



Detecting Breast Cancer in Histopathology with Deep Neural Networks

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Received: September 02, 2025

Published: October 14, 2025

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Abstract

Breast cancer is a disease that has existed for thousands of years[1], and affects millions of people yearly[2]. There were 8.8 million cancer deaths and 684,996 breast cancer deaths in 2020 alone[3]. Any amount of work that we do to reduce the number of deaths by early diagnosis of breast cancer is going to be crucial in saving several lives in a year. We set out to be able to design an easier way to diagnose breast cancer, using machine learning to help. A patient who is at risk of having breast cancer is suggested to have a biopsy. The AI tool we have created aids in the process of the biopsy and helps with the diagnosis. This would increase the efficiency of the patient workflow by adding the ML models in the loop before it gets to the physician, lowering cost and increasing the number of people they would be able to look at. The data we initially tried to use was from mammograms, but due to the large number of existing research using mammography images, we switched to using histopathology images.

Histopathology images are images of small portions of tissue under a microscope, sampled from a biopsy. Histopathology images are also complex in terms of disease classification for an untrained eye which could add a lot of false classifications. Hence the tool could aid in assisting technicians to physicians in their diagnosis. After testing with several different machine learning models, we landed on MobileNet V2 which gave an accuracy of 91.2% across the dataset. This tool could add a lot of value in clinical diagnosis during the patient pathway.

Keywords: Breast Cancer; Histopathology; Neural Networks

Introduction

Breast cancer has been in recorded history for a long time, with matching records stretching back to 3000 BCE [1]. Some of the most common types of breast cancer are lobular carcinoma in situ, ductal carcinoma in situ (the most common), infiltrating lobular carcinoma, and infiltrating ductal carcinoma [4]. 2.3 million women were diagnosed with breast cancer and 670,000 people died from breast cancer in 2022 [2]. In the USA, there are 287,850 cases diagnosed yearly, 43,250 deaths, and 51,400 of the cases are ductal

carcinoma [5]. For people who have their cancer discovered early before it has spread, there is a 99% survival rate.

Instead, if the breast cancer is not found until after it has spread, the survival rate decreases to a range of 30-86% [6]. Breast cancer treatment can include a combination of several different methods. These methods include; surgery to remove the cancerous cells; chemotherapy, which uses medicines to shrink and kill the cancer; hormonal therapy, used to block cancer from getting hormones that it requires to continue expanding; biological therapy, which

works with the body's immune system to either fight the cancer cell directly or combat side effects from other treatments; and radiation therapy, where radiation is used to target and eliminate cancer cells.

Mammography is the process of using X-rays to check for breast cancer. Histopathology is using a microscope to observe small sections of tissue [7].

There has been a lot of research into developing models to identify breast cancer. The majority of these use mammography or ultrasound datasets. Additionally, the CNNs most commonly used are AlexNet, VGG, ResNet, DenseNet, Inception (GoogleNet), LeNet, and UNet [8]. Some studies have found that the main issue with trying to accomplish the task of creating an applicable model for any type of image is the dataset. Due to the lack of significant portions of data, there could be overfitting or general accuracy issues that arise. Some of these issues can be solved by either manipulating the data or finding a large enough dataset [9]. The dataset we chose was large, likely helping us with these issues. In histopathology, using AI has shown to be promising. There have been studies that have shown that a model can score several percentage points higher than a professional pathologist when it comes to identifying cancer [10].

Dataset

We decided to use a histopathology dataset for the presence of breast cancer. The histopathology dataset came from 162 slides of 162 patients at a 40x zoom. 555,048 patches were gathered, with 397,476 identified not to have cancer and 157,572 positively identified to have cancer. This data specifically includes data on the most common type of breast cancer, Invasive Ductal Carcinoma [11]. The images gathered were of resolution 50 by 50. There were some inconsistencies, leading to some resizing being necessary, but the majority were 50 by 50. We resized the images to 75 by 75 for compatibility with the models we were using.

Some possibilities for the dataset could have been a dataset containing mammography, or ultrasounds. We chose not to use those two as mammography already had extensive research on it. There were at least 90 studies, at least 3 of which accomplished a high level of optimization [12]. For ultrasounds, there are also a large number of studies, with there being at least 58, a majority of which lead to the conclusion that AI in ultrasounds is a good prospect

[13]. Histopathology is also considered to be the “gold standard” for diagnosing cancer [14]. For these reasons, in addition to the histopathology dataset being uniform and high quality, we decided to use it.

Sample malignant pathology images

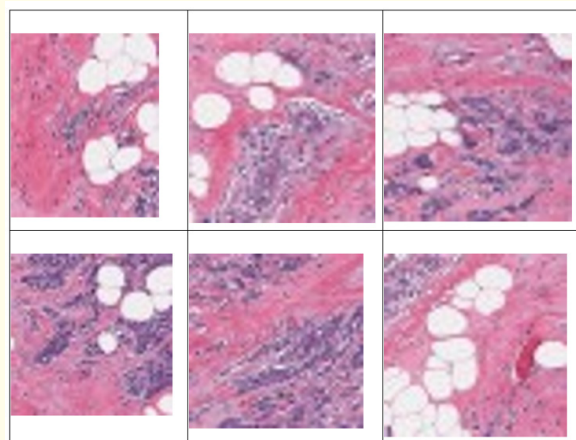


Figure a

Sample benign pathology images

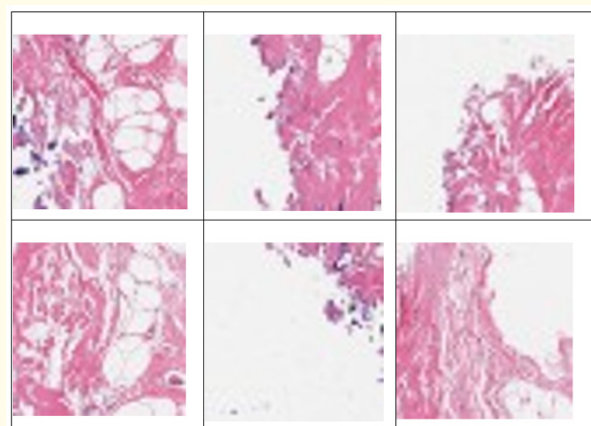


Figure b

Preprocessing

We did three main steps of preprocessing. We first resized all of the images, because even though they were mostly 50 by 50, some

were not consistent sizes, so we resized them all to 50 by 50 pixels. Next, we edited the targets with one hot encoding. We got whether the image depicted a cancerous cell or not from the file's title, which had a number 0 or 1 representing this. This made sure the model could output and train based on this. Last, before running the model, we did a train test split. The train test split splits the dataset in two. These are two unequally sized parts of the data. This is so that the model can check its accuracy from training with the train part of the split, with the test of the split. It makes sure that it is not overfitting.

Experimental methodology

We used several types of model architectures. The first type we used was a basic homegrown convolution model. It had 3 convolutional layers of 16, 64, then 128. It then had 3 layers of dense layers of 128, 64, and 32. We did 10 epochs, and it gave the final values of the training loss being 0.3777, training accuracy being 0.8371, validation loss being 0.4030, and validation accuracy being 0.8348. We then used proper models. We did transfer learning, taking previously trained models and adjusting the model's architecture slightly to fit our data better.

The transfer learning models that were used in this experiment were ResNet 50, ResNet 101 V2, VGG16, VGG 19, and MobileNetV2. The MobileNetV2 model gave us the most accuracy of all the different models. The training accuracy was recorded to be 92.72% and the validation accuracy was recorded to be 91.2% The accuracy and loss charts for the MobileNet V2 model for 50 epochs are shown below

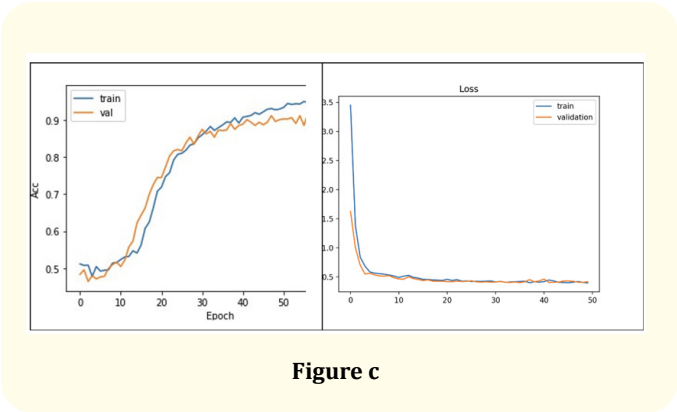


Figure c

The accuracy (left) and the loss (right) charts for both the training and validation sets for the MobileNetV2 model are given above

Results

The best model in training was the ResNet101 model, while the two VGG models did better in validation. The ResNet101 model had an accuracy of 0.9175176024436951 and a loss of 0.2315249890089035 in training, while during validation, the VGG19 model had an accuracy of 0.7260429263114929 and the VGG16 model had a loss of 0.776662290096283. We ended up with a precision of 0.65, a recall of 0.61, and an F1-score of 0.63.

	precision	recall	f1-score	support
0	0.85	0.87	0.86	79772
1	0.65	0.61	0.63	31238
accuracy			0.80	111010
macro avg	0.75	0.74	0.74	111010
weighted avg	0.79	0.80	0.79	111010

Figure d

The precision recall score table is given above

The goal we were going for was that of higher sensitivity, as that would mean the model would have fewer false negatives at the cost of more false positives. This would be beneficial as this would mean that fewer people had a false sense of security, as it would be easier and more likely to detect false negatives later on rather than false positives. However, we ended up with a higher specificity, as we tended towards having more false negatives.

Conclusion

This model would be used in a live diagnostic situation. A doctor might have a histopathology sample under a microscope, and then this model would be implemented in a way so that it would return a result of whether or not it detected cancer. This implementation would make the diagnosis system more efficient and streamlined, as it removes the limiting factor of needing a doctor to review. This would not be the final diagnosis situation, as it would be a secondary step post-screening. Approximately 1 in 8 women will

develop breast cancer at some point in their lives, and 1 in 39 will die from the disease [15]. Additionally, while the survival rate for breast cancer when diagnosed early is 99%, if diagnosed later it can drop down to 30% [6].

Due to this, we hope that adding this step of plugging in a sample of tissue can create a more efficient workflow so that cancer can be more easily caught. A few next steps would be to get additional data to test and train the model on, as to get extra information about its possible use cases and limitations. Next, we could run a clinical trial and test the model with a specific controlled study group.

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