Classification Of Histopathological Image for Predication of Breast Cancer Using Pre-Trained Resnet 50 Model

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APPROVAL

This is the thesis titled " **Classification of Histopathological image for prediction of breast cancer using pre-trained RESNET Model**" submitted by Rabeya Tasnin Raha to the department of Information and Communication Engineering, Daffodil International University, has been accepted as satisfactory for the partial fulfilment of the requirement for the degree of Bachelor of science in Electronics and Telecommunication Engineering and approved as to its style and contents.

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I hereby declare that this project has been done by me under the supervision of **Md. Taslim Arefin**, Associate Dean & Associate Professor & Head, Department of ICE **Daffodil International University**. I also declare that neither this project nor any part of this project has been submitted elsewhere for award of any degree or diploma.

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Rabeya Tasnin Raha

ABSTRACT

One of the most common and deadly types of cancer that affects women globally is breast cancer. Accurate diagnosis and early detection are essential for enhancing patient outcomes. Recent developments in deep learning and computer vision have demonstrated promising outcomes in the processing of medical images. To improve the precision of breast cancer detection, this project offers a study on the categorization of breast cancer images usingtransfer learning techniques and the ResNet50 model. In terms of classification accuracy and reliable feature extraction, this project showed ResNet50 to perform better than CNNs, highlighting its higher potential for precise breast cancer prediction from CT-SCAN images. The significance of deep learning architectures like ResNet50 in enhancing medical picture classification tasks is highlighted by these findings.

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CHAPTER 1: Introduction

1.1 Introduction

Breast cancer is a common and difficult disease that affects millions of people worldwide. It is aform of cancer that starts in the cells of the breast. While the precise causes of breast cancer are unknown, it is known that genetics, hormone imbalances, environmental influences, and lifestyle decisions all play a role in its development. Early detection and medical research discoveries have dramatically improved the prognosis for people diagnosed with breast cancer. Regular self-examinations, clinical screens, and mammograms are critical for discovering the illness early on, allowing for more effective treatment options and better outcomes.

Breast cancer awareness programs have been helpful in teaching people about the significanceof early detection, risk factors, and available support systems. These efforts have not only raisedawareness but also lessened the stigma associated with the disease, fostering open dialogue and empowering individuals to take care of their health.

Each year, breast cancer claims hundreds of thousands of lives globally. The death rate can be considerably decreased by early diagnosis and treatment. However, traditional manual diagnosis requires heavy labor, and pathologists' protracted workload makes diagnostic errors more likely to occur. Automatic histopathological picture recognition is essential for accelerating diagnosis and raising diagnostic accuracy.Breast cancer treatment techniques differ based on the stage and kind of cancer, and may involve surgery, chemotherapy, radiation therapy, targeted medicines, and hormonal therapies. Personalized treatment regimens that are tailored to each patient's specific needs are critical forincreasing quality of life and overall survival rates.

To help those afflicted by the disease, resources, emotional support, and guidance have been made available via support networks and organizations committed to breast cancer research, patient care, in addition to medical advancements. The combined efforts of researchers, medical professionals, breast cancer survivors, and advocates continue to advanceour understanding of the disease and enhance the lives of the people it affects.

It is critical that we keep funding research, raising awareness, and creating a welcoming atmosphere for people and families living with breast cancer as we move forward. Our efforts toincrease awareness, promote early diagnosis, and fund ongoing research can help create a world in which breast cancer is not only better understood but also more successfully preventedand treated in the future.

Breast cancer is a frequent illness in women and one of the leading causes of mortality in women worldwide, accounting for 627,000 deaths out of 2.1 million diagnosed cases in 2018.

Invasive ductal carcinoma (IDC) accounts for approximately 80% of all diagnosed cases of breastcancer. Early, accurate diagnosis is critical to selecting the best treatment plan and improving patient survival rates. Microscopic examination of histopathologic stained tissue and subsequent digitalization have become increasingly viable as slide scanning technology has advanced, as has the cost of digital storage in recent years. Automatic histopathological picture recognition is essential for accelerating diagnosis and raising diagnostic accuracy [1]. There are several benefits to digital pathology, including remote diagnosis, rapid archival access, and simplified consultation procedures with experts.

1.2 Motivation

Clinicians can use the richness of information in histopathology images to help them make precise diagnostic and prognostic judgments. However, analyzing these images requires a pathologist's knowledge and can be difficult and time-consuming. The goal of our research is touse machine learning to create reliable and accurate categorization models that can assist pathologists in their evaluations.

We are attempting to classify images of breast cancer histopathology with the goal of providing clinicians with cutting-edge tools that not only speed up analysis but also improve accuracy.Such technology has a wide range of possible advantages, from assisting in early detection toforecasting disease aggression, which could ultimately result in more specialized and efficienttreatment approaches.

Our drive is also fueled by the chance to close the gap between medical knowledge and

technological advancement. Data scientists and medical practitioners working together can create ground-breaking solutions that directly improve patient care. We want to create a synergy between human knowledge and artificial intelligence as we train models to recognizepatterns and subtleties in histopathological images.

1.3 Research Objective

1. To SLN assessment's challenges are Illustrated this demonstrates the need for advancements in the detection and treatment of cancer.

2. To deep learning algorithms for Proposing a Solution using the ResNet-50 deep learning architecture. The specific objectivesof this study are as follows.

3. To data preparation and augmentation with the ResNet-50 architecture and enhance the model's ability to generalize.

4. To implement ResNet-50 architecture to accommodate the specific classification task and the number of classes involved.

5. To transfer learning and pretraining ResNet-50 model on the breast cancer histopathology images dataset.

6. Hyperparameter Tuning and Optimization for mitigate overfitting and ensure the model's generalization capability.

7. Model Evaluation and Performance Metrics.

8. Interpretability and Visualization.

9. Comparative analysis of using ResNet-50 for breast cancer histopathologyimage classification.

1.5 Project Outline

In Chapter 1 briefly introduced about breast cancer, scope and limitation, Research Objective.

In Chapter 2 remaining sections are organized as follows:
The relevant research in deep learning, transfer learning, and breast cancer imaging is reviewed.

In Chapter 3 the approach is described in full, including information on data collection, preprocessing, and the ResNet50 design.

In Chapter 4 the dataset and experimental setup, including data sources and preparation methods, are presented.

In Chapter 5 a thorough study of the outcomes and performance measures is provided.

In Chapter 6 the findings, consequences, difficulties, and prospective directions for the futureare covered.

Chapter 2: Background Study

2.1 Breast Cancer and Imaging Modalities

Breast cancer is a type of cancer that originates in the cells of the breast. It is one of the mostcommon cancers diagnosed in women, but it can also occur in men. Early detection and accurate diagnosis are crucial for effective treatment and improved outcomes. Imaging modalities play a significant role in both the detection and diagnosis of breast cancer. Breast cancer can be grouped in several ways, including by its histologic type, clinical characteristics, and expression of tumor markers. Ductal and lobular carcinomas account for roughly 75 and 15% of all invasive breast cancer cases in the US, respectively, and are the twomost prevalent histologic categories [7]. Here are some commonly used imaging modalities for breast cancer:

Mammography:

Mammography is the most common and widely used imaging modality for breast cancer screening. It involves taking X-ray images of the breast tissue. Mammograms can detect abnormalities such as calcifications or masses in the breast tissue, often before they can be feltduring a physical examination. Digital mammography has become the standard, allowing for better image manipulation and storage.

Ultrasound (Sonography):

Breast ultrasound uses high-frequency sound waves to create images of the breast tissue. It is often used to further evaluate abnormalities found on mammograms or physical examinations. Ultrasound can differentiate between solid masses and fluid-filled cysts, aiding in the diagnosis and characterization of breast lesions.

Magnetic Resonance Imaging (MRI):

Breast MRI is a powerful imaging technique that uses a strong magnetic field and radio waves tocreate detailed images of the breast tissue. It is particularly useful in certain situations, such as assessing the extent of disease in high-risk individuals and characterizing suspicious lesions found on mammograms or ultrasound.

Computed Tomography (CT) Scan:

While not commonly used for routine breast imaging, CT scans can be used to assess the chestand surrounding areas for signs of metastasis (spread of cancer to other parts of the body). CTscans provide detailed cross-sectional images of the body.

Positron Emission Tomography (PET) Scan:

PET scans can be used to detect areas of increased metabolic activity in the body, which can indicate the presence of cancer cells. In breast cancer, PET scans are often used to evaluate theextent of disease and identify potential metastases.

Molecular Breast Imaging (MBI):

MBI is a specialized imaging technique that uses a small amount of radioactive material tocreate images of breast tissue. It is particularly useful in dense breast tissue, where mammography may be less effective at detecting abnormalities.

Each imaging modality has its strengths and limitations, and the choice of modality depends onfactors such as the patient's risk profile, the type of lesion being evaluated, and the purpose of the imaging (screening, diagnosis, staging, etc.). Often, a combination of different imaging techniques may be used to get a comprehensive view of the breast tissue and any potential cancerous lesions.

2.2 Deep Learning in Medical Image Analysis

Deep learning has achieved remarkable success in medical image analysis and has demonstrated its potential in various applications. Deep learning has the ability to organize and extract discriminative information from data without the need for a domain expert to construct featureextractors [8].Its success is evident in the following area.

Disease Detection and Diagnosis:

Disease detection and diagnosis Deep learning models have demonstrated great accuracy in identifying a variety of diseases from medical photos. They have been employed, for example, to detect malignancies (breast, lung, and skin), neurological problems (Alzheimer's, Parkinson's), cardiovascular conditions (heart disease, aneurysms), and more.

Localization and Segmentation:

Deep learning has made it possible to precisely segment and locate structures of interest inside medical images. Planning treatments, operations, and interventions depends on this. Segmenting organs, tumors, blood vessels, and lesions are someexamples.

Image classification:

Deep learning algorithms can accurately classify medical photos into several categories. They can distinguish between various skin lesions, classify retinal images toidentify diabetic retinopathy, and identify lung nodules in CT scans, among other things.

Radiomics and Predictive Modeling: Complex features from medical images are extracted usingdeep learning to enable the development of predictive models. Based on the study of imaging data, these models can forecast disease development, treatment response, and patient outcomes.

Screening and early detection: Deep learning is useful for early disease detection and screeningprograms because of its capacity to recognize subtle abnormalities. Deep learning algorithms, for instance, assist mammography in identifying breast cancer in its early stages.

Image Reconstruction and Enhancement: Medical picture quality has been improved usingdeep learning approaches, which also reduce noise and artifacts. Additionally, they help in picture reconstruction from sparse or noisy data, increasing the diagnostic utility of subpar scans.

Personalization and customization: Deep learning models can be trained to identify traits unique to a patient and adjust treatment strategies accordingly. This method is very useful in precision medicine, where therapies are tailored to each patient's distinct profile.

Resource Optimization: By automating operations like image preparation, quality evaluation,and anomaly identification, deep learning can enhance the effectiveness

medical imagingworkflows while saving time and resources for medical personnel. Even though deep learning has had great success, there are still issues to be resolved. Large anddiverse datasets are required; there are issues with model interpretation and generalization to new data; there may be biases in model predictions; there are legal issues to think about; and AIsystems are now being integrated into clinical practice. Deep learning's effectiveness in medicalpicture processing is evidence of its potential to revolutionize healthcare, but its sustained development and appropriate application depend on ongoing study and cooperation between AI scientists and medical professionals.

2.3 Transfer learning and Resnet 50 Transfer learning

A machine learning technique called transfer learning makes use of information obtained whiletraining one model and applies it to a separate but related job. It's a potent method that has gained popularity recently because of its capacity to improve model performance, shorten training times, and frequently use less labeled data. Here is a thorough justification of transferlearning:

The idea that models might use the knowledge acquired from addressing one problem to help solve another, related problem more successfully is the main driving force behind transfer learning.

For each new job in classical machine learning, models are trained from the start, requiring asignificant amount of labeled data and computer power. The transfer learning process overview shown figure 2.1.

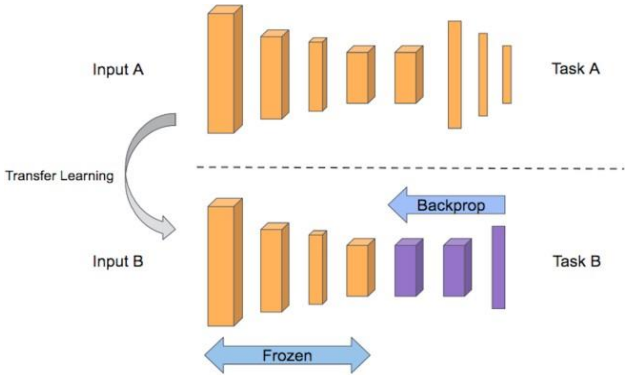


Fig 2.1: Transfer Learning

Two main steps are often involved in transfer learning:

Pre-training: A model learns to extract meaningful features or representations from the input data by being trained on a sizable dataset. A neural network, such as a convolutional neural network for images, or other machine learning models can be used as this pretrained model.

Fine-tuning: By further training the pretrained model on a smaller dataset associated with the new issue, the model is modified (fine-tuned) for the target job. Only the model's top layers arechangeable during this stage; the lower layers, which are in charge of feature extraction, are frequently kept frozen.
Based on the connection between the source and target tasks, transfer learning can be dividedinto many types:

a. Inductive Transfer Learning: The most typical type of transfer learning is inductive, where thesource and target tasks are distinct but the learned information is used to enhance the target task. Using a large image dataset for pretraining and fine-tuning for a particular image classification task, for instance,

Transductive Transfer Learning: In this scenario, the source and target tasks are identical, butthe source domain information and target domain information could be different. For instance, utilizing insights from one camera's photos to enhance performance on photographs from another

c. Unsupervised Transfer Learning: This occurs when the source and target tasks (such asclustering or dimensionality reduction) are both unsupervised.

Added advantages of transfer learning:
Better Performance: When there is a lack of data, transfer learning frequently produces modelsthat perform better than those that are trained from scratch.

Less Labeled Data Needed: Compared to training from scratch, fine-tuning requires less labeleddata.

Faster Training: Because the feature extraction layers of pre-trained models have alreadyacquired relevant representations, training time is reduced.

Domain Adaptation:
Transfer learning can customize models for various domains, strengthening their resistance to variations in data distribution. Resources are saved, including the processing power and knowledge necessary for large-scale model training.

The use of transfer learning

Transfer learning is frequently employed in various disciplines, including computer vision andnatural language processing. Examples comprise:

1.Using ResNet, VGG, or BERT deep neural networks that have been pretrained for a variety ofapplications.
2.Language models for sentiment analysis, translation, and other uses are being fine-tuned.
3.using 3. Transfer learning to diagnose diseases using medical imaging.
4.Utilizing pre-trained models for fraud detection, recommendation engines, and sentimentanalysis.

Challenges and Things to Think About

1.Transfer learning is effective, but it can be difficult to choose the best pretrained model, specify the fine-tuning technique, and handle domain differences.
2.The amount of adaptation versus reuse must be balanced. Avoid over-adapting to the sourcedomain or job.
3.When transferring knowledge from one domain to another, especially when working withsensitive material, ethical and privacy considerations are crucial.

Transfer learning involves using the knowledge gained and quick advancement from a source task to enhance learning and growth for a new target task. Utilizing the properties and traits ofthe source task, which will be applied and mapped onto the target work, is how know ledge isapplied.

Negative transfers, on the other hand, happen when the transfer mechanism causes the performance of the new target task to decline. Being able to give and ensure the positive transfer between activities that are connected while avoiding the negative transfer betweentasks that are unrelated is one of the main issues when using transfer learning methods.

Resnet 50:

ResNet stands for Residual Network and is a specific type of convolutional neural network (CNN) introduced in the 2015 paper "Deep Residual Learning for Image Recognition" by He Kaiming, Zhang Xiangyu, Ren Shaoqing, and Sun Jian. CNNs are commonly used to power computer visionapplications. To solve the issue of vanishing gradients in deep neural networks, ResNet-50 was created. The degradation problem, wherein adding more layers resulted in higher training errors, affected networks as they grew deeper. This problem is reduced by the inventive designof ResNet. Residual learning serves as the foundation of ResNet. ResNet introduces shortcut connections, often referred to as skip connections or residual connections, in place of explicitly attempting to learn the appropriate mapping from input to output.

Information can go swiftly from one layer to a subsequent layer in the network thanks to theseshort-cut connections. In essence, the network learns residual functions, which facilitate optimization. The residue block process overview shown figure 2.2:

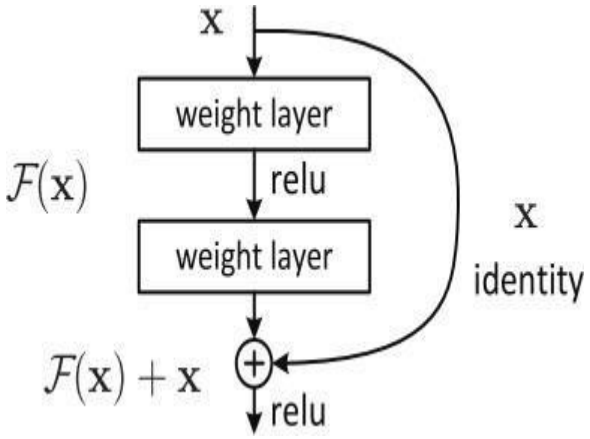


Fig 2.2: Residue block

By basically "skipping" the layers in between, the output of the preceding layer is added (element-wise) to the output of the remainder block. ResNet-50 has 50 layers, the majority of which are residual blocks. There are numerous stages to the architecture, each with a different number of residual blocks. It consists of a convolutional layer at the beginning and max poolingafter that. With different numbers of residual blocks, there are four steps. pooling of global averagesa categorization layer that is completely connected.

ResNet-50's residual blocks are organized in a "bottleneck" fashion. This indicates that there arethree convolutional layers—1x1, 3x3, and 1x1 convolutions—within each residual block. The dimensionality is decreased by 1x1 convolutions, then increased by a further 1x1 convolution after a 3x3 convolution extracts features. This design maintains expressiveness while lowering the computational cost. computer vision tasks, such as object identification, and picture segmentation, have demonstrated ResNet-50 to produce outstanding results It is renowned for its capacity to train extremely deep neural networks—even ones withmore than 1000 layers—without encountering the vanishing gradient issue.

ResNet-50 has gained popularity as a pre-trained model in transfer learning applications because of its great performance and stability. ResNet-50 is a 50-layer convolutional neural network Residual neural networks are a type of artificial neural network forms networks by stackingresidual blocks.

Applications:

Applications including image classification, object recognition, fine-grained classification, andeven medical image analysis make extensive use of ResNet-50 and its derivatives.

In many transfer learning instances where pre-trained ResNet models are improved on certaintasks, it acts as a feature extractor.

2.4 Related Studies on Breast Cancer Classification

Certainly, here are a few studies that focus on breast cancer classification using various techniques, including deep learning, machine learning, and other image analysis methods:

"Deep Learning for Breast Cancer Histopathological Image Analysis: A Comprehensive Review"(2021):

This review paper provides an extensive overview of the recent advances in applying deep learning techniques to breast cancer classification using histopathological images. It covers various deep learning architectures, data augmentation strategies, and challenges in the field.

"Classification of Breast Cancer Histology Images Using Convolutional Neural Networks" (2016):

This study investigates the use of convolutional neural networks (CNNs) for classifying breast cancer histology images. It explores different CNN architectures and evaluates their performance on a publicly available dataset.

"Breast Cancer Histopathology Image Classification: An In-Depth Analysis and Review" (2018):

This review paper provides an in-depth analysis of various image analysis techniques applied to breast cancer classification using histopathological images. It covers traditional image analysis methods as well as machine learning and deep learning approaches.

"Breast Cancer Histopathological Image Classification: A Comprehensive Review" (2020): Similar to the previous study, this paper provides a comprehensive review of the methodologies employed in breast cancer histopathological image classification. It covers feature extraction techniques, machine learning algorithms, and deep learning models.

"Breast Histopathology Image Classification with Deep Neural Networks" (2017): This study focuses on using deep neural networks for breast cancer histopathology image classification. It compares different neural network architectures and discusses the challengesand opportunities in the field.

"Breast Cancer Classification Using Machine Learning and Thermal Images" (2020):
This study explores the use of thermal images and machine learning techniques for breast cancer classification. It demonstrates the potential of non-invasive methods for early cancerdetection.

"A Comparative Study on Breast Cancer Histopathology Image Classification" (2019):
This study performs a comparative analysis of different machine learning algorithms for breast cancer histopathology image classification. It evaluates the performance of traditional and deeplearning models on the dataset.

"Ensemble of Deep Learning Models for Breast Cancer Histology Image Classification" (2021): This research explores the use of ensemble techniques to combine multiple deep learning models for improved breast cancer histology image classification accuracy.
These studies represent a mix of approaches, including deep learning, traditional machine learning, and a variety of imaging modalities. They provide insights into the state-of-the-artmethods and advancements in breast cancer classification using medical images.

CHAPTER 3: Methodology

This chapter has shown the methodology of the work. Here, Dataset Acquisition and Preprocessing, Transfer learning concept, architecture of ResNet50 model, Training process of the model, Misclassified photographs has been discussed.

3.1 Dataset Acquisition and Preprocessing

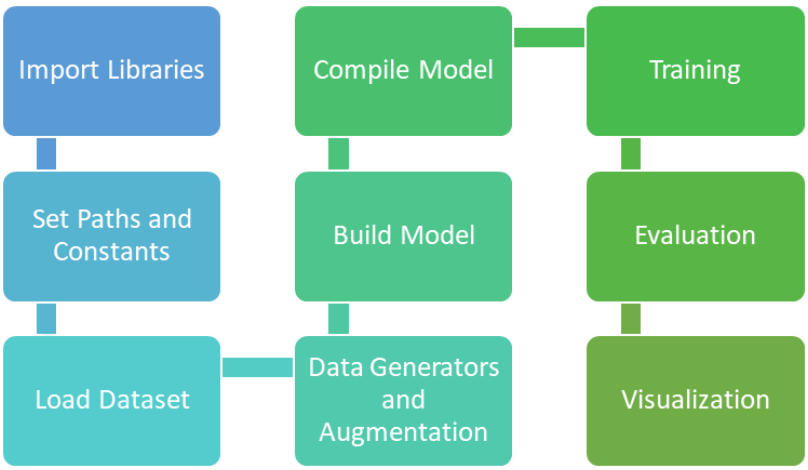


Fig 3.1: Dataset process

Figure 3.1 shows the sheet dataset process.

Import Libraries:

Import necessary libraries including TensorFlow, Keras, Pandas, scikit-learn, and matplotlib.It Paths and Constants:

img_dir: Specifies the directory's path where the images for the dataset are located.

Class names ('benign' and malignant) are defined by class_names.

image_size: Defines the desired size for the images' input. The batch size for training and validation data is specified by batch_size. Figure 3.2 shows how to import the libraries.

```
import os
import numpy as np
import pandas as pd

import tensorflow as tf
from tensorflow.keras import layers
from tensorflow.keras.models import Model
from tensorflow.keras.applications.resnet50 import ResNet50
import tensorflow_addons as tfa

from sklearn.metrics import *
import scikitplot as skplt

from functools import partial
import albumentations as A
import matplotlib.pyplot as plt
import seaborn as sns

AUTOTUNE = tf.data.experimental.AUTOTUNE
data = pd.read_csv('../input/breakhis/Folds.csv')
img_dir = '../input/breakhis/BreaKHis_v1/'
class_names = ['benign', 'malignant']
```

Fig 3.2: code to import libraries

Setup Dataset:

uses Pandas to read dataset information from the CSV file "Folds.csv". This file probably contains information about the names of the image files and any associated CL.Utilizing Image Data Generator, create data generators for training and validation. Set up some hyperparametersand make sure they are optimized for our particular issue [14].

The training data is subjected to picture augmentation techniques such as rotation, shifting, shearing, zooming, and horizontal flipping. asses, and the training and validation datasets split. Based on the validation_split argument, it divides the data into training and validationsubgroups. Both normal and cancerous photos can be found in the dataset. Automated classification of these photos into two classifications is the task connected with this dataset,which would be a useful computer-aided diagnosis tool for the doctor [2].

Create Model:

combines pretrained ImageNet weights with a base ResNet-50 model (ResNet50). Removes thetop classification layer from the ResNet-50 model (include_top=False), since custom classification layers will take its place. Adds fully connected layers and global average pooling forclassification. Figure 3.3 shows how to create the model.

```
# train_loader = tf.data.Dataset.from_tensor_slices((img_dir+train_df.path, train_df.label_int))
# valid_loader = tf.data.Dataset.from_tensor_slices((img_dir+valid_df.path, valid_df.label_int))

train_loader = tf.data.Dataset.from_tensor_slices((img_dir + train_df.path, train_df.label_in
t))
valid_loader = tf.data.Dataset.from_tensor_slices((img_dir + valid_df.path, valid_df.label_in
t))


train_ds = (
    train_loader.shuffle(len(train_df))
    .map(parse_image, num_parallel_calls=AUTOTUNE)
    .map(partial(augmentor),num_parallel_calls=AUTOTUNE)
    .batch(BATCH_SIZE)
    .prefetch(AUTOTUNE)
)
valid_ds = (
    valid_loader.shuffle(len(valid_df))
    .map(parse_image, num_parallel_calls=AUTOTUNE)
    .map(resize_rescale, num_parallel_calls=AUTOTUNE)
    .batch(BATCH_SIZE)
    .prefetch(AUTOTUNE)
)
```

Fig 3.3: Code to create the model.

Build Model:

Assembles the model using the categorical cross-entropy loss function and the Adam optimizer.

Accuracy tracking metrics are configured for training. Figure 3.4 shows how to build the model.

```
tf.keras.backend.clear_session()

def build_network(input_size):
    base_model = ResNet50(weights='imagenet', include_top=False, input_shape=(input_size, inp
ut_size, 3))
    x = base_model.output
    x = layers.GlobalAveragePooling2D()(x)
    predictions = layers.Dense(1, activation='sigmoid')(x)
    model = Model(inputs=base_model.input, outputs=predictions)
    return model

model = build_network(IMAGE_SIZE)

checkpoint_cb = tf.keras.callbacks.ModelCheckpoint("best_model.h5", save_best_only=True)
clr_scheduler = tfa.optimizers.CyclicalLearningRate(
    initial_learning_rate=2e-1,  maximal_learning_rate=7e-3,
    step_size=3*(SAMPLE_SIZE//BATCH_SIZE),
    scale_fn=lambda x: 1 / (2.0 ** (x - 1)),
    scale_mode='cycle'
)
METRICS = [
    'accuracy',
    tf.keras.metrics.Precision(name='precision'),
    tf.keras.metrics.Recall(name='recall'),
]
```

```
# remove 600 from dataset for testing
test_df = data.groupby('label').sample(n=300)
train_df = data.drop(test_df.index).reset_index(drop=True)
test_df = test_df.reset_index(drop=True)

# split training and validation set
valid_df = train_df.sample(frac=0.2)
train_df = train_df.drop(valid_df.index).reset_index(drop=True)
valid_df = valid_df.reset_index(drop=True)

test_df['set'] = 'test'
train_df['set'] = 'train'
valid_df['set'] = 'valid'
data_new = pd.concat([train_df,valid_df, test_df])

ax = sns.displot(data=data_new, x='label', col='set')

print('Training set')
print(train_df.label.value_counts())

print('\nValidation set')
print(valid_df.label.value_counts())

print('\nTest set')
```

Fig 3.4: Build the model

Training:

1. Utilizes the training data generator to train the model.
2. The performance of the validation during training is tracked using the validation datagenerator.
3. With the stated number of epochs, the fit procedure is called.
4. Evaluation: Without rearranging the data, create a test data generator for the validation subset.uses the training model to forecast class probabilities for the validation data.
5. selects the class index with the highest likelihood to be used in computing the anticipatedclasses.
6. uses the scikit-learn classification report function to provide a classification report thatincludes precision, recall, and an F1 score.

Visualization:

1. using matplotlib to plot the training and validation accuracy over epochs.
2. uses the confusion_matrix function from scikit-learn to create a confusion matrix and theheatmap feature of Seaborn to display it.
3. The code shows an entire workflow for developing, training, assessing, and visualizing a breastcancer histopathology image classification model based on ResNet-50. Remember that this codeoffers a fundamental framework and can be improved further with hyperparameter tuning, more complex evaluation metrics, and other upgrades.

3.2 Transfer Learning Concept

The following code snippet illustrates the idea of transfer learning, a deep learning technique frequently used to apply previously trained models to new tasks. Training from scratch may be better replaced by transfer learning. In transfer learning, a network that has been trained for one task is tweaked and used for another, related task. Transfer learning can be used as a baseline or a feature generator, respectively [10]. The transfer learning idea is used in this codein the following ways:

Base Pre-trained Model:

A pre-trained ResNet-50 model with weights learned from the ImageNet dataset is first loadedinto the program. This acts as the fundamental model. The ImageNet dataset, which contains avariety of objects and textures, has taught the pre-trained model to recognize a wide variety offeatures.

Feature Extraction:

The ResNet-50 model's fully connected classification layer is taken out (include_top=False),leaving only the layers in charge of feature extraction. These layers are kept around becausethey are good at extracting important details from pictures.

Custom Classification Head:

On top of the underlying model that has already been trained, a new custom classification headis added. This comprises one or more fully connected layers for classification and a global average pooling layer to summarize the geographic data. The final classification layer has the same number of neurons as the classes (benign and malignant) in the target dataset.

Compile Model:

Adam, an optimizer, and categorical cross-entropy, a loss function, are used in the constructionof the complete model. The model is prepared for training in this step.

Data Generators and Augmentation:

The dataset is loaded and expanded using an ImageDataGenerator in the code. Applying different transformations to the training images, such as rotation, flipping, and shifting, is known as data augmentation. The model's capacity to generalize to fresh, untried images isimproved by this phase.

Training:

Using the obtained augmented data, the model is trained on the training dataset. In order to prevent the pre-trained weights from being drastically altered, the base layers (feature extraction layers) are frozen during training. The customized classification head has

been conditioned to adjust to the classification task of classifying histopathological imagesof breast cancer.

Measurement and Evaluation:

On a portion of the dataset used for validation, the trained model is assessed. Calculating classification metrics like accuracy, precision, recall, and F1-score is part of the evaluation process. The confusion matrix was also created to give information on performance by class.

Fine-tuning (Not Included):

The process of fine-tuning follows transfer learning. It entails continuing training on the targetdataset while unfreezing a few of the pre-trained base model's top layers. The fine-tuning procedure is not included in this code, though.

The provided code illustrates the transfer learning idea by starting with a pre-trained ResNet-50model, customizing it to a new task (classifying breast cancer histopathology images), and training the model on a particular dataset with data augmentation. This method reduces training time and makes use of the knowledge that the feature extraction skills of the pre- trained model have been able to capture.

3.3 Architecture of ResNet50 Model

Kaiming He, Xiangyu Zhang, Shaoqing Ren, and Jian Sun introduced ResNet-50, a deep convolutional neural network architecture, in their 2015 publication titled "Deep Residual Learning for Image Recognition." It is renowned for its outstanding performance in image classification tasks and is a member of the ResNet (Residual Network) family of models.

I can provide you with a streamlined illustration of the ResNet-50 architecture. Please be aware that this figure is only a high-level representation and does not provide particular information regarding the number of filters or layer dimensions. The resnet50 process overview shown figure 3.5.

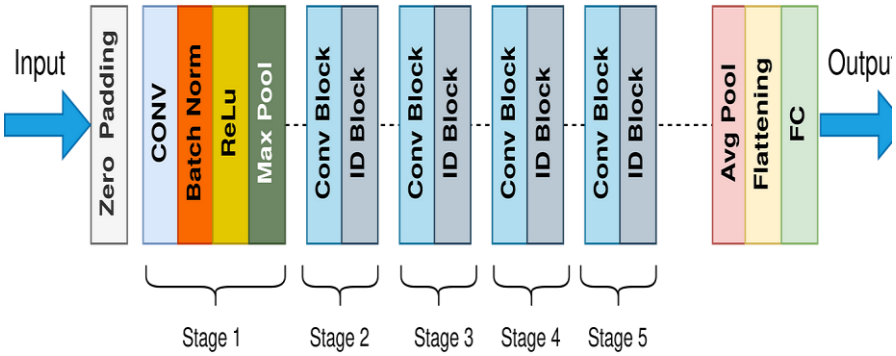


Fig 3.5: ResNet50 Model Architecture

The following diagram shows the data flow across the main model components and gives a high-level overview of the ResNet-50 architecture. According to the previous response, each "residual block" in the diagram depicts a stack of convolutional layers with skip connections. This simplified model does not take into account the precise information regarding filter sizes,dimensions, and the number of layers in each block.

Here is an overview of the architecture of the ResNet-50 model:

Input layer: The model accepts an RGB image as input, usually one that is 224x224 pixels in size.

Pooling and Convolutional Layers:7x7 convolution with 64 filters makes up the first layer, whichis followed by a 3x3 max-pooling layer with a stride of 2.

Residual Blocks: ResNet-50 consists of a number of residual blocks. These blocks are organizedas follows:

1. 2.3x3 convolutional layer filters
2. 3.1x1 filters on a convolutional layer are used to restore dimensionality.
3. connection shortcut or skip that omits one or more layers. The main innovation of ResNet is this. The skip connection facilitates the training of extremely deep networks and aids in preventing the vanishing gradient problem. After every convolutional layer, batch normalizationand ReLU activation are used.

Residual Blocks Configuration:

There are four residual blocks that make up esNet-50 specifically, and each one has a distinctnumber of layers:

1.64 filters in one block

2.128 filters on 2 blocks

3.three blocks, 256 filters

4.512 filters across 5 blocks

global averages: Global average pooling is used to shrink the spatial dimensions to 1x1 after thefinal residual block.

Fully connected layer: Classification is performed using a fully connected layer with 1000 outputunits (equivalent to 1000 ImageNet classes).

SoftMax Activation: Class probabilities are obtained by applying a softmax activation function tothe fully connected layer's output.

Output: The end result is a probability distribution over the classes, and the prediction is theclass with the highest probability.

In comparison to other deep neural network architectures, ResNet-50 was created to be deep while still being computationally effective and simpler to optimize. Since they are essential for training very deep networks, the skip connections in the residual blocks have been incorporatedinto several cutting-edge deep learning architectures.

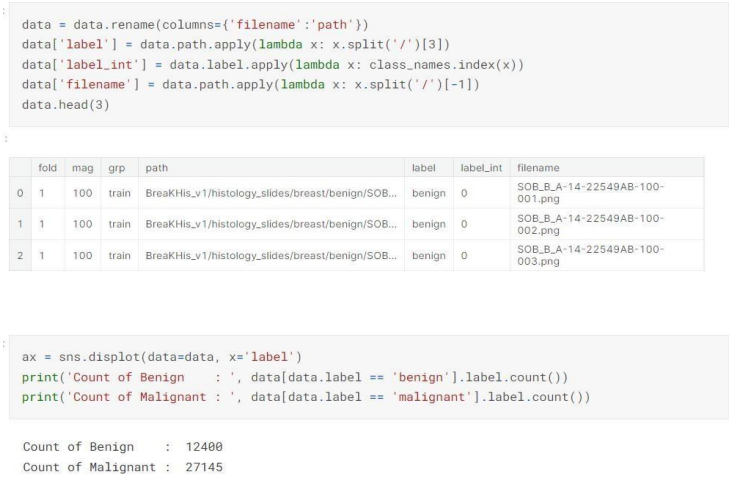
It's important to keep in mind that ResNet-50 is only one version of the ResNet architecture; there are also ResNet-18, ResNet-34, and other versions with various numbers of layers andfilter sizes. Widely utilized for a range of computer vision tasks, ResNet-50, with its 50 layers,maintains a balance between accuracy and computational complexity.

3.4 Training Process of the model

This code's training procedure is an essential step in developing a deep learning model for categorizing images using TensorFlow and Keras. We produce tensor image data in batches using real-time data augmentation. With this kind of data augmentation, we want to make surethat every time our network is trained, it sees fresh iterations of our data [11]. Let's outline thetraining procedure in detail:

Data preparation and loading:

Data loading and preparation are the first steps in the training process. A CSV file called "Folds.csv" that contains data on picture paths and labels (benign or malignant) is used to loadthe dataset. Training, validation, and test sets of data are divided up. Adenosis, fibroadenoma, phyllodes, and tubular adenoma are further subtypes of the benign tumor. Ductal carcinoma, lobular carcinoma, mucinous carcinoma, and papillary carcinoma are subcategories of the malignant tumor type [3]. The training sets class distribution is balanced using an oversamplingtechnique. The Augmentations library is used to create data augmentation pipelines that preprocess photos for the training and validation sets. Figure 3.6 shows how to train the model.



```
data = data.rename(columns={'filename':'path'})
data['label'] = data.path.apply(lambda x: x.split('/')[3])
data['label_int'] = data.label.apply(lambda x: class_names.index(x))
data['filename'] = data.path.apply(lambda x: x.split('/')[-1])
data.head(3)
```

	fold	mag	grp	path	label	label_int	filename
0	1	100	train	BreaKHis_v1/histology_slides/breast/benign/SOB...	benign	0	SOB_B_A-14-22549AB-100-001.png
1	1	100	train	BreaKHis_v1/histology_slides/breast/benign/SOB...	benign	0	SOB_B_A-14-22549AB-100-002.png
2	1	100	train	BreaKHis_v1/histology_slides/breast/benign/SOB...	benign	0	SOB_B_A-14-22549AB-100-003.png

```
ax = sns.displot(data=data, x='label')
print('Count of Benign    : ', data[data.label == 'benign'].label.count())
print('Count of Malignant : ', data[data.label == 'malignant'].label.count())
```

```
Count of Benign    :  12400
Count of Malignant :  27145
```

Fig 3.6: Training Process of the model

Model Building:

The deep learning model is built using the ResNet50 architecture, which is pre-trained on ImageNet. The model is customized for binary classification by adding a global average pooling layer (toreduce spatial dimensions) and a dense layer with a sigmoid activation function (to producebinary classification output).

Optimizer and callbacks:

To track and manage the training process, callbacks are used.

The optimal model weights are saved using Model Checkpoint during training.

The learning rate is modified during training using a cyclical learning rate scheduler fromTensorFlow Addons.

The binary cross-entropy loss function, which is appropriate for binary classification, the stochastic gradient descent (SGD) optimizer, and evaluation measures such as accuracy, precision, and recall are all used in the model's construction.

Model Training:

The actual training process occurs in this step.

The model.fit() method is called with the following parameters:

train_ds: The training dataset, which is a TensorFlow dataset containing preprocessed imagesand labels.

epochs: The number of training epochs (in this case, 12).

batch_size: The batch size used for training (64 in this code).6.verbose: Controls the verbosity of training output.

callbacks: List of callbacks to be used during training, including model checkpointing andcyclical learning rate scheduling.

validation_data: The validation dataset (valid_ds) for monitoring model performance duringtraining.

Training History:

The training history, which includes metrics such as loss, accuracy, precision, recall, etc., is stored in the history variable. This history can be used for further analysis and

visualization.

Model assessment:

The model is assessed on the test dataset after training.

Preprocessed test data is fed into the trained model to make predictions.

Scikit-learn routines are used to compute classification metrics such as precision, recall, F1-score, and accuracy.

Scikit-plot is used to illustrate the confusion matrix.

3.5 Misclassified Photographs

The filenames, actual labels, and anticipated labels for mislabeled photos are all stored in aData Frame.

Images that have been incorrectly labeled are those in which the actual label differs from theexpected label.

The training procedure aims to minimize the loss function, repeatedly update the model's weights and biases using the training data and enhance the model's accuracy in classifying breast histopathology images. The optimizer directs the training process, which is tracked byvarious metrics and callbacks to make sure the model generalizes well to new input.

The following evaluation measures are employed in this code to gauge how well the picturecategorization model performs:

Accuracy: A typical indicator called accuracy counts the percentage of samples in the test setthat were properly identified.

Precision:

Out of all the positive predictions the model makes, precision is the percentage of true positive predictions (properly anticipated positives). It's outlined as:

Precision is equal to TP/(TP+ FP).

Precision is calculated in the context of this code for both the "benign" and "malignant" classifications.

Sensitivity or True Positive Rate of Recall:

1.Recall quantifies the percentage of accurate positive samples (true positive predictions)among all positive samples.

2.Recall is TP / (TP + FN).

Recall can also be calculated.

F1-Score:

The harmonic mean of recall and precision, known as the F1-score, provides a balanced evaluation of a model's performance. It's outlined as:

The F1-Score is calculated by multiplying the precision and recall scores by two.Both 'benign'and malignant classes are used to calculate the F1-score.

Uncertainty Matrix:

1.A table that lists the categorization outcomes of the model is known as a confusion matrix. Itdisplays the total number of true positives, true negatives, false positives, and false negatives.

2.This code uses the scikit-plot module to display a confusion matrix.

The 'benign' and malignant classes of these measurements are calculated and published separately. Additionally, the method determines an overall accuracy and a micro-averaged F1-score that take into account both classes' performance. These metrics provide a thorough assessment of the model's capacity to separate benign from malignant breast histopathologyimages. Earlier detection to breast cancer as whether it is being benign or malignant can be stimulated and classified and thus save life and efforts [6].

CHAPTER 4: Dataset And Experimental Setup

Dataset And Experimental Set The 9,109 histopathological images of breast tumor tissue collected from 82 patients using various magnification factors (40X, 100X, 200X, and 400X) make up the Breast Cancer Histopathological Image Classification (BreakHis). It now has 5,429 malignant samples and 2,480benign samples (700x460 pixels, 3-channel RGB, 8-bit depth per channel, PNG format). In cooperation with the P&D Laboratory for Pathological Anatomy and Cytopathology, Parana, Brazil (http://www.prevencaoediagnose.com.br), this database was created. This database enables future benchmarking and evaluation; therefore, we think researchers will find it beneficial.

4.1 Description of Dataset

The Breast Cancer Histopathological Image Classification (BreakHis) database is a valuable resource for researchers and healthcare professionals involved in breast cancer detection andclassification. The description of dataset overview shown in figure 4.1.

	fold	mag	grp	path	label	label_int	filename
0	1	100	train	BreaKHis_v1/histology_slides/breast/benign/SOB...	benign	0	SOB_B_A-14-22549AB-100-001.png
1	1	100	train	BreaKHis_v1/histology_slides/breast/benign/SOB...	benign	0	SOB_B_A-14-22549AB-100-002.png
2	1	100	train	BreaKHis_v1/histology_slides/breast/benign/SOB...	benign	0	SOB_B_A-14-22549AB-100-003.png

Fig 4.1: Description of Dataset

The database consists of 9,109 microscopic images of breast tumor tissue. These images are collected from 82 patients and are taken at different magnifying factors, including 40X, 100X, 200X, and 400X.The dataset contains both benign and malignant samples, with a total of 2,480benign and 5,429 malignant samples. This diversity in tumor types makes it suitable for variousresearch purposes, particularly in the field of breast cancer diagnosis. The images in the database are in the PNG format and have a resolution of

700X460 pixels. Each image is in 3- channel RGB format with an 8-bit depth in each channel. This high-quality imaging data is essential for accurate analysis and classification. The database was created in collaboration with the P&D Laboratory – Pathological Anatomy and Cytopathology in Parana, Brazil. This collaboration ensures the reliability and authenticity of the data for research purposes.

Researchers can use this database to develop and evaluate computer-aided diagnosis (CAD) systems, deep learning models, and other image processing techniques for breast cancer detection and classification. It can aid in improving the accuracy and efficiency of breast cancer diagnosis, ultimately benefiting patients. Overall, the database is a valuable resource that contributes to the ongoing efforts to improve breast cancer diagnosis and treatment.

Researchers in the field of medical imaging and pathology can leverage this dataset to develop innovative solutions for breast cancer detection and histopathological classification.

Important facts regarding the data it contains, such as information about its origin, composition, format, and purpose, are included in the description of the BreakHis dataset. Let's examine the main components of the dataset description in more detail:

A total of 9,109 microscopic images of breast tumor tissue are included in the dataset. These photos were taken from 82 different patients.

Tumor Types: The dataset includes two main kinds of breast tumors:

Benign Samples: 2,480 photos of benign breast tumor tissue are available.

Malignant Samples: There are 5,429 photos of breast tumor tissue that is malignant.

Magnification: The photographs are taken at various magnifications, such as 40X, 100X, 200X, and 400X. These magnification settings are essential for viewing various granularities and levels of tissue detail.

Image Specifications:

Resolution: The pixels in each image have a resolution of 700 by 460. This offers the level of clarity and detail required for microscopic investigation.

The red, green, and blue channels each include color information because the images

are in a 3-channel RGB format. As a result, color changes in the tissue samples can be represented. Each color channel has an 8-bit depth, allowing it to express 256 distinct color shades. This depth is usual for RGB photos in general.

Format: The PNG (Portable Network Graphics) format is used to store the images in the collection. PNG is a popular standard for lossless image compression that preserves high-qualityimages without causing information loss

Data Source: I collected these data from Kaggle. And it was from the Parana, Brazil-based P&DLaboratory for Pathological Anatomy and Cytopathology was involved in the creation of the dataset. A publicly accessible dataset called BreaKHis contains microscopic biopsy images of both benign and malignant breast cancers[9].

The BreakHis dataset was created primarily as a helpful resource for scholars. It makes a varietyof duties for identifying and classifying breast cancer easier. This dataset can be used by researchers to evaluate and assess the effectiveness of algorithms and models created for the early detection of breast cancer.

In conclusion, the BreakHis dataset description offers a thorough overview of the data's content,structure, and origin. For academics planning to use the dataset for their studies, this information is crucial. Although histopathologists have tried to come up with methods to dividethe disease into meaningful categories and are aware of the diversity of breast cancer [4]. As it helps them understand the dataset's suitability for their specific research needs in the field of breast cancer histopathological image classification. The samples of dataset overview shown in figure 4.2.

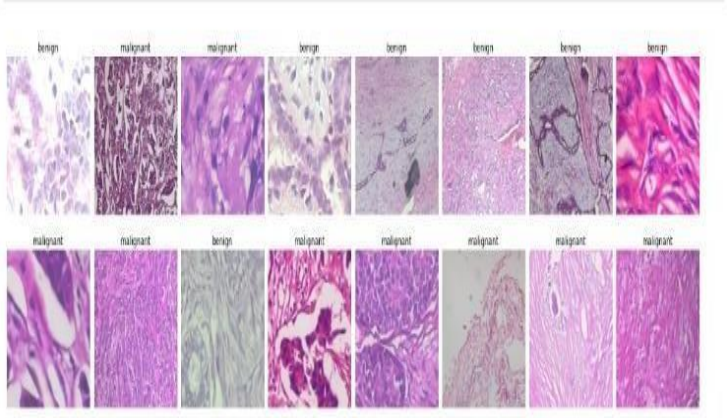


Fig 4.2: Samples of dataset

4.2 Data Preprocessing Techniques

The classification of histological images was done by processing many patches of a specified size. Histological characteristics that can be seen up close separate cancer cells. The cytoplasm may also exhibit atypia, and the nucleus is frequently big and atypical. Additionally, there are obvious structural variations between healthy and sick tissues [5]. Here is an example of data preprocessing for the BreakHis dataset:

Data collection: The BreakHis dataset includes 9,109 microscopic pictures of breast tumor tissue that were gathered from 82 patients, as was previously mentioned. The photos in the data, which were taken at various magnifications (40X, 100X, 200X, and 400X), are kept in PNGformat.

It is crucial to inspect the dataset to comprehend its structure, features, and any potential problems before beginning any preprocessing. This entails:

examining the PNG file format.

confirming the photos' (700 x 460 pixel) dimensions.3.examining the bit depth (8 bits per channel).

Data Cleaning: For the BreakHis dataset, the following actions may be taken:

Taking Care of Missing Photographs: Verify that every one of the 9,109 photographs is there andthat none are missing. Then Check the photos for any anomalies, corruption, or artifacts that could taint the analysis as part of the quality control process. Visual inspection or automated quality checks may be used in this.

Removing Unwanted Photographs: Any photographs that are deemed unnecessary or of poorquality may be taken out of the dataset.

Data Transformation: You might need to do the following to get the photos ready for machinelearning:

Normalization: To guarantee uniformity in data representation, normalize pixel values, typicallyto a range between 0 and 1 for each channel. Encode labels onto the photos according to whether they show benign or malignant tumors. For tasks involving supervised learning, theselabels are necessary. Splitting the data into sets for training, validation, and testing. Usually, a sizeable chunk is set aside for training (for example,

70–80%), a smaller piece for validation (for example, 10-15%) to allow for hyperparameter tuning, and a third portion (for example, 10- 15%) to test the model and assess its performance.

Data Augmentation:

You might use data augmentation techniques to fictitiously expand your training dataset, depending on the application. Rotation, flipping, and zooming are common image enhancements.

Data balancing: If the classes are significantly out of balance (for example, there are more malignant than benign examples), you might want to use methods like oversampling, under sampling, or creating synthetic samples. Keep a log of all preprocessing decisions and actions, as well as information about image scaling, normalization, and any data augmentationthat was used.

Depending on the application, you may use data augmentation techniques to fictitiously expandthe size of your training dataset. Rotation, flipping, and zooming are common image enhancements. Figure 4.3 shows the data balancing.

```
# upsampling training dataset
max_count = np.max(train_df.label.value_counts())
min_count = np.min(train_df.label.value_counts())
train_df = train_df.groupby('label').sample(n=max_count, replace=True)
train_df = train_df.reset_index(drop=True)
train_df.label.value_counts()

ax = sns.displot(data=train_df, x='label')
```

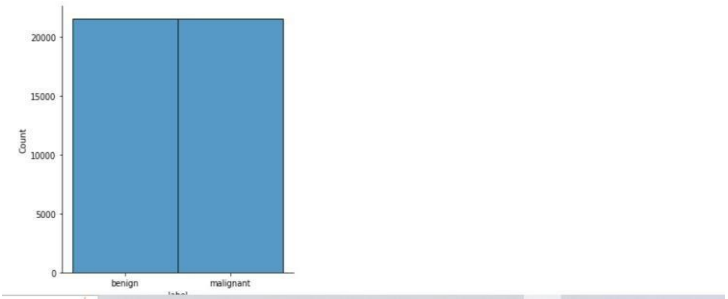


Fig 4.3: Code to Data balancing

Exploratory Data Analysis (EDA): Use EDA to learn more about the dataset by exploring relationships, visualizing distributions, and looking for any trends or potential

problems. In order to effectively use the BreakHis dataset for breast cancer histopathology image classification tasks, data preprocessing is a crucial step. It guarantees that the data is in the proper format and quality to be used for developing artificial intelligence models or performing more research, ultimately resulting in accurate and valuable findings.

4.3 Implementation Details

There are various implementation details that must be taken into consideration in order to use the Breast Cancer Histopathological Image Classification (BreakHis) dataset efficiently for research or machine learning activities. The BreakHis dataset can be properly prepared and used for machine learning or research on the histopathological image categorization of breast cancer by adhering to these implementation specifications. Accurate and relevant results require proper data handling a

Data Collection: Download the BreakHis dataset from a reputable repository or directly from the publisher's website (http://www.prevencaoediagnose.com.br).And make sure you have 9,109 PNG files representing the tissue from breast tumors. The advancement of machine learning and computer vision may provide more accurate categorization techniques for the histological evaluation of hematoxylin and eosin-stained sections. These techniques have great classification rates for automatically categorizing breast tissues[12]

Data Storage:

Create distinct directories for benign and malignant samples in the dataset's structure. Depending on your processing needs and capabilities, store the dataset on your computer locally or in a cloud-based storage system.

Data Loading:

1.To read and load photos from the dataset into your analytic or machine learning environment,create data loading functions or scripts. Then manage picture loading, you can utilize libraries for image processing such as OpenCV or PIL.

Data Splitting:

Create training, validation, and testing sets from the dataset. 70% for training, 15% for validation, and 15% for testing are typical splits to prevent class imbalance issues, make sure thesplits retain a comparable distribution of benign and malignant samples.

Data Balancing:

In order to balance the classes in the training set, check for class imbalance and, if necessary, use strategies like oversampling, undersampling, or synthetic data generation.

Batching and data loading:

During model training and evaluation, create data loading pipelines that effectively load andpreprocess batches of photos. Use these pipelines to implement data transformation and augmentation.

Data documentation and versioning:

in order to track alterations or updates over time, keep version control for the dataset. Make areport that details the dataset, its source, the preprocessing procedures, and any alterations that were made.

Data Security and Privacy:

Make sure that the dataset is stored securely and that only people with permission are allowed access.Handle the dataset in accordance with privacy laws and industry best practices if it contains sensitive patient data.

Exploration and visualization of data:

Learn more about the distribution of benign and cancerous samples, magnification factors, andother pertinent aspects by exploring the collection through visualizations.

Data Logging and Monitoring:

Implement logging and monitoring to track data access, changes, and any issues that may ariseduring data processing.

Data quality control:

Implement data quality tests to find and correct any anomalies, mistakes, or outliers in thedata. Optimization of data storage, if applicable:

Consider data storage optimization approaches to cut storage costs, depending on the size ofthe dataset.

Backup and recovery of data:

Create regular backups of the dataset to guard against data loss due to hardware malfunctionsor other unforeseen circumstances

.

4.4 Experimental Design

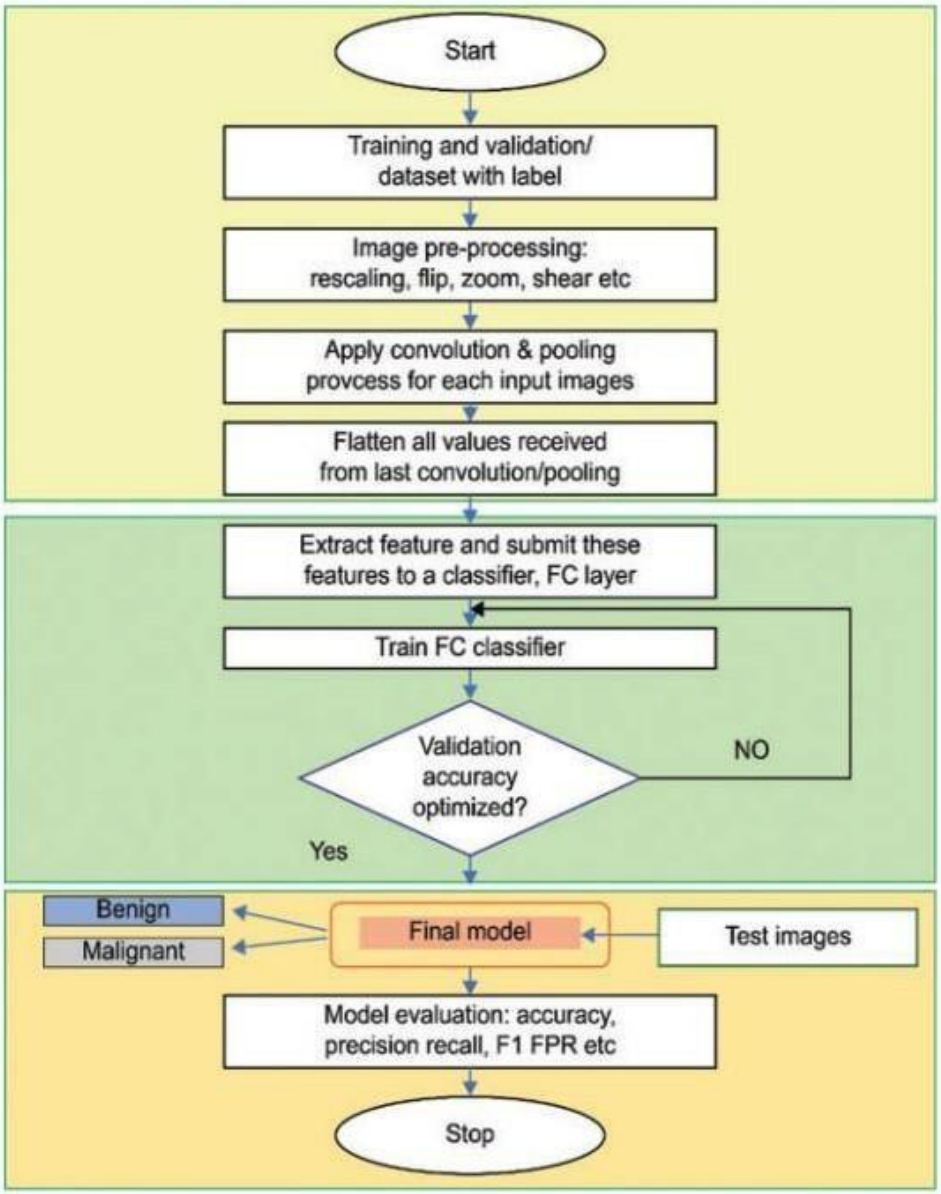


Fig 4.4: Experimental Design

CHAPTER 5: Results and Analysis

This chapter has shown the result and analysis of the work. Here, experimental result and images prediction has been discussed.

5.1 Results and Analysis

The accuracy rate of the model's classification is the primary metric used to assess its usefulness. To analyze the extra quality parameters, such as precision, the confusion matrix isused.

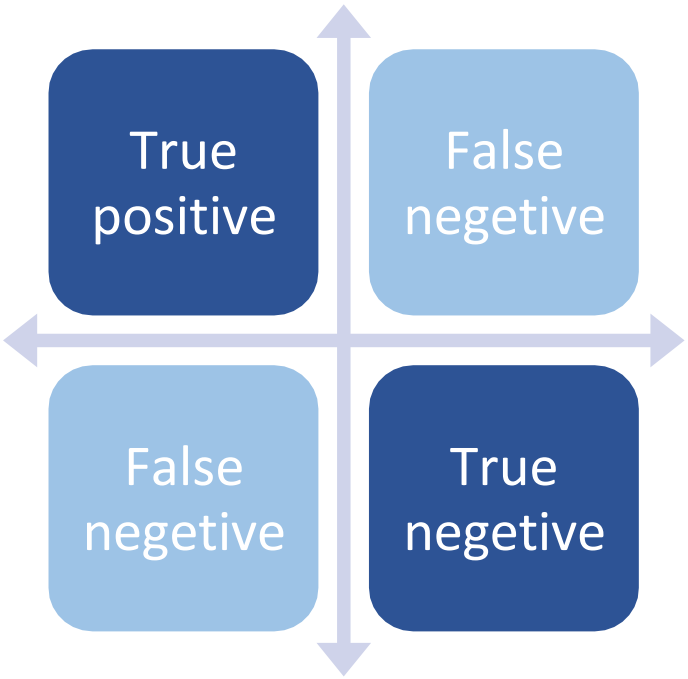


Fig 5.1: Results and Analysis

Positive class 0 and Negative class 1 The true positive (TP), false negative (FN), false positive (FP), and true negative (TN) values are each represented by a different cell element in this example. The terms "TP" and "FP" stand for "true positive class" and "cases where there is an actual negative class," respectively. FN displays a positive class, while TN refers to the negativelyprojected negative class. Mistakenly classifying as a negative class. Figure 5.1 shows the result and analysis.

In training set

Malignant 21528

Benign 9628

Name: label, dtype: int6

Set of validation

malignant 5317

benign 2472

Name: label, dtype: int64

Test set

malignant 300

benign 300

Name: label, dtype: int64

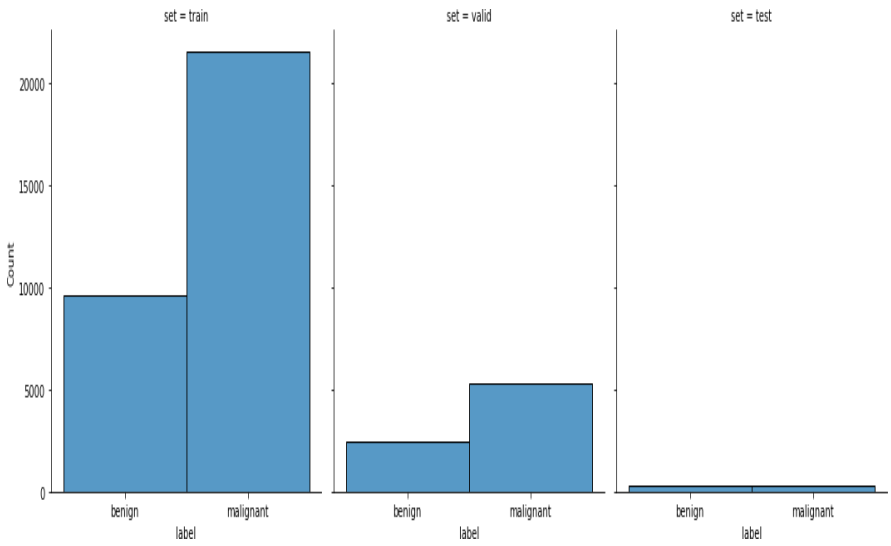


Fig 5.2: Training set and Validation set and Test set

Figure 5.2 shows the three types of data given as training data with which I will trained the model. Valid data, with which to learn my model. Test data with which to test the performance of my model.

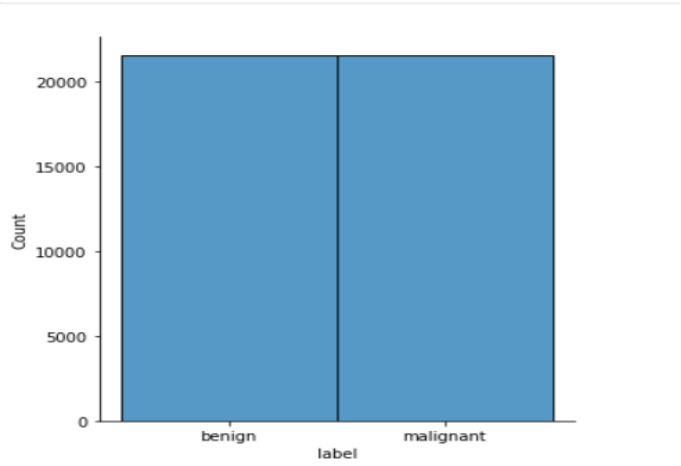


Fig 5.3: Upsampling Training Dataset

In this figure 5.3, we're using groupby to group the DataFrame by the 'label' column and then using sample to randomly sample with replacement, ensuring each class has the maximum count of samples**.**

5.2 Experimental Results

Confusion matrices were used for performance evaluation in order to draw conclusions. There are six main steps in this study: (a) Data and picture pre-processing (a) feature extraction, (b) network training and FC layer fine-tuning, (c) model augmentation, and (d)accuracy assessment utilizing the validation dataset, model finalization, and final performance evaluation of accuracyand other criteria using test data that hasn't been seen before.

Image processing is a crucial stage since it improves image quality and gets input ready. pictures for teaching a network. Data augmentation was required because there were feweravailable photographs that were subsequently separated into train, validation, and test datasets.

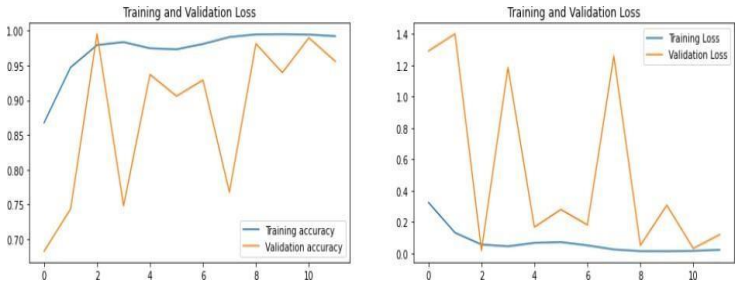


Fig 5.4 : Construct neural network & start training

Figure 5.4 shows us training and validation losss.The pre-built model Resnet50 has been used to extract features. The network layers have beenkept trainable, and the original pre-trained weights have been loaded, allowing the model to learn new patterns.using the supplied unpublished medical dataset. Redefining the parametersallowed for fine-tuning.Multiple runs have been used to fine-tune the hyper- and FC-layer parameters for the best possible accuracy on datasets for training and validation.

	precision	recall	f1-score	support
benign	0.93	0.97	0.95	300
malignant	0.97	0.93	0.95	300
accuracy			0.95	600
macro avg	0.95	0.95	0.95	600
weighted avg	0.95	0.95	0.95	600

f1_score : 0.9466666666666667
accuracy_score : 0.9466666666666667

Fig 5.5: score of models.

The assessment of a binary classification model, which typically uses input data to forecast which of two classes will be present. The terms "benign" and "malignant," which are frequentlyemployed in the context of medical diagnosis, such as the detection of cancer, are utilized in thisinstance. Let's analyze the outcomes:

For samples classified as "benign," the precision is 0.93, which indicates that 93% of the time the model's "benign" classification predictions are accurate. In other words, only 7% of the samples classified as "benign" actually are.For the class labeled "malignant," precision is 0.97, meaning that 97% of the time the model's classification of a sample as "malignant" is accurate.False positives only occur in 3% of the samples classified as "malignant".When the cost of false positives is substantial, as it is in medical diagnosis when you don't want to inform someone they have a sickness when they don't, high precision is crucial. Figure 5.5 shows the score of the model.

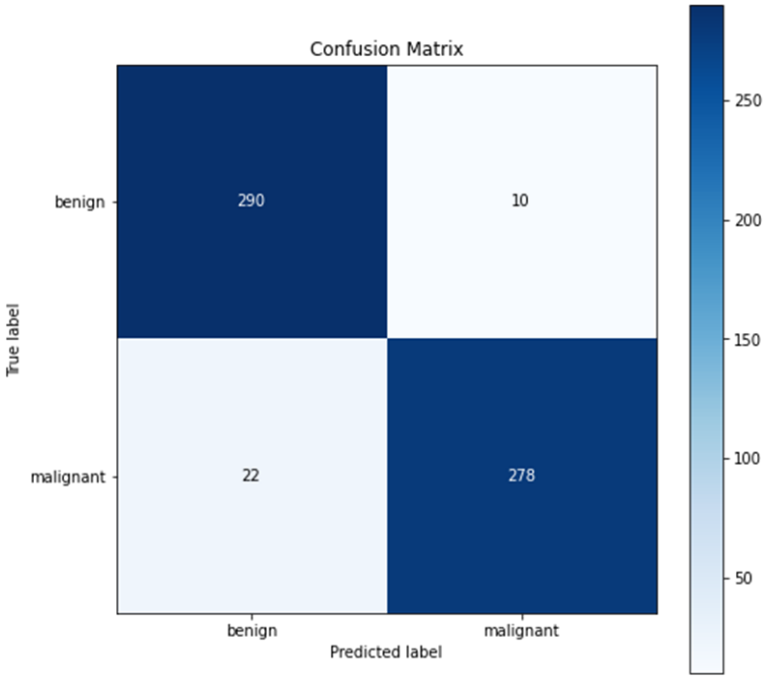


Fig 5.6: Evaluate neural network performance.

Recall:

1.Recall for the "benign" class is 0.97, which indicates that 97% of the actual "benign" samples are correctly identified by the model. Only 3% of cases that are deemed "benign" are actually false negatives.2.The recall for the "malignant" class is 0.93, meaning that 93% of the real "malignant" samples are correctly identified by the model. False negatives, which account foronly 7% of "malignant" cases, are incorrectly labeled as something else.

When the cost of false negatives is substantial, as it is when making a medical diagnosis, andyou want to make sure you find as many cases of the disease as you can, strong recall is essential.

F1-score : The F1-score strikes a compromise between recall and precision. It is the harmonic mean of these two numbers and is very helpful when you just have one measure to gauge howwell a model is working. The F1-score in this instance is roughly 0.947, showing a reasonable balance between recall and precision.

Accuracy: The model's overall accuracy is around 94.7%. This indicates that the model classifiesapproximately 94.7% of all samples correctly. But accuracy by itself can be deceptive, particularly in cases of class imbalance (unequal distribution of classes). The high accuracy in this instance indicates that the model functions well in both classes. Figure 5.6 shows the Evaluate neural network performance

Macro Average: The macro-average computes the mean by averaging the precision, recall, andF1 scores for each class separately. It's roughly 0.95 in your case, which indicates solid performance across the board for both classes.

Weighted Average: The weighted average takes into account how many samples are included ineach class. The model appears to perform well across both classes while accounting for class imbalances because it is also close to 0.95.

The findings imply that the binary classification model is operating effectively. It has a high F1-score for both "benign" and "malignant" classes, great precision, recall, and overall accuracy. This suggests that the model is proficient at differentiating between these two classes, which issignificant in instances involving medical diagnosis when precision is crucial. Figure 5.7 shows 30 images that predict breast cancer. Figure 5.8 are shows some wrong images.

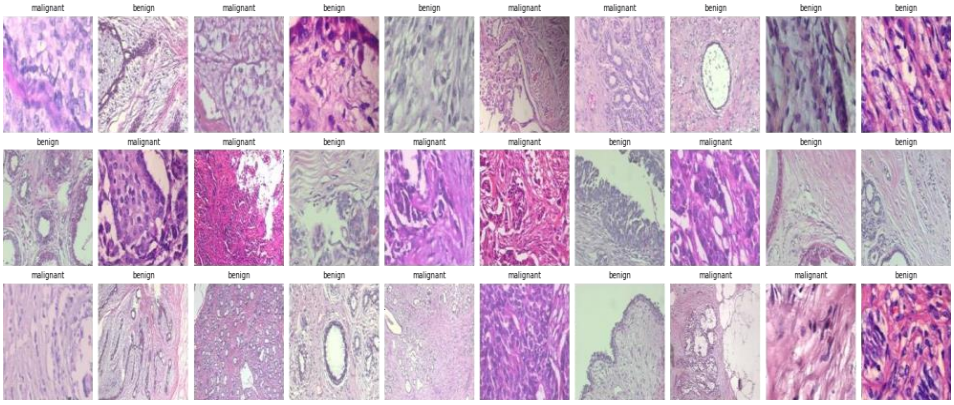


Fig 5.7: view first 30 predictions of image

Wrong prediction:

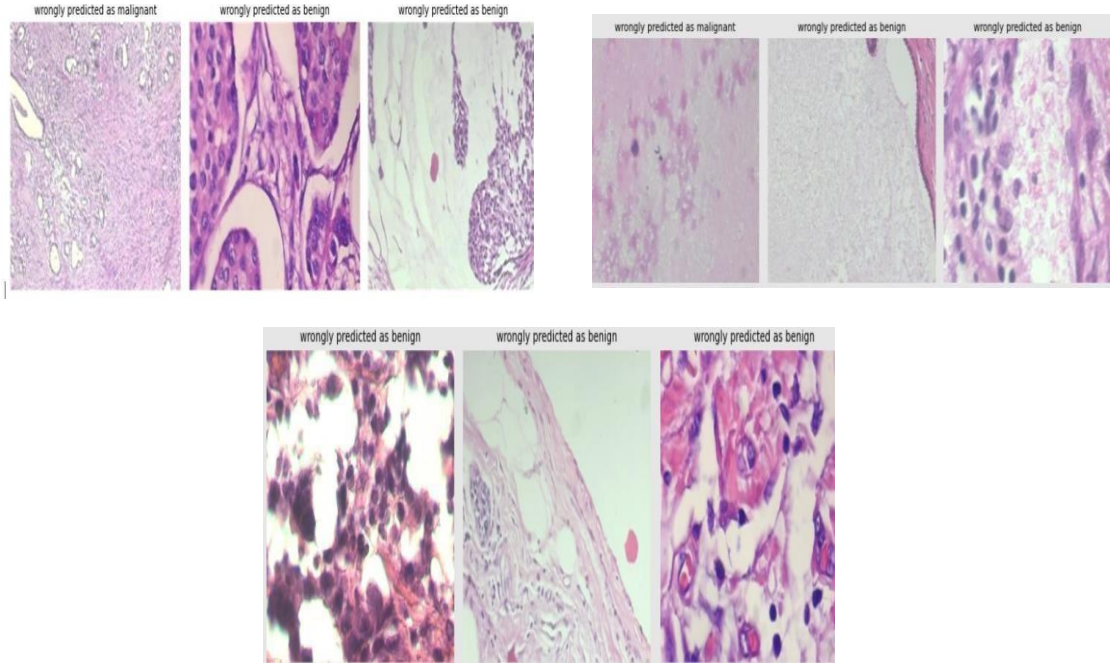


Fig 5.8: view some wrong prediction image

5.3 performance and Comparison

Compare Breast Cancer Histopathology image classification through assembling multiple compact CNNs and Breast Cancer Histopathology Images Classification through resNet50.The Statement (Performance of a Multi-Model Assembling Strategy):

1.This statement is about a different method that employs a multi-model assembly strategy.

2.It achieves 87.5% accuracy at the patient level and 84.4% accuracy at the image lever [1].

3.However, specific metrics like precision, recall, and F1-score are not provided here.

The statement highlights the use of this method for patient-level and image-level classification.Performance Metrics for a Binary Classification Model, First Statement:

1.The model performs admirably overall, with an accuracy of roughly 95%.

2.The model is doing well in both classes ("benign" and "malignant"), as evidenced by itsexcellent precision, recall, and F1-score.

3.It uses a weighted average to correct for class imbalances while still producing a high score ofroughly 0.95.

4.According to the assertion, the model exhibits a balanced trade-off between recall and precision, pointing to strong overall classification performance.

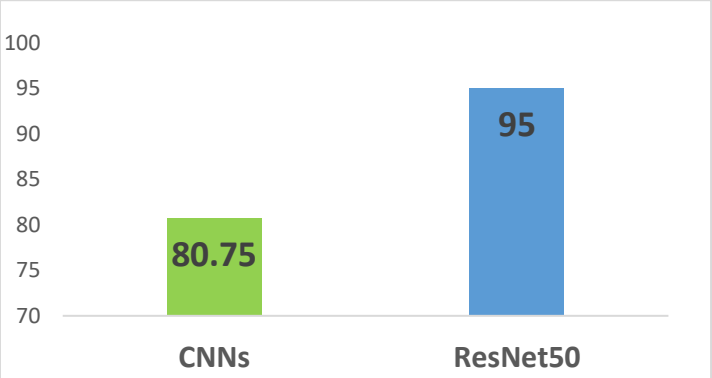


Fig 5.9: Comparison between CNNs and ResNet50

In this Figure 5.9 shows the first statement reports a higher accuracy of approximately 95%, while the second statement reports slightly lower accuracies of 87.5%. First statement provides more comprehensive information regarding the model's performance, including class-wise metrics, while the second statement emphasizes a multi-model assembly strategy with accuracy figures at different levels but lacks detailed performance metrics.

CHAPTER 6: Conclusion

6.1 Conclusion

A significant and fruitful line of investigation in the realm of medical image analysis and healthcare is the classification of breast cancer histopathology images using the ResNet-50 model. Breast cancer histopathology image categorization using deep learning, more specifically the ResNet-50 architecture, has shown incredible promise for increasing the precision and effectiveness of cancer detection. It is the most prevalent cancer in America, where women are anticipated to have up to 30% more diagnoses of it in 2019[13]. In histopathology photos, the deep convolutional neural network ResNet-50 has demonstrated outstanding accuracy in differentiating between malignant and benign breast tissue. It is a good choice for this job because it can capture fine details in the photographs. ResNet-50 reduces human interpretation's subjectivity by automating the classification process. Although radiologists' extensive knowledge is a major factor in their ability to successfully identify malignant tumors from histopathological pictures, specialists occasionally disagree with their conclusions. A second option for picture diagnosis is provided by computer-aided diagnosis, which can increase the accuracy of experts' judgment.

Large datasets can be used to train deep learning models like ResNet-50, making them flexible for a variety of populations and capable of identifying different cancer subtypes. For dealing with the variety of breast cancer cases, this scalability is essential. ResNet-50 and comparable models can still be difficult to use in practical clinical settings, despite their promise. Continuous hurdles include ensuring robustness, addressing data privacy concerns, and integrating new models into the current healthcare infrastructure. ResNet-50 and other deep learning models frequently lack transparency in their decision-making. It is necessary to make an effort to improve interpretability so that clinicians can understand the rationale behind a specific classification. ResNet-50's success is highly dependent on the caliber and variety of the training data. It is important to make an effort to ensure that the training datasets are impartial and representative.

Breast cancer histopathology image categorization using ResNet-50 holds significant promise for enhancing the precision, effectiveness, and objectivity of cancer diagnosis. Even if there are still issues and concerns, more research and advancement in this area

have the potential to have a big influence on early breast cancer diagnosis and treatment, leading to better patient outcomes. In this study, ResNet50 was rated as the best model for performance and accuracy in the identification and classification of breast cancer using transfer learning. ResNet50 is a wonderful and effective predictor in the field of health [15].

6.2 Future Study

It is accepted that the pursuit of a flawless, 100% accurate output through fine-tuning is an admirable goal in the context of this undertaking. The current endeavor, however, is unable to do the thorough investigation and improvement necessary to achieve such a degree of precision due to time restrictions. As a result, it is anticipated that future research projects will offer the chance to devote the required amount of time and money to this effort, potentially leading to superior results in terms of accuracy and performance.

6.3 Limitations

Data Availability and Diversity: The effectiveness of the classification models heavily dependson the quality, diversity, and size of the dataset. Limited availability of high-quality labeled histopathology images could impact the generalization and performance of the models.

Data Imbalance: Imbalance among different subtypes and grades of breast cancer could lead tobiased classification results, favoring the majority class. Addressing data imbalance is crucial toensure fair and accurate predictions.

Complexity of Breast Cancer: Breast cancer is a complex disease with various subtypes and grades, making accurate classification challenging. Models might struggle with distinguishingsubtle differences among closely related classes.

Interpreting Deep Learning Models: While efforts will be made to enhance interpretability, deep learning models can still be challenging to interpret comprehensively. The exact decision-making process within the models might not be fully transparent.

Clinical Variability: The clinical relevance of the classification models might vary depending on factors such as the specific patient population, the availability of additional clinical data, and evolving medical guidelines.

Ethical Considerations: Implementing models in a clinical setting requires careful considerationof patient privacy, informed consent, and potential biases that could affect different demographic groups.

External Validation: Due to the unique characteristics of different medical institutions andpatient populations, the developed models might need to be externally validated before widespread adoption.

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