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A FRAMEWORK FOR ENHANCED RESNET50-BASED DEEP LEARNING ARCHITECTURE FOR PROSTATE CANCER DIAGNOSIS SURVIVABILITY

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ABSTRACT

Prostate cancer has become one of the commonly diagnosed non-skin malignancies in men and another foremost source of death in cancer related ailment. It is projected that in every six American men, one is likely to be affected by this illness throughout their lifespan. The major issue confronted with during the development of prostate cancer management comprises of enlarged size of prostate biopsies and a shortage of urological pathologists, this is a constrain on the diagnosis of prostate cancers. Prostate cancer is one of the most commonly types of cancer in men, and it is estimated that 1 out of 9 men will be diagnosed with prostate cancer at some point during their lifetime. There are some challenges associated with using AI for prostate cancer detection. AI algorithms cannot accurately distinguish between benign and malignant tumours due to their complexity. In this study, a framework for Prostate Cancer Detection Model (PCDM) will be developed, using the modified ReseNet, it's a faster Regional Convolutional Neural Network (R-CNN) mask and dual optimizers. It will be developed for detecting prostate cancer and will be applied on Prostate Cancer dataset. The model will be evaluated using following evaluation metrics, such as accuracy, precision, recall, and F1 score.

KEYWORDS: *Prostrate Cancer, Optimizer, Regional Convolutional Neural Network, Tumor, Diagnose and Cancer Detection*

INTRODUCTION

Prostate cancer can often be treated successfully if it is detected early, so it is important for men to get regular screenings to check for any signs or symptoms (Wang *et al*., 2023; Shao *et al*., 2023; 2020; Elmuogy *et al*., 2021; Hassan *et al*., 2021). AI techniques are being used to detect prostate cancer to improve accuracy and reduce costs, such as Machine Learning (ML) and Deep Learning (DL), which are used to analyze MRI scans and CT scans to analyze patient data such as age, race, family history, and lifestyle factors. The use of DL for prostate cancer detection can help reduce costs by reducing the need for expensive biopsies and other tests. It can also help improve accuracy by providing more accurate results than traditional methods (Bygari *et al*., 2023).

DL has the potential to revolutionize prostate cancer detection and provide more accurate results than traditional methods (Hassan *et al*., 2022). PCDM model combines the power of DL with the accuracy of traditional methods to provide an effective method for detecting prostate cancer (Du *et al*., 2022; De *et al*., 2021). The modified ReseNet model is used to extract features from the images, while the Faster R-CNN model is used to classify them. The dual optimizers are used to enhance the parameters of the models, ensuring that they can accurately detect prostate cancer. The results of this technique have been impressive (Hassan *et al*., 2022; Kandel *et al*., 2020; Dogo *et al*., 2022; Du *et al*., 2022; De *et al*., 2021; Hassan *et al*., 2022). It has been shown to be more accurate than traditional methods in detecting prostate cancer, with a sensitivity of up to 95%. Furthermore, it has been shown to be faster than traditional methods, taking only a few minutes for each image for quickly and accurately detecting prostate cancer in patients. In this study, the modified ReseNet framework model will be developed for extracting features from the images, while the Faster R-CNN model is used to classify them.

LITERATURE REVIEW

A deep learning model based PCDM based on MRI images to accurately detect prostate cancer. The new architecture advances the current Deep Learning literature by proposing a modified version of the ResNet architecture. The proposed PCDM uses ReseNet to effectively handle complex features, which could be crucial in detecting cancerous cells and achieving high accuracy in detecting prostate cancer cells.

Prostate cancer is a major health concern among men, with an estimated one million new cases diagnosed each year worldwide (Ahmad *et al*., 2023). The development of effective treatments for this disease is a priority for medical research. Recently, the use of DL algorithms has become increasingly popular in the diagnosis of prostate cancer (Xu *et al*., 2023; Rostami *et al*., 2021).

This literature review focuses on the related works that are based on three models: the modified ResNet model, the faster R-CNN model, and the dual optimizers Adam and SGD. The ResNet model is a Convolutional Neural Network (CNN) that has been used to detect prostate cancer from MRI images (Naik *et al*., 2022; Yaqoob *et al*., 2021; Minaee *et al*., 2021; Zhang *et al*., 2019). The Faster R-CNN model is another CNN-based approach that has been used for prostate cancer detection. Dual optimizers are use as fixed learning rates throughout training. Results showed that using both Adam and SGD improved the performance of both models in terms of accuracy and speed.

Yu *et al*. (2023) introduces a PI-RAD-SAI model for prostate cancer detection based on MRI. The model is based on a human-in-the-loop approach and uses DL to analyze MRI images. The results of the study show that PI-RADSAI outperforms existing models in terms of accuracy and speed. Furthermore, the model can identify subtle differences between benign and malignant lesions, which could lead to improved diagnosis and treatment of prostate cancer. (Bygari *et al*., 2023) proposed an algorithm for classifying prostate cancer that consists of three stages, all involving ensemble deep neural networks. A UNet is used to segment the histopathological image that is superimposed on the original image to highlight the important areas in determining the grade of cancer. The ensemble model is composed of Xception and EfficientNet-b7. This method has achieved a classification accuracy of 92.38%, outperforming many existing methods.

Provenzano *et al.* (2023) examine the accuracy of a machine learning algorithm in classifying prostate MRI lesions using single- and multi-institutional image data. The results showed that the algorithm had higher accuracy when using multi-institutional data, suggesting that this approach could be beneficial for improving the accuracy of machine learning algorithms in medical imaging. (Xiang *et al.*, 2023) discuss the use of weakly supervised learning to automatically diagnose and grade prostate cancer from whole slide images. The authors propose a supervised learning method that combines CNN with a multi-task learning framework. This method is tested on two datasets and compared to existing methods. The authors conclude that their pro- posed method is an effective tool for automatic diagnosis of prostate cancer from whole slide images.

Zhu *et al.* (2023) present a DL approach to accurately predict the origin of bone metastatic cancer using digital pathological images. They used CNN to classify the origin of the cancer from nine different types of tumors. The results showed that the CNN model achieved an accuracy of 95.2%, which is higher than other existing methods. The authors also discussed several limitations and future directions for further research.

Esteva *et al.* (2022) discusses the use of DL to personalize prostate cancer therapy. They suggest an approach that could be used to improve treatment outcomes for prostate patients. Salman *et al.* (2022) explain the importance of early detection and accurate diagnosis of prostate cancer, as well as the limitations of current diagnostic methods. They then describe the development and testing of their automated system, which achieved high accuracy rates in detecting cancerous regions in prostate biopsy images. The authors conclude that their system has the potential to improve the efficiency and accuracy of prostate cancer diagnosis.

Hosseinzadeh *et al.* (2021) propose a DL model for detecting prostate cancer on bi-parametric MRI, specifically examining the minimum training data size required. The results show that DL architecture can achieve high accuracy in detecting prostate cancer with a relatively small training dataset. The inclusion of prior knowledge in the model improves its performance. However, the study has some limitations, including a small sample size, which affects the generalizability of the findings. Nonetheless, the study highlights the potential benefits of using DL architecture for prostate cancer diagnosis Li *et al.* (2022).

Artificial Neural Network in Biomarker Diagnosis and Risk Stratification

Diagnosis and prognosis of prostate cancer have been guided by PSA level testing. However, concerns about absolute accuracy can sometimes lead to patients being given invasive treatment options when active surveillance might provide better outcomes in these men Choyke (2017).

Over the past 10 years, avalanches of biomarkers have been identified and are put into clinical assays (Jin *et al.*, 2020). While several of these biomarkers have been studied and characterized, there is no standard overlap between all of these assays due to the function of each assay, and there is no absolutely perfect list of biomarkers to look at when predicting diagnosis and prognosis. Thus, it is important to be able to identify and evaluate any new biomarkers for their clinical significance in a way that is both meaningful and accurate. Therefore, ANNs can play an instrumental role in analyzing and validating the biomarkers. For example, one study suggested that Ki67 is an important marker of survival and disease progression (Fruge *et al*., 2020).

Green *et al*. (2016) created an ANN that was designed to validate Ki67 gene expression while comparing it to another potential candidate in DLX2. Univariate analysis showed that both Ki67 and DLX2 were significant in predictiveness of future metastases. Nevertheless, only 6.8% of prostate cancer patients have high expression of Ki67. Thus, this study showed that these 2 biomarkers could be used to identify candidates for targeted therapy only.

Kim *et al.* (2016) developed a novel approach by combining targeted proteomics with computational biology to discover new potential proteomic signatures for prostate cancer. The study started with 133 differentially expressed proteins that were evaluated with synthetic peptides in a 74-patient cohort. Then they applied machine learning approaches to develop clinical predictive models using these candidates. Results showed that computationally guided proteomics can be used to discover novel non-invasive biomarkers. Overall, there are numerous studies which reflect the potential of AI ANNs to allow more effective identification and validation of biomarkers to aid in prostate cancer surveillance (Green *et al*., 2016).

Patients diagnosed with prostate cancer often remain confused due to treatment options that are available to them. Thus, understanding how certain therapies are put into place may allow for ease of mind and improvements in patient satisfaction. Auffenberg *et al*. (2019) developed a registry that used ANN to better allow patients to take charge of their care. This registry, which is called askMUSIC, takes data from 45 urology practices within the Michigan Urological Surgery Improvement Collaborative (MUSIC). This registry data is used to create a random forest machine learning model which could predict prostate cancer treatment options. Patients can go to askMUSIC website and interact with the registry data and predicted treatment to show therapy options to alleviate fear about a given therapy from the patient perspective (Auffenberg *et al*., 2019).

Alitto *et al.* (2017) developed a PRODIGE project; it used an Umbrella Protocol that focused on standardization of data sharing. Within this protocol, a standardized knowledge sharing process is implemented using semi-formal ontology representing clinical variables. This process can be adapted to use with machine learning or traditional statistics. The standardization of these techniques supports the multifactorial decision support systems (DSS) which can be seen as the basis for future patient-level support therapy decisions. Together, there are multiple studies which reflect the potential of AI ANNs to allow the development of effective patient-centric tools to help with educating the patients about the treatment options and disease progression/regression.

De Vente *et al*. (2021) present a DL architecture approach for detecting and grading prostate cancer in MRI. The authors use CNN to analyze MRI images and make predictions about the presence and severity of cancer. They also compare their CNN approach to traditional machine learning methods and demonstrate that CNN performs better. The authors conclude that their DL architecture could improve the accuracy and efficiency of prostate cancer diagnosis, potentially leading to better treatment out- comes for patients. Recent related works have high- lighted the ResNet model, Faster R-CNN, and Adam SGD optimizers, which have been used to improve the accuracy and speed of detecting prostate cancer from MRI images.

SYSTEM DESIGN

The ResNet architecture for image classification tasks, have the ability to handle deeper networks without suffering from vanishing gradients. The modified ResNet50 architecture includes changes such as adding or removing layers, changing activation functions, or using regularization techniques. The dataset will be divided into 80% of the data used for training the model and 20% of the data used for testing its performance. The number of times an experiment is repeated will be dependent on factors such as variability in the data or randomness in the initialization of weights in neural networks. Typically, learning curves are performed to ensure that results are consistent and reliable.

Algorithm of the Design

$F(x) := H(x) - x$ which gives $H(x) := F(x) + x$ (1)

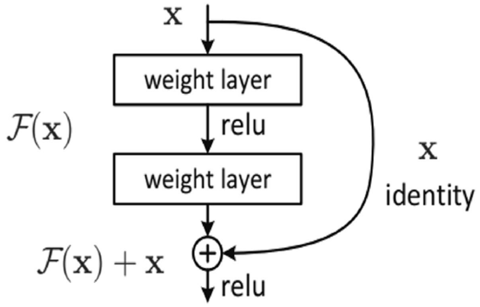

Fig. 1: Algorithm of the general layer description

Process Development Description

Input layer: The prostate dataset, the weights wk, λa, λs, learning rate η, weight decay γ
Stage 1 - Residual Blocks
Residual block 1 (Bottleneck):
Convolutional layer: filters, kernel size 1 × 1
Batch normalization layer
ReLU activation layer
Convolutional layer: filters, kernel size 3 × 3
Batch normalization layer
ReLU activation layer
Convolutional layer: filters, kernel size 1 × 1
Batch normalization layer
Shortcut connection
ReLU activation layer
Repeat step 6 for residual blocks 2 and 3
Stage 2—Residual Blocks
Residual block 4 (Bottleneck):
Same as step 6, but with stride 2 in the second convolutional layer and filters
Repeat step 6 for residual blocks 5, 6, and 7, but with filters in the first and second convolutional layers
Stage 3—Residual Blocks
Residual block 8 (Bottleneck):
Same as step 6, but with stride 2 in the second convolutional layer, filters in the first and second convolutional layers, and filters in the third convolutional layer
Repeat step 6 for residual blocks, but with filters in the first and second convolutional layers, and filters in the third convolutional layer

Stage 4—Residual Blocks
Residual block (Bottleneck):
Same as step 6, but with stride 2 in the second convolutional layer, filters in the first and second convolutional layers, and filters in the third convolutional layer
Repeat step 6 for residual blocks in the first and second convolutional layers, and filters in the third convolutional layer
Region Proposal Network (RPN) layer
RPN classification layer
RPN regression layer
RoIAlign layer
Convolutional layer with 1024 filters and a kernel size of 3 × 3
Mask classification layer
Mixed optimizer:
Adam for first 10 epochs: learning rate is expected to be 0.001
SGD for remaining epochs: learning rate is expected to be 0.01
For each batch:
Update weights with mixed optimizer:

The performance of the proposed modified ResNet50- based architecture for prostate cancer diagnosis was evaluated using several commonly used metrics, including accuracy, sensitivity, specificity, and F1-score. Accuracy measures the proportion of true positives and true negatives in relation to all predictions made by the model. It can be calculated as in Eq. (1). Sensitivity, also known as recall, measures the proportion of true positives in relation to all actual positive cases, while specificity measures the proportion of true negatives in relation to all actual negative cases. Sensitivity can be calculated as in Eq. (2). Specificity can be calculated as in Eq. (3).

The F1-score is a harmonic means of precision and recall, and it provides a balanced assessment of a model's accuracy in detecting both positive and negative cases. F1-score can be calculated as in Eq. (4).

$$\text{Accuracy (ACC)} = (TP + TN)/(P + N) \quad (1)$$

$$TPR = TP/(TP + FN) \quad (2)$$

$$SPC = TN/(FP + TN) \quad (3)$$

$$PPV = TP/(TP + FP) \quad (4)$$

Where True Positive (TP), True Negative (TN), False Positive (FP), False Negative (FN).

The models will be evaluated using four different metrics, namely accuracy, precision, recall, and F1 score.

Bygari *et al.* (2023) present an innovative approach to grading prostate cancer using deep neural networks, the limitations in the dataset, feature selection, generalizability, and potential biases of the method need to be taken into consideration. Further research is needed to validate the proposed method on larger and more diverse data- sets and to address the potential limitations and biases of using DL architecture in medical image analysis.

Additional to Zhu *et al.* (2023) suggest a model to predict the origin of bone metastatic cancer using DL architecture on digital pathological images, the limitations in the dataset, the focus on bone metastatic cancer only, the lack of detailed explanation of the features used, the absence of comparison with other models, and the potential limitations and biases of using DL architecture in medical image analysis need to be taken into consideration. Further research is needed to validate the proposed method on larger and more diverse datasets and to address the potential limitations and biases of using DL architecture in medical image analysis (Albahri *et al.*, 2023; Hassan 2023).

DISCUSSION

The Model utilization of Rectified Linear Unit (ReLU) activation functions in the convolutional layers, this plays a crucial role in promoting robust feature learning, leading to enhanced classification accuracy. A major aspect that will be used in the experiments is the effect of varying model configurations. The impact of changing the number of layers in the modified ResNet50 architecture is evident that the "More Layers" configuration outperforms the "Fewer Layers" configuration across all metrics. This suggests that a deeper network with additional layers enhances the model's ability to distinguish between cancerous and non-cancerous regions within MRI images. The advantage of the modified ResNet50 architecture lies in its adaptability to accommodate these variations, allowing for optimization based on specific diagnostic needs.

Hyperparameter Sensitivity

The sensitivity in the model will be attributed to various hyperparameters, which includes learning rate, batch size, and dropout rate, was also explored in our ablation experiments. While these hyperparameters may seem subtle, their impact on model performance is significant.

Through systematic adjustments and evaluations, these hyperparameters will help to achieve optimal results. This sensitivity analysis highlights the importance of careful hyperparameter selection in the design of deep learning architectures for medical image analysis.

Interpretability and visualization

Achieving high metrics is essential, but understanding why the model makes certain predictions is equally crucial, particularly in medical applications. To address this aspect, we utilized visualization techniques such as gradient-weighted class activation maps (Grad-CAM). These visualizations provide insights into which regions of the MRI images the model focuses on when making predictions. By enhancing interpretability, these techniques not only aid in comprehending the model's decision-making process but also contribute to better performance. The experiments when developed will demonstrates high value of interpretability in fine-tuning the model and improving its accuracy.

CONCLUSION

The use of a modified ResNet50 architecture and Faster R-CNN for automatic diagnosis of prostate cancer through medical imaging represents a significant advancement in the field of computer-aided diagnosis. Specifically, the use of dual optimizers facilitates faster convergence and improved generalization, ultimately resulting in higher overall performance.

The utilization of Heterogeneous Information Networks (HINs) presents an intriguing research avenue. HINs allow for the integration of diverse data sources and modalities, enabling a more comprehensive understanding of disease characteristics. By incorporating HINs into deep learning architectures, researchers can develop models that leverage a broader spectrum of patient information, ultimately advancing the state-of-the-art in medical diagnosis and treatment.

This approach allows for the representation of medical data as graphs, where nodes represent entities like patients or medical records, and edges capture relationships and dependencies between them. Leveraging graph-based deep learning techniques can enable the discovery of intricate patterns and correlations within large-scale medical data- sets. This, in turn, could lead to more accurate disease prediction and treatment recommendations.

HINs enable the fusion of diverse data sources, such as electronic health records, genomics, and clinical imaging, into a unified network structure. Deep learning on HINs can facilitate comprehensive patient profiling and personalized medicine by considering the multifaceted aspects of an individual's health.

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