

## Design of Convolutional Neural Networks Model for Fine-Grained Classification of Cervical Cells

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### Abstract

One of the most prevalent cancers in the world and one of the most harmful to human life is cervical cancer (CC). This procedure was created to increase the diagnostic accuracy of CC in such dataset pictures in order to better detect and forecast illness. Therefore, we attempted to demonstrate a convolution neural network-based classification framework for CC that is intelligent and effective and has a comparatively basic architecture in comparison to others. Additionally, we offered a simple and useful technique for CC classification from cytological pictures using effective feature extraction or accurate cell image segmentation effort. The outcomes of automatic cell detection are contrasted with those of other cutting-edge cell detection methods as well as hand annotation of the underlying data. Many of the procedures for cell detection and categorization are still being worked on. This procedure's primary goals are to pinpoint the cell area and increase segmentation precision. With an F1 score of 0.96, the suggested approach has the highest cell detection accuracy.

**Keywords:** Cervical Cancer, Fine-Grained Classification, Convolution Neural Network, Automatic Cell Detection.

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### 1. Introduction

As previously indicated, one of the three factors (the other two being tubule development and nuclear pleomorphism) for evaluating breast cancer tissue slides is the proportion of mitotic cells seen in breast histopathology photographs. The biological heterogeneity of mitotic cells makes it difficult to detect them, making automatic identification and counting of mitotic cells a tough undertaking. The relevance of analyzing the mitotic count is due to the fact that it assesses the tumor's aggressiveness. Mitotic cells have the capacity to duplicate all of their chromosomes, divide the chromosomes in their nuclei into two identical sets, place each set in a separate new nucleus, and produce two new cells as a result.

The mitotic process's first phase is known as prophase. Nucleoli vanish during this stage, and chromatin (DNA and related proteins) may be seen under a light-based microscope. Two sister chromatids that share the same genetic material make up the chromosome. The centromere serves as the link between the two sisters chromatids. The spindle fibres from each centriole connect to each chromosome at a specific protein structure known as the kinetochore when they reach the opposite ends of the cell. Each chromosome's centromere contains the kinetochore. Other spindle fibres also extend, but they interact with the spindle from the other pole rather than joining to chromosomes.

The chromosomes will be positioned along the centre of the cell nucleus. The line that results is known as the metaphase plate. This procedure will make it more likely that after the aligned chromosomes are split, each new nucleus will include a copy of each chromosome in the following stages.

One of the most useful tools for pathology investigations is histopathology slides. Even skilled pathologists find it difficult and time-consuming to see these types of slides, therefore computerising this process enables the professionals to analyse more cases per day and more quickly. This article suggests an automated mitotic detection system (AMDS) for histopathology slide pictures of breast cancer. The main components of an autonomous image-based analyzer are taken into consideration in the proposed AMDS, and in each phase, certain unique innovations are used. 2D anisotropic diffusion filters are used in the pre-processing stage to more precisely segment the raw digital histopathology pictures. Using maximum likelihood estimation, the histopathology slide pictures are segregated during the training segmentation phase according to the RGB contents of respective pixels. The potential mitosis and non-mitosis possibilities are next processed, leading to the object-wise extraction of their finished local binary patterns. Two afterwards non-linear support vector machine classifiers are trained on the pixel- and object-levels, respectively, for the classification phase. Some object and region-based metrics are used for the proposed AMDS' assessment. After calculating the assessment criteria, we can see that our suggested approach outperforms other competitors' methods in the Mitos-ICPR2012 contest for breast cancer histopathology

pictures, according to the f-measure metric (70.94% for Aperio XT scanning images and 70.11% for Hamamatsu images). The experimental findings demonstrate that the suggested AMDS performs better than other competitor systems put out for the MitoS-ICPR2012 challenge.

By five-fold cross-validation with patient-level splitting, the suggested technique is assessed on the Herlev cervical dataset. The findings demonstrate that greater classification accuracy may be attained generally by using cytoplasm and nucleus masks as raw morphological information into appearance-based CNN learning. The four CNN models achieve classification accuracies of 94.5%, 71.3%, and 64.5% for two-class (abnormal versus normal), four-class ('The Bethesda System'), and seven-class ('World Health Organization classification system') classification tasks, respectively. GoogLeNet fed with both morphological and appearance information achieves these classification accuracies. In order to manage contacting cells, we offer the suggested cell identification approach, which is based on sparse reconstruction using simple templates. A probability map that denotes the existence of cells is created using the sparse reconstruction error of a sliding window over the whole testing picture. Clustering using weighted mean-shift is carried out utilising the probability map to provide the final detection findings. Our approach shows that integrating cervical cell shape with visual cues can enhance classification performance.

## 2. Literature Survey

This study proposes a method for analysing PAP smear pictures of the cervical area based on an examination of the distribution and size and shape of the cell nuclei. An effective and simple approach to find any abnormalities in cervical cells is the PAP smear test. However, analysing a lot of PAP smear photos by hand is a laborious operation and human inspection is not always gratifying. This study's objectives include automating the screening procedure and providing detailed statistical information that will be useful in identifying anomalies in the cervical area. In MATLAB®, a sophisticated, interactive environment for data visualisation, analysis, and computing, the suggested technique is put into practise. The digitised pictures were segmented, and different statistical statistics were calculated using the MATLAB® Image Processing Toolbox. It is possible to programme MATLAB® to discriminate between normal and suspect cervical cells by analysing cell nuclei distribution and accounting for shape and size parameters. RGB colouring is used for images. Three-dimensional and hence challenging to process is the matrix that corresponds to a colour picture. Although all cell nuclei are not spherical, we solely took their round form into consideration when segmenting them. The procedure might be automated using a computer utilising a histogram or fuzzy logic, or it could be made interactive so that a pathologist can input his own grayscale threshold [1].

One of the most serious health issues the world is now dealing with is lung cancer. The development of automatic lung cancer diagnosis has advanced medical technology. The Morphing Sobel Approach is a novel strategy that makes use of morphed X-ray scan pictures. Morphological operators, Gaussian filters, de-noising, and a straightforward Sobel operator are all used in the morphing Sobel technique. The Morphed Sobel Approach first applies a Gaussian filter, then applies a soft threshold to smooth out the picture, and then employs binarization to reduce noise. The segmentation procedure produces better results, and simulation is also quite effective. However, the threshold value used in this segmentation procedure will remain the same, making it difficult to obtain an exact result value [2].

Because image analysis of cancer cells is acknowledged as the most effective and efficient approach to detect its genesis, it is crucial for breast cancer diagnosis and treatment. To increase the accuracy of breast cancer identification from stained tissues of biopsy pictures, I suggest an approach depending upon pixel-wise posterior probability of co-occurrence of cell components. In lieu of long calculations and complex mathematical theory, the double threshold offers a straightforward and straightforward method of handling the segmentation problem. A potential contender for the advance identification of breast cancer is microwave-induced thermal acoustic imaging (TAI), which combines the high contrast of microwave imaging and the high resolution of ultrasound imaging. Since cancer cells were found in this project's earlier stages, the beginning stage can also be treated using this strategy. The next step will be to optimise a number of random threshold settings and import the image into the MATLAB workspace for the most accurate and effective image recognition [3].

One of the most complex and developing areas of study nowadays is medical image processing. Multispectral MRI has become a viable alternative to ultrasound (US) for the accurate detection of cancer in the breast, prostate,

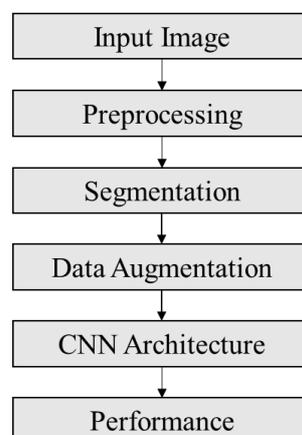
liver, and other organs in recent years. The proposed method is described in this work for identifying and removing prostate cancer cells from an MRI scan picture of the prostate organ. The system has been tested on a variety of patient MRI data that included pictures of prostate cancer. The basic application of morphological procedures is based on some presumptions regarding the size and form of the malignancy. In order to make the cancer apparent in the picture, the cancer cells are ultimately mapped into the original grey scale image with 255 intensity. The morphological procedure and Gaussian filter are coupled to provide an output that is enhanced and noise-free. One of the flaws in this project is that the region is not contoured to be separated, therefore noise reduction is the sole action conducted [4].

Cervical cancer incidence and death have unquestionably decreased as a result of the traditional Pap smear. However, a few issues have come to light, including the lack of qualified pathologists and the growing workload brought on by more people having access to preventative healthcare, which will eventually render the screening process time-consuming and extremely prone to human error. An automated cervical cancer cell identification method has been created to address this issue. The morphology of the cells and level set procedures are used to identify cervical cancer cells. Test results demonstrate that the system can distinguish between malignant and normal cells using a categorization of colour intensity. It is hoped that this system would assist the pathologist in reducing workload and minimising human mistake while preserving and enhancing system accuracy. It is hoped that this system would assist the pathologist in reducing workload and minimising human mistake while preserving and enhancing system accuracy. Despite several attempts to improve the image, this project has certain shortcomings. Cancer stages won't be able to be identified in this experiment [5].

### 3. Proposed System

Five-fold cross-validation with patient-level splitting is used to assess the proposed approach on the Herlev cervical dataset. The findings demonstrate that improved classification accuracy may be attained in general by using cytoplasm and nucleus masks as raw morphological information in appearance-based CNN learning. For the two-class (abnormal vs normal), four-class, and seven-class activities that need classification, GoogLeNet fed with both morphological and appearance information has the greatest classification accuracies of 94.5%, 71.3%, and 64.5%. We outline the suggested cell detection algorithm in this section, which uses sparse reconstruction and simple templates to handle touching cells. A probability map that denotes the existence of cells is created using the sparse reconstruction error of a sliding window (equivalent to an image patch) over the whole testing picture. The use of weighted mean-shift clustering to the probability map yields the final detection findings. Our approach shows that integrating cervical cell shape with visual cues can enhance classification performance. The following are some benefits of the suggested strategy:

- The CNN is more accurate than other methods.
- More is Feature Stability.



**Fig 1: Flow Diagram**

Various steps that are involved during implementation of proposed approach are being explained under following section:

## 1. Input Image

The image that has RGB colour channels is referred to as the input image. The dataset image is the image that was used as input. The dataset picture is always used as the input image, making all of the images' pixel values and intensities essentially identical. In comparison to other photographs that were acquired from different web pages, the input image that was collected from the dataset will produce higher results. Because the dataset picture was chosen, the procedure' accuracy has enhanced.

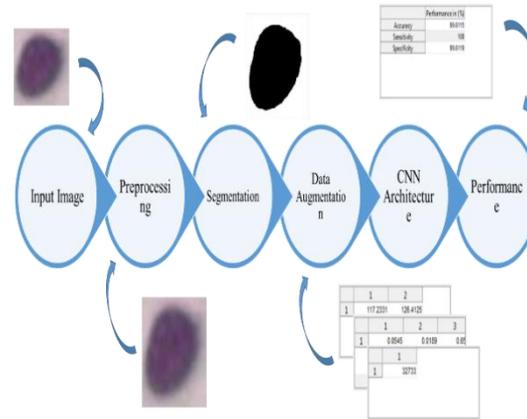


Fig 2: System Architecture

## 2. Preprocessing

Resampling is the process of enlarging or decreasing the size of an image using software. When a picture is resized, its pixels for width and height are either increased or decreased. Other methods of resizing an image include cropping it to a smaller size. As a result, the image is scaled in this procedure to 256 X 256, where 256 is the number of pixels in the row and 256 is the number of pixels in the column.

## 3. Segmentation

Segmentation divides a picture into discrete areas that each include pixels with comparable characteristics. The areas should have a close relationship to the portrayed items or interesting aspects in order to be relevant and beneficial for picture analysis as well as interpretation. From low-level image processing that splits a grayscale or High-resolution image is transformed into a colour image and one or more supplementary images. description that identifies features, objects, and scenes, meaningful segmentation is the first step. The accuracy of segmentation determines how well an image analysis will turn out, however correct picture partitioning is typically a very difficult subject. The latter assemble pixels in a groups depending upon some global property, such as grey level or colour, and ignore the spatial connections between components in a picture.

## 4. Data Augmentation

*Centroid Feature Extraction:* It determines the centroid of each zone and computes the distance and angle between the beginning point and the centroid as well as the ending point and centroid. Consider a log-polar location grid that has 17 location bins altogether, 3 distinct radii, 8 angular directions for 2 of them, and 3 different radii. Create a 16-bin gradient histogram. Create a feature vector with a 272-dimension (17\*16) size. Reduce the dimensionality of the space and project the characteristics onto a 128-dimensional space.

## 5. CNN Architecture

Convolutional neural networks, often known as ConvNets, are MLP versions that draw inspiration from biology. They feature multiple types of layers, each of which functions differently from the typical MLP layers. Convolutional neural networks (CNN, or ConvNet) are a kind of deep neural networks employed most frequently to analyse visual vision in deep learning. Multilayer perceptron derivatives, or CNNs, are regularised variants. Typically, the term "multilayer perceptron" refers to networks that have all of their neurons linked to those in the layer above them, or fully connected networks. These networks are prone to over fitting data owing to their "fully-connectedness." The regularisation process is approached differently by CNNs, who take use of the hierarchical structure of the data to piece combining increasingly complex patterns from modest, straightforward ones. So, on a scale of connectedness and complexity, CNNs are at the lower end.

#### 4. Results

We outline the suggested cell identification approach, which uses sparse reconstruction and easy-to-use templates to handle contacting cells. A probability map that identifies the existence of cells is created using the sparse reconstruction error of a sliding window (equivalent to an image patch) over the whole testing picture. Weighted mean-shift clustering is utilized to the probability map to provide the final detection findings. By integrating cervical cell morphology with visual cues, our technique shows that classification accuracy may be increased. For the identification and categorization of cells, several processes are still being worked on. Finding the cell area and increasing segmentation accuracy are the key goals of this approach. With an F1 score of 0.96, the suggested technique achieves the highest level of cell detection precision.

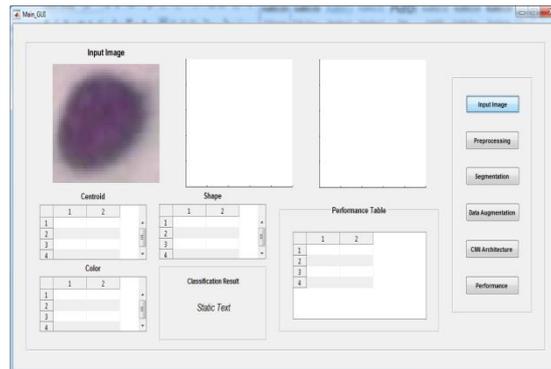


Fig 3: Input Image

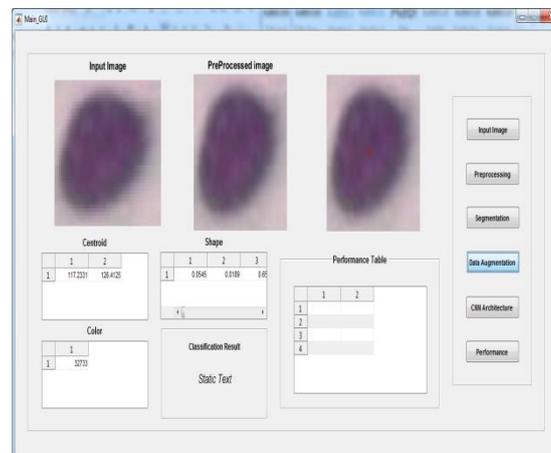


Fig 4: Data Augmentation

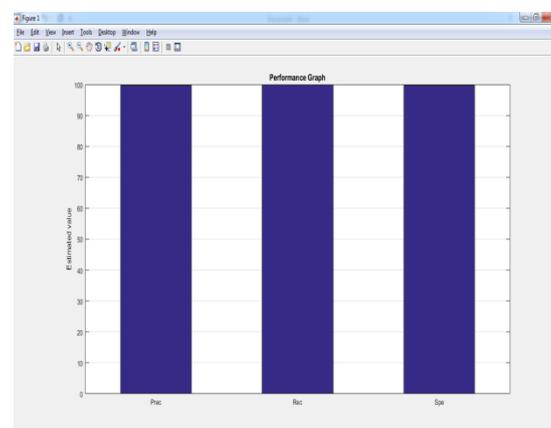


Fig 5: Performance Analysis

## 5. Conclusion

One of the most prevalent cancers in the world that endangers human life the most is cervical cancer (CC). This procedure was devised in order to increase the diagnostic accuracy of CC in such dataset pictures, which would help with illness identification and prediction. So, using a convolutional neural network (CNN) with a relatively basic architecture in comparison to others, we attempted to present an intelligent and effective classification model for CC. Additionally, using effective feature extraction or accurate cell image segmentation work, we developed a simple and useful approach for the categorization of CC from cytological pictures. The outcomes of comparing automated cell identification against manually labeled underlying data along with other cutting-edge cell detection techniques. With an F1 score of 0.96, the suggested technique achieves the highest level of cell detection precision.

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