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Cervical Cancer Papsmear Classification through Meta-Learning Technique using Convolution Neural Networks

Mahendra[1*], *Jumadi*[2], *and Dwiza Riana*[3]

[1,2,3] *Universitas Nusa Mandiri, Indonesia*

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CORRESPONDING AUTHOR
14220029@nusamandiri.ac.id

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ABSTRACT

This study uses convolutional neural networks (CNNs) and meta-learning techniques to create an accurate and efficient model for classifying the risk factors of cervical cancer. The dataset includes four types of cervical lesions, and the main objective is to categorize these lesions as either benign or malignant. This classification is essential for early and succesfull treatment of cervical cancer. The challenge arises from the complexity and variations in the images, resulting in the inability of conventional machine learning and deep learning approaches to provide correct classifications. Meta ensemble learning approaches are employed to improve the model's classification accuracy. The dataset of cervical cancer risk factors is preprocessed before being used to train and evaluate numerous CNNs utilizing pre-trained models and various architectures. Subsequently, a meta-learning is employed to optimize the learning process, and used to aggregate the outputs of the multiple CNNs. Moreover, the assessment findings show the model achieves high accuracy and effectiveness. Finally, the suggested model's accuracy score will be contrasted against the current cutting-edge methods used by other existing systemsh.

1. Introduction

Cervical cancer classification has made significant advancements in recent years, especially with the utilization of deep learning methods. Researchers have developed various models and techniques to accurately detect and classify early cervical cancer cells. For example, Goncalves et al . devised a method based on convolutional neural networks to extract deep learning features from cervical pictures and classify early cervical cancer cells. These deep learning features were then used in conjunction with extreme learning machines for accurate classification.

Additionally, various international research teams have also focused on deep learning techniques for the identification and classification of cervical cancer. In the United States, an organization at Utah State University utilized a quicker region convolutional neural network with an amazing AUC of 0.91 can automatically identify the cervical region in cervicography pictures and diagnose dysplasia and malignancy. Similarly, a research group in Japan developed a neural network to classify 500 photos of cervical cancer classified into three categories, demonstrating the possibilities of deep learning in this field, despite the early stages of development.

Furthermore, Lu et al [1] conducted research on cervical cancer detection and classification, highlighting the relevance of utilizing CNNs for feature extraction and classification of cervical cancer images. These studies collectively showcase the promising role using CNNs and other deep learning techniques in improving the accuracy and efficiency of cervical cancer classification. The development of convolutional neural networks has greatly contributed to the automation of image analysis in order to identify cervical cancer. These deep learning-based models have shown impressive progress in accurately classifying both normal and cancer cells in cervical images. Xiang et al [2], for instance, developed CNN-based models using YOLOv3 as the baseline model, achieving high classification accuracy and adding a classifier particular to a job to further improve performance.

As the field of cervical cancer research continues to evolve, The possibilities of deep learning methods, particularly CNNs, for the detection and classification of cancer cells becomes increasingly apparent. The use of CNNs to categorize cells and extract deep characteristics has proven to be instrumental in enhancing cervical cancer accuracy detection. Moreover, the development of faster-region convolutional neural networks has led to automatic detection of cervical regions in cervicography images, ultimately enabling the classification of dysplasia and cancer with remarkable precision.

The aforementioned studies underscore the transformative impact of deep learning methods, particularly CNNs, in the realm of cervical cancer classification. In light of these advancements, it is evident that the integration of deep learning techniques holds great promise for the continued improvement of cervical cancer detection and classification. The ability of deep learning methods to accurately classify both normal and cancer cells in cervical images is a significant advancement in the field of cervical cancer research. These methods have not only shown high accuracy in the classification of early cervical cancer cells but have also contributed to the automation of image analysis for the detection of cervical cancer.

Moreover, the research conducted by Ghoneim et al [1]. highlights the importance of feature extraction in cervical cancer detection and classification. Their study emphasizes the relevance of using CNNs for feature extraction and classification, further solidifying the pivotal role of deep learning techniques in this domain.

With the continuous evolution of the field, it is crucial to recognize the potential of deep learning methods, especially CNNs, in the detection and classification of cancer cells. The utilization of CNNs for feature extraction and cell classification has significantly improved the accuracy of cervical cancer detection, paving the way for enhanced diagnostic capabilities.

In conclusion, the incorporation of deep learning methods, particularly CNNs, has revolutionized the landscape of cervical cancer research. As these methods continue to advance, they offer unprecedented opportunities for improving the accuracy and efficiency of cervical cancer detection and classification. This progress holds tremendous promise for enhancing medical imaging technologies and, ultimately, improving patient outcomes. The development and application of convolutional neural networks in the field of cervical cancer research have significantly elevated the classification accuracy and automation of image analysis for the detection of cervical cancer. With the potential showcased in the studies mentioned, it is evident that deep learning, particularly the use of CNNs, plays a crucial role in advancing the field of cervical cancer classification.

2. Research Method

2.1. Convolutional Neural Network

One kind of deep neural network that results from the multilayer perceptron (MLP) is the convolutional neural network (CNN) [3]. What sets CNNs apart from MLPs is their capacity to identify and detect objects in picture formats. The convolutional layer, which is added to CNNs and is made up of neurons with activation functions, bias, and weight, is what gives CNNs their superior performance over neural networks (NNs) [4]. The fully-connected layer and feature extraction are the two main components of CNN [5]. Illustration of CNNs is shown in figure 1 [6].

2.1.1. Feature Extraction Layer

The layer responsible for feature extraction "encodes" a picture by taking the shape of the object it represents. Therefore, CNNs are theoretically a multi-stage design with many arrays and maps in each input and output process. The extraction layer is divided into two halves separately.

a. Convolutional layer

A convolutional neural network's (CNN) central structure is called the convoluted layer. Using a filter or fixed-size kernel, this layer transforms inputs into a format that is easily processed without sacrificing crucial convulsed properties [7]. Each unit in this layer takes input from the layer above, and there are filters (kernels) that cover the whole input. As a result, the input map is created by convolution between each filter, after which the input is shifted and the total of the dot products is used.

b. Pooling

Using the use of two popular methods, average and maximum pooling, pooling is a strategy for lowering dimensionality [8]. When the highest value is used, this technique is referred to as max pooling; average pooling utilizes the medium value. Next comes the process of flattening, which is the reconfiguration of a pooling structure into a one-dimensional vector for use in classification in fully-connected neural networks, or MLPs.

c. MLP layers

The classification process is carried out using a fully linked multi-layer perceptron called MLP layers.The input, output, and hidden layers are the three layers that make up an MLP. The rectified linear unit (ReLU), which is widely used in deep learning because of its simplicity, is used by the activation function.

2.1.2. Fully-connected layer

The multidimensional array that is the feature extraction layer, which is the foundation for fully-connected layer operations, is flattened (reshaped) in the vector feature map [9], [10]. Additionally, much as in neural networks, all of the activated neurons from the preceding layer are connected to the following layer. Therefore, every activation (of the preceding) has to be transformed into 1-D data in order for the connection to function effectively. These often process data using the MLP term, which is classified appropriately [11]. In the meanwhile, neurons that are coupled to a particular input region contrast with convolution layers, which are fully-connected in nearly every section. But both still carry out "dot product" procedures, thus there's not much of a difference between their roles in Figure 1.

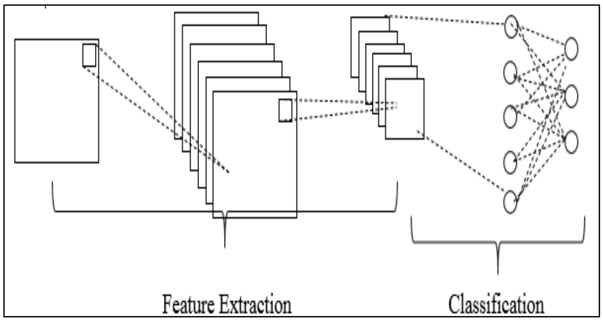


Figure 1. Illustration of Convolutional Neural Network

2.2. Confusion Matrix

One of the primary metrics used to assess the effectiveness of a categorization is accuracy [12]. refers to the accuracy-meauring confusion matrix's proportion of accurate responses during the testing phase. Accuracy: the ratio of correctly classified points (correct predictions) to the total number of predictions made [13].

The accuracy formula is presented in Equation (1) [13] and Table 1.

$$\text{Accuracy} = \frac{TP+TN}{TP+TN+FP+FN} \quad (1)$$

Where TP is Quantity of cervical cancer samples and accurate classification, TN is the quantity of fit people that were accurately identified, FP is the quantity of healthy people who are mistakenly diagnosed with cervical cancer, and FN is the quantity of cervical cancer samples that are mistakenly identified as healthy.

Table 1. Matrix of Confusion

	Prediction	
	Positive	Negative
Positive	T_P	F_P
Negative	F_N	T_N

3. Result and Discussion

3.1. Data

The dataset Papsmear in this paper consisted of 24.712 informations with 4 features used. Specifically, there are 7.357 normal cells in this dataset; 6.051 koilocyt cells are abnormal squamous epithelial cells that exhibit characteristic changes associated with human papillomavirus (HPV) infection; 5.663 low-grade squamous intraepithelial lesion (L-Sill) cells are considered to be mid-level abnormal changes in cervical cells and are considered to be precanceraous; and 5.641 high-grade squamous intraepithelial lesion (H-Sill) cells are considered to be more significant abnormal changes in cervical cells and are considered to be an advanced stage of dysplasia and carry a higher risk of cervical cancer. The data distribution can be seen in Figure 2.

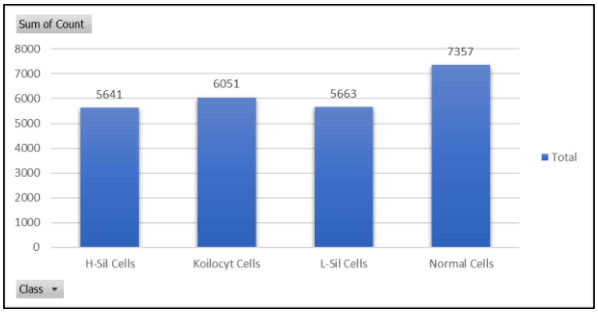
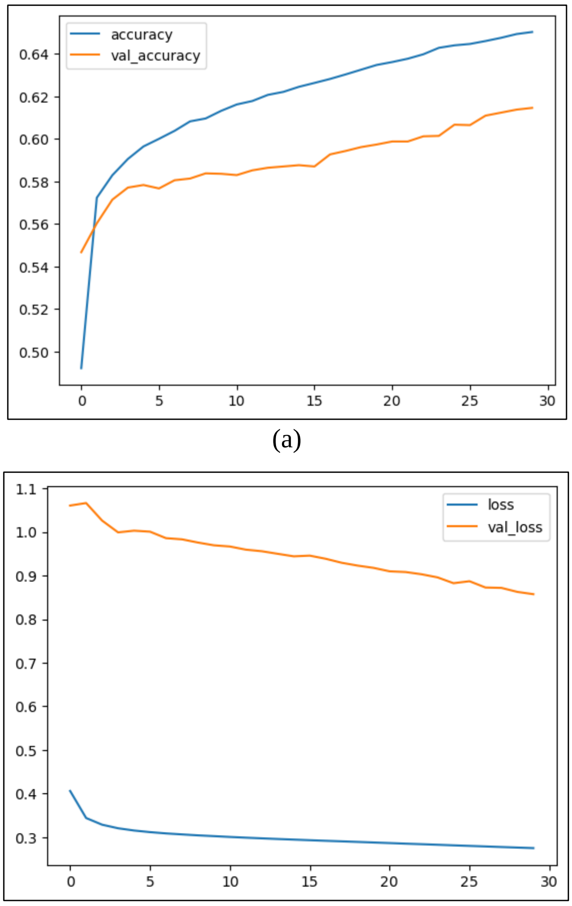


Figure 2. Data Distribution

3.2. Results

Figure 3 and Figure 4 display the outcomes of this investigation, which employed a convolutional neural network with 30 epochs. Figure 3(a) showed an increase in accuracy of 65,42%, while the testing data's orange line indicated an accuracy value of 61,45%. Figure 3(b) demonstrated that when the number of epochs reduces, the number of losses (errors) also decreases. On training data, the error was 0, whereas on test data, it was 0.8573.



(a)

(b)

Figure 3. Convolutional Neural Network, (a) Model Accuracy of CNN, and (b) Model Loss of CNN

The confusion matrix shown in Figure 4 was used to evaluate the performance of a classification model on the Cervical Cancer Pap Smear Classification dataset. This matrix shows the relationship between the true labels (on the Y-axis) and the predicted labels by the model (on the X-axis). Each element in the matrix represents the number of data points predicted with a specific combination. The main diagonal of the matrix (164, 300, 517, and 655) indicates the number of correct predictions for each class, while the off-diagonal elements represent the number of incorrect predictions. For instance, 164 data points with the true label H-Sil were correctly predicted as H-Sil, while 312 data points with the true label H-Sil were incorrectly predicted as L-Sil.

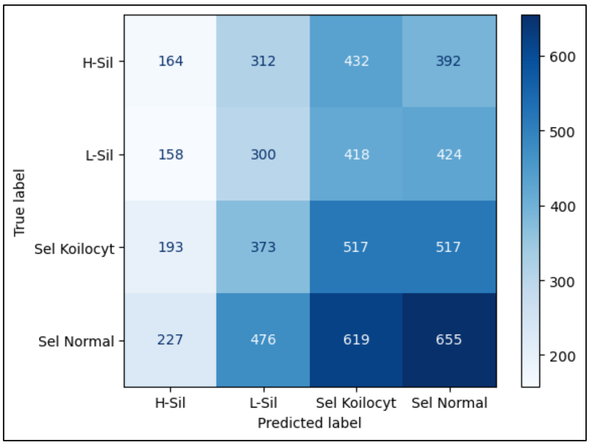


Figure 4. Confusion Matrix

From this matrix, it is evident that the model struggles to distinguish certain classes. For example, 392 H-Sil data points were misclassified as Sel Normal, and 517 Sel Koilocyt data points were also misclassified as Sel Normal. On the other hand, the Sel Normal class has the highest number of correct predictions (655), indicating relatively better performance for this class compared to others. Conversely, the H-Sil class has a lower number of correct predictions (164), suggesting that the model requires improvement to better recognize this class.

The possibility of data imbalance across classes should also be considered, as it could affect the model's performance. To improve classification accuracy, several steps can be taken, such as balancing the data across classes, refining the features used by the model, or optimizing the classification algorithm.

4. Conclusion

Medical professionals may more easily classify ailments by utilizing machine learning to detect and anticipate sickness. Early disease identification is critical because it enables patients to obtain the appropriate therapy promptly, improving their chances of recovery and lowering their risk of illness. Thus, with x data gathered and x factors noted, this study focuses on cervical cancer, a prevalent health issue. Convolutional neural networks and classifiers were combined in the methodology. The experimental findings demonstrated that the data were appropriately and accurately anticipated by the employed approaches. According to research, Convolutional neural network model performs the best when it comes to classifying data related to cervical cancer. Therefore, in order to get better results for predicting and categorizing various diseases, this technology is being developed to deliver more accuracy and to employ a bigger database in future study.

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