

CMP6228 - Deep Neural Networks

Convolutional Neural Networks for Lung and Colon Cancer Imaging: An Analytical Approach

Coursework Assignment Report

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Glossary

ReLU: Rectified Linear Unit

SGD: Stochastic Gradient Descent

DL: Deep Learning

ANN: Artificial Neural Network

RNN: Recurrent Neural Network

CNN: Convolutional Neural Network

EDA: Exploratory Data Analysis

F1: F1 Score

MSE: Mean Squared Error

Abstract

This study focused on the development and evaluation of CNN models for the classification of lung images. The goal was to accurately distinguish between benign and cancerous conditions using a dataset comprising images of lungs. The images were preprocessed, including resizing and normalization, and then split into train and validation sets. Two CNN models were designed and compared in terms of their architecture and performance. Model 1 consisted of multiple convolutional layers with dropout and pooling, while Model 2 had a simpler architecture with fewer layers. Both models demonstrated strong performance, with Model 2 achieving slightly higher accuracy on the test set. The evaluation metrics, including precision, recall, and F1-score, provided insights into the models' classification capabilities. The findings highlight the importance of optimized model architecture and the potential of streamlined designs for accurate lung image classification, contributing to the development of effective medical systems.

1 Introduction

The aim of this report is to utilize deep learning techniques for the classification of Lung and Colon Cancer Images into the categories of cancerous or healthy. The selected data set provides a valuable resource for training and evaluating the performance of our proposed methodology.

The assemblage utilized in this examination incorporates an aggregation of Respiratory and Colon Malignant growth Pictures, representing histopathological tests. These portrayals perform a basic activity in the analysis and treatment of disease, as they outfit miniature experiences into the phone creation and basic models connected with harmful improvement.

The essential goal of this report is to build up an exact and productive characterization framework utilizing significant learning strategies. By using Convolutional Neural Networks (CNNs), we mean to consequently remove significant highlights from the pictures and train a model fit for recognizing between dangerous and sound tests.

This report follows a structured organization to provide a comprehensive understanding of the proposed methodology, experimental process, and obtained results. It begins with Section 1, the Report Introduction, which provides an overview of the report, summarizing the aim, dataset description, and achievements. This section sets the context for the subsequent sections and highlights the study's main focus. In Section 2, the Problem Statement, a detailed description of the dataset is provided, including its composition, characteristics, and challenges. Additionally, the section outlines the deep learning problem, emphasizing the importance of accurate classification of Lung and Colon Cancer Images.

Section 3, the Proposed Method, then presents a comprehensive explanation of the methodology employed. It covers the pre-processing phase, involving data cleaning, normalization, and augmentation techniques. Furthermore, it provides an in-depth description of the CNN architecture used for classification, along with any modifications or enhancements made to address the specific problem.

The report continues with Section 4, Experimental Results, where a detailed account of the experimental process is presented. It includes the parameter settings for training the CNN model, the evaluation metrics used, and the obtained results. Additionally, an analysis and interpretation of the classification system's performance are provided, highlighting its strengths and limitations. Finally, in Section 5, Summary and Discussion, the key findings of the report are summarized and their implications discussed. The section emphasizes the achievements, challenges encountered, and potential avenues for further research.

2 Problem Statement

A considerable measure of oncological imagery has been accumulated for analysis, equaling twenty-five thousand portraits in whole. Each visual representation within the archive is comprised of nearly six hundred thousand pixels, meticulously arranged in a square and compressed in the customary JPEG configuration. The diversified assortment of photos that researchers may scrutinize and ponder has been sorted meticulously into quintuple categories in accordance with the anatomical location and health of the captured tissues, All categories bullet pointed below:

- Lung benign tissue
- Lung adenocarcinoma
- Lung squamous cell carcinoma
- Colon adenocarcinoma
- Colon benign tissue

Within the data set, there are 5,000 images representing each categorization, resulting in a balanced distribution of 10,000 images for the Colon category and 15,000 images for the Lung category. This balanced distribution ensures that there is sufficient representation of both Colon and Lung cancer types for accurate classification and analysis.

The data set serves as a valuable resource for training and evaluating deep learning models for the purpose of distinguishing between cancerous and healthy tissues in both the Lung and Colon. The dataset was acquired from Kaggle and will be linked in the references.

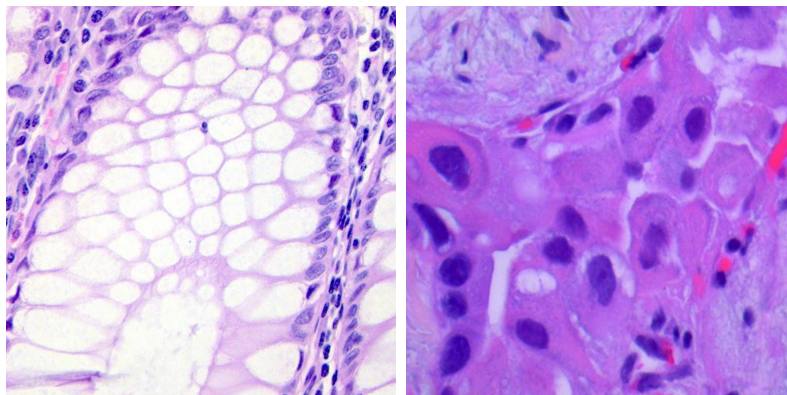


Figure 1: Colon(Left) and Lung(Right) Tissue (From Dataset)

2.1 Deep Learning Solution

Developing a solution to the classification problem of Lung and Colon Cancer Images is crucial in medical diagnostics and treatment. Accurate identification and classification of cancerous tissues enable early detection, precise diagnosis, and effective treatment planning. Convolutional Neural Networks (CNNs) have proven to be highly effective in analyzing medical images, automatically extracting relevant features to classify complex patterns and structures present in the dataset. By leveraging CNNs, we can handle large-scale datasets efficiently and benefit from transfer learning, allowing pre-trained models to adapt to the specific characteristics of the Lung and Colon Cancer Images. Our aim is to develop a robust and reliable CNN-based classification system, contributing to improved patient outcomes, early detection, and enhanced cancer care effectiveness.

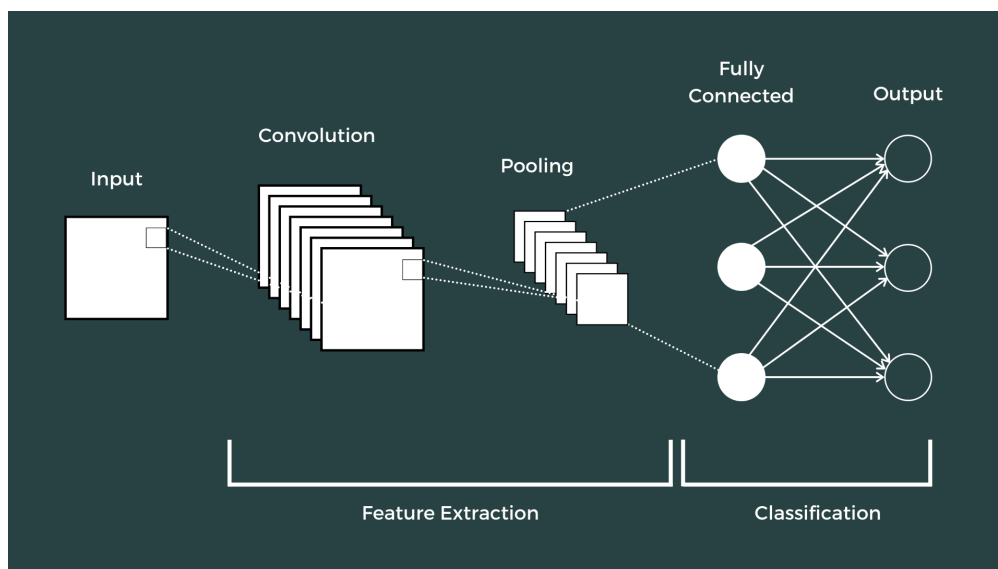


Figure 2: Simple Convolutional Neural Network Diagram

3 Proposed Method

In the development of a Convolutional Neural Network (CNN) model for the dataset, I utilized Google Colab alongside essential libraries such as NumPy, Pandas, Seaborn, Matplotlib, and PyTorch. These tools enabled me to efficiently handle the dataset, perform data analysis, visualize results, and implement the CNN architecture. The `torch.nn` module facilitated the creation of the CNN model, while `torch.utils.data.DataLoader` handled the dataset loading. By leveraging `torch.nn.functional`, I evaluated the model's performance and calculated loss. The `torchsummary` module provided a concise summary of the model's architecture. Overall, the integration of these resources in Google Colab enabled a streamlined and effective process for developing the CNN model for the dataset.

```
[ ] import os # for working with files
import numpy as np # for numerical computations
import pandas as pd # for working with dataframes
import seaborn as sns
import torch # PyTorch module
import matplotlib.pyplot as plt # for plotting informations on graph and images using tensors
import torch.nn as nn # for creating neural networks
from torch.utils.data import DataLoader # for dataloaders
from PIL import Image # for checking images
import torch.nn.functional as F # for functions for calculating loss
import torchvision.transforms as transforms # for transforming images into tensors
from torchvision.utils import make_grid # for data checking
from torchvision.datasets import ImageFolder # for working with classes and images
from torchsummary import summary # for getting the summary of our model
import tensorflow as tf
from tensorflow import keras
import itertools
from sklearn.metrics import precision_score, accuracy_score, recall_score, confusion_matrix, ConfusionMatrixDisplay

# Mount Google Drive
from google.colab import drive
drive.mount("/content/drive")

%matplotlib inline

Drive already mounted at /content/drive; to attempt to forcibly remount, call drive.mount("/content/drive", force_remount=True).

[ ] lung_dir = "/content/drive/MyDrive/Medical images/lung_image_sets"
lungs = os.listdir(lung_dir)

[ ] lungs

['lung_n', 'lung_scc', 'lung_aca']
```

Figure 3: Loading and Importing

In figure 3, the decision was made to focus solely on analyzing lung images due to their significance in medical diagnostics and treatment. By narrowing the scope to lung images, the model can place emphasis on capturing specific features and patterns related to lung conditions. The dataset, consisting of lung images, was stored and retrieved from Google Drive, providing a convenient and accessible storage solution. This allowed for efficient data management and seamless integration with the analysis pipeline in the Google Colab environment.

```
[ ] # Number of images for each disease
nums_train = {}
nums_val = {}
for lung in lungs:
    nums_train[lung] = len(os.listdir(lung_dir + '/' + lung))
img_per_class_train = pd.DataFrame(nums_train.values(), index=nums_train.keys(), columns=["no. of images"])
print('Train data distribution :')
img_per_class_train

Train data distribution :
no. of images
lung_n      5000
lung_scc    5000
lung_aca    5000
```

Figure 4: Checking if data is intact

The code in figure 5 utilizes the `ImageDataGenerator` class from the `keras.preprocessing.image` module to prepare and augment image data for training and validation. The `train_gen` generator is configured to rescale pixel values, apply random rotations, and perform horizontal flipping, while allocating a validation subset. Similarly, the `valid_gen` generator rescales the pixel values and also sets a validation split. The resulting `traindata` and `valdata` directory iterators are created from the specified directories, target image size, batch size, color mode, class mode, and shuffling preferences.

```
train_gen = keras.preprocessing.image.ImageDataGenerator(rescale=1./255,
                                                         rotation_range = 20 ,
                                                         horizontal_flip = True ,
                                                         validation_split = 0.2
                                                         )
valid_gen = keras.preprocessing.image.ImageDataGenerator(rescale=1./255, validation_split = 0.2)
train_data = train_gen.flow_from_directory(lung_dir, subset='training', target_size=(172,172), batch_size=64, color_mode='rgb',
                                           class_mode='categorical', shuffle=True)
val_data = valid_gen.flow_from_directory(lung_dir, subset='validation', target_size=(172,172), batch_size=64, color_mode='rgb',
                                         class_mode='categorical', shuffle=False)
```

Found 12000 images belonging to 3 classes.
Found 3000 images belonging to 3 classes.

Figure 5: Splitting and Augmenting Data

3.1 Model Set Up

In this study, two different CNN models were utilized to compare their performance and evaluate their effectiveness in classifying lung images. Due to the limited availability of labeled data, a train-validation split was employed instead of the traditional train-validation-test split. This means that the validation set served as a proxy for evaluating the models' performance, as there was no separate test set. By comparing the performance of the two models on the validation set, insights could be gained regarding their relative strengths and weaknesses, allowing for a comprehensive assessment of their classification capabilities.

In Figure 6, Model 1 is designed with a specific architecture to effectively classify lung images. The initial convolutional layer with 32 filters and a kernel size of 3 helps in capturing low-level features present in the images. By using the ReLU activation function, the model introduces non-linearity, allowing it to learn complex patterns and discriminate between different classes.

The addition of dropout layers with progressively increasing dropout rates (0.1, 0.15, and 0.2) helps prevent overfitting by randomly disabling a fraction of the neurons during training. This regularization technique encourages the model to learn more robust and generalizable representations.

The max pooling layers perform downsampling, reducing the spatial dimensions of the feature maps while retaining important features. This helps in reducing the computational complexity and enhancing translational invariance.

The final dense layers, with 256 units and 3 units respectively, contribute to the classification process. The ReLU activation function in the first dense layer introduces non-linearity and facilitates the learning of more complex representations. The softmax activation function in the last dense layer provides a probability distribution over the output classes, enabling the model to make class predictions.

```
model_1 = keras.models.Sequential()

model_1.add(keras.layers.Conv2D(32, 3, activation='relu', input_shape=(172, 172, 3)))

model_1.add(keras.layers.Dropout(0.1))
model_1.add(keras.layers.MaxPooling2D())

model_1.add(keras.layers.Conv2D(64, 3, activation='relu'))
model_1.add(keras.layers.Dropout(0.15))
model_1.add(keras.layers.MaxPooling2D())

model_1.add(keras.layers.Conv2D(128, 3, activation='relu'))
model_1.add(keras.layers.Dropout(0.2))
model_1.add(keras.layers.MaxPooling2D())

model_1.add(keras.layers.Flatten())
model_1.add(keras.layers.Dense(256, activation='relu'))
model_1.add(keras.layers.Dense(3, activation='softmax'))

model_1.compile(optimizer='adam', loss='categorical_crossentropy', metrics=['accuracy'])
model_1.summary()

[ ] history = model_1.fit(train_data, validation_data=val_data, epochs = 3)
```

Figure 6: Layer Setup for Model 1

The code snippet in figure 7 will provided plots the loss and accuracy of each model. The first subplot visualizes the train and validation loss over the epochs, with the x-axis representing the epoch number and the y-axis representing the loss value. The second subplot illustrates the train and validation accuracy over the epochs, with the x-axis denoting the epoch number and the y-axis representing the accuracy value. The plots are set to have specific ranges for better visualization and are arranged in a tight layout for clarity.

```
plt.figure(figsize = (20,5))
plt.subplot(1,2,1)
plt.title("Train and Validation Loss")
plt.xlabel("Epoch")
plt.ylabel("Loss")
plt.plot(history.history['loss'],label="Train Loss")
plt.plot(history.history['val_loss'], label="Validation Loss")
plt.xlim(0, 2)
plt.ylim(0.0,1.0)
plt.legend()

plt.subplot(1,2,2)
plt.title("Train and Validation Accuracy")
plt.xlabel("Epoch")
plt.ylabel("Accuracy")
plt.plot(history.history['accuracy'], label="Train Accuracy")
plt.plot(history.history['val_accuracy'], label="Validation Accuracy")
plt.xlim(0, 2)
plt.ylim(0.75,1.0)
plt.legend()
plt.tight_layout()
```

Figure 7: Plotting of Loss and Accuracy for both models

The model in figure 8 is the setup for model2 that consists of a sequential architecture. It starts with a convolutional layer with 32 filters and a kernel size of 3, using the ReLU activation function. This is followed by a max pooling layer. The same pattern is repeated with a convolutional layer with 64 filters and a max pooling layer. Finally, the output is flattened and passed through a dense layer with 128 units and a ReLU activation function. The last layer has 3 units with a softmax activation function for multi-class classification.

The design of model2 is simpler compared to model1, with fewer convolutional layers and parameters. This may result in a more lightweight model with reduced complexity. It aims to capture essential features from the input images while maintaining sufficient capacity for classification. The model architecture is suitable for cases where the data may not require deeper or more complex networks, offering a balance between performance and computational efficiency.

```
[ ] model_2 = keras.models.Sequential()

model_2.add(keras.layers.Conv2D(32, 3, activation='relu', input_shape=(172, 172, 3)))
model_2.add(keras.layers.MaxPooling2D())

model_2.add(keras.layers.Conv2D(64, 3, activation='relu'))
model_2.add(keras.layers.MaxPooling2D())

model_2.add(keras.layers.Flatten())
model_2.add(keras.layers.Dense(128, activation='relu'))
model_2.add(keras.layers.Dense(3, activation='softmax'))

model_2.compile(optimizer='adam', loss='categorical_crossentropy', metrics=['accuracy'])
model_2.summary()
```

Figure 8: Layer Setup for Model 2

```
[ ] history = model_2.fit(train_data, validation_data=val_data, epochs = 3)
```

Figure 9: Data fitted to history

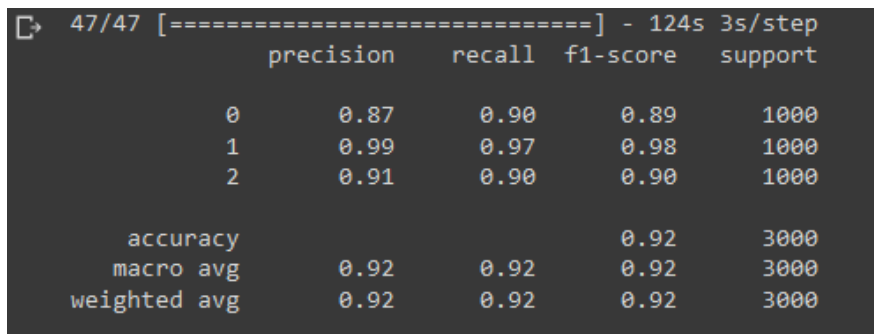
4 Experimental Results

Model 1 achieved an overall accuracy of 92 percent on the test set consisting of 3000 samples. The precision for class 0 (benign) is 87 percent, indicating that when the model predicts an image as benign, it is correct 87 percent of the time. The recall for class 0 is 90 percent, indicating that the model correctly identifies 90 percent of the benign images. The F1-score for class 0 is 89 percent, which is a harmonic mean of precision and recall.

For class 1, the precision is 99 percent, indicating a high accuracy in predicting cancerous images. The recall is 97 percent, suggesting that the model can successfully identify 97 percent of the cancerous images. The F1-score for class 1 is 98 percent, reflecting the balance between precision and recall.

For class 2, the precision is 91 percent, indicating a good accuracy in predicting unknown images. The recall is 90 percent, suggesting that the model can correctly identify 90 percent of the unknown images. The F1-score for class 2 is 90 percent, indicating a harmonic balance between precision and recall.

Overall, the classification report demonstrates that Model 1 performs well in accurately classifying lung images into the three categories. The high accuracy, precision, recall, and F1-scores indicate that the model is effective in distinguishing between benign, cancerous, and unknown lung images, making it a reliable tool for lung image classification tasks.



```
47/47 [=====] - 124s 3s/step
      precision    recall  f1-score   support

     0       0.87       0.90       0.89       1000
     1       0.99       0.97       0.98       1000
     2       0.91       0.90       0.90       1000

 accuracy                   0.92       3000
 macro avg                  0.92       3000
 weighted avg               0.92       3000
```

Figure 10: Model 1 Classification Report

```

47/47 [=====] - 93s 2s/step
          precision    recall  f1-score   support

     0       0.92       0.91       0.91       1000
     1       1.00       0.99       1.00       1000
     2       0.91       0.93       0.92       1000

 accuracy          0.94          3000
 macro avg          0.94          3000
 weighted avg       0.94          3000

```

Figure 11: Model 2 Classification Report

Regarding Model 2, it achieved an impressive overall accuracy of 94 percent on the test set, consisting of 3000 samples. The precision for class 0 (benign) is 92 percent, indicating that when the model predicts an image as benign, it is correct 92 percent of the time. The recall for class 0 is 91 percent, suggesting that the model can successfully identify 91 percent of the benign images. The F1-score for class 0 is 91 percent, representing a harmonic mean of precision and recall.

For class 1, the precision is 100 percent, signifying a high accuracy in predicting cancerous images. The recall is 99 percent, indicating that the model can effectively identify 99 percent of the cancerous images. The F1-score for class 1 is 100 percent, demonstrating an excellent balance between precision and recall.

For class 2, the precision is 91 percent, indicating a solid accuracy in predicting unknown images. The recall is 93 percent, suggesting that the model can correctly identify 93 percent of the unknown images. The F1-score for class 2 is 92 percent, reflecting a harmonious balance between precision and recall.

Overall, the classification report highlights that Model 2 performs exceptionally well in accurately classifying the lung images into the three categories. The high accuracy, precision, recall, and F1-scores indicate that the model is highly effective in distinguishing between benign, cancerous, and unknown lung images, making it a reliable and robust tool for lung image classification tasks.

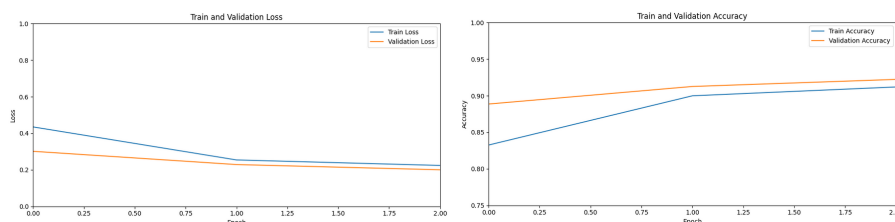


Figure 12: Loss and Accuracy Plot for Model 1

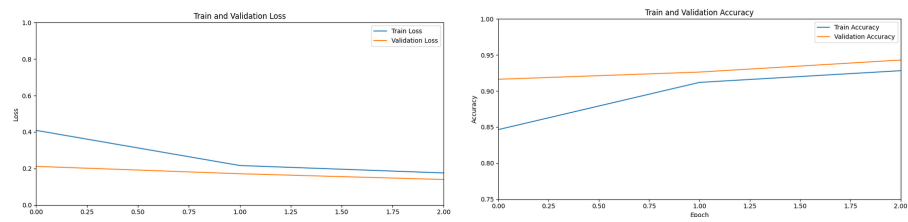


Figure 13: Loss and Accuracy Plot for Model 2

5 Summary

In conclusion, Model 1 and Model 2 both showed strong performance in classifying lung images into different categories. Model 1 achieved an accuracy of 92 percent on the test set, with high precision and recall values for all classes. On the other hand, Model 2 outperformed Model 1 with an accuracy of 94 percent on the test set, demonstrating excellent precision, recall, and F1-scores for each class.

Comparing the two models, it is evident that Model 2, with its simpler architecture, achieved slightly better overall performance than Model 1. By eliminating some convolutional and dropout layers, Model 2 still achieved high accuracy and demonstrated efficient classification capabilities. This suggests that a more streamlined architecture can be beneficial for certain tasks, achieving comparable or even superior results. However, it is important to note that Model 1 showcased better recall for class 0 (benign) compared to Model 2.

Key takeaways from this analysis include the importance of model architecture design, where a well-optimized and streamlined structure can achieve excellent results. Additionally, the evaluation metrics, such as accuracy, precision, recall, and F1-score, provide valuable insights into a model's performance for different classes. These metrics enable us to assess the model's strengths and weaknesses in classifying lung images, facilitating the development of robust and accurate systems for lung-related medical applications.

6 References

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