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ORIGINAL

Robust Deep Learning Approach for Automating the Epithelial Dysplasia Detection in Histopathology Images

Enfoque robusto basado en aprendizaje profundo para automatizar la detección de displasia epitelial en imágenes de histopatología

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ABSTRACT

Automated image analysis using deep learning techniques helped diagnose epithelial dysplasia in normal tissues. This study examined a hybrid approach that combined traditional image processing methods with deep learning for accurate tissue classification. A diverse, annotated dataset of epithelial dysplasia histology images was created and processed. To mitigate overfitting, a pre-trained convolutional neural network (CNN) model was finetuned with optimized hyperparameters. Performance metrics, including accuracy and precision, were assessed using an independent test dataset. The Structural Similarity Index (SSIM) was applied to enhance image contrast. The optimized deep learning model outperformed conventional methods in diagnostic accuracy. The hybrid approach demonstrated significant effectiveness in distinguishing epithelial dysplasia in medical images. The results highlighted the potential of integrating deep learning algorithms with traditional image processing techniques for automated medical diagnostics. This method showed promise for future applications in enhancing diagnostic accuracy and efficiency.

Keywords: Evolutionary Optimization; Metaheuristic; Engineering Design; Leadership.

RESUMEN

El análisis automatizado de imágenes mediante técnicas de aprendizaje profundo ayudó a diagnosticar la displasia epitelial en tejidos normales. Este estudio examinó un enfoque híbrido que combinó métodos tradicionales de procesamiento de imágenes con aprendizaje profundo para una clasificación precisa de los tejidos. Se creó y procesó un conjunto de datos diverso y anotado de imágenes histológicas de displasia epitelial. Para mitigar el sobreajuste, se ajustó un modelo de red neuronal convolucional (CNN) preentrenado con hiperparámetros optimizados. Se evaluaron métricas de rendimiento, incluidas la precisión y la exactitud, utilizando un conjunto de datos de prueba independiente. Se aplicó el Índice de Similitud Estructural (SSIM) para mejorar el contraste de las imágenes. El modelo optimizado de aprendizaje profundo superó a los métodos convencionales en precisión diagnóstica. El enfoque híbrido demostró una eficacia significativa en la diferenciación de la displasia epitelial en imágenes médicas. Los resultados resaltaron el potencial de integrar algoritmos de aprendizaje profundo con técnicas tradicionales de procesamiento de imágenes para el diagnóstico médico automatizado. Este método mostró potencial para futuras aplicaciones en la mejora de la precisión y eficiencia diagnóstica.

Palabras clave: Optimización Evolutiva; Metaheurística; Diseño de Ingeniería; Liderazgo.

INTRODUCTION

RECENTLY, medical imaging manifested a prominent effort to develop automated systems for detecting and analysing microscopic histology images. This field has traditionally relied on the discerning expertise of pathologists, who diagnose diseases qualitatively. Digital image processing has enabled the possibility of computer-aided diagnosis.[1] The formulation of efficient, reliable algorithmic, and automated methods significantly enhances data collection, facilitates research, and aids in diagnosing abnormal tissue changes, notably in cancer and epithelial dysplasia. Histopathological tests are important for diagnosing Infectious, Inflammatory, and Cancer diseases. Epithelial tissues, which form the linings of internal and external body surfaces, frequently manifest pathological abnormalities. Microscopic imaging of these tissues yields critical insights into cellular and tissue morphologies, providing valuable information on disease presence, progression, and potential prognoses.[2] Central to this endeavor is the accurate analysis of cell morphology, a task greatly augmented by image processing techniques. Image processing, an integral part of the broader field of signal processing, focuses on manipulating digital images. Cancer is the designation employed for a vast array of illnesses with a shared characteristic forming irregular cells that impact existing cells and disseminate throughout the organism, as shown in figure 1. In simple terms,[3] the human physique continues to generate fresh cells. Occasionally, the proliferation is so rapid that these fresh cells develop in regions where the former cells have not yet perished, and this phenomenon is identified as cancer.

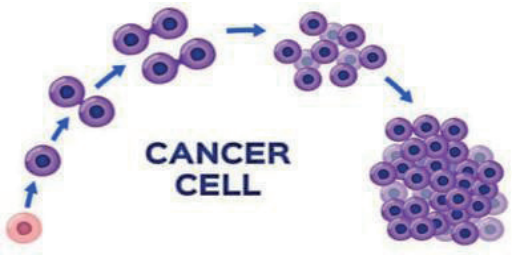

Figure 1. The expansion of unusual cells that affect preexisting cells

The primary goals encompass improving visual characteristics, extracting relevant data, and interpreting these characteristics for various purposes, from healthcare to surveillance. Image processing is a powerful tool for converting unprocessed visual information into an easier format to understand, analyze, or utilize through mathematical and computational algorithms.[4] The 21st century has witnessed notable progress in imaging technologies and computational techniques. These advancements have resulted in adopting image-processing methods, especially in histopathological assessments. Histopathological images play a vital role in medical analysis, necessitating advanced tools for accurate interpretation.[5] Image segmentation techniques are particularly important for processing these images, enabling individual cell analysis to distinguish healthy from pathological cells.[6] Features extraction, such as cell shape, size, and texture, is crucial for understanding cellular abnormalities. Automation in medical imaging, driven by Deep Learning (DL), is gaining traction to improve scalability and reduce human error in diagnosing diseases like cancer with early cellular indicators.[7] The internal and external surfaces of the Epithelial cell line of the body are often linked to epithelial cancers, characterized by uncontrolled cell growth and the ability to spread to other tissues. The development of epithelial cancers usually starts with a precursor condition called dysplasia. However, current methods face challenges in detecting and diagnosing various forms of dysplasia. Present screening methods mostly involve visually examining suspicious tissues, followed by more invasive procedures like biopsies. Biopsy samples are then analyzed histopathologically to identify markers of dysplasia and cancer.[8] These markers include metabolic activity, cell thickness, architectural features (depth and density), and nuclear characteristics (size, density, and shape). Detecting abnormal tissue changes, like epithelial dysplasia, through histology image analysis presents challenges. Visual detection methods have limitations: Dysplasia is not always visible, leading to unnecessary biopsies, and diagnosing it can be complex. Hence, image processing techniques are needed to assess the disease state in tissue samples accurately. These techniques can achieve higher accuracy in dysplasia detection, reducing the need for invasive procedures and improving diagnostic precision.

The main aim of this study is to investigate the approaches utilized in examining the morphological features of cells in microscopic histopathological images. This investigation seeks to advance significantly in the medical and computer vision domains by introducing an automated image-processing method for detecting epithelial dysplasia using Artificial Intelligence and Deep Learning.[9] This research utilizes medical images from the Pathology Department at the Jordan University Hospital. This paper proposes a novel approach for computer-aided medical diagnostics, leveraging DL with image processing to automatically diagnose epithelial dysplasia in histopathological images.[10] The methodology integrates traditional techniques with deep learning algorithms for image analysis. While the paper acknowledges the role of laboratory preparation and image preprocessing,

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the core focus shifts to applying a deep learning model for accurate tissue classification. This reduces the weakness of the adaptive thresholding and mathematical calculations based on pixel intensity.

The research explores the optimization of the deep learning model's hyperparameters to achieve superior diagnostic accuracy compared to conventional methods.[11] To achieve the objectives of this study, a series of systematic steps and procedures should be considered. Firstly, the initial phase involved a comprehensive examination of existing literature and studies in microscopic histology image analysis. This evaluation aimed to pinpoint deficiencies in current methodologies that necessitate further exploration and investigation.[12] Secondly, the collection of data and sample preparation involves gathering data from archived patient records. Five hundred digital tissue images representing both normal and cases of epithelial dysplasia were obtained from the Jordan Hospital Pathology Department. These images encompass a range of diagnosed cases of epithelial dysplasia, such as tubular adenoma polyps with various grades of dysplasia, tubular adenomatous dysplasia, and serrated adenoma with low-grade dysplasia. Thirdly, A novel algorithm based on AI DL was created to process and automatically diagnose microscopic histology images of epithelial dysplasia.[13] Fourthly, the image processing tool available in MATLAB was utilized to apply the analysis and processing. Finally, testing the proposed approach reveals the efficiency and accuracy of the selected data sample.

The structure of this paper is organized into sections: The section "LITERATURE REVIEW" discusses a comprehensive literature review and critical analysis of previous techniques used in analyzing and automating microscopic histology image diagnostics. Section "CLASSIFICATION TECHNIQUES FOR HISTOPATHOLOGICAL IMAGES" explores novel methods to automate the diagnosis of histopathological images depicting epithelial dysplasia, detailing their development and theoretical underpinnings. Sections "METHOD" and "RESULTS" present the proposed approach and the results for diagnosing epithelial dysplasia based on efficiency and accuracy. The final section proposes areas for future research in the automated diagnosis of histopathological images.

Literature Review

This section gives a comprehensive overview of image processing tools and medical concepts essential for the automated diagnosis of histopathological images. It covers digital image processing principles, fuzzy and shock filters, histogram equalization, and adaptive threshold techniques. It also discusses pathology, histology, and epithelial dysplasia in the context of medical diagnosis. In[14], the Deep Learning model for oral epithelial dysplasia grading using ResNet50 achieved 85,30 % accuracy in training but showed low generalization (60 % accuracy) on independent testing, indicating potential limitations. Also, in[15], Deep learning, specifically EMODplus, claimed the automation of oral epithelial dysplasia detection and grading in histopathology images with high accuracy, aiding pathologists in clinical practice, where they used Deep learning with convolutional neural networks and EMODplus system combining feature detection and logistic model. The literature also covers the techniques in Histopathological Image Analysis, including a survey of research methodologies and technological approaches used to analyse microscopic histopathological images. Also, the section reviews current literature and significant studies, emphasizing key contributions and identifying areas requiring further research. The aim is to place the novel methodology introduced in the paper within the existing research and technological landscape of histopathological image analysis. This section establishes a strong framework for the paper, offering a detailed understanding of the technical tools and medical background necessary for comprehending the complexities of automated diagnostic processes in histopathological images.

Image Processing

Digital image processing manipulates images using computers. As indicated in[16], it involves detecting, sensing, and analyzing digital images, building on prior. In[1], it was explained that digital image processing uses pixels with values representing image parts. The process begins with image acquisition and enhancement to improve relevant details. The work introduced in[17] shows that object classification and segmentation can be applied to get finer details.

This paper discusses specific image processing methods in research, explaining their application and importance. As described in[18], the concept of fuzzy filters is based on representing elements visually as a cluster of points without clear borders. Fuzzy logic grades each element between 0 and 1. Fuzzy filters can be used to handle images with unclear details and borders. Fuzzy filters are effective at preserving borders where traditional filters have difficulty. They handle blurred edges and variations in image data at the pixel level, making them well-suited for complex tasks requiring high accuracy and detailed information extraction.

The research presented in[19] showed that Shock filters can be utilized to apply morphological operations like dilation or erosion on individual pixels based on their location in minimum or maximum intensity regions identified using the sign function and Laplacian operator. The effects of these filters create sharp transitions between regions but may struggle with specific noise types like Gaussian noise. Research suggests improvements like using a "soft" Laplacian to enhance performance against such noise. As a type of morphological image

enhancement technique, shock filters can modify flow patterns, correct image artefacts, and improve overall clarity, making them a valuable tool in digital image processing.

In[20], the histogram equalization technique was described by adjusting pixel intensities to create a more even distribution. They claimed that this nonparametric procedure is particularly effective for medical digital images with brightness variations, improving the visibility of bone structures in X-ray images, for example. It can enhance various image types, making it useful for detailed analysis of microscopic or thermal images. However, histogram equalization can disproportionately increase contrast, especially in images with subtle variations. While it efficiently emphasizes high-contrast regions, it may not be ideal for all situations. However, histogram equalization remains a powerful tool in digital image processing, improving image interpretability and diagnostic utility in many applications.

In[21], adaptive thresholding was discussed to convert grayscale images to binary by assigning foreground or background values based on pixel intensity. In[22], smaller image windows were employed for uniform illumination, dividing the image into sub-images to establish optimal thresholds. The mean of local intensity values is commonly used as the threshold. In[23], it was confirmed that the adaptive thresholding adjusts the threshold dynamically for each pixel, making it effective for images with varying lighting conditions. It can be applied to color and grayscale images, producing a binary image that outlines divisions. Adaptive thresholding requires consideration of appropriate foreground and background pixels. Fast mechanisms like the means of regional focus and distribution play a crucial role in this process, emphasizing the importance of selecting the right neighborhood size for successful adaptive thresholding in digital image processing.

Medical Applications

The research presented in[24] highlighted that digital image processing involves a broad spectrum of applications, which was briefly explained in various disciplines, such as radiology, astronomy, and biology. These applications are categorised depending on the sources of the images being processed. Digital image sources, including electronic, ultrasonic, and other types, serve as the fundamental origins of the images and are utilized across a diverse range of applications. The work of[25] pointed out that medical image processing is a notable area. Digital image processing was employed in various diagnostic and therapeutic contexts in the medical domain. For instance, bone scans use gamma rays to detect pathological bone changes. This application of gamma rays exemplifies the critical role of digital image processing in medical diagnostics. In[26], a further illustration of using X-rays in medical diagnoses under the umbrella of digital image processing applications was introduced. X-ray imaging is a prominent example of using digital image processing to visualize, analyze, and interpret medical data, thereby aiding accurate disease diagnosis and patient management. In[27], cancer diagnosis can be achieved by applying digital image processing to analyze histological images. Enabling detailed analysis of cellular structures improves diagnostic efficiency and accuracy. Integrating image processing techniques in histology is essential for accurate disease detection, effective treatment planning, and improved patient care. In[26], pathology was defined as the study and diagnosis of diseases, focusing on causative factors and disease progression. Pathologists regularly distinguish between normal and abnormal tissues. Histology, a subset of pathology, includes studying microscopic tissue and cell structure. Histological diagnosis is based on analyzing tissue slides under a microscope to determine appropriate treatments for illnesses by assessing cellular abnormality. Several cellular samples from biological sources may lack adequate contrast under normal lighting conditions for effective microscopic examination. To address this, staining techniques enhance contrast, aiding in observing specific cellular components like organelles, cell membranes, and nuclei. In[28], indicating that the hematoxylin and Eosin (HE) staining is the most widely used in pathology. This preference is attributed to its cost-effectiveness. HE staining imparts distinctive colors to various tissue components, aiding their identification and analysis. The basic dye hematoxylin colors cell nuclei blue, starkly contrasting the acidic eosin, which stains the cytoplasm and other cell components in shades of pink. Consequently, pathologists can better differentiate, observe, and evaluate the intricate details of cellular structures, significantly contributing to accurate disease diagnosis and understanding.

Epithelial Dysplasia

In[29], epithelial dysplasia is characterized as a disorder in the differentiation of epithelial cells, which carries the potential to progress into invasive carcinoma. In pathology, dysplasia is a term used to describe an anomaly in cellular development, typically marked by abnormal alterations in immature cells. Frequently, dysplasia indicates an early neoplastic process, signaling the onset of potential malignant transformation. In[30], it was noted that aggressive esophageal squamous cell carcinomas developed through dysplasia or intraepithelial neoplasia. The transformation from normal epithelial tissues to potentially malignant states is converted gradually. Squamous cell carcinomas, often representing a later stage in this progression, are usually preceded by a phase of epithelial dysplasia. In[31], epithelial dysplasia was categorized into distinct stages based on the severity of cellular abnormalities, classifying these stages as low-grade, moderate, and severe, as shown in

figure 2. This classification categorizes epithelial tissue based on the severity of abnormal cell changes and tissue structure. By identifying the stage of dysplasia, doctors can better assess and manage these changes. The classification framework helps predict the potential for the condition to progress and guides the selection of suitable treatment options.

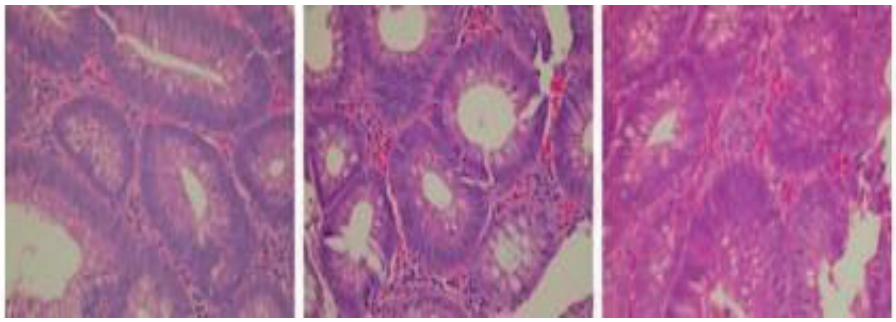

Figure 2. A gradation in the extent of cellular atypia and architectural disorganization within the epithelial tissue

As reported in[24], a diverse stream of epithelial dysplasia types was meticulously examined. These include a tubular adenomatous polyp with maximum stage dysplasia, two tubular adenomas with moderate stage dysplasia, tubular adenomatous dysplasia, one tubular adenomatous polyp with minimum stage dysplasia, three tubular adenoma polyps with minimum stage dysplasia, tubular villous with mitigated stage dysplasia, tubular adenoma with minimum stage dysplasia, tubular adenoma with mitigated dysplasia, two serrated adenomas with minimum stage dysplasia, and villous adenoma with minimum stage dysplasia. In[32], various epithelial dysplasia manifestations presented abnormalities in epithelial cells, different from normal mucosa. Normal tissue and dysplastic changes should be distinguishable for accurate diagnosis. Investigating stages and types of dysplasia provides insights into lesion progression and potential for malignancy. An overview of techniques used in analyzing histopathological images, focusing on automation of diagnosis and quantitative analysis, was also illustrated.

Quantitative Histopathological Image Analysis

The analysis of histopathological quantitative images is important to provide a well-structured overview of the research and techniques applied to histology tissue images from the disease diagnosis and grading perspective. In[33], the work revealed several techniques to analyze the histopathological images that help analyze tissue images to diagnose or grade diseases. This complexity and variability require sophisticated analysis methods to accurately interpret the cellular and tissue structures in the histopathological images. In[34], image analysis can enhance the quality control of histological sections, aiding in accurate interpretation and reducing recuts. For specific diagnoses like Invasive Ductal Carcinoma (IDC) in breast cancer, spatial recurrence analysis methodologies leveraging machine learning techniques have shown promising results, achieving high detection performances.

The research of[35] shows that the key aspect of histopathological image analysis is color normalization, particularly vital for images with uneven histopathological staining. Color discrepancies in stained images offer challenges in histopathological image analysis. This requires further discussion of the methods employed to standardize the color in images, addressing the challenges posed by variability in staining processes. Color normalization ensures consistency across images, enhancing subsequent analyses' reliability. Several methods indicated in[36], such as stain normalization, aim to standardize colour appearance for accurate analysis. Different stain normalization techniques like Macenko and Vahadane methods were proposed to enhance model performance in classifying metastatic tissue slides. Additionally, it was confirmed in[37] that utilizing multiple slides to construct a representative reference for color normalization has shown promising results in improving computational pathology robustness and integrity. Color stain normalization plays a crucial role in tasks like image retrieval, where differences in colorization can impact the accuracy of analysis. In summary, color normalization techniques are vital for enhancing the reliability and effectiveness of histopathological image analysis.

Methods for Analyzing Microscopic Histopathology Images

Image preprocessing, segmentation, and morphological analysis are traditional image processing techniques that can be replaced/integrated with the DL approaches in terms of complexity for a cancer diagnosis. DL is rapidly becoming the leading method for analyzing microscopic histopathology images due to its high accuracy and ability to handle complex tasks.[38] However, traditional techniques still have a place, especially for situations with limited data or a need for interpretable results. Noise reduction, contrast enhancement, and stain normalization are the initial steps to prepare the image for analysis. Segmentation isolates objects of

interest such as cytoplasm, nuclei, or specific tissue structures) from the background. Classification and/or diagnosis can be achieved using thresholding, edge detection, and watershed.[39] DL architecture is particularly well suited for image analysis. CNNs can learn complex patterns directly from the image data, eliminating the need for manual feature extraction. They excel at tasks like tissue classification for normal or abnormal. Also, the disease prognosis can be identified to predict the types of cells.[40]

In summary, DL is the leading method for analyzing microscopic histopathology images to guarantee accuracy in medical image diagnosis due to its ability to handle complex tasks, as shown in table 1. However, traditional techniques still have a place, especially for situations with limited data or a need for interpretable results. Extracting meaningful data from the images can be achieved by quantitative analysis.[41] This involves the assessment of tissue, the measurement of cellular features, and the quantification of staining patterns. The integration of these quantitative measures into the diagnostic process aids in the development of more standardized and reproducible diagnostic criteria.

Classification techniques for histopathological images

Histopathological image analysis can handle large-scale, high-density images and extensive databases. To address this, many researchers have turned to machine learning algorithms, which can be broadly categorized into supervised and unsupervised learning methods. These approaches are crucial in managing and interpreting the vast amounts of data generated in histopathological studies.

Traditional methods combine depth with efficient computation and result interpretation from feature contributions analysis. The approach requires extensive manual feature development work but struggles to identify advanced image changes properly. At present, deep learning methods deliver precise results and enhance the management of image complexities, and they automatically extract features during end-to-end learning processes, starting from raw image inputs and continuing to diagnosis outputs. Implementing these methods faces limitations because they both require extensive datasets and expensive computational resources.

In[42], SVM was used in histopathological image analysis. This technique involves manual labelling of the images to train the classifier, which then applies this learned knowledge to new labels and unseen tissue regions in slide images. On the other hand, unsupervised learning, such as clustering algorithms, does not require prelabeled data and instead identifies patterns and structures within the data independently. In[43], unsupervised classification was illustrated, and the K-means clustering algorithm was employed, followed by a dimensionality reduction technique, to extract texture features in renal histopathological samples. SVM methods have been extensively evaluated in the processing of digital histopathological images. SVM is a popular supervised classifier algorithm in this field. Researchers such as the work introduced in[44] and[45] employed SVM classifiers to distinguish between normal and abnormal histology tissue cells. SVMs' ability to handle high-dimensional data makes them particularly suitable for analyzing complex histopathological images. In[46], the SVM was used to diagnose specific conditions, such as differentiating adenocarcinoma from benign carcinoma in histopathological images. SVM provided accurate and reliable diagnostic results on various histopathological concepts. In summary, supervised and unsupervised machine learning algorithms are prominent in histopathological image analysis. Their ability to process and analyze large datasets accurately makes them indispensable tools in modern pathology, enhancing the diagnosis and understanding of various diseases at the tissue and cellular levels.

METHOD

The proposed method focuses on automating epithelial dysplasia diagnosis based on histopathology images using a combination of image processing techniques and machine learning algorithms. Key techniques include image restoration, feature extraction, and deep learning (DL). Image segmentation isolates regions of interest (ROIs) within tissue samples, such as individual cells or cell clusters. Feature extraction quantifies various aspects of these regions, including shape, size, texture, and color. Convolutional Neural Networks (CNNs) are then employed to analyze these features and identify potential pathological changes, classifying them into diagnostic categories such as benign or cancerous.

The methodology is structured into distinct phases, each contributing to the accurate detection and analysis of tissue images, as illustrated in figure 3. The main stages of the proposed technique include image segmentation, feature extraction, DL based analysis, and classification, ensuring a comprehensive and precise diagnostic process. Quantitative analysis involves statistical and computational tools to extract data from images, measure cellular features, assess tissue architecture, and quantify staining patterns, thereby enhancing the diagnostic criteria.

Data Acquisition and Preprocessing

A large collection of high-quality histopathological images encompassing normal and dysplastic epithelial tissues was collected from the Pathology Department at the Jordan University Hospital. This dataset comprises representatives of various severities and types of dysplasia. The dataset includes 500 digital images classified

into 300 normal and 200 with dysplastic epithelial tissues of various levels, as samples shown in figure 4. The levels are classified into adenomatous polyps with high-grade dysplasia, adenomatous polyps with moderate-grade dysplasia, and adenomatous polyps with low-grade dysplasia. The data is annotated with manual label regions of interest (ROIs) within the images, specifying areas with normal and dysplastic epithelium that are considered crucial for training the deep learning model. Also, to ensure consistency within the dataset, color normalization, sharpening filter, and noise reduction, shown in figure 5, are applied using a fuzzy filter. After applying this step, the result is shown in figure 6, which illustrates the clear difference between the input and output images. In microscopic histology images, the fuzzy filter is very helpful for removing noise based on our experiments. By considering the nearest data to remove the noise, the fuzzy filter was employed because of its ability to perform edge preservation. It distinguishes between local variations of noise and image structures. The result of the previous step is then converted into a grayscale mode to reduce the computational requirements and to prepare for the segmentation step. This step is important as a preprocess for the next phase, which applies an adaptive threshold represented in equation (1).

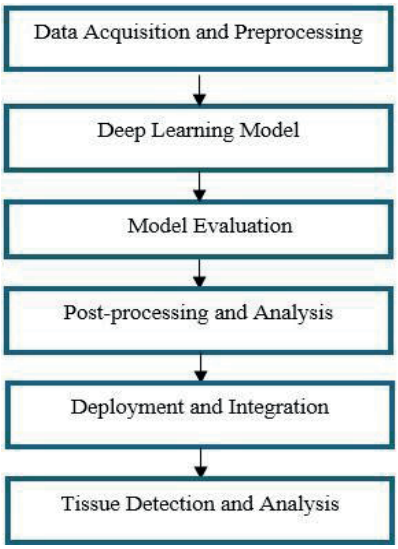

Figure 3. The flow chart of the proposed methodology

$$T(x,v) = \{\ 1 \quad if\ I(x,y) > T(x,y)\ 0 \quad otherwise \qquad (1)$$

Where T (x, y) is the threshold value at pixel (x, y).

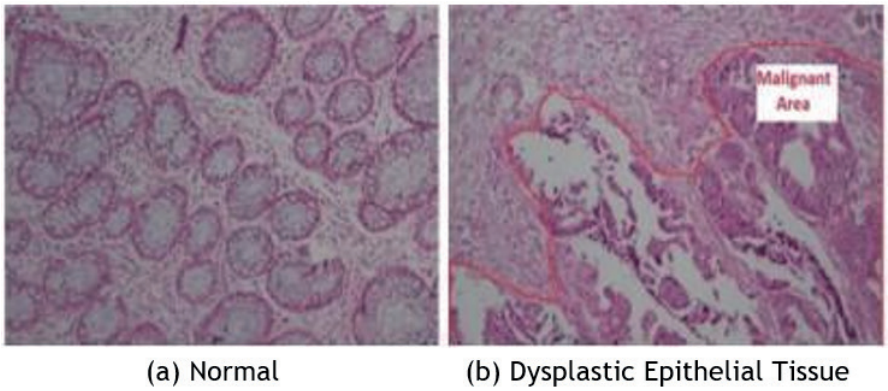

Figure 4. Microscopic images of (a) normal, and (b) dysplastic epithelial tissue samples

Almost all cameras produce soft images, as though digital images of microscopic tissue images are considered soft as well.[1] There is a need to sharpen the image. This can be applied using the shock filter, as shown in figure 7. It was selected because it is ideal for applying it locally in either the dilation or erosion process, depending on whether the pixel belongs to the influence zone of a maximum or a minimum. This is the case in epithelial dysplasia images where there is variation in the image structure. As indicated in[47], applying the Shock filter enhanced the image and produced a sharp discontinuity called shock at the borderline between the objects and the background. Microscopic specimens can be hard to see clearly due to low contrast. This is because they don't absorb light well, leading to blurry differences between the object and background. Histogram equalization[48] adjusts image brightness for better contrast.

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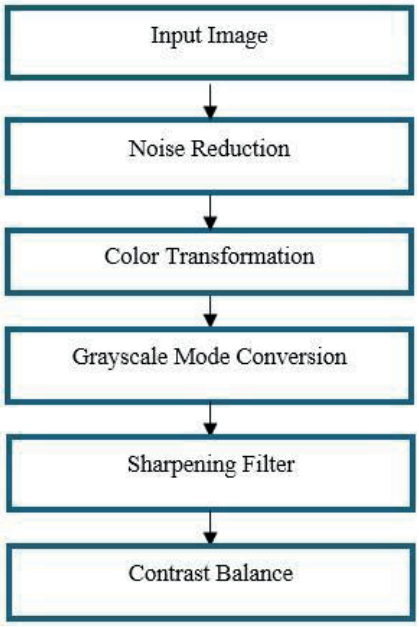
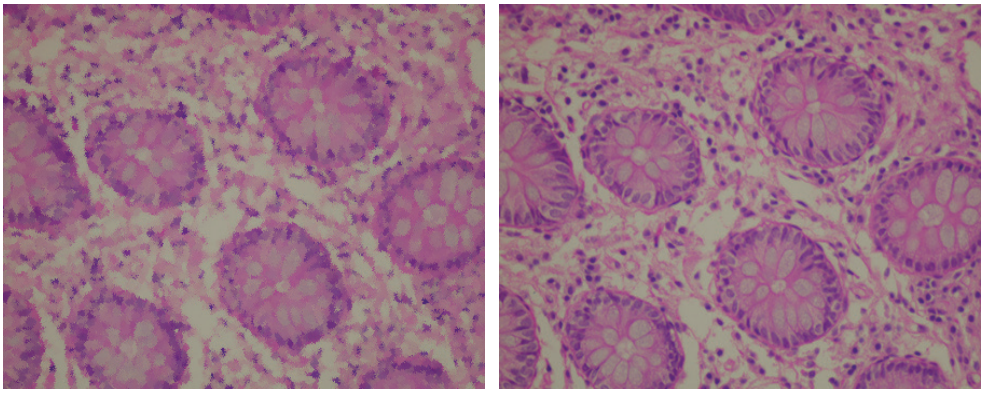


Figure 5. Preprocessing stage



(a) Poor quality image of normal mucosal glands, (b) Image restoration after applying noise reduction, color transformation, and image scaling

Figure 6. The results (a) before and (b) after the preprocessing

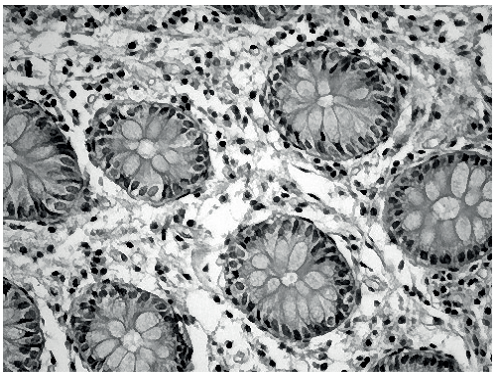


Figure 7. The performance of the shock filter

Deep Learning Model

Convolutional Neural Networks (CNNs) are particularly well-suited for this task. As indicated in[49], CNNs offer several advantages over traditional methods for analyzing microscopic histopathological images, particularly in detecting and classifying epithelial dysplasia. Popular choices include VGG16, ResNet, or even custom architectures designed for medical image analysis. Convolution is the essential operation of CNNs in which a kernel (filter) is applied to the input image to produce the output feature map. Mathematically, it can be written as shown in equation (2):

$$F(I * K, x, y) = \sum \quad \sum \quad I(m - x, n - y)K(m, n) \qquad (2)$$

Where *I* is the input image, K is the kernel, m and n are the width and height of the input image, respectively, and (x,y) is the coordinate of the feature map.

This operation helps the network learn small local patterns of the image, such as edges, textures, and many more spatial hierarchies within the image. After this operation, an activation function is applied to impose nonlinearity in the model so that complex, higher-level patterns may be learned. The ReLU activation is one of the most commonly used activation functions in CNNs, which can be written in equation (3):

$$F\ (x, y)\ =\ Max(0, x) \qquad (3)$$

ReLU activation helps address the vanishing gradient problem and allows the model to converge faster by only passing positive values through the network.

The labeled datasets are divided into training, validation, and testing sets. The training set is used to train the model, the validation set helps finetune hyperparameters to prevent overfitting, and the testing set evaluates the final model performance. These represent abstract concepts or objects within the image and are learned by the later convolutional layers. They are often task-specific and depend on the training data. The CNN model is then trained based on the training set using the labeled ROIs. This involves feeding the images into the network and adjusting its internal parameters (weights and biases) to accurately differentiate between normal and dysplastic tissues based on the provided labels. The hyperparameters are finetuned using learning rate, optimizer settings, and number of training epochs to optimize the model's performance and prevent overfitting (learning patterns specific to the training data that don't generalize well to unseen images).

Model Evaluation

The model's performance was assessed based on the testing set using metrics like accuracy and F1Score. The accuracy metric measures how well the model can correctly identify normal and dysplastic tissues using equation (4). True Positives (TP) represent correctly classified dysplastic images, True Negatives (TN) represent correctly classified normal images, and Total Images is the total number of images in the testing set. While high accuracy is desirable, it might not be the most informative metric in imbalanced datasets (unequal numbers of normal and dysplastic images).

Where: TP: True Positives TN: True Negatives FP: False Positives FN: False Negatives.

$$Accuracy = (TP + TN)/TI \qquad (4)$$

Where: TI is the total images (TP + TN + FP + FN)

The F1-Score metric provides a balanced view of precision and recall, combining them into a single score, as shown in equation (5), considering the False Positives (FP).

$$F1 - Score\ =\ 2\ *\ (Precision\ *\ Recall)/(Precision\ +\ Recall) \qquad (5)$$

Where:

$$Precision\ =\ TP/(TP\ +\ FP) \qquad (6)$$
$$Recall\ =\ TP/(TP\ +\ FN)$$

Data augmentation is applied to enhance the performance of the proposed method. The trained dataset is normalized based on the best matches of the structure similarity index (SSIM) used in[50] among the related group dataset by applying the equation (7). Normalization is applied based on the similarity of two images by integrating image contrast, structural difference, and brightness. The SSIM index combines three comparisons into a value between 0 (no similarity) and 1 (perfect similarity). Nested loops were applied to get the best match for each image.

$$SSIM(x, y)\ =\ [l(x, y)\ *\ c(x, y)\ *\ s(x, y)]\ /\ [L\ *\ C\ *\ S] \qquad (7)$$

Where: L,C, and S are stabilization factors to avoid division by 0.

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Postprocessing and Analysis

Morphological operation improves the accuracy of ROI segmentation within the images. A saliency map visualizes which image regions contribute most to the model's predictions. This step is crucial to identifying the proposed method's drawbacks and future work.

Deployment and Integration

The trained and validated model is integrated with the software system that was implemented using MATLAB. This involves creating a user interface for pathologists to upload images and receive automated results. Consequently, a robust deep learning-based system was developed and tested to automate detecting and analysing epithelial dysplasia in histopathological images. This can improve efficiency, accuracy, and consistency in diagnosing normal and dysplastic images.

RESULTS

Figure 8. Mucosal gland low-quality image (HEstain, 400X)

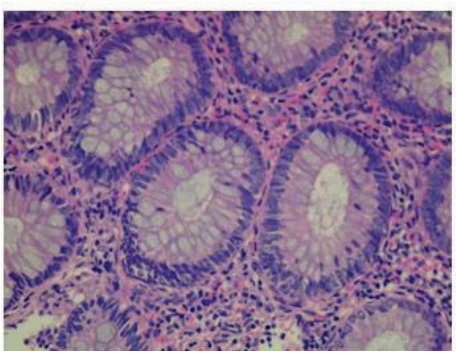

Figure 9. A low-grade dysplasia image

This study evaluated a deep learning model integrated with traditional image processing for detecting epithelial dysplasia in histopathological images. The model achieved many true positives (451 out of 500), correctly identifying many dysplastic images. However, there were also 30 false positives, where normal images were incorrectly classified as dysplastic. While the number of true negatives (19) indicates the model effectively identified some normal images, the low number suggests room for improvement in correctly classifying all normal tissues and the false positives (30). To gain a more comprehensive understanding of the model's performance, the F1Score was calculated, which considers both precision and recall. After substituting the values shown in equation (3), the Precision= 451 / (451 + 30) = 0,938. Recall metric measures the proportion of actual positive cases (dysplasia) that the model correctly identifies, and if it equals 451 / (451 + 50) = 0,902, then the F1-score will be equal to 2* (0,938 * 0,902) / (0,938 + 0,902) = 0,920. The high precision (0,938) indicates that the model is good at identifying true dysplasia cases, with only a small number of false positives (30). This suggests that the model effectively avoids misclassifying normal tissues as dysplastic, which is crucial to prevent unnecessary biopsies or procedures. The F1Score of 0,920 further reinforces this positive evaluation. It demonstrates a good balance between precision and recall, meaning the model performs well in identifying true positives and minimizing false positives and negatives (assuming a moderate number of False Negatives). While some samples appear low quality and inconspicuous, as seen in figure 8, the automated technique successfully diagnosed them. This is attributed to the preprocessing phase, which effectively enhanced these images. The proposed automated technique misdiagnosed three samples, all of which were cases of low-grade tubular dysplasia. Low-grade dysplasia exhibits subtle tissue changes compared to high-grade or moderate dysplasia, making it more

challenging for the algorithm to detect. Figure 9 illustrates an example of a low-grade dysplasia image that resulted in a false positive diagnosis.

Evaluation

The results of the proposed approach were compared with the competitive methods shown table 1. Traditional image processing and machine learning methods offer interpretable results and require less computational power. However, they often require manual feature engineering and may struggle with complex image variations, leading to lower accuracy in detecting epithelial dysplasia compared to deep learning approaches. Convolutional Neural Networks (CNNs) excel in this task, achieving superior accuracy and handling image complexity effectively. However, they necessitate large datasets for training and can be computationally expensive. Additionally, CNNs are often considered "black boxes" making it challenging to understand their decision-making process.

Table 1. Comparison table summarizing the characteristics of various methods for detecting epithelial dysplasia in histopathological images

Method	Advantages	Disadvantages
Traditional Image Processing + Machine Learning	Interpretable results Computationally efficient	Lower accuracy compared to deep learning. Requires feature engineering expertise
Support Vector Machines (SVM)	Good performance for some datasets	May struggle with complex image variations
Convolutional Neural Networks (CNNs)	High accuracy	Requires large datasets for training
The Proposed Method	High accuracy Handles image complexity	Requires large datasets for training

Ensemble learning approaches can improve accuracy by combining multiple models, but they introduce additional complexity and require careful selection and training of individual models. As explained in table 2, the results reveal that the proposed approach has outperformed the related works in Precision, Recall, and F1Score, respectively. The table demonstrates a clear trend: Deep learning-based methods outperform traditional image processing and machine learning approaches in epithelial dysplasia detection.

Table 2. Comparison table summarizing the performance of various methods for detecting epithelial dysplasia in histopathological images

Method	Precision	Recall	F1Score
Traditional Image Processing	0,750	0,770	0,791
Support Vector Machines	0,830	0,820	0,850
CNNs	0,910	0,891	0,912
Ensemble Learning	0,920	0,895	0,918
The Proposed Approach	0,938	0,902	0,920

The traditional image processing method achieves a moderate F1Score of 0,791. While it offers interpretable results, it might struggle with complex image variations, leading to lower accuracy than deep learning approaches. SVMs show improvement over traditional methods with an F1Score of 0,850. However, they may struggle with highly diverse image data. CNNs significantly outperform previous methods, achieving an F1Score of 0,912. Their ability to learn complex features from data makes them well-suited for this task. Ensemble Learning combines multiple models (potentially including CNNs) and yields an F1Score of 0,918, comparable to CNNs alone. However, this approach can be more complex and computationally expensive. The proposed method achieves the highest F1Score of 0,920 and has a slightly higher recall (0,902) compared to other methods; it maintains a high precision (0,938), indicating a good balance between identifying true positives (dysplasia) and minimizing false positives (normal tissues misclassified as dysplastic).

CONCLUSIONS

DL and image processing techniques were integrated to have highly accurate rates in detecting epithelial dysplasia images. The proposed model reveals promising results with a high F1Score, suggesting a good balance between precision and recall. However, further analysis with a larger dataset and investigation into false negatives can provide future work research to identify potential areas for improvement. The results confirm

the benefits of the DL method, particularly CNNs, in its accuracy in the detection of epithelial dysplasia. The proposed method demonstrates promising results, achieving the best overall Precision, Recall, and F1Score. Future work requires additional datasets to improve the model's ability to differentiate between normal and abnormal dysplastic tissues. Also, analysing the types of images causing false positives and negatives can help identify areas for improvement in the model or data preprocessing techniques. Also, Adapting the proposed method for broader cancer detection.

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CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

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