Defeat Cancer with CNNs

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1 Introduction

In the coming years, artificial intelligence is set to revolutionize the field of medicine with its far-reaching and transformative effects. Within a short span of time since the initial groundbreaking showcases of AI algorithms that can accurately detect diseases from medical images at a level comparable to human experts, the realm of medical AI has advanced significantly. In this paper, we will provide a short introduction of the role of AI in medicine, and we will then focus on its application in detecting Breast Cancer using deep learning models such as CNNs and ResNet-32.

2 AI algorithms in medicine

Recent progress in the deployment of AI algorithms in medicine has shown promising results in retrospective studies. However, critics argue that the real-world application of AI systems may be less effective than anticipated. Challenges include issues of speed, complexity, and potential complications arising from human-AI interactions. To bridge the gap between theory and practice, randomized controlled trials (RCTs) and prospective studies are being conducted to demonstrate the quantifiable positive impact of AI models in real healthcare settings. Deep learning has made significant advancements in the interpretation of medical images, particularly in radiology, pathology, gastroenterology and ophthalmology. AI systems have improved accuracy in tasks such as mammography interpretation, cardiac function assessment, lung cancer screening and pathology diagnosis. They have the potential to not only aid in diagnosis but also enhance risk prediction and treatment planning. Overall, the progress in deploying AI algorithms in medicine offers promising prospects for improving healthcare outcomes. Continued research, standardization and validation efforts are crucial to harness the full potential of AI in clinical practice.[1][2]

2.1 Deep Learning for medical images

Medical AI research has traditionally focused on image classification using supervised learning, where AI systems are trained on labeled data and evaluated against human experts. Firstly, researchers are looking beyond image data and exploring non-image data sources such as text, chemical and genomic sequences. These data types offer rich medical insights and have been leveraged for various applications, such as understanding biomolecules, detecting cancer with noninvasive procedures, predicting gene editing, identificating antibiotic resistance in pathogens. Secondly, researchers are moving beyond traditional supervised learning approaches and considering problem formulations that involve unlabeled or imperfect data. Unsupervised learning techniques have been employed to find novel patterns and categories, leading to insights into disease manifestation and patient subgroups. Other formulations, such as weakly supervised learning and image reconstruction, have allowed researchers to achieve excellent results even with limited or noisy data. What we must not forget is the importance of collaboration between AI systems and human experts. Rather than competing against humans, AI systems are designed to work alongside them, augmenting their capabilities. This collaborative approach aims to achieve better performance by combining the strengths of both AI and human expertise. By leveraging artificial intelligence's analytical power and humans' interpretive skills, healthcare professionals can make more accurate diagnoses, develop personalized treatment plans and improve patient care.[1]

3 Detecting Breast Cancer

Breast cancer is a major cause of cancer-related deaths in women. It accounts for a significant percentage of cases and deaths globally. The most common type is Invasive Ductal Carcinoma (IDC), which spreads aggressively. Early detection through mammography screening is crucial for reducing morbidity and mortality. Currently, the diagnosis involves manual examination of tissue samples, which is time-consuming and subjective. AI algorithms in medical image analysis have shown promise in surpassing human performance: they can detect subtle abnormalities in mammograms, leading to earlier detection. AI can also assist radiologists in accurately identifying and categorizing breast lesions, reducing false positives and negatives. Additionally, AI algorithms can determine tumor origin and detect mutations, improving medical diagnostics. AI is not meant to replace healthcare professionals but to provide valuable support and second opinions. It can bridge the gap in regions with limited expertise, improving patient outcomes. Furthermore, AI systems can continuously learn and improve from new data, enhancing their diagnostic capabilities. In conclusion, AI integration in medical image analysis can significantly improve breast cancer detection, accuracy, and patient outcomes.[3]

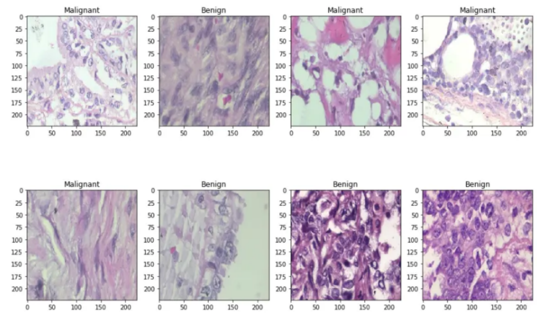

Figure 1: Benign vs malignant samples

3.1 CNNs for breast cancer detection

Convolutional Neural Networks (CNNs) are the most popular deep learning technique that has been utilized in several studies for breast cancer detection. They have become a widely adopted approach due to their capability to automatically learn important features from image data, facilitating accurate and efficient classification of diseases. CNNs excel at capturing local patterns and spatial relationships within images, making them particularly well-suited for analyzing medical images and detecting subtle abnormalities. The success of CNNs in image disease diagnosis is evident from the numerous models that have been developed and applied to various medical conditions. These models leverage the power of CNNs to achieve remarkable results in terms of diagnostic accuracy and have shown potential to outperform human-level performance in certain tasks. These models often incorporate advanced techniques, including residual learning, attention mechanisms and transfer learning, to further enhance their performance.[4] The model presented in the paper *A Novel Method for IDC Prediction in Breast Cancer Histopathology Images using Deep Residual Neural Networks*[5] introduces a novel approach for accurately diagnosing Invasive Ductal Carcinoma in breast cancer by leveraging deep learning techniques. The authors propose a model based on deep residual neural networks to overcome challenges such as vanishing gradients and accuracy degradation that commonly occur as the model depth increases. The model architecture utilizes 2D-convolutional layers, which are known for their effectiveness in processing image data. However, as the model becomes deeper, there is a tendency for the loss to saturate at a higher value, resulting in decreased accuracy. To address this, the authors employ residual learning, a technique that involves incorporating residual blocks into the model. The proposed model consists of four residual blocks, each comprising three convolutional layers and a residual connection with a single convolutional layer. The convolutional layers within the residual blocks are activated using the ELU function. Importantly, the convolutional layer in the shortcut connection does not employ an activation function. The output of each residual block is obtained by adding the shortcut connection to the last convolutional layer and passing it through a ReLU activation layer. After the residual blocks, a global average pooling operation is performed to obtain a 1D-vector representation. This vector is then passed through a fully connected layer (FC) for classification. The model's optimization is guided by monitoring various evaluation metrics, including accuracy, loss, AUROC score, precision, recall, and F1 score. Additionally, the authors employ Grad-CAM (Gradient weighted class activation mapping) to visualize and better understand the model's decision-making process. The dataset used in this study was sourced from the Kaggle *Breast Cancer Histopathology Images*. It comprises a total of 277,524 patches, each measuring 50x50 pixels. Among the extracted images, 198,738 were diagnosed as IDC negative, indicating the absence of Invasive Ductal Carcinoma, while 78,786 were diagnosed as IDC positive, indicating the presence of Invasive Ductal Carcinoma. For the proposed methodology, a subset of 7,500 images was selected from the dataset. This subset consisted of 3,000 IDC positive images and 4,500 IDC negative images. By utilizing a subset of images instead of the entire dataset, the researchers addressed the issue of memory errors that could occur due to the large volume of data. In terms of performance, the proposed model achieves outstanding results. It attains a 99.29 % accuracy in predicting IDC in histopathology images. Specifically, for the affected class (IDC), the model achieves a precision of 0.9969, recall of 0.9889, specificity of 0.9969, and an F1 score of 0.99294. Similarly, for the normal class, the model achieves a precision of 0.9889, recall of 0.9969, specificity of 0.9889, and an F1 score of 0.99296. Furthermore, the model exhibits an impressive AUROC score of 0.9996, indicating its high discriminatory power in distinguishing IDC cases from non-IDC cases.

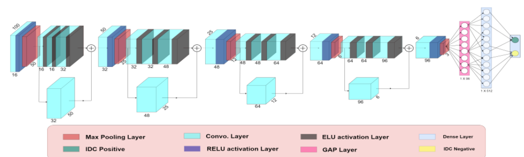

Figure 2: Model architecture

3.2 ResNet-32 and FastAI

To address the challenge of limited medical images, it is possible to use transfer learning by fine-tuning a well-established deep neural network, ResNet. This pre-trained network was initially trained on millions of natural, non-medical images and was then fine-tuned using thousands of biomedical images. By leveraging the knowledge learned from a large dataset, this approach effectively reduced the number of training samples required and achieved successful results.

The article *ResNet-32 and FastAI for Diagnoses of Ductal Carcinoma from 2D Tissue Slides*[6] explores the effectiveness of Residual Networks and FastAI technology in accurately identifying ductal carcinoma from 2D tissue slides. ResNet-32, a 32-layer Convolutional Neural Network (CNN), is utilized in combination with FastAI to achieve precise classification results with efficient computational efforts. ResNet is known for its ability to handle the issue of vanishing gradients and effectively learn intricate features. Compared to Recurrent Neural Network models, ResNet models offer superior performance in classifying tumors while avoiding complex training procedures. By stacking residual connections, ResNet builds a network that remains efficient even as the architecture becomes more complex, making it a preferred choice over alternative models. FastAI, a comprehensive deep learning package, offers researchers and specialists various libraries and packages that accelerate deep learning outcomes, including GPU acceleration and a faster callback mechanism. This combination results in faster model execution with less code and improved precision in classifying tissue slides. The proposed FastAI-driven ResNet-32 model outperforms other existing models in terms of sensitivity, specificity, accuracy, and F1-score. According to the statistical analysis presented in the paper, the model achieves a confidence level of 98.6%.

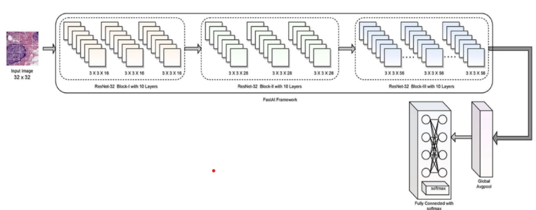

Figure 3: Layered architecture of ResNet-32 for classifcation

4 Our implementations

Despite the difficulties encountered due to the large amount of images contained in the considered dataset, we tried ourselves to build a model that could work for this classification problem. It is a very standard deep model, which usually works well in these kind of situations. We initialized a sequential model and we added the first convolutional layer, which takes an input of shape (64, 64, 3), corresponding to images with a height and width of 64 pixels and 3 color channels (RGB). The layer applies a number of filters, with ReLU as activation function. We then added another convolutional layer with the same number of filters and kernel size, we performed maxpooling on the feature maps and applied dropout regularization after each convolutional layer to reduce overfitting. This pattern of adding convolutional, pooling, and dropout layers is repeated twice more, each time with a different number of filters to capture increasingly complex features. We then flatten the output from the previous convolutional layers into a 1-dimensional vector, preparing it for input to a fully connected layer. A fully connected (dense) layer is added with 256 units and a ReLU activation function. Dropout regularization is then applied to the output of the dense layer. Finally, the model is completed by adding the final dense layer with 2 units, representing the number of classes to be predicted (binary classification). The activation function used for this layer is softmax, which produces probabilities for each class.

The obtained results are not particularly good: in fact, the model has an accuracy on the test set that is around 86 % and the loss function does not have particularly low values. In this analysis we must certainly consider some limitations: due to the reduced capacities of our machines, we could not use the entire dataset, but only a reduced version; we also had to stop at a limited number of epochs (equal to 20).

5 Conclusions

In conclusion, the field of breast cancer detection has witnessed remarkable progress with the application of CNNs. These advanced models have exhibited exceptional performance in accurately identifying and classifying tumors from 2D tissue slides. The potential of CNNs in revolutionizing medical image analysis for breast cancer detection cannot be overstated. By effectively extracting pertinent features from intricate medical images, CNNs provide healthcare professionals with valuable insights to make informed decisions and improve patient outcomes. However, it is important to acknowledge the challenges that accompany the adoption of CNNs in breast cancer detection.[7] Ensuring the quality and representativeness of training data remains a critical concern. Additionally, addressing privacy issues and implementing secure mechanisms for data sharing are essential to maintain patient confidentiality while facilitating collaborative research. To fully harness the potential of CNN-based breast cancer detection, further research and development efforts are necessary. Integration of additional "omics-based" data, such as genomic and proteomic information, can enhance the accuracy and precision of diagnoses. Simplifying the models and optimizing their clinical applicability will enable seamless integration into existing healthcare workflows. Moreover, establishing robust frameworks for data sharing is vital for fostering collaboration among researchers and institutions. By pooling resources and knowledge, we can accelerate advancements in breast cancer detection and treatment, leading to more effective and personalized patient care.

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