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Detection of Cervical Lesions: A Region-based Approach for Analyzing Microscopic Images

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ABSTRACT: Cervical cancer is a widespread issue globally, with the majority of deaths occurring in lower-resource countries. To address this challenge, recent technological advancements have focused on automating the screening process. However, there remains a critical need for affordable and portable solutions that can reach underserved populations. This study proposes a novel approach: a low-cost microscopy device that uses smartphones to analyze liquid-based cytology samples. The device operates autonomously, capturing images and identifying cervical lesions without the need for extensive human intervention. The research evaluates various deep learning models designed for object detection to find the most suitable architecture. Additionally, the study explores transfer learning from conventional cytology datasets to enhance the robustness of lesion detection in images acquired by mobile technology. Initial tests on the SIPAKMED dataset report promising detection metrics, albeit with room for improvement before clinical deployment. Notably, the proposed system can analyze a cytological sample in approximately 4 minutes, indicating practicality for use in healthcare settings. Overall, while further refinements are necessary, this research marks a significant step toward developing an affordable and effective IoT-based framework for expanding cervical cancer screening coverage worldwide.

KEY WORDS: Cervical cancer, SIPAKMED and Cytological

I. INTRODUCTION

Ranking as the fourth most common cause of cancer inci- dence and mortality in women worldwide, cervical cancer continues to constitute a major public health problem. In 2018, approximately 84% of all cervical cancers and 88% of all deaths caused by cervical cancer occurred in lower- resource countries [1]. Moreover, the mean age at diagnosis of cervical cancer is quite low compared with that of most other major cancer types, generating a proportionally greater loss of life-years.

In order to reduce mortality rates, the worldwide adoption of both early detection and screening programs is essential [2]. Examples of screening methods recommended by the World Health Organization (WHO) are: i) visual inspection of with acetic acid (VIA); ii) cervical cytology through con- ventional (PAP) test or liquid-based cytology (LBC); iii) Hu- man papillomavirus (HPV) testing for high-risk HPV types. The first method has been more adopted in low-resource settings, due to its cost, in spite of its limited accuracy for the detection of pre-cancerous lesions. The second method has been the standard method for screening, being linked to drastic reductions of mortality rates after its adoption in many countries, with LBC being used in more developed countries and conventional Pap tests otherwise. Finally, in more recent years HPV tests have been used for screening, either alone or in combination with Pap tests, since most cervical cancers are caused by HPV

In recent years, efforts have been underway to improve cervical cancer screening by developing automated microscopy solutions such as the ThinPrep Imaging System (TIS) and the BD FocalPoint GS Imaging System (FocalPoint™) [3]. These systems are effective but come with high costs, which restrict their widespread use. There is a critical need for more affordable alternatives that can automatically capture images of cytology samples and assist in identifying cervical lesions using computer-aided diagnosis (CAD) systems [4]. Finding such solutions could significantly enhance screening efforts by improving accuracy, reducing the workload of cytotechnologists, lowering screening program expenses, and ultimately decreasing the incidence and mortality rates associated with cervical cancer [4].

In response to these challenges, Fraunhofer AICOS has developed an innovative solution known as the µSmartScope—a fully automated 3D-printed microscope that integrates with smartphones. This device serves as a cost-effective alternative to traditional microscopes, particularly beneficial in regions with limited access to healthcare services. Controlled entirely by a smartphone, the µSmartScope uses a motorized stage for autonomous

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image capture. Its primary aim is to lessen the reliance on onsite microscopy experts by facilitating integration with Artificial Intelligence (AI) systems. Initially used for diagnosing malaria through automated analysis of blood smears [6], [7], the µSmartScope is currently being redesigned for cervical cancer screening. Its focus is on accurately examining liquid-based cytology samples.

This study proposes an innovative framework based on Internet of Things (IoT) technology. It leverages the µSmartScope for capturing microscopic images of cervical samples and integrates deep learning models for automated detection and classification of cervical lesions from these images. Despite advancements in smartphone processing capabilities, the computational complexity of state-of-the-art detection models hinders their deployment directly on mobile devices. Therefore, the proposed system advocates for a cloud-based approach to process images, underscoring the role of IoT in integrating AI algorithms into practical decision support systems for cervical cancer screening

1 depicts a novel mobile-based framework designed to detect cervical lesions:
(A) Shows the µSmartScope device with a smartphone attached, housing a liquid-based cytology (LBC) sample.
(B) Displays sequential screenshots from a smartphone app, illustrating the revised solution:
(i) Inserting the cervical sample.
(ii) Aligning the optic disk and initiating image capture via the app.
(iii) Demonstrating potential visual feedback for automated lesion detection.

To enhance detection accuracy, three deep neural network architectures for object detection were optimized and compared. Given limitations in the dataset collected via portable microscopy, a thorough analysis was first conducted using the SIPAKMED dataset, a publicly available repository of conventional cytology [8]. This initial investigation aimed to identify the most effective models and establish a baseline for performance in the detection pipeline.

II. RELATED WORK

One of the main tasks encompassed by the analysis of cer- vical samples is the identification of cervical lesions in the microscopic fields. As a consequence, this is a pivotal step for the development of a successful computer-aided cervical cancer screening system. In spite of the myriad algorithmic methodologies to achieve it reported in the literature [9], only the main lines of research are mentioned in this section.

Many studies focus on segmenting cells in images to categorize them based on abnormalities, a crucial step in developing effective systems for computer-aided cervical cancer screening. This segmentation aims to locate cells for detailed analysis and to extract clinically significant features such as cell shape, dimensions, and inner structures. Some researchers, like Byju et al. [10], employ traditional image analysis techniques such as customized Laplacian of Gaussian (LoG) filters to detect cell nuclei contours. More sophisticated approaches, as seen in [11], tackle challenges like segmenting individual cells that may appear clustered or overlapping. Effective pipelines often start with segmenting nuclei to establish shape priors, using refined active contour algorithms to segment cytoplasm regions. Methods may iteratively adjust intensity thresholds based on object properties like area and eccentricity. Alternatively, machine learning models are used for pixel-wise classification to distinguish cell regions from backgrounds. For instance, [12 have applied such models successfully to single-cell images, though broader application to entire microscopic fields remains a challenge.

In studies focusing on individual cells, datasets like the Herlev dataset [14] are pivotal, providing images categorized by cervical intraepithelial neoplasia (CIN) levels. These studies extract features like statistical measurements, perimeter, and intensity variations to predict CIN levels using machine learning models such as k-NN, Bayesian networks, J48 trees, and multi-layer perceptrons (MLP). For instance, [16] combines these features into a vector fed into classifiers, achieving superior performance with k-NN while maintaining efficient computational times. Overall, these methodologies aim to enhance clinical decision-making by automating cell analysis, leveraging both traditional techniques and advanced machine learning to improve cervical cancer screening processes.

III. DATASETS AND DATA PREPARATION

This section describes the used image datasets and the re- spective data preparation procedures. The creation of the mobile HFF regions dataset, detailed in section III-A, was motivated by the lack of a benchmark dataset for the

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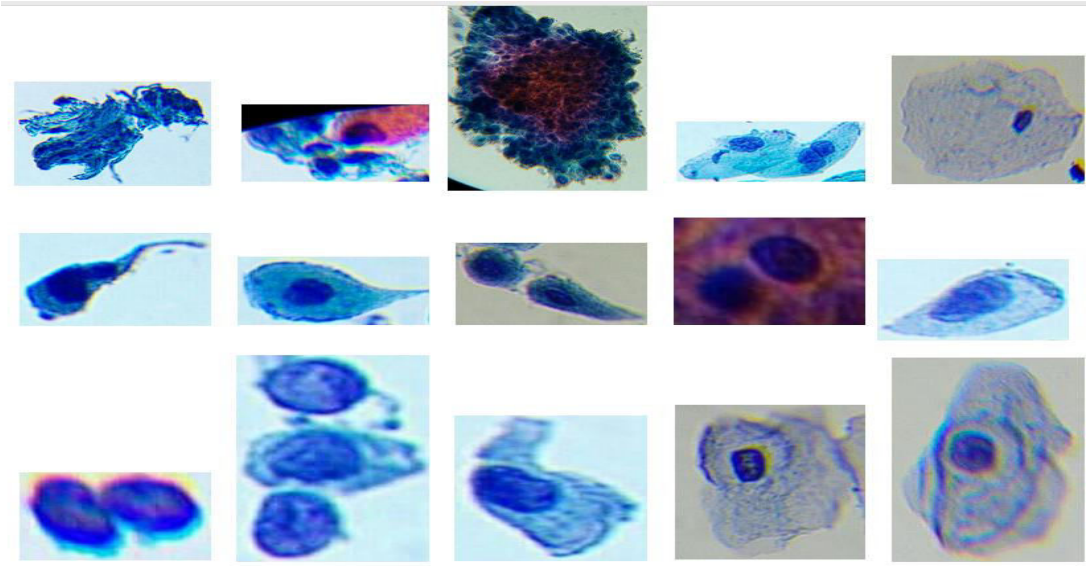
local- isation of cervical lesions in microscopic fields of liquid- based cytology samples and their stratification according to the abnormality levels of the Bethesda system. Although there are many public datasets based on images of cervical cytology, some of them only provide images of previously separated single cells and classify them according to CIN levels instead of the Bethesda system's classes (e.g., the Herlev dataset [14]), while the ones that include images of microscopic fields of view either do not provide abnormality classification labels for each cell/region or separate the existing cells in relation to their type and not abnormality level (as it is the case of the SIPAKMED dataset, char- acterised in section III-B), besides including images from conventional cytology preparations instead of LBC samples.

The mobile HFF regions dataset was specially curated for this research using the µSmartScope prototype paired with a smartphone. It contains 21 LBC samples from Hospital Fernando Fonseca, each meticulously annotated by a specialist to identify abnormal cells or clusters indicating cervical lesions. Annotations are marked with bounding boxes around these regions and categorized according to the Bethesda System's classification: ASC-US, LSIL, ASC-H, HSIL, and SCC. Figure 2 in the paper displays examples from each category, demonstrating the varying structures associated with different lesion levels and similarities between cells of consecutive levels.

1.Subset division

The separation of the data instances in the train, validation and test subsets was performed in 2 phases:



ASC-US LSIL ASC-H HSIL SCC

TABLE 1: Mobile HFF regions dataset sample and annota- tion distribution (training, test and total).

Number	ASU-US	LSIL	ASU-H	HSIL	SCC	Total
Samples	4	3	4	3	2	16
Train annot	352	58	79	203	13	705
Test Annot	125	38	30	29	0	222
Total annot	477	96	109	232	13	927

i) Initially, the dataset was split into training and test sets at the sample level, ensuring that all images from the same patient sample remained in either the training or test subset. This approach prevented overlap between training and test data, maintaining diversity across the dataset. The division was carefully done based on visual inspection of the different structures within each class across samples. This method aimed for an 80/20 train/test ratio to account for limited annotated images and the varied morphological properties present in abnormal regions.

ii) Multiple train/validation splits were created using a stratified k-fold cross-validation method applied to each training sample individually. This procedure ensured that each class within the dataset was equally represented in both training and validation subsets. Each sample's images were divided into k exclusive subsets, with one subset

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chosen for validation and the rest for training. A k value of 5 was selected to balance validation instances and provide ample training data. The final training and validation sets for each split were formed by combining subsets from all samples included in that particular split.

2.Image patches extraction

To obtain images of fixed dimensions, required for the ap- plication of some of the detection models and to restrain the computational resources used during training, the images acquired with the µSmartScope were divided into adjacent patches. The extraction of each patch was executed taking into account the annotated regions contained in its area, through a procedure detailed in Appendix A and illustrated in Figure 3. These steps were applied after pre-processing the acquired images to segment the optic disk (according to the steps described in [7]) and crop the main field of interest in accordance with the segmented region. The dimensions of the extracted patch images were one of the settings optimised during the tuning process, as later specified in Section IV-B

3.Addressing the main limitations of the dataset

Although the mobile HFF regions dataset is fairly even concerning the proportion of samples for each diagnosis outcome, the distribution of abnormal regions is not balanced for all lesion levels, as it is clear from Table 1. Furthermore, the amount of clinical cases of each class is scarce, and the total number of microscopic fields with abnormal regions may be insufficient to train complex neural network models. In addition to this, the number of patch images without annotated objects (henceforth referred to as empty patches) surpasses substantially the number of patch samples that con- tain actual regions of interest: the annotated patches comprise approximately $3 - 7\%$ depending on the size of the extracted patches. This imbalance could lead to many training steps be- ing performed using mainly images without bounding boxes from which the network can learn, dampening the learning process.

Therefore, to address these shortcomings, efforts were made in terms of pre-processing operations, as described next:

i) **Merging similar classes**: Due to the under-representation of SCC and similarities in clinical management with HSIL, these classes were merged into a single category called HSIL-SCC.

ii) **Down-sampling empty images**: To balance the dataset, empty patches without annotated objects were reduced in number. This was achieved through detailed phases described in Appendix B, ensuring a more even distribution between empty patches and those containing annotated regions. Initially, only 3-5% of patches were annotated, but after downsampling, this increased significantly to approximately 60-67%.

iii) **Achieving uniform class distribution**: Addressing the imbalance among classes critical for model learning, data augmentation techniques were applied. These included geometric transformations such as flips and rotations, intensity adjustments like blurring and sharpening to simulate varying focus levels, and gamma correction across RGB channels. Additional images were generated based on the difference in representation between classes, ensuring each class had sufficient training instances. This approach was guided by the number of patches annotated with each class, assuming an average of one object per annotated image.

SIPAKMED DATASET

The SIPAKMED dataset [8] is composed of 966 images of conventional cytology samples acquired using a CCD cam- era (Infinity 1 Lumenera) adapted to an optical microscope (OLYMPUS BX53F), as well as expert annotations concern- ing the cytoplasmatic and nuclear contours of each cell type. The images contain 5 types of cells - superficial/intermediate (Sup.-Int.), parabasal (Parab.), koilocytotic (Koiloc.), dysker- atotic (Dysk.) and metaplastic (Metap.), corresponding to distinct types of epithelium and including abnormal and nor- mal cell classes. Despite the diversity of cell types that are a part of the dataset, each image only encompasses annotations of a specific cell class, even if the captured microscopic field includes cells of some of the other classes. Some examples of each class are included in Figure 4, and the per-class distributions of the images and cell objects are presented in Table 2.

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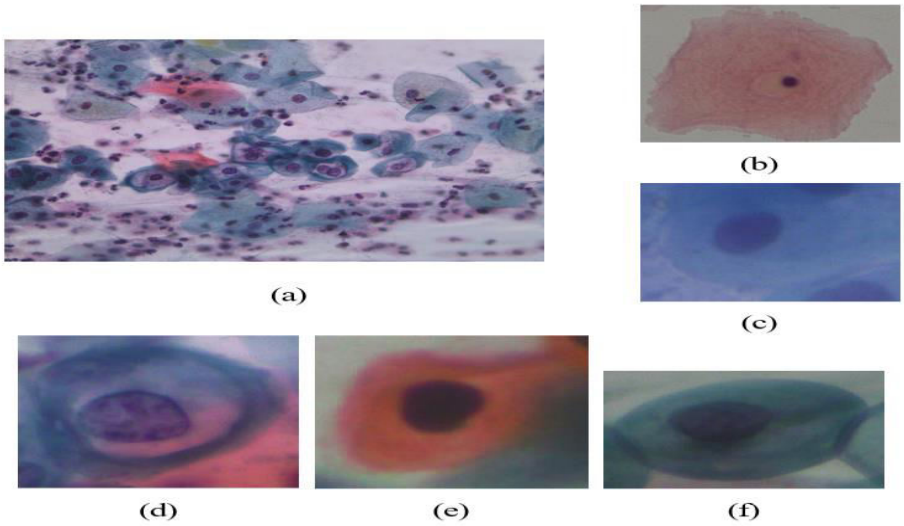
There is a slight imbalance in the number of images



Images from the SIPAKMED dataset were utilized for developing detection algorithms. Figure (a) shows an image featuring koilocytotic cells, while other images depict examples of superficial/intermediate cells (b), parabasal cells (c), koilocytotic cells (d), dyskeratotic cells (e), and metaplastic cells (f).

The SIPAKMED dataset naturally exhibited a balanced distribution of some classes, particularly parabasal and superficial/intermediate cells, with each image containing multiple instances of cells from these classes. This inherent balance avoided the necessity for additional data augmentation strategies to equalize class representation.
Annotations in the SIPAKMED dataset initially outlined cell and nuclei contours, requiring transformation into bounding boxes for detection algorithms. Ground truth bounding boxes were consequently defined as the smallest rectangular boxes encompassing the entire cytoplasmic contour of each cell.

To align processing methodologies between datasets, the SIPAKMED images underwent most of the preprocessing steps detailed in Section III-A2 for the mobile HFF regions data. However, due to the distinct characteristics of conventional cytology images, certain operations such as optic disk segmentation and specific augmentation transformations were not applicable. These steps ensured methodological consistency across datasets while adapting approaches to suit the unique attributes of the SIPAKMED dataset, facilitating accurate detection algorithm development for cervical lesion analysis.

TABLE 2: SIPAKMED dataset image and cells distribution.

Number	Sup-Int	Parab	Koiloc	Dysk	Metap	Total
Images	126	108	238	271	223	966
Cells		787	825	793	813	4049

IV. METHODOLOGY

The main goal of this work was to develop a model able to locate and classify cervical lesions in images of microscopic fields of LBC samples. Despite the pre-processing efforts employed to handle the restricted volume of images and the peculiarities of the mobile HFF regions dataset, these short- comings still hindered the successful development of robust pipelines based on deep learning models. For this reason, the construction of the main region detection approach was first conducted using the public SIPAKMED dataset [8]. Even though it is composed by conventional cytology samples and its classification labels correspond to cell types instead of abnormality levels, both datasets are from cervical cytol- ogy preparations and the corresponding annotations divide them according to morphological properties relevant for the identification of cervical lesions. Thus, two distinct region detection studies were conducted:

1. the search for the optimal model for region detec- tion and identification of the associated type of cells,

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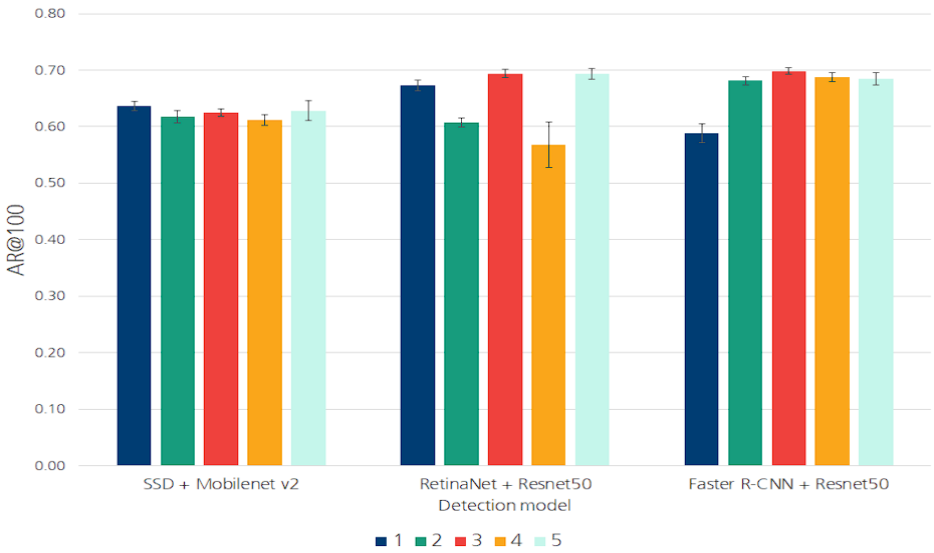
based on the conventional microscopy samples of the SIPAKMED dataset (using models pre-trained in the COCO dataset);

2. the investigation of the knowledge transfer utility be- tween the two types of cytology preparations, through the application of the best meta-architecture and back- bone network resulting from the SIPAKMED studies to the mobile HFF regions images.

V. RESULTS AND DISCUSSION

The mobile detection of cervical lesions: a region-based approach for the analysis of microscopic images" likely focuses on developing a method for detecting cervical lesions using region-based techniques applied to microscopic images. Here's a summary of what the results section might include based on the title and typical research objectives:

1. **Method Evaluation**: The paper would likely evaluate the effectiveness of the region-based approach proposed. This evaluation would involve metrics such as precision, recall, accuracy, and possibly the F1 score to measure how well the method detects cervical lesions compared to existing approaches.
2. **Performance Metrics**: Results would present quantitative measures of the model's performance, including sensitivity (recall), specificity, and possibly the area under the receiver operating characteristic curve (AUC-ROC). These metrics provide insights into how well the model distinguishes between different classes of cervical lesions.
3. **Comparison with Baselines**: The paper might compare the region-based approach with other methods or baselines, such as traditional image processing techniques or state-of-the-art deep learning models. This comparison would highlight the advantages of the proposed approach in terms of accuracy, computational efficiency, or robustness.
4. **Dataset Insights**: Results would discuss insights gained from the dataset used (e.g., mobile HFF regions dataset), including challenges encountered (e.g., class imbalance) and how preprocessing steps (e.g., merging classes, downsampling) addressed these challenges to improve model performance.
5. **Qualitative Analysis**: Alongside quantitative metrics, the paper might include qualitative analysis, showcasing visual examples of correct and incorrect lesion detections. This provides a deeper understanding of how the model performs in practical scenarios.
6. **Discussion of Findings**: The results section would conclude with a discussion of the implications of the findings. This might include recommendations for future research directions, limitations of the current approach, and practical implications for mobile cervical lesion detection systems.



Average 5-fold cross-validation AR@100 re- sults obtained in the SIPAKMED dataset with the dif- ferent hyperparameter settings tested for each meta- architecture/backbone combination. The represented values were obtained as the average validation results for the five cross-validation splits. The error bars correspond to the standard deviation over all splits.

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Overall, the results to demonstrate the efficacy and potential of the region-based approach in advancing the field of mobile cervical lesion detection, providing a comprehensive evaluation of the proposed methodology.

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