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AUTOMATIC SEGMENTATION OF COLON CANCER USING SAM AI

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SUMMARY

The third most prevalent form of cancer globally in both men and women is colon cancer which affects the digestive tract and occurs in the human body's greater intestine develops from certain polyps are tiisues that grow inside the colon of various sizes which at later stage can develop into a cancer cell. The tissues are taken from colon using biopsy method and cured. Under a microscope, histopathology images are categorised as a manual screening of colon the study tissue. Size of the nucleus and form of the glands are accepted standards for identifying colon cancer cells. The images obtaimed using colonscopy are converted into gray scale images where feature extraction done by conventional techniques and classified. To improve diagnosis methods for processing images and AI characteristics are also used. The automatic thresholding approach known as Otsu's Method, image thresholding, image enhancement, and edge detection techniques are used in the many processing procedures for an image. The SAM AI model is utilised to extract the malignancy characteristic of colon cancer. For the diagnostic images, metrics like resolution and peak signal to noise ratio are acquired.

Key words: *artificial intelligence, SAM AI, otsu's method, grey-level slicing, automatic thresholding, edge detection.*

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INTRODUCTION

Colorectal cancer ranks as the third most prevalent diagnosis and the second deadliest disease for individuals of both genders. According to WHO data, around 1.9 million new colorectal cancer cases are anticipated globally in 2020, leading to over 930,000 deaths. Significant regional variations in incidence and mortality rates were observed. The highest incidence rates were found in Europe, Australia, and New Zealand, with Eastern Europe reporting the steepest fatality rates. By 2040, it is projected that the annual incidence of colorectal cancer will rise to 3.2 million new cases (a 63% increase) and 1.6 million deaths (a 73% increase). Recently, the number of cancer patients has surged due to various factors, including poor dietary habits, smoking, obesity, heredity, age, and others. In rare cases, it can be inherited from parents through their genetic material. Colon cancer is a form of tumor that develops within the colon or rectum, which are parts of the large intestine in the digestive system

[1]. Colorectal cancer can be diagnosed by several methods, like colonoscopy, biopsy, and colon capsule endoscopy (CCE), a safe and effective way to recognize polyps and colorectal cancer. AI is a powerful tool that holds significant potential for replacing traditional methods in the detection of colon cancer [2]. We employ the Segment Anything model (SAM) and digital image processing to classify colon images. Capturing images is the first step in image processing, a method that involves gathering data from various domains. Images were taken from The Cancer Genome Atlas which offers images for different types of cancers [16]. Histopathology images are used to analyze and assess tissue ailments using a microscope. Images of the size is 768×768 are in JPEG format. Image quality is measured using comprehensive reference measures such as MSE (Mean Square Error)-[3] It is a popular full-reference picture quality indicator; lower values imply higher quality. The average squared deviation between the estimated and real picture is measured, which takes into account both the estimator's bias and variance [4]. PSNR (Peak Signal to Noise Ratio) compares signal strength to noise in dB. Lossless compression methods and human perceptual approximations are the most commonly used for image compression. Utilizing a logarithmic scale and the peak-to-MSE ratio, higher PSNR values (30-80 dB) correspond to higher quality. Recently, further complete reference measures called SSIM (Structured Similarity Indexing Method) - Using structural information changes, such as brightness and contrast masking, SSIM assesses the quality of images. Variants include 3-SSIM, which emphasizes the role of edge areas in perception, and MS-SSIM, which evaluates similarity at many scales have emerged, in contrast to MSE and PSNR [5]. This study primarily focuses on comparing several image quality criteria to provide a holistic view. Image processing techniques to detect malignancies linked with colon cancer in histopathology pictures [6] [12]. For feature extraction and segmentation, [17] we look specifically at the Otsu approach, Power law, and Edge detection filters such as Sobel and Roberts. With the help of these kinds of filters, we hope to uncover essential traits such as Bizzare nuclei- This tumor has aberrant histologic characteristics, including uneven forms, varying diameters, hyperchromatism, and irregular chromatin distribution. Its abnormal nuclei have been linked to several diseases, including malignancy. This tumor is sometimes misdiagnosed as leiomyosarcoma [7]. Prominent nucleus **-** A visible nucleus under a microscope shows an active cell doing major biological activities such as DNA replication or protein synthesis, which aids in cell identification and categorization. Vesicular nucleus **-** Actively synthesizing or proliferating cells have vesicular nuclei, also known as open-phase nuclei, which have prominent nucleoli, a lot of nucleoplasm, and not much chromatin material. Usually, a DNA-containing nucleolus is found in the centre of it.

Proliferation **-** Proliferation is the reproduction or multiplication of cells by division, which is essential for tissue development and repair [10]. Abnormal proliferation is a characteristic of cancer. Atypical mitotic figure **-** An atypical mitotic figure is anything other than the standard form of normal mitosis, which includes anaphase bridge, multi-polar, ring, scattered, asymmetrical, and lag-type mitoses. Pleomorphism **-** Pleomorphism is the variety in the form and structure of cells or organisms within a species, which includes the capacity to change shapes or forms over the life cycle or under different environmental conditions [7]. Stratification **-** Biological structures, tissues, or populations can be categorized or organized according to their positional hierarchy through the use of layers or strata, which is known as stratification. It appears as stratified tissue, which is made up of many layers of epithelial cells. In cellular analysis N-C ratio is a quantitative metric that represents morphological traits that can change in both normal and pathological circumstances [8]. Context is important in evaluating this ratio because it is only one factor examined by pathologists and histologists, which are important indications of malignancy in colon cancer [20].

METHODOLOGY

The diagnosis of colorectal Cancer performed the image processing algorithms for good accuracy and resolution for the identification of Vesicular nucleolus, Hyper chromatic nuclei, Nuclear cytoplasmic ratio, Abnormal Mitotic division, Proliferation, Stratification, Bi-Nucleation, Multi-nucleation, Prominent double nucleus, cytoplasm contains mucin, Cells Elongation, Atypical Mitotic figures. The algorithms performed are Power Law Transformation, [9] Grey-level Slicing, Otsu's Method, Roberts, Sobel, Thresholding. For noise reduction and unique identification of cancer using Segment Anything Model it is an AI model used for the Separation of tumour characteristics. Figure 1 shows tthe schemetatic diagram of the work carried in this paper below.

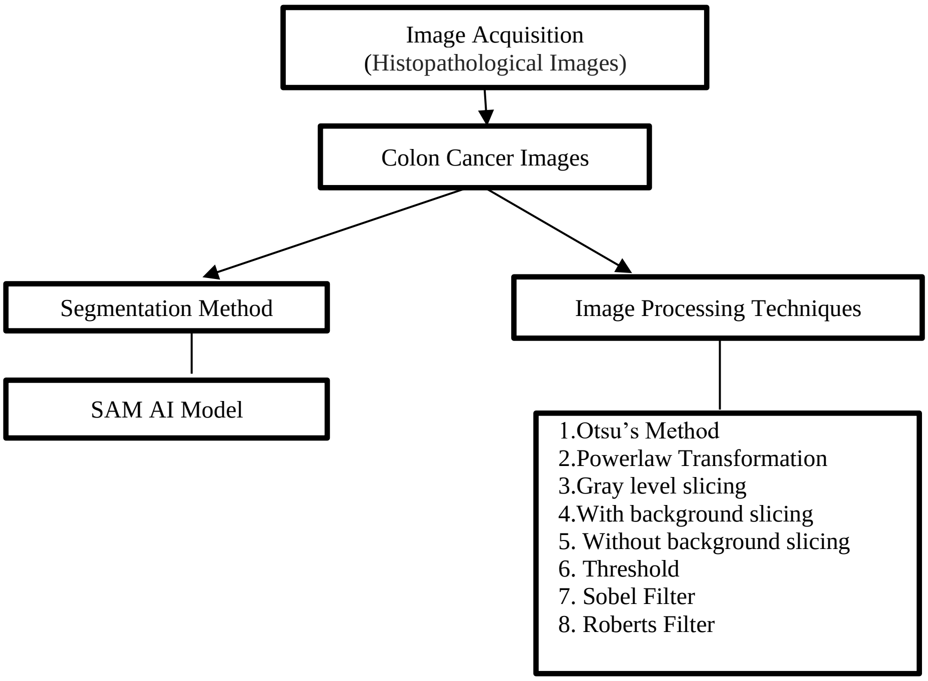


Figure 1. Schemetatic diagram of the work carried in this paper

ALGORITHM

Power Law Transformation

An Enhancing method of image processing algorithms for different types of display areas of an image which adjusts the numerical values like pixel of an image. The numerical value is termed as gamma. By changing the value of gamma in a transformation the feature of Bi - nucleation, Multi-nucleation and Prominent double nucleus are enhanced clearly [18] the gamma value is 1.1.

$$s=cr\gamma \tag{1}$$

Where, c is any constant and r, s are normalized input and output pixel values. Let c=1 then s in equation (1).

Gray-Level Slicing

Image threshold is a method in image processing that highlights a specific range of gray levels in an image. This pixel value of this ranges from 0 (black) to 255 (white). With background and without background methods are used in equation (2).

$$s = L-1 \text{ for } a < r < b \tag{2}$$

Here, a and b define some specific range of gray levels. with background slicing, it displays the background of an image at a high range of 255 (white) and the original gray level values in other areas, so that feature of abnormal mitotic division, the nucleus having bi-nucleation and multi-nucleation. The prominent double nucleus is the feature of malignancy. The background information is discarded fully. After the feature of abnormal mitotic division only shown.

Threshold

Threshold is a simple and effective method for splitting an image into foreground and background. Type of picture segmentation method. Adjust the pixel size for easy examination. Extract the area of the image that contains all of the information. Here, the hard-thresholding method is used. Pixels with an intensity less than the threshold T are set to zero, whereas pixels with an intensity greater than the threshold are set to 255 or kept unchanged, depending on the desired effect. It will get a binary image. The threshold value, t, is determined to be 120 to 160. 160 is chosen to show off the features of colon cancer, such as aberrant mitotic division, bi-nucleation and multi-nucleation, and the vesicular nucleus equation (3) [11].

$$\text{If } f(x, y) > T \text{ then } f(x, y) = 0 \text{ else } f(x, y) = 255. \quad (3)$$

Otsu's Method

This approach reduces intra-class variance, often known as the weighted sum of the variances of two classes. It uses a histogram and probability for each intensity level. The histogram works quite well. It follows a bimodal distribution, with a deep and abrupt valley between the two peaks. The grayscale histogram of a picture is used to establish an appropriate threshold value that divides the foreground and background regions with the greatest inter-class variance. The equation stated earlier illustrates Otsu's Method, functioning like a histogram to highlight the clear valleys in the problematic areas of an image [19].

Sobel Filter

Edge detection methods in image processing. The Sobel kernel relies on center differences but provides more weight to the core pixels when averaging. Applying two 3*3 convolutional filters called kernels to the first derivatives of Gaussian kernel.

$$Gx = (a2 + 2a3 + a4) - (a0 + 2a7 + a6) \ \& \ Gy = (a6 + 2a5 + a4) - (a0 + 2a1 + a2) \quad (4)$$

The above two equations (4) are partial derivates of the Sobel operator. The characteristics of colon cancer, including the boundary of the vesicular nucleus and the contours of irregular mitotic division.

Roberts Filter

Edge detection filters in image processing detect edges based on applying a horizontal and vertical filter in order. These two filters are convolution filters in the form [13]. Calculates the difference between adjacent pixels. The Roberts filter is in practice, too small to reliably, find edges in the presence of noise.

SAM AI

The Segment Anything Model (SAM) is an image segmentation method developed by Meta AI it is based on foundation models that had a significant impact on NLP. And focuses on promptable segmentation tasks. By merely clicking or interactively choosing which points to include or remove from an object, [14] SAM is able to segment objects. Using a polygon tool, you may also make segmentations by segmenting regions or bounding boxes, and the tool will snap to the object. When SAM cannot positively identify the item to be segmented, it can generate numerous valid masks. SAM can automatically recognize every object in a picture and create a mask for it. SAM allows, real-time interaction with the project by instantaneously providing a segmentation mask for every prompt once the image embedding have been pre-computed [15].

RESULT AND DISCUSSIONS

In the field of computer vision, the Segment Anything Model (SAM) represents an important change. This leading-edge instance segmentation model displays an incredible ability for carrying out demanding image segmentation tasks with unprecedented correctness and adaptability. Although useful in certain contexts, earlier models frequently required a great deal of retraining in order to adjust to novel or varied tasks.SAM constitutes an innovation in computer vision, making these models more flexible and efficient. Workflow Diagram of Segment Anything Model AI and Image 1-Vesicular Nuclues, Image 2-Hyper Chromatic Nuclei, Image 3- Stratification, Image 4-Pleomorphisim shown in Figure 2, 3, 4, 5, 6. The Performance Metrics shown in Table 1, 2, 3, 4.

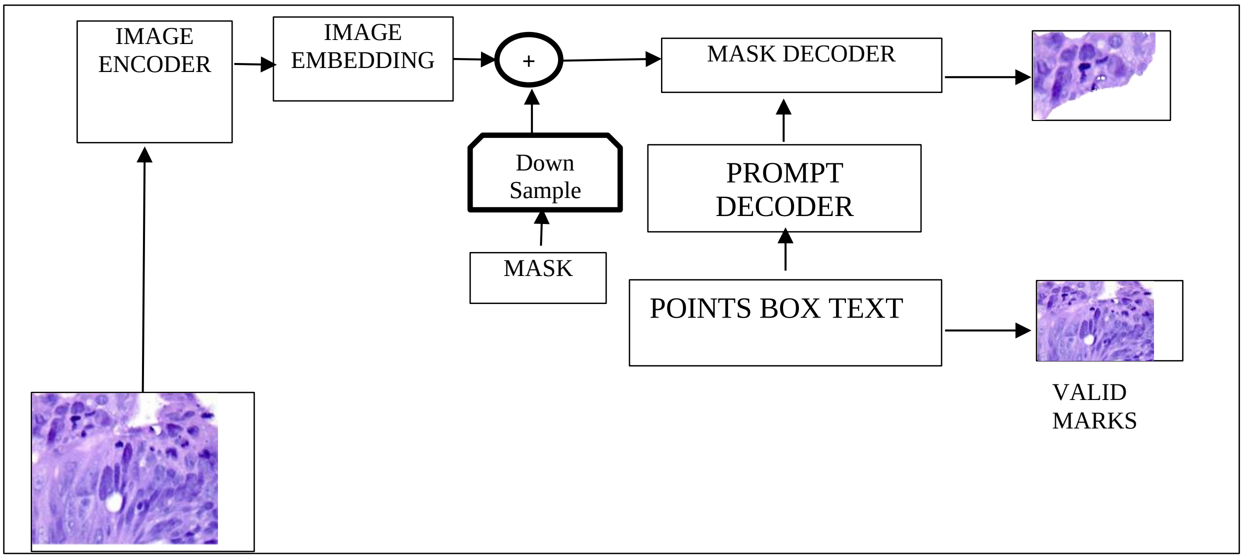
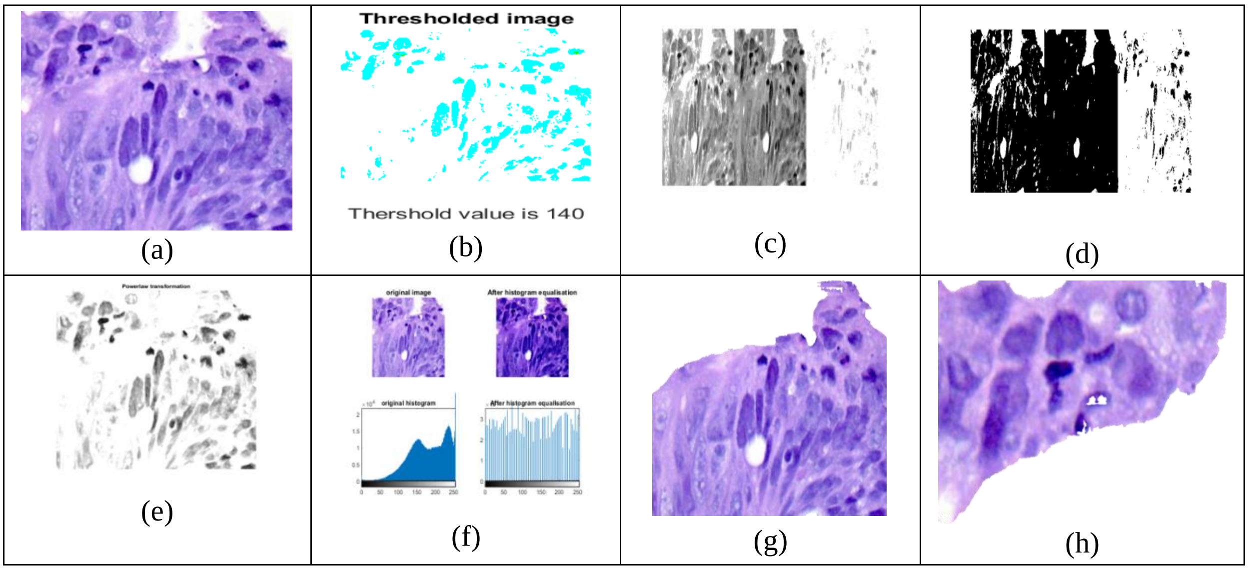


Figure 2. Workflow Diagram of Segment Anything Model AI

Image 1-Vesicular Nuclues



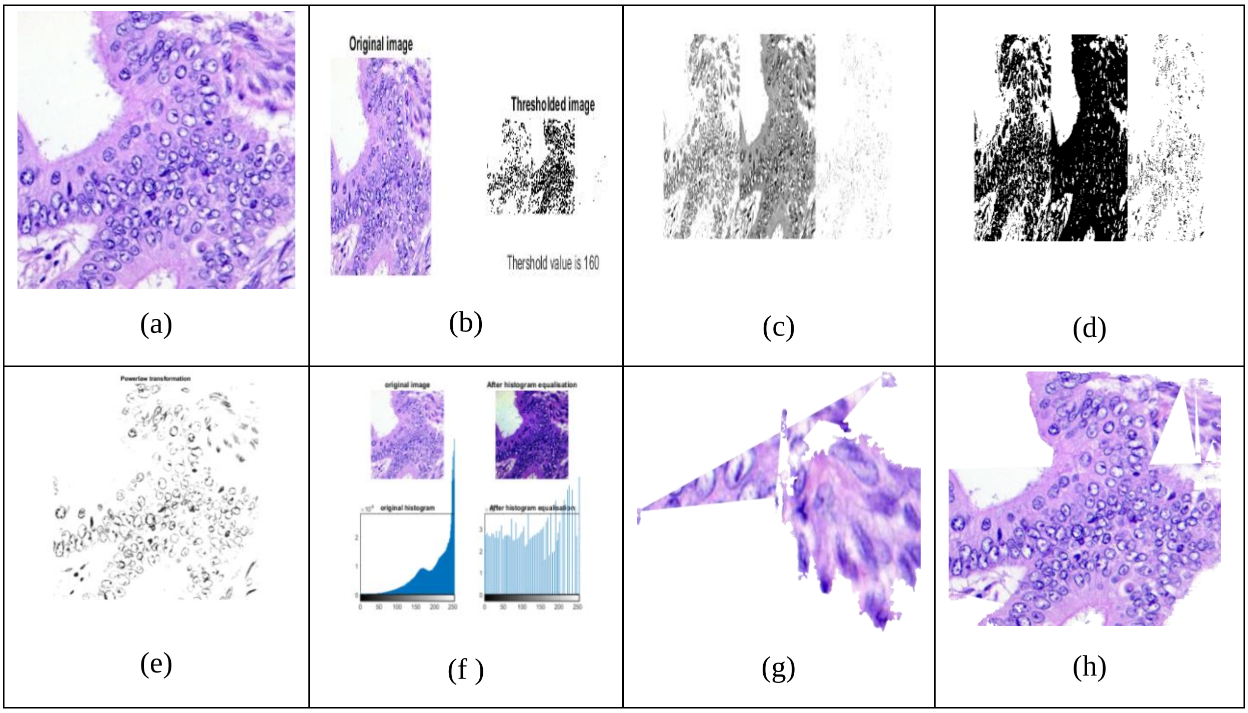
(a) (b) (c) (d) (e) (f) (g) (h)

Figure 3. (a) Original Image (b) Threshold Image (c) With Background slicing (d) Without Background Slicing (e) Power Law Transformation (f) Otsu’s Method (g) Abnormal Mitotic Figure (h) SAM AI of Vesicular Nucleus

Table 1: The Performance Metrics of Image 1Vesicular Nucleus

Image 1	**Resolution**	**PSNR**	**MSE**	**SSIM**
Original Image	0.589	34.2027	24.7064	0.9910
Threshold	0.0679	19.8942	666.286	0.8330
With background	0.328	27.8561	109.5303	0.9049
Without background	0.328	19.626	708.623	0.8645
Power Law Transformation	0.415	29.3284	75.8998	0.9486
Otsu’s Method	0.235	18.4482	929.5301	0.8351
Roberts filter	0.415	21.3314	478.5651	0.8684
Sobel filter	0.415	20.0645	640.6612	0.8284
Abnormal Mitotic figure	0.587	34.5252	22.9380	0.9940
Vesicular Nucleolus	0.151	31.0047	51.5952	0.9869

Image 2-Hyper Chromatic Nuclei



(a) (b) (c) (d)

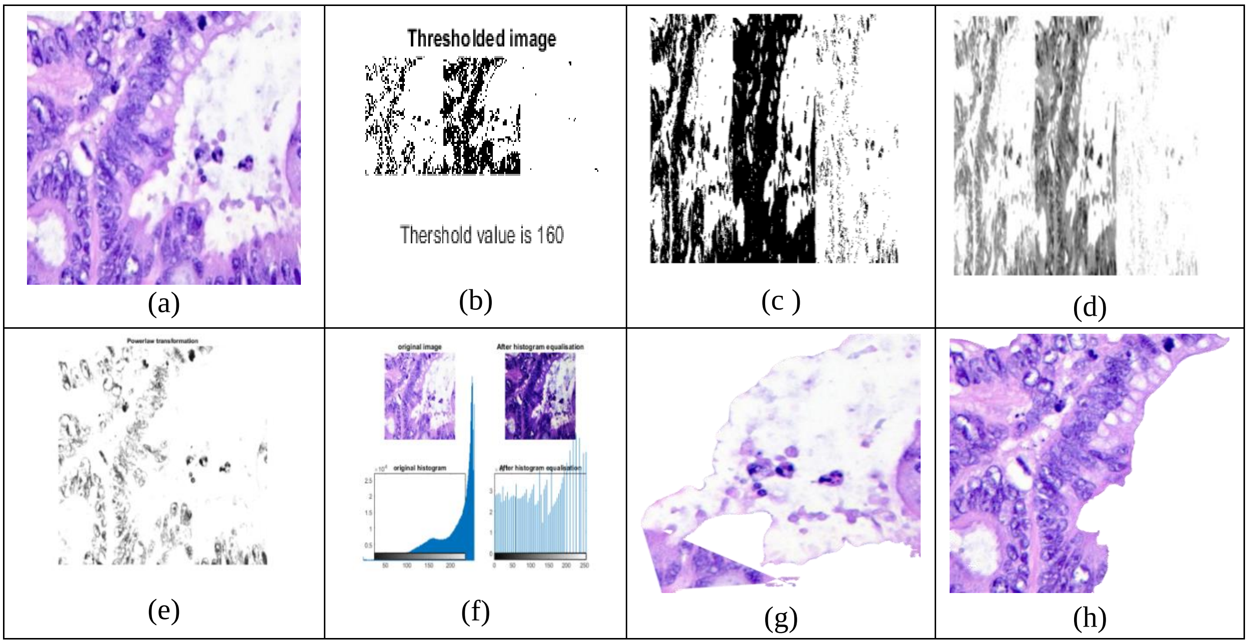
(e) (f) (g) (h)

Figure 4. (a) Original Image (b) Threshold Image (c) With Background slicing (d) Without Background Slicing (e) Power Law Transformation (f) Otsu's Method (g) Epithelial Cells Figure (h) SAM AI of Hyper Chromatic Nuclei

Table 2: Performance Metrics of Segmented Hyper Chromatic Nuclei

Image 2	**Resolution**	**PSNR**	**MSE**	**SSIM**
Original Image	0.589	32.1666	39.4839	0.9820
Threshold	0.235	21.6108	448.7432	0.9157
With background	0.328	25.1098	200.4914	0.8510
Without background	0.328	0.0164	1.4859	0.0008
Power Law Transformation	0.415	27.3771	118.9506	0.9325
Otsu's Method	0.235	18.2163	980.5027	0.8105
Roberts filter	0.415	19.4591	736.5042	0.8352
Sobel filter	0.415	18.3397	736.5042	0.7907
Epithelial cells.	0.119	29.9827	65.2844	0.9827
Hyper-chromatic nuclei	0.589	29.6350	70.7256	0.9832

Image 3- Stratification

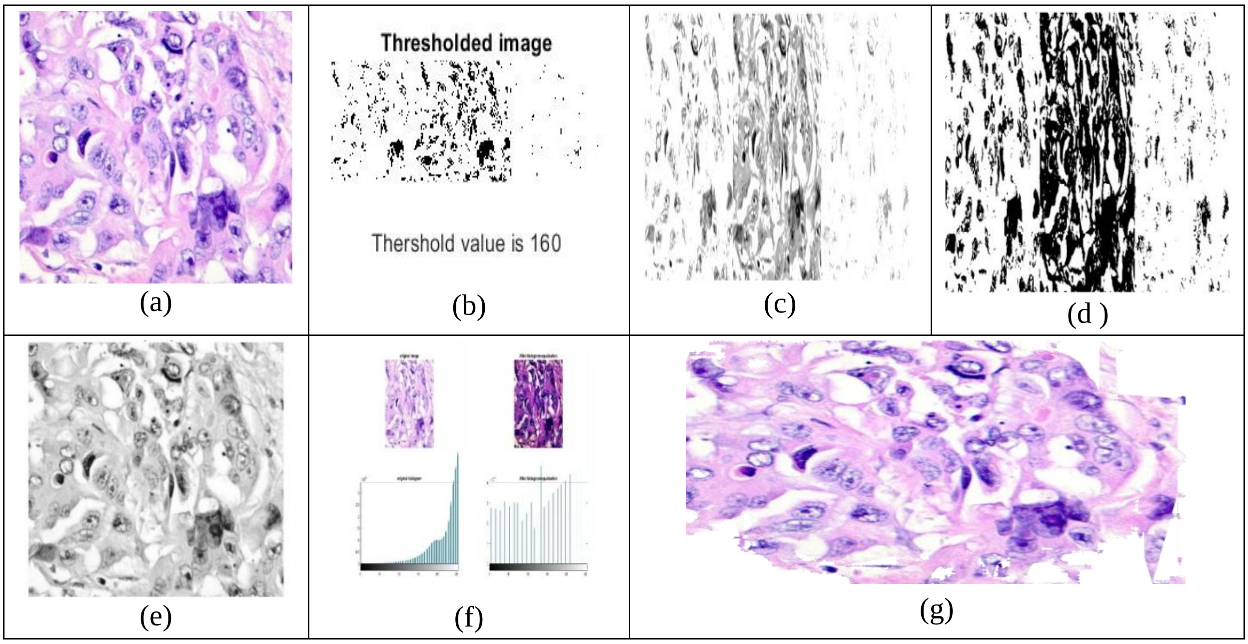


(a) (b) (c) (d)

(e) (f) (g) (h)

Figure 5. (a) Original Image (b) Threshold Image (c) With Background slicing (d) Without Background Slicing (e) Power Law Transformation (f) Otsu's Method (g) Gland Variation in size and shape (h) Stratification

Image 4-Pleomorphisim



(a) (b) (c) (d)

(e) (f) (g)

Figure 6.(a) Original Image (b) Threshold Image (c) With Background slicing (d) Without Background Slicing (e) Power Law Transformation (f) Otsu's Method (g) SAM AI of Pleomorphism

Table 3. Image metrics for stratification

Image 3	**Resolution**	**PSNR**	**MSE**	**SSIM**
Original Image	0.5898	33.4844	29.1501	0.9862
Threshold	0.2352	22.7200	347.5969	0.9243
With background	0.3287	26.4125	148.5356	0.8791
Without background	0.3287	0.0178	1.0824	0.0008
Power Law Transformation	0.4150	28.5319	91.1774	0.9450
Otsu’s Method	0.2352	18.3525	950.2339	0.8127
Roberts filter	0.4150	20.2570	612.8871	0.8414
Sobel filter	0.4150	18.8696	843.5605	0.7927
Gland variation	0.3694	32.9264	33.1464	0.9859
Stratification	0.4815	33.1763	31.2929	0.9912
Vesicular nucleus	0.0131	28.8330	85.0701	0.9721

Table 4. Performance Metrics of Pleomorphism

Image 4	Resolution	PSNR	MSE	SSIM
Original Image	0.5898	32.6197	35.5723	0.9808
Threshold	0.3675	24.2352	245.2203	0.9314
With background	1.2662	18.7307	870.9757	0.8746
Without background	0.3513	26.4292	147.9651	0.8794
Power Law Transformation	0.3675	31.1749	49.6122	0.9667
Otsu’s Method	1.7779	20.4238	589.7960	0.8640
Roberts filter	0.8377	19.0621	806.9918	0.8357
Sobel filter	0.8387	19.0621	806.9918	0.8357
Pleomorphism	0.02856	29.5422	72.2533	0.9789

CONCLUSION

In this work, four histopathological images of colon cancer were taken. Image enhancement method, Image segmentation methods for Abnormal Mitotic, Pleomorphism, Vesicular nucleus, and Hyper-chromatic nuclei. Peak-to-signal-Noise-ratio, Mean Square Error Metric, and Structural Similarity Index have been discussed. It has been found that the Segment Anything Model performs very well and the data shows the performance metrics of algorithms performed in this paper. The Performance and the details obtained are compared with conventional methods of Image Processing Methods. Medical image analysis is now more efficient because of the automatic segmentation of colon structures and lesions made possible by the integration of sophisticated algorithms and machine learning techniques like the Segment Anything Model. This approach also reduces the need for manual involvement. This enhances the repeatability and dependability of the results in addition to expediting the diagnostic procedure.

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