original = cv2.resize(img_original, target_size)
    cv2.imwrite(os.path.join(final_path, 'M', img), img_original)
```

In [21]:

```
print('Total number of normal images: {}'.format(len(os.listdir(os.path.join(final_path, 'N')))))
print('Total number of benign images: {}'.format(len(os.listdir(os.path.join(final_path, 'B')))))
print('Total number of malignant images: {}'.format(len(os.listdir(os.path.join(final_path,
'M')))))
```

```
207
1093
1316
```

In [ ]:

Setup

In [1]:

```
from google.colab import drive
drive.mount('/content/gdrive')
```

```
Mounted at /content/gdrive
```

In [2]:

```
%cd /content/gdrive/My Drive/Cornell/2020-2021/Biomedical ML Final Project - Melted
Paper/Datasets/archive/all-mias
```

```
/content/gdrive/.shortcut-targets-by-id/13OShW0589KdYJRWaN9GrhtF2vtwdrUUW/Biomedical ML Final
Project - Melted Paper/Datasets/archive/all-mias
```

Baseline Standard ML Classifiers

k-NN, SVM, Random Forest, Logistic Regression, MIAS

Importing Necessary Libraries

In [4]:

```
import numpy as np
import cv2, os, sys, random, pickle, h5py
import matplotlib.pyplot as plt
import matplotlib.image as mpimg
import tensorflow as tf
from tensorflow import keras
import pandas as pd
from sklearn.preprocessing import LabelEncoder
from sklearn.model_selection import train_test_split

import warnings
warnings.filterwarnings(action="ignore", message="^internal gelsd")
```

Importing Labels and Images

Info.txt lists the films in the MIAS database and provides specific information about the images.

- 1st col: MIAS database reference number
- 2nd col: Character of background tissue

```
F - Fatty
G - Fatty-glandular
D - Dense-glandular
```

- 3rd col: Class of abnormality present

```
CALC - Calcification
CIRC - Well-defined/circumscribed masses
SPIC - Spiculated masses
MISC - Other, ill-defined masses
ARCH - Architectural distortion
ASYM - Asymmetry
NORM - Normal
```

- 4th col: Severity of abnormality

```
B - Benign
```

```
        M - Malignant
        N - Normal
```

- 5th, 6th col: (x, y) image coordinates of center of abnormality
- 7th col: Approximate radius (in pixels) of a circle enclosing the abnormality

In [5]:

```
df = pd.read_table('Info.txt', delimiter=' ')
df.SEVERITY = df.SEVERITY.fillna('N')
df = df[df.columns[:-1]]
df.head()
```

Out[5]:

	REFNUM	BG	CLASS	SEVERITY	X	Y	RADIUS
0	mdb001	G	CIRC	B	535.0	425.0	197.0
1	mdb002	G	CIRC	B	522.0	280.0	69.0
2	mdb003	D	NORM	N	NaN	NaN	NaN
3	mdb004	D	NORM	N	NaN	NaN	NaN
4	mdb005	F	CIRC	B	477.0	133.0	30.0

In [6]:

```
# visualizing different classifications
df_grouped = df.groupby(['CLASS','SEVERITY'])[['REFNUM']].count()
df_grouped
```

Out[6]:

		REFNUM
CLASS	**SEVERITY**	
ARCH	**B**	9
	M	10
ASYM	**B**	6
	M	9
CALC	**B**	15
	M	15
CIRC	**B**	21
	M	4
MISC	**B**	7
	M	8
NORM	**N**	207
SPIC	**B**	11
	M	8

LabelEncoder can be used to transform non-numerical labels (as long as they are hashable and comparable) to numerical labels.

In [7]:

```
le = LabelEncoder()
for col in ['BG', 'CLASS', 'SEVERITY']:
    df[col] = le.fit_transform(df[col])
df['RADIUS'] = df['RADIUS'].fillna(-0)
df['X'] = df['X'].fillna(-1)
df['Y'] = df['Y'].fillna(-1)
df.head()
```

Out[7]:

	REFNUM	BG	CLASS	SEVERITY	X	Y	RADIUS
0	mdb001	2	3	0	535.0	425.0	197.0
1	mdb002	2	3	0	522.0	280.0	69.0
2	mdb003	0	5	2	-1.0	-1.0	0.0
3	mdb004	0	5	2	-1.0	-1.0	0.0
4	mdb005	1	3	0	477.0	133.0	30.0

In [8]:

```
# Extracting Features
X = df.drop(columns=['REFNUM','SEVERITY'])
X.head()
```

Out[8]:

	BG	CLASS	X	Y	RADIUS
0	2	3	535.0	425.0	197.0
1	2	3	522.0	280.0	69.0
2	0	5	-1.0	-1.0	0.0
3	0	5	-1.0	-1.0	0.0
4	1	3	477.0	133.0	30.0

In [9]:

```
# Creating target values
y = df['SEVERITY'].values
print(y[0:5])
```

```
[0 0 2 2 0]
```

In [10]:

```
le_name_mapping = dict(zip(le.classes_, le.transform(le.classes_)))
print(le_name_mapping)
```

```
{'B': 0, 'M': 1, 'N': 2}
```

In [11]:

```
#split dataset into train and test data
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=1, stratify=y
)
```

K Nearest Neighbors (referenced https://towardsdatascience.com/building-a-k-nearest-neighbors-k-nn-model-with-scikit-learn-51209555453a)

In [12]:

```
from sklearn.neighbors import KNeighborsClassifier
# Create KNN classifier
knn = KNeighborsClassifier(n_neighbors = 3)
# Fit the classifier to the data
knn.fit(X_train,y_train)
```

Out[12]:

```
KNeighborsClassifier(algorithm='auto', leaf_size=30, metric='minkowski',
                     metric_params=None, n_jobs=None, n_neighbors=3, p=2,
                     weights='uniform')
```

In [13]:

```
#show first 5 model predictions on the test data
knn.predict(X_test)[0:5]
```

Out[13]:

```
array([2, 2, 0, 0, 2])
```

In [15]:

```
#check accuracy of our model on the test data
print('k-NN accuracy: {}'.format(knn.score(X_test, y_test)))
```

```
k-NN accuracy: 0.8939393939393939
```

Logistic Regression

In [19]:

```
from sklearn.linear_model import LogisticRegression
lr = LogisticRegression(random_state = 0)
lr.fit(X_train, y_train)
lr.predict(X_test)[0:5]
print('Logistic regression accuracy: {}'.format(lr.score(X_test,y_test)))
```

```
Logistic regression accuracy: 0.8484848484848485
```

```
/usr/local/lib/python3.6/dist-packages/sklearn/linear_model/_logistic.py:940: ConvergenceWarning:
lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
  extra_warning_msg=_LOGISTIC_SOLVER_CONVERGENCE_MSG)
```

Support Vector Machine

In [20]:

```
from sklearn.svm import SVC
svc = SVC(kernel='linear', random_state=0)
svc.fit(X_train, y_train)
svc.predict(X_test)[0:5]
print('SVM accuracy: {}'.format(svc.score(X_test,y_test)))
```

```
SVM accuracy: 0.803030303030303
```

Random Forest

In [21]:

```
from sklearn.ensemble import RandomForestClassifier
rf = RandomForestClassifier(n_estimators = 10, criterion = 'entropy', random_state =0)
rf.fit(X_train, y_train)
rf.predict(X_test)[0:5]
print('Random forest accuracy: {}'.format(rf.score(X_test,y_test)))
```

```
Random forest accuracy: 0.803030303030303
```

In [ ]:

In [1]:

```
from google.colab import drive

drive.mount('/content/gdrive')
```

```
Mounted at /content/gdrive
```

In [9]:

```
%cd /content/gdrive/My Drive/Courses/ECE/ECE 5970/Biomedical ML Final Project - Melted Paper
```

```
/content/gdrive/.shortcut-targets-by-id/13OShW0589KdYJRWaN9GrhtF2vtwdrUUW/Biomedical ML Final
Project - Melted Paper
```

Baseline Transfer Learning

VGG-16, MIAS

In [10]:

```
import os, time, cv2, random
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import matplotlib.image as mpimg
import seaborn as sns
import skimage as sk
import skimage.transform
from sklearn.metrics import auc, roc_curve
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import LabelEncoder
from sklearn.utils import class_weight
from tensorflow.keras.utils import to_categorical
from tensorflow.keras.optimizers import Adam
from tensorflow.keras.losses import CategoricalCrossentropy
from tensorflow.keras.metrics import CategoricalAccuracy
from tensorflow.keras.applications import VGG19, VGG16
from tensorflow.keras.layers import Concatenate, Dense, Dropout, Flatten, Input
from tensorflow.python.keras import Sequential
```

In [11]:

```
df = pd.read_table('Datasets/archive/all-mias/Info.txt', delimiter=' ')
df.SEVERITY = df.SEVERITY.fillna('N')
lookUp = df[['REFNUM', 'SEVERITY']].set_index('REFNUM').T.to_dict()
df.head(5)
```

```
/usr/local/lib/python3.6/dist-packages/ipykernel_launcher.py:3: UserWarning: DataFrame columns are
not unique, some columns will be omitted.
  This is separate from the ipykernel package so we can avoid doing imports until
```

Out[11]:

	REFNUM	BG	CLASS	SEVERITY	X	Y	RADIUS	Unnamed: 7
0	mdb001	G	CIRC	B	535.0	425.0	197.0	NaN
1	mdb002	G	CIRC	B	522.0	280.0	69.0	NaN
2	mdb003	D	NORM	N	NaN	NaN	NaN	NaN
3	mdb004	D	NORM	N	NaN	NaN	NaN	NaN
4	mdb005	F	CIRC	B	477.0	133.0	30.0	NaN

In [12]:

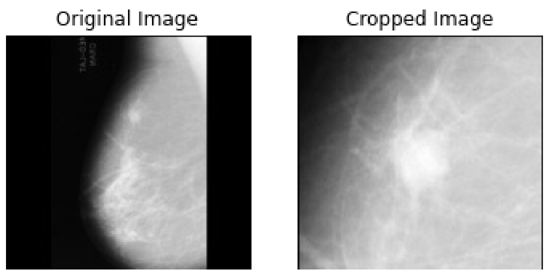
```
def get_roi(path, df, le):
  images, labels = [], []
  lookUp = {}
  for row in df.iterrows():
    # Read the image.
    image = cv2.imread(os.path.join(path, str(row[1][0]) + '.jpg'), cv2.IMREAD_GRAYSCALE)
    image = image.reshape((image.shape[0], image.shape[1], 1))
    label = str(row[1][3])

    # If abnormal, crop around the tumor
    x2, y2 = 0, 0
    edge = image.shape[0] # mias is default 1024x1024
    if label != 'N' and str(row[1][4]) != 'nan':
      x, y = int(row[1][4]), int(row[1][5])
      x1 = x - 112
      if x1 < 0:
        x1, x2 = 0, 224
      if x2 != 224:
        x2 = x + 112
        if x2 > edge:
          x1, x2 = edge - 224, edge

      y1 = edge - y - 112
      if y1 < 0:
        y1, y2 = 0, 224
      else:
        y2 = edge - y + 112
        if y2 > edge:
          y1, y2 = edge - 224, edge

    # Normal case: crop around centre of image.
    else:
      x1, x2 = int(edge / 2 - 112), int(edge / 2 + 112)
      y1, y2 = int(edge / 2 - 112), int(edge / 2 + 112)

    images.append(image[y1:y2, x1:x2, :])
    labels.append(label)
    lookUp[str(row[1][0])] = (image[y1:y2, x1:x2, :], label)

  labels = to_categorical(le.fit_transform(labels))
  return images, labels, lookUp
```

In [13]:

```
le = LabelEncoder()
images, labels, img_dict = get_roi('Datasets/archive/all-mias', df, le)
```

In [14]:

```
mdb023 = mpimg.imread('Datasets/archive/all-mias/mdb023.jpg')
img = img_dict['mdb023'][0]
# display images
fig, ax = plt.subplots(1,2)
ax[0].imshow(mdb023, cmap='gray');
ax[0].set_title('Original Image')
ax[0].get_xaxis().set_visible(False)
ax[0].get_yaxis().set_visible(False)
ax[1].imshow(img.reshape((img.shape[0], img.shape[1])), cmap='gray');
ax[1].set_title('Cropped Image')
ax[1].get_xaxis().set_visible(False)
ax[1].get_yaxis().set_visible(False)
plt.show()
```



In [15]:

```
# 60-20-20 train-val-test split
X_train, X_test, y_train, y_test = train_test_split(images, labels, test_size=0.20, stratify=labels
, shuffle=True)
X_train, X_val, y_train, y_val = train_test_split(X_train, y_train, test_size=0.25, stratify=y_trai
n, shuffle=True)
X_train, X_val, X_test = np.array(X_train), np.array(X_val), np.array(X_test)
y_train, y_val, y_test = np.array(y_train), np.array(y_val), np.array(y_test)
```

In [16]:

```
def calculate_class_weights(y_train, le):
    y_train = le.inverse_transform(np.argmax(y_train, axis=1))
    weights = class_weight.compute_class_weight("balanced", np.unique(y_train), y_train)
    return dict(enumerate(weights))
    # return class_weights
```

In [17]:

```
class_weights = calculate_class_weights(y_train, le)
print(class_weights)
```

```
{0: 1.6097560975609757, 1: 2.0625, 2: 0.528}
```

In [18]:

```
def get_class_count(labels):
  num_classes = len(labels[0])
  counts = np.zeros(num_classes)
  for label in labels:
    for i in range(num_classes):
      counts[i] += label[i]
  return counts.tolist()
```

In [19]:

```
def random_shearing(img):
  tf = sk.transform.AffineTransform(shear=random.uniform(-0.3, 0.3))
  return sk.transform.warp(img, tf, order=1, preserve_range=True, mode='wrap')

def random_noise(img):
  return sk.util.random_noise(img)

def random_rotation(img):
  return sk.transform.rotate(img, random.uniform(-30, 30))

def horizontal_flip(img):
  return img[:, ::-1]
```

In [20]:

```
transformation_functions = {
  'shear': random_shearing,
  'rotate': random_rotation,
  'noise': random_noise,
  'horizontal_flip': horizontal_flip,
}
```

In [21]:

```
def transform_images(img, transforms: dict):
  num_transformations = random.randint(0, len(transforms))
  transformed_image = img
  for i in range(num_transformations):
    key = random.choice(list(transforms))
    transformed_image = transforms[key](img)
  return transformed_image
```

In [22]:

```
def generate_more_images(images, labels, transformation_functions):
  more_images = images
  more_labels = labels

  class_balance = get_class_count(labels)
  img_to_add = [max(class_balance) - i for i in class_balance]

  for i in range(len(img_to_add)):
    if int(img_to_add[i]) == 0:
      continue
    label = np.zeros(len(img_to_add))
    label[i] = 1
    class_label_indices = [i for i, x in enumerate(labels) if np.array_equal(x, label)]
    class_images = [images[i] for i in class_label_indices]

    for k in range(int(img_to_add[i])):
      transformed_image = transform_images(class_images[k % len(class_images)],
transformation_functions)
      transformed_image = transformed_image.reshape(1, 224, 224, 1)

      more_images = np.append(more_images, transformed_image, axis=0)
      more_labels = np.append(more_labels, label.reshape(1, len(label)), axis=0)
  return more_images, more_labels
```

In [23]:

```
y_train_before = y_train
X_train, y_train = generate_more_images(X_train, y_train, transformation_functions)
```

In [24]:

```
print('Training data size BEFORE augmenting: {}'.format(len(y_train_before)))
print('Training data size AFTER augmenting: {}'.format(len(y_train)))
```

```
Training data size BEFORE augmenting: 198
Training data size AFTER augmenting: 375
```

In [25]:

```
def create_vgg16_model():
  input = Input(shape=(224, 224, 1))
  img_conc = Concatenate()([input, input, input])

  # VGG19 model with pre-trained ImageNet weights.
  model = Sequential()

  # Base convolutional layers
  model.add(VGG16(include_top=False, weights="imagenet", input_tensor=img_conc))

  # FC layers
  model.add(Flatten())
  FC = Sequential(name='FullyConnected')
  FC.add(Dropout(0.2, seed=16, name='Dropout'))
  FC.add(Dense(units=512, activation='relu', name='Dense1'))
  FC.add(Dense(units=64, activation='relu', name='Dense2'))
  FC.add(Dense(3, activation='softmax', kernel_initializer="random_uniform", name='Output'))
  model.add(FC)
  print(model.summary())
  print(FC.summary())
  return model
```

In [26]:

```
model_16 = create_vgg16_model()
```

```
Downloading data from https://storage.googleapis.com/tensorflow/keras-
```

```
applications/vgg16/vgg16_weights_tf_dim_ordering_tf_kernels_notop.h5
58892288/58889256 [==============================] - 1s 0us/step
Model: "sequential"
_________________________________________________________________
Layer (type)                 Output Shape              Param #   
=================================================================
vgg16 (Functional)           (None, 7, 7, 512)         14714688  
_________________________________________________________________
flatten (Flatten)            (None, 25088)             0         
_________________________________________________________________
FullyConnected (Sequential)  (None, 3)                 12878595  
=================================================================
Total params: 27,593,283
Trainable params: 27,593,283
Non-trainable params: 0
_________________________________________________________________
None
Model: "FullyConnected"
_________________________________________________________________
Layer (type)                 Output Shape              Param #   
=================================================================
Dropout (Dropout)            (None, 25088)             0         
_________________________________________________________________
Dense1 (Dense)               (None, 512)               12845568  
_________________________________________________________________
Dense2 (Dense)               (None, 64)                32832     
_________________________________________________________________
Output (Dense)               (None, 3)                 195       
=================================================================
Total params: 12,878,595
Trainable params: 12,878,595
Non-trainable params: 0
_________________________________________________________________
None
```

In [27]:

```
batch_size=20
max_epoch_frozen=20
max_epoch_unfrozen=20

def train_model(model, X_train, X_val, y_train, y_val, class_weights, epoch, batch_size):
  # Only train fully connected layers by freezing CNN layers
  model.layers[0].trainable = False
  compile_model(model, 1e-5)
  history1 = fit_model(model, X_train, X_val, y_train, y_val, class_weights, epoch, batch_size)
  training_results(history1, frozen=True)

  return history1

def compile_model(model, learning_rate):
  model.compile(optimizer=Adam(learning_rate), loss=CategoricalCrossentropy(),
metrics=[CategoricalAccuracy()])

def fit_model(model, X_train, X_val, y_train, y_val, class_weights, epoch, batch_size):
  history = model.fit(
      x=X_train,
      y=y_train,
      class_weight=class_weights,
      batch_size=batch_size,
      steps_per_epoch=len(X_train) // batch_size,
      validation_data=(X_val, y_val),
      validation_steps=len(X_val) // batch_size,
      epochs=epoch,
  )
  return history
```

In [28]:

```
def training_results(history, frozen) -> None:
  fig = plt.figure()
  n = len(history.history["loss"])
  plt.figure()
  plt.plot(np.arange(0, n), history.history["loss"], label="train set")
  plt.plot(np.arange(0, n), history.history["val_loss"], label="validation set")
```

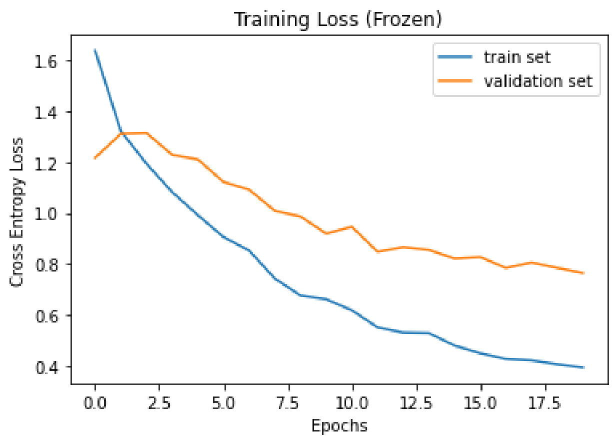
```
    plt.title('Training Loss ' + ('(Frozen)' if frozen else '(Unfrozen)'))
    plt.legend(loc='upper right')
    plt.xlabel('Epochs')
    plt.ylabel('Cross Entropy Loss')
    plt.savefig('output/training-loss-baseline.png')
    plt.show()

    fig = plt.figure()
    n = len(history.history["loss"])
    plt.figure()
    plt.plot(np.arange(0, n), history.history["categorical_accuracy"], label="train set")
    plt.plot(np.arange(0, n), history.history["val_categorical_accuracy"], label="validation set")
    plt.title('Training Accuracy ' + ('(Frozen)' if frozen else '(Unfrozen)'))
    plt.legend(loc='upper right')
    plt.xlabel('Epochs')
    plt.ylabel("Accuracy")
    plt.ylim(0, 1)
    plt.savefig('output/training-accuracy-baseline.png')
    plt.show()
```

In [29]:

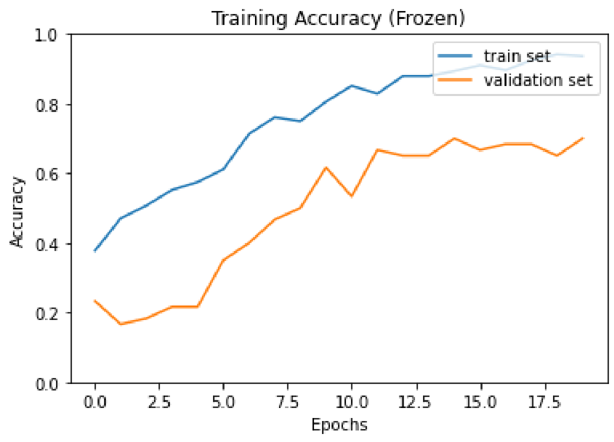
```
batch_size = 20
max_epoch = 20
history_frozen = train_model(model_16, X_train, X_val, y_train, y_val, class_weights, max_epoch, ba
tch_size)
```

```
Epoch 1/20
18/18 [==============================] - 2s 121ms/step - loss: 1.6364 - categorical_accuracy: 0.37
78 - val_loss: 1.2166 - val_categorical_accuracy: 0.2333
Epoch 2/20
18/18 [==============================] - 2s 102ms/step - loss: 1.3206 - categorical_accuracy: 0.47
04 - val_loss: 1.3106 - val_categorical_accuracy: 0.1667
Epoch 3/20
18/18 [==============================] - 2s 101ms/step - loss: 1.1933 - categorical_accuracy: 0.50
70 - val_loss: 1.3134 - val_categorical_accuracy: 0.1833
Epoch 4/20
18/18 [==============================] - 2s 102ms/step - loss: 1.0819 - categorical_accuracy: 0.55
21 - val_loss: 1.2280 - val_categorical_accuracy: 0.2167
Epoch 5/20
18/18 [==============================] - 2s 101ms/step - loss: 0.9913 - categorical_accuracy: 0.57
46 - val_loss: 1.2103 - val_categorical_accuracy: 0.2167
Epoch 6/20
18/18 [==============================] - 2s 101ms/step - loss: 0.9058 - categorical_accuracy: 0.61
13 - val_loss: 1.1217 - val_categorical_accuracy: 0.3500
Epoch 7/20
18/18 [==============================] - 2s 101ms/step - loss: 0.8524 - categorical_accuracy: 0.71
27 - val_loss: 1.0913 - val_categorical_accuracy: 0.4000
Epoch 8/20
18/18 [==============================] - 2s 102ms/step - loss: 0.7426 - categorical_accuracy: 0.76
06 - val_loss: 1.0083 - val_categorical_accuracy: 0.4667
Epoch 9/20
18/18 [==============================] - 2s 102ms/step - loss: 0.6767 - categorical_accuracy: 0.74
93 - val_loss: 0.9861 - val_categorical_accuracy: 0.5000
Epoch 10/20
18/18 [==============================] - 2s 102ms/step - loss: 0.6618 - categorical_accuracy: 0.80
56 - val_loss: 0.9192 - val_categorical_accuracy: 0.6167
Epoch 11/20
18/18 [==============================] - 2s 102ms/step - loss: 0.6187 - categorical_accuracy: 0.85
07 - val_loss: 0.9462 - val_categorical_accuracy: 0.5333
Epoch 12/20
18/18 [==============================] - 2s 103ms/step - loss: 0.5516 - categorical_accuracy: 0.82
82 - val_loss: 0.8481 - val_categorical_accuracy: 0.6667
Epoch 13/20
18/18 [==============================] - 2s 103ms/step - loss: 0.5309 - categorical_accuracy: 0.87
89 - val_loss: 0.8661 - val_categorical_accuracy: 0.6500
Epoch 14/20
18/18 [==============================] - 2s 103ms/step - loss: 0.5291 - categorical_accuracy: 0.87
89 - val_loss: 0.8553 - val_categorical_accuracy: 0.6500
Epoch 15/20
18/18 [==============================] - 2s 103ms/step - loss: 0.4800 - categorical_accuracy: 0.89
30 - val_loss: 0.8213 - val_categorical_accuracy: 0.7000
Epoch 16/20
18/18 [==============================] - 2s 104ms/step - loss: 0.4500 - categorical_accuracy: 0.90
99 - val_loss: 0.8272 - val_categorical_accuracy: 0.6667
```

```
Epoch 17/20
18/18 [==============================] - 2s 105ms/step - loss: 0.4279 - categorical_accuracy: 0.89
58 - val_loss: 0.7846 - val_categorical_accuracy: 0.6833
Epoch 18/20
18/18 [==============================] - 2s 104ms/step - loss: 0.4222 - categorical_accuracy: 0.92
39 - val_loss: 0.8058 - val_categorical_accuracy: 0.6833
Epoch 19/20
18/18 [==============================] - 2s 104ms/step - loss: 0.4071 - categorical_accuracy: 0.94
08 - val_loss: 0.7848 - val_categorical_accuracy: 0.6500
Epoch 20/20
18/18 [==============================] - 2s 107ms/step - loss: 0.3943 - categorical_accuracy: 0.93
61 - val_loss: 0.7645 - val_categorical_accuracy: 0.7000


<Figure size 432x288 with 0 Axes>
```



```
<Figure size 432x288 with 0 Axes>
```



In [30]:

```
from sklearn.metrics import accuracy_score, confusion_matrix
def evaluate_model(prediction, y_true, le):
  true_y = le.inverse_transform(np.argmax(y_true, axis=1))
  pred_y = le.inverse_transform(np.argmax(prediction, axis=1))

  # Calculate accuracy
  accuracy = float('{:.4f}'.format(accuracy_score(true_y, pred_y)))
  print("Accuracy = {}\n".format(accuracy))

  cm = confusion_matrix(true_y, pred_y)
  cm_norm = cm.astype('float') / cm.sum(axis=1)[:, np.newaxis]
  cm_norm[np.isnan(cm_norm)] = 0
  plot_confusion_matrix(cm_norm, le)
```

In [31]:

```
def plot_confusion_matrix(cm, le):
  fig, ax = plt.subplots(figsize=(6, 4))
  sns.heatmap(cm, annot=True, ax=ax, fmt='.2f', cmap=plt.cm.Blues, vmin=0, vmax=1)  # annot=True to
```

```
annotate cells

  # Set labels, title, ticks and axis range.
  ax.set_xlabel('Predicted Classes')
  ax.set_ylabel('True Classes')
  ax.set_title('Confusion Matrix')
  ax.xaxis.set_ticklabels(le.classes_)
  ax.yaxis.set_ticklabels(le.classes_)
  plt.tight_layout()
  bottom, top = ax.get_ylim()
  plt.show()
  plt.savefig('output/confusion_mat.png')
```

In [36]:

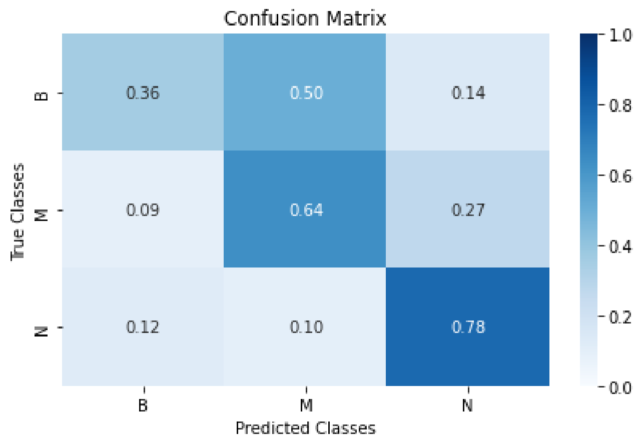
```
def plot_roc(y_true, y_pred, le):
  fpr, tpr, roc_auc = {}, {}, {}

  for i in range(le.classes_.size):
      fpr[i], tpr[i], _ = roc_curve(y_true[:, i], y_pred[:, i])
      roc_auc[i] = auc(fpr[i], tpr[i])

  all_fpr = np.unique(np.concatenate([fpr[i] for i in range(len(le.classes_))]))

  mean_tpr = np.zeros_like(all_fpr)
  for i in range(le.classes_.size):
      mean_tpr += np.interp(all_fpr, fpr[i], tpr[i])

  mean_tpr /= le.classes_.size

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

  fpr['micro'], tpr['micro'], _ = roc_curve(y_true.ravel(), y_pred.ravel())
  roc_auc['micro'] = auc(fpr['micro'], tpr['micro'])
  plt.figure(figsize=(8, 5))

  plt.plot([0, 1], [0, 1], 'k--', color='black', lw=2)
  plt.annotate('Random Guess', (.54, .49), color='black')

  plt.plot(fpr['micro'], tpr['micro'],
           label='Micro-Average ROC curve (area = {0:0.2f})'
                 ''.format(roc_auc["micro"]),
           color='red', linestyle=':', lw=3)

  plt.plot(fpr['macro'], tpr['macro'],
           label='Macro-Average ROC curve (area = {0:0.2f})'
                 ''.format(roc_auc['macro']),
           color='black', linestyle=':', lw=3)

  colors = ['#3972ba', '#ab923e', '#3bb300']
  for i, color in zip(range(len(le.classes_)), colors):
      plt.plot(fpr[i], tpr[i], color=color, lw=2,
               label='ROC of Class {0} (area = {1:0.2f})'
                     ''.format(le.classes_[i], roc_auc[i]))

  plt.xlim([0.0, 1.0])
  plt.ylim([0.0, 1.0])
  plt.xlabel('False Positive Rate')
  plt.ylabel('True Positive Rate')
  plt.title('ROC Curve')
  plt.legend(loc='lower right')
  plt.savefig('output/ROC.png')
  plt.show()

  plt.figure(figsize=(8, 5))
  plt.plot(fpr['micro'], tpr['micro'],
           label='Micro-Average ROC curve (area = {0:0.2f})'
                 ''.format(roc_auc["micro"]),
           color='red', linestyle=':', lw=3)

  plt.plot(fpr['macro'], tpr['macro'],
           label='Macro-Average ROC curve (area = {0:0.2f})'
                 ''.format(roc_auc['macro']),
           color='black', linestyle=':', lw=3)
```

```
colors = ['#3972ba', '#ab923e', '#3bb300']
for i, color in zip(range(len(le.classes_)), colors):
    plt.plot(fpr[i], tpr[i], color=color, lw=2,
             label='ROC of Class {0} (area = {1:0.2f})'
                   ''.format(le.classes_[i], roc_auc[i]))

plt.xlim(0, 0.2)
plt.ylim(0.8, 1)
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('ROC Curve (Top Left)')
plt.legend(loc='lower right')
plt.savefig('output/ROC-top-left.png')
plt.show()
```

In [32]:

```
# validation
prediction = model_16.predict(X_val, batch_size=20)
evaluate_model(prediction, y_val, le)
```

```
Accuracy = 0.6667
```



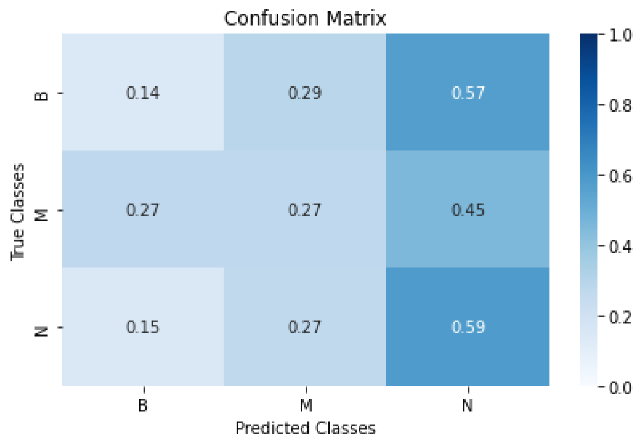
```
<Figure size 432x288 with 0 Axes>
```

Testing

In [33]:

```
predictions = model_16.predict(x=X_test)
evaluate_model(prediction, y_test, le)
```

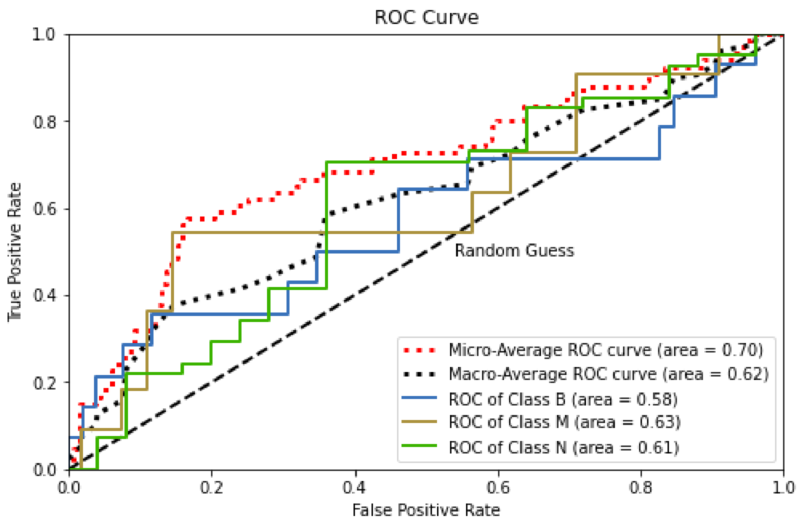
```
Accuracy = 0.4394
```

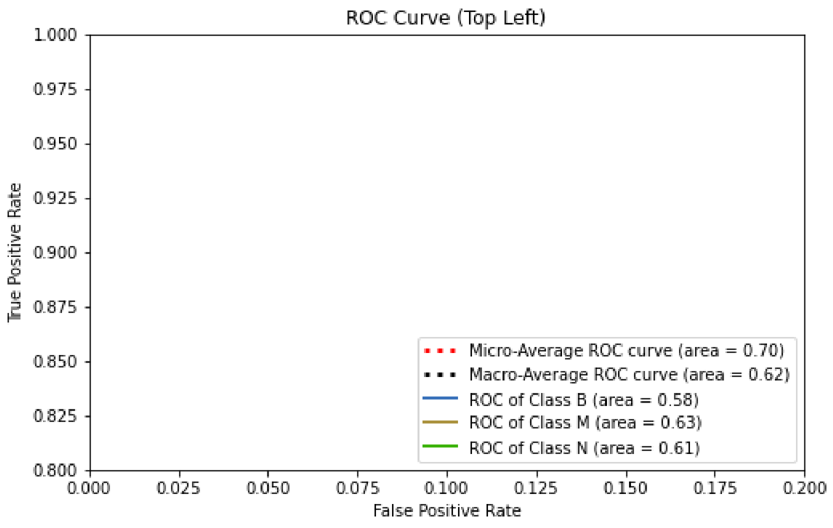


```
<Figure size 432x288 with 0 Axes>
```

In [37]:

```
plot_roc(y_test, predictions, le)
```





In [1]:

```
from google.colab import drive

drive.mount('/content/gdrive')
```

```
Mounted at /content/gdrive
```

In [2]:

```
%cd /content/gdrive/My Drive/Courses/ECE/ECE 5970/Biomedical ML Final Project - Melted Paper
```

```
/content/gdrive/My Drive/Courses/ECE/ECE 5970/Biomedical ML Final Project - Melted Paper
```

Final Transfer Learning Model

VGG-16, MIAS, DDSM, INbreast

In [3]:

```
import os, time, cv2, random
import matplotlib.pyplot as plt
import matplotlib.image as mpimg
import numpy as np
import pandas as pd
import seaborn as sns
from sklearn.metrics import auc, roc_curve
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import LabelEncoder
from sklearn.utils import class_weight
from tensorflow.keras.applications import VGG19, VGG16
from tensorflow.python.keras import Sequential, regularizers
from tensorflow.keras.layers import Concatenate, Dense, Dropout, Flatten, Input
from tensorflow.keras.losses import CategoricalCrossentropy
from tensorflow.keras.optimizers import Adam
from tensorflow.keras.metrics import CategoricalAccuracy
from tensorflow.keras.utils import to_categorical
```

In [4]:

```
normal_images_path = os.path.join('Datasets', 'final-dataset-augment', 'N')
benign_images_path = os.path.join('Datasets', 'final-dataset-augment', 'B')
malignant_images_path = os.path.join('Datasets', 'final-dataset-augment', 'M')
```

In [5]:

```
normal_images = os.listdir(normal_images_path)
benign_images = os.listdir(benign_images_path)
malignant_images = os.listdir(malignant_images_path)
```

In [6]:

```
images, labels = [], []
```

In [7]:

```
for img in normal_images:
  labels.append('N')
  image = cv2.imread(os.path.join(normal_images_path, img), cv2.IMREAD_GRAYSCALE)
  image = image.reshape((image.shape[0], image.shape[1], 1))
  images.append(image)
```

In [8]:

```
for img in benign_images:
  labels.append('B')
  image = cv2.imread(os.path.join(benign_images_path, img), cv2.IMREAD_GRAYSCALE)
  image = image.reshape((image.shape[0], image.shape[1], 1))
  images.append(image)
```

In [9]:

```
for img in malignant_images:
  labels.append('M')
  image = cv2.imread(os.path.join(malignant_images_path, img), cv2.IMREAD_GRAYSCALE)
  image = image.reshape((image.shape[0], image.shape[1], 1))
  images.append(image)
```

In [10]:

```
le = LabelEncoder()
labels = to_categorical(le.fit_transform(labels))
```

Split Data 60-20-20 for training-validation-testing

In [11]:

```
X_train, X_test, y_train, y_test = train_test_split(images, labels, test_size=0.20, stratify=labels
, shuffle=True)
X_train, X_val, y_train, y_val = train_test_split(X_train, y_train, test_size=0.25, stratify=y_trai
n, shuffle=True)
X_train, X_val, X_test = np.array(X_train), np.array(X_val), np.array(X_test)
y_train, y_val, y_test = np.array(y_train), np.array(y_val), np.array(y_test)
```

In [12]:

```
print(len(y_train), len(y_test), len(y_val))
```

```
2316 773 773
```

In [13]:

```
def calculate_class_weights(y_train, le):
  y_train = le.inverse_transform(np.argmax(y_train, axis=1))
  weights = class_weight.compute_class_weight("balanced", np.unique(y_train), y_train)
  return dict(enumerate(weights))
  # return class_weights
```

In [14]:

```
class_weights = calculate_class_weights(y_train, le)
print(class_weights)
```

```
{0: 1.0052083333333333, 1: 0.9784537389100126, 2: 1.0171277997364954}
```

VGG16 with L1L2 Regularization

In [15]:

```
def create_vgg16_model():
  input = Input(shape=(224, 224, 1))
  img_conc = Concatenate()([input, input, input])

  # VGG19 model with pre-trained ImageNet weights.
  model = Sequential()

  # Base convolutional layers
  model.add(VGG16(include_top=False, weights="imagenet", input_tensor=img_conc))

  # FC layers
  model.add(Flatten())
  FC = Sequential(name='FullyConnected')
  FC.add(Dense(units=512, kernel_regularizer=regularizers.l1_l2(l1=.001,l2=.001), activation='relu'
, name='Dense1'))
  FC.add(Dense(3, activation='sigmoid', kernel_initializer="random_uniform", name='Output'))
  model.add(FC)
  print(model.summary())
  print(FC.summary())
  return model
```

In [16]:

```
model = create_vgg16_model()
```

```
Downloading data from https://storage.googleapis.com/tensorflow/keras-
applications/vgg16/vgg16_weights_tf_dim_ordering_tf_kernels_notop.h5
58892288/58889256 [==============================] - 1s 0us/step
Model: "sequential"
_________________________________________________________________
Layer (type)                 Output Shape              Param #   
=================================================================
vgg16 (Functional)           (None, 7, 7, 512)         14714688  
_________________________________________________________________
flatten (Flatten)            (None, 25088)             0         
_________________________________________________________________
FullyConnected (Sequential)  (None, 3)                 12847107  
=================================================================
Total params: 27,561,795
Trainable params: 27,561,795
Non-trainable params: 0
_________________________________________________________________
None
Model: "FullyConnected"
_________________________________________________________________
Layer (type)                 Output Shape              Param #   
=================================================================
Dense1 (Dense)               (None, 512)               12845568  
_________________________________________________________________
Output (Dense)               (None, 3)                 1539      
=================================================================
Total params: 12,847,107
Trainable params: 12,847,107
Non-trainable params: 0
_________________________________________________________________
None
```

In [17]:

```
def train_model(model, X_train, X_val, y_train, y_val, class_weights, epoch, batch_size, title=""):
  # Only train fully connected layers by freezing CNN layers
  model.layers[0].trainable = False
  compile_model(model, 1e-5)
  history1 = fit_model(model, X_train, X_val, y_train, y_val, class_weights, epoch, batch_size)
  training_results(history1, True, title)

  # Unfreeze all layers
  model.layers[0].trainable = True
  compile_model(model, 1e-5)
  history2 = fit_model(model, X_train, X_val, y_train, y_val, class_weights, epoch, batch_size)
  training_results(history2, False, title)

  return history1, history2

def compile_model(model, learning_rate):
  model.compile(optimizer=Adam(learning_rate), loss=CategoricalCrossentropy(),
metrics=[CategoricalAccuracy()])

def fit_model(model, X_train, X_val, y_train, y_val, class_weights, epoch, batch_size):
  history = model.fit(
      x=X_train,
      y=y_train,
      class_weight=class_weights,
      batch_size=batch_size,
      steps_per_epoch=len(X_train) // batch_size,
      validation_data=(X_val, y_val),
      validation_steps=len(X_val) // batch_size,
      epochs=epoch,
  )
  return history
```

In [18]:

```
def training_results(history, frozen, title):
    fig = plt.figure()
    n = len(history.history["loss"])
    plt.figure()
    plt.plot(np.arange(0, n), history.history["loss"], label="train set")
    plt.plot(np.arange(0, n), history.history["val_loss"], label="validation set")
    plt.title('Training Loss' + (' (Frozen)' if frozen else ' (Unfrozen)'))
    plt.legend(loc='upper right')
    plt.xlabel('Epochs')
    plt.ylabel('Cross Entropy Loss')
    plt.savefig('output/training-loss-' + str(frozen) + '-' + title + '.png')
    plt.show()

    fig = plt.figure()
    n = len(history.history["loss"])
    plt.figure()
    plt.plot(np.arange(0, n), history.history["categorical_accuracy"], label="train set")
    plt.plot(np.arange(0, n), history.history["val_categorical_accuracy"], label="validation set")
    plt.title('Training Accuracy ' + ('(Frozen)' if frozen else '(Unfrozen)'))
    plt.legend(loc='upper right')
    plt.xlabel('Epochs')
    plt.ylabel("Accuracy")
    plt.ylim(0, 1)
    plt.savefig('output/training-accuracy-' + str(frozen) + '-' + title + '.png')
    plt.show()
```

In [19]:

```
from sklearn.metrics import accuracy_score, confusion_matrix
def evaluate_model(prediction, y_true, le, title=""):
    true_y = le.inverse_transform(np.argmax(y_true, axis=1))
    pred_y = le.inverse_transform(np.argmax(prediction, axis=1))
    print(len(pred_y))
    # Calculate accuracy
    accuracy = float('{:.4f}'.format(accuracy_score(true_y, pred_y)))
    print("Accuracy = {}\n".format(accuracy))

    cm = confusion_matrix(true_y, pred_y)
    cm_norm = cm.astype('float') / cm.sum(axis=1)[:, np.newaxis]
    cm_norm[np.isnan(cm_norm)] = 0
    plot_confusion_matrix(cm_norm, le, title)
```

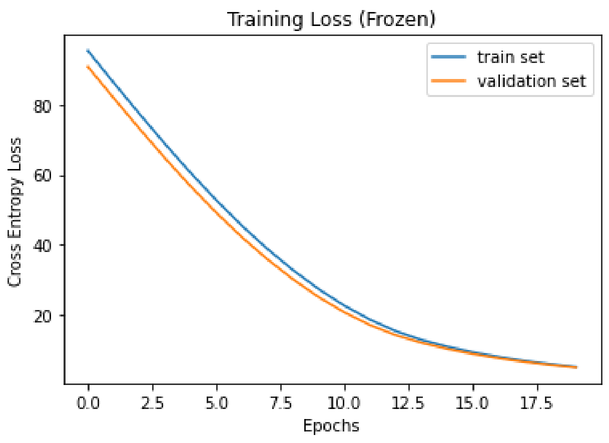
In [20]:

```
batch_size = 20
max_epoch = 20
history_frozen, history_unfrozen = train_model(model, X_train, X_val, y_train, y_val, class_weights
, max_epoch, batch_size, '-l2=0.01')
```

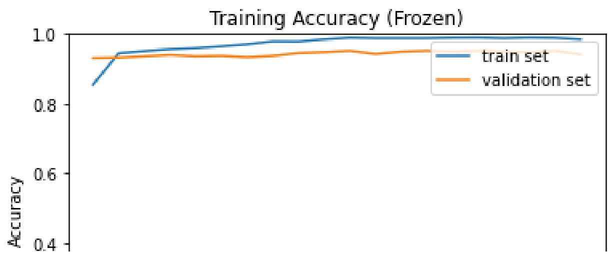
```
Epoch 1/20
115/115 [==============================] - 14s 122ms/step - loss: 95.4280 - categorical_accuracy:
0.8539 - val_loss: 90.8369 - val_categorical_accuracy: 0.9303
Epoch 2/20
115/115 [==============================] - 14s 123ms/step - loss: 86.3343 - categorical_accuracy:
0.9443 - val_loss: 81.9584 - val_categorical_accuracy: 0.9316
Epoch 3/20
115/115 [==============================] - 14s 123ms/step - loss: 77.4560 - categorical_accuracy:
0.9503 - val_loss: 73.1924 - val_categorical_accuracy: 0.9355
Epoch 4/20
115/115 [==============================] - 14s 125ms/step - loss: 68.8088 - categorical_accuracy:
0.9560 - val_loss: 64.7476 - val_categorical_accuracy: 0.9395
Epoch 5/20
115/115 [==============================] - 15s 126ms/step - loss: 60.5226 - categorical_accuracy:
0.9591 - val_loss: 56.6818 - val_categorical_accuracy: 0.9355
Epoch 6/20
115/115 [==============================] - 15s 128ms/step - loss: 52.6966 - categorical_accuracy:
```

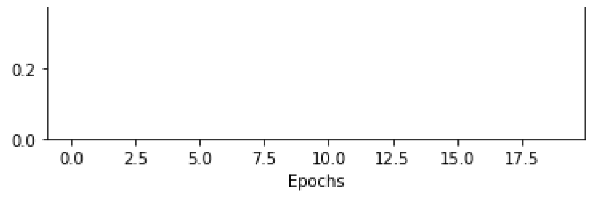
```
0.9643 - val_loss: 49.1168 - val_categorical_accuracy: 0.9368
Epoch 7/20
115/115 [==============================] - 15s 130ms/step - loss: 45.4051 - categorical_accuracy:
0.9699 - val_loss: 42.1260 - val_categorical_accuracy: 0.9329
Epoch 8/20
115/115 [==============================] - 15s 132ms/step - loss: 38.7062 - categorical_accuracy:
0.9782 - val_loss: 35.7482 - val_categorical_accuracy: 0.9368
Epoch 9/20
115/115 [==============================] - 15s 133ms/step - loss: 32.6363 - categorical_accuracy:
0.9778 - val_loss: 29.9990 - val_categorical_accuracy: 0.9447
Epoch 10/20
115/115 [==============================] - 15s 134ms/step - loss: 27.2281 - categorical_accuracy:
0.9843 - val_loss: 24.9445 - val_categorical_accuracy: 0.9474
Epoch 11/20
115/115 [==============================] - 15s 134ms/step - loss: 22.5098 - categorical_accuracy:
0.9891 - val_loss: 20.5992 - val_categorical_accuracy: 0.9513
Epoch 12/20
115/115 [==============================] - 16s 137ms/step - loss: 18.5088 - categorical_accuracy:
0.9878 - val_loss: 16.9545 - val_categorical_accuracy: 0.9421
Epoch 13/20
115/115 [==============================] - 16s 138ms/step - loss: 15.2521 - categorical_accuracy:
0.9878 - val_loss: 14.0905 - val_categorical_accuracy: 0.9487
Epoch 14/20
115/115 [==============================] - 16s 139ms/step - loss: 12.7495 - categorical_accuracy:
0.9878 - val_loss: 11.9355 - val_categorical_accuracy: 0.9513
Epoch 15/20
115/115 [==============================] - 16s 139ms/step - loss: 10.8281 - categorical_accuracy:
0.9891 - val_loss: 10.1889 - val_categorical_accuracy: 0.9487
Epoch 16/20
115/115 [==============================] - 16s 139ms/step - loss: 9.2512 - categorical_accuracy: 0
.9895 - val_loss: 8.7588 - val_categorical_accuracy: 0.9513
Epoch 17/20
115/115 [==============================] - 16s 139ms/step - loss: 7.9262 - categorical_accuracy: 0
.9878 - val_loss: 7.5420 - val_categorical_accuracy: 0.9487
Epoch 18/20
115/115 [==============================] - 16s 139ms/step - loss: 6.8079 - categorical_accuracy: 0
.9895 - val_loss: 6.5113 - val_categorical_accuracy: 0.9474
Epoch 19/20
115/115 [==============================] - 16s 139ms/step - loss: 5.8648 - categorical_accuracy: 0
.9887 - val_loss: 5.6345 - val_categorical_accuracy: 0.9513
Epoch 20/20
115/115 [==============================] - 16s 139ms/step - loss: 5.0551 - categorical_accuracy: 0
.9843 - val_loss: 4.8965 - val_categorical_accuracy: 0.9408
```

```
<Figure size 432x288 with 0 Axes>
```



```
<Figure size 432x288 with 0 Axes>
```

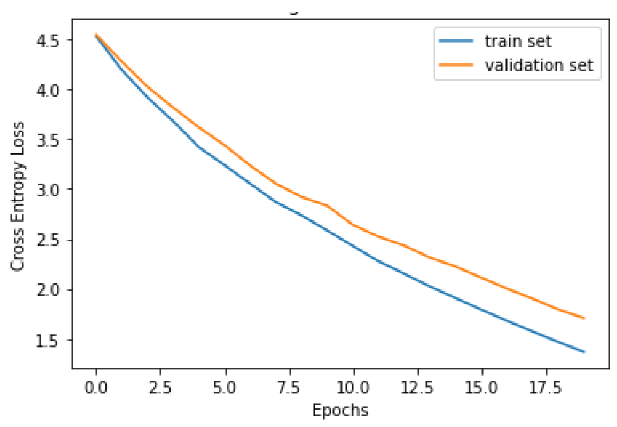




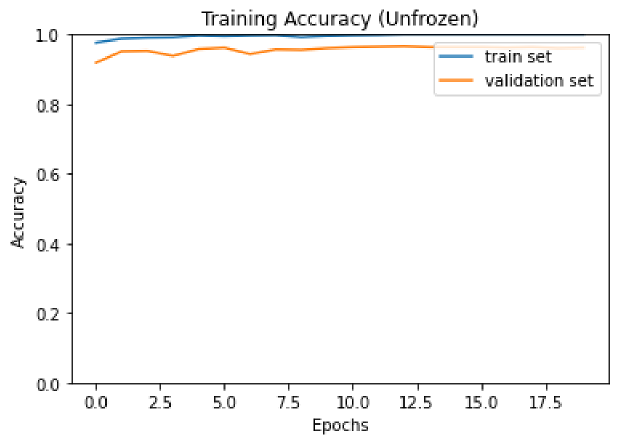
```
Epoch 1/20
  2/115 [.............................] - ETA: 18s - loss: 4.7241 - categorical_accuracy:
1.0000WARNING:tensorflow:Callbacks method `on_train_batch_end` is slow compared to the batch time
(batch time: 0.1058s vs `on_train_batch_end` time: 0.2187s). Check your callbacks.
115/115 [==============================] - 40s 347ms/step - loss: 4.5306 - categorical_accuracy: 0
.9761 - val_loss: 4.5458 - val_categorical_accuracy: 0.9184
Epoch 2/20
115/115 [==============================] - 40s 344ms/step - loss: 4.1914 - categorical_accuracy: 0
.9878 - val_loss: 4.2751 - val_categorical_accuracy: 0.9513
Epoch 3/20
115/115 [==============================] - 40s 346ms/step - loss: 3.9180 - categorical_accuracy: 0
.9904 - val_loss: 4.0244 - val_categorical_accuracy: 0.9526
Epoch 4/20
115/115 [==============================] - 40s 345ms/step - loss: 3.6786 - categorical_accuracy: 0
.9913 - val_loss: 3.8157 - val_categorical_accuracy: 0.9382
Epoch 5/20
115/115 [==============================] - 40s 344ms/step - loss: 3.4200 - categorical_accuracy: 0
.9970 - val_loss: 3.6167 - val_categorical_accuracy: 0.9579
Epoch 6/20
115/115 [==============================] - 40s 345ms/step - loss: 3.2401 - categorical_accuracy: 0
.9948 - val_loss: 3.4402 - val_categorical_accuracy: 0.9618
Epoch 7/20
115/115 [==============================] - 40s 345ms/step - loss: 3.0535 - categorical_accuracy: 0
.9970 - val_loss: 3.2359 - val_categorical_accuracy: 0.9434
Epoch 8/20
115/115 [==============================] - 40s 345ms/step - loss: 2.8692 - categorical_accuracy: 0
.9978 - val_loss: 3.0546 - val_categorical_accuracy: 0.9566
Epoch 9/20
115/115 [==============================] - 40s 344ms/step - loss: 2.7367 - categorical_accuracy: 0
.9917 - val_loss: 2.9212 - val_categorical_accuracy: 0.9553
Epoch 10/20
115/115 [==============================] - 40s 346ms/step - loss: 2.5842 - categorical_accuracy: 0
.9956 - val_loss: 2.8321 - val_categorical_accuracy: 0.9605
Epoch 11/20
115/115 [==============================] - 40s 345ms/step - loss: 2.4297 - categorical_accuracy: 0
.9974 - val_loss: 2.6413 - val_categorical_accuracy: 0.9632
Epoch 12/20
115/115 [==============================] - 39s 343ms/step - loss: 2.2757 - categorical_accuracy: 0
.9983 - val_loss: 2.5224 - val_categorical_accuracy: 0.9645
Epoch 13/20
115/115 [==============================] - 39s 342ms/step - loss: 2.1514 - categorical_accuracy: 1
.0000 - val_loss: 2.4331 - val_categorical_accuracy: 0.9658
Epoch 14/20
115/115 [==============================] - 39s 341ms/step - loss: 2.0245 - categorical_accuracy: 1
.0000 - val_loss: 2.3129 - val_categorical_accuracy: 0.9632
Epoch 15/20
115/115 [==============================] - 39s 341ms/step - loss: 1.9081 - categorical_accuracy: 1
.0000 - val_loss: 2.2236 - val_categorical_accuracy: 0.9632
Epoch 16/20
115/115 [==============================] - 39s 340ms/step - loss: 1.7924 - categorical_accuracy: 1
.0000 - val_loss: 2.1131 - val_categorical_accuracy: 0.9632
Epoch 17/20
115/115 [==============================] - 39s 340ms/step - loss: 1.6806 - categorical_accuracy: 1
.0000 - val_loss: 2.0033 - val_categorical_accuracy: 0.9618
Epoch 18/20
115/115 [==============================] - 39s 339ms/step - loss: 1.5729 - categorical_accuracy: 1
.0000 - val_loss: 1.9023 - val_categorical_accuracy: 0.9632
Epoch 19/20
115/115 [==============================] - 39s 339ms/step - loss: 1.4684 - categorical_accuracy: 1
.0000 - val_loss: 1.7943 - val_categorical_accuracy: 0.9605
Epoch 20/20
115/115 [==============================] - 39s 339ms/step - loss: 1.3689 - categorical_accuracy: 1
.0000 - val_loss: 1.7078 - val_categorical_accuracy: 0.9618
```

```
<Figure size 432x288 with 0 Axes>
```

Training Loss (Unfrozen)



```
<Figure size 432x288 with 0 Axes>
```



In [21]:

```python
def plot_roc(y_true, y_pred, le):
  fpr, tpr, roc_auc = {}, {}, {}

  for i in range(le.classes_.size):
      fpr[i], tpr[i], _ = roc_curve(y_true[:, i], y_pred[:, i])
      roc_auc[i] = auc(fpr[i], tpr[i])

  all_fpr = np.unique(np.concatenate([fpr[i] for i in range(len(le.classes_))]))

  mean_tpr = np.zeros_like(all_fpr)
  for i in range(le.classes_.size):
      mean_tpr += np.interp(all_fpr, fpr[i], tpr[i])

  mean_tpr /= le.classes_.size

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

  fpr['micro'], tpr['micro'], _ = roc_curve(y_true.ravel(), y_pred.ravel())
  roc_auc['micro'] = auc(fpr['micro'], tpr['micro'])
  plt.figure(figsize=(8, 5))

  plt.plot([0, 1], [0, 1], 'k--', color='black', lw=2)
  plt.annotate('Random Guess', (.54, .49), color='black')

  plt.plot(fpr['micro'], tpr['micro'],
           label='Micro-Average ROC curve (area = {0:0.2f})'
                 ''.format(roc_auc["micro"]),
           color='red', linestyle=':', lw=3)

  plt.plot(fpr['macro'], tpr['macro'],
           label='Macro-Average ROC curve (area = {0:0.2f})'
                 ''.format(roc_auc['macro']),
           color='black', linestyle=':', lw=3)

  colors = ['#3972ba', '#ab923e', '#3bb300']
```

```
    for i, color in zip(range(len(le.classes_)), colors):
        plt.plot(fpr[i], tpr[i], color=color, lw=2,
                 label='ROC of Class {0} (area = {1:0.2f})'
                       ''.format(le.classes_[i], roc_auc[i]))

    plt.xlim([0.0, 1.0])
    plt.ylim([0.0, 1.0])
    plt.xlabel('False Positive Rate')
    plt.ylabel('True Positive Rate')
    plt.title('ROC Curve')
    plt.legend(loc='lower right')
    plt.savefig('output/ROC.png')
    plt.show()

    plt.figure(figsize=(8, 5))
    plt.plot(fpr['micro'], tpr['micro'],
             label='Micro-Average ROC curve (area = {0:0.2f})'
                   ''.format(roc_auc["micro"]),
             color='red', linestyle=':', lw=3)

    plt.plot(fpr['macro'], tpr['macro'],
             label='Macro-Average ROC curve (area = {0:0.2f})'
                   ''.format(roc_auc['macro']),
             color='black', linestyle=':', lw=3)

    colors = ['#3972ba', '#ab923e', '#3bb300']
    for i, color in zip(range(len(le.classes_)), colors):
        plt.plot(fpr[i], tpr[i], color=color, lw=2,
                 label='ROC of Class {0} (area = {1:0.2f})'
                       ''.format(le.classes_[i], roc_auc[i]))

    plt.xlim(0, 0.2)
    plt.ylim(0.8, 1)
    plt.xlabel('False Positive Rate')
    plt.ylabel('True Positive Rate')
    plt.title('ROC Curve (Top Left)')
    plt.legend(loc='lower right')
    plt.savefig('output/ROC-top-left.png')
    plt.show()
```

In [22]:

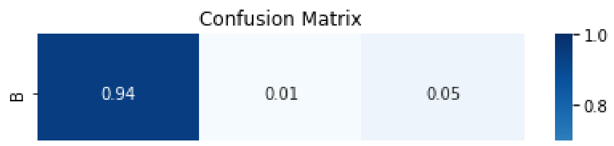
```
def plot_confusion_matrix(cm, le, title=""):
    fig, ax = plt.subplots(figsize=(6, 4))
    sns.heatmap(cm, annot=True, ax=ax, fmt='.2f', cmap=plt.cm.Blues, vmin=0, vmax=1)

    # Set labels, title, ticks and axis range.
    ax.set_xlabel('Predicted Classes')
    ax.set_ylabel('True Classes')
    ax.set_title('Confusion Matrix')
    ax.xaxis.set_ticklabels(le.classes_)
    ax.yaxis.set_ticklabels(le.classes_)
    plt.tight_layout()
    bottom, top = ax.get_ylim()
    plt.show()
    plt.savefig('output/confusion_mat' + title + '.png')
```

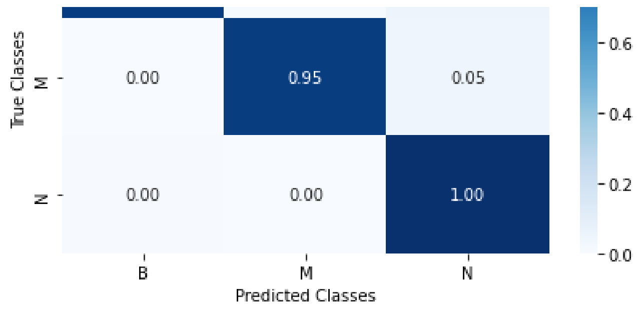
Validation

In [23]:

```
prediction = model.predict(X_val, batch_size=20)
evaluate_model(prediction, y_val, le, '-val-l2=0.01')
```

```
773
Accuracy = 0.9612
```





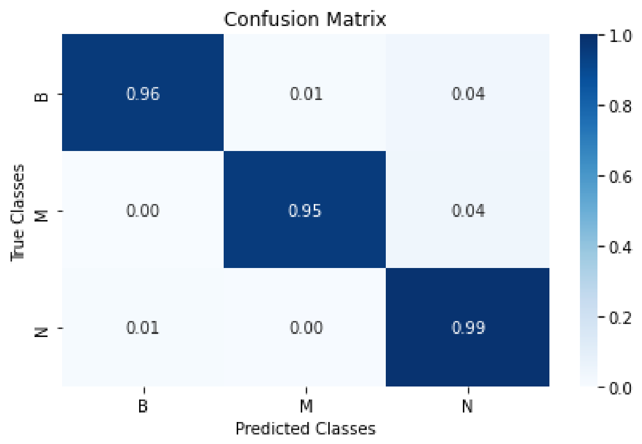
```
<Figure size 432x288 with 0 Axes>
```

Testing

In [24]:

```
predictions = model.predict(x=X_test)
evaluate_model(predictions, y_test, le, '-test-l2=0.01')
```

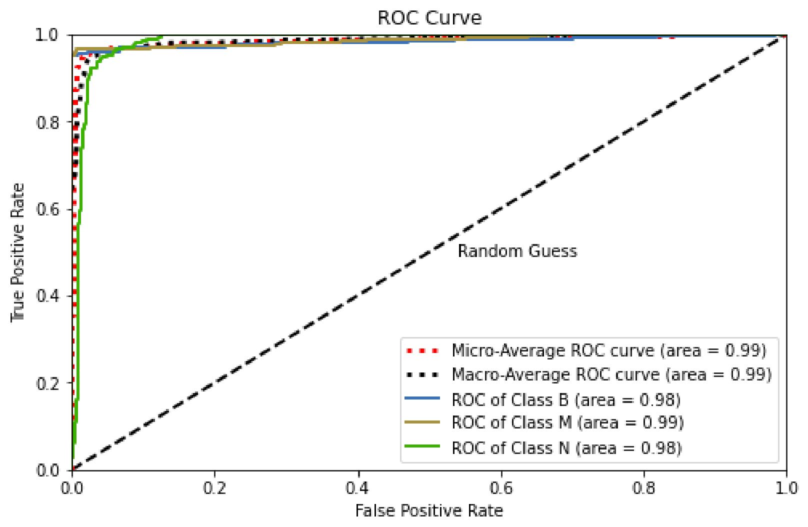
```
773
Accuracy = 0.9664
```

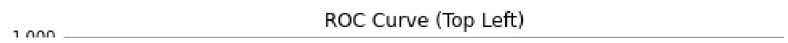


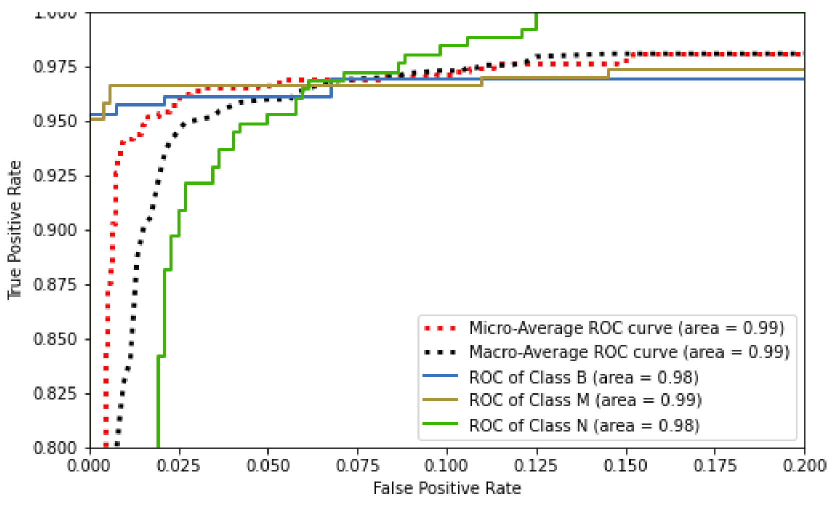
```
<Figure size 432x288 with 0 Axes>
```

In [25]:

```
plot_roc(y_test, predictions, le)
```






1.000
0.975
0.950
0.925
0.900
0.875
0.850
0.825
0.800
True Positive Rate
0.000
0.025
0.050
0.075
0.100
0.125
0.150
0.175
0.200
False Positive Rate
Micro-Average ROC curve (area = 0.99)
Macro-Average ROC curve (area = 0.99)
ROC of Class B (area = 0.98)
ROC of Class M (area = 0.99)
ROC of Class N (area = 0.98)

```
In [ ]:
```