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Deep Learning based Cervical Cancer Detection using CNN

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ABSTRACT
Cervical cancer is a type of cancer that originates in the cervix, a part of the women's reproductive system and this cancer has an ability to progress to other parts of their body including lungs, liver, bladder etc. About 190,000 deaths are due to cervical cancer each year in the US. This gives rise to the importance of early stage detection of cervical cancer. Many studies found that cervical cancer is caused by infection with Human Papilloma Virus(HPV) and this is preventable at it's early stages with several vaccines. Our work aims to develop a mechanism to detect early stage cervical cancer by analysing the Magnetic Resonance Imaging(MRI) images of the cervix. Noise reduction techniques are applied at the preprocessing stage which involves the usage of a mean filter to remove certain types of noise from the image. Then the segmentation is applied on the preprocessed image using CNN. Deep features extracted are then classified using a support vector machine (SVM).
Keywords: Cervical cancer,Linear Gaussian filter,MRI,Segmentation,Support Vector Machine.

I. INTRODUCTION

In females, one of the leading cancer related deaths are caused by cervical cancer, which is the abnormal growth of cells in the cervix. Early stage detection is not possible as there are no symptoms shown in the beginning of the disease. However it can be diagnosed earlier through routine check-ups like papanicolaou (PAP) smear test,which is costly and time consuming. Studies show that the average age of patients is between 45 to 50 yrs. There exists a clear link between cervical cancer and sexual life[2]. Many experts reported sexual transmission due to contamination by papillomavirus[3]. In addition to sexual transmission, there exists other possibilities like tobacco use, immune deficiency, poor nutrition status,a history of having several marriages, child birth at young ages etc. There are many symptoms for cervical cancer including pain in pelvis and abdomen, irritation while urination, abnormal vaginal discharge etc. Almost 90% of the cervical cancer cases are due to the infection with human papillomavirus(HPV). HPV types can be of low risk or high risk. This classification is based on their oncogenic potential. High risk strains are said to be oncogenic and low risk strains are generally asymptomatic. The Human Papilloma Virus(HPV) is initially affected by skin cells and at the starting stage the cancer cells start growing till the cervix lining. It then slowly spread to the lymph nodes of the cervical cells and spread to bladder and other body parts at the worst stage.

The papanicolaou (Smear) was one of the globally accepted screening test for cervical cancer which was introduced in the beginning of 1940's. This test can detect the disease at an early stage of

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cell abnormal growth. A brush is needed to perform the PAP test. The brush is smoothly used to scrape the xcellular materials from the cervix portion and then smeared into a glass slide.

As the existing methods are time consuming and costly, analysts started thinking about Artificial Intelligence [4] based cervical screening methods in the beginning of 2010s as it was progressing into many health care analysis areas. One of the most advanced aspects of AI was Machine Learning and Computer Vision. The researchers started developing Machine Learning algorithms that have the ability to extract meaningful information from clinical/health care images without any compromise in the accuracy. During initial stages, they collected many malignant cell MRI images from different data sources and started factorizing the malignant images. Such systems detected malignant images from new MRI scanned results but they produced low accuracy. One of the first successful screening was done in Mexico in 2010 that classified the cervical images into negative and positive by using K-Nearest Neighbor (KNN) methods which produced 71% accuracy[5]. A recent study done in Indonesia in the second quarter of 2020, used image processing techniques to differentiate cancerous and non-cancerous images and then used Support Vector Machine(SVM) for its classification[8]. This method was more accurate and generated 90% accuracy in its classification.

II. RELATED WORKS

Mango discussed the use of computer-based algorithms to detect cancerous cells in the cervix.Herecommended thePAPNET cytological screening system for the detection of abnormal cells. Mango's solution is based on a conventional PAP smear test and an artificial neural network(ANN) model. The ANN model allows the automatic detection of the precancerous tests. More Elaborate solutions require a detection module to extract the cell nuclei region from cervigrams. For Instance, Bamford and Lovell employed an active contour method to extract the cell nuclei region. Bamford and Lovell identified the RoI are prior to extracting a specific number of contours.Then, only the most relevant contours are retained for further processing. Feature extractions schemes have been also recommended in the literature. A conventional region growing algorithm is modified by Mat-Isa et al. [12]. The proposed modification, called the seeded region growing features extraction (SRGFE), infers the size and grayscale levels of a specific RoI in the cervigramimage. Another approach is attributed to Chang et al. where the size and deformation of a cell nuclei are used to categorize it as abnormal. Chang et al. pre-processed the cervigramimage to remove the noisy parts prior to the extraction of the cell nuclei region [13]. Then, two complementary approaches are suggested to classify the cells using the grayscale level and energy,respectively. The resulting classifier is able to discriminate the abnormal cells. A data-driven solution is described in which Kim and Huang used an optimized bounding box (OBB) method to detect the RoI in cervigram images. The RoI is usually a BB rectangle centered around the cervix. Several BB regions with different locations and scales are extracted from similar images using a similarity metric. Then, the "best" BB region is retained using a combination of Euclidean Distance and intersection over union (IoU) metrics. Finally, a two-variant classifier is built on majority voting method and support vector machine (SVM) model. Both classifiers are trained using engineered (or hand-crafted) features. These features are constructed using cervical colour and texture representations. Song et al. used first a Sobel filter to detect the cervix RoI. Then, amulti-modal approach is proposed for the cervical cancer classification. The latter approach collects information from the cervigrams and the clinical tests. This classification decision is based on the collected information. Song et al. evaluated a similarity measure based on the classifier information to extract a label for the cervigram under consideration.

It is noteworthy to mention that Kimand Huang assessed the performance of two different categories of cancer classifiers. In the first category, classifiers are designed and trained using hand-crafted features. These features, well tested in the computer vision field, are standard image descriptors. Such descriptors include pyramids of local binary patterns (PLBP), pyramid color histogram in the L*a*b* color space (PLAB) and pyramid histogram of orientated gradients (PHOG). In the second classifier category, auto-extracted features are used to train the cervical cancer classifier. These features are directly inferred during learning by a random forest, SVM or convolutional neural network (CNN) model.Using a publicly available patient data, Adem et al. classified four different target variables including the Schiller, Cytology, Biopsy and Hinselmann features. These features represent potential cervical cancer risks. Unlike our proposed model, Adem et al. used a small sized dataset consisting of patient historical data. The deep learning classifier consists of a stacked autoencoder model. Correct classification rates reached 0.978 which highlights

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the superiority of deep learning models in patient diagnostic support systems.

Fernandes et al. predicted cervical cancer risks and subjective quality assessment scores from colposcopic images based on different modal-ities and human experts. The prediction model relies on a regularization-based transfer learning strategy. Such strategy enables the source and target models to share the same model pa-rameters and reduces the size of the required training data. In addition, the model trained onone expert/modality subset can be easily extended thanks to the transfer learning strategy. Us-ing only nucleus-level texture features, Phoulady et al. classified cervical tissue as normal or cancer. The proposed features are processed using a two-step nucleus-level analysis. In the first step, nucleus-level information is captured using an adaptive multilevel thresholdingsegmentation.Then, the shape of the segmented regions is approximated using an ellipse fitting algorithm. The Two-step classifier, called adaptive nucleus shape modeling (ANSM) algorithm, achieved a classi-fication accuracy of 0.933 with zero false negative rates. Thanks to its performance, the ANSMmodel can improve the overall performance of cervical histology image analysis tools.Devi et al. surveyed and analyzed several ANN architectures used in the classification of cervical cancer. The most efficient architectures are recommended for the binary classification of cervical images as normal or abnormal cervical cells. The performance of these architectures are contrasted to that of the manual screening methods such as the PAP smear and liquid cytology based (LCB)tests.To mitigate the image segmentation challenges, Zhang et al. proposed a segmentation-free classifier for cervical cancer. Unlike previous models, Zhang et al. trained a deep learning model using automatic features. To cope with the limited size of the training data, Zhang et al.trained their model using a two-stage approach. In the first stage, the deep learning model is pre-trained on a natural image dataset. Then, the trained model is tuned using nuclei-centered patches extracted from adaptively resampled cervical images. Despite its good performance, this model requires accurately extracted image patches

III. MATERIALS AND METHODS

The main steps involved in the proposed methodology for cervical cancer detection includes:

- Collection of data
- Preprocessing of images
- Feature learning through convnet
- Classification using SVM

One of the most efficient data collections is the Herlev University Hospital dataset called Herlev dataset. The dataset was created together by the Herlev University Hospital and Technical University of Denmark. Hervlev pap smear dataset is selected for training and learning purpose.TheHervlev pap smear dataset is an open access publicly available dataset which contain two groups of cell images diagnosed by different doctors.The groups are divided into 7 classes as described in Figure 1.

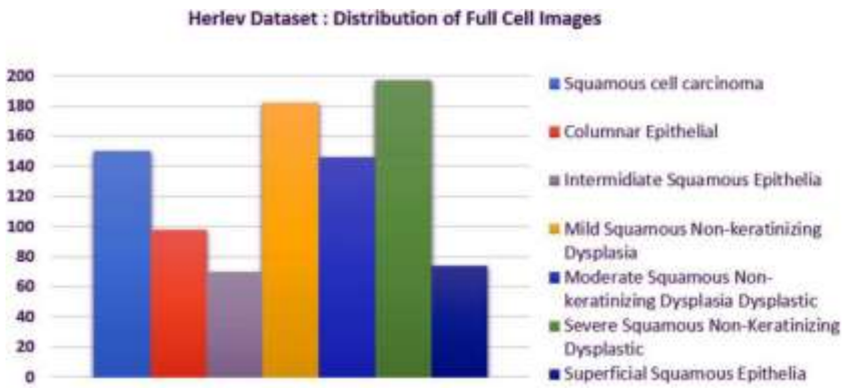

Figure 1 Herlev dataset distribution

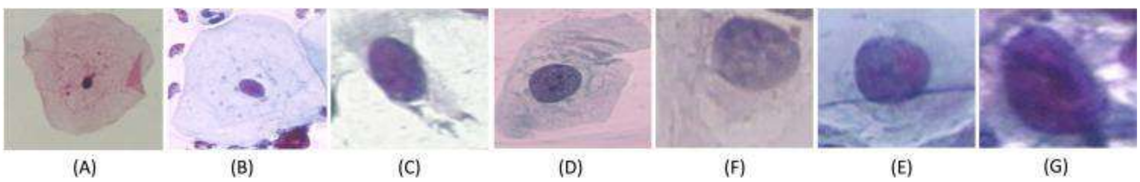

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Figure 3 The cells are classified into 7 classes**:**(A) superficial squamous epithelia, (B) intermediate squamous epithelia, (C) columnar epithelial, (D) mild squamous non-keratinizing dysplasia, (E) moderate squamous non-keratinizing dysplasia, (F) Severe squamous non-keratinizing dysplasia, (G) squamous cell carcinoma in which (A),(B),(C) are considered to be normal and (D),(D),(F),(G) are considered to be abnormal.

Table 1 shows the characteristics of cells in the dataset

Numbers(Cells)	Cell description	Type
70	Intermediate	Normal
74	Superficial	Normal
98	Columnar	Normal
146	Mild	Abnormal
182	Moderate	Abnormal
197	Severe	Abnormal
150	Squamous	Abnormal

As noisy images create problems for machine learning and vision based approaches a good noise reduction technique needs to be applied before further processing. Filtering methods like spatial filters can be used for removing noise but generally these methods result in shift variance and over smoothing. A linear Gaussian filter is applied on the images to remove noise, but this method lacks accuracy. A mean filtering method is used for reducing the noise of pap smear images in this work. Mean filter is also known as Box filter. The basic idea of a box filter is to replace each pixel value with the mean value of its nearest neighbours. After the l filter is applied, data augmentation is performed to make it ready for training. The purpose of the augmentation process may go through a number of rotations and translations.

The convnets are applied to learn the features automatically.The deep features extracted are used for further classification.Deep features are extracted from the outer layer of convent for the classification. Classification is a complex procedure.A support vector machine (SVM) which is a supervised learning model is then applied to generate the classification score.

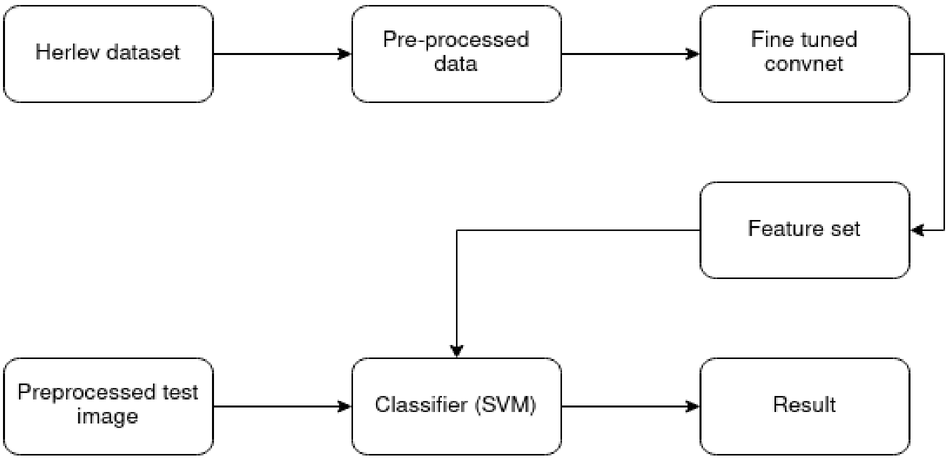

Figure 4 CNN architecture

IV. RESULTS AND DISCUSSION

30 epochs are used on the Herlev dataset for the classification of normal and abnormal cells using Convnet. It took 12 epochs to reach the validation accuracy to its maximum value. The maximum of validation accuracy achieved is 0.9940 . The table below represents the classification time needed on three different experiments. All the images in the Herlev dataset are feeded to classifiers to measure the classification accuracy of each category. The classification accuracy of normal and abnormal classes are 97.79 and 99.20 respectively.

Table 2 shows the characteristics of cells in the dataset

Experiment	Result	Response time (In seconds)

Experiment 1	Normal	14.25
Experiment 2	Abnormal	12.13
Experiment 3	Abnormal	12.4321
Experiment 4	abnormal	13.210

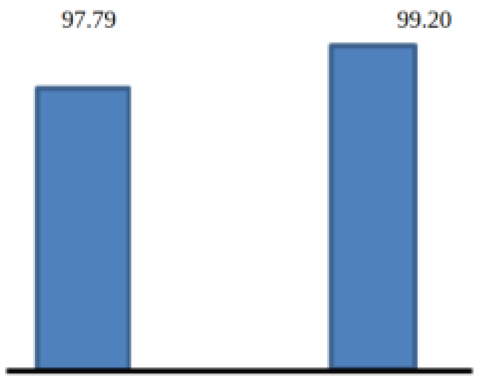

Figure 5 shows the characteristics of cells in the dataset

V. CONCLUSIONS

This work proposes an automatic cervical cancer detection system using convolutional neural networks. The proposed system is much needed as the manual scanning mechanism is time consuming and costly. The proposed work performs well on testing sessions also with 97.79% accuracy on normal sets and 99.20% accuracy on abnormal sets. In future work we intend to generate more classes to normal and abnormal cells so as to classify the cells based on their severity.

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