



NEAR EAST UNIVERSITY
INSTITUTE OF GRADUATE STUDIES
DEPARTMENT OF COMPUTER INFORMATION SYSTEMS

CERVICAL CANCER DIAGNOSIS USING VERY DEEP NETWORKS
OVER DIFFERENT ACTIVATION FUNCTIONS

PhD THESIS

KHALED MABROUK AMER ADWEB

Nicosia
December, 2022

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PROF. DR. NADIRE CAVUS

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Abstract

Cervical Cancer Diagnosis Using Very Deep Networks Over Different Activation Functions

Mabrouk Amer Adweb, Khaled

PhD, Department of Computer Information Systems

Prof. Dr. Nadire Cavus (Supervisor)

Assoc. Prof. Dr. Boran Sekeroglu (Co-Supervisor)

December, 2022, 97 pages

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Keywords: Cervical cancer, deep learning, residual learning, deep network, activation functions

Özet

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Mabrouk Amer Adweb, Khaled

Doktora, Bilgisayar Enformatik Anabilim Dalı

Prof. Dr. Nadire Çavuş

Doç. Dr. Boran Şekeroğlu

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Anahtar Kelimeler: Rahim ağzı kanseri, derin öğrenme, Artık öğrenme, derin ağ, aktivasyon fonksiyonları



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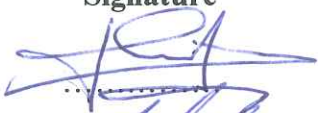






ASSOC. PROF. DR. BORAN SEKEROGLU

Nicosia

December, 2022

Approval

We certify that we have read the thesis submitted by Khaled Mabrouk Amer Adweb titled “Cervical Cancer Diagnosis Using Very Deep Networks Over Different Activation Functions” and that in our combined opinion it is fully adequate, in scope and in quality, as a thesis for the degree of PhD of Computer Information Systems.

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Declaration

I hereby declare that all information in this document has been obtained and presented in accordance with academic rules and ethical conduct. I also declare that, as required by these rules and conduct, I have fully cited and referenced all material and results that are not original to this work.

Khaled Mabrouk Amer Adweb

.... ./.../2022

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Khaled Mabrouk Amer Adweb

Abstract

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List of Abbreviations

ReLU: Rectified Linear Unit

Leaky ReLU: Leaky Rectified Linear Unit

PReLU: Parametric Rectified Linear Unit

HPV: Human Papillomavirus

PAP: Papanicolaou

ResNet: Residual neural Network

CSCC: Cervical Squamous Cell Carcinoma

TZ: Transformation Zones

CNN: Convolutional Neural Network

VGGNets: Visual Geometry Group Neural Networks

TP: True Positive

TN: True Negative

FP: False Positive

FN: False Negative

CHAPTER I

INTRODUCTION

This chapter introduces the entire thesis presented in this report. The introductory chapter presents the overview of the study which includes the motivation of the research from its proposal, the aims and objectives of the research, the significance of the study and an outline of the study's methodology as it was designed for the study. At the end of the chapter the overall outline of the entire thesis is also presented with a description of each chapter.

1.1 Overview

Cervical cancer is a tumor that grows in the cervix which is the narrow entrance of the uterus. Such type of cancer is more likely to hit the women aged between 30 and 45, who are sexually active (Dong et al., 2020). Cervical cancer is the most common deadly cancer for women in America (Dong et al., 2020) after the breast cancer. Up to date, cervical cancer is still considered incurable in case it reaches its severe later stages. Moreover, it is found by the statistics of the World Health Organization (WHO) that this type of cancer is the fourth most prevalent cancer globally, with a reporting rate of 5,70,000 new cases in 2018, accounting for 7.5% of all women cancer deaths (CDC, 2021). Currently, there are about 85% of the women who face death every year due to cervical cancer in the developing care where professional medical care is not well available.

This toll of deaths can be reduced or stopped by granting the developing world countries the access to better technology and healthcare systems in this field. This includes the availability of regular screening tests, which can help in providing an effective treatment for the cervical precancer stage. On the other hand, cervical cancer can be hard to be detected or diagnosed in its earlier stages as it has no clear and visible signs in its early stage (Zhang et al., 2020). This makes the regular screening and checkup very significant in order to prevent such disease as this earlier identification can increase the 5-years survival rate of this cancer to 66% (Dhawan et al., 2021).

The current methods available for screening cervical cancer are mainly the following: HPV testing, PAP smear testing, colposcopy, and biopsy (American Cancer Society, 2020). The most used screening technique for the diagnosis and treatment of cervical cancer is the PAP smear. However, this technique has several drawbacks: It needs big number of microscopic examinations to for the diagnosis of cancer and noncancer patients, in addition, it is time consuming and requires trained professionals. Nevertheless, PAP smear and HPV testing are considered very expensive treatment and they provide low sensitivity in detecting cervical cancer (Adweb et al., 2021).

Thus, the development of computer aid systems that can detect the precancerous stages of cervical cancer are in need. Such systems that rely only on images can be used as tools to assist medical experts in diagnosing the early stages of cervical cancer and whether or there is a probability of malignant cancer transformations.

Deep learning has proved itself as a powerful method in analyzing medical images (Shen et al., 2021). Starting from classification to segmentation, deep learning methods have made a sharp progress in that field, making identification and detection of diseases easier and sooner. However, going deeper and deeper, problems like vanishing gradients have appeared. Residual learning was however proposed as a solution to very deep networks. Residual learning (He et al., 2016) is a deep learning method that uses identity mapping and skip connections to improve the performance of a very deep network designed to perform complex medical images classification tasks such as chest x-rays diseases detection and others.

Some medical image analysis and classification can be very challenging such as the cervical pre-cancerous stage identification. This can be due to the complexity of the healthy and cervical cancerous types. Cervical has some pre-cancer stages which are not considered as cancer, but they can transform into cancer. These stages are three and they are referred as the three different types named as: type 1, type 2, and type 3. Each of these types have some different features however, they can also be very similar or hardly visible by human naked eye. Thus, this makes it challenging for a deep network to extract the most accurate features that describe each type. The motivation of such work is to prevent the cervical transformation by detecting when a cervical colposcopy image is normal or

abnormal (type 1, type 2, type 3) which can help medical doctors to take helpful precautions and provide the rightful treatments to patients which can prevent the cervical cancer transformation.

1.2 Statement of the Problem

Cervical cancer is a very dangerous disease which continues to challenge both patients and the medical health community. Like every other forms of diseases in humans the best possible case for treatment and management is the case of an early detection to ensure the adequate management and treatment processes are applied to patients. Early detection of cancer cases (Buskwofie et al., 2020; Johnson et al., 2019; Bouvard et al., 2021; Wentsensen et al., 2021; Lin et al., 2021; Boon et al., 2022; Wilailak et al., 2021) especially cervical cancer needs adequate early recognition of the symptoms of the disease, and the mere eye observation of precancerous images in diagnosis may not be efficient enough, and can be highly complemented by the use of computer vision solutions such as the research application presented here in this study.

1.3 Purpose of the Study

This study was proposed and implemented as a research effort in the field of computer vision to complement the medical field in the diagnosis of cervical cancer in the early stages of it being precancerous to enable adequate and proper management of the disease. The study was proposed to apply different models of deep learning models to enable an evaluation of the best performing model for the diagnosis of precancerous cervical images. The study is also carried out to contribute to the existing body of academic literature, and a possible real case implementation of the proposed model in diagnosis of precancerous cervical images in the health institutions.

1.4 Research Questions

The proposal of this research and the proposed methodologies of this study in the use of three different models of deep learning is faced with answering a research question of:

RQ1: Which of the models performs better in the classification of precancerous cervical images. Also,

RQ2: Whether or not any of the proposed models performs optimally to serves as a significant performance improvement in the applications of deep learning for precancerous image classification.

1.5 Thesis Objectives

It is seen that the studies that focus on diagnosing cervical cancer and distinguishing it from the healthy cervical colposcopy using deep learning methods are quite limited, and the studies that worked in that field used datasets that are not public, hence they can't be validated or reproduced. of diagnosing cervical cancer using deep learning are quite limited. Hence, applying deep networks in detecting the pre-cancerous cervical colposcopy is in an urge need as it may help in preventing their transformation into cancer. In this context, our main goal of this study was drawn, and it is to develop a classification deep learning model that has the capability of classifying the colposcopy cervical images into pre-cancerous or healthy colposcopy images. We selected the residual learning-based model due to their efficiency in case of very deep models which is needed in our case because we need to extract very deep and unique features from the images. For that purpose, we selected to use a ResNet18 architecture and train it from using precancerous and healthy images collected from public datasets which eventually should be capable of identifying the patients who have pre-cancerous cervical colposcopy. This network is designed from scratch; hence we evaluated its performance over different activation functions such as: rectified linear unit (ReLU), Leaky rectified linear unit (Leaky-ReLU), and parametric rectified linear unit (PReLU). Hence, to find the function that best fit our model, we replicated the same network's architecture and tested each replica over different activation function and finally evaluated each model's performance.

1.6 Significance of the Study

Cervical cancer screening is an effective stage to prevent the abnormalities transformation into cervical cancer. Hence, a deep learning model trained for detecting the abnormalities in cervical colposcopy images can help medical physicians in accurately identifying cervixes that may be abnormal and those that may more likely transform into cancer. In short, our contribution of this thesis is:

- A cervical screening residual learning based model that is trained on raw colposcopy images and has the capability of accurately identify whether a cervix is healthy or there is a chance of a cancer transformation was developed
- The proposed models in this thesis have shown performance improvement compared to other deep learning models proposed in related studies.
- The adoption of ResNet18 architecture to build the proposed models have shown the efficiency of the deep learning architecture in extraction of unique features to improve overall classification performance of healthy cervical images vs precancerous cervical images.
- A comprehensive report of the proposed methodology and the application of all the deep learning models have been made to show the impact of different activation functions on the performance of ResNet.

1.7 Limitations

This study like all researches is bound by some research limitations. The implementation of the study is limited to the underlying subject of the research. All literature reviews to form the background of the research are limited to published academic research literatures on the subject of deep learning, machine learning, image processing and precancerous cervical image computer classification. The research is also limited on the experimental dataset available to this research obtained from the health institutions and their classification of the images based on their observations.

1.8 Definition of Terms

- **Rectified Linear Unit (ReLU):** This is a piecewise function characterized as a linear function, ReLU has the ability to directly output an input if it is found to be positive, else it will be output as a zero. ReLU has become a prominent and default activation function for several neural network models because of its ease of training and good performance (Agarap, 2018).
- **Leaky Rectified Linear Unit (Leaky ReLU):** This is a variation of ReLU activation function that is primarily used for negative values that have a small

slope contrary to a flat slope. In Leaky ReLU, the coefficient of the slope is predetermined before training commences. ReLU is a prominent in classification tasks that have a challenge of sparse gradients (Wang et al., 2018).

- **Parametric Rectified Linear Unit (PReLU):** This is also a variation of the ReLU function which is used to carry out a generalized application of a slope for negative values in a traditional ReLU rectified linear unit (Wang et al., 2022).
- **Papanicolaou (PAP):** This is a medical health test that is carried out to collect cells from the human cervix for closer look and observation to distinguish and diagnose cancer and precancerous in the cervix (McDonald et al., 2022).
- **Residual neural Network (ResNet):** This is an artificial neural network (ANN) that can be in two variants; either gated or non-gated. ResNet is the first ANN with hundreds of layers of deep neural networks (Fang et al., 2021).
- **Cervical Squamous Cell Carcinoma (CSCC):** This is a rare form of cervix glassy cell carcinoma, it is characterized as a very aggressive uterine cervix tumor (Cheng et al., 2020).
- **Convolutional Neural Network (CNN):** This is a class of ANN that are commonly applied in the computer analysis and classification of images (Desai & Shah., 2021).

1.9 Thesis Overview

This thesis is structured as follows:

- **Chapter one:** This is an introduction of the thesis which also shows the problem that is detected and studies in this thesis, as well as the scope, objective and the significance of the study.
- **Chapter two:** This includes theoretical background about neural networks. It also explains deep learning, transfer learning concepts in addition to discussing the convolutional neural network and how can transfer learning is accomplished.

- **Chapter three:** This is the methodology chapter of the thesis, where the research tools, materials and methods are discussed for the experimental setup of the study.
- **Chapter four:** This chapter presents the results of the designed experiments presented in the proposed methodology.
- **Chapter five:** This is the discussion chapter of the thesis, where all the reported results are discussed relative to the performance and the design of the proposed methodology of this research.
- **Chapter six:** This is the conclusion chapter of the thesis. In this chapter a conclusion statement is made, and recommendations based on the findings of the study are also presented.

CHAPTER II

LITERATURE REVIEW

This chapter presents a comprehensive literature review carried out to provide a robust theoretical background of the study. The literature reviews covers literature findings on the subject of cervical cancer diagnosis in the healthcare systems across the globe and the best practices relating to the state of the art methods used. Also, the literature review covers the subject of deep learning classification methods, related researches to our study, and their respective findings.

2.1 Theoretical Background

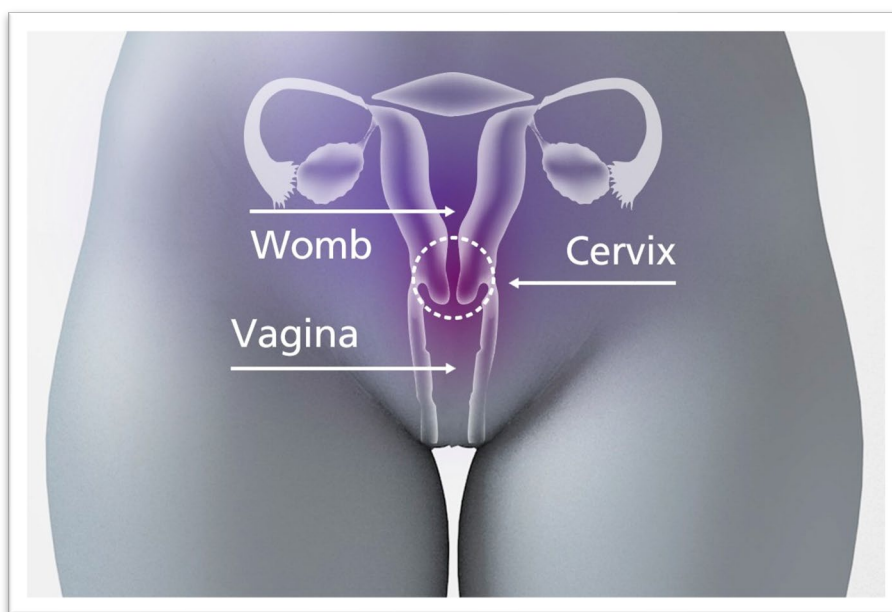
2.1.1 Cervical cancer

Cervical cancer is a cancer it's determined anywhere inside the cervix which is the hole among the vagina and the womb (uterus). Cervix is also a part of the reproductive system and is sometimes known as the neck of the womb (ASCO, 2020). Nearly all cervical cancers are due to an infection from certain kinds of human papillomavirus (HPV). It can often be averted by way of attending cervical screening, which pursuits to find and deal with modifications to cells earlier than they become cancer (Birdsong, 1996). Cervical cancer generally grows very slowly, and its growth far relies upon on how massive it is and whether it has spread to all parts of the body in addition to the individual's standard health situation (Lu et al., 2020).

Cervical cancer affects about 14,000 people in the United States each year. Cervical cancer is most commonly detected in people between the ages of 35 and 44. At the time of diagnosis, the average patient is 50 years old. Cervical cancer claims the lives of about 4,000 people each year. Because of screenings and the HPV vaccine, this percentage is decreasing. Figure 2.1 shows the cervical structure (NHK, 2021).

Figure 1.1.

Cervix structure (NHK, 2021)



2.1.2 Cervical cancer types

Cervical cancer is divided into two types: squamous cell carcinomas and adenocarcinomas. Squamous cell carcinomas account for 80 to 90 percent of cervical malignancies, while adenocarcinomas account for 10 to 20 percent (CDC, 2020). The squamous cell carcinoma (CSCC) can be defined as the second most common form of skin cancer. It begins in the epidermis, or skin's outer layer of cells. SCCs are more commonly detected on sun-exposed areas of the skin. Hands, face, arms, legs, ears, mouths, and even bald areas on the top of the head all fall under this category. SCCs can develop in mucus membranes and the genitals, among other places (NHK, 2021).

Adenocarcinoma is a cancerous tumor. It starts in the glands that line your organs and grows from there. Breast, stomach, prostate, lung, pancreatic, and colorectal cancers are all common types of adenocarcinoma. This form of cancer can affect a number of different body parts, including:

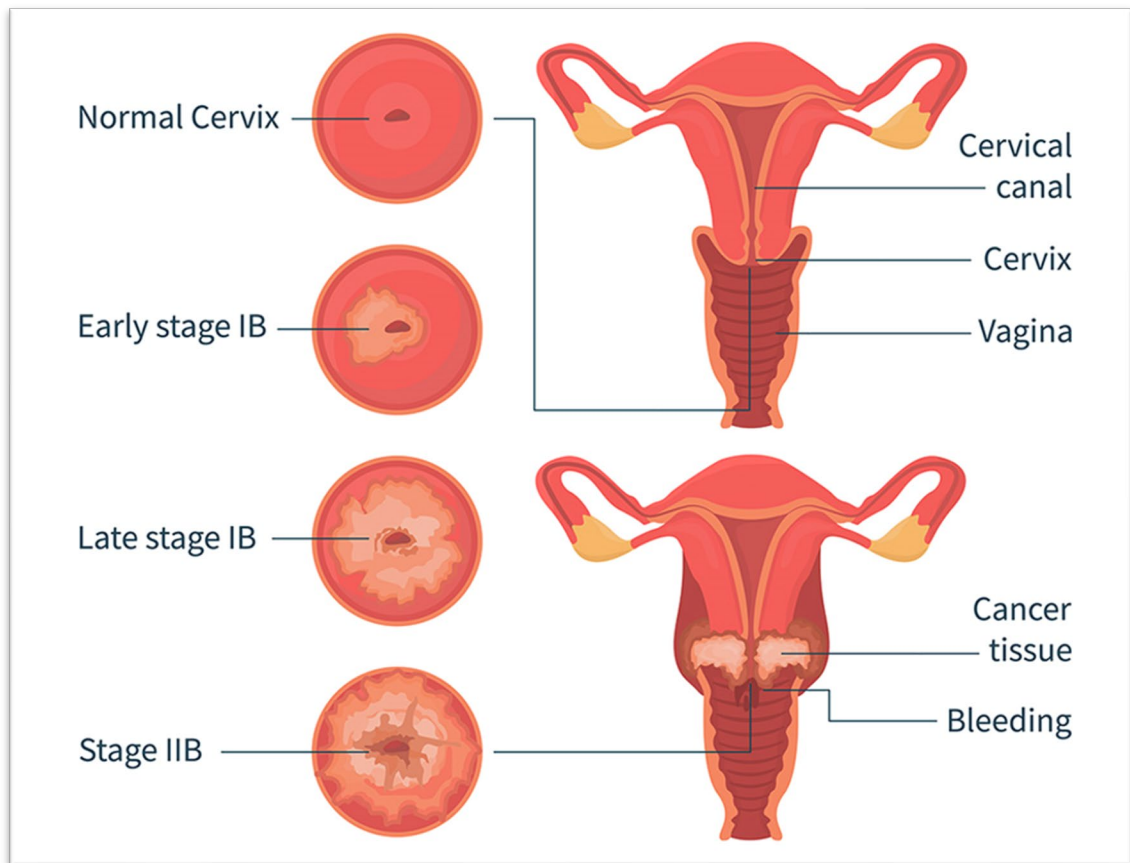
- Breast.
- Prostate.

- Pancreas.
- Esophagus.
- Colon/rectum.
- Stomach.

Adenocarcinoma is a cancer that originates in the glands that line your organs (glandular epithelial cells). Mucus, digestive juices, and other liquids are secreted by these cells. Tumors might arise if your glandular cells start to alter or expand out of control. Some tumors discovered in glandular cells are benign and do not cause malignancy. Adenomas are the medical term for these tumors. Some tumors that grow in glandular cells, however, are malignant. Adenocarcinomas are the medical term for these tumors (Gorantla et al., 2019). Adenocarcinomas start off as tumors in the glands that line the organs, but they can migrate to other parts of the body. The brain, liver, lungs, lymph nodes, bone, and bone marrow are all possible targets. Figure 2.2 shows the different stages of cervical cancer.

The cervical cancer grade informs medical doctor about the cancer's prognosis and treatment options. Cervical cancer cells are graded on a scale of 1 to 3:

- Grade 1 (low grade) cells resemble regular cells the most.
- Grade 2 cells resemble normal cells in appearance.
- Grade 3 (high grade) look aberrant and unrelated to normal cells

Figure 2.2.*Stages of cervical cancer (Lyndhurst, 2022)*

2.1.3 Symptoms of cervical cancer

Many women with cervical cancer are unaware that they have it until it has progressed to the point where symptoms appear. When symptoms do occur, they're frequently misdiagnosed as menstrual cycles or urinary tract infections (UTIs). Symptoms of cervical cancer include:

- Between cycles, after sex, or after menopause, strange bleeding can happen.
- Vaginal discharge that is different in appearance or scent than typical
- Pelvic discomfort
- Requiring more frequent urination
- Urinary discomfort

2.1.4 Causes of cervical cancer

The sexually transmitted human papillomavirus is responsible for the majority of cervical cancer cases (HPV). The virus that causes genital warts is the same one that causes this. There are over 100 distinct HPV strains. Cervical cancer is caused by only a few varieties. HPV-16 and HPV-18 are the two most frequent kinds that cause cancer.

Cervical cancer is not inevitable if you are infected with a cancer-causing strain of HPV. The vast majority of HPV infections are cleared by the immune system within two years. Other malignancies can be caused by HPV in both men and women. These are some of them:

- Cancer of the vulvar,
- Cancer of the uterus,
- Cancer of the penis,
- Cancer of the anal,
- Cancer of the rectal mucosa,
- Cancer of the throat.

2.1.5 Cervical cancer treatment

Cervical cancer can be easy to be treated in case it was detected early. The four main treatments are (Netmetds, 2021):

- *Surgery*: The goal of surgery is to get rid of as much cancer as possible. The doctor may be able to remove only the part of the cervix that has cancer cells. Surgery to remove the cervix and other pelvic organs may be required if the cancer is more extensive.
- *Radiation therapy*: High-energy X-ray beams are used to kill cancer cells. It can be administered by a machine that is external to the body. A metal tube implanted in the uterus or vaginal canal can also be used to deliver it from within the body.
- *Chemotherapy*: This technique is a treatment that employs chemicals to kill cancer cells all over the body. This treatment is given in cycles by doctors. Chemo will

be administered to you for a length of time. After that, you'll discontinue the treatment to allow your body to heal.

- *Targeted therapy:* Bevacizumab (Avastin) is a newer medicine that differs from chemotherapy and radiation in how it works. It prevents the formation of new blood vessels, which aid cancer growth and survival. This medication is frequently used in conjunction with chemotherapy.

2.2. The Transformation Stage

Cervical cancer can be easy to prevent if discovered in its early stages. Hence, every woman, regardless of where she lives, should have access to effective, life-saving treatment. Women in low-resource situations around the world are now benefiting from programs that diagnose and cure cancer in a single visit (Zhang et al., 2014). However, one of the most difficult aspects of these cervical cancer screen and treat programs is establishing the optimal mode of treatment, which might vary depending on patients' physiological characteristics, in part owing to a lack of experience in the sector.

In order to prevent the transformation stage or cervical cancer, cervixes should be diagnosed and divided into three types: type 1, type 2, and type 3. These three types help medical doctors find the transformation zones that are more susceptible to convert the cervix tumor into cancer. Thus, detecting these zones can help in providing the best treatments that may prevent the cancer. All these types are not cancerous (Normal).

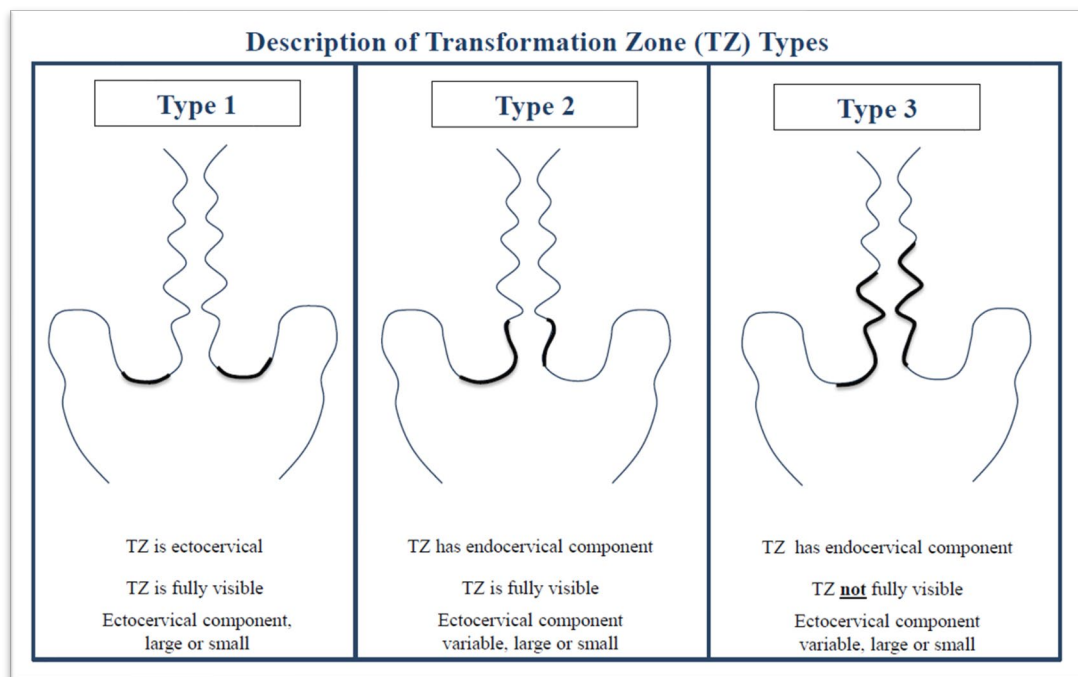
To identify the type of colposcopy images, the colposcopist can do an assessment of the following (Netmeds, 2021):

- Adequate/inadequate indicates whether the cervix has been visualized and, if not, why (e.g. vaginal stenosis, cervix obscured by inflammation, bleeding, scarring)
- Visibility of the squamocolumnar junction: the internal edge of the TZ that is totally visible, somewhat visible, or not visible.
- According to the visibility of all or part of the squamocolumnar junction's upper limit, TZ should be classified as Types 1,2, or 3:
 - **Type 1:** In this type, all the transformation zone (TZ) is ectocervical in addition to the upper limit

- **Type 2:** For this type, the transformation zone's upper limit is partially or totally visible in the canal and is fully visible around 360 degrees.
- **Type 3:** In the canal, only a portion or the complete upper limit of the TZ is visible. The outer limit of Type 3 TZ may be evident on the ectocervix, in the canal, or not apparent at all (Figure 2.3).

Figure 2.3.

Types of cervical pre-cancerous transformation zones (Cancer, 2020)



2.3 Deep learning

Deep learning is essentially a subset of a neural network composed of more than three hidden layers of neurons. These neural networks try to mimic human brain behavior in more accurate way than the traditional three layers networks. However, they are far from fulfilling its ability unless they are trained using large amount of data which allows such deep networks to “learn” low- and high-level features from large amounts of input data (LeCun et al., 2015). Although a neural network of one or very few hidden layers can

still achieve approximate predictions, adding more hidden layers can also help to create deeper models which can optimize and refine for better accuracy (Lu et al., 2019).

Recently, deep learning methods and models drive many artificial intelligence applications and services due to its strong ability of improving automation and performing analytical and physical tasks better than human in some cases (Shen et al., 2017). Convolutional neural networks are mainly described by a sequence of several layers that work together to extract meaningful features from an image in order learn an output related to the input image. These layers are the following (Lecun et al., 2015):

- *Input Layer*: This is the first layer in which a 2D or 3D image is fed into a network to be processed by several consecutive layers.
- *Convolution*: The typical CNN architecture is shown in Figure 2.5. as seen the first layers are usually the convolution layers, pooling layers and then these two are followed by some fully connected layers where images are classified. In convolution layer, the image undergoes n convolution filters of size $k \times k$ to generate n convolution maps ($C1$) of size $i \times i$.

An image, in general, can be mathematically represented as a tensor with the following dimensions:

$$\dim(image) = n_H, n_W, n_C$$

Where:

- n_H : the size of the Height
- n_W : the size of the Width
- n_C : the number of Channels

In case of a RGB image, for instance, we have $n_C = 3$, Red, Green and Blue. In convention, we consider the filter K to be squared and to have an odd dimension denoted by ff which allows each pixel to be centered in the filter and thus consider all the elements around it.

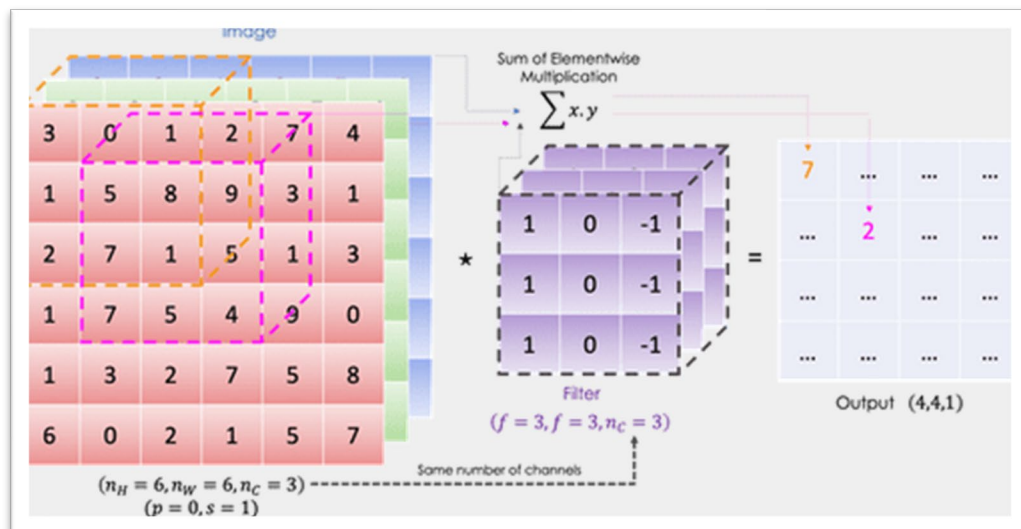
When operating the convolutional product, the filter/kernel K must have the same number of channels n_c the image, this way we apply a different filter to each channel. Thus the dimension of the filter is as follows:

$$\dim(\text{filter}) = f, f, n_c$$

The convolutional product between the image and the filter is a 2D matrix where each element is the sum of the elementwise multiplication of the cube (filter) and the subcube of the given image as illustrated in Figure 2.4:

Figure 2.4.

Basics of convolutions operation (Lecun et al., 2015)



Mathematically speaking, for a given image I_I and filter k_k we have:

$$\text{Conv}(I, K)_{x,y} = \sum_{i=1}^{n_H} \sum_{j=1}^{n_W} \sum_{k=1}^{n_C} K_{i,j,k} I_{x+i,-1,y+j-1,k}$$

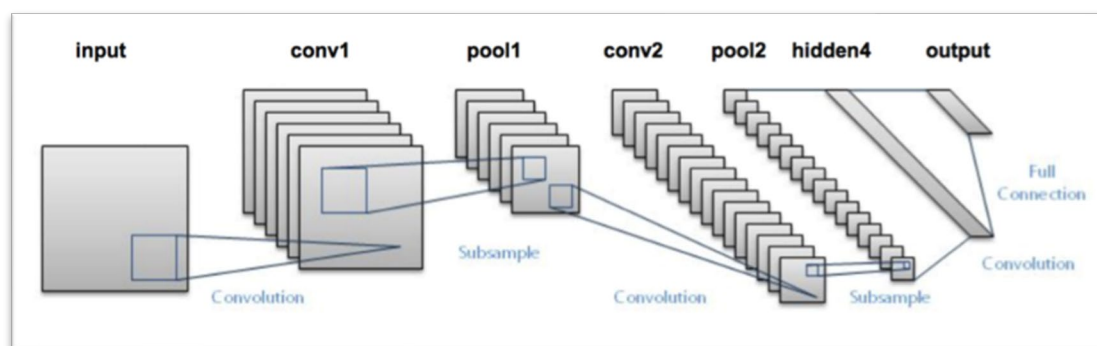
- *Maximum pooling*: The convolution layer is followed by a pooling layer in which the features maps computer I this layer are than sub-sampled a pooling (sub-sampling) operation on the convolution maps using a window size of $b \times b$.

Down-sampling is accomplished with a max pooling layer, which divides the input into rectangular pooling regions and computes the limit of each region.

- *Batch Normalization*: A batch normalization layer uses a mini batch to standardize each and every input channel. Batch normalization layers are used between convolutional layers and nonlinearities, such as the ReLU layers, to speed up convolutional neural network training and reduce sensitivity to network initialization. The layer first standardizes the activations of each channel by taking away the mini-batch mean and dividing it by the mini-batch standard deviation. Then, the layer moves the input by a learnable offset β and measures it by a learnable scale factor γ . A batch normalization standardizes its inputs x_i by first computing the mean μ_B and variance σ_B^2 over a mini-batch and over each input channel. Then, it computes the normalized activations as the new inputs.

Figure 2.5.

Basic convolutional neural network architecture (Lecun et al., 2015)



2.3.1 Residual Learning

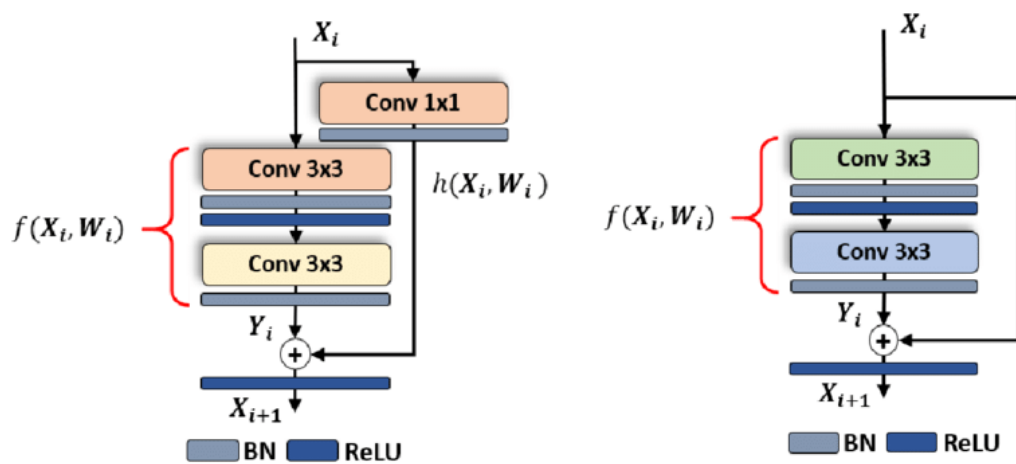
Deep networks have recently begun to go deeper, i.e., to include numerous hidden layers. This "extreme" depth appeared to be linked to some optimization issues throughout the network learning process. When a network is trained with a stochastic gradient descent approach, this problem is known as vanishing gradients (He et al., 2016; Oyedotun et al., 2018). The notion is that as the networks become more complex, the estimated gradient of the loss function begins to fall exponentially as it propagates back to the starting layers. As a result, it may approach zero at some layers, making the network difficult to train. Weights

and biases may not be properly tuned during each training pass if the gradient is small or zero, resulting in less convergence and a high error value.

He et al. (2016) developed a residual learning idea for simply creating and training very deep networks without having to deal with the vanishing gradients problem. Instead of connecting layers in a shallow way, residual networks (ResNets) established a new idea of connections termed the skip or identity connections over some layers. This is built on residual units in the network, where the identity of input is mapped from lower to higher hidden layers. As a result, rather of learning the underlying input mapping, the network is permitted to fit its residual mapping, as illustrated in Figure 2.6a.

Figure 2.6.

Residual units and identity mappings (Owais et al., 2019)



(a) 1 X 1 convolutional map based ResNet

(b) Identity map based ResNet

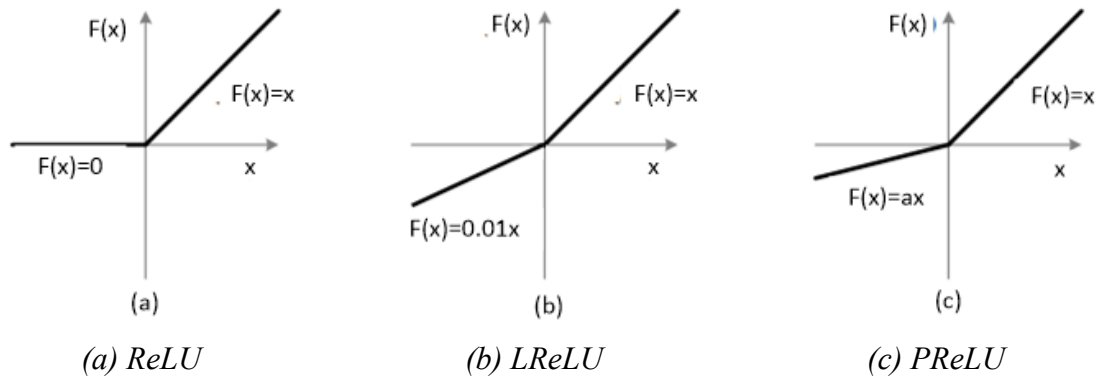
Residual mappings can be divided into two categories. The identity mapping-based shortcut connectivity (Figure 2.6a) is the first one and it is when the input is plainly exposed to a skip or short connection without having to go via the convolution layer (He et al., 2016; Oyedotun et al., 2017). The convolutional based identity mapping is the second residual block, in which a brief link of input hits a 1x1 convolution layer along the shortcut path (Figure 2.6.b). The residual units of a residual network structure are shown in Figure 2.6.

In terms of computational complexity and training time, more identity mapping-based shortcut connectivity leads to better network performance. Moreover, identity

mapping based on convolution can help in better propagation of information during the forward and backward passes of network learning.

Figure 2.7.

Activations functions



Furthermore, each residual unit has two convolutional layers with a 3x3 filter size, as shown in Figure 2.6. These filters save the learnable parameters that are optimized during the network's training phase. Each unit additionally has a batch normalization (BN) layer that normalizes the features map and a rectified linear unit (ReLU) layer that serves as the network's activation function. The following are the inputs and outputs (He et al., 2016):

$$Y_i = h(X_i) + f(X_i + W_i) \quad (1)$$

$$X_{i+1} = F(Y_i)$$

(2)

The identity mapping of input X_i is represented by $h(X_i)$, while the residual function is represented by F . The input, weight, and output are represented by X , W , and Y , respectively. As a result, the identity mapping (Figure 2.7a) is defined as $h(X_i) = X_i$ in the case of identity mapping-based shortcut connection. However, in the case of convolutional based identity mapping (Figure 2.7b), the identity mapping is defined as $h(X_i, W_i)$ and is not the same as input because a 1x1 convolution layer is used to exceed it. The following are the input-output computations in this case:

$$Y_i = h(X_i, W_i) + f(X_i + W_i) \quad (3)$$

$$X_{i+1} = F(Y_i) \quad (4)$$

Where $h(X_i, W_i)$ represents the convolutional based identity mapping.

2.3.2 Activation functions

The three activation functions used in this study, namely ReLU (Simonyan and Zisserman, 2014), Leaky-ReLU (Xu et al, 2015), and PReLU (He et al., 2017), will be addressed in depth in this section. The functions that set a specific output or "activation" for a given input based on its weight are known as activations functions. Non-linear transform functions that can learn complex mapping functions are preferred transform functions (Agarap, 2018). To perform well with the Sigmoid activation function, traditional and shallow neural networks with one or a few hidden layers are used. The input values are transformed into a range of 0 and 1 using this non-linear activation function. As a result, the output is between 0 and 1 for any given positive or negative input. When employing the Sigmoid function, however, one important issue arises. With a given big positive value, the sigmoid function saturates.

- ***Rectified Linear Unit (ReLU)***

After that, a rectified linear unit (ReLU) was proposed to solve the Sigmoid activation function problem (Simonyan and Zisserman, 2014; Szegedy et al., 2015). It has gained a lot of traction in deep learning networks and has led to a lot of ground-breaking applications in various disciplines (Simonyan and Zisserman, 2014; Szegedy et al., 2015; Oyedotun et al., 2018). As seen in equations 5 and 6, it is simply threshold at zero input values, i.e., it zeros the negative input values while keeping the positive input values.

$$F(x) = \max(0, X) \quad (5)$$

Which has the gradient of

$$F'(x) = \begin{cases} 0 & \text{if } x \leq 0 \\ x & \text{if } x > 0 \end{cases} \quad (6)$$

Where F is the ReLU activation output, and x is the input value.

ReLU improved the performance of deep convolutional neural networks by allowing them to converge more quickly and avoid the vanishing gradient problem. ReLU, on the other hand, can occasionally experience “dying ReLU”, in which the ReLU neuron's input values are trapped at negative levels. ReLU output is always 0 in this situation, which deactivates the majority of the neurons (Lu et al., 2019). As a result, the network's learning is harmed, resulting in poor convergence and performance (Nwankpa et al., 2018). Setting the learning rate to minimal values can help, but other modified versions of ReLU have also been proposed to avoid zeros being generated for negative input values.

- ***Leaky-ReLU***

Xu et al. (2015) introduced Leaky ReLU (Leaky-ReLU) as a new activation function to improve and alter the traditional ReLU and solve more complex and non-linear functions. The major goal of Leaky-ReLU was to eliminate the problem of "dying ReLU," which was linked with ReLU. As a result, this method indicates a little information loss in the section where output is always 0. Because the weights will be modified, the gradient will be minimal but not zero, and neurons will not be dormant. This function proposes that in the case of negative input, the output will be the input multiplied by a little value (0.01) so that the neurons are not turned off (Equation 7 and 8).

$$F(x) = \begin{cases} \alpha x & \text{if } x \leq 0 \\ x & \text{if } x > 0 \end{cases} \quad (7)$$

Which has the gradient of

$$F'(x) = \begin{cases} \alpha & \text{if } x \leq 0 \\ 1 & \text{if } x > 0 \end{cases} \quad (8)$$

- ***PRELU***

Applying Leaky-ReLU to CNNs (Clevert et al., 2015; Nwankpa et al., 2018; Goodfellow et al., 2013) revealed that this function has several advantages over ReLU, such as eliminating the zero-gradient aspect of the vanishing gradient problem and speeding up network learning and convergence. However, several research (Maas et al., 2013; Clevert et al., 2015; Xu et al., 2015) have found that Leaky-ReLU has a small impact on network accuracy; as a result, He et al. (2015) presented a new modified version of Leaky-ReLU. A

parametric rectified linear unit (PReLU) is a new approach that is comparable to Leaky-ReLU. Instead of having a predetermined slope value of 0.01 for negative inputs, PReLU lets the network to learn this coefficient, just like weights and biases, during training. The following is the function's output:

$$F(x) = \begin{cases} \alpha x & \text{if } x \leq 0 \\ x & \text{if } x > 0 \end{cases} \quad (9)$$

This function has the gradient of

$$F'(x) = \begin{cases} \alpha & \text{if } x \leq 0 \\ 1 & \text{if } x > 0 \end{cases} \quad (10)$$

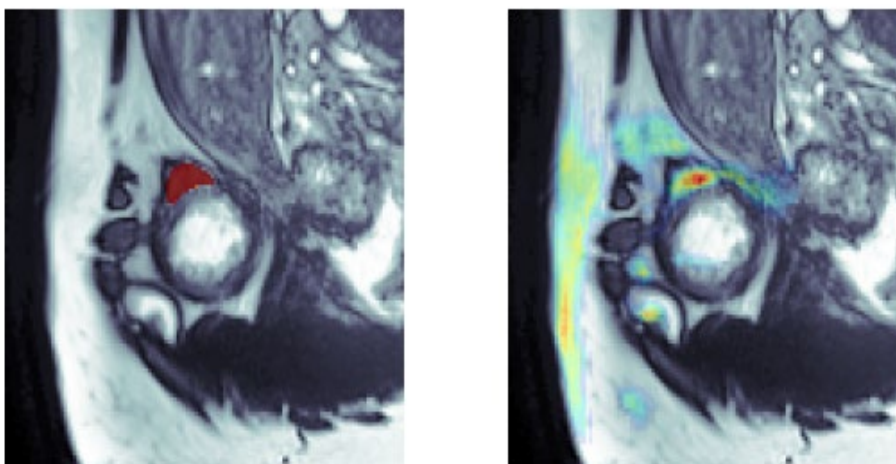
Where F is the leaky PReLU activation function, x denotes the input value, and α denotes the learnable coefficient. The three different activation functions are shown in Figure 2.7. It can be observed that depending on the coefficient value, which is learnable in this case, PReLU can contain them all:

- If $\alpha=0$; F becomes ReLU
- If $\alpha>0$; F becomes Leaky-ReLU
- If α is a learnable parameter, F becomes PReLU

These three activation functions are used in a residual network constructed for the detection of cervical cancer in this research. In order to choose the best function for such a residual network's classification task, the network's performance is compared across the three aforementioned functions in terms of accuracy.

Figure 2.8.

An example of the effects of different Transfer function on the medical image's segmentation (Nieradzik et al., 2021)



(a) Left: Leaky ReLU

(b) Right: Parametric ReLU

2.3.4 Residual Networks Architectures

The ResNet model was quite successful, as evidenced by the fact that its ensemble took first place in the ILSVRC 2015 classification competition with a 3.57 percent error rate (He et al., 2016). It also won first place in the ILSVRC and COCO contests in 2015 for ImageNet detection, ImageNet localization, COCO detection, and COCO segmentation.

2.3.4.1 The significance of ResNet in computer vision

Machine learning professionals add extra layers when working with deep convolutional neural networks to tackle an issue in computer vision. These additional layers aid in the faster resolution of complicated problems since the individual layers can be trained for different jobs to produce highly accurate outcomes (Jastrzębski et al., 2018).

While the number of stacked layers might enhance the model's features, a deeper network can reveal the degradation issue. To put it another way, as the number of layers

in a neural network grows, the accuracy levels may become saturated and gradually decline. As a result, the model's performance degrades on both training and testing data.

ResNet was built specifically to address this issue. Residual blocks are used in deep residual nets to increase model accuracy. The strength of this form of neural network is the concept of “skip connections”, which is at the heart of the residual blocks.

There are two ways that these skip connections work. First, they solve the problem of vanishing gradients by creating an alternate path for the gradient to follow. They also allow the model to learn an identity function. This ensures that the model's upper levels perform equally well as the lower layers.

In short, residual blocks make learning identity functions much easier for the layers. As a result, ResNet boosts the performance of deep neural networks by adding more neural layers while lowering the error rate. To put it another way, skip connections combine the outputs of prior layers with the outputs of stacked layers, allowing for far deeper network training than previously feasible.

2.3.4.2 ResNets architecture

The ResNet-34 was the first ResNet architecture, which included inserting shortcut connections within a plain network to transform it into its residual network counterpart. The plain network was influenced by VGG neural networks (VGG-16, VGG-19) in this case, with 3 filters in the convolutional networks. ResNets, on the other hand, have fewer filters and are less sophisticated than VGGNets. The 34-layer ResNet reaches 3.6 billion FLOPs in comparison to 1.8 billion FLOPs for smaller 18-layer ResNets (He et al., 2016).

It also followed two simple design rules: Each layer had the same number of filters for the same output feature map size, and the number of filters was doubled if the output feature map size was halved to keep the time complexity per layer the same.

This plain network was enhanced using shortcut connections. Despite the fact that the input and output dimensions were identical, the identity shortcuts were applied immediately. There were two options to consider when the dimensions were increased (Oyedotun et al., 2018). The first was that the shortcut would still execute identity mapping while padding the dimensions with extra zero entries. To match dimensions, the

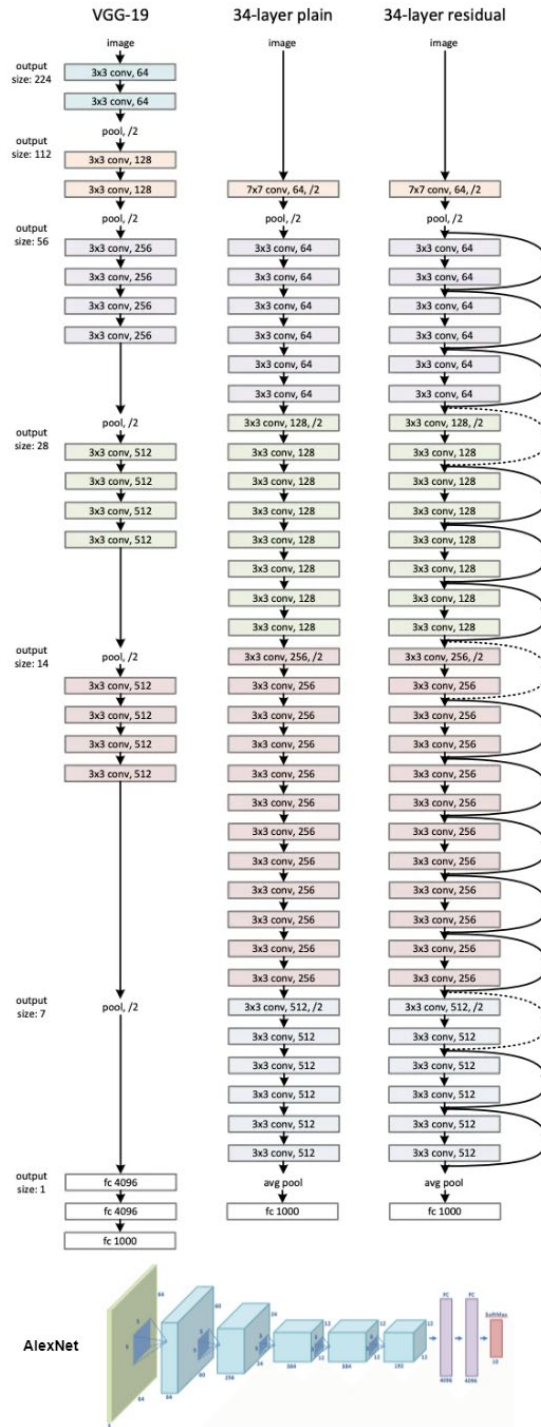
alternative option was to employ the projection shortcut. Figure 2.9 shows the architecture of ResNet in addition to the skip connections included in it versus other structure such as the plain structure and the VGG architecture.

2.4 Related Research

It is noticeable from the review that most of cervical cancer screening studies were conducted using hepatological or microscopic images (Bengtsson & Malm, 2014; Ghoneim et al., 2020; Zhang & Zhao, 2019), while a few have been conducted to diagnose cancer using colposcopy images (Dhawan et al., 2021; Adweb et al., 2021; Chandran et al., 2021). This may be either because of the lack of the public datasets or the complexity of classifying or screening cervical pre-cancer types using colposcopy images. In general, most of the studies propose used microscopic input images in order to classify them into cancerous or non-cancerous. These studies produced significant results, but they used different modality databases for training and testing their models. A deep learning method was proposed to classify the colposcopy images into type 1, type 2, and type 3 in (Chandran et al., 2021).

Figure 2.9.

The ResNet's architecture versus different types of deep models' architectures (He et al., 2016)



Similar to our work, popular cervical screening dataset is used for training and testing the network presented. The authors in this work proposed a deep network named as Colposcopy Ensemble Network (CYENET) to classify cervical cancer automatically

from colposcopy images. It is noticed that such deep network was capable of achieving significant results when compared to other models such as VGG16 and VGG19. When tested, the CYENET presented in this work reached an accuracy of 92.3%. However, this study aims to classify the three different types of cervical pre-cancerous stages in contrast to our work which combines these three types as 1 type: abnormal.

Another study for the classification based deep learning method was proposed by Mustafa and Dauda (2021). Their method uses three different deep convolutional neural networks (DCNNs), each with different optimizers such as stochastic gradient descent (SGD), Root Mean Square Propagation (RMSprop), and Adaptive Moment Estimation (Adam), for the classification of cervical images into healthy or cancerous. This model was then trained and tested cancerous and healthy cervical images and the best optimizer based on the one that leads to the best performance of the network.

Moreover, Yuan et al. (2020) proposed a method for the recognition of cervical squamous intraepithelial lesions recognition in colposcopy images. The authors used different deep learning models such as U-Net network in order to segment the lesion in a cervix and feeding this segmented cervix part into a ResNet to be then classified as positive or negative in which positive means cancer. Experimentally, this study achieved a relatively good classification accuracy of 84.10% in classifying positive and negative colposcopy cervical cancer images.

Haidar et al. (2017) conducted a study for the classification of uterine cervical cancer using images of digital histology. Different several steps were adopted in this study which include division of images into 10 groups, subdivision of groups into 3 parts (top, middle, and bottom with an average of 0.5551, 0.5362, and 0.3847 respectively), chunk extraction, as well as the classification of various segments of the images. However, the experimental data was 65 images in total. 32 images were classified from the data set as normal cells (32 images), CIN1 cells (7 images), CIN2 cells (17 images), and CIN3 cells (10 images). However, the results indicated that the algorithm utilized in this study has a better result (77.37%) compared to a previously adopted method (75.75%) with the same data set.

Another study conducted by Wasswa et al. (2019) used a proposed methodology of fuzzy c means algorithm to carry out the classification of pap smears. The study aimed at mitigating lack of accuracy a precision in the Pap-smear technique through an automated technique. The enhancement of images was carried out through a “contrast adaptive histogram” and the segmentation of cells was accomplished using a “Trainable Weka Segmentation classifier”. Three different data sets were used in analyzing the classifier. Which consist of single and multiple cell images as well as slide images from Pap smear. The specificity, precision and accuracy observed from each of the analyzed data sets were “98.88%, 99.28% as well as 97.47%” for single cell images, “97.64%, 98.08% as well as 97.16%” for multiple cell images and “96.80%, 98.40% and 95.20%” for Pap smear slide images. However, the results observed from this study clearly shows a better accuracy and precision as opposed to other algorithms based on false results on positivity (2.53%), false results on negativity (0.72%) as well as errors observed during classification of data in cancer analysis.

Another study by Pegah et al. (2018) used deep CNN for the discrimination of pathology images. This study focused on distinguishing between two kinds of lungs cancer, bladder cancer and different four kinds of biomarkers as well as five breast cancer biomarkers. Deep learning approach was utilized in the analysis and detection of different subgroups of cancer. The accuracy of the results from this analysis was 69%, 95%, 92% and 100% for the identification of different subgroups of cancer and biomarkers.

Henning et al. (2018) carried out an analysis on nuclei detection using deep learning methods, in their proposed method, a combination of PMap techniques were applied. The effort of training, detection and image quality of different data sets were analyzed in this study. Moreover, from the report it was observed that post processing of PMap had the highest quality during the detection. Hematoxylin and Eosin (H & E) strained views had the best performance (f1 measure – 0.816) of “colorectal adenocarcinomas” as well as Ki-67 measure (0.819) in breast cancer imaging. This detection was processed and analyzed at 4.15 mega-pixels. This method of detection proved to be of high quality as well as high precision.

Siti et al. (2015) proposed a cervical cancer image classification for neural Pap system using an improved feature extraction method. The use of Neural-Pap in detection analyses has several limitations, but in this study several strategies were used to eliminate these limitations. “Adaptive Fuzzy-k-Means (AFKM)” is a proposed algorithm for this study. However, the proposed algorithm for this study was observed to be more effective than the single Neural-Pap algorithm. Hence, the combination of these algorithms has been found to increase the detection and imaging of cervical cancer with 76.35% as opposed to Neural-Pap (73.40%).

Peng et al. (2019) studied the application of deep learning algorithms on cervical cancer MRI images. The study was focused on cervical cancer segmentation technology, through the use of wireless network and deep learning algorithm in the analysis. During the study two different types of deep learning analysis (traditional and optimized algorithms) was carried out on five different test groups. However, results obtained from the different five rest groups showed that the traditional algorithm is not an idea test method as seen with the low accuracy and data’s not exceeding 90%. For an accurate MRI analysis of cervical cancer, as reported by Peng et al. (2019), the optimized algorithm and wireless network gave a result with an accuracy of about 98%. Hence the use of this technique and method is highly effective in the detection of cervical cancer.

Noha et al. (2019), proposed a deep learning method of ad carcinoma detection. The purpose of this study was to carry out an adaptation measure on different deep learning techniques in the detection of esophageal adenocarcinoma. In detecting the “high-definition white light endoscopy” region of esophagus, different detection methods were used via “convolutional neural networks (CNNs). The different techniques utilized involve “fast R-CNN”, “Faster R-CNN”, “Regional based convolutional neural network; R-CNN”, “Single shot multi-box detector (SSD)”. During the analysis, a total of 100 images were gotten from 39 patients. However, results from this study revealed that SSD as well as Faster R-CNN (accuracy – 0.83) had the best imaging quality with a sensitivity, specificity, and F-measure of 0.96, 0.92 and 0.94 respectively for SSD. The method utilized in this study revealed its effectiveness in the detection of abnormal regions of esophageal adenocarcinoma.

An early diagnosis and progression of cervical cancer using deep learning was proposed by Nguyen et al. (2017). In their study a total of 8 datasets consisting of “202 cancer”, “115 cervical intraepithelial neoplasia”, and “105 normal samples”. Deep learning technique was introduced in the analysis of the datasets, as well as analysis on the viability of cells. The records from the analysis revealed an accuracy ready of 97.96%, sensitivity (99.01%) and a specificity reading (95.65%). However, this analysis will help open new avenues with effective readings for cancer cell staging. Ramin and Zahra (2017), also carried out a similar study using methods for the adaptive brachytherapy treatment based on the classification cervical cancer images and their progression.

Cox models of deep learning was applied in a study by Matsuo et al. (2019) for prediction of outcomes of survival of patients of cervical cancer. The main focus of this study was to make comparison between “cox model” and “neural network model” in the diagnosis of cervical cancer. Samples containing 40 demo graphs of cancer were grouped into 3 groups. The results observed for deep learning and cox technique were 0.695 and 0.787 for the concordance index. This study revealed deep learning technique to be more suitable in cervical cancer diagnosis.

Liyuan et al. (2019) applied a hybrid method of cervical tumor segmentation and classification using anatomic prior and deep learning. A machine learning technique was proposed in this study which was integrated with a convolutional neural networking system. This was carried out by fabricating a spatial convolutional neural system which helped to map the PET image at (-1, 0 and 1) pixels. From the 50 samples used from cervical tumor patience, a diced coefficient of 0.84 was obtained. It was however noted that this technique was highly accurate in cervical tumor diagnosis.

Miao et al. (2018) proposed cervical cancer image classification by applying CNN deep learning models on cytological cervical images. Two datasets were used in this study: original image (3012) and augmented image (108432). “Three folding cross validation” technique was applied in this study. The results showed an overall accuracy of 93.33% (original image group) and 89.48% (augmented image group). An improvement of 3.85% was achieved using augmented images. However, this technical of diagnosis is very effective in cervical cancer staging.

Ali et al. (2021) proposed a cervical cancer classification based on a proposed application of machine learning algorithms with a technique of transformations using sine function, z-score, and log. The classification of the cancer images using the applied transformations and Random Forest machine learning instance reported a classification accuracy of 98.33% for biopsy cervical images and 98.65% for cytology cervical images. Their proposed technique of transformations is reported as a significant contribution to the efficient identification and prioritization of risk factors in cervical cancer patients. Gupta and Gupta (2021) applied an ensemble approach of machine learning models for cervical cancer classification, in their study they used k-nearest neighbours to balance oversampled and missing values in the dataset they experimented on. This approach was further used to extract the identified most significant and viable features from the cervical images, the stacking architecture used in this study was reported to have the best performing accuracy compared to previous studies that experimented on the same dataset.

Identifying colposcopy as a very effective technique of medical healthcare institution diagnosis of cancer in patients, a study reported by Chandran et al. (2021), proposed deep learning model application of cancer classification based on colposcopy cervical images. In their study they proposed the application of two distinct deep learning models which they eventually evaluated for better performance on classification on colposcopy images, the applied deep learning models are VGG19 and CYENET deep learning models. The experiments carried out were reported with performance accuracy of 73.3% and 92.3% for VGG19 and CYENET respectively. The superior performance of the CYENET deep learning model was attributed to the model having a higher sensitivity and specificity in the classification of colposcopy cervical images. Another study by Tanimu et al. (2022) proposed the classification of cervical cancer images using a decision tree (DT) machine learning algorithm for the classification of risk factors in subjects. Their study also used applications of feature selection techniques based on selection operator and least absolute shrinkage, and recursive feature elimination (RFE). The applied feature selection was applied in tandem with oversampling balancing techniques known as SMOTETomek. The proposed study reported a better performance accuracy in contrast to a non-application of the feature selection techniques with a sensitivity performance of 100% and accuracy performance of 98.72%.

2.4.1 The Gap in the Literature

The reviewed literature on related works on the subject of cervical cancer classification, recognition and detection have shown some gaps in the study that need further research to improve upon. Some of the research gaps found are the majority of cervical cancer classification using deep learning models and computer vision application are proposed and experimented on using full blown cancer image datasets, hence this leaves a gap of enabling early detection of the disease as is desirable in medical diagnosis best practices which also applies to cervical cancer diagnosis, treatment and management. Another identified research gap is the use of few cervical cancer images in majority of studies and research of both cancerous and precancerous cervical cancer. The use of limited or few datasets does not enable deep learning models to reach their robust potential of optimal training which leads to better classification and recognition of images which also applies to the case of classification of precancerous or cancerous cervical cancer images.

CHAPTER III

MATERIALS AND METHODS

This chapter reports the proposed research methodology of this thesis regarding the experiments and the experimental setup of the thesis. The chapter comprehensively outlines the deep learning models applied for classification experiments, the description of the precancerous dataset used in the experiments of this research, the experimental setup and data pre-processing applied for all the experiments carried out in this research. The comprehensive adequacy of this chapter considers reproducibility of the experiments of any further researches or related work that might seek to carry out the experiments of this research for validation and further analysis.

3.1 Methodology

Some image classification tasks are considered simple as the classes are very distinctive (Yuan et al., 2020). However, others can be very challenging for a deep neural network. Cervical cancer diagnosis task is an example of a very challenging medical image classification task due to the healthy versus pre-cancerous colposcopy images complexity and similarity (Yuan et al., 2020).

For a deep network to be capable of extracting very distinctive features between two or more classes it should be very deep in order to extract low to high level features of the images. However, in recent years, training very deep networks seemed to be associated with computation time and consuming and difficulty in training. Moreover, another serious problem had been shown with training very deep networks which is called the vanishing gradient (Oyedotun et al., 2017). Such a problem appears when a very deep network is trained using backpropagation algorithm, the value of the product of derivative decreases until at some point the partial derivative of the loss function reaches a value close to zero, and then partial derivative vanishes (Li et al., 2021). The residual learning approach was proposed to solve such problem of training very deep networks without reaching the vanishing gradient phenomenon (He et al., 2016). In this work our classification task can be challenging and very deep and distinctive features extraction of features that distinguish the pre-cancerous from the healthy cervical raw images is needed.

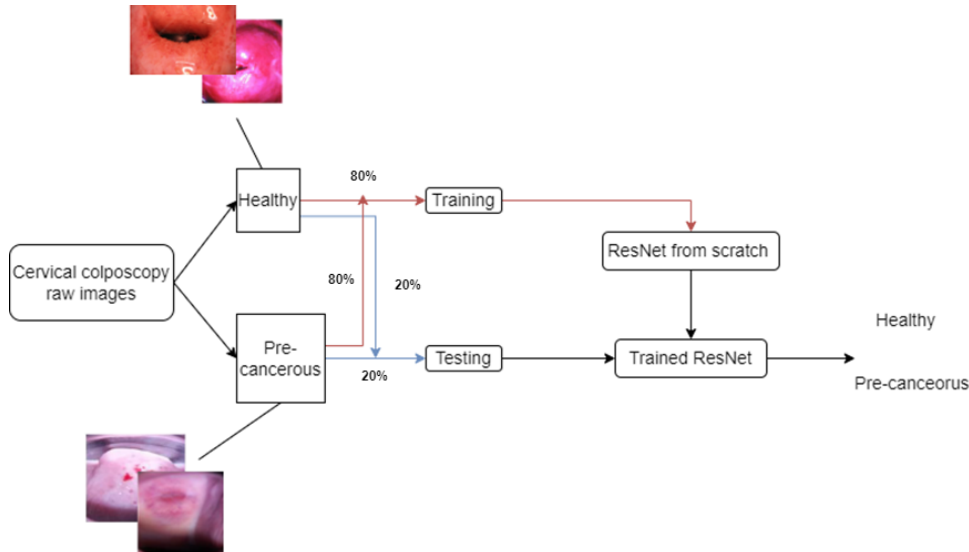
Hence, we opt to use a residual learning approach that can make it easier to train the presented deep models in addition to achieving better results than other traditional deep learning models.

In practice, building a residual deep convolutional neural network and training it from scratch created from scratch can be a tedious task in particularly if a huge dataset is not available as such models require training on huge benchmarks in order to tune their hyperparameters. Training time can also be a challenge when training very deep models from scratch due to the very big number of parameters such models can have like the filters learning, weights update, and calculation of errors (Shafiq et al., 2022).

In this thesis, a relatively huge dataset was available hence we built a residual convolutional neural network from scratch. Moreover, we attempted to study the effects of various activation functions of the performance of a newly built residual network. Figure 3.1 shows the process of splitting our dataset into training and validation/testing using a learning scheme of 80:20 which uses more testing images than other schemes in the literature review studies which used a few testing images, this makes our results more robust and accurate. It is important to mention that our ResNet model was replicated into three copies, each uses a different activation function which aims to discover which function can cause a slight impact on the network's accuracy using this specific colposcopy dataset (Kaggle dataset, 2020).

Figure 3.1.

A simple block diagram of the training and testing process of the ResNet. The data is split into training and testing with respect to our learning scheme which is: 80:20



3.2 Dataset

In this study, three residual networks of 18 layers are designed as discussed above. For each model we used different activation function. the next step is to train and test these models to be capable of diagnosing the colposcopy raw cervical images that have a probability of transforming into cervical cancer. Hence, for this purpose, we needed images of healthy cervical images that are normal and don't have a transformation zone. We also needed cervical images of cervixes that can be transformed into cancer, and they are three types: type 1, type 2, and type 3 depending on their transformation zone as explained in Chapter 2. Note that all three types are not cancerous, but they are most likely to transform into cervical cancer if not diagnosed and treated early, which is the main goal of this work. As for the pre-cancerous stage cervical images, they are collected from the public dataset: Intel and MobileODT Cervical Cancer Screening, which is a competition launched on Kaggle (Kaggle dataset, 2020) to classify three types of cervical pre-cancer images (earlier stages of cervical abnormalities that may transform into cancer). In this study, we considered all three types as one class which is the “pre-cancerous” as our aim

is to classify precancerous and healthy images. Regarding the normal cervical images, we collected them from the Tripoli Hospital Center, Libya.

Thus, by grouping all three types as one class and getting the healthy images we made a good dataset of healthy and pre-cancerous cervical colposcopy images that can be used to train deep models to perform cervical screening which can help in preventing the occurrence of cervical cancer. The number of healthy and pre-cancerous cervical images collected from both datasets is shown in Table 3.1. We used 3897 cervical pre-cancerous images from the first dataset (Kaggle dataset, 2020), while the number of images obtained from the second dataset was 800.

Table 3.1.

Datasets before data augmentation

	Healthy	Pre-cancerous
Dataset 1	-	3897
Dataset 2	800	-

For training and testing the models, we used a learning scheme of 80:10:10, i.e., 80 % of the images are used for training the network, 10% for validation, and the remaining are used for testing purposes. On the other hand, it was noticed that there is an imbalance in the dataset as due to the biggest number difference between both classes, i.e., the number of abnormal cervical images number is \sim four times more than normal images in the created dataset. Thus, this may result in overfitting and lead the models to exhibit a bias towards the majority class (Pre-cancerous cervixes), which is practically not desirable. In order to overcome and avoid such problems a data preprocessing of data augmentation technique was applied on the dataset.

3.2.1 Data pre-processing

The original size and dimension of the cervical cancer image dataset has a variation of sizes with no standard image sizes, the variation of image sizes varies from 480 X 640 pixels to the maximum size of 3096 X 4128 pixels of images. Data preprocessing was applied to the images to ensure all dataset images are uniform in

dimension, also we carried out data augmentation for the balancing of the proportion of the dataset. The final pixel dimension of the dataset after pixel resizing and data augmentation is saved as 150 X 150 pixels for each image.

Data augmentation and resizing was carried out using the MATLAB image data augmenter function to create shift translation and scale variance for the image data used in this study. This leads to increasing the number of healthy images to 3984 by rotating some original images at angle 90° and 180° and translating up to two pixels horizontally and vertically of some other images. Overall, a dataset of 3984 healthy cervical images was formed as shown in Table 3.2. Figure 3.2 shows a sample of some augmented images. The augmented data is not considered in the test phase, and the testing performed only the original images in order to avoid bias.

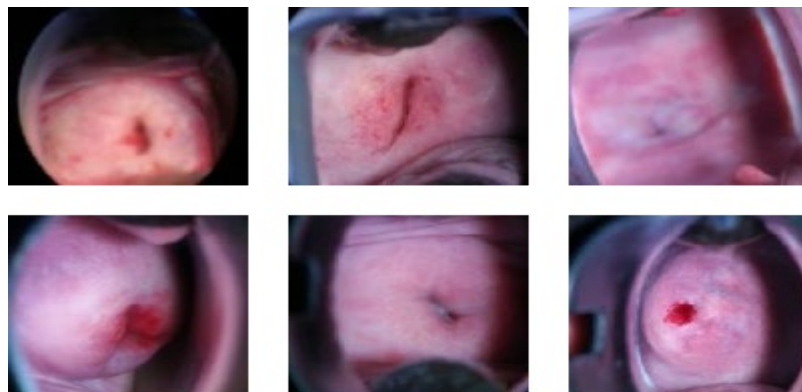
Table 3.2.

Datasets after augmentation and data splitting

	Healthy	Pre-cancerous
Dataset 1	-	3897
Dataset 2	3984	-
Total		7881

Figure 3.2.

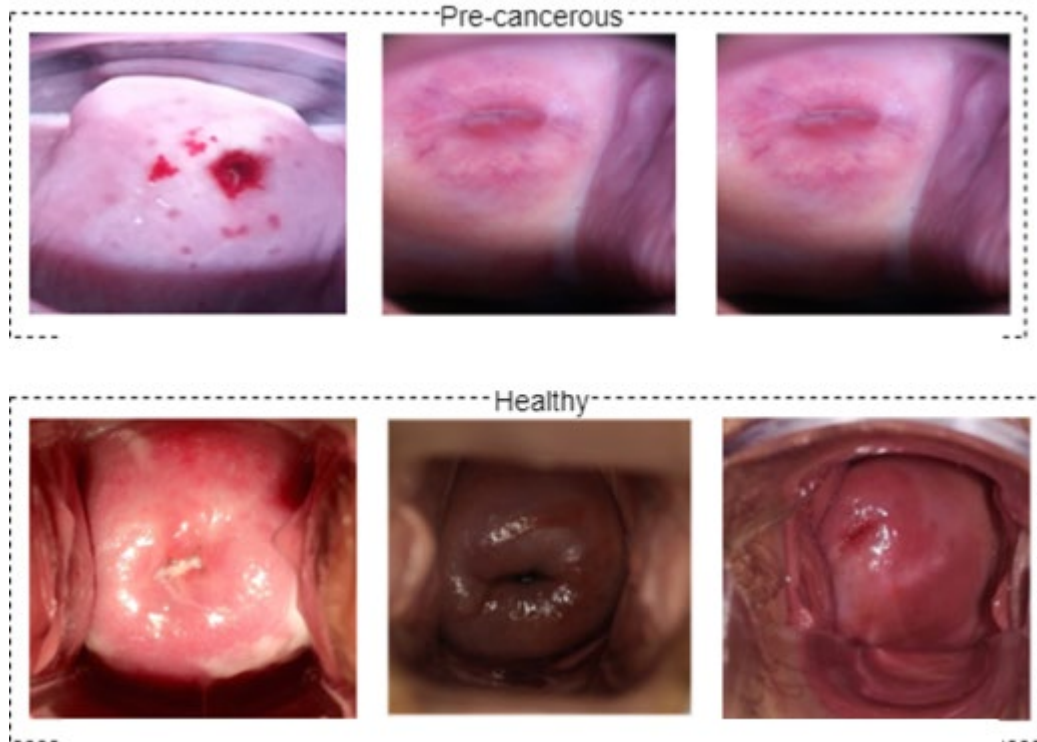
A sample of augmented cervical images



A sample of our healthy and pre-cancerous cervical colposcopy images is shown in Figure 3.3. As seen the first row shows three pre-cancerous raw images which were all considered as pre-cancerous while the second row shows three different healthy examples of cervical colposcopy cervixes.

Figure 3.3.

A sample of healthy and pre-cancerous cervical colposcopy images from our dataset



3.3 Results Evaluation Metrics

The trained ResNet deep convolutional neural networks are evaluated by calculating their testing accuracies as given below (Adweb et al., 2021):

$$\text{Accuracy} = \frac{N}{T} \quad (11)$$

Where N is the number of correctly classified images, while T represents the total number of images. In addition to the accuracy metric, more evaluations metrics such as sensitivity, specificity, are also used to evaluate the ResNet models:

$$\text{Sensitivity} = \frac{TP}{TP+FN} \quad (12)$$

$$\text{Specificity} = \frac{TN}{TN+FP} \quad (13)$$

Where TP stands for true positive, and it indicates the number of correctly predicted positive classes (i.e., Pre-cancerous). TN stands for true negative, and it indicates the number of correctly predicted negative classes (i.e., Healthy). FP refers to false positive, and it indicates the number of incorrectly predicted positive data samples, while FN is the false negative, and it indicates the number of incorrectly predicted negative data samples.

3.4 Deep Residual Network-Based Cervical Cancer Diagnosis

To diagnose cervical cancer, three deep residual networks with three different activation functions are used. As shown in Figure 3.4, our network architecture is based on the ResNet18 structure and consists of 50 layers with four residual and convolution blocks. There are 1 x 1 and 3 x 3 convolution operations (Conv) and rectified linear unit (ReLU) functions in each residual and convolution block. Furthermore, batch normalization (BN) and dropout layers are employed in the development of more viable designs as well as the improvement of model generalization. Due to the figure's simplicity, certain layers are not revealed. The output of all these layers of residual blocks undergoes a 3 x 3 max-pooling procedure before being transmitted to the global averaging pooling layer (Lin et al., 2013). This layer takes the role of the fully connected layer, converting each feature map into a value. Because our cervical screening task is a binary classification task, the obtained values are subsequently input into a Sigmoid function. It's worthy to mention that various research studies have indicated that using global average pooling lowers overfitting because there are no parameters to optimize in this layer (Lin et al.,

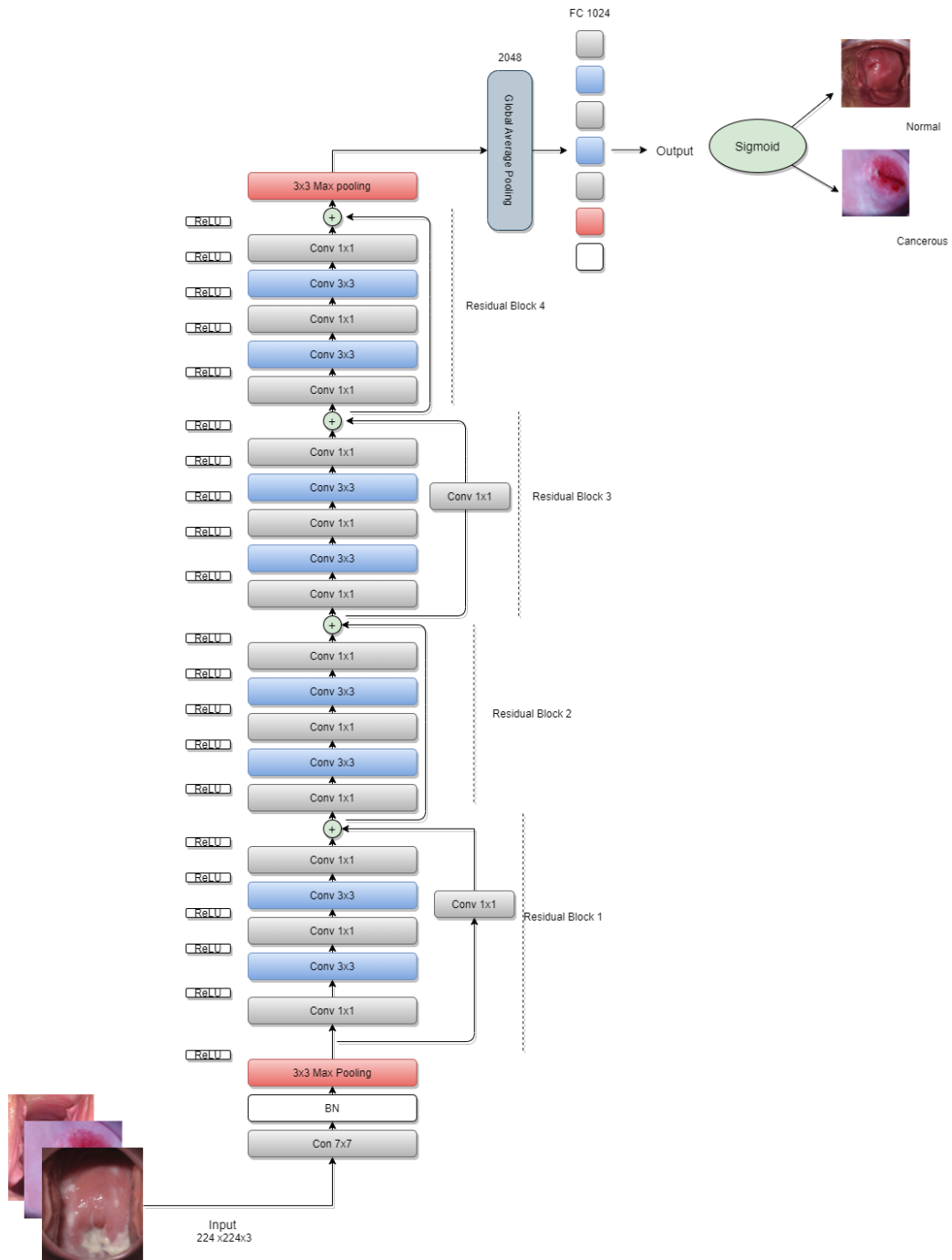
2013; He et al., 2016; Oyedotun et al., 2018). Furthermore, this approach to spatial translation is more robust and efficient, and the shift of the input for it sums the spatial information of the input data. Our study investigates the effects of activation functions on a residual neural network on a specific and challenging medical classification task. As a result, three models are created, each with a different activation function. Figure 3.4 only displays the ReLU-based ResNet design; however, two more similar networks, one with Leaky-ReLU and the other with PReLU, are also developed using the same architecture but with different activation functions. These functions are used in the residual blocks, but not in the main blocks.

3.5 Hardware Setup Specification

The specifications of hardware used for the experiments of this study are given as follows: the experiments were carried out on a personal computer with an Intel core i7 processor running at 2.60 Ghz. With an installed RAM of 16 gigabytes. The computer is running a windows 11 operating system on a x64 based processor. The computer hardware setup is also running a dedicated graphic processing unit with the following specification: NVIDIA GeForce TX 1660 Ti with Max-Q design of 4 gigabytes.

Figure 3.4.

The structure of the employed ResNet18 model with ReLU activation function



CHAPTER IV

RESULTS

This chapter reports the experimental results of the defined and presented proposed methodology, and also the chapter presents charts, figures and tables observed and reported throughout the course of the experiments carried out in the study. The chapter also ensured training results are reported to complement the actual test results of the trained models to enable comparison of efficiency and performance for precancerous cervical images classification.

4.1 Training the Residual Models

Three different residual models used in this work are all trained using the same healthy and pre-cancerous images, as previously stated. The three developed models are trained and tested using 80:20 learning method. This means that 80% of the data (6305 images) is used for training, and 20% is used as a hold-out test (1576). Training data was used to fine-tune the networks' hyper parameters and reduce overfitting. On a MATLAB 2020a, all models were trained for 80 epochs on the training dataset with a learning rate of 0.01, 0–1 input image normalization, cross entropy loss function, growth rate of 12, and block depth of 6. This hyper parameter selection was based on the grid-hyper parameters search, which was influenced by Huang et al., (2016). The learning parameters of the three distinct networks are defined in Table 4.1. To optimize the proposed models, a stochastic gradient descent method is employed to train the networks with a mini batch size of 55 iterations per epoch, this leads to a maximum of 4400 iterations for all 80 epochs of training and validation process. The number of Epoch required for training is chosen depending on the variances in accuracy and validation error. In other words, the number of epochs is chosen based on the validation error and network performance, as these can be linked to optimization issues, i.e., if they are high, overfitting may occur. As a result, a maximum of 80 epochs is chosen.

All models experimented on in this research have similar structures, however they have distinct activation functions and that gives a significant variation in their training duration and completion time. When the training time of all three models is compared, the

lowest training completion time was of ReLU ResNet with a completion time of 50 minutes, the second highest completion time was of Leaky ReLU ResNet with 67 minutes, and the highest was observed in the completion time of PReLU ResNet with a completion time of approximately 100 minutes. Figure 4.1, Figure 4.2, and Figure 4.3 illustrate the training process of the ReLU ResNet, Leaky ReLU ResNet, and PReLU ResNet respectively.

Table 4.1.

Learning parameters of the three different models

	ReLU-ResNet	Leaky ReLU- ResNet	PReLU-ResNet
Training ratio	80%	80%	80%
Learning rate	0.01	0.01	0.01
Number of epochs	80	80	80
Training accuracy	85.41%	98.6%	98.6%
Training time (mins)	50	67	100

Figure 4.1.

Learning curves of the ReLU ResNet model

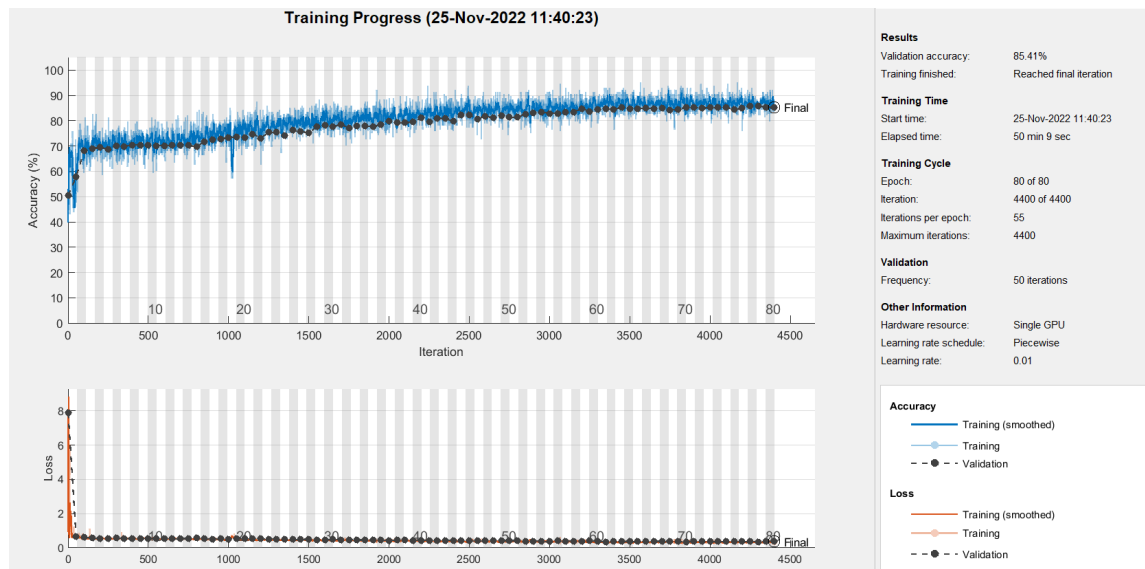


Figure 4.2.

Learning curves of the Leaky ReLU ResNet model

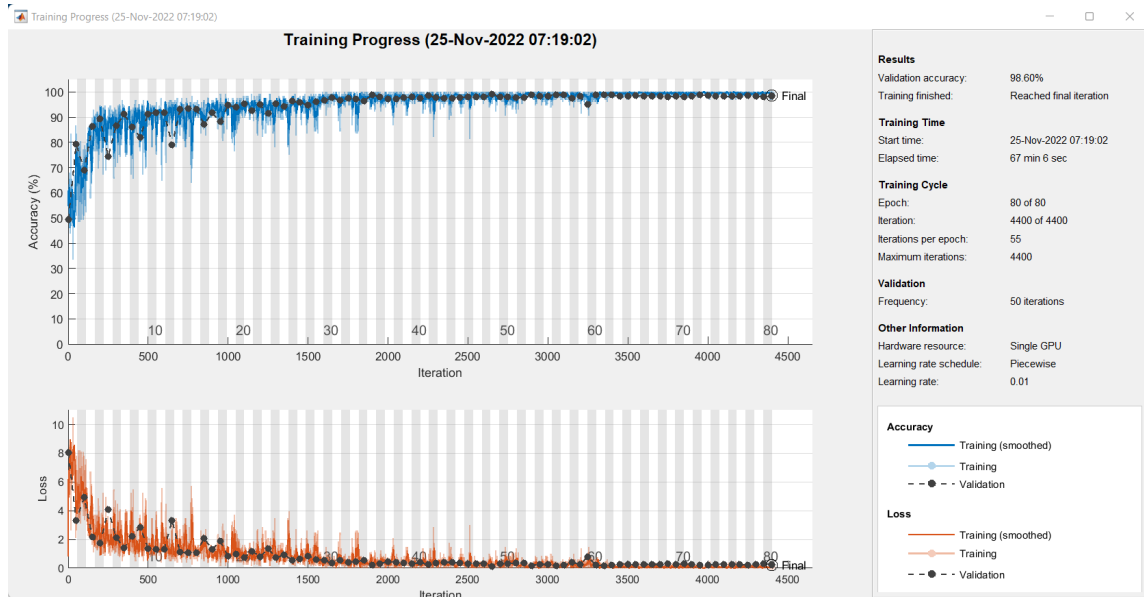
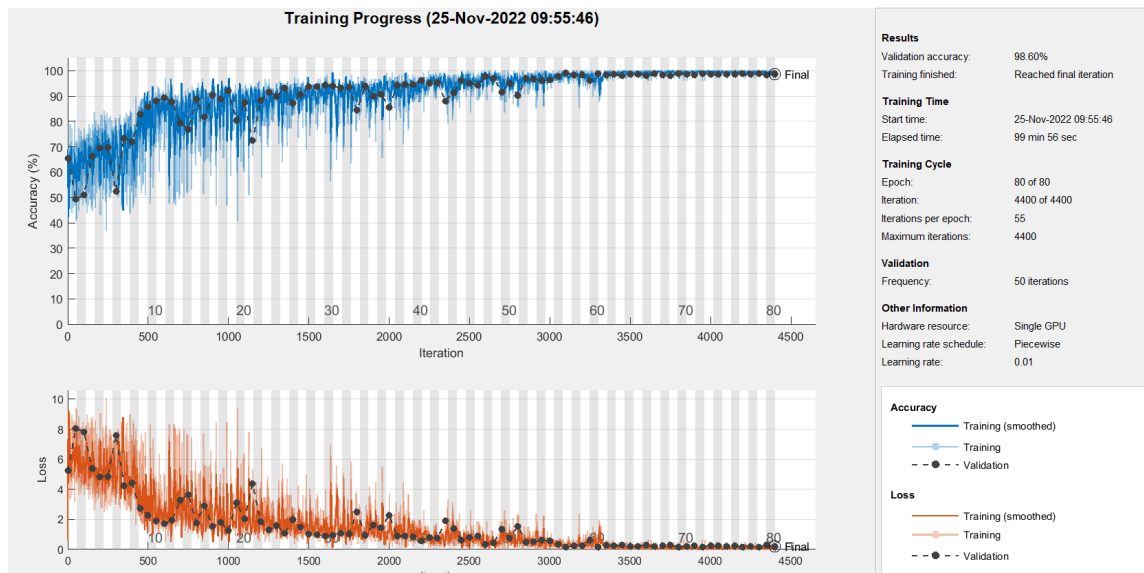


Figure 4.3.

Learning curves of the PReLU ResNet model



4.2 Test Experiment Results

The test experiment results of this study were reported for all three models that were previously trained, the models were also evaluated for misclassification to see where the misclassification of images were made because in diagnosis of precancerous or cancerous images the misclassification of images is as important as the accurate classification of cervical images due to the severe repercussions associated with misdiagnosis that may stem from misclassification. The performance of the accuracy evaluation was reported for the three models with performance accuracy of 89.72%, 98.60%, and 98.60% for ReLU ResNet, Leaky ReLU ResNet, and PReLU ResNet respectively, the performance accuracy of all three models is given in Table 4.2 below.

Table 4.2.

Overall classification accuracy of all three models

Model	Accuracy (%)
ReLU ResNet	89.72
Leaky ReLU ResNet	98.60
PReLU ResNet	98.60

The network test results were also evaluated for specificity and sensitivity as part of the chosen evaluation metrics of this research experiments. The specificity and sensitivity of the three models were calculated with the aid of the confusion matrix generated for the three models to show the rates of true positive (TP), true negative (TN), false positive (FP), and false negative (FN). The confusion matrix of all three models are illustrated in Figure 4.4, Figure 4.5, and Figure 4.6 for Relu ResNet, Leaky ReLU ResNet, and PReLU ResNet respectively. The results for the sensitivity and specificity of all three models is also shown in Table 4.3.

Table 4.3*Sensitivity and specificity performance for all three models*

Model	Specificity (%)	Sensitivity (%)
ReLU ResNet	89.72	89.71
Leaky ReLU ResNet	98.49	98.71
PReLU ResNet	98.74	98.46

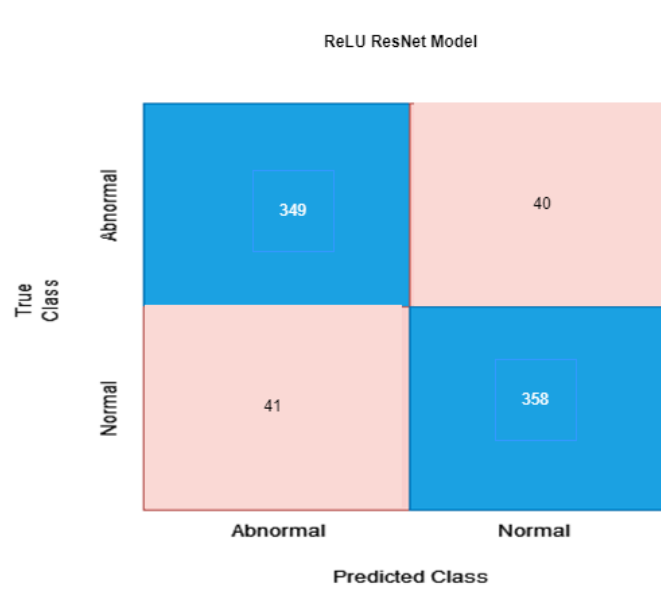
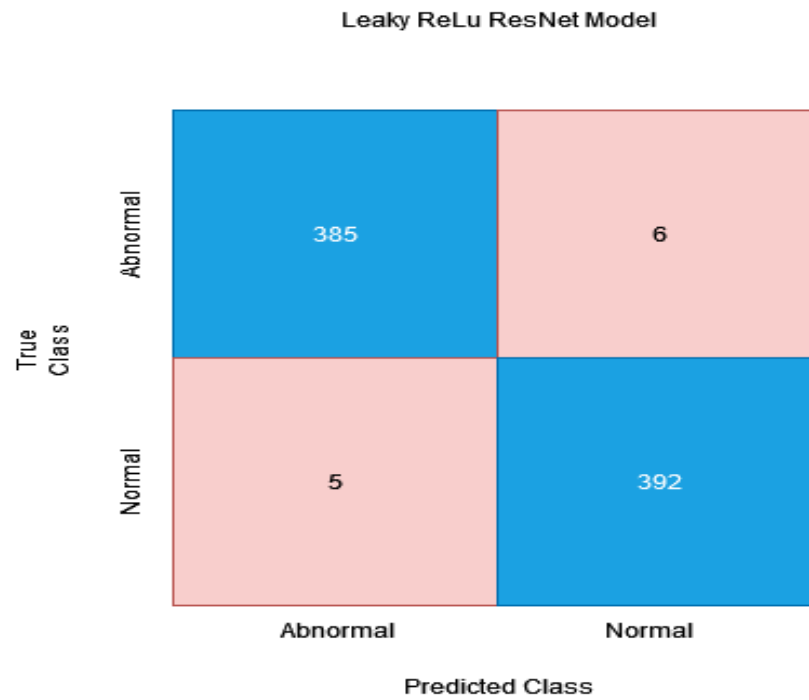
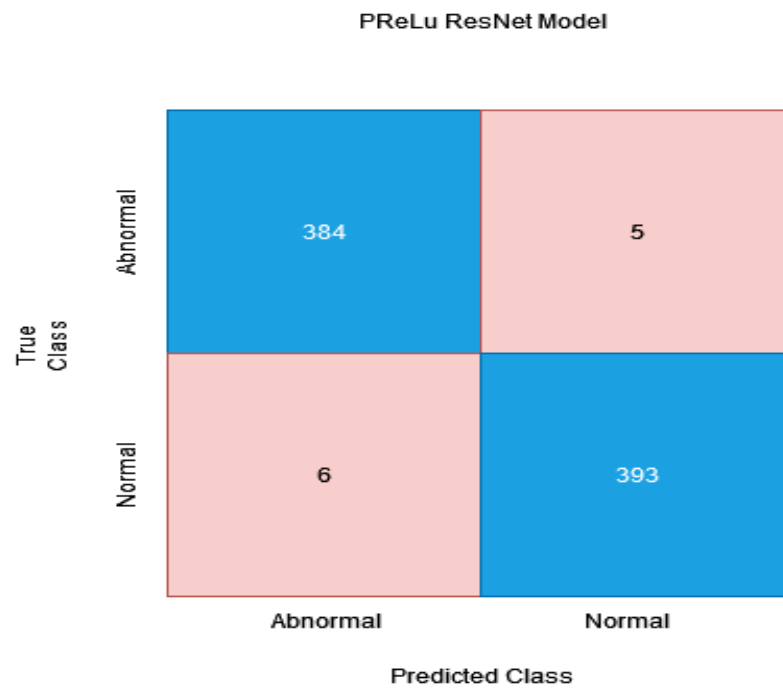
Figure 4.4*Confusion matrix of ReLU ResNet test experiment*

Figure 4.5

Confusion matrix of Leaky ReLU ResNet test experiment

**Figure 4.6**

Confusion matrix of PReLU ResNet test experiment



Misclassification of the images done by all three models was also observed and reported. The total misclassified images using the ReLU ResNet model was 81 images, the misclassification of Leaky ReLU ResNet was 11 images and the misclassification of PReLU ResNet was also 11 images. The number of misclassified images is reported in Table 4.4.

Table 4.4

Misclassification rates of all three models

Model	Total No. of misclassified images
ReLU ResNet	81
Leaky ReLU ResNet	11
PreLU ResNet	11

4.3 Statistical Tests

After the test experiments, statistical tests were also carried out on the final output results of the classification of all three models experimented on. The statistical test applied on our test result is the McNemar's test of matched pairs, the test is applied to pairs of the three models experimented with in our thesis to compare the performance of the models based on statistical test significance. The significance is evaluated for the test with significance value of 0.05 (5%). Table 4.5 shows the p value between each pair of models. The p values for all three paired tests between the models showed were observed greater than 0.05.

Table 4.5

Statistical tests p-value results of all three models paired

Model	p - value
ReLU ResNet/ Leaky ReLU ResNet	1.0
ReLU ResNet/ PReLU ResNet	1.0
Leaky ReLU ResNet / PReLU ResNet	0.75

CHAPTER V

DISCUSSION

This chapter reports a discussion of the findings of this study based on the results of the experiments of all three models as reported in the results chapter. The results of the experiments are further analysed for an adequate discussion of the findings in the results chapter.

5.1 Models Evaluation Results

In order to evaluate the feasibility of the models when tested on unseen colposcopy images, we conducted several experiments of testing the models on 20% of the data that were not used during the training stage. The results achieved when testing the three different models are shown in Table 5.1. As seen, the models with different activation functions performed differently in which the ReLU-ResNet achieved lower accuracy, sensitivity, specificity than other networks with Leaky-ReLU and PReLU. This lower performance can be because of its dying gradient problem caused by its ReLU activation function which consequently leads to a poor learning during the training results in bad performance when tested.

Table 5.1

Overall classification evaluation metrics results of all three models

Model	Accuracy (%)	Specificity (%)	Sensitivity (%)
ReLU ResNet	89.72	89.72	89.71
Leaky ReLU ResNet	98.60	98.49	98.71
PReLU ResNet	98.60	98.74	98.46

According to the results of the test experiments of all three models, the least performing is the ReLU ResNet model which is associated with a dying gradient as discussed in the literature section and methodology section. The overall accuracy of Leaky ReLU ResNet and PReLU ResNet models have been observed to have the same performance in accuracy evaluation, but with further evaluation of misclassified images

in the confusion matrix the sensitivity of both models as well as the specificity of the models both show insignificant varying differences as shown in Table 5.1. The confusion matrix of the two models was observed for analysis to see the number of misclassifications and which classes of the images were classified according to each model's experiment. Figure 5.1 and Figure 5.2 show the confusion matrix of PReLU and Leaky ReLU.

Figure 5.1

Leaky ReLU ResNet confusion matrix

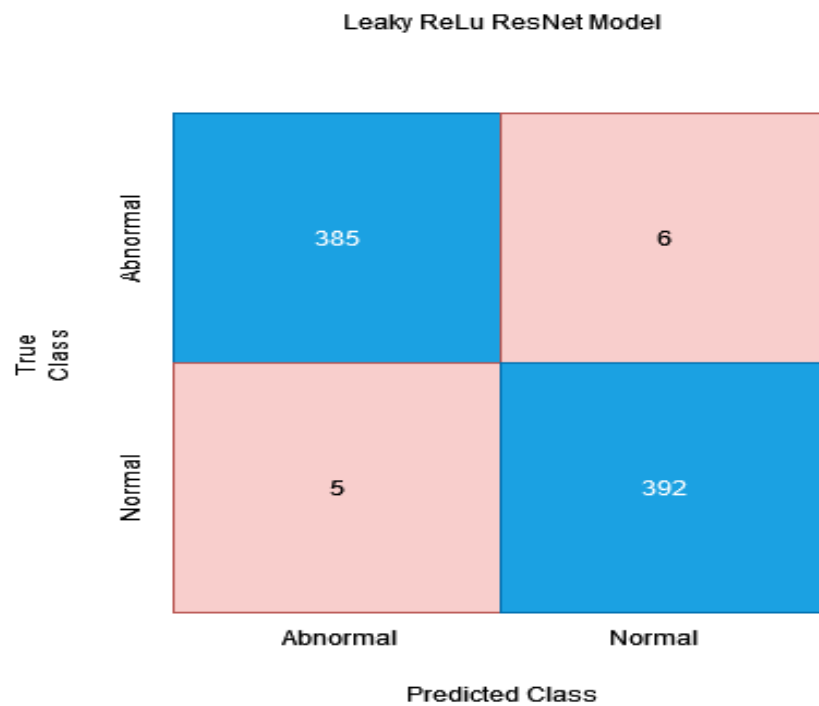
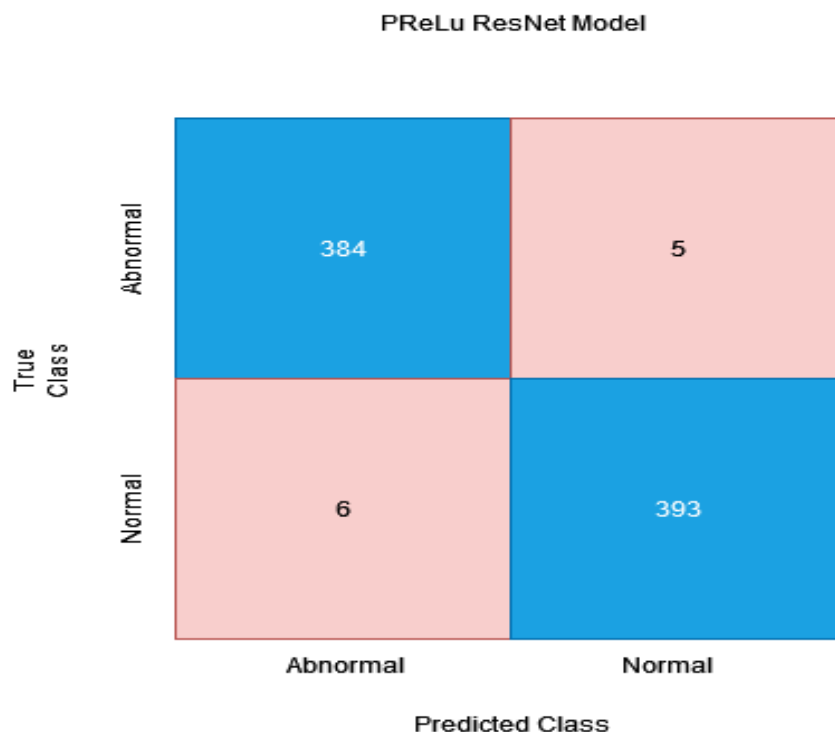


Figure 5.2*PReLU ResNet confusion matrix*

From the confusion matrix it can be observed that both PReLU and Leaky ReLU models had the same misclassification rate due to their equal number of misclassified images, with each model having 11 misclassified images; both precancerous and healthy images. There is however a difference in their misclassification, and that led to the varying rates in specificity and sensitivity, Leaky ReLU has a higher misclassification of healthy cervical images with 6 misclassified healthy cervix images as precancerous cervix images, and 5 misclassified precancerous cervix images as healthy images. Whereas in PReLU ResNet experiments there was a lower misclassification rate of healthy cervix images as precancerous with a total of 5 images misclassified, and 6 precancerous images misclassified as healthy cervix images.

Table 5.2 shows the misclassification rate of all three models used in test experiments of this study, also Figure 5.3, and 5.4 show the misclassified images, for

Leaky ReLU ResNet model, Figure 5.5 and Figure 5.6 show the misclassification images for PReLU ResNet model. In the ReLU ResNet model test experiments it had a higher misclassification rate with a total of 81 misclassified images; 40 healthy cervix images and 41 precancerous cervix images. In the Leaky ReLU model 6 of the healthy cervix images were misclassified as precancerous images, and 5 of the precancerous cervix images were misclassified as healthy images. For PReLU ResNet 5 of the healthy cervix images were misclassified as precancerous cervix images and 6 of the precancerous cervix images were misclassified as healthy cervix images.

Table 5.2

Misclassification rates of all three model's test experiments

Model	No. of misclassified normal images	Misclassification of normal images (%)	No. of misclassified abnormal images	Misclassification of abnormal images (%)	Overall misclassification (%)
ReLU ResNet	40	10.1	41	10.5	10.28
Leaky ReLU ResNet	6	1.5	5	1.3	1.4
PReLU ResNet	5	1.3	6	1.5	1.4

Figure 5.3.

Misclassified abnormal images of Leaky ReLU ResNet test experiment

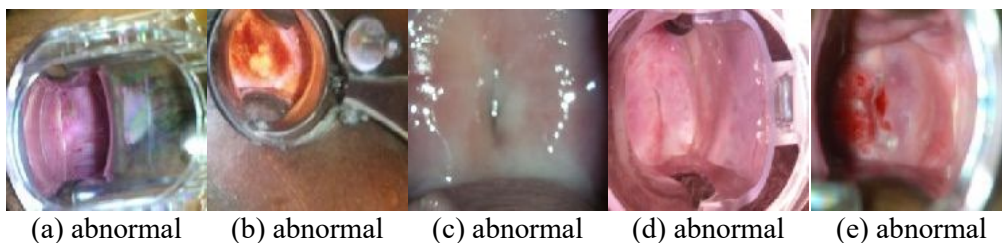
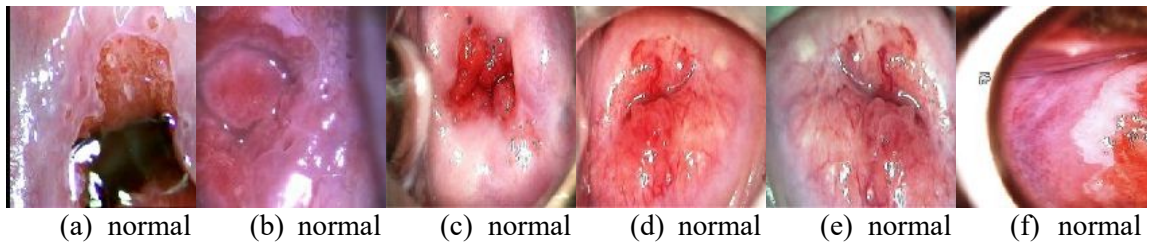
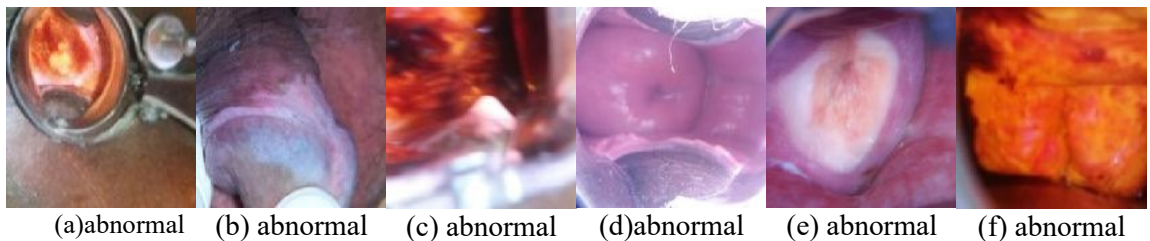


Figure 5.4.

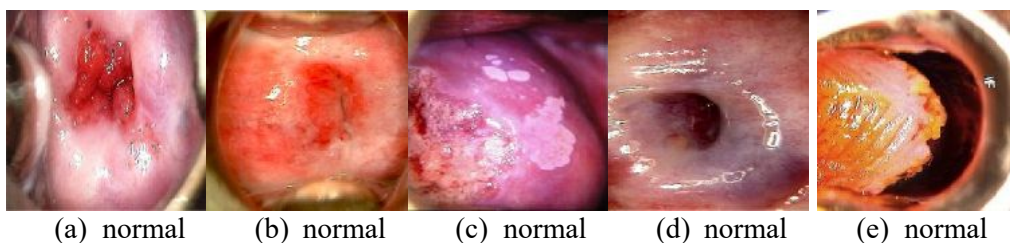
Misclassified normal images of Leaky ReLU ResNet test experiment

**Figure 5.5.**

Misclassified abnormal images of PReLU ResNet test experiment

**Figure 5.6.**

Misclassified normal images of PReLU ResNet test experiment



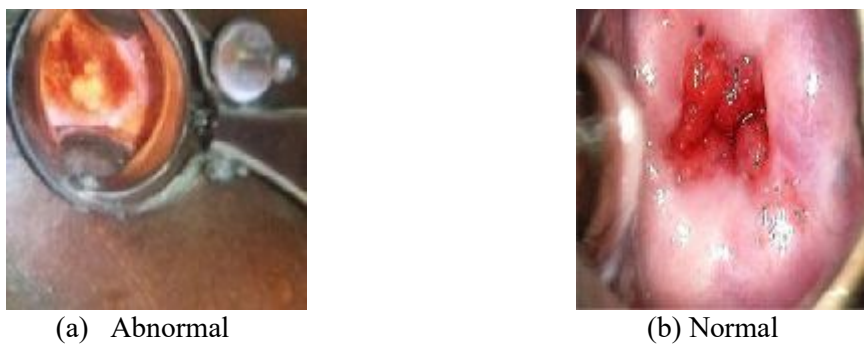
The misclassified images of both Leaky ReLU and PReLU ResNet models were traced in the test images used in the test experiments for observation with the naked eye. However, the misclassified images of both PReLU and Leaky ReLU ResNet were different from each other except for two images we found in common in their misclassification, each model had 9 different images except two images, for the two images shown in Figure 5.7 as the same images misclassified by PReLU and Leaky ReLU ResNet models. Naked eye observation of the precancerous misclassified images of Leaky

ReLU ResNet model showed the images as seen in Figure 5.3a, 5.3b, and 5.3c looked like healthy cervix images and only the image in Figure 5.3d, and 5.3e looked like precancerous images. For Leaky ReLU misclassification of healthy images, all the healthy cervix images misclassified look like they had some form of inflammation and actually looked like some precancerous images in the dataset. The misclassified images in the PReLU ResNet model on the other hand showed some different observations compared to the Leaky ReLU misclassification of precancerous images, all the precancerous cervix images misclassified in PReLU ResNet looked similar to precancerous images in the dataset except for one in Figure 5.5d. Whereas the images misclassified in PReLU ResNet test experiments showed all images looked like they were actually precancerous images from observations of the nature of cancerous images in the dataset.

Observation of the two images both PReLU and Leaky ReLU ResNet misclassified looked like they were both belonging to the misclassified classes they were mapped to during test experiments, as both precancerous and healthy images looked like they belonged in the opposite classes of the dataset, this can be seen in the illustration of the two images misclassified by both PReLU and Leaky ReLU ResNet in the test experiments.

Figure 5.7

The two images misclassified by both Leaky ReLU and PReLU ResNet models



Based on the naked eye observations of the images misclassified by both PReLU and Leaky ReLU ResNet shows some of the images might have been subject to mislabeling during the dataset collection processes before our experiments used them. Figure 5.8 depicts the learnt activations of PReLU-ResNet, at the first convolution and max-pooling layers, it displays the learned activations. The network learned gradients and

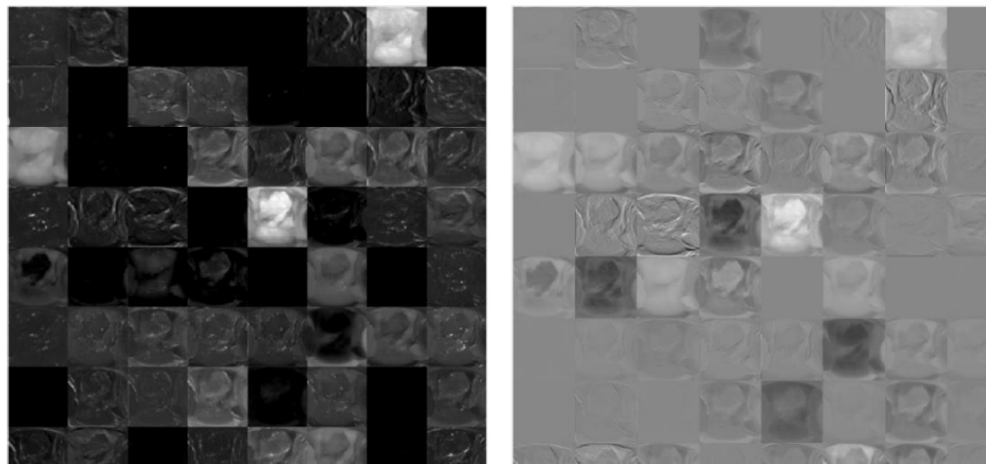
different degrees of abstraction in these two layers, but since learning is still in the first layers, those features are limited to color, orientations, and edges.

However, as we go deeper (Figure 5.8), networks appear to learn increasingly complex and meaningful features, such as objects and whole pieces of cervixes; learnt features are built up by mixing features from prior layers, as in deeper layers. We display the learnt features at a deeper layer and at the activation layer of each network in Figure 5.9. As a result, we select each network's seventh activation function layer and visualize its leaning properties. When compared to other networks with leaky-ReLU (Figure 5.9c) and PReLU functions (Figure 5.9b), which appear to learn more abstract and intricate features, the network with ReLU activation function (Figure 5.9a) appears to learn no significant information.

As shown in Figure 5.9a, ReLU-ResNet appears to be unable of extracting the proper features from cervical images that help in determining whether the cervix is healthy or pre-cancerous, which has an impact on the learning performance of the networks. This is most likely why this network has lower accuracy and error than others.

Figure 5.8.

Learned features of PReLU-ResNet.

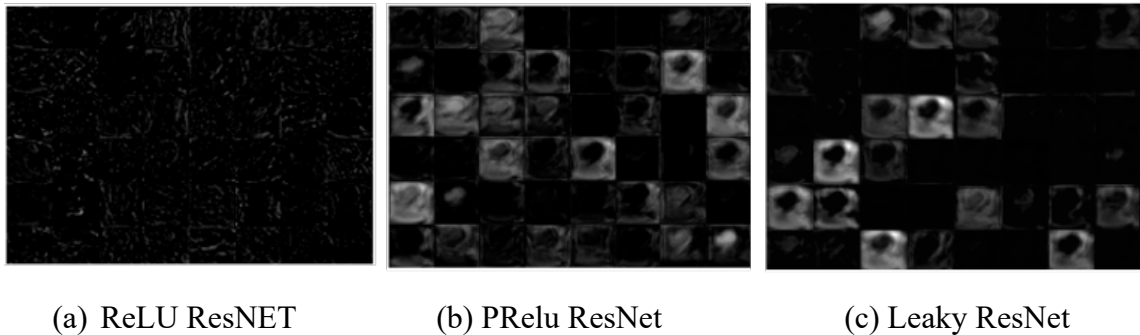


(a) Pooling layer 1

(b) Convolution layer 1

Figure 5.9.

Learned features at activation function layers of all networks at layer 7



5.2 Results comparison

Several studies (Bengtsson and Malm, 2014; Gorantla et al., 2019; Lu et al., 2020; Zhang et al., 2019; Guo et al., 2020) have been undertaken to diagnose cervical cancer, but only a handful have employed raw cervical pictures. The majority of these studies (Bengtsson and Malm, 2014; Guo et al., 2020) employed microscopic data as inputs to their systems. These studies generated significant findings, but they cannot be compared to ours because the database they used to validate the network's performance is made up of different types of data than ours. Furthermore, several other research have used the same Kaggle database as ours, but for other purposes, such as classifying the three forms of cervical precancerous (Gorantla et al., 2019) or segmenting the uterine cervix (Ghoneim et al., 2020). As a result, some studies with the same sort of dataset and goal have to be sought in order to make a fair comparison (application).

One approach of this work was proposed after a lengthy search, and it discusses the classification of cervical images as pre-cancerous or healthy. Mustafa and Dauda (2019) discussed the classification of colposcopy cervical images into cancerous or healthy. Three alternative deep convolutional neural networks (DCNNs) are used in their study, each with its own set of optimizers, including stochastic gradient descent (SGD), Root Mean Square Propagation (RMSprop), and Adaptive Moment Estimation (Adam). Those networks were all trained and evaluated on malignant and healthy cervical pictures, and the results were compared to determine which optimizer was the best. According to the authors, the CNN based on Adam had the maximum accuracy of 90%. Yuan et al. (2020) examined the detection of cervical squamous intraepithelial lesions in colposcopy

images in another investigation. The U-Net model for segmenting the lesion in the cervix and the ResNet model for categorizing positive and negative colposcopy cervical cancer images were among the applications provided in this study. However, we are primarily interested in their ResNet classification model in this comparison because it has a similar applicability to ours. Yuan et al. (2020) found that their ResNet model was 84.10% accurate in distinguishing between positive and negative colposcopy cervical cancer images.

Table 5.3 compares the suggested networks addressed in this research to the related studies cited earlier. It shows that in terms of accuracy, our generated residual learning-based networks outperform the plain and standard Adam convolution neural network (Mustafa and Dauda, 2019). By comparing the two approaches, it is found that the residual learning strategy can have a significant positive impact on a CNN by increasing its generalization capability. More recent studies as referenced in the related works section of the literature such as the work of Gupta and Gupta (2021) in which they applied a KNN stacking method for classification has shown our proposed methodology has a performance improvement, also the study of Chandran et al. (2021) which applied CYENET deep learning model reported 92.3% performance accuracy which is also significant improvement using our proposed models.

Table 5.3

Performance comparison with other related works

Model	ReLU-ResNet	Leaky-ReLU-ResNet	PReLU-ResNet	Adam based CNN (Mustafa and Dauda, 2019)	ResNet (Yuan et al., 2020)	KNN Stacking (Gupta & Gupta, 2021)	CYENET Chandran et al. (2021)
Accuracy	89.72%	98.6%	98.6%	90%	84.1%	95%	92.3%

CHAPTER VI

CONCLUSION AND RECOMMENDATIONS

This is the final chapter of this thesis, it presents a conclusion statement based on the findings and discussions presented in the earlier chapters of the thesis. Also, the chapter presents recommendation remarks and recommendations for future studies on the same subject of the thesis; classification of precancerous cervical images.

6.1 Conclusion

This study was carried out as an effort to contribute to the research efforts and body of literature in the diagnosis and treatment management of cervical cancer. The study was motivated by early diagnosis of cervical cancer as a preferred form of diagnosis of the disease for a better treatment and management of the disease in patients. Hence, the study proposed the use of the ReLU ResNet architecture of deep learning with modifications to the activation functions as reported in other studies of image classifications as potential techniques of improving the classification accuracy of the deep learning architecture.

In experiments, it was discovered that all networks had strong generalization power for proper cervical cancer diagnosis; however, the network with the ReLU activation function had lower accuracy than the other networks with the Leaky-ReLU and PReLU activation functions. The ReLU-ResNet was also shown to have a problem extracting the relevant and complicated properties that distinguish the two cervical classes, resulting in poor generalization. Finally, it was demonstrated that the activation functions of Leaky-ReLU and PReLU might be used as a performance enhancer for residual learning-based networks. This is mostly due to their capacity to resolve the 'dying ReLU' issue that plagues the ReLU activation function. The network achieved higher accuracies in categorizing pre-cancerous and healthy cervical data when PReLU activation was utilized in this investigation. Also, it was identified that that the activation functions of Leaky-ReLU and PReLU may be used to increase the performance of a residual learning-

based network. The ability to tackle the “dying ReLU” problem connected with the ReLU activation function is largely responsible for their improved performance.

Overall, this study demonstrates that a deep learning system can perform challenging medical classification tasks, such as cervical screening. Such methods can aid medical professionals in diagnosing this disease and determining its pre-shape before it progresses to cervical cancer. This technique can also be used to distinguish between the three forms of cervical cancer. Such a sophisticated technology could be extremely useful because it can stage cervical cancer, which aids in the development of treatment plans suited to patients’ individual cancer types.

The limitations of the activation functions are also examined in this thesis, and three distinct functions are used to investigate the impact of the activation function on ResNet performance. As a result, three networks with three different networks were created. A collection of raw cervical images was used to train and test all networks.

6.2 Recommendations

The following are recommendations which are based on the results and findings of the study, the recommendations are made for two disciplines; for the computer vision research community and for the healthcare institutions.

6.2.1 Recommendations for Researchers

In this study the classification of precancerous cervical images was done for three types of precancerous stages of cervical cancer as one class. We recommend further studies to be carried out to distinguish the three types of precancerous cervical images against healthy cervical images. Also observations of the misclassifications of the images of this study have indicated a possible error in data labelling because of the uncontrolled nature of the datasets formation, hence we recommend the design and collection of cervical cancer images in a controlled environment to eliminate data mislabelling which is a significant cause of misclassification and error in most machine learning problem solving efforts.

6.2.2 Recommendations for Healthcare Institutions

This study recommends the mainstream healthcare institutions to carry out proper and adequate archiving of diagnosis images of cervical cancer, precancerous and healthy cervical images with intentions of sharing it with the computer vision community to contribute to research efforts carried out for automating the diagnostics process of their professions. In doing so the computing research community will have less data mislabelling that increases misclassification and error in experiments.

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APPENDICES

Appendix A
Ethics Committee Permission



ETHICAL APPROVAL DOCUMENT

Date: 19/01/2022

To the Institute of Graduate Studies,

For the thesis project entitled as “CERVICAL CANCER DIAGNOSIS USING VERY DEEP NETWORKS OVER DIFFERENT ACTIVATION FUNCTIONS” the researchers declare that they did not collect any data from human/animal or any other subjects. Therefore, this project does not need to go through the ethics committee evaluation.

Title: Prof. Dr.

Name Surname: Nadire Çavuş

Signature: 

Role in the Research Project: Supervisor

Title: Assoc. Prof. Dr.

Name Surname: Boran Şekeroğlu

Signature: 

Role in the Research Project: Co-Supervisor

Appendix B
Turnitin Similarity Report

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by Khaled Mabrouk Amer Adweb

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DEPARTMENT OF COMPUTER INFORMATION SYSTEMS

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CERVICAL CANCER DIAGNOSIS USING VERY DEEP NETWORKS
OVER DIFFERENT ACTIVATION FUNCTIONS

PhD THESIS

KHALED MABROUK AMER ADWEB

SUPERVISOR

PROF. DR. NADIRE CAVUS

CO-SUPERVISOR

ASSOC. PROF. DR. BORAN SEKEROGLU

Nicosia

December, 2022

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Appendix C

Dataset

The screenshot shows the Kaggle website interface. At the top, there is a search bar and buttons for 'Sign In' and 'Register'. The left sidebar contains navigation options: 'Create', 'Home', 'Competitions', 'Datasets', 'Code', 'Discussions', 'Learn', and 'More'. The main content area features a banner for the 'Intel & MobileODT Cervical Cancer Screening' competition, which is a 'Featured Prediction Competition' with a '\$100,000 Prize Money'. The banner text asks 'Which cancer treatment will be most effective?' and mentions 'Intel' and '848 teams · 5 years ago'. Below the banner are tabs for 'Overview', 'Data', 'Code', 'Discussion', 'Leaderboard', and 'Rules', along with a 'Join Competition' button.

Dataset Description

Warning: This data contains graphic contents that some may find disturbing.

In this competition, you will develop algorithms to correctly classify cervix types based on cervical images. These different types of cervix in our data set are all considered normal (not cancerous), but since the transformation zones aren't always visible, some of the patients require further testing while some don't. This decision is very important for the healthcare provider and critical for the patient. Identifying the transformation zones is not an easy task for the healthcare providers, therefore, an algorithm-aided decision will significantly improve the quality and efficiency of cervical cancer screening for these patients.

To understand more about the background of how these cervix types are defined, please refer to this document.

Files
8734 files
Size
46.53 GB
Type
jpg, csv, 7z

Cervix type

EN English (United Kingdom) **Team 1**

مستشفى طرابلس المركزي
Tripoli Central Hospital



2022/12/27 م

إلى من يهمه الأمر
بعد التحية

تحققنا من أن الطالب خالد مبروك عامر الدويب جاء إلينا في عام 2020 للحصول على مجموعة بيانات حول صور التنظير المهبل لعنق الرحم ، وقد أعطيناها إذنا شفهيًا أثناء تقديم مجموعة البيانات. هذه الرسالة عبارة عن تأكيد خطي للإذن باستخدام مجموعة البيانات المقدمة من مؤسستنا الصحية.

أطيب التحيات.



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To Whom it May Concern

Greetings ,,,,,,

We verified that the student : Khaled Mabrouk Amer Adweb has come to us in 2020 to get a set of data concerned colposcopy cervical healthy images , and we gave him verbal permission , when he submitted the set of these data herein . This letter is deemed as written evidence of permission to use the given set of data that , submitted by our healthy institution .

Stamped & Signed By:
Hospital general manager



Appendix D

Source Code

```

%
% dataFolder = 'D:\dataset';
% categories = {'abnormal', 'Normal'};
% imds = imageDatastore(fullfile(dataFolder, categories), ...
%   'LabelSource', 'foldernames');
% trainingImages = imresize(imds.read(), [32 32]);
% validationImages=imresize(imds.read(), [32 32]);
% [trainingImages,validationImages] = splitEachLabel(imds,0.8,'ran');%%%
% %%%%Create a random partition for a stratified 10-fold cross-validation.

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

%%
% There are now 55 training images and 20 validation images in this very
% small data set. Display some sample images.
numTrainImages = numel(trainingImages.Labels);
YValidation=validationImages.Labels
% YTrain=trainingImages.Labels
idx = randperm(numTrainImages,16);
figure
for i = 1:16
    subplot(4,4,i)
        I = readimage(trainingImages,idx(i));
        imshow(I)
end

imageSize = [32 32 3];
pixelRange = [-4 4];

netWidth = 16;

layers = [
    imageInputLayer([150 150 3],'Name','input')
    convolution2dLayer(3,netWidth,'Padding','same','Name','convInp')
    batchNormalizationLayer('Name','BNInp')

    eluLayer('Name','relu1')
    convolutionalUnit(netWidth,1,'S1U1')
    additionLayer(2,'Name','add11')
    eluLayer('Name','relu11')
    convolutionalUnit(netWidth,1,'S1U2')
    additionLayer(2,'Name','add12')
    eluLayer('Name','relu12')

    convolutionalUnit(2*netWidth,2,'S2U1')
    additionLayer(2,'Name','add21')
    eluLayer('Name','relu21')
    convolutionalUnit(2*netWidth,1,'S2U2')
    additionLayer(2,'Name','add22')
    eluLayer('Name','relu22')

```

```

convolutionalUnit(4*netWidth,2,'S3U1')
additionLayer(2,'Name','add31')
eluLayer('Name','relu31')
convolutionalUnit(4*netWidth,1,'S3U2')
additionLayer(2,'Name','add32')
eluLayer('Name','relu32')

averagePooling2dLayer(8,'Name','globalPool')
fullyConnectedLayer(2,'Name','fcFinal')
softmaxLayer('Name','softmax')
classificationLayer('Name','classoutput')
];

lgraph = layerGraph(layers);
figure('Units','normalized','Position',[0.2 0.2 0.6 0.6]);
plot(lgraph);

lgraph = connectLayers(lgraph,'relu1','add11/in2');
lgraph = connectLayers(lgraph,'relu11','add12/in2');

figure('Units','normalized','Position',[0.2 0.2 0.6 0.6]);
plot(lgraph);

skip1 = [
    convolution2dLayer(1,2*netWidth,'Stride',2,'Name','skipConv1')
    batchNormalizationLayer('Name','skipBN1')];
lgraph = addLayers(lgraph,skip1);
lgraph = connectLayers(lgraph,'relu12','skipConv1');
lgraph = connectLayers(lgraph,'skipBN1','add21/in2');

lgraph = connectLayers(lgraph,'relu21','add22/in2');

skip2 = [
    convolution2dLayer(1,4*netWidth,'Stride',2,'Name','skipConv2')
    batchNormalizationLayer('Name','skipBN2')];
lgraph = addLayers(lgraph,skip2);
lgraph = connectLayers(lgraph,'relu22','skipConv2');
lgraph = connectLayers(lgraph,'skipBN2','add31/in2');

lgraph = connectLayers(lgraph,'relu31','add32/in2');

figure('Units','normalized','Position',[0.2 0.2 0.6 0.6]);
plot(lgraph)

numUnits = 9;
netWidth = 16;
net=resnet18
figure('Units','normalized','Position',[0.1 0.1 0.8 0.8]);
plot(net)

%Train network
miniBatchSize = 128;
learnRate = 0.1*miniBatchSize/128;
valFrequency = floor(size(trainingImages,4)/miniBatchSize);
options = trainingOptions('sgdm', ...

```

```

'InitialLearnRate',learnRate, ...
'MaxEpochs',80, ...
'MiniBatchSize',miniBatchSize, ...
'Shuffle','every-epoch', ...
'Plots','training-progress', ...
'Verbose',false, ...
'ValidationData',{validationImages,YValidation}, ...
'LearnRateSchedule','piecewise', ...
'LearnRateDropFactor',0.1, ...
'LearnRateDropPeriod',60);

doTraining = true;
if doTraining
    trainedNet = trainNetwork(trainingImages,lgraph,options);
else
    load('CIFARNet-20-16.mat','trainedNet');
end
YPred = classify(trainedNet,validationImages);
YTest = validationImages.Labels;
accuracy = sum(YPred == YTest)/numel(YTest)
cm = confusionchart(YTest,YPred);
cm.Title = 'Confusion Matrix for Test Data';
cm.RowSummary = 'row-normalized';
%%%%%%%%%% Metric Evaluation %%%%%%%%%%%
cmc = confusionmat(YTest, YPred);
cmc = cmc';
precision = diag(cmc)./sum(cmc,2);
overall_precision = mean(precision)
recall= diag(cmc)./sum(cmc,1)';
overall_recall = mean(recall)
fscore = (2*(overall_recall*overall_precision))/(overall_recall+overall_precision)
%%%%%%%%%% ADDED CODES FOR TRUE
CLASSIFICATION%%%%%%%%%%

RightlyPredictedF = find(YPred == YTest);
realcount = validationImages.Labels;
realcount = nominal (realcount);
realcount = cellstr(realcount);

%realcount is the labels of all test set
%rightlypredicted is the index of all rightly predicted
abnormalcount = 0;
normalcount = 0;
abnormal = {'abnormal'};
for i = 1:length(RightlyPredictedF)
    idx = RightlyPredictedF (i, 1)
    foundlabel = realcount{idx,1}
    if isequal (foundlabel, abnormal{1,1})
        abnormalcount = abnormalcount + 1;
    else
        normalcount = normalcount + 1;
    end
end

disp ('number of correctly classified abnormal: TP');
disp (abnormalcount);
disp ('number of correctly classified normal: TN');

```

```

disp (normalcount);

end
%%%%% ADDED CODES FOR MISCLASSIFICATION ANALYSIS %%%%%

wronglyPredictedF = find(YPred ~= YTest);
validationImages.Files{wronglyPredictedF}

abnormalcount = 0;
normalcount = 0;
abnormal = {'abnormal'};
for i = 1:length(wronglyPredictedF)
    idx = wronglyPredictedF (i, 1)
    foundlabel = realcount{idx,1}
    if isequal (foundlabel, abnormal{1,1})
        abnormalcount = abnormalcount + 1;
    else
        normalcount = normalcount + 1;
    end

    disp ('number of misclassified abnormal:FN');
    disp (abnormalcount);
    disp ('number of misclassified normal: FP');
    disp (normalcount);
end

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
function layers = convolutionalUnit(numF, stride, tag)
layers = [
    convolution2dLayer(3,numF,'Padding','same','Stride',stride,'Name',[tag,'conv1'])
    batchNormalizationLayer('Name',[tag,'BN1'])
    eluLayer('Name',[tag,'relu1'])
    convolution2dLayer(3,numF,'Padding','same','Name',[tag,'conv2'])
    batchNormalizationLayer('Name',[tag,'BN2'])];
end

```


Appendix E

Curriculum Vitae CV

PERSONAL INFORMATION

Surname, Name: Adweb, KHALED Mabrouk Amer

Nationality: Libyan

Date and Place of Birth: 10 January, 1980, Libya

Marital Status: Married



EDUCATION

Degree	Institution	Year of Graduation
M.Sc.	Near East University (NEU), North Cyprus.	2016
B.Sc.	Higher Institute of Science and Technology, Algarabulli. Libya.	2002

WORK EXPERIENCE

Year	Place	Enrollment
2006 - Present	Higher Institute of Science and Technology, Algarabulli. Libya.	Lecturer

LANGUAGES

- Arabic and English.

PUBLICATIONS IN INTERNATIONAL REFEREED JOURNALS (IN COVERAGE OF SCI/SCIE/SSCI)

- Adweb, K. M. A., Cavus, N., & Sekeroglu, B. (2021). Cervical cancer diagnosis using very deep networks over different activation functions. *IEEE Access*, 9, 46612-46625. DOI: 10.1109/ACCESS.2021.3067195

THESIS

Master

- Adweb, (2016). *Self-Efficacy of University Students' Towards Mobile Phone Security*. Master Thesis, Near East University (NEU), Department of Computer Information Systems, Applied Science.

Undergraduate Project

- Adweb, (2002). *Salary System for Educational Institution*. Unpublished Undergraduate project, Higher Institute of Science and Technology, Algarabulli, Libya, Department of Computer.

SPORTS

- Football, Basketball.

HOBBIES

Reading, Research, Movies.