

The Application of AI in healthcare with focus on detecting diseases at early stages

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Early disease detection is very important in healthcare because many conditions, like Pneumonia, and Cardiomegaly often start with small signs that are hard to spot. Chest X-rays are a common tool for diagnosing these diseases, but interpreting them can be challenging and time-consuming, especially in busy hospitals or areas with fewer medical professionals. This project uses artificial intelligence (AI) to analyze X-rays and identify conditions like Edema more quickly and accurately. By helping doctors detect diseases earlier, AI reduces their workload and makes better healthcare available to more people.

Solution 1 – SimpleCNN with implementations

This solution uses the base model of the CNN architecture, with an SE networks implementation that selectively emphasises the most important features in the given data.

Implementation Process:

The images are loaded from the specified directory, converted to grayscale, and pre-processed with transformations such as resizing, random augmentations, and normalization. These processed images are then converted into tensors and fed into the model via a DataLoader for batch processing during training or evaluation. The model uses these images to learn features through convolutional layers, enhanced by a Squeeze-and-Excitation (SE) block, for classification.

```
class SEBlock(nn.Module):
    def __init__(self, channels, reduction=16):
        super(SEBlock, self).__init__()
        self.fc1 = nn.Linear(channels, channels // reduction)
        self.fc2 = nn.Linear(channels // reduction, channels)
        self.sigmoid = nn.Sigmoid()

def forward(self, x):
    # Global Average Pooling
        se_input = torch.mean(x, dim=[2, 3], keepdim=False)
        se_output = self.fc1(se_input)
        se_output = torch.relu(se_output)
        se_output = self.fc2(se_output)
    # Reshape to match the feature map size
        se_output = self.sigmoid(se_output).unsqueeze(2).unsqueeze(3)
        return x * se_output # Scale the feature map
```

Model Training:

Training was conducted on the NIH dataset, using 5000 images for training and validation and 1000 images for testing.

The model is trained using a K-fold cross-validation approach, where the dataset is split into 5 folds, and the model is trained and validated on each fold. For each fold, the model undergoes multiple epochs, during which it learns by optimizing the weights using the Adam optimizer and minimizing the CrossEntropy loss. The learning rate is adjusted with a scheduler, and data augmentation techniques are applied during training to increase robustness. The model's performance is evaluated after each epoch on a validation set, and the best model (based on training accuracy) is saved. This process is repeated for each fold, and the final performance is averaged across all folds to determine the model's overall effectiveness.

Solution 2 – ResNet-50

This solution uses an AI model based on ResNet-50 to analyse chest X-rays and predict diseases. It is designed for multi-label classification, meaning it can identify multiple diseases in a single image.

Implementation Process:

This model processes chest X-ray images by resizing them to 224x224 pixels to ensure all images are the same size and normalizing them to help the model work better with different types of data. It uses techniques like resizing and normalization to handle variations in the images, making it more reliable. Horizontal flipping is avoided to keep important medical details, like differences between the left and right lungs, accurate. As seen in this small snippet of code below.

```
from torchvision import transforms
normalize = transforms.Normalize(mean=[0.485, 0.456, 0.406],

std=[0.229, 0.224, 0.225])

# transforms.RandomHorizontalFlip() not used because some disease might be more likely to the present in a specific lung (lelf/rigth)

transform = transforms.Compose([transforms.ToPILImage(),

transforms.Resize(224),

transforms.ToTensor(),

normalize])
```

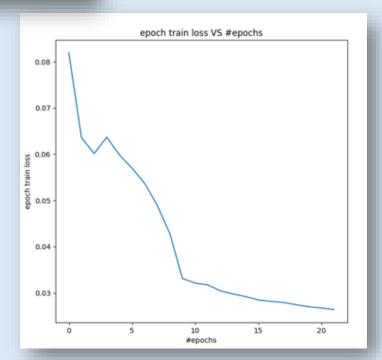
Model Training:

Training was conducted on the NIH dataset, using **86,524 images** for training and validation and **25,596 images** for testing. Focal Loss was applied to handle class imbalance effectively. The model was trained in stages:

Stage 1: Fine-tuned deeper layers with a lower learning rate for initial training stability.

Subsequent Stages: Gradually unlocked and fine-tuned additional layers for improved performance.

The graph from the training process shows that the model's loss decreases over time. This happens because of staged fine-tuning, where layers are gradually trained, optimized learning rates, and the use of Focal Loss, which helps the model handle class imbalances better.



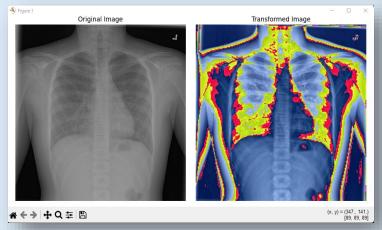
Solution 2 – ResNet-50

Testing and Evaluation:

The model's performance is measured using ROC-AUC (Receiver Operating Characteristic - Area Under Curve), which shows how well it distinguishes between diseased and non-diseased cases. An overall ROC-AUC score of 74.7% indicates strong accuracy, with high performance for diseases like Emphysema (87.2%), Cardiomegaly (83.5%), and Hernia (83.7%), though some conditions like Infiltration (62.9%) and Pneumonia (65.0%) had lower scores. This can be seen from the testing results on the right.

Testing on New Images:

I tested the trained model on a few random X-ray images by applying the same preprocessing steps used during training, such as resizing and normalization. The model provided predictions for each class, and when I compared them to the actual labels, the results were quite accurate with only a small percentage of errors. This gave me confidence in the model's reliability and performance.



Predictions: Atelectasis: Probability: 0.5794 (Positive) Consolidation: Probability: 0.0275 (Negative) Infiltration: Probability: 0.6299 (Positive) Pneumothorax: Probability: 0.0303 (Negative) Emphysema: Probability: 0.0196 (Negative) Fibrosis: Probability: 0.9341 (Positive) Effusion: Probability: 0.0850 (Negative) Pneumonia: Probability: 0.3242 (Negative) Pleural_thickening: Probability: 0.2710 (Negative) Cardiomegaly: Probability: 0.2855 (Negative) Nodule: Probability: 0.1925 (Negative) Mass: Probability: 0.2417 (Negative) Hernia: Probability: 0.1604 (Negative) No findings: Probability: 0.0495 (Negative)

Class 0 (Atelectasis): ROC-AUC = 0.7214 Class 1 (Cardiomegaly): ROC-AUC = 0.8349 Class 2 (Consolidation): ROC-AUC = 0.6666

Class 3 (Edema): ROC-AUC = 0.8017 Class 4 (Effusion): ROC-AUC = 0.7824 Class 5 (Emphysema): ROC-AUC = 0.8722

Class 6 (Fibrosis): ROC-AUC = 0.7576 Class 7 (Hernia): ROC-AUC = 0.8371

Class 9 (Mass): ROC-AUC = 0.7468 Class 10 (No Finding): ROC-AUC = 0.7011

Macro-Average ROC-AUC: 0.7469 Script completed in 0h 7m 1s!

Visualizing transformations...

Overall Metrics:

Class 11 (Nodule): ROC-AUC = 0.6754

Class 13 (Pneumonia): ROC-AUC = 0.6502

Class 14 (Pneumothorax): ROC-AUC = 0.8099

Class 8 (Infiltration): ROC-AUC = 0.6296

Class 12 (Pleural_Thickening): ROC-AUC = 0.7159

IMAGE_PATH = r"D:\Multi_label_NIH\sample_xrays\00025075_007.png" # Path to your sample image 95377 00025075_007.png Atelectasis | Fibrosis 25075 12 F 2020 0.194311 0.194311

Overall: This model uses advanced techniques like image augmentation, balanced loss functions, and staged training to accurately predict diseases from chest X-rays. It effectively handles class imbalance, ensures reliable predictions for rare conditions, and provides robust performance metrics, making it highly suitable for real-world medical diagnostics.

Solution 3 - DenseNet121

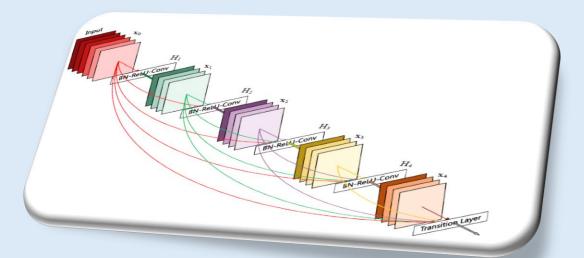
DenseNet121:

Connects each layer to every other layer, to ensure dense connectivity as in Figure 1.

Reduced parameters compared to ResNet.

Combines features via concatenation instead of summation.

Facilitates gradient flow and feature reuse.



Figuere1 (Huang et al., 2017)

Dataset and Preprocessing:

Dataset composed of Chest X-ray images with 14 conditions reduced to 2 conditions (Mass, Pneumothorax).

Images resized 224x224 avoiding different sizes, CenterCrop has been applied for robust classification.

Balanced dataset: 3:1 ratio of healthy to unhealthy images to imitate a real scenario.

Model Implementation:

Pre-trained CheXNet model modified, trained new model for 2 classes (Mass and Pneumothorax).

Image cropping using CenterCrop instead then TenCrop as the dataset are front chest X-rays.

Data script have been modified for binary classification.

Prediction, precision, recall, F1-score, and confusion matrix have been added for a better performance evaluation.

Solution 3 - DenseNet121

Challenges:

The model was working with a previous version of python, some of the features, function and libraries were outdated.

The model was detecting 14 diseases, modification to identify 2 conditions led to compatibility issues.

Balancing the validation, training and test list. With no appropriate ratio and labels the model result inaccurate.

Computational challenges when training the model, working with the CPU had major effect on time complexity.

Results:

From the AUROC score (Area Under Receiver Operating Curve) the model has a good ability to distinguish between the positive and negative classes, 82% for Mass and 81% for Pneumothorax .

Single images was taken online and tested for prediction; both cases have been tested, and the model is able to distinguish the conditions.

Precision measures the corrected prediction, the result shows 0.59% positive Mass, and 0.76% Pneumothorax in the given data. The model has higher results with Pneumothorax.

Recall measures the correct positive prediction.

F1-Score is an harmonic mean between precision and recall.

Support is the number of given data.

Classification	Report:			
	precision	recall	f1-score	support
Mass	0.59	0.86	0.70	413
Pneumothorax	0.76	0.70	0.73	438
micro avg	0.65	0.78	0.71	851
macro avg	0.67	0.78	0.71	851
weighted avg	0.67	0.78	0.71	851
samples avg	0.65	0.66	0.65	851

Confusion Matrix:

[[478 84] [143 295]]

Macro-Averaged AUROC: 0.8240

AUROC for Mass: 0.8057

AUROC for Pneumothorax: 0.8424

Predicted probabilities for single image:

Mass: 72.87%

Pneumothorax: 50.64%

Predicted probabilities for single image:

Mass: 53.82%

Pneumothorax: 67.24%

Using Autoencoder in My Solution 4

For my solution, I am utilizing an autoencoder, a specialized type of artificial neural network designed for unsupervised learning. Autoencoders are particularly effective for learning efficient coding's of unlabelled data.

It consists of two parts:

- **Encoder**: Compresses the input into a smaller latent representation.
- •Decoder: Reconstructs the original input from the latent representation.

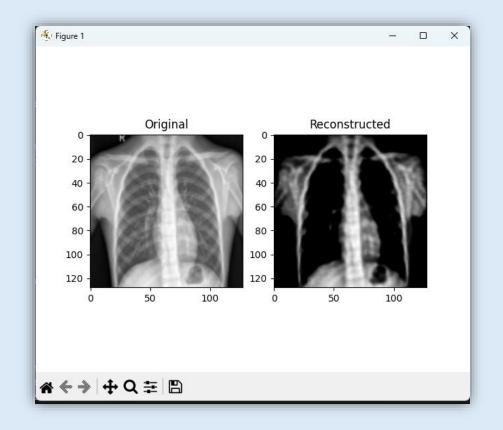
The encoder uses **convolutional layers** to compress the input image.

```
import os
import cv2
import numpy as np
import matplotlib.pyplot as plt
import torch
import torch.nn as nn
import torch.optim as optim
from torch.utils.data import Dataset, DataLoader
from torchvision import transforms
```

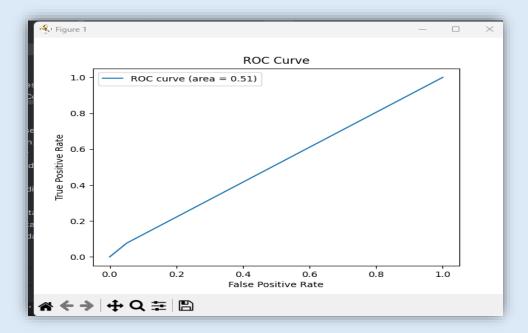
```
self.decoder = nn.Sequential(
nn.ConvTranspose2d(in_channels: 128, out_channels: 64, kernel_size=3, stride=2, padding=1, output_padding=1), # 64 x 32 x 32
nn.ReLU(),
nn.ConvTranspose2d(in_channels: 64, out_channels: 32, kernel_size=3, stride=2, padding=1, output_padding=1), # 32 x 64 x 64
nn.ReLU(),
nn.ConvTranspose2d(in_channels: 32, out_channels: 1, kernel_size=3, stride=2, padding=1, output_padding=1), # 1 x 128 x 128
nn.Sigmoid()
)
```

The model's True Positive Rate (Sensitivity) and False Positive Rate (1-Specificity) are traded off in this Receiver Operating Characteristic (ROC) curve.

The model's performance is indicated by the Area Under the Curve (AUC) value. The AUC in this case is 0.51, which is really near to the 0.5 for random guessing.



Solution 4



The reconstruction closely matches the original for normal X-rays when the autoencoder learns patterns typical of normal chest X-rays. Any discrepancy between the original and recreated image indicates anomalies, such as pneumonia symptoms.

Conclusion

These methods allow us to pick the right approach for different needs, from simple setups to advanced diagnostics. Combining them could further improve reliability and accuracy in disease detection.

Looking ahead, there's potential to integrate these algorithms into real-world clinical systems, like combining them with electronic health records for personalized diagnostics. Future work could focus on creating hybrid models or ensembles that bring together the best of these techniques. There's also room to explore how these methods perform with larger and more diverse datasets, improving their generalization and making them even more effective in healthcare.

These advancements can make early disease detection faster, more accurate, and accessible, ultimately improving patient care and saving lives.

References

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