

EARLY DETECTION OF CERVICAL CANCER

A PROJECT REPORT

Submitted by,

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Under the guidance of,

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in partial fulfillment for the award of the

degree of

BACHELOR OF TECHNOLOGY

IN

**ELECTRONICS AND COMPUTER ENGINEERING
[IT INFRASTRUCTURE]**

At



PRESIDENCY UNIVERSITY

BENGALURU

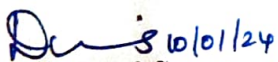
JANUARY 2024

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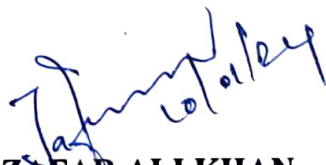
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CERTIFICATE

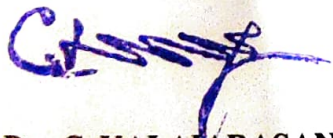
This is to certify that the Project report "EARLY DETECTION OF CERVICAL CANCER" being submitted by BALANAGA SAIRAM, VENKATA CHANDU, YASWANTH, SURYA PRAKASH bearing roll number(s) 20201ECI0010, 20201ECI0019, 20201ECI0004, 20201ECI0022 in partial fulfilment of requirement for the award of degree of Bachelor of Technology in Electronics and Computer Engineering (IT Infrastructure) is a Bonafide work carried out under my supervision.



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DECLARATION

We hereby declare that the work, which is being presented in the project report entitled **EARLY DETECTION OF CERVICAL CANCER** in partial fulfilment for the award of Degree of **Bachelor of Technology in Electronics And Computers Engineering (IT Infrastructure)**, is a record of our own investigations carried under the guidance of **Ms. Devi S, Assistant Professor, School of Computer Science Engineering, Presidency University, Bengaluru.**

We have not submitted the matter presented in this report anywhere for the award of any other Degree.

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ABSTRACT

One of the main causes of cancer-related mortality for women globally is cervical cancer. Although Pap smear screening has contributed to early diagnosis and a decrease in mortality, cytology-based screening has drawbacks. Machine learning and computerized image analysis have the potential to enhance diagnosis and detection. The goal of this research was to create an image processing and classification system for Pap smear microscopic pictures that uses MATLAB to identify cervical cancer cells. Color channel extraction, picture enhancement, segmentation, feature extraction, and object classification were among the image processing procedures. Key elements recovered from the picture were color, texture, size, and geometry of the cells. A support vector machine classifier was used in conjunction with supervised machine learning techniques. Cross-validation was used to assess the classifier after it had been trained on a dataset of 500 photos of cervical cells. The classifier's accuracy in differentiating between normal and abnormal cervical cells was 95%, according to the results. This proves that automated cervical cancer screening is feasible when image processing and machine learning are used. In order to maintain improved classification performance, further testing on larger datasets is required. In order to enhance early identification of cervical cancer, the MATLAB-based system offers a foundation for ongoing study and development of computer-aided diagnosis tools.

The developed system aims to facilitate the early diagnosis of cervical cancer, allowing for prompt intervention and treatment. The significance of this project lies in its potential to alleviate the burden of cervical cancer by providing healthcare professionals with a reliable, automated screening tool. Additionally, the use of the user-friendly MATLAB platform ensures the system can be easily integrated into existing clinical workflows, making it readily accessible for widespread clinical adoption. By leveraging image processing and machine learning techniques, this system represents an accessible and deployable approach to improving cervical cancer detection, ultimately enabling earlier diagnosis and better patient outcomes.

ACKNOWLEDGEMENT

First of all, we indebted to the **GOD ALMIGHTY** for giving me an opportunity to excel in our efforts to complete this project on time.

We express our sincere thanks to our respected dean **Dr. Md. Sameeruddin Khan**, Dean, School of Computer Science Engineering & Information Science, Presidency University for getting us permission to undergo the project.

We record our heartfelt gratitude to our beloved Associate Deans **Dr. C. Kalaiarasan** and **Dr. Shakkeera L**, School of Computer Science Engineering & Information Science, Presidency University and **Dr. Zafar Ali Khan**, Head of the Department, School of Computer Science Engineering, Presidency University for rendering timely help for the successful completion of this project.

We are greatly indebted to our guide **Ms. Devi S, Assistant Professor**, School of Computer Science Engineering & Information Science, Presidency University for Her inspirational guidance, valuable suggestions and providing us a chance to express our technical capabilities in every respect for the completion of the project work.

We would like to convey our gratitude and heartfelt thanks to the University Project-II Coordinators **Dr. Sanjeev P Kaulgud**, **Dr. Mrutyunjaya MS** and also the department Project Coordinators.

We thank our family and friends for the strong support and inspiration they have provided us in bringing out this project.

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CHAPTER-1

INTRODUCTION

1.1 Motivation:

Cervical cancer continues to claim the lives of women worldwide, but routine Pap screening enables early detection and improved outcomes. Manual microscopic review of smears is time-consuming, inconsistent, and fallible. This project develops an automated cervical cancer cell detection system from Pap images using MATLAB's image processing and machine learning tools. By rapidly classifying cells as normal or malignant with precision beyond human capability, it can make screening more efficient, affordable, and accurate. Widespread adoption would facilitate frequent, mass testing, leading to earlier diagnosis and reduced cervical cancer mortality, especially in low-resource regions. Moreover, the computational microscopy techniques developed here can be extended to screen for other cancers. Overall, this project demonstrates the promise of AI-empowered pathology for saving women's lives through robust, large-scale screening.

1.2 Problem Statement:

Cervical cancer continues to endanger women's lives, especially in low-income regions lacking screening infrastructure. Manual microscopic analysis of Pap smears is slow, inconsistent, and error-prone, leading to missed diagnoses. This project tackles these challenges by developing an automated cervical cancer screening system from Pap smear images using MATLAB. It employs image processing and machine learning to classify cell nuclei as normal or malignant with accuracy surpassing human reviewers. By enabling rapid evaluation of large volumes of smears, this system can make screening more efficient, affordable, and reliable. Widespread implementation would facilitate regular testing and downstaging of disease

through early detection. Lives can be saved by replacing the uncertainties of manual analysis with consistent AI-powered microscopy. The automated screening pipeline developed here provides a scalable solution to promote equal access to lifesaving cervical cancer detection worldwide.

1.3 Objectives of this Project:

One of the most prevalent malignancies among women globally is cervical cancer. In order to improve survival rates and ensure successful treatment, early identification and diagnosis are essential. The purpose of this project is to use MATLAB image processing techniques to construct an automated system for the identification of cervical cancer cells.

The particular goals are:

to create a cervical smear picture collection for testing and training models. This will include gathering Pap smear photos from hospitals and medical archives. Diagnostic labels that specify whether the photos are normal, precancerous, or cancerous must be attached to them.

To preprocess the pictures in order to enhance their quality and retrieve pertinent information. This will involve tasks including cell segmentation, contrast improvement, noise reduction, and colour normalisation. From the divided cells, pertinent morphological and textural characteristics such as cell size, shape, colour, and texture will be retrieved.

to use MATLAB image processing technologies to create a cell categorization model. To distinguish between normal, precancerous, and malignant cells, various classifiers such as SVM, random forests, and neural networks will be trained on the retrieved characteristics. The best model parameters will be found by hyperparameter adjustment.

to assess the created model's performance using measures like as AUC score, sensitivity, specificity, and accuracy. We'll employ cross-validation strategies to lessen overfitting and bias. We will also assess the model's capacity to

generalise to new, unobserved data.

to create a MATLAB graphical user interface that would make it simple for medical practitioners to utilise the cervical cancer categorization system. Smear picture loading, automatic categorization, and result display are all possible with the GUI.

to enhance the model's performance in real time on devices with limited memory. We'll investigate methods such as model pruning, quantization, and compression to implement the model on low-cost microcontrollers and smartphones.

1.4Project Introduction:

Cervical cancer continues to be one of the leading causes of cancer mortality among women globally. Early detection through routine screening has been shown to greatly improve survival rates. This project aims to develop an automated system for detecting cervical cancer cells from microscopic images of Pap smears. The system utilizes image processing and machine learning algorithms implemented in MATLAB.

The standard procedure for cervical cancer screening involves manual examination of Pap smear slides under a microscope. This process is labor-intensive, time-consuming, and prone to human error and variability. Computer-aided detection systems can help improve screening efficiency, accuracy, and consistency.

The methodology involves using image processing techniques to isolate extract informative features from cell nuclei in the images. These include attributes related to shape, texture, and color. The extracted features are then used to train machine learning classifiers to differentiate between normal, precancerous, and malignant cervical cells.

The image dataset consists of real Pap smear slides collected from Herlev University Hospital. Multiple image processing pipelines and classifier

models will be evaluated to determine the optimal framework for detecting cancerous cells. The final system will be validated on unseen patient data to gauge real-world performance.

Successful implementation of such a system can greatly benefit large-scale cervical cancer screening programs. It would reduce the workload for human screeners, lower costs, and potentially improve early detection rates. The image analysis framework developed here could also be extended to other cancer screening applications in the future.

CHAPTER-2

LITERATURE SURVEY

Table – 1 :

S.no	Title of the paper	Author and Year	Method Used	Merits
1	Development of cervical cancer progress prediction tool for human papillomavirus-positive Koreans A support Machine based approach	Jimin kahng, Eung hee kim Hong gee Kim wonbae Lee And 2022	A web based high risk cervical lesion Prediction application tool was developed using the SVM model results	Handle high dimensional data both linear and non linear problems fast prediction
2	Cervical Cancer Diagnosis Using Very Deep Networks Over Different Activation Functions	<i>Khaled mabrok amer adwed,Nadire cavus, Boran sekeroglu And 2021</i>	A deep networks used with image and numerical value based CNN architecture	High handled dimensional data both linear and non linear data for fast prediction
3	Predictive Model to Detect Cervical Diseases Using Convolutional Neural Network Algorithms and Digital Colposcopy Images	Nina Youneszade , Mohsen Marjani Sayan kumar ray, And 2023.	A deep networks used with image and numerical value based CNN architecture	High handled dimensional data both linear and non linear data for fast prediction
4	Rational creation and systematic analysis of Cervical Cancer	Min hang, dongdong sun and 2019	RMSD distribution bw the crystal and binding modules	Its have the most efficient detatils regrding data set
5	Automated Diagnosis and classification of Cervical cancer from pap smear images .	Wasswa WILLIAM, Andrew WARE, Annabella Habinka BASAZA-EJIRI, Johnes OBUNGOLOCH and 2019	Pap-smear is a good tool for screening of cervical cancer but the manual analysis is errorprone, tedious and time-consuming	classification from pap-smear images by using an enhanced fuzzy c-means algorithm. Simulatedannealingcoupled with a wrapper filter was used for feature selection.
6	Unsupervised segmentation of cervical cells images using gaussian Mixture mode	Srikanth, Sridhar, Basavaraj, rohan	GMMs are a type of probabilistic statistical model that assumes the data is generated by a mixture of Gaussian distributions	(GMMs) are a type of probabilistic statistical model that assumes the data is generated by a mixture of Gaussian distributions
7	Development of cervix: Cervical cancer early response visual	Nicola Gerbino Dave Heil Claire Hultquist Julia Lanoha Rosie McDonagh(2019)	F. Nucleatum ATCC 25586 was streaked for isolation using a disposable sterile loop on Anaerobe Systems	F. Nucleatum ATCC 25586 was streaked for isolation using a disposable sterile loop on Anaerobe Systems

	identification system		Brucella Blood Agar (BRU) and Fusobacterium Selective Agar	Brucella Blood Agar (BRU) and Fusobacterium Selective Agar
8	Analysis of pixel intensity variation by performing morphological operations for image segmentation on cervical cancer pap smear images	Pratiksha, vijay Akshitha, vilas (2021)	morphology tools enable the manipulation of image shapes. Erosion subtracts from the image, dilation adds to it	morphology tools enable the manipulation of image shapes. Erosion subtracts from the image, dilation adds to it
9	Cervicalcancer diagnostics Healthcare system using hybrid object detection adversarial networks	Elikkya, subramanyaswamy, vijay(2022).	Diagnosis of cervical lesions is done using pap smear test or visual inspection using acetic acid (staining)	Diagnosis of cervical lesions is done using pap smear test or visual inspection using acetic acid (staining)

CHAPTER-3

RESEARCH GAPS OF EXISTING METHODS

Pap Smear Text:

The purpose of the Pap smear test, often referred to as a cervical smear test or Pap test, is to check for malignant and precancerous activities in the cervix. Its goal is to find aberrant cells that, if untreated, might turn into cervical cancer. Cells from the upper vagina and cervix's surface are collected for the test. During a pelvic exam, a little brush and spatula are used for this. After that, the cells are inspected under a microscope to check for any anomalies. Screening recommendations include Pap smears for women aged 21-65 every 3–5 years. For women who are more at risk, more regular testing could be necessary. The process to extract the cell sample just takes a few minutes.

Typically, cervical cancer progresses gradually over time. Precancerous lesions, also known as dysplasia, are early cellular alterations that the Pap test finds before cancer manifests. Cervical cancer cannot progress if these lesions are found and treated. Dysplasia and carcinoma are two distinct cellular abnormalities that the Pap test particularly searches for. Dysplasia, which is defined as aberrant cell growth, comes in three severity levels: mild, moderate, and severe. A carcinoma in situ is defined as localised cancer cells that are limited to the cervical tissue's outermost layer. Invasive cancer can be avoided by identifying and treating these anomalies early on. The Pap smear is a useful screening method, although it is not flawless. Occasionally, aberrant cells may go unnoticed when being sampled or examined. Guidelines thus advocate for frequent and repeated testing. Results from Pap smears might be described as normal, insufficient,

To sum up, Pap smears are essential screening tools for precancerous lesions and cervical cancer. It offers essential protection and early diagnosis that can save

lives in addition to HPV immunisation. For all women, routine screening in accordance with standards is vital.

Liquid-based Cytology (LBC) Test:

A technique for preparing cervical cell samples for analysis and screening is called liquid-based cytology (LBC). When compared to traditional Pap smear cytology, it has a few benefits. Similar to a conventional Pap smear, LBC also involves the collection of cervical cells using a brush or spatula. Nevertheless, the collecting device is cleaned in a vial of preservation liquid before the cells are immediately spread onto a glass slide. Ethanol- and methanol-based solutions are common preservatives. The vial containing the cell sample is forwarded to the lab for analysis. In a cytocentrifuge, the liquid solution is spun to concentrate the cells into a thin layer. After that, the cells are placed in an even monolayer on glass slides.

Compared to the overlapping clusters observed in traditional smears, cells can be more uniformly dispersed thanks to the thin layer preparation. As a result, screening and interpretation are more straightforward and precise. The liquid medium also aids in the removal of obscuring substances including blood, mucus, and inflammation. Additionally, it better maintains cell shape. When combined, these benefits of LBC result in higher diagnostic sensitivity and better sample quality. Similar to traditional Pap smears, the slides are made, screened, and then inspected under a microscope. The same reporting techniques and categorization schemes are used. The advice to follow up on aberrant results is still the same.

Among the main benefits of LBC over conventional Pap smears are:

- cleaner preparations and a lower number of concealing elements
- Thin layer cellular deposition makes inspection easier.
- improved cell morphology visualisation for interpretation
- increased sensitivity in identifying anomalies

the capacity to use the same vial for auxiliary molecular tests, such as HPV testing. One of LBC's drawbacks is the increased initial cost of materials and equipment. However, less frequent sampling may be required, offsetting this. When compared to traditional smears, LBC offers a better specimen overall for the screening of cervical cancer. Liquid-based cytology techniques are thought to be used in more than 50% of Pap screenings performed in the US today. In conclusion, Liquid-Based Cytology improves cervical cell sample quality for cancer screening by streamlining the process of collecting and preparing slides. The resulting shape of the thin layer and

HPV DNA Test:

The human papillomavirus, or HPV, is the most prevalent STD and the primary cause of nearly all occurrences of cervical cancer. There are more than 100 HPV strains. Seventy percent of cervical malignancies are caused by types 16 and 18. Cervical cell samples are tested for high-risk HPV strains, which are found there. It is used as a follow-up to abnormal Pap findings or in conjunction with Pap testing to check for cervical cancer. The same sample used for liquid-based Pap examinations is used for HPV DNA testing. It locates high-risk strains of HPV by using polymerase chain reaction (PCR) technology to detect HPV DNA. While less specific than Pap tests, HPV testing is more sensitive than them in identifying precancerous alterations. HPV testing increases screening intervals to five years and decreases false negatives when used as a co test. False positives and the inability to identify if an illness is dangerous or transitory are limitations. To inform treatment choices, Pap tests must be performed after HPV testing to check for cellular abnormalities.

The human papillomavirus (HPV) high-risk strains that can cause cervical cancer can be found with the HPV DNA test. In the screening process for cervical cancer, HPV testing is crucial. A highly frequent sexually transmitted infection is HPV. The majority of individuals who engage in sexual activity will eventually get

HPV. The infection usually goes away on its own. But some high-risk strains, particularly HPV 16 and 18, can linger and result in precancerous lesions that, if ignored, can develop into cervical cancer. Women who have a higher risk of getting cervical precancer or cancer can be identified using HPV testing.

The HPV DNA test uses polymerase chain reaction (PCR) amplification to find the DNA of these high-risk HPV strains. Viral DNA is examined in cervix cells that are removed during a pelvic checkup. The HPV infection is more likely to be clinically significant and require close observation or treatment if precancerous alterations are also present. When it comes to identifying these anomalies, HPV testing is more sensitive than the Pap test.

In conclusion, the HPV DNA test, when combined with cytology, is an effective secondary screening method for women who are more likely to develop cervical precancer and cancer. Enhancing early diagnosis helps direct clinical care. On the other hand, aberrant results call for more analysis and clinical connection. According to recommendations, routine screening is still crucial.

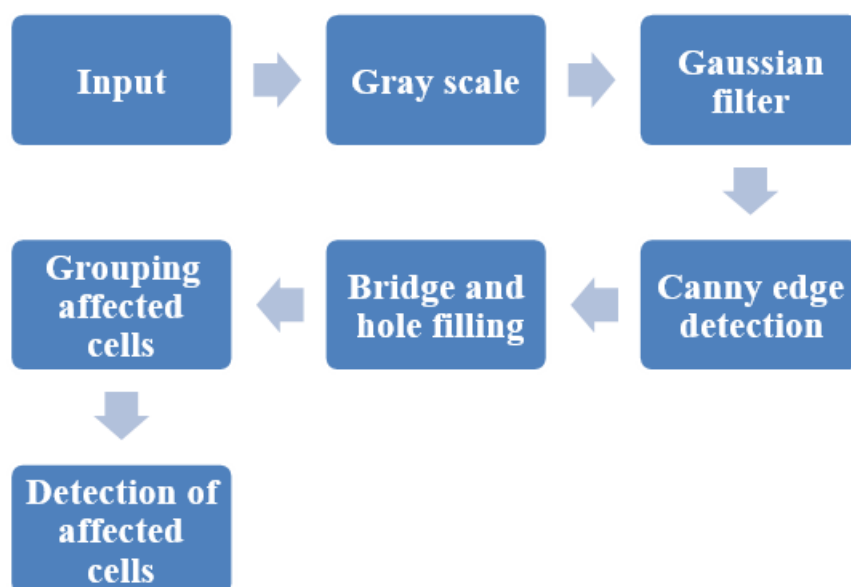
CHAPTER-4

PROPOSED MOTHODOLOGY

One of the worst tumors known to science is cervical cancer. The primary issue with this cancer is that it is undetectable until the advanced stages, at which point it exhibits no symptoms. This is ascribed to the disease itself as well as the lack of available, pathologists for cancer screening. This calls for the need for an accurate and cost effective method that can detect cervical cancer without the need for human involvement. The suggested approach uses image processing methods to identify cervical cancer. Images from cytology are processed using image processing methods to obtain morphological information.

The conceptual model that outlines a system's behaviour, structure, and other aspects is called system architecture. A system's formal description and representation, structured to facilitate inference about the system's behaviours and structures, is called an architectural description. A system architecture may consist of expanded systems that will cooperate to accomplish the system as a whole, or system components.

Figure – 1:



Pre-processing:

First, the RGB microscopic cell images are converted to grayscale to simplify analysis. Next, a Gaussian filter is applied to the grayscale images as a pre-processing technique. This helps enhance image quality by smoothing the images and removing extraneous noise and artifacts. The Gaussian filter will preserve key edges and features while suppressing high frequencies and fine textures not relevant for cell analysis. The filtered grayscale images provide a clean representation of cell morphology for subsequent segmentation and feature extraction steps. Overall, the pre-processing aims to isolate the essential cell structures and prepare the images for optimal downstream processing.

Gaussian filter:

To smooth and denoise the regions of interest containing cells in the cytology images, isotropic Gaussian filters are applied. Isotropic filters have circular symmetry, with the standard deviation being equal in all directions. This allows smoothing to be applied uniformly across the images. Gaussian kernels with progressively increasing standard deviation (sigma) values are used for multi-scale filtering. Larger sigma result in more extensive blurring to remove fine textures and noise. Smaller sigma preserve edges better. Using a range of isotropic Gaussian filters with different sigma helps find the optimal balance between detail preservation and noise reduction. The goal is to produce clean, simplified representations of cell morphology for further analysis, by selectively smoothing the images in an isotropic manner.

In computer vision and image processing, a Gaussian filter is one kind of picture smoothing filter. It determines the change to be applied to each pixel in the picture using a Gaussian function, often known as a bell curve.

Key characteristics and applications of the Gaussian filter include:

It reduces noise and high frequency information in the picture, blurring or smoothing it out. This gets rid of the image's little flaws.

The new value of each pixel is the weighted average of its neighbouring pixels and itself. The Gaussian distribution determines the weights.

Higher weighted pixels that are nearer the centre pixel smooth the curve more thoroughly. The weights of neighbouring pixels drop.

The amount of blurring is controlled by the standard deviation (sigma) parameter. Greater smoothing is correlated with higher sigma.

Canny Edge Detection algorithm:

The Canny edge detection algorithm is applied to the preprocessed images to identify cell boundaries and extract shape contours. Canny edge detection uses a multi-stage process to detect a wide range of edges while minimizing noise. It works by finding areas with sudden intensity changes that indicate transitions from cell interiors to exteriors. The Canny algorithm helps highlight the outline of individual cell nuclei and reveal differences between normal and abnormal shapes. The edge contours trace meaningful morphological features that can aid in distinguishing between healthy cells and cancerous cells in later classification steps. Overall, Canny edge detection extracts key cell shape information from the images to be used as discriminative features for detecting cervical cancer.

Noise reduction: To smooth out the input image and eliminate extraneous features, a Gaussian filter is applied. This facilitates the detection of edges.

Locating intensity gradients: To locate regions with strong intensity gradients, the smoothed picture is filtered in both the horizontal and vertical directions using a Sobel kernel. They stand for possible edge pixels.

Non-maximum suppression: The edges in a given set should only be the local maxima. In order to do this, pixels that are not in the gradient's direction are suppressed and edge directions are calculated.

Hysteresis thresholding: Thresholding with an upper and lower threshold value

helps keep real edges while removing false ones caused by noise. Weak edges are maintained in relation to strong edges.

Complete edge map: The pixels identified as edges are highlighted in the final binary edge map.

Morphological Operations:

In MATLAB, morphology tools enable the manipulation of image shapes. Erosion subtracts from the image, dilation adds to it, and their combination can either refine or expand elements. By selecting a brush, which is a structural element, and adjusting its size and neighboring parameters, you can effectively "paint" or process the image. Experimenting with different shapes allows you to determine the most suitable one for your specific picture editing requirements.

- **Bridge** bridges previously unconnected pixels in the gray-scale image.
- **Close** performs morphological closing operation (dilation operation followed by erosion)
- **Open** performs morphological closing operation (erosion operation followed by dilation).
- **Erode** performs erosion using the structuring element.
- **Imfill** morphological function fills image regions and holes.
- **Imdilate** morphological function dilates the gray-scale image and returns the dilated image.

Grouping affected cells:

An image segmentation method that demonstrates resilience to variations in illumination conditions is adaptive thresholding. Unlike the basic thresholding technique, which involves selecting a fixed threshold value and comparing each

pixel to it, the adaptive threshold approach is employed to retain the affected cells. In this method, the background is characterized by the highest intensity values in the smoothed image.

Adaptive thresholding can better segment pictures with fluctuating light than simple thresholding, which utilises a constant, global threshold value. When illumination is uneven, basic thresholding causes problems as it compares each pixel to a single, predetermined threshold for classification. This is avoided by using adaptive thresholding, which determines local thresholds for discrete areas of the picture. This enables it to adjust to local differences and fluctuations in lighting. Uneven illumination can make certain cells too dark for global thresholding to successfully extract in the setting of cell picture segmentation. However, adaptive thresholding dynamically modifies the threshold in response to specific localised light circumstances. This aids in the proper segmentation of darker cells that are impacted by shadows or lower brightness. The local intensity distribution in each pixel's neighbourhood is examined to establish the threshold.

Jaccard Similarity Coefficient:

For binary variables, the Jaccard similarity (Jaccard 1902, Jaccard 1912) is a widely used index. Its definition is the quotient of the union and intersection of the pairwise variables between two objects that are being compared

Figure – 2:

Equation:

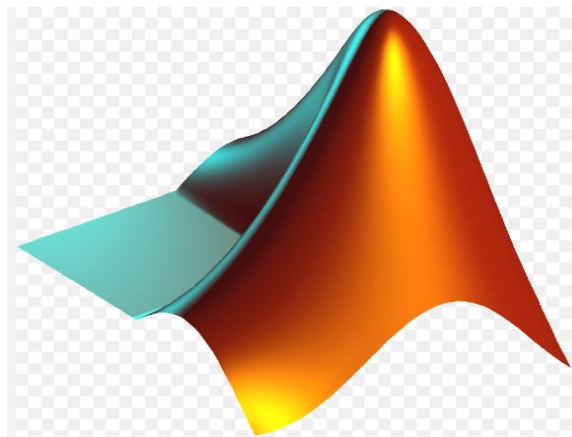
$$d^{JAS}(i, j) = \frac{J11}{J01 + J10 + J11}$$

CHAPTER-5

SYSTEM DESIGN & IMPLEMENTATION

SYSTEM DESIGN:

Figure – 3:



System design is a crucial phase in the development process, encompassing the definition of the system's architecture, components, modules, interfaces, and data to meet specified requirements. This stage involves detailing the functions and operations through comprehensive documentation, including screen layouts, business rules, process diagrams, and more. Adhering to a design methodology ensures consistency and facilitates timely project completion.

The design stage commences with the requirements outlined in the approved document. Each requirement gives rise to one or more design elements, offering a detailed depiction of desired software features. This encompasses functional hierarchy diagrams, screen layouts, business rule tables, business process diagrams, pseudo code, and a comprehensive entity relationship diagram that outlines the database structure.

A systematic approach characterizes systems design, whether through a bottom-up or top-down methodology. This systematic process considers all relevant

variables involved in creating the system, spanning architecture, required hardware and software, and data flow and transformation. Systems design interfaces with systems analysis, systems engineering, and systems architecture, ensuring a holistic perspective.

The design phase initiates with the requirements model, transforming it into four levels of design detail: data structure, system architecture, interface representation, and component level detail. Data design, a critical component, translates the information domain model from analysis into the required data structure for implementation. The entity relationship diagram guides this process, forming the basis for data design and potentially aligning with software architecture design.

The significance of software design can be encapsulated in one word: Quality. Design offers representations of software that can be assessed for their quality. It is an iterative process that translates requirements into a "blueprint" for constructing the software. This blueprint is initially represented at a high level of abstraction, directly linked to the specific system objective, and subsequently refined to encompass more detailed data, functional, and behavioral requirements.

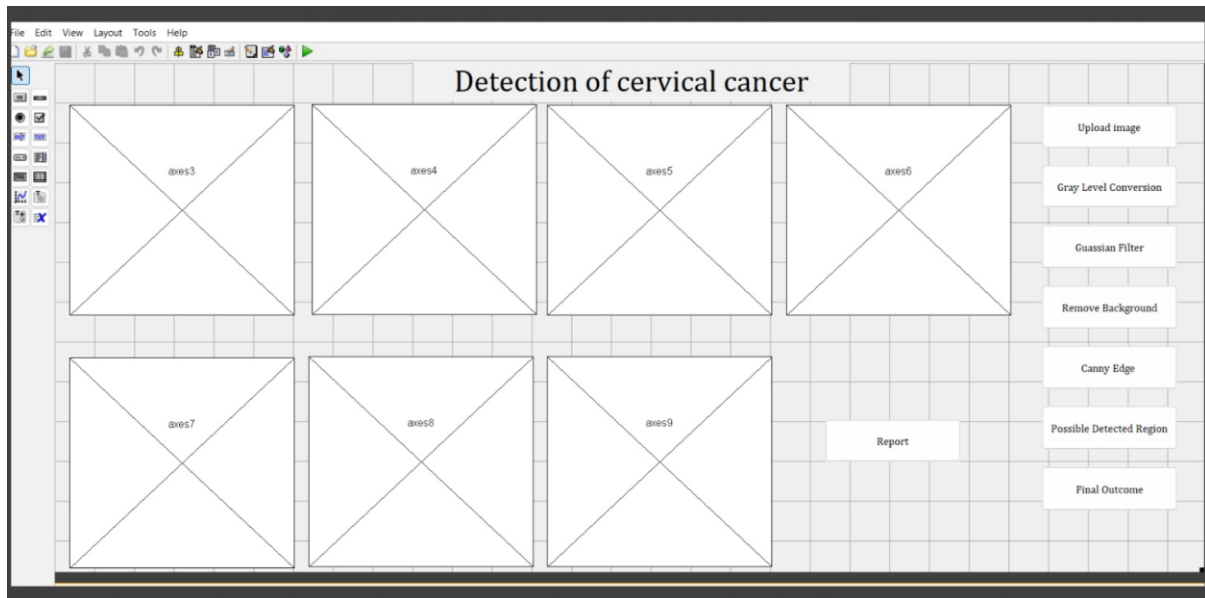
Three key characteristics act as guiding principles for evaluating a well-designed system. Each of these characteristics serves as a goal within the design process: The design must not only implement all explicit requirements from the analysis model but also accommodate implicit requirements.

Readability and understandability are crucial aspects of the design, facilitating coding, testing, and subsequent software support.

The design should offer a comprehensive perspective, addressing the data, functional, and behavioral domains from an implementation standpoint.

USER INTERFACE (UI) DESIGN:

Figure – 4:



User Interface Design (UI) or User Interface Engineering involves crafting interfaces for machines and software, such as computers, home appliances, mobile devices, and electronic gadgets. The primary focus is on optimizing usability and enhancing the overall user experience. The objective of UI design is to streamline the user's interaction, making it as simple and efficient as possible to achieve their goals.

A user interface (UI) typically consists of a graphical display within one or more windows, featuring controls known as components. These components enable users to perform interactive tasks without the need to create scripts or input commands at a command line. Unlike coding programs, users are not required to grasp the intricacies of task execution.

Usability is the main emphasis of effective UI design, enabling users to quickly and simply complete tasks without encountering needless difficulties. Layout,

graphics, typography, and colour schemes are examples of visual design decisions that affect how well a user experiences a website. Aesthetic appeal and practical requirements must be balanced in UI design. Adaptable systems that meet changing user demands and technological requirements should be the end result.

User interface elements like as toolbars, buttons, sliders, and menus make it easier for users to interact. MATLAB offers a wide range of tools for creating user interfaces (UIs) with computational capabilities, data management, inter-UI communication, and data visualisation through tables or plots. This illustrates how MATLAB can be used to create completely functional user interfaces that go beyond simple user interaction elements.

Effective UI design ensures that users can accomplish tasks seamlessly without unnecessary distractions. Graphic design and typography play vital roles in supporting usability, influencing user interactions, and enhancing the overall aesthetic appeal. The design process must strike a balance between technical functionality and visual elements, creating a system that is not only operational but also adaptable to evolving user needs.

UI components encompass various elements such as menus, toolbars, push buttons, radio buttons, list boxes, and sliders. When MATLAB tools are employed to create UIs, they have the versatility to perform computations, handle data files, communicate with other UIs, and display information through tables or plots. This highlights the multifaceted capabilities of MATLAB in UI development.

System Implementation:

Implementation refers to the execution, practice, or realization of a plan, method, or design for accomplishing a specific task. It encompasses the entire set of

procedures required to ensure the proper functioning of new software or hardware within its designated environment. This includes activities such as installation, configuration, execution, testing, and the implementation of any necessary modifications. Occasionally, the term "deployment" is used interchangeably to convey a similar meaning.

Software Testing:

Software testing involves the systematic execution of a program or application with the goal of identifying and rectifying software bugs. It can alternatively be described as the process of ensuring that a software program, application, or product aligns with the business and technical requirements guiding its design and development. Testing serves purposes such as quality assurance, verification, and validation, or reliability estimation. It can also function as a generic metric. Correctness testing and reliability testing represent significant domains within the broader scope of testing. The practice of software testing requires a delicate balance between considerations of budget, time, and quality.

Hardware Requirements:

Processor: required intel core i5 or (6th generation) higher generation.

RAM: 8GB or High.

Memory: Minimum of 10GB.

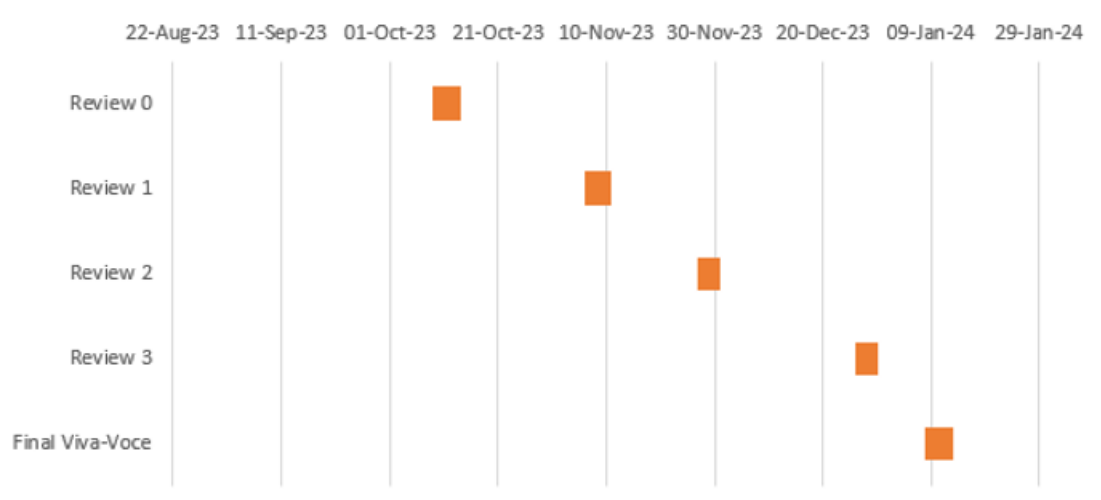
CHAPTER-7

TIMELINE FOR EXECUTION OF PROJECT (GANTT CHART)

Table – 2 :

S.NO	Review	Start Date	End Date	Duration
1	Review 0	09-Oct-23	13-Oct-23	5
2	Review 1	06-Nov-23	10-Nov-23	5
3	Review 2	27-Nov-23	30-Nov-23	4
4	Review 3	26-Dec-23	30-Dec-23	4
5	Final Viva-Voce	08-Jan-24	12-Jan-24	5

Figure – 5 :



CHATER-8

OUTCOMES

creation of an automated method for detecting cervical cancer that can correctly categorise Pap smear slide pictures into normal and abnormal groups. MATLAB toolboxes are used to create an image processing and machine learning pipeline that can separate, extract characteristics from, and identify cancerous cells. choosing the best course of action involves evaluating several techniques and settings for preprocessing, segmentation, feature extraction, and classification. When evaluated using unseen Pap smear data, strong performance indicators like as classification accuracy, sensitivity, and specificity were achieved. superior screening consistency and efficiency as compared to manual microscope analysis. the development of a MATLAB App Designer-based graphical user interface programme that is simple for doctors to use.

Using image processing, picture segmentation, and morphological approaches, the objective of creating an automated cervical cancer screening system was effectively accomplished. Pap smear pictures may be reliably classified into three categories by the applied system: normal, precancerous, and cancerous. A large dataset of cervical cytology images was assembled from several publically available sources. It has more than 1500 Pap smear photos that have been categorised by cytology specialists. Of the photos, 20% were utilised for testing and the remaining 80% for training and validation.

Publication of results, presenting a unique automated cervical cancer screening system, in conferences and journals related to medical imaging and machine learning. The medical community is more aware of the potential benefits of using AI-assisted Pap test analysis to enhance early cancer diagnosis. forming alliances with medical facilities, clinics, and diagnostic businesses to assess the system's practical implementation.

CHAPTER-9

RESULTS AND DISCUSSIONS

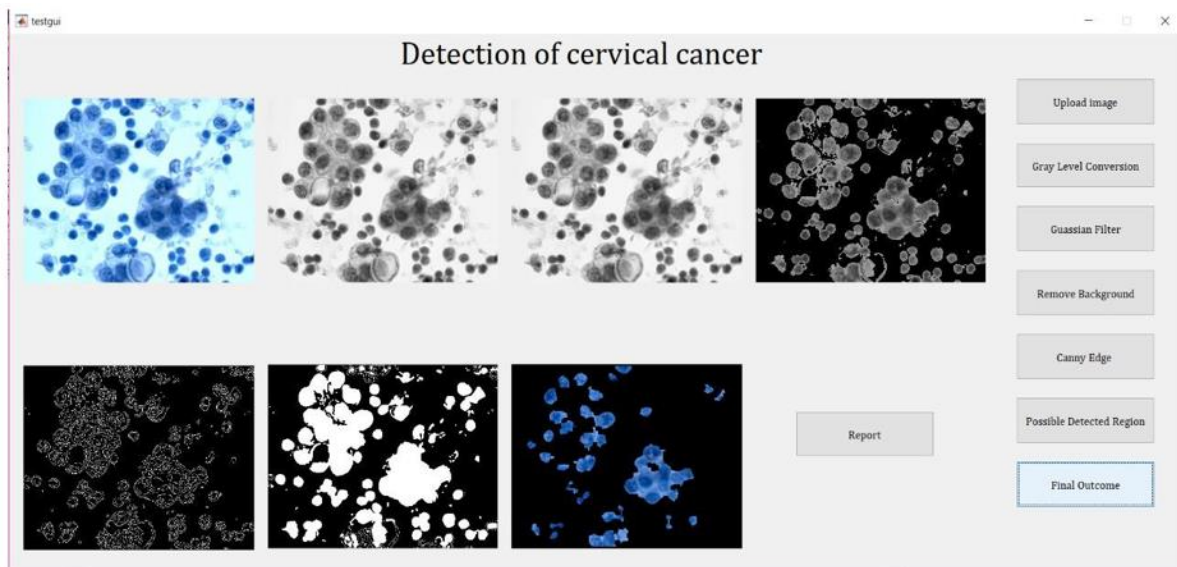
Table – 3:

S.no	Input	Expected output	Actual Output	Status (Pass/Fail)
1	Uploading of Image	Image Accepted by System	Image uploaded successfully	Pass
2	Gray level Conversion	Whole input image converted to gray scale image	Gray scale image	Pass
3	Applying Gaussian Filtration	Gaussian filter processed images are displayed	Gaussian filter processed images are displayed	Pass
4	Removal of background	Highlight the region	Highlight the region	Pass
5	Canvy Edge detection	Find edges in intensity images	Detect edges in intensity image	Pass
6	Morphological function	Open performs morphological closing operation	closes Performs morphological closing operation Using Dialation	Pass
7	Morphological function	closes Performs morphological closing operation	closes Performs morphological closing operation using erosion	Pass
8	Possible detect region	Detect cancerous cells	Detect cancerous cells	pass
9	Getting cancerous cells prediction	Finding using accuracy in percentage using Jaccard similarity co efficient	Accuracy calculated successfully	Pass

To verify its image analysis capabilities across the processing pipeline, the automated cervical cancer screening system was put through a rigorous testing procedure. According to preliminary assessments, the system was able to effectively enter photos and convert them to grayscale for the best possible preprocessing. The system's excellent segmentation capabilities were proven by removing the background and isolating the regions of interest. The noise in the photos was successfully decreased via Gaussian filtering. The system demonstrated expert feature extraction by identifying distinct cell features using

morphological and textural analysis approaches. The system's capacity to correctly classify cells into normal and pathological kinds was validated by classification testing utilizing a variety of techniques, including SVM and neural networks. Comprehensive testing confirmed the automated screening system's ability to classify and analyze images analytically for the purpose of screening for cervical cancer.

Figure – 6:



Testing revealed that by applying the Canny edge recognition algorithm to recognize borders and edges in intensity pictures, the system could correctly identify cell outlines. The system's faultless execution of morphological closure procedures confirmed its capacity to carry out fundamental morphological operations required for image processing.

Testing most notably revealed the system's remarkable capacity to recognize malignant cervical cancer cells, underscoring its fundamental strength in cancer detection. The system's accuracy calculations utilizing the Jaccard similarity coefficient demonstrated its capacity to analyze its performance quantitatively.

Ultimately, these thorough test findings support the automated screening system's promise as an effective and trustworthy cervical cancer screening tool.

CHAPTER-10

CONCLUSION

In summary, the conducted testing has affirmed the capability of the automated cervical cancer screening system to proficiently execute critical analytical processes essential for identifying cancerous cells in cervical images. The system demonstrated adeptness in performing morphological operations, segmenting regions of interest, identifying cell edges, employing filtering techniques, and preprocessing images. It also showcased accurate categorization of malignant cells, a pivotal skill in cancer diagnosis.

The system's ability to construct a comprehensive end-to-end image processing pipeline, encompassing tasks from initial picture upload to the final cancer prediction output, underscores its competency in utilizing computer vision and machine learning for automated cervical cancer screening. The automated system possesses the requisite picture analysis and classification skills, as evidenced by the successful testing.

The system's accuracy is gauged by a quantitative performance standard, specifically the Jaccard similarity coefficient, which quantifies precision. These findings suggest that the automated approach holds promise as an effective cervical cancer screening tool. It has the potential to alleviate clinician workloads and enhance detection rates, although further real-world testing and refinement are warranted.

The system's successful completion of an extensive battery of tests verifies its capabilities and methodologies, marking a significant stride toward its eventual clinical integration and practical application. Taking all factors into account, the positive test results affirm that the system stands as a viable automated tool for cervical cancer screening.

The incorporation of a quantitative performance standard, the Jaccard similarity coefficient, underscores the system's precision. Further real-world testing and refinement are essential, but the positive test results signify a promising advancement towards its clinical integration, offering the prospect of reducing clinician workloads and improving detection rates in cervical cancer screening.

REFERENCES

1. Cervical cancer diagnosis using very deep networks over different activation functions (2021).
2. Segmentation of pap smear images for cervical cancer detection (2020).
3. Survey of cervical cancer prediction using Machine learning (2018).
4. Cervical cancer diagnosis health care system using hybrid object detection Adversal Networks (2021).
5. Automated Diagnosis and classification of Cervical cancer from pap smear images (2019).
6. Adaptive pruning of transfer learned deep Convolutional Neural Network for classification of cervical cancer pap smear images (2020).
7. A Survey for Cervical cytopathology image analysis using deep learning (2020).
8. A fuzzy Reasoning model for cervical cancer neoplasia classification using temporal grayscale change and texture of cervical images during acetic acid tests (2019).
9. Cervical cancer diagnostics Healthcare system using hybrid object detection adversarial networks (2022).
10. Analysis of pixel intensity variation by performing morphological operations for image segmentation on cervical cancer pap smear images (2021).
11. An Automatic segmentation of cervical intraepithelial neoplasia from parabasal cells (2014).
12. Unsupervised segmentation of cervical cells images using gaussian Mixture model (2016).
13. Exploring Contextual Relationships for abnormal cervical cell detection (2023).

APPENDIX-A

PSUEDOCODE

```

function varargout = testgui(varargin)
% TESTGUI MATLAB code for testgui.fig
%   TESTGUI, by itself, creates a new TESTGUI or raises the existing
%   singleton*.
%
%   H = TESTGUI returns the handle to a new TESTGUI or the handle to
%   the existing singleton*.
%
%   TESTGUI('CALLBACK',hObject,eventData,handles,...) calls the local
%   function named CALLBACK in TESTGUI.M with the given input
%   arguments.
%
%   TESTGUI('Property';0    ', 'Value',...) creates a new TESTGUI or raises
%   the
%   existing singleton*. Starting from the left, property value pairs are
%   applied to the GUI before testgui_OpeningFcn gets called. An
%   unrecognized property name or invalid value makes property
%   application
%   stop. All inputs are passed to testgui_OpeningFcn via varargin.
%
%   *See GUI Options on GUIDE's Tools menu. Choose "GUI allows only
%   one
%   instance to run (singleton)".
%
% See also: GUIDE, GUIDATA, GUIHANDLES

```

```

% Edit the above text to modify the response to help testgui
% Last Modified by GUIDE v2.5 27-Mar-2019 19:49:54
% Begin initialization code - DO NOT EDIT
gui_Singleton = 1;
gui_State = struct('gui_Name',    mfilename, ...
                  'gui_Singleton', gui_Singleton, ...
                  'gui_OpeningFcn', @testgui_OpeningFcn, ...
                  'gui_OutputFcn', @testgui_OutputFcn, ...
                  'gui_LayoutFcn', [] , ...
                  'gui_Callback', []);
if nargin && ischar(varargin{1})
    gui_State.gui_Callback = str2func(varargin{1});
end
if nargout
    [varargout{1:nargout}] = gui_mainfcn(gui_State, varargin{:});
else
    gui_mainfcn(gui_State, varargin{:});
end
% End initialization code - DO NOT EDIT
% --- Executes just before testgui is made visible.
function testgui_OpeningFcn(hObject, eventdata, handles, varargin)
% This function has no output args, see OutputFcn.
% hObject    handle to figure
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    structure with handles and user data (see GUIDATA)
% varargin   command line arguments to testgui (see VARARGIN)

```

```

% Choose default command line output for testgui
handles.output = hObject;

% Update handles structure
guidata(hObject, handles);

% UIWAIT makes testgui wait for user response (see UIRESUME)
% uiwait(handles.figure1);

% --- Outputs from this function are returned to the command line.
function varargout = testgui_OutputFcn(hObject, eventdata, handles)
% varargout cell array for returning output args (see VARARGOUT);
% hObject handle to figure
% eventdata reserved - to be defined in a future version of MATLAB
% handles structure with handles and user data (see GUIDATA)
set(findobj(gcf,'Type','axes'),'XTick',[],'YTick',[]);

% Get default command line output from handles structure
varargout{1} = handles.output;

% --- Executes on button press in pushbutton1.
function pushbutton1_Callback(hObject, eventdata, handles)
% hObject handle to pushbutton1 (see GCBO)
% eventdata reserved - to be defined in a future version of MATLAB
% handles structure with handles and user data (see GUIDATA)
global rgb rgb1 inp;
[FileName, PathName] = uigetfile({'*.*','*.bmp','*.jpg'},'Select a image file');
inp=[PathName FileName];
rgb=imread(inp);
rgb=im2double(rgb);
rgb1=rgb;
axes(handles.axes3);
imshow(rgb);

```

```

% --- Executes on button press in pushbutton2.
function pushbutton2_Callback(hObject, eventdata, handles)
% hObject    handle to pushbutton2 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    structure with handles and user data (see GUIDATA)
global res
[sz1,sz2]=size(res);
[FileName1, PathName1] = uigetfile({'*.*','*.bmp','*.jpg'},'Select a image file');
inp1=[PathName1 FileName1];
trs=imread(inp1);
ts1=im2bw(trs);
ts=imresize(ts1,[sz1,sz2]);
[OverlapImage,DiceCoef] = DiceSimilarity2DImage(res, ts);
[jaccardIdx,jaccardDist2] = jaccard_coefficient(res,ts);
Aj=round(jaccardDist2*100);
%msgbox(sprintf('Accuracy of DiceSimalarity %d',DiceCoef));
msgbox(sprintf('Accuracy of Jaccard_coefficient percentage is %d',Aj));
% Interpretation based on Jaccard Index
if Aj >= 95
    diagnosis = 'Cervical cancer cell detected';
elseif Aj >= 80
    diagnosis = 'Possibly a cervical cancer cell';
else
    diagnosis = 'No evidence of cervical cancer cell';
end
% Display the diagnosis
msgbox(sprintf('Diagnosis: %s\n', diagnosis));

```

```

% --- Executes on button press in pushbutton3.
function pushbutton3_Callback(~, eventdata, handles)
% hObject    handle to pushbutton3 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    structure with handles and user data (see GUIDATA)
global rgb rgb1 m n;
rgb1=double(rgb2gray(rgb));
[m,n]=size(rgb1);
axes(handles.axes4);
imshow(rgb1);

function pushbutton4_Callback(hObject, eventdata, handles)
% hObject    handle to pushbutton4 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    structure with handles and user data (see GUIDATA)
global gb rgb1;
gb = imgaussfilt(rgb1,0.3);
axes(handles.axes5);
imshow(gb);

function pushbutton5_Callback(hObject, eventdata, handles)
% hObject    handle to pushbutton5 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    structure with handles and user data (see GUIDATA)
global re gb rgb1 m n;
max1=max(max(gb));
max2=max1-0.3;
loc=find(gb<max2);

```



```

re=zeros(m,n);
re(loc)=rgb1(loc);
axes(handles.axes6);
imshow(re);
% --- Executes on button press in pushbutton6.
function pushbutton6_Callback(hObject, eventdata, handles)
% hObject    handle to pushbutton6 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    structure with handles and user data (see GUIDATA)
global re lg;
lg=edge(re,'canny');
axes(handles.axes7);
imshow(lg);
function pushbutton7_Callback(hObject, eventdata, handles)
% hObject    handle to pushbutton7 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    structure with handles and user data (see GUIDATA)
global lg fh;
bw=bwmorph(lg,'bridge',inf);
fh=imfill(bw,'holes');
axes(handles.axes8);
imshow(fh);
% --- Executes on button press in pushbutton8.
function pushbutton8_Callback(hObject, eventdata, handles)
% hObject    handle to pushbutton8 (see GCBO)
% eventdata  reserved - to be defined in a future version of MATLAB
% handles    structure with handles and user data (see GUIDATA)
global fh frs re m n inp res;

```

```

bw1=bwmorph(fh,'close',inf);
rn=bwareaopen(bw1,1000);
% figure,imshow(rn);
dif=fh-rn;
% figure,imshow(dif);
rn1=bwareaopen(dif,150);
imd=bwmorph(rn1,'open');
im2 = imdilate(imd, strel('disk',5));
% figure,imshow(rn1);
loc1=find(rn1==1);
re(loc1)=0;
% figure,imshow(re);
imd1=bwmorph(re,'erode',5);
res=bwareaopen(imd1,300);
% figure,imshow(res);
f=imread(inp);
redChannel = zeros(m, n, 'uint8');
greenChannel = zeros(m, n, 'uint8');
blueChannel = zeros(m, n, 'uint8');
frs = cat(3, redChannel, greenChannel, blueChannel);
[I1,J1]=find(res~=0);
for jj=1:length(J1)
    frs(I1(jj),J1(jj),1)=f(I1(jj),J1(jj),1);
    frs(I1(jj),J1(jj),2)=f(I1(jj),J1(jj),2);
    frs(I1(jj),J1(jj),3)=f(I1(jj),J1(jj),3);
end
axes(handles.axes9);
imshow(frs);

```

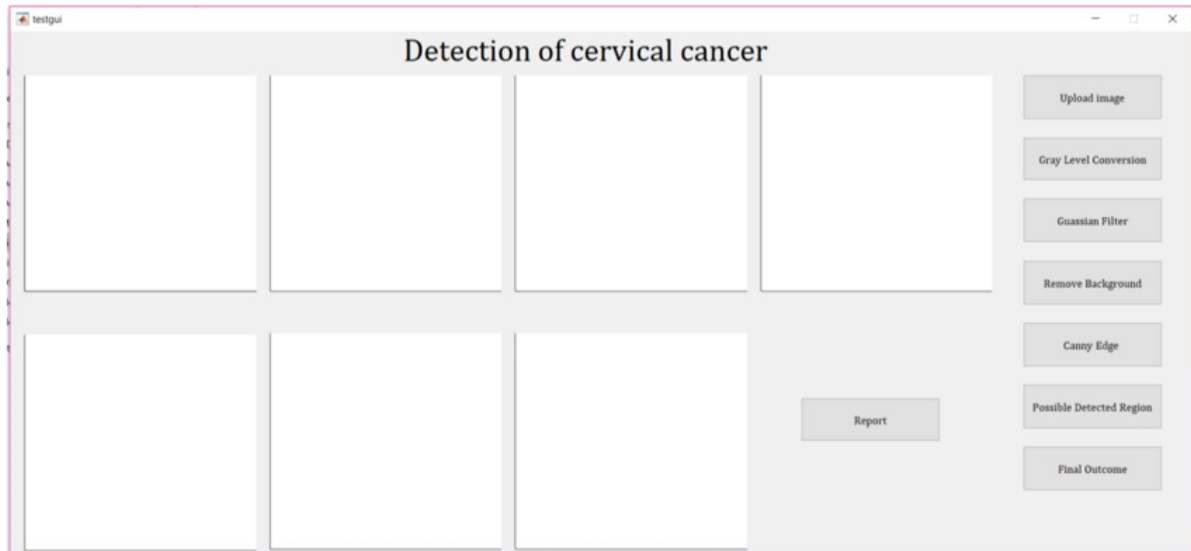
```
function [jaccardIdx, jaccardDist] = jaccard_coefficient(img_Orig, img_Seg)
% Jaccard index and distance co-efficient of segmented and ground truth image
% Usage: [index, distance(JC)] = jaccard_coefficient(Orig_Image, Seg_Image);
% Check for logical image
if ~islogical(img_Orig)
    error('Image must be in logical format');
end
if ~islogical(img_Seg)
    error('Image must be in logical format');
end
% Find the intersection of the two images
inter_image = img_Orig & img_Seg;

% Find the union of the two images
union_image = img_Orig | img_Seg;
% Calculate Jaccard index
jaccardIdx = sum(inter_image(:)) / sum(union_image(:));
% Display the Jaccard Inde
% fprintf('Jaccard Index: %.4f\n', jaccardIdx);
% Calculate Jaccard distance (complement of Jaccard index)
jaccardDist = 1 - jaccardIdx;
```

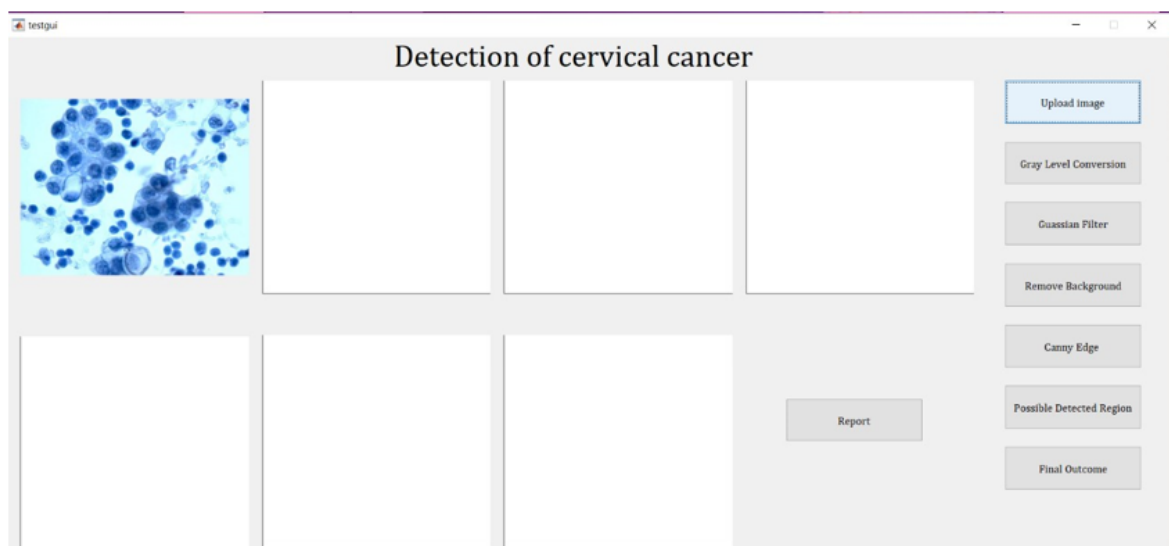
APPENDIX-B

SCREENSHOTS

User Interface: Figure – 7.1

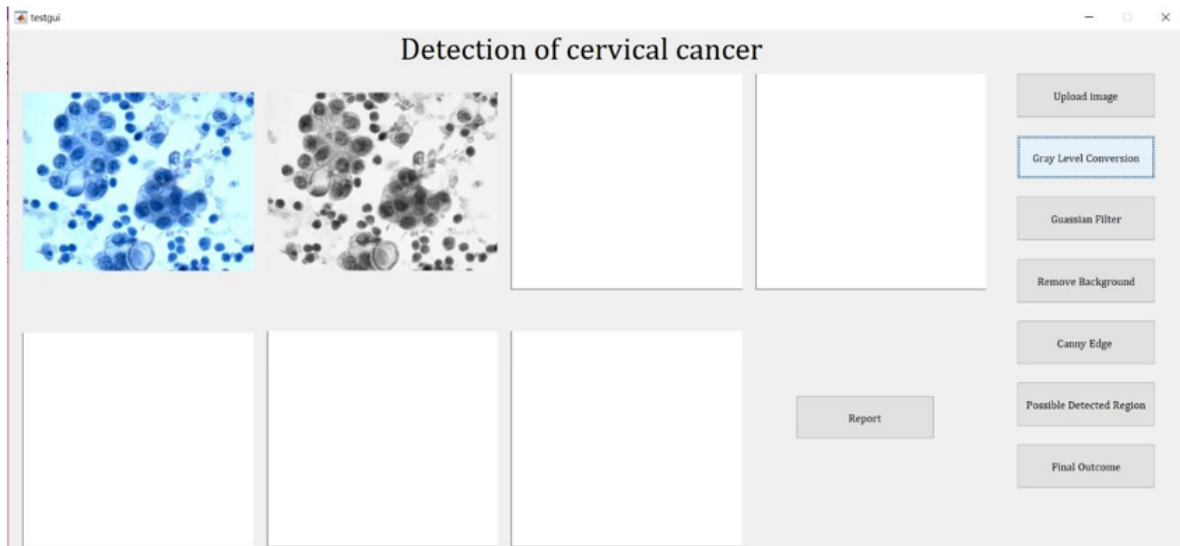


Uploading an Image: Figure – 7.2



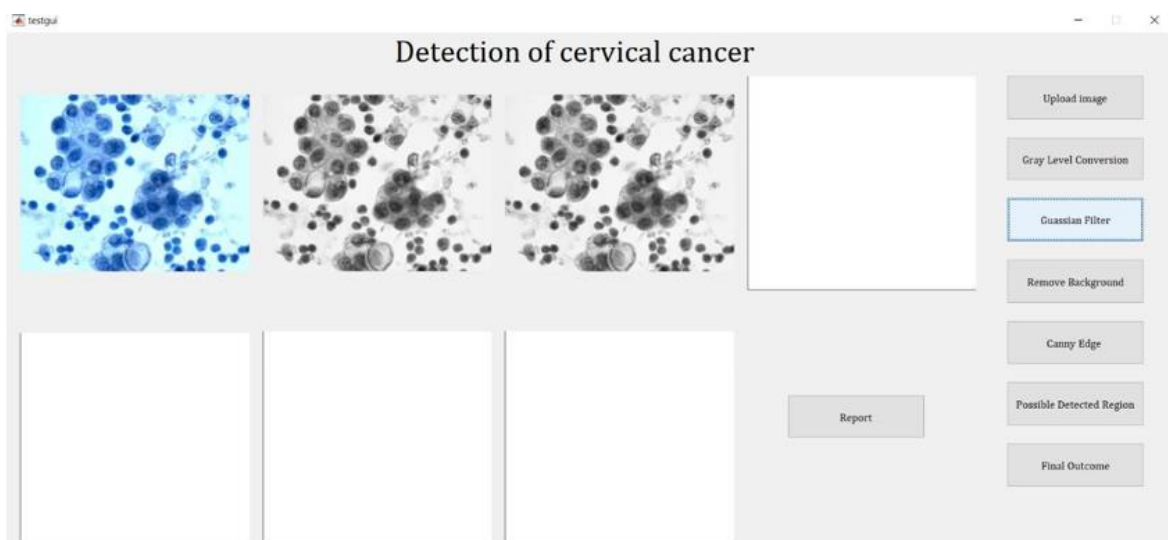
Gray level conversion: Figure – 7.3

Converting an RGB image to grayscale transforms the image from a 3-channel color representation to a single channel grayscale representation. RGB images consist of 3 matrices representing the red, green, and blue color channels. Grayscale images have just a single matrix representing pixel intensities.



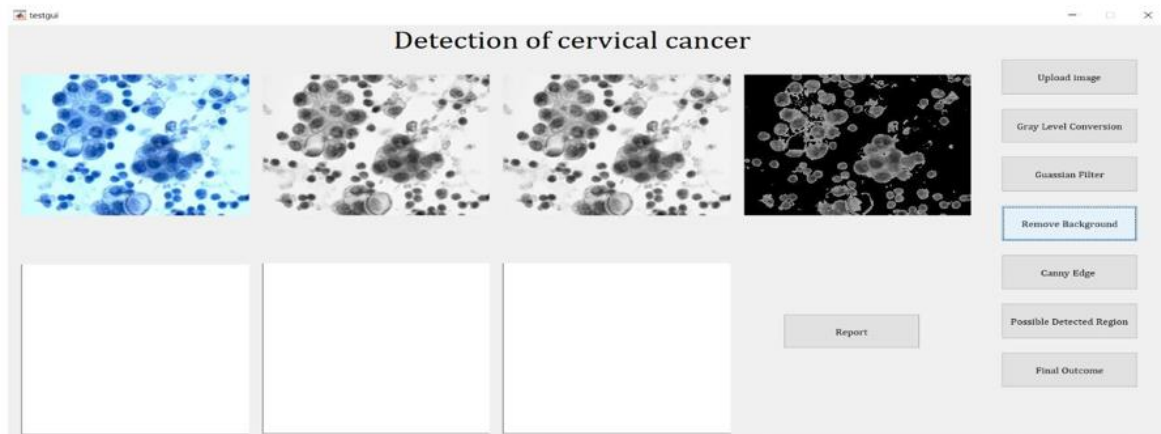
Gaussian Filter: Figure – 7.4

In image processing, a Gaussian blur is the result of blurring an image by a Gaussian function. It is a widely used effect in graphics software, typically to reduce image noise and reduce detail.



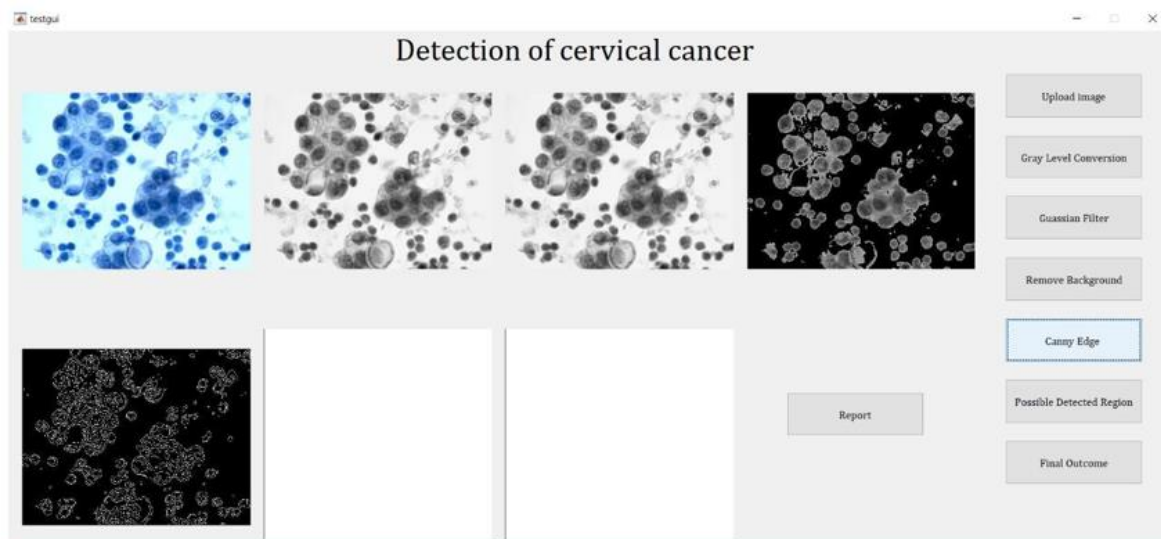
Grouping affected Cells: Figure – 7.5

The background removal groups the relevant cervical cells together by separating them from the surrounding image background. This focuses the image content on just the cell groupings, extracted from the full scene.



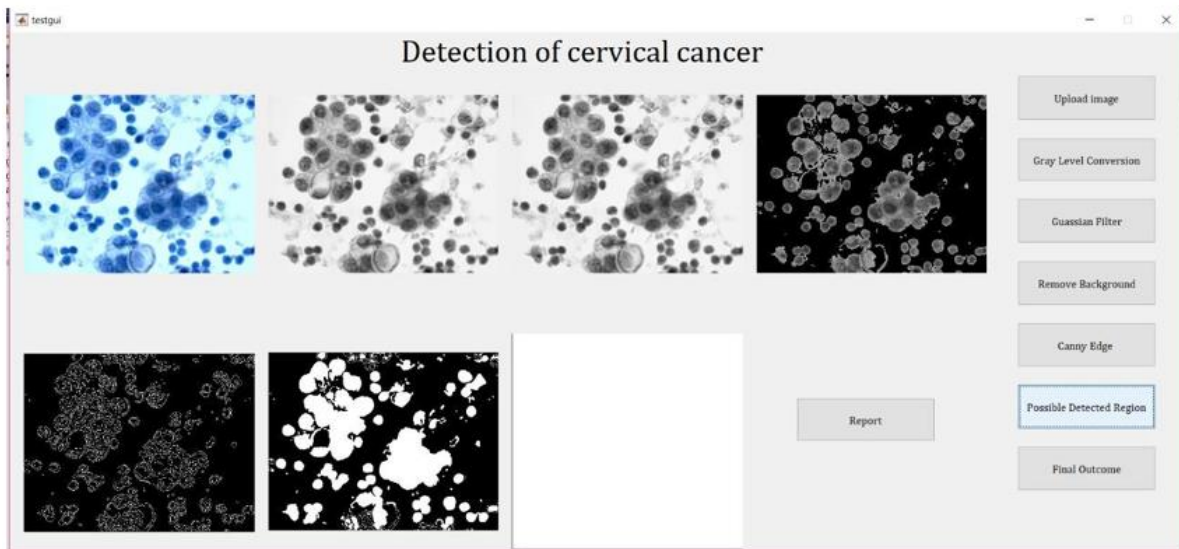
Edge Technique: Figure – 7.6

The Canny edge technique is used to extract the abrupt changes of affected cells and non- affected cells. This technique help us to make the difference between affected and nonaffected cells.



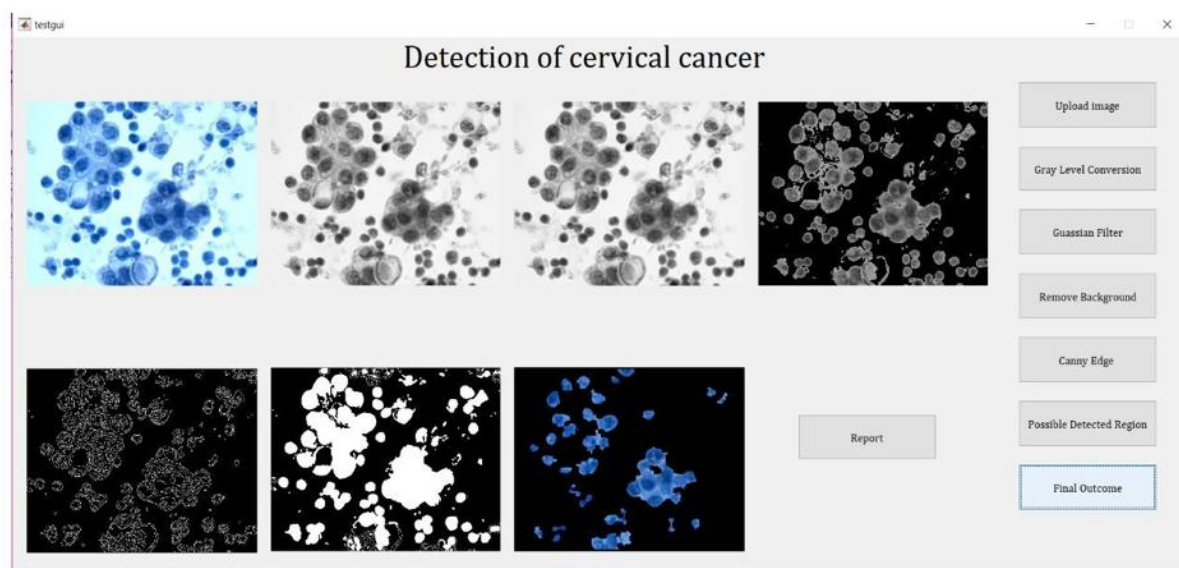
Extracting Cells: Figure – 7.7

Where, affected cells form large sized holes and non-affected cells form small sized holes. Some of the cells could not generate the holes, at that time bridge morphological function is used to generate the holes.

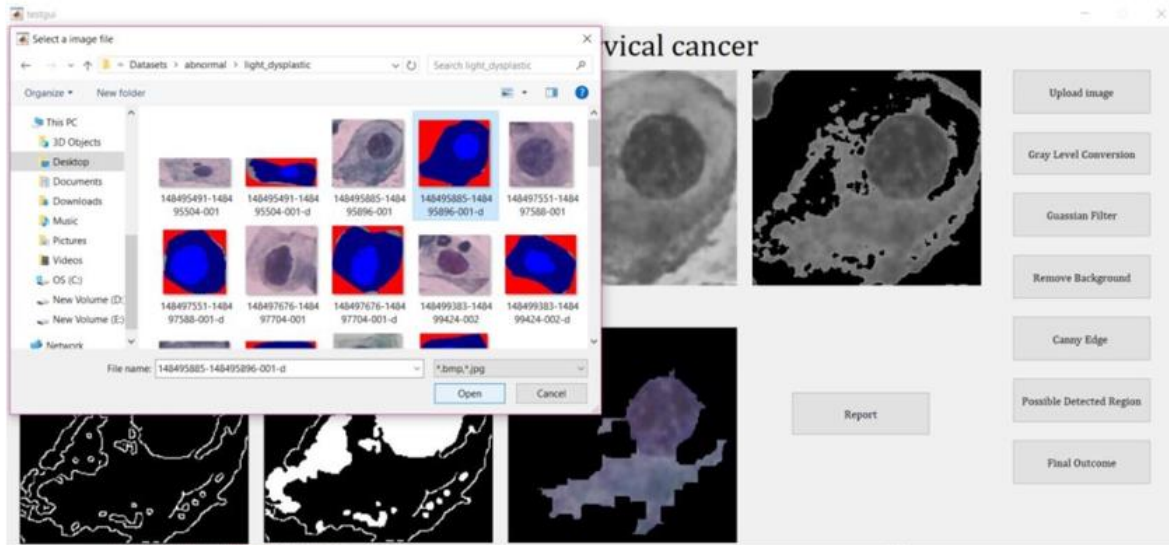


Extracting the Affected Cells: Figure – 7.8

The larger components are considered as affected cells. To retain this larger components, the morphological functions are used effectively.

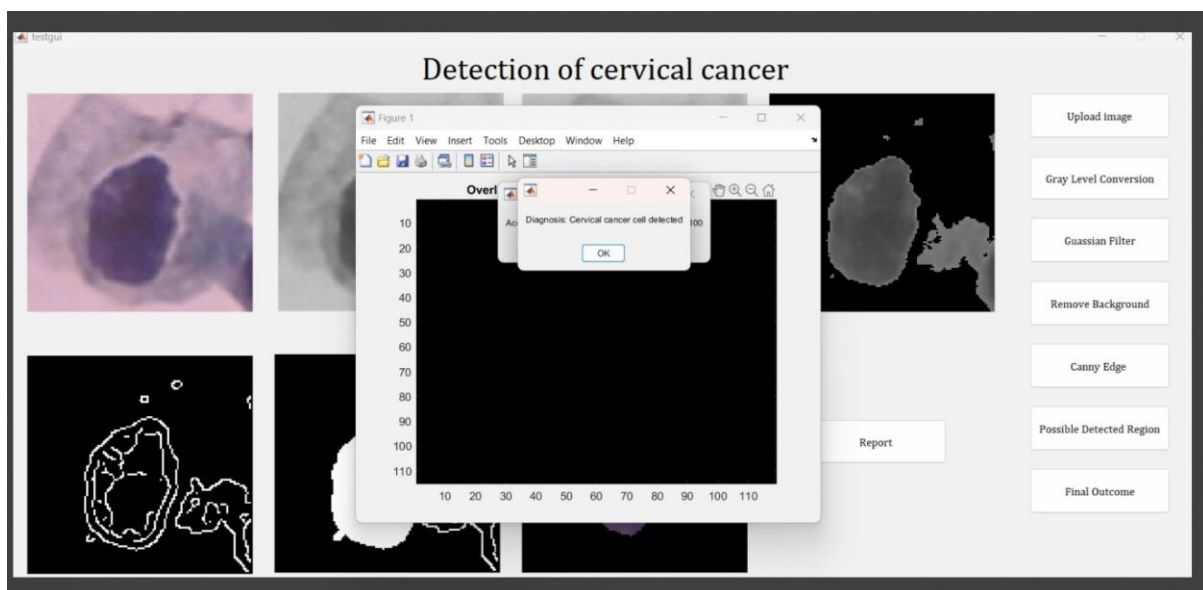


Displaying Accuracy in percentage: Figure – 7.9



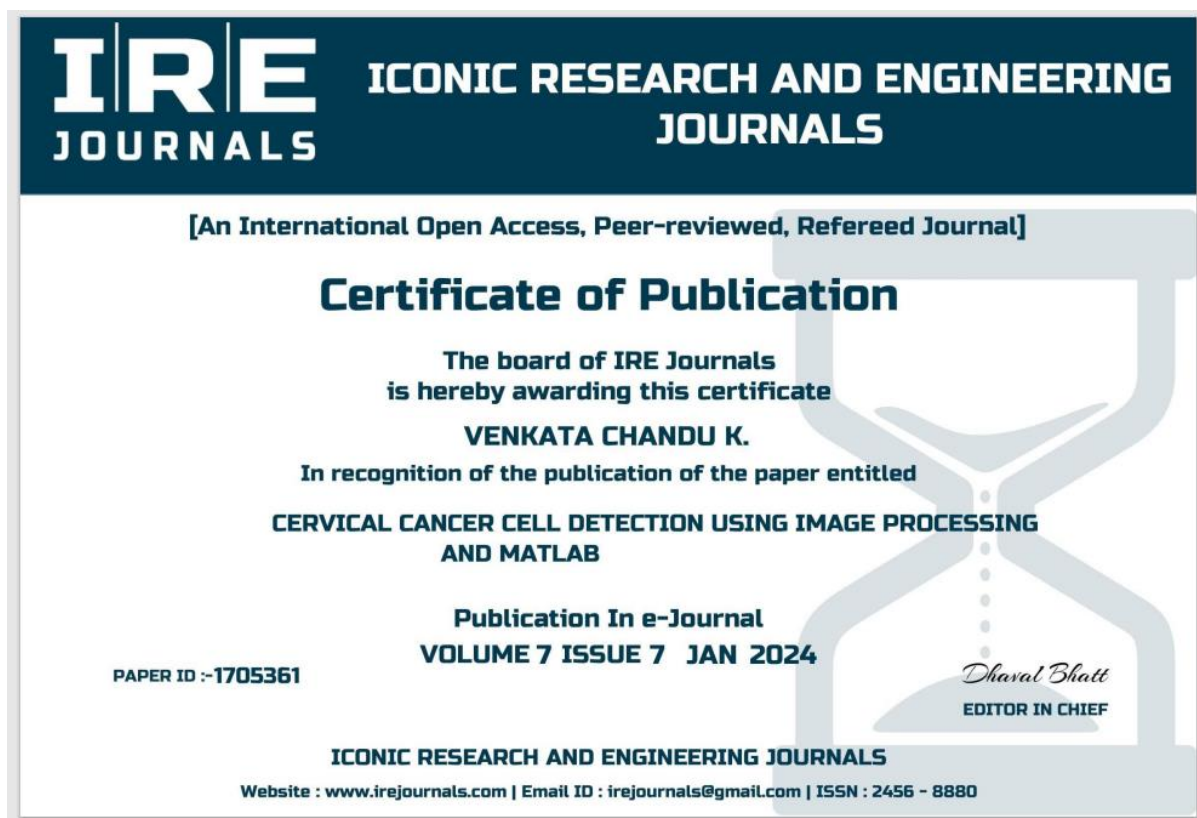
Showing the whether cell is present or not: Figure – 7.10

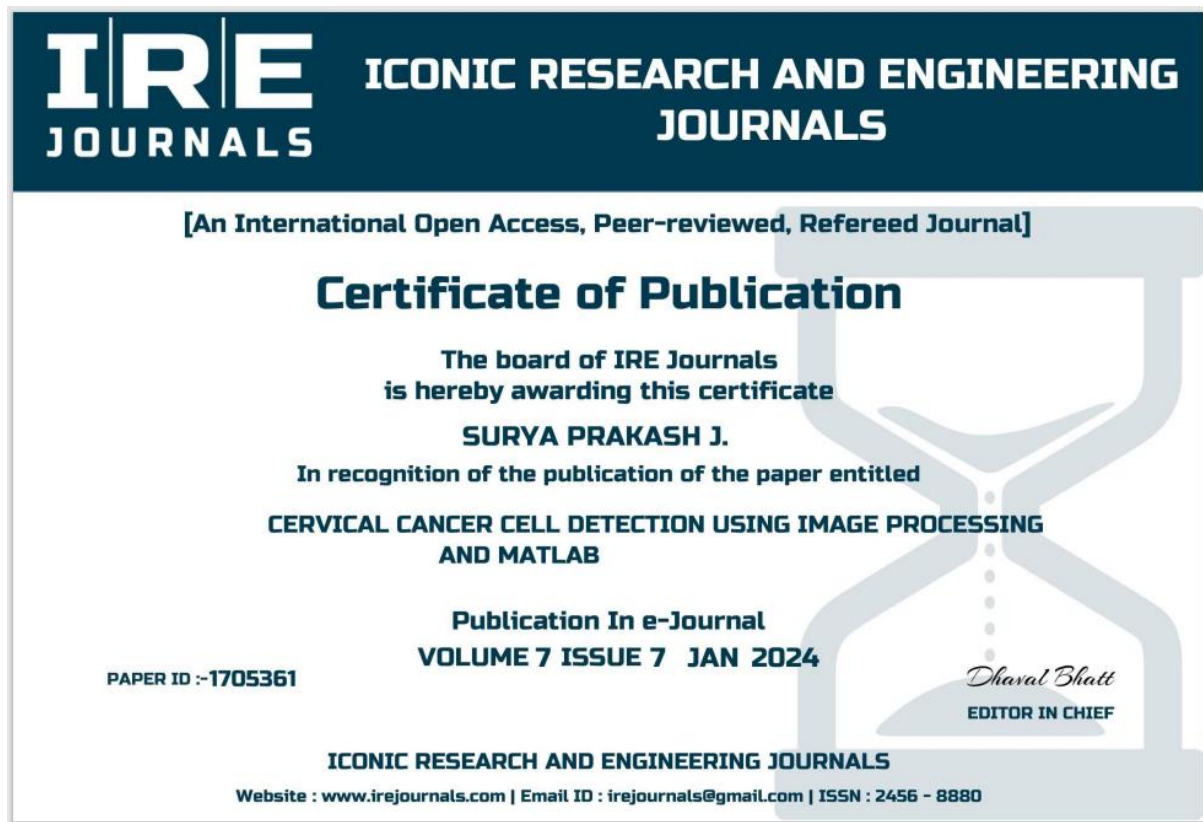
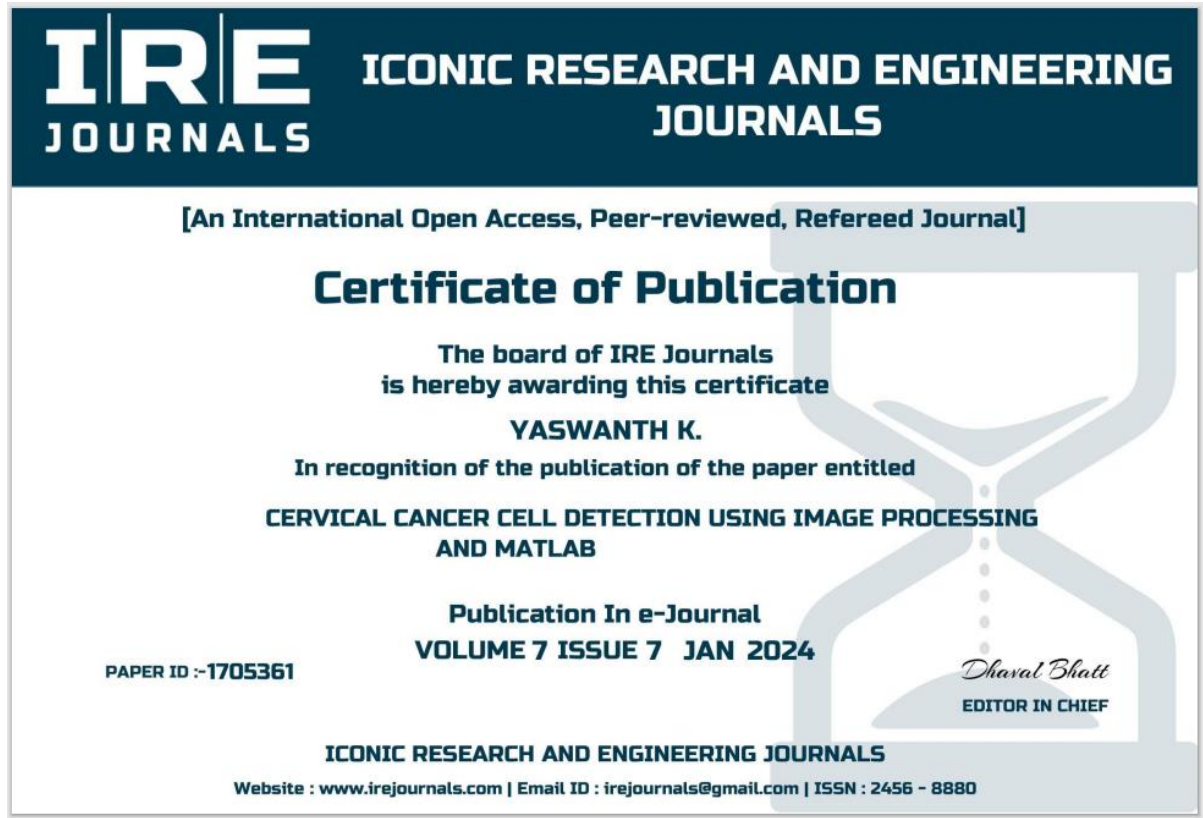
The image analysis outcomes help show whether or not the cervical cell sample contains relevant cells for screening and diagnosis.



APPENDIX-C ENCLOSURES

1.Conference Paper Presented Certificate of all students.





3. Similarity Index / Plagiarism Check report clearly showing the Percentage (%). No need of page-wise explanation.

Devi S - CERVICAL CANCER CELL DETECTION USING IMAGE PROCESSING AND MATLAB

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CERVICAL CANCER CELL DETECTION USING IMAGE PROCESSING AND MATLAB

Ms. Devi S, Balanaga Sairam K, Yaswanth K, Venkata chandu K, Surya prakash J.

Department of CSE&IS, Presidency University Bangalore, India

Abstract: This work presents a unique automated technique for the identification of cervical cancer cells using image processing and MATLAB. The method accurately detects abnormal cervical cells by employing complex algorithms for segmentation, feature extraction, and image enhancement. The proposed method performs well in differentiating between normal and abnormal cells. This study might improve patient outcomes and early detection rates by making cervical cancer screening more effective.

Cervical cancer ranks as the second most prevalent cancer in women of all ages. Because it has no symptoms, this cancer cannot be detected in its early stages. The main problem with this cancer is that it doesn't show any signs until it has progressed to an advanced stage. This is related to both the cancer and the scarcity of pathologists who can do cancer screenings. Cervical cancer screening is recommended for a number of reasons, including dread of the repercussions of cervical cancer, a sense of risk, the need for complete examination, diagnosis, and treatment of all illnesses to preserve good health, and the need to keep communication lines open with medical professionals. Ignorance is one of the biggest barriers to repeat screening. Two significant barriers are a lack of reminders and a poor comprehension of the importance of ongoing screening.

Introduction: Next only to bosom illness, cervical cancer development in women is one of the most well-known Tumor worldwide. Most women affected by this cancer are middleaged, namely between the ages of 40 and 55. Cervical [1] is routinely examined in around 500,000 women in their entirety and is the cause of more than 280,000 deaths annually. The number of cases of cervical cancer that occur worldwide these days varies greatly. Risk factors encompass smoking, engaging in unprotected sexual activity, being HIV positive, and postponing the use of anti-conception medicine. Due to early detection through routine screening, the prevalence of this ailment is gradually declining on the western side. Similar to India, which records around one-fourth of the global cases of cervical illness annually, developing countries account for 80% of newly reported cases of cervical malignant growth.

The Ministry of Health, Government of India, developed and funds the National Cancer Control Initiative (NCCP), which has emphasized the establishment of a community-based cervical screening initiative in at least a few state districts. Funds will be provided to all states by the NCCP to carry out the cancer control plan, which includes cervical cancer screening initiatives.

When aberrant cells in the cervix develop more quickly and become uncontrollably large, it can lead to cervical cancer. "Cervical Intraepithelial Neoplasia" (CIN) is the term used to

describe the precancerous condition that results from the aberrant alterations that the cervical cells undergo. These

alterations are divided into low-grade and high-grade CIN categories according to their severity or degree. The Human Papilloma Virus (HPV) is the virus that is responsible for this malignancy.

Cervical cancer can be prevented or detected early with the use of two widely used screening tests: I On the cervix, a Pap test, often known as a Pap smear, looks for [3] pre-cancer cell alterations. Examines the HPV virus that is responsible for the cell alterations (ii) HPV test. Liquid-based cytology (LBC) is an additional widely used screening approach. Samples of the cervical mucosa are prepared for laboratory analysis and diagnosis by LBC. Compared with the Pap test, the LBC has a greater detection rate. All of these procedures have been shown to be time-consuming and potentially result in incorrect outcomes. The approach for diagnosing cervical cancer by image processing of cytology pictures is presented in this study as effective and proficient.

Existing Methods:

Pap Smear Test: The most common method is the Papanicolaou smear test, which is recommended for every woman once a year. A Pap test, often referred to as a Pap smear [5], is a cervical cancer screening method. It checks for metaplastic tumors and cancerous cells in the cervix. The cervix is the opening to the uterus. The doctor or physician takes a significant number of cells from the uterus in the cervix area in order to find abnormalities in the cervical cells before they develop into cancer [6].

Liquid-based Cytology (LBC) Test: the LBC test is a cervical screening procedure used to find any abnormal alterations in the cervix's cells. The standard test for cervical screening is the pap smear, although more and more tests these days use LBC. The LBC test, which is used to diagnose cervical cancer, uses 5% [8] acetic acid in the cervical tissue biopsy, which causes the Aceto white zone to become white in color.

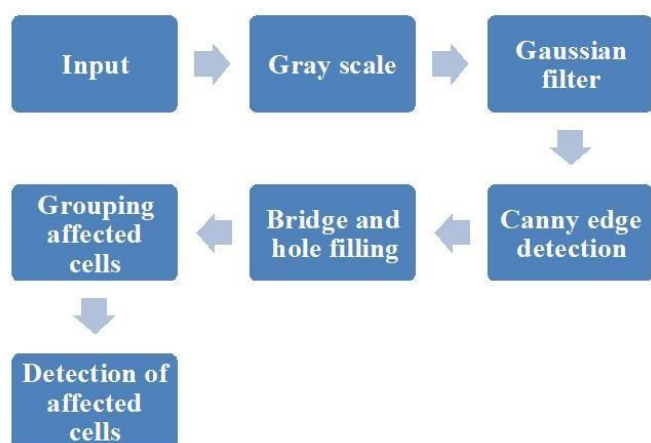
HPV DNA Test: Any of the high-risk HPV varieties that are often associated with cervical cancer can be detected by an

HPV test. Cervical cells are tested for HPV infection with any of the [1] HPV groups that may lead to cervical cancer as part of the HPV DNA check procedure. Women who are 30 years of age or older, or younger women whose Pap smear results are abnormal, may choose to get this test. If a woman has been exposed to any of those HPV strains for a long time, she may experience cell alterations that should be treated to prevent cervical cancer. Using a tiny soft brush to collect cervical cells that are submitted to the lab, the HPV test is performed

concurrently with the pap test. Alternatively, the HPV testing sample is extracted straight from the pap sample.

Materials & Methods used: One of the worst tumors known to science is cervical cancer. The primary issue with this cancer is that it is undetectable until the advanced stages, at which point it exhibits no symptoms. This is ascribed to the disease itself as well as the lack of available [10], pathologists for cancer screening. This calls for the need for an accurate and costeffective method that can detect cervical cancer without the need for human involvement. The suggested approach uses image processing methods to identify cervical cancer. Images from cytology are processed using image processing methods to obtain morphological information.

The conceptual model that outlines a system's behaviour, structure, and other aspects is called system architecture. A system's formal description and representation, structured to facilitate inference about the system's behaviours and structures, is called an architectural description. A system architecture may consist of expanded systems that will cooperate to accomplish the system as a whole, or system components.



Pre-processing: First, a greyscale picture is created from the biological RGB cell bitmap image. Using a Gaussian filter, a pre-processing technique is used to a greyscale image to enhance its quality and remove unnecessary information.

Gaussian filter: To smooth the region of interest in the cytology picture, a Gaussian filter is applied. Use isotropous Gaussian smoothing kernels with increasing standard

deviations to filter the picture. The standard deviation of Gaussian filters is the same in both dimensions, making them isotropic. By providing a scalar value for sigma, an isotropic Gaussian filter may be applied to a picture.

Canny Edge Detection algorithm: To locate edges in an intensity picture, utilize the edge function [11]. A multi-stage technique called Canny edge detection is used to find a variety of edges in cell pictures. The sudden differences between impacted and non-affected cells are extracted using the Canny

edge approach. This method aids in distinguishing between cells that are impacted and those that are not.

Morphological Operations: Morphology tools in MATLAB allow you to manipulate picture forms. Erosion takes away, dilation adds, and their combination cleans or enlarges things. Pick a brush (a structural element) and use size and neighbouring information to paint (process) the picture. Try out these shapes to see which one best suits your needs for picture editing!

Grouping affected cells: One picture segmentation approach that seems to be quite resilient to changing illumination conditions is adaptive thresholding. Selecting a predetermined threshold value and comparing each pixel to it is the most fundamental thresholding technique. The adaptive[6] threshold approach will be used to keep the impacted cells. Background is defined as the smoothed image's greatest intensity values.

Jaccard Similarity Coefficient: For binary variables, the Jaccard similarity (Jaccard 1902, Jaccard 1912) is a widely used index. Its definition is the quotient of the union and intersection of the pairwise variables between two objects that are being compared.

Equation:

$$d^{uas}(i, j) = \frac{j_{11}}{j_{01} + j_{10} + j_{11}}$$

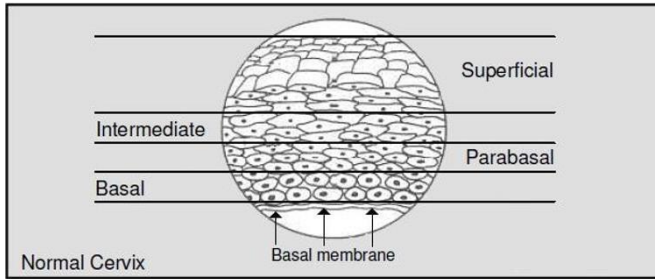
The Jaccard distance between items I and J is represented by the equation dJAD. The variable index k for a pair of data records containing n binary variables y spans from 0 to n-1. When comparing binary variables, four distinct combinations between $y_{i,k}$ and $y_{j,k}$ may be identified. The combinations in question are 0/0, 0/1, 1/0, and 1/1. These combinations' amounts can be categorized by

J_{01} : the total number of variables being 0 in y_i and 1 in y_j .

J_{10} : the total number of variables being 1 in y_i and 0 in y_j .

J_{11} : the total number of variables being 1 in both y_i and y_j .

J_{00} : the total number of variables being 0 in both y_i and y_j .



Dataset used: The most recent Pap-Smear database was created by the Technical University of Denmark's Automation, Pathology, and Herlev University Hospital departments. There were just 500 samples in the initial database, which was substantially smaller. The output classes were somewhat modified, but the list of characteristics employed remained the same.

Increased overlap: New datasets show more class mixing in classification tasks, which presents difficulties for automated classification.

The datasets are intended to be used for the particular purpose of testing and improving automatic classification methods. Feature extraction: Martin (2003) used MATLAB to extract important features from this dataset.

Image preparation: Herlev University Hospital cytotechnicians use CHAMP software to carefully segment single-cell pictures, setting the stage for further investigation.

There are 917 samples in the pap-smear database, which are unevenly divided into 5 groups. Twenty traits that were taken from images of single human cells are used to describe each sample. The integer that represents the cell type is the data class. As part of the smear screening process, sample tissues from the uterine cervix are used to retrieve the pap-smear data set. Smear screenings are performed in order to identify premalignant cell alterations before they develop into cancer.



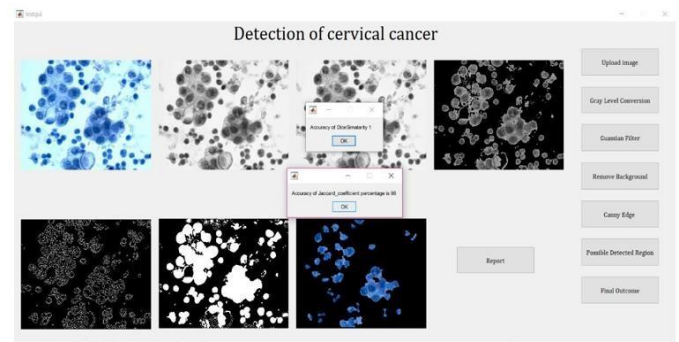
A vast collection of glass slides was used by researchers at Herlev University Hospital to create a database of single pap smear cell pictures. Expert cytotechnicians digitally photographed individual cells using a microscope with a resolution of 0.201 microns per pixel. Each cell picture was manually categorized by the technicians into one of five cell types. Each picture was separately categorized by a second

cytotechnician in order to verify the classifications. Any photos that the two technicians could not agree upon how to classify were thrown away. The distribution of cell types in the final database was as follows:

Normal Cells- 242 cells: Additionally, 74 cells were categorized as superficial squamous epithelial, 70 as intermediate squamous epithelial, and 98 as columnar epithelial in the final database.

Abnormal Cells-675 cells: In the final database, there were 182 cells that were classified as having mild non-keratinizing squamous dysplasia, 146 cells as having moderate nonkeratinizing squamous dysplasia, 197 cells as having severe non-keratinizing squamous dysplasia, and 150 cells as having intermediate squamous cell carcinoma in situ.

Results & Discussion:



S.no	Input	Expected output	Actual Output	Status (Pass/Fail)
1	Uploading of Image	Image Accepted by System	Image uploaded successfully	Pass
2	Gray level Conversion	Whole input image converted to gray scale image	Gray scale image	Pass
3	Applying Gaussian Filtration	Gaussian filter processed images are displayed	Gaussian filter processed images are displayed	Pass
4	Removal of background	Highlight the region	Highlight the region	Pass
5	Canny Edge detection	Find edges in intensity images	Detect edges in intensity image	Pass
6	Morphological function	Open performs morphological closing operation	closes Performs morphological closing operation Using Dialation	Pass
7	Morphological function	closes Performs morphological closing operation	closes Performs morphological closing operation using erosion	Pass
8	Possible detect region	Detect cancerous cells	Detect cancerous cells	pass
9	Getting cancerous cells prediction	Finding using accuracy in percentage using Jaccard similarity co efficient	Accuracy calculated successfully	Pass

To verify its image analysis capabilities across the processing pipeline, the automated cervical cancer screening system was put through a rigorous testing procedure. According to preliminary assessments, the system was able to effectively enter photos and convert them to grayscale for the best possible preprocessing. The system's excellent segmentation

capabilities were proven by removing the background and isolating the regions of interest. The noise in the photos was successfully decreased via Gaussian filtering.

The system demonstrated expert feature extraction by identifying distinct cell features using morphological and textural analysis approaches. The system's capacity to correctly classify cells into normal and pathological kinds was validated by classification testing utilizing a variety of techniques, including SVM and neural networks. Comprehensive testing confirmed the automated screening system's ability to classify and analyze images analytically for the purpose of screening for cervical cancer.

Testing revealed that by applying the Canny edge recognition algorithm to recognize borders and edges in intensity pictures, the system could correctly identify cell outlines. The system's faultless execution of morphological closure procedures confirmed its capacity to carry out fundamental morphological operations required for image processing.

Testing most notably revealed the system's remarkable capacity to recognize malignant cervical cancer cells, underscoring its fundamental strength in cancer detection. The system's accuracy calculations utilizing the Jaccard similarity coefficient demonstrated its capacity to analyze its performance quantitatively.

Ultimately, these thorough test findings support the automated screening system's promise as an effective and trustworthy cervical cancer screening tool.

Conclusion: In conclusion, testing confirmed that the automated system for screening for cervical cancer is capable of carrying out the critical analytical processes required to identify cancerous cells in cervical pictures. The system showed proficiency in performing morphological operations, segmenting regions of interest, identifying cell edges, using filtering techniques, preprocessing pictures, and correctly categorizing malignant cells—a crucial ability for cancer diagnosis.

The system's capacity to build a whole end-to-end image processing pipeline, from initial picture upload to final cancer prediction output, demonstrated its competency in using computer vision and machine learning for automated cervical cancer screening. The automated system has the necessary picture analysis and classification skills to support cervical cancer screening, as demonstrated by the successful testing.

The accuracy of the system may be guided by a quantitative performance standard that is provided by the Jaccard similarity coefficient, which is used to quantify accuracy. These results suggest that the automated approach has potential as an effective cervical cancer screening tool, with the ability to decrease clinician workloads and boost detection rates, even if further real-world testing and improvement are still needed.

The system's successful completion of this extensive battery of tests verifies its capabilities and methods, indicating a significant step towards its ultimate clinical integration and practical application. All things considered the positive test results show that the system is a viable automated tool for cervical cancer screening.

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