DeepCervix: enhancing cervical cancer detection through transfer learning with VGG-16 architecture

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ABSTRACT

Cervical cancer remains a significant global health concern, emphasizing the urgent need for improved detection methods to ensure timely treatment. This research introduces a sophisticated methodology leveraging recent advances in medical imaging and deep learning algorithms to enhance the accuracy and efficiency of cervical cancer detection. The proposed approach comprises meticulous data preprocessing to ensure the integrity of input images, followed by the training of deep learning models including ResNet-50, AlexNet, and VGG-16, renowned for their performance in computer vision tasks. Evaluation metrics such as accuracy, precision, recall, and F1-score demonstrate the efficacy of the methodology, with an outstanding accuracy rate of 98% achieved. The model's proficiency in accurately distinguishing healthy cervical tissue from cancerous tissue is underscored by precision, recall, and F1-score values. The primary strength of this deep learning-based approach lies in its potential for early detection, promising significant impact on cervical cancer diagnosis and treatment outcomes. This methodology contributes to advancements in medical imaging techniques, facilitating improved outcomes in cervical cancer detection and treatment.

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1. INTRODUCTION

Cervical cancer ranks as the fourth most prevalent cancer in women worldwide and remains a leading cause of cancer-related mortality, with projections estimating 604,000 new cases and 342,000 deaths globally in 2020 [1]. The high mortality rate primarily stems from late diagnoses, emphasizing the critical importance of early detection and screening initiatives. While traditional screening methods like Pap smear tests have demonstrated efficacy in reducing cervical cancer risk, they are inherently reliant on the expertise of healthcare professionals and can be subject to subjective interpretation, leading to potential false negatives or positives [2]–[4]. In recent years, deep learning (DL) algorithms have garnered increasing attention for their potential role in automating the identification and diagnosis of cervical cancer [5], [6]. DL leverages artificial neural networks to analyze data and generate predictions, exhibiting notable success across various domains, particularly in medical imaging. DL algorithms excel in recognizing subtle patterns and details

within images, surpassing human perceptual capabilities and enhancing the precision and reliability of cancer diagnosis [7]–[9].

Litjens et al. [10] surveyed the use of deep learning in image analysis, underlining the prospect of this technique for enhancing diagnostic accuracy and treatment in a variety of medical specialties. Xue et al. [11] offered an extensive review of the utilization of DL methods in the detection of cervical cancer. They discussed the advantages and challenges associated with these approaches, including the requirement for a lot of good data, the potential for bias and overfitting, and the importance of interpretability and transparency in medical decision-making using multi-parametric magnetic resonance imaging (MRI) data. Jiang et al. [12] developed DL-based radiomic algorithms to distinguish between vessel invasion and non-vessel invasion in cervical cancer. Novitasari et al. [13] proposed a cervical cancer diagnosis system that uses gray level cooccurrence matrix techniques. The system achieved an accuracy of 95% using a gaussian kernel in detecting abnormal cells, demonstrating its potential as a useful tool for cervical cancer screening. Paul et al. [14] employed an adaptive median filter to effectively eliminate impulse noises present in Pap smear images. Subsequently, they utilized a bi-group enhancer to differentiate between nucleus pixels and other object pixels. Following this, a segmentation methodology was applied to isolate the nucleus regions within the cervical smear images. The methodology demonstrated an impressive accuracy rate of 98.37%. Chankong et al. [15] introduced a method for automatic segmentation and classification of cervical cancer cells, employing the fuzzy C-means (FCM) clustering technique. They validated their approach using artificial neural networks (ANNs), achieving accuracies of 93.78% for the 7-class problem and 99.27% for the 2-class problem

While previous studies have highlighted the potential of DL techniques in enhancing the precision and effectiveness of cervical cancer screening, diagnosis, and classification [16], [17], there are still several gaps in the literature that need to be addressed. One major gap is the lack of extensive research specifically focusing on the utilization of DL for cervical cancer identification, particularly in terms of its practical implementation and comparative analysis with traditional screening methods. Additionally, there is a need for more studies that investigate the scalability and feasibility of integrating DL algorithms into existing screening processes, especially in regions with limited access to healthcare resources.

Our study addresses these research gaps by proposing a methodology for utilizing DL specifically for cervical cancer identification. We contribute by developing a comprehensive approach that includes data pre-processing, model training, and model evaluation using various metrics. By employing well-known convolutional neural network architectures like ResNet-50, AlexNet, and visual geometry group (VGG)-16, we provide insights into the comparative effectiveness of these models for cervical cancer identification. Additionally, we highlight the potential benefits of integrating DL algorithms into existing screening processes, such as increased screening efficiency, objectivity in analysis, and the ability to identify precancerous lesions at earlier stages. Our research contributes to advancing the understanding of DL's role in cervical cancer screening and provides practical implications for improving patient outcomes, particularly in resource-constrained settings.

2. METHODS AND MATERIAL

The primary objective of this study is to enhance the accuracy and automation of cervical cancer detection and diagnosis through the utilization of DL approaches. By harnessing the capabilities of these advanced methods, our aim is to streamline the process of early detection and treatment of cervical cancer, ultimately contributing to a reduction in its mortality rate. Figure 1 illustrates the workflow of our proposed work, showcasing the various stages involved in our approach to leveraging DL for cervical cancer detection and diagnosis. Through this comprehensive workflow, we seek to establish a robust framework that enables efficient and accurate identification of cervical cancer, thereby improving patient outcomes and advancing the field of cancer detection and treatment.

The proposed methodology comprises key steps, including database collection, processing, feature extraction, and classification, with a focus on utilizing the Harlev benchmark database for cervical cancer detection. Rigorous pre-processing was conducted to eliminate potential noise and artifacts, ensuring accurate image analysis. In the subsequent phase, ResNet-50, AlexNet, and VGG-16 convolutional neural network (CNN) architectures were employed to train the DL model. Binary cross-entropy loss function and the Adam optimizer were utilized for binary classification problems, allowing the model to identify optimal weights and biases to minimize classification errors. The adaptive learning rate optimization feature of the Adam optimizer contributed to enhanced model performance. The third phase involved a thorough evaluation of the trained model's performance using key metrics such as accuracy, precision, recall, and F1-score. Receiver operating characteristic (ROC) and area under the curve (AUC) curves were generated to assess the model's ability to differentiate between cervical cancer and normal cervical tissue, providing a visual representation

of its performance in differentiating true positive and false positive rates. This methodology has been meticulously designed to address challenges related to data variability, model complexity, and interpretability, essential for developing a clinically relevant and dependable cervical cancer detection model. Visual representations of cancerous and non-cancerous images in Figures 2 and 3 further illustrate the outcomes of the proposed approach. In summary, the methodology aims to advance medical image analysis and diagnosis, offering a comprehensive framework for automated cervical cancer detection.

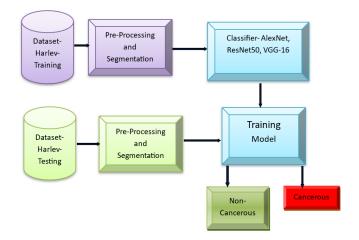


Figure 1. Workflow of proposed work

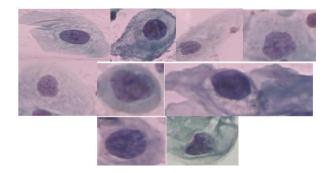


Figure 2. Cancerous images

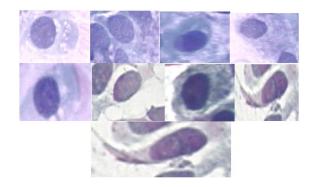


Figure 3. Non-cancerous images

2.1. Database: Herlev dataset

The Herlev dataset, developed by Herlev University Hospital, is a significant resource for research in cervical cancer detection and diagnostics [18]. This dataset is readily accessible for research purposes and offers a robust foundation for developing and testing automated detection systems. The Herlev Pap smear

dataset comprises 917 single-cell cervical images, captured at a high resolution of 0.201 µm per pixel using advanced microscopes and digital cameras. The images are obtained through conventional Pap smear staining and processing methods, ensuring consistency and reliability in the data. The dataset includes seven distinct stage classifications to facilitate accurate diagnosis:

- i) Superficial Squamous 74: normal cells.
- ii) Intermediate Squamous 70: normal cells.
- iii) Columnar Squamous 98: normal cells.
- iv) Mild dysplasia 182: abnormal.
- v) Moderate dysplasia 146: abnormal.
- vi) Severe dysplasia 197: abnormal.
- vii)Carcinoma in situ 150: abnormal.

These classifications are further grouped into two main categories: benign (classes 1-3) and malignant (classes 4-7). This categorization supports the development of models that can distinguish between healthy and potentially cancerous cells. One of the key features used for classification within the Herlev dataset is the significant size difference in the nuclei of abnormal or malignant cells compared to normal cells. Malignant cells often exhibit larger nuclei with irregular shapes and increased chromatin content, which are critical indicators for automated detection systems.

2.2. Segmentation

In Pap smear cell images, both the nucleus and cytoplasm are present, and the characteristics of the nucleus, such as size and shape, play a crucial role in determining whether a cell is pathological or normal. To analyze the properties of the nucleus, a specific portion of the image needs to be extracted, and segmentation is employed to identify the region of interest [19], [20]. The extraction of background, cytoplasm, and nucleus from single-cell Pap smear images involves a segmentation process. The smear cell image typically consists of three regions: cytoplasm, nucleus, and background. For a more detailed analysis, it is imperative to segment the cytoplasm and nucleus regions. The nucleus areas are segmented using the k-means clustering technique, followed by morphological procedures.

The k-means clustering technique utilizes the Euclidean distance metric to partition items into two groups. Initially, K cluster centers are chosen, and data points are divided into K clusters based on their proximity to these centers. The Euclidean distance metric is employed to determine proximity. The process is iterated until there are no further changes to the cluster centers. The stages of the k-means algorithm include:

- 1) Create a histogram of intensity levels.
- 2) Set K cluster centers' random intensities to K for each cluster.
- 3) Repeat steps 1-3 until the cluster centers remain the same.
- 4) For each pixel, determine the distance between each cluster's center and the signal intensity, assigning the signal to the closest cluster.
- 5) Determine the new cluster centers by averaging all cluster members.

The outcome of the k-means method is the segmentation of the nucleus region from the cervical cell image. This result undergoes morphological processes, specifically erosion and morphological reconstruction, to accurately segment the nucleus region. These processes contribute to a refined analysis of the cellular components, aiding in the diagnosis and study of pathological conditions.

2.3. Network architectures

2.3.1. VGG-16

The VGG-16 network architecture gained prominence when it was introduced by the visual geometry group at Oxford University for the ImageNet ILSVRC-2014 competition. Notably, VGG-16 stood out among its contemporaries due to its remarkable depth, a characteristic that resulted in a substantial increase in the number of parameters. To manage this parameter increase, VGG-16 adopted a strategic approach by using small 3×3 convolutional filters with a stride of 1 and padding of 1 for all its convolutional layers. This design choice ensured that the spatial dimensions of the input were not significantly reduced [21].

In the VGG-16 architecture, the convolutional layers were structured into clusters comprising two or three layers. After each cluster, max pooling was applied to downsample the input, contributing to the network's ability to capture and learn hierarchical features effectively. Towards the latter part of the VGG-16 network, three fully connected (FC) layers were incorporated, followed by a SoftMax layer. These FC layers played a crucial role in learning high-level features and making predictions based on the learned representations. The SoftMax layer produced the final probability distribution across different classes in the classification task. Overall, VGG-16 gained widespread recognition for its depth and parameter efficiency, achieved through the utilization of small filters, the preservation of input dimensions, and the incorporation of clustered convolutional layers followed by max pooling, as depicted in Figure 4.

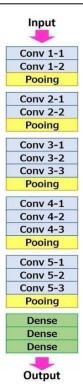


Figure 4. VGG-16 architecture

2.3.2. AlexNet

AlexNet, a deep convolutional neural network (DCNN) architecture depicted in Figure 5, was initially introduced in the ImageNet ILSVRC-2012 competition. It revolutionized deep learning for image categorization problems with its innovative design. The architecture of AlexNet comprises three fully connected layers, rectified linear unit (ReLU) activation, max pooling, local response normalization (LRN), three convolutional layers with varying filter sizes, dropout for regularization, and a softmax layer for classification [22].

The sequence of layers in AlexNet performs feature extraction and classification, paving the way for advancements in deep learning for image analysis. Its deep convolutional architecture, utilization of ReLU activation, incorporation of max pooling, LRN, and dropout techniques have significantly influenced the field of CNNs. AlexNet's groundbreaking design fundamentally changed the landscape of deep learning, contributing to its success in addressing image classification challenges. The introduction of AlexNet marked a significant milestone in the evolution of deep learning, setting the stage for subsequent developments and innovations in CNN architectures. Its impact continues to resonate in the field, shaping the trajectory of research and applications in image analysis and classification tasks.

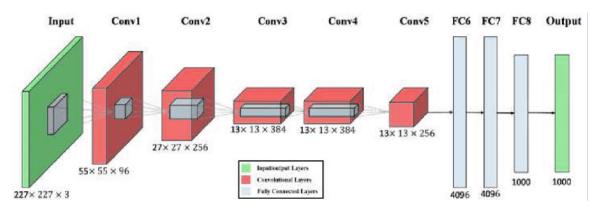


Figure 5. AlexNet architecture

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2.3.3. ResNet-50

ResNet-50, a DCNN architecture unveiled by Microsoft Research, is depicted in Figure 6. It introduces a groundbreaking concept known as residual connections, which enable the network to learn residual functions, thereby addressing the challenge of training deep networks effectively. With a total of 50 convolutional layers, ResNet-50 is composed of multiple convolutional layers organized into phases. To enhance computational efficiency, the architecture incorporates bottleneck and residual blocks [23], [24].

For classification purposes, a fully connected layer is utilized, and global average pooling is employed to reduce spatial dimensions. The distinguishing feature of ResNet-50, the inclusion of residual connections, has propelled its popularity across various computer vision applications. These residual connections enable the training of deeper and more accurate networks, contributing to improved performance and robustness in complex tasks. Overall, ResNet-50 stands out as a significant advancement in DL architectures, offering enhanced capabilities for training deep neural networks and achieving superior performance in computer vision applications [25]. Its innovative design and utilization of residual connections have solidified its position as a preferred choice for a wide range of tasks in the field of computer vision.

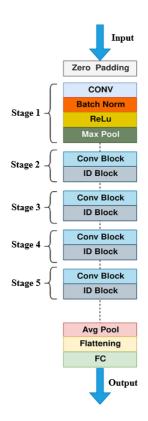


Figure 6. ResNet-50 architecture

3. RESULTS AND DISCUSSION

The results of our study demonstrate the effectiveness of our proposed DL model in the context of cervical cancer detection shown in Table 1. Our model, trained on a dedicated dataset of cervical images, achieved a remarkable accuracy rate of approximately 98%. The higher AUC values further underscore the superior performance of our approach.

The success of our DL model in accurately identifying cases of cervical cancer is a key highlight. With an accuracy of 98%, our model showcases its robustness in distinguishing between cancerous and noncancerous instances in Pap smear images. The evaluation metrics, including F1-score, accuracy, and recall, further validate the model's proficiency, with values of 98%, 99%, and 98%, respectively. In the context of the accuracy versus validation accuracy curve as shown in Figure 7 and the loss versus validation loss curve as shown in Figure 8, our model exhibits consistent and favorable performance. These visual representations provide insights into the model's learning process, highlighting its ability to generalize well and minimize loss during validation.

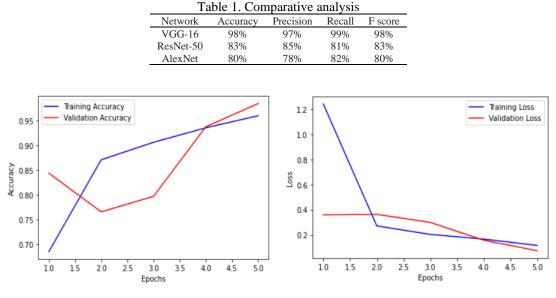


Figure 7. Accuracy vs validation accuracy

Figure 8. Loss vs validation loss

The discussion of these results emphasizes the potential and significance of DL techniques in early cervical cancer detection. Achieving a high level of accuracy, our DL model addresses a critical aspect of healthcare by offering a reliable and automated screening method. This not only showcases the capabilities of DL in medical image analysis but also underscores the importance of leveraging advanced technologies for the timely diagnosis and management of diseases.

Furthermore, our study enhances the broader landscape of cervical cancer detection research by offering a detailed comparison of the latest advancements in existing literature, as summarized in Table 2. This provides context for our findings, highlighting the novelty and effectiveness of our proposed DL methodology. Results and discussion collectively affirm the success of our DL model in automated cervical cancer detection. The high accuracy rates, along with robust evaluation metrics and visual representations, validate the model's efficacy and underscore its potential for real-world clinical applications.

Table 2. Comparison with the state of the art

Author	Methodology	Accuracy
Hussain et al. [21]	AlexNet, VGG-16, and 19, ResNet-50 and 101, GoogleLeNet	90%
Sompawong et al. [26]	Mask regional CNN	91.70%
Wu et al. [27]	DCNN	93.33%
Proposed model	VGGNet-16	98%

4. CONCLUSION

In this research, we introduced a DL approach for the early detection of cervical cancer utilizing cervical images. Our methodology, which includes data pre-processing, feature extraction, and classification stages, demonstrated a high accuracy rate of 98% in experiments conducted on a dataset of cervical images. Central to our approach is the utilization of CNNs, specifically the VGGNet-16 architecture. This choice provides a fast and accurate method for detecting cervical cancer in its early stages, holding significant implications for cancer screening and diagnosis.

Our study builds upon previous research in the field of medical imaging and cancer detection. While earlier studies have explored various machine learning and image processing techniques, our work distinguishes itself by leveraging the advanced capabilities of CNNs, particularly the VGGNet-16 architecture, to achieve superior accuracy. This advancement aligns with the growing trend of employing deep learning in medical diagnostics to enhance early detection and treatment outcomes.

Looking ahead, potential future research directions include expanding the dataset and testing the model on different imaging modalities to further validate its performance and robustness. Additionally, exploring other CNN architectures and integrating multi-modal data could provide deeper insights and improve the model's generalizability. By continuously refining and improving our DL approach, we aim to enhance its applicability and effectiveness in real-world clinical settings.

In summary, our deep learning approach for detecting cervical cancer using cervical images has exhibited a high level of accuracy, holding promise for application in other cancer detection tasks. This methodology has the potential to significantly impact cancer screening and diagnosis practices. Through continued research and development, we aspire to contribute to the advancement of medical imaging technologies and improve outcomes in cancer detection and treatment.

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