

Literature Review on Artificial Intelligence in Radiology
Comparison on Breast Cancer and Covid-19 CNN's
Assignment 2

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Table of Contents

Introduction	3
Digital Pathology	4
Digital Pathology in Relation to Breast Cancer.....	4
Digital Pathology in Relation to Covid-19 Detection.....	4
Digital Pathology in Relation to AI.....	4
Digital Pathology in Relation with Machine Learning and Deep Learning.....	4
Digital Pathology in Relation with Neural Networks	5
What are Convolutional Neural Networks	5
Research Problem	5
Methods and Materials.....	6
Determination of Data and Convolutional Neural Networks.....	6
Breast Cancer Detection	6
Covid-19 Detection	7
Data Availability and Image Sizing.....	7
Python Libraries	7
Mask R-CNN	8
AlexNet.....	9
Breast Cancer – Code Set	9
Data Set	9
Part A – Dataset Cleaning.....	9
Part B – Model Training.....	11
Part C – Model Execution	12
Covid-19 – Code Set	13
Data Set	13
Part 1 – Classifier Modelling.....	13
Part 2 – Classifier Evaluation	13
Part 3 – Classifier Interface	14
Results.....	14
Discussion and Conclusion	15
References.....	16

Table of Figures:

Figure 1: Mask R-CNN Architecture, (Cruz-Roa et al., 2018).....	5
Figure 2: Dataset for Breast Cancer Recognition, (Suckling et al., 1994).....	6
Figure 3: Python Libraries, (Zhao, 2020)	8
Figure 4: Mask R-CNN Framework, (He et al., 2017)	8
Figure 5: Mask R-CNN Framework, (He et al., 2017)	9
Figure 6: AlexNet for Breast Cancer Detection, (Ragab et al., 2019)	9
Figure 7: Proportion of Mammograms with and without Tumour	10
Figure 8: Distinct abnormalities	10
Figure 9: Distinct abnormalities	11
Figure 10: Various Abnormalities	11
Figure 11: Epoch Model Performance	12
Figure 12: Plots detecting Breast Cancer	12
Figure 13: Plots detecting Breast Cancer	13
Figure 14: CNN with a 10-fold cross validation, (Zhao, 2020)	13
Figure 15: Output detecting negative results, (Zhao, 2020)	14
Figure 16: Challenges Encountered - Code Execution.....	15

Introduction

Digital Pathology

High-resolution photographs of pathology slides are digitally captured and saved in the discipline of digital pathology, (Cruz-Roa et al., 2018). In traditional pathology, diseases and anomalies are identified by looking at physical slides under a microscope. These slides are transformed into digital images by digital pathology, allowing for archiving, sharing, and computer-based tool analysis, (Cruz-Roa et al., 2018). This convergence illustrates the seamless integration between computer science and health informatics disciplines.

Digital Pathology in Relation to Breast Cancer

Digital pathology is on the verge of becoming a mainstream option for routine diagnostics, marking a significant advancement in everyday clinical practice for diagnosing diseases and conditions, (Nithya & Santhi, 2011). This advancement comes at a critical time as Breast Cancer remains the second leading cause of death in women worldwide, (Kelly et al., 2021). Early detection through routine mammograms has proven to be the most effective prevention strategy in improving Breast Cancer outcomes, (Kelly et al., 2021). Timely detection, particularly in the early stages, is strongly linked to better prognosis, underscoring the need for enhanced and timely screening strategies, (Ahmad, 2019). In health care and radiology, digital pathology establishes a DICOM standard that seamlessly aligns with clinicians' workflows. These digital images play a pivotal role in diagnosis and treatment planning within the health informatics domain, significantly enhancing the efficiency and accuracy of the process.

Digital Pathology in Relation to Covid-19 Detection

Digital pathology is also frequently utilised while analysing chest c-rays, especially when using COVID-19. This is due to the fact that digital pathology gives pathologists and researchers the chance to examine, review, and diagnose slides remotely, (Cruz-Roa et al., 2018). This method also facilitates collaborations, as multiple experts can simultaneously view and discuss the same slide without the need of being in the same place physically. Overall, this improves efficiency and enables the use of computer-aided analysis, (Cruz-Roa et al., 2018).

Digital Pathology in Relation to AI

The fields of pathology and medical imaging have benefited greatly from the integration of digital pathology with AI. Digital pathology images can be automatically analysed and interpreted using AI methods like deep learning and machine learning. AI algorithms can recognise patterns, features, and anomalies in the images, making it possible to diagnose many diseases accurately and quickly, (Cruz-Roa et al., 2018).

Digital Pathology in Relation with Machine Learning and Deep Learning

Machine learning and deep learning are the two main AI techniques used in radiology (Zhao, 2020). Machine learning models are trained to apply mathematical techniques to find patterns in data and produce predictions, either under supervision or independently. In order to simulate extremely complicated interactions between inputs and outputs, deep learning is a subclass of machine learning that uses deep neural networks (Zhao, 2020). Additionally, manually derived features from photos with a texture resembling a tumour are used to train statistical machine learning models. Following training, they are able to categorise the conditions of patients in order to "support clinical decision making" (Hosny et al., 2018).

Digital Pathology in Relation with Neural Networks

Recent research has shown remarkable progress in the field of digital pathology, with Convolutional Neural Networks (CNNs) emerging as the leading representation learning method for computer vision tasks, (Cruz-Roa et al., 2018). CNNs have demonstrated considerable success in digital pathology applications, including tumor and mitosis detection, highlighting their potential to revolutionize cancer diagnosis and treatment, (Cruz-Roa et al., 2018).

What are Convolutional Neural Networks

Convolutional Neural Networks (CNNs) are a particular kind of deep learning architecture made specifically for processing and analysing visual data, including images, (Cruz-Roa et al., 2018). Due to their ability of automatically learning hierarchical features from incoming images, CNNs are very good at tasks like image classification, object recognition, and segmentation. As a result, CNNs are frequently used in the healthcare sector for a variety of purposes, including their effectiveness in managing data from medical imaging and other tasks.

Mask R-CNN is an extension of the Faster R-CNN architecture, (He et al., 2017). In contrast to Faster R-CNN, the main Mask R-CNN strategy has many more sub-strategies, including instance segmentation, bounding-box object detection, and person keypoint detection, (He et al., 2017). The precise number of layers in a mask R-CNN depends on the implementation and particular requirements. Figure 1, illustrates the architecture for Mask R-CNN.

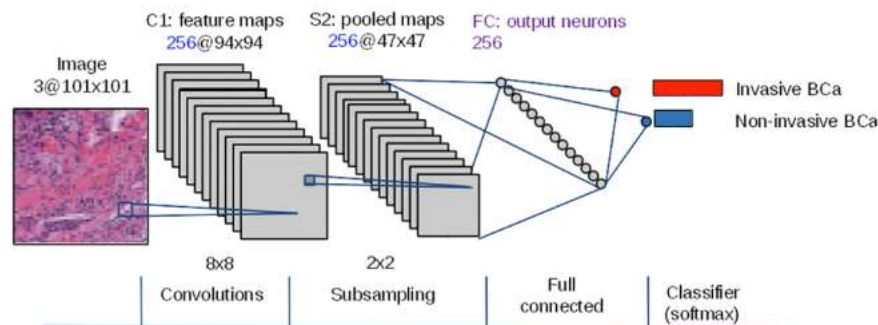


Figure 1: Mask R-CNN Architecture, (Cruz-Roa et al., 2018)

One of the most popular neural networks is called AlexNet. AlexNet has five convolution layers, three pooling layers, and two fully connected layers with approximately 60 million free parameters, (Ragab et al., 2019).

Research Problem

In this paper, I delved into a comprehensive discussion of CNNs, exploring their architecture and functionality to demonstrate their pivotal role in anomaly identification. The research problem lies in the intricate correlation between computer science and health informatics in utilizing AI techniques for cancer detection through pattern recognition.

I took a multi-disciplinary approach, reviewing and implementing existing CNNs, emphasizing their functionality in pattern recognition for anomaly identification. To assess the effectiveness of CNNs in pattern recognition, I compared two distinct CNN structures, MASK R-CNN and AlexNet, using multiple DICOM images of different image types, including chest x-rays and breast mammograms.

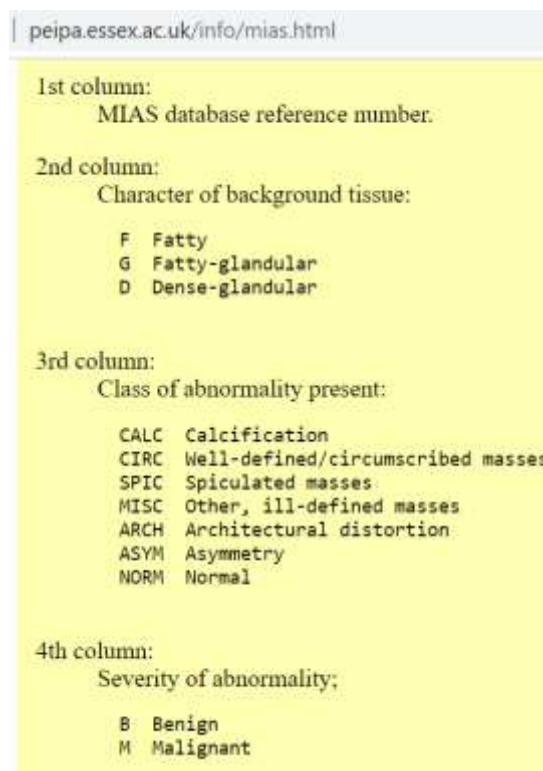
Methods and Materials

Determination of Data and Convolutional Neural Networks

The selection of the CNN's was carefully based on two essential criteria. Firstly, we prioritized datasets that were publicly available, ensuring easy access for replication and validation. Secondly, our focus was on datasets that utilize powerful CNN models like Mask R-CNN and AlexNet. Additionally, we considered the coding language used in the implementation, with a preference for Python. Python's versatility, coupled with the availability of essential extensions through Anaconda, made it an ideal choice. Furthermore, Python's seamless integration with Jupyter Notebook provided a user-friendly and efficient coding platform for our analyses.

Breast Cancer Detection

Using the Mask R-CNN neural network, we analyzed a dataset for breast cancer recognition in mammogram images (Figure 2). Mask R-CNN is an extension of Faster R-CNN specifically designed for tumor detection. The code's classifications successfully located tumors and identified their types. We employed CNN layers with 1 to 4 hidden convolution layers, containing 10 to 128 filters, and 1 to 5 dense layers with 120 to 2000 nodes for this implementation, (Kelly et al., 2021).



The image is a screenshot of a web browser displaying the MIAS database information page. The URL in the address bar is peipa.essex.ac.uk/info/mias.html. The page content is organized into four columns, each with a title and a list of categories or values. The first column is for the MIAS database reference number. The second column is for the character of background tissue, with options F (Fatty), G (Fatty-glandular), and D (Dense-glandular). The third column is for the class of abnormality present, with options CALC (Calcification), CIRC (Well-defined/circumscribed masses), SPIC (Spiculated masses), MISC (Other, ill-defined masses), ARCH (Architectural distortion), ASYM (Asymmetry), and NORM (Normal). The fourth column is for the severity of abnormality, with options B (Benign) and M (Malignant).

1st column:	MIAS database reference number.
2nd column:	Character of background tissue:
	F Fatty
	G Fatty-glandular
	D Dense-glandular
3rd column:	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 column:	Severity of abnormality;
	B Benign
	M Malignant

Figure 2: Dataset for Breast Cancer Recognition, (Suckling et al., 1994)

Covid-19 Detection

For the detection of Covid-19, the dataset utilized AlexNet. This python code source from GitHub is used to develop a prototype that categorises and determines whether chest x-rays for covid-19 are positive or negative. To prevent computational complexity, the number of layers and parameters is decreased. Two convolutional layers, two max-pooling layers, one hidden layer, and one output layer makes up this structure. Batch normalisation is used to normalise the produced data in between layers.

Data Availability and Image Sizing

The DICOM images and Python code used in the study were made publicly available on GitHub. These data sources had distinct structures. For tumor detection, the images had predetermined sizes ranging from 100x100 to 1024x1024, (Kelly et al., 2021). On the other hand, for COVID detection, the images were resized to 244x244 pixels as required by the code's structure, (Zhao, 2020).

Python Libraries

Some of the key libraries utilized in Breast Cancer detection from Mammograms included:

- TensorFlow 1.15.0: A powerful deep learning library.
- Keras 2.3.1: A high-level API for building neural networks.
- Pandas 1.3.5: Employed for data manipulation and analysis in Python.
- Scikit-learn 1.0.2: A versatile machine learning library for tasks like classification and regression.
- Seaborn 0.12.2: Utilized for creating appealing data visualizations, built on top of Matplotlib version 3.5.3.
- NumPy 1.21.6: Utilised to handle big arrays and matrices in numerical computations.
- SciPy 1.7.3: Used for scientific computing and technical computing. In this case, it was utilized as it contains modules for image processing
- Pillow 9.5.0: Is an image library in python, used for opening, manipulating, and saving many different image file formats
- Cython 0.29.36: Primarily utilized to enhance the performance of Python code
- Scikit-image 0.19.3: Utilized in this situation as it offers a variety of image-processing capabilities and methods, including image filtering, segmentation, feature extraction, and picture transformations.
- OpenCV-Python 4.8.0.74: Used as it provides a wide range of functions and tools for working with images and videos
- H5Py 3.8.0: Used because it offers a user interface for interacting with the HDF5 (Hierarchical Data Format 5), which was the format for many of the data files used in this project.\
- Imgaug 0.4.0: Python library used for image augmentation.

Additionally, the Mask R-CNN extension, mrcnn-tf115, was installed to enable proper utilization of Mask R-CNN capabilities.

When comparing the Python library extensions between the two code sets, for the detection of Covid-19, AlexNet was utilized and required fewer additional extensions. It was also implemented in Python and leveraged TensorFlow and Keras, alongside Scikit-learn, NumPy, Matplotlib and a few others. Please refer to Figure 3, to see the details on the python libraries.

```

import tensorflow as tf
from tensorflow import keras
from tensorflow.keras.layers import Dense
from tensorflow.keras.layers import Conv2D
from tensorflow.keras.layers import MaxPooling2D
from tensorflow.keras.layers import BatchNormalization
from tensorflow.keras.layers import Flatten
import numpy as np
import matplotlib.pyplot as plt

```

Figure 3: Python Libraries, (Zhao, 2020)

Overall, both code sets utilized essential libraries to support their deep learning tasks, with slight variations in the required extensions based on the chosen neural network architecture.

Mask R-CNN

The method of CNN's called Mask R-CNN extends the Faster R-CNN as mentioned earlier on in the paper. But in this extension, we add a branch for prediction segmentation masks on the region of interest also known as ROI, (He et al., 2017). This is added in parallel with the existing branches for the classification and bounding box regression. Please reflect to Figure 4 and 5, to see clearly how this framework is organized. Mask R-CNN is an advanced version of Faster R-CNN, which is a model that has the ability to detect and locate objects in images, (He et al., 2017). While Faster R-CNN tells us what objects are in the image and where they are located with bounding boxes, Mask R-CNN goes one step further and adds a third output, which is the exact shape of each object, like a precise outline or mask, (He et al., 2017). The Mask R-CNN is simple to implement, and train given the Faster R-CNN framework. Additionally, Mask R-CNN is conceptually simple to understand. To give an easier example, image we were to feed the model images of breast mammographs with tumors present. In this case the Faster R-CNN can tell you there is tumor present on the mammographs. But Mask R-CNN can also draw the outline of where the tumor exists in each of the mammographs. Which is why Mask R-CNN is so useful in health care. To see an example of how Mask R-CNN creates these boundaries on images, please refer to Figure 5. However, this process of creating these outlines is more challenging because it requires very detailed information about the anomaly's boundaries, (He et al., 2017). Mask R-CNN uses a technique called "pixel-to-pixel alignment" to figure out these exact shapes accurately.

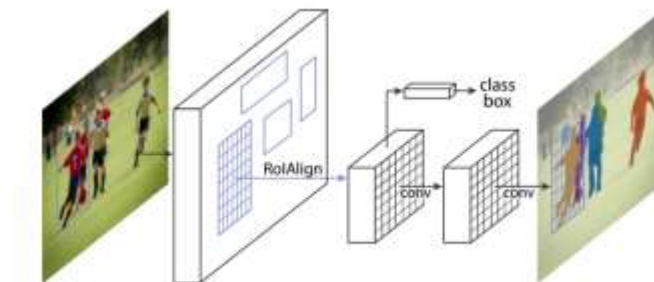


Figure 4: Mask R-CNN Framework, (He et al., 2017)



Figure 5: Mask R-CNN Framework, (He et al., 2017)

AlexNet

AlexNet, often referred to as the "pioneer" of CNNs, holds the distinction of being optimized for classifying a thousand different classes, (Zhao, 2020). However, it also demands a tremendous amount of memory and computational power during training due to the large number of mathematical operations involved, (Zhao, 2020). This deep learning architecture called AlexNet has made substantial advancements in computer vision. As mentioned earlier in the paper, AlexNet is a convolutional neural network (CNN) consisting of five convolutional layers, followed by three fully connected layers, (Zhao, 2020). In this project, AlexNet is employed to determine whether chest images fed into the model contain COVID-19 or not. However, if we were to utilize AlexNet for identifying benign or malignant breast cancer, the model's structure would resemble the one depicted in Figure 6.

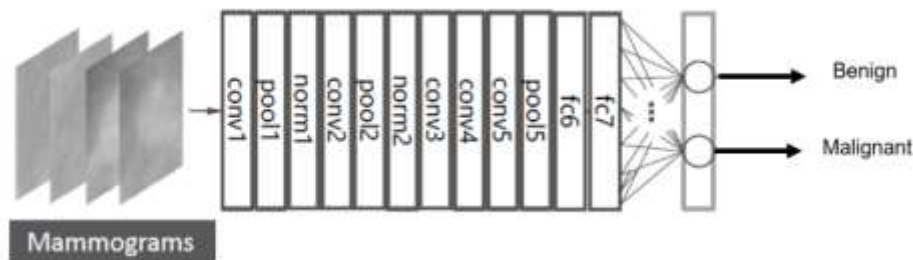


Figure 6: AlexNet for Breast Cancer Detection, (Ragab et al., 2019)

Breast Cancer – Code Set

Data Set

In this code set, 322 mammograms from the Mammographic Image Analysis Society, or MIAS, were used from a total of 161 patients. Every image utilised from this dataset is 1024 by 1024 pixels and has a 200 micron pixel edge reduction. There were a few factors in this dataset that were crucial to take into account. The characteristics of the background tissue, for instance, were divided into three categories: Fatty, Fatty-glandular, and Dense-glandular. In addition, a wide range of types of abnormalities, including calcification, well-defined/circumscribed masses, spiculated masses, poorly defined masses, architectural distortion, asymmetry, and normal, were taken into account. Finally, it's critical to classify these photos according to the severity of the anomaly, depending on whether the mass is benign or malignant.

Part A – Dataset Cleaning

There are three primary sections to this code set. We will concentrate on Part A in this section, which deals with dataset cleaning. Here, we read image files and pull-out essential information. Our main goal is to locate tumour-containing photos and eliminate duplicates to ensure a clean dataset. Creation of visuals is possible to help us understand the data when the cleaning procedure is finished, and duplicates

have been eliminated. The graph, which is displayed in Figure 7, demonstrates the proportion of photos with and without tumours.

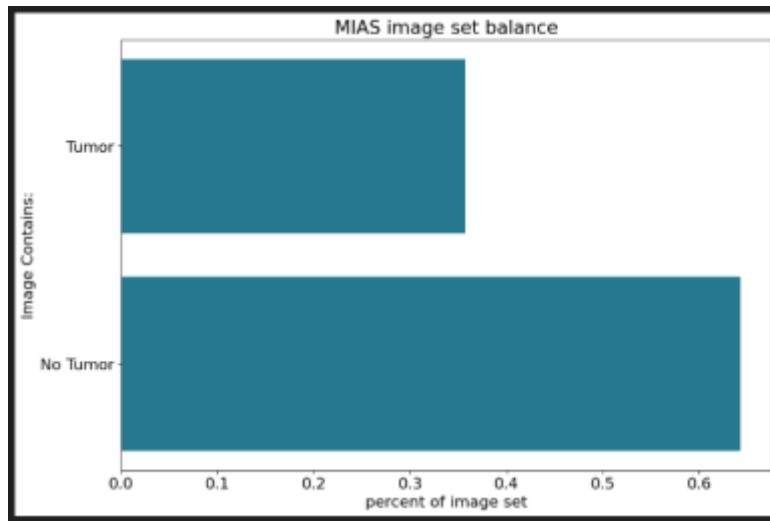


Figure 7: Proportion of Mammograms with and without Tumour

In addition, we have the capability to generate various graphs illustrating data on distinct types of abnormalities, along with background tissue references. For more details, please refer to Figures 8 and 9.

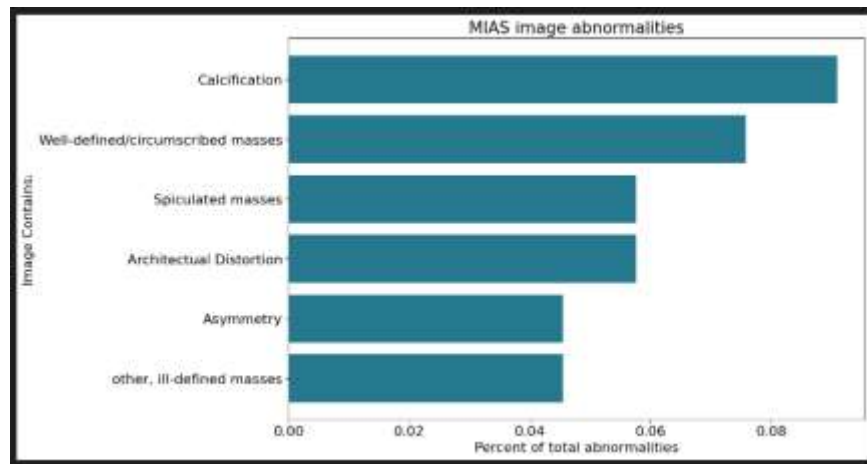


Figure 8: Distinct abnormalities

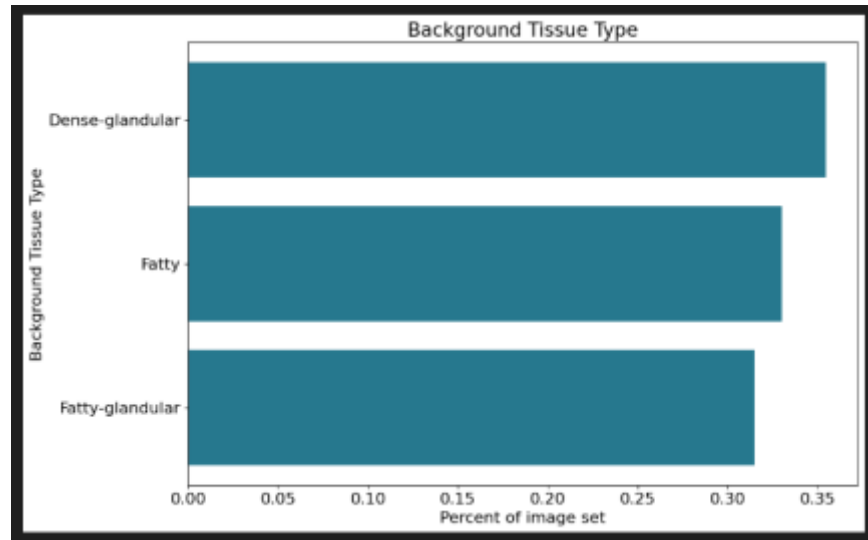


Figure 9: Distinct abnormalities

To enhance data comprehension and enable a focused comparison between tumor and non-tumor cases, as well as various abnormalities, we generated specific visuals (see Figure 10).

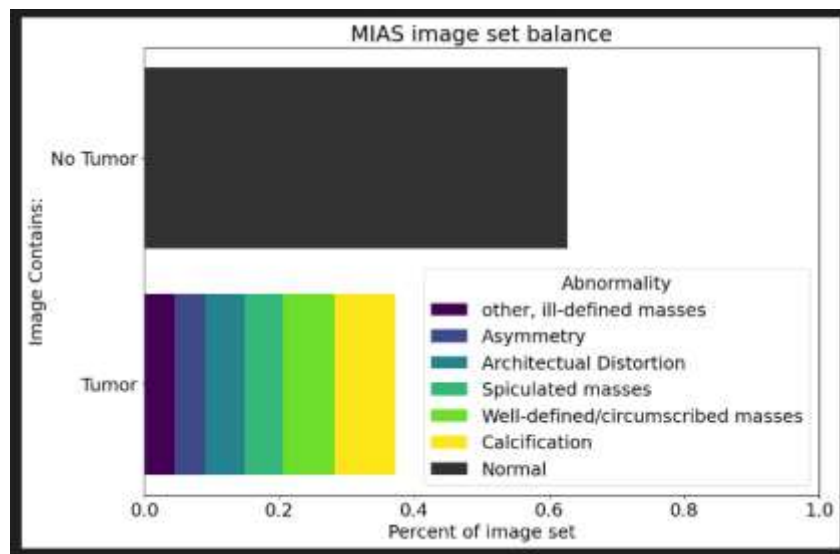


Figure 10: Various Abnormalities

Part B – Model Training

Moving on to part B, the training procedure is carried out using the "cnn.fit" approach in this section. We randomly divide the data using a random seed, and we can then determine how many epochs are required for this model to produce reliable findings. In the context of machine learning, epochs refer to the number of times a model examines and absorbs information from the entire training dataset, (Zhao, 2020). In other words, an epoch is a single time when the model iterates over the dataset. Figure 11 displays the model's performance accuracy as well as the loss in terms of the epochs' historical development.

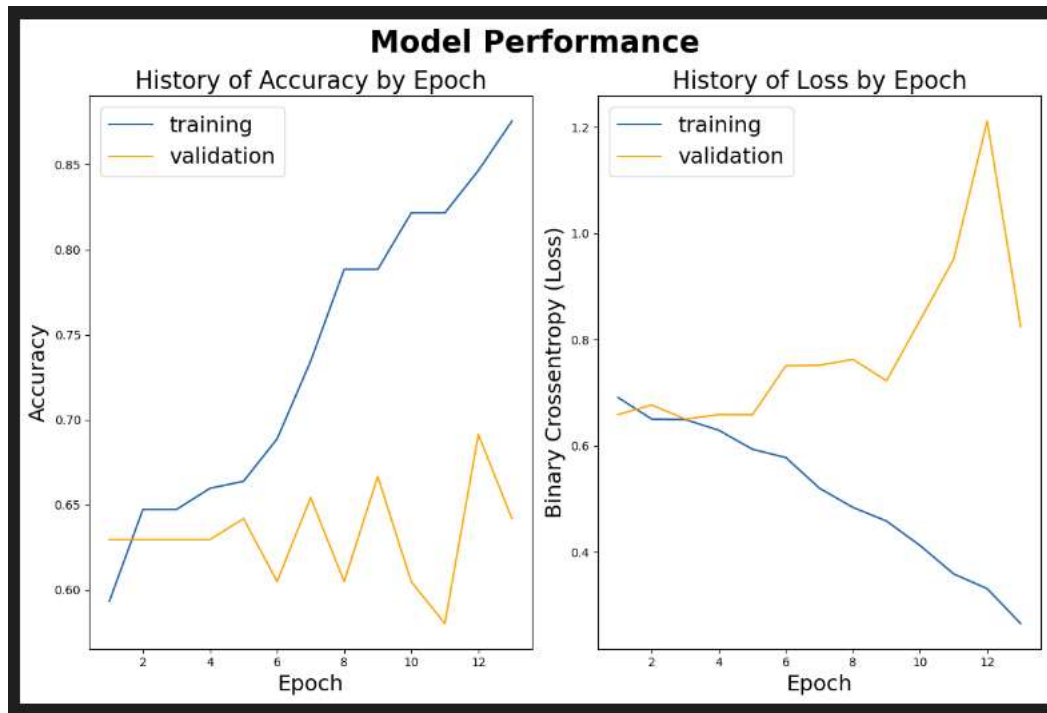


Figure 11: Epoch Model Performance

Part C – Model Execution

Moving on to part C, we do the mask fit and import the coco dataset, (Abdulla, 2019) from Mask R-CNN as a base in this step. In order to train the model, this phase executes the fifteen epochs. We are able to load this fit once the model has been trained and executed. The plots that are produced after the model has been trained show both the original breast photos and the output images with the ROI (region of interest) boxes. The ROI's are the bounding boxes that indicate the areas that have the chance of containing tumor. An illustration of one of the plots is shown in Figure 12 and 13.

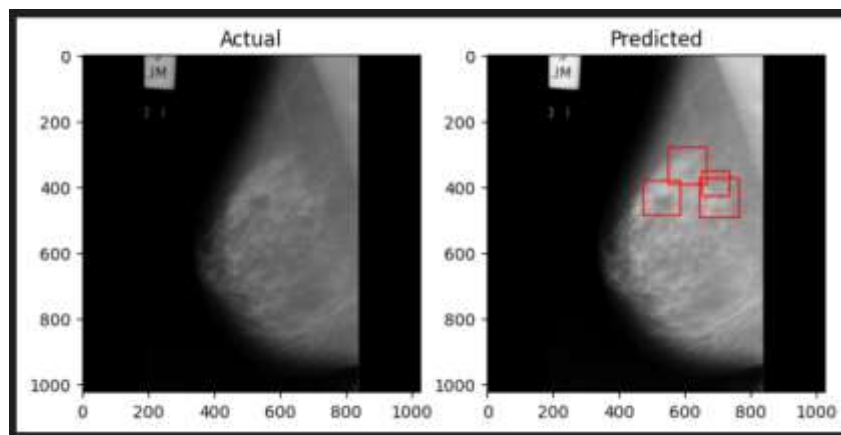


Figure 12: Plots detecting Breast Cancer

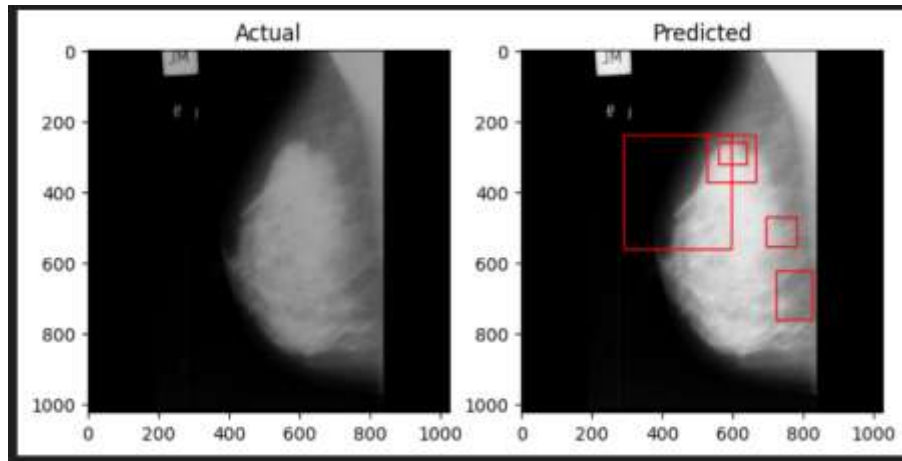


Figure 13: Plots detecting Breast Cancer

Covid-19 – Code Set

Data Set

The data sets used to train and run this code base are from the University of Montreal (Cohen, 2020) and from Kaggle (Chest X-Ray Images, n.d.). This project only used 50 DICOM x-ray images for training and testing of the model.

Part 1 – Classifier Modelling

In this section of the code, we categorize data into pairs of images and labels, convert images to greyscale and reshape images to have a dimension recognizable by the CNN, (Zhao, 2020). In addition to this, in this section we also build the neural network. After that we are able to train and test the CNN with a 10-fold cross validation, (Zhao, 2020). Figure 14 reflects the visualization of these 10-fold cross validation process. This includes training the model with five iterations, these iterations are also known as epochs, (Zhao, 2020).

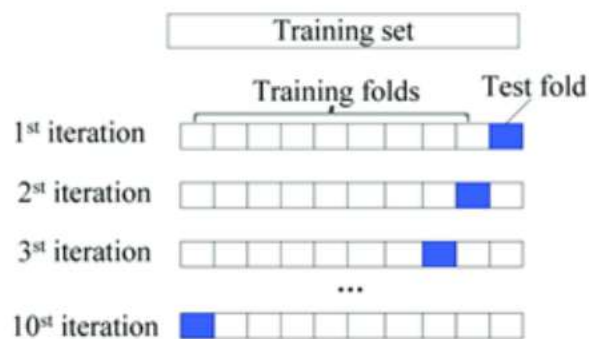


Figure 14: CNN with a 10-fold cross validation, (Zhao, 2020)

Part 2 – Classifier Evaluation

In this section we load the trained model and import and process the data.

Part 3 – Classifier Interface

In this section the user is able to select an image from their saved folders. This is done by using the Tk class which represents the main window of a Tk application. After the user selects the image, the model is used to predict the selected image and inform the output to the user. An example of the output is shown in Figure 15.

```
[INFO] LOADING TRAINED MODEL.....  
[INFO] MODEL LOADED! Please select an x-ray image.  
  
PROBABILITY: 0.0008239746  
RESULT: COVID19 not detected.
```

Figure 15: Output detecting negative results, (Zhao, 2020)

Results

In this section, I will outline the timelines for different aspects of the project. Let's begin by discussing the epoch timelines that were used to train the convolutional neural networks.

For the breast cancer detection, the code set underwent a total of 15 epoch iterations. Table XX provides a detailed overview of the timeline for each iteration. In contrast, the COVID-19 detection model required only 5 epoch iterations to achieve effective training, remarkably completing in approximately 30 minutes. This impressive reduction in training time clearly demonstrates a significant advantage over the breast cancer detection model.

Table 1: Epochs Iteration Time Stamps

Epoch / Iteration Number	Approximate Time Iteration Required	Approximate Time Iteration Ended
1	2 Hours 48 Minutes	5:50 PM
2	2 Hours 48 Minutes	8:31 PM
3	2 Hours 48 Minutes	11:23 PM
4	2 Hours 48 Minutes	1:40 AM
5	2 Hours 48 Minutes	3:20 AM
6	2 Hours 48 Minutes	5:30 AM
7	2 Hours 48 Minutes	7:40 AM
8	2 Hours 48 Minutes	9:55 AM
9	2 Hours 48 Minutes	12:10 PM
10	2 Hours 48 Minutes	2:55 PM
11	2 Hours 48 Minutes	5:25 PM
12	2 Hours 48 Minutes	7:43 PM
13	2 Hours 48 Minutes	9:58 PM
14	2 Hours 48 Minutes	12:30 AM
15	2 Hours 48 Minutes	3:20 AM

Furthermore, this section includes a Gantt chart, providing an insightful overview of the challenges encountered during the execution of both code sets. Additionally, it offers a detailed breakdown of the

time dedicated to various aspects of assignment two. For more comprehensive information, please refer to Figure 16.



Figure 16: Challenges Encountered - Code Execution

Discussion and Conclusion

In this section, I will thoroughly examine the limitations and successes of this project, focusing on the utilization of two distinct convolutional neural network structures.

The visual results presented in the results section clearly indicate that running epochs in the breast cancer detection code set demanded significantly more time and complexity compared to the COVID-19 detection code set. This discrepancy holds implications and limitations that warrant closer examination. When training a model, “we expect the loss to decrease and accuracy to increase as the number of epochs increases”, (baeldung, 2023). Therefore, running a sufficient number of epochs is crucial for optimal model performance.

While using Mask R-CNN for breast cancer detection, we were able to perform the necessary number of epochs to achieve the highest accuracy. Moreover, the visual representations from parts A and B of the code set confirmed the model's accuracy. However, in the case of the code set using AlexNet for COVID-19 detection, a limitation arose as there was no function to allow running epochs to their maximum for increased accuracy. Instead, the value of 5 was predetermined as the number of epoch iterations. This discrepancy in the number of epoch iterations could pose challenges when comparing the two code sets, as they had varying inputs in terms of how many epochs each model could run.

During the project review with Dr. William, several additional limitations came to light. Among them, one of the key concerns emphasized by Dr. William was the usage of only one angle for running the breast cancer mammograms. In a real-life hospital setting, radiologists and oncology specialists typically require multiple angles of the breast tissue to gain a comprehensive understanding of whether cancer is present

or not. This limitation could potentially be a limitation in the implementation of this project in a real-world hospital scenario.

Another notable limitation highlighted by Dr. William was that the testing was conducted solely using one dataset, specifically the MIAS dataset. To attain more robust and reliable results, running the model on different and multiple datasets would have been beneficial. The inclusion of diverse datasets would have provided clearer insights into the accuracy and effectiveness of the neural network model's outputs.

I am aware that there are publicly available datasets, such as the Curated Breast Imaging Subset of Digital Database for Screening Mammography (CBIS-DDSM), which could have been utilized. However, due to the constraints of the project timeline, I regrettably could not proceed with running the model on this dataset. Nonetheless, it is critical to acknowledge that in future implementations of this project, exploring various datasets will be crucial to gain more of a comprehensive understanding of the model's performance and accuracy.

Overall, in the context of digital health and health informatics, the utilization of DICOM Images and AI has proven highly effective in image analysis and anomaly detection. These advancements are closely linked to improving patients' well-being, facilitating vital support from doctors throughout the diagnostic process. The integration of AI with medical imaging has the potential to revolutionize radiology workflows, leading to significant advancements in healthcare practices and benefiting patients on a considerable scale.

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