Image processing and analysis for intelligent diagnostic colonoscopic instrumentation system

Marta Patricia Tjoa

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Image Processing and Analysis for intelligent Diagnostic Colonoscopic Instrumentation System

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A thesis submitted to the Nanyang Technological University
in fulfilment of the requirement for the degree of
Doctor of Philosophy

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*To my dear parents, sister, and brothers,
for their love and encouragement.*

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Summary

Colorectal cancer is a common cancer prevalent in Singapore and other countries. The early detection of colorectal cancer in patients by frequent check-ups is important to reduce mortality rate. Minimally invasive colonoscopic procedures are increasingly employed for screening, diagnostic and surgical purposes as well as initiation appropriate follow-up actions.

Generally the expert physician performs the clinical colonoscopic examination coupled with the visual and qualitative analysis of the colonoscopic images for the preliminary detection of abnormalities related to cancer. It has some limitations such as tending to be time-consuming, subject to variations in interpretation, and being unsuitable for comparative evaluation. Computer-aided image processing and analysis systems would prove to be a valuable assistant to the physician in detecting abnormalities. The main objective of the present research is to develop a computer-aided scheme to help physicians perform the tasks of colonoscopic image analysis and subsequent abnormality detection for clinical diagnosis. The effort to solve this problem has resulted in four major research contributions in colonoscopic image processing and analysis presented in this thesis.

First, new techniques for segmentation have been developed. The newly proposed segmentation methods for colon abnormality detection are based on texture, homogeneity index, and clustering algorithm. The texture information is measured with a method based on linear binary pattern and magnitude. The main advantages of the proposed method are the absence of any requirement of prior knowledge of the image to be processed and the parameter values not being sensitive to different

images. The new homogeneity index method is a segmentation algorithm comprising two stages of segmenting the image in the hue and intensity domains. Region merging based on $L^*a^*b^*$ colour space is adopted to overcome the resultant over-segmentation problem. The clustering algorithm, Fuzzy C-means, is also applied to segment the colonoscopic image. This algorithm minimises the objective function, which is the weighted sum-of-squared errors within groups, to cluster the pixels in the image into different segments or regions. The proposed methods are able to segment the image into a number of major regions, which can be used for prompting the physician on the possible presence of abnormal regions during the colonoscopy.

Second, a new method of extracting the lumen of the colon from the colonoscopic image has been developed. The proposed method is a modification of the modified deformable region model approach to determine the lumen from the colonoscopic image by deforming an approximate boundary plan to the real boundary iteratively by employing a growing and shrinking operation. A connected component labelling algorithm is applied on the inverse intensity to eliminate small regions inside the lumen. The results obtained showed that the proposed modified deformable region model method detects the lumen contour faster and more accurately than the snake and minimum variance region growing methods.

Third, a set of new quantitative features based on shape, texture, and colour features are defined constituting a novel method of quantitative characterisation of the colon. The limits on the quantitative parameters singly or in combination correlate to abnormalities in the colon and are hence used to assist the endoscopist in the detection of abnormalities. Subsequently a selection based on principal component analysis or clinical input is employed with artificial neural networks, namely, back propagation neural network and self-organising method to come up with a new scheme for

detection of colon abnormalities.

Finally, a pseudo real-time intelligent diagnostic colonoscopic instrumentation system has been designed and implemented. In order to work with physicians in a clinical setting, it is essential that real-time image capture, processing, and analysis have to be carried out. A new method was developed for archiving the real-time image capture coupled with intelligent image processing leading to pseudo real-time colonoscopic image processing and analysis. This new method facilitates computer-assisted decision making by the physician. It is expected that the proposed technique would be of great value in medical training where different types of abnormalities can be detected if a series of images is presented and corresponding analysis is made available.

The present work forms part of an innovative effort in new applications of image processing, image segmentation, and extraction of meaningful parameters, thus formulating a new paradigm of quantitative characterisation of the colon leading to an intelligent technique for analysis and diagnosis to determine the presence of abnormalities. It is envisioned that the proposed technique will pave the way to new methods of intelligent endoscopy, including colonoscopy, oesophagoscopy, bronchoscopy, etc., which will facilitate the physicians in clinical diagnosis particularly in a screening mode. It is therefore considered that the intelligent system developed from the present work can be a key to aiding the clinicians by computer-assisted endoscopy for cancer screening,

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Chapter 1

INTRODUCTION

1.1 Motivation

Cancer has been the leading cause of death in Singapore since 1991 [1]. In 2002, it accounted for 28 % of all deaths [2]. Colorectal cancer, the second leading cause of cancer, has been increasing in both males and females especially in those over 45 years of age. On 27th February 2001, “TODAY” newspaper reported that 1000 new cases of colorectal cancer are detected each year in Singapore.

People considered to be at high risk of colorectal cancers are those with a history of colorectal polyps or previous colorectal cancer, those with an immediate relative previously diagnosed with colorectal cancer before the age of 45, those with two or three immediate relatives diagnosed with colorectal cancer at any age, and those with a family known to have familial adenomatous polyposis [3].

Each of the sections of the colon and rectum has several layers of tissue.

Colorectal cancer starts in the innermost layer and can grow through some or all of the other layers. Lymph is a clear fluid that contains tissue waste products and immune system cells. Lymphatic vessels carry this fluid to lymph nodes (small, bean-shaped collections of immune system cells important in fighting infections). Most lymphatic vessels of the colon or rectum lead to regional lymph nodes in the vicinity. Cancer cells may enter lymph vessels and spread out along these vessels to reach lymph nodes, where they continue to grow. If cancer cells have multiplied in these lymph nodes, they are more likely to have spread to other organs of the body as well. Some examples of a colonoscopic view of the colon are shown in Figure 1.1. Polyp is characterised by its surface which is smooth in small polyps and lobular in large polyps, the covering mucosa appears normal or slightly erythematous with a pale yellow colour. The ulcers are characterised by the patches-like regions and reddish colour.

(a) Normal Colon

(b) Abnormal Colon (Polyps)

(c) Abnormal Colon (Ulcers)

Figure 1.1: Colonoscopic view of colon

Colon cancer can be prevented if polyps that lead to the cancer are detected and removed. The earlier the colorectal cancer is detected and treated, the greater the chance for a full recovery and a return to normal life. Several major studies have conclusively reported that frequent check-ups reduce mortality from colorectal cancer.

The simplest way to detect a rectal cancer is by the insertion of the doctor's finger into the rectum, i.e. a rectal examination. This can be done at the outpatient clinic, taking less than 5 minutes and causing minimal discomfort. However, this can only detect cancers in the last 5 to 8 cm of the rectum. An X-ray examination called a barium enema may also be performed to examine the whole length of the large intestine. A dye is inserted into the rectum and allowed to coat the length of the intestine. Multiple X-rays are subsequently taken from various portions of the large intestine. Hence, the abnormal areas are identified. A suspicious area must then be biopsied using a colonoscope or sigmoidoscope. For cancers, which are even further along the large intestine, a sigmoidoscope or endoscope examination can be performed. These scopes have longer fibre optic flexible tubes which are inserted up the rectum into the colon. Through these scopes, removal of a small piece of growth for pathological testing is possible. The insertion of this scope can be performed with minimal anaesthesia in an outpatient clinic. Although uncomfortable, the procedure lasts less than 30 minutes.

The colonoscope utilises a video chip and strobe light to capture an image which is then displayed on a video monitor. This allows careful visual inspection of the entire surface lining of the organ being examined. The operation of a colonoscope requires special skills acquired through years of training. The colon has a very flexible structure with bends and twists that make navigation of the colonoscope within the colon difficult. An inexperienced physician may insert the scope in the wrong direction, causing injury to the colon wall. In addition, while the inexperienced physician is concentrating on the determination of insertion direction and the operation of the colonoscope, the physician may overlook abnormalities present on the colon surface. During and after the clinical colonoscopic examination, essential analysis of the colonoscopic images is generally performed qualitatively which is time-

consuming, subject to variation in interpretation and is not suitable for comparative evaluation.

In the colonoscopic procedures, the physician inserts the long tube into the large intestine from the rectum while simultaneously watching the monitor to observe the inside of the colon. There are some difficulties in the existing colonoscopic procedures, including diagnosis of colonoscopic images and path planning for the navigation of the colonoscope. Therefore, the need for computer-based image processing and diagnostic systems is constantly increasing.

Image processing techniques have become increasingly important in a wide variety of applications in the medical field with the advent of information technology. These techniques can be used to assist the physician in diagnosis, treatment, and research because much of the experts' knowledge can be embedded in the computer-based systems. However, the image processing techniques are mainly applied to Magnetic Resonance Imaging (MRI), Computed Tomography (CT) and Positron Emission Tomography (PET) images as well as ultrasound images in the areas of enhancement and segmentation [4]-[7]. Only in recent years, the processing and analysis of colonoscopic images have gained importance and only a few researchers are working in this area [8]. Image processing and analysis can be applied to colonoscopic images in a number of areas, with very good potential for future clinical applications. The typical areas are:

- a. Enhancement of the colonoscopic image for better viewing and understanding. This includes brightness enhancement, contrast enhancement, noise removal, edge sharpening, pseudo-colours, etc.
 - b. Identification of tumours and abnormal tissues at an early stage: using the technique of image segmentation or pattern recognition, the image processing
-

- system can aid the clinicians in identifying and extracting the abnormal tissues from the normal tissues.
- c. Quantification of diagnostic information. These can be used for teaching, preoperative surgical review, comparison of findings, measurement of pathology size, and characterisation of the pathological features.
 - d. Computer-assisted diagnosis. It is hoped that an intelligent, computer-assisted clinical diagnosis can be achieved with a consistent level of performance. This could be possible with software that is capable of image analysis, such as identifying the lumen geometry with appropriate spatial parameters.

Computer-aided diagnostic system for colonoscopic images conceptually consists of the following subsystems or stages as shown in Figure 1.2.

Figure 1.2: An automated computer-aided diagnostic system

The images are acquired from an endoscope during the endoscopy. The pre-processing of the images is then performed to improve the quality of the input images. This includes noise reduction, contrast enhancement, histogram equalisation, etc. The images are then decomposed into regions, each of which holds properties distinct from those of their neighbours. This is an essential part of image analysis and is a basic requirement for the identification and classification of objects in an image. The

classification part characterises the features in the image with the kind of abnormality and labels each of these regions by type, for example, identifying the lumen, bleeding, ulcer, etc. At the end of this stage, all the abnormal areas on the image are marked. Then the decision making comes as an instruction or suggestion to the clinicians based on the results of classification. For instance, it could be a suggestion that a big lump exists on the surface of the tissue and it needs to be thoroughly examined to see whether it is benign or malignant. The analysis results can be saved and organised, so that the information can be used for reference and comparison in the future.

Literature review shows that increasing attention has been devoted to detecting abnormalities with the aid of computer vision system and image processing technique in recent years [9]-[13]. However, most of them concentrate their interests in identifying the skin tumour and lung cancer. On the other hand, in the area of colonoscopic image processing and analysis, it appears that reported research interests are focused on autonomous guidance systems to navigate the instrument in the human colon and the method for detecting boundary of colon lumen [14]-[18].

High-resolution digital colonoscopic images captured from the endoscope can lead to more accurate diagnosis and greater ease in documentation and analysis. The use of digital image processing and analysis on colonoscopic images would produce objective interpretations, together with quantitative measurements. Therefore, computer-assisted image processing is essential to assist the colonoscopic diagnosis, which can provide essential critical features for confirmation, comparison and evaluation of the suspicious signs. However, the image processing techniques developed for colonoscopic diagnosis are based on some specific characteristic domains. Generally, one single technique to efficiently detect different types of abnormalities related to gastro-intestinal cancers is not available.

1.2 Objectives

The objective of the present research is to develop a computer-aided scheme for the operation of an endoscope with the focus set on helping the physicians in the diagnosis of the colonoscopic images. The potential benefit of this research work is to facilitate diagnostic colonoscopy by developing computer-assisted methods in image processing and analysis. The objectives of the proposed project are:

- To develop new methods of colour image segmentation for the colour colonoscopic images, which are essential for alerting the physicians on possible abnormalities in the colon.
- To extract the quantitative parameters from the colonoscopic images to facilitate the classification of colon state and to classify the colonoscopic image into normal or abnormal state in order to help the physicians in doing the screening procedure.
- To design and implement the pseudo real-time colonoscopic image analysis which would be of great value in for detection of abnormalities.

1.3 Major Contributions of the Thesis

The main contributions of the present research work are described in the following section.

- New methods are proposed for segmentation of the colour colonoscopic image using texture information, colour-based method and clustering method. The texture information is measured with a method based on linear binary pattern and

magnitude. The colour-based segmentation uses a homogeneity index measure. The clustering algorithm utilises Fuzzy C-means.

- A new method for extracting the lumen of the colonoscopic image is proposed. The method is based on a modified deformable region model for the purpose of navigating the endoscope.
- A set of new quantitative features has been formulated for the analysis of the colonoscopic images to distinguish between normal and abnormal colon. The features are based on the shape, texture and colour information of the colonoscopic image.
- New application of feature selection coupled with artificial intelligence is proposed for classifying the colon state intelligently.
- Development of an intelligent classification method for detection of abnormalities in the colon, thus an intelligent colonoscopic instrumentation system by utilising colonoscopic images.
- New methods of endoscopic pseudo real-time image processing and analysis system have been developed.

1.4 Organisation of the Thesis

The organisation of the thesis is as follows. Introductory aspects of the research work and the objectives are included in Chapter 1. The relevant literature and a description of the proposed methods are reviewed in Chapter 2. Techniques for segmenting colour

colonoscopic images for medical diagnosis are proposed in Chapter 3. The methods for extracting the lumen for medical diagnosis are shown Chapter 4. The feature extraction and classification of the colonoscopic image for diagnosis are explained in Chapter 5. The extended application for the intelligent colonoscopic instrumentation system is described in Chapter 6. The summary of the achievements, major contribution made by the present work, and recommendations for future research is provided in Chapter 7, followed by the author's publications and the bibliography.

Chapter 2

LITERATURE REVIEW AND PROPOSED METHODS

In this chapter, the techniques and development of computer-aided diagnostics for the colonoscope are reviewed and summarised. Colonic anatomy and pathological features of colonoscopic images are mentioned in Section 2.1 and Section 2.2, respectively. Diagnostic endoscopy is given in Section 2.3. Selected image segmentation algorithms and colonoscopic image processing algorithms are described in Section 2.4 and Section 2.5, respectively.

2.1 Colonic Anatomy of the Colon

The anatomy of a normal colon has considerable variations from individual to individual. Therefore colonoscopists need to be aware of the normal anatomy and its common variations. It is useful to divide the colon into distinct sections as each part

has its own colonoscopic characteristics (Figure 2.1).

The colon is comprised of the cecum, ascending colon, transverse colon, descending colon, sigmoid colon, and finally the rectum. The cecum is mobile and its mobility depends on its posterior peritoneal attachment. The sigmoidal colon and the transverse colon are free to move on the mesenteries. The mobility of these sections of the colon is a function of their length and the elasticity of their mesenteries.

Figure 2.1: Gastrointestinal tract

A detailed description of the colon is as follows. The rectum is recognised by its location adjacent to the anus, its ample lumen compared to the other parts of the colon (short of the cecum), its semicircular valves and a characteristic mucosal translucency. Due to the flexibility of the endoscope, the internal end of the anal canal can be

inspected using a reflexion manoeuvre. It is important to become familiar with the normal appearance of the anus so that normal veins and venous cushions are not mistaken for haemorrhoids or rectal varices. The sigmoid colon loops anteriorly with the curve of the sacrum and then posteriorly to join the descending colon, which lies retroperitoneally in the left paracolic gutter. The mobile sigmoid colon is one of the keys to a successful colonoscopy. Excessive force applied to a rigid sigmoid colon is painful and may cause perforation.

The descending colon is usually easy to negotiate as it runs a straight course up the left paracolic gutter before turning medially and anterior. Frequently, a blue discolouration is seen at the splenic flexure where the spleen abuts the thin-walled colon. The transverse colon runs adjacent to the anterior abdominal wall, then turns posteriorly to enter the hepatic flexure, which turns down into the right paracolic gutter. The ascending colon runs retroperitoneally down the right paracolic gutter to enter the cecum.

A large number of abnormalities may be observed during colonoscopy, such as colitis, ischemic colitis, strictures, diverticula, polypoid lesions, and colonic malignancy (See details in Section 2.2). Many of these were discussed with the physicians and are well illustrated in endoscopic atlases [19]–[21].

2.2 Pathological Features of Colonoscopic Images

The operation of a colonoscope requires a high level of skill and experience to avoid injury to the patient. The major risks of colonoscopy are bleeding and perforation.

- Bleeding is most commonly seen after colonoscopic polypectomy; it can be
-

immediate or delayed. Local methods of haemostasis (injection, heater probe) may solve this problem.

- Perforation is the most serious of colonoscopic complications. Colonoscopy is contraindicated when the bowel is severely inflamed or when recent perforation is suspected. Pneumatic perforation due to excessive insufflations of the bowel proximal to a distal stricture is a rare event. However, this type of complication is an obvious risk in the presence of high-grade bowel obstruction. Forcing the colonoscope tip through a tight stricture also invites trouble. Perforation can occur in a normal colon. A colonoscope can exert enormous forces on the bowel wall. Sometimes these shearing forces are sufficient to cause a transmural tear, often at a distance from the colonoscope tip. A classic scenario is the sigmoidal colon tear resulting from excessive force applied to overcome looping, this type of perforation always requires surgical repair.

A large number of abnormalities may be seen during colonoscopy. Some of the more common abnormalities are briefly described below.

- *Colitis*
Normal colonic mucosa has luster and translucency. In certain areas, particularly the rectum, sub-mucosal vessels are clearly visible. Loss of these characteristics is an early sign of mucosal inflammation. Friability (ease of bleeding) is another sign of colitis. The colonic epithelium is packed with mucus-secreting goblet cells; mucus secretion increases when the mucosa is irritated. This protective mechanism is responsible for the characteristic mucous quality of colitic diarrhoea. Severe inflammation generates exudates giving the mucosa a mottled red and white (strawberry and cream) appearance.
-

Acute colitis may be focal or diffuse. Focal colitis is often limited to the rectum (proctitis), where a sharply demarcated border exists between the normal and abnormal mucosa. Most patients with ulcerative colitis also have rectal involvement. Rectal sparing, patchy ('skip') lesions, aphthous ulcers, ileal strictures, perianal fissures and fistulae are all suggestive of Crohn's disease. Infectious colitides tend to have non-specific appearances. However, pseudomembranous colitis (associated with *Clostridium siffficile* infection) is easily recognised: multiple cream-coloured or yellow pseudomembranes dots on the surface of the bowel. Cytomegalovirus (CMV) colitis may be suspected in immunosuppressed patients when large, flat, circumscribed red lesions are seen. These are different from, and should not be confused with, the nodular lesions of Kaposi's sarcoma complicating acquired immune deficiency syndrome (AIDS).

(a) Ulceration in active ulcerative colitis

(b) Loss of inter-haustral fold pattern in chronic ulcerative colitis

(c) Tabularisation of the colon occurs in long-standing ulcerative colitis

Figure 2.2: Ulcerative colitis

● *Ischemic colitis*

Colonic ischemia is a microvascular phenomenon principally affecting so-called 'watershed' areas of arterial blood supply, such as where the superior and inferior mesenteric artery territories overlap. The classical presentation,

usually an elderly man, is of acute abdominal pain accompanied by a bloody stool. A plain abdominal radiogram showing indentation or 'thumb-printing' of the colonic gas pattern; evidence of mucosal edema, is a strong indication used in the diagnosis. As the condition is almost always self-limiting, endoscopy is only utilised if the diagnosis is seriously in doubt. The appearances of ischemic colon range from subtle to dramatic; at the severe end of the spectrum the mucosa has a dusky, purplish hue. Once a diagnosis of colonic ischemia has been confirmed, the colonoscope should be withdrawn. Attempting total colonoscopy may risk a mucosal tear or perforation.

- ***Strictures***

Benign colonic strictures may be post-surgical or due to a variety of conditions, including diverticular disease, Crohn's colitis, intestinal ischemia and tuberculosis. Contrast studies are often more useful for evaluating strictures than colonoscopy. The information provided by inspecting the lumen is often limited. It is unwise to push blindly through a tight colonic stricture, as this risks perforation. Some benign colonic strictures are amenable to colonoscopic dilatation using balloon catheters. Malignant strictures may be obvious on barium enema examination. Occasionally, malignant colon strictures are extrinsic rather than intrinsic; locally metastatic tumour (e.g. gastric) encases the colon, causing narrowing but rarely complete obstruction.

- ***Diverticula***

There are outpouchings of mucosa at sites of weakness in the colon wall. They are easily recognised on barium enema. The presence of extensive diverticulosis on a contrast study should set off mental alarm bells and

colonoscopy may be difficult. The sigmoid colon often becomes rigid as a result of the fibrous reaction to diverticulitis; this loss of mobility renders colonoscopy difficult, if not impossible. Other causes of a rigid pelvic colon include previous pelvic inflammatory disease, peritonitis, gynaecologic surgery (especially abdominal hysterectomy) and pelvic irradiation. The colonoscope tip should never be pushed ahead blindly if diverticula are present. The trick to distinguishing the lumen from the opening of a diverticulum is to follow the folds. Folds radiate from the lumen but not from a diverticulum.

Figure 2.3: Diverticular disease

- ***Polypoid Lesions***

Colonic polypoid lesions are the most common pathology found during colonoscopy. They may be single or multiple, and of epithelial or nonepithelial origin. The epithelial polyps include adenomatous polyps, hyperplastic polyps, juvenile polyps, and inflammatory polyps. The characteristic appearance of colonic adenomas varies. Histologically, adenomas are composed predominantly of branching tubules packed closely together surrounded by lamina propria, and are often pale-yellow. Hyperplastic polyps are small sessile excrescences, usually less than 5 mm in diameter, most commonly found in the rectum. The tiny mucosal excrescences or slightly larger mamillations can be

pale or the same colour as the surrounding mucosa. Juvenile polyps, a type of hamartoma, are prevalent in children and adolescents. The typical colonoscopic finding is that of a 1.5 to 3 cm sessile lesion with an intensely erythematous, friable, eroded, ulcerated surface. Inflammatory polyps or pseudopolyps occur in the setting of inflammatory changes in the colon. Lipoma is the most frequently encountered lesion of submucosal tumours. One diagnoses a lipoma by the colour, the smooth surface, and by determining whether the lesion is soft and indents when pressed by an accessory such as closed biopsy forceps. Leiomyoma are rare submucosal tumours in the colon, ranging in size from 2 mm to 4 cm. At colonoscopy they appear smooth and sessile, and may be covered with reddish, stretched mucosa. Carcinoid tumours may be found in the rectum but are rare in the colon. Usually a carcinoid appears as a smooth, sessile lesion with a glistening surface mucosa, which is of a pale-yellow colour.

(a) A flat, sessile, villous polyp which developed around a valve of Houston

(b) Conglomerate of innumerable small polyps covers the colon wall like a carpet

(c) Minute polyps scattered over the colon wall

Figure 2.4: Polyps

- *Colonic Malignancy*

Colonic malignancy includes epithelial malignancies and nonepithelial

malignancies. The epithelial malignancies include adenocarcinoma, and epidermoid cancer. The nonepithelial malignancies include lymphoma, and kaposi's sarcoma. Adenocarcinomas may occur throughout the rectocolon but are most common within the distal 40 cm. An ulcerated mass is a commonly encountered configuration of adenocarcinoma. The ulcer is irregular, deep, and grey or pink, with a necrotic appearance. The surrounding mucosa is heaped up, red, and friable, and accounts for the bleeding which occurs in the majority of these lesions. Epidermoid or squamous-cell carcinoma originating from the anal verge may occasionally invade the distal rectum.

Various abnormalities in the colon have been described in the earlier section. In present research work, new methods are developed to enable computer-assisted analysis and diagnosis of a few commonly occurring abnormalities. The results of the present work can be extrapolated to include larger number and types of abnormality.

2.3 Diagnostic Endoscopy

Colonoscopic examination today is a common and safe technique used in medical treatment and is even more essential than X-ray examination in gastroenterology. Colonoscopic diagnosis of diseases occurring in the gastrointestinal tract has already used the endoscope, and various colonoscopic treatments are now used.

Some research works have been done to improve the endoscope for different functions, including the small intestine diagnosis and therapy [23], paranasal sinus surgery [24], and rigid neuroendoscope navigation for minimally invasive surgery [25]. The fundamental limitation of current flexible endoscopes is the inability to know the position and orientation of all parts of the device [26]. As a consequence the

movement of the endoscope is difficult with the possibility of damage to the walls of the colon. The computer control of an endoscope was shown to be feasible using the mathematical tools for manipulating highly redundant and flexible robots. The computer-controlled endoscope uses air actuation of a multi-link mechanism with sensory feedback provided by a 3-D magnetic sensor placed in the biopsy channel of the gastroenterological endoscope [27]. A virtual endoscope system (VES) with force sensation [28] has also been developed.

The fibre optic endoscopes have been widely used for diagnosis and therapy of digestive diseases [29]. The fibre scope examination gives a reliable diagnosis of early gastric cancer. Recently, fibre optic endoscopes have been replaced by video endoscopes. A video endoscope contains a charge couple device (CCD) camera to capture the image of the colon, and the captured image is transmitted to a large colour monitor where the colonoscopic image is displayed. It has several advantages compared to the fibre optic endoscopes including high resolution, high image quality, and better diagnosis of abnormalities. There are two types of imaging systems available in video endoscopes:

- A simultaneous colour television system

Each picture element of the CCD is provided with a colour filter array arranged in mosaic form, and the three RGB colour signals are obtained simultaneously. The advantages are that the image is sharp, and that colour registration is perfect even for rapidly moving objects. The disadvantage is that there is a limitation to the extent of miniaturisation possible.

- A field sequential type

The light source is provided with rotating red (R), green (G), and blue (B)

filters. A sequence of these three colours reaches the object, and the reflected light is converted into R, G, and B electric signals, which are then transmitted to a TV monitor. In this case, it is easier to miniaturise the CCD, and the production of the three primary colours has high fidelity. Colour registration is difficult for rapidly moving objects and it is complicated by short exposure time.

Video endoscopes provide advantages for monitoring, documenting, and processing the image. Image processing is considered to hold great potential for future applications, particularly for the detection of early stage lesions. As the image obtained is in the form of electronic signals, it can be changed, manipulated, enhanced, transmitted, and merged with an entire array of other electronic media and databases using computer technology. One of technical advances possibly made by video endoscopes is the application of software processing of digital images and hardware improvement.

Image processing for the colonoscopic images can be divided into two sub-categories: image enhancement and image analysis. The image enhancement technique improves the visual clarity of an image without generating any new information about it. This includes various techniques such as edge enhancement and colour enhancement. Image analysis produces additional information about an image and encompasses techniques such as pattern recognition and feature extraction. Both techniques can be processed by individual operations (e.g. contrast enhancement) or by neighbourhood operations (e.g. edge enhancement). In individual pixel operations, calculations are performed on the values of each single pixel, independent of the value of other pixels in the image. In neighbourhood operations, the value of a pixel is replaced by a value that is modified by the values of neighbouring pixels [22].

2.4 Selected Image Segmentation Algorithms

Image segmentation is the first and the most difficult task in analysing an image with a view to object detection, feature extraction, object recognition, scene interpretation, and image coding. The principal goal of the segmentation process is to partition an image into regions (also called classes, or subsets) that are homogeneous with respect to one or more characteristic features. Image segmentation is an ongoing research area and a number of approaches have been proposed in the literature. Despite the large number of segmentation techniques available, no one general method is available to handle a large and diverse set of imagery. Research efforts are geared towards developing a segmentation scheme which is most appropriate for a given application [30].

2.4.1 Thresholding Methods

Thresholding is an important technique for image segmentation and is used in many image processing applications. A thresholding procedure attempts to determine an intensity value, called the threshold, which separates the desired classes. The segmentation is then achieved by grouping all pixels with intensity greater than the threshold into one class, and all other pixels into other classes. Thresholding is often used as an initial step in a sequence of image processing operations. Its simplest form can only generate two classes. Thresholding typically does not take into account the spatial characteristics of an image. This causes it to be sensitive to noise and intensity inhomogeneities, which can occur in magnetic resonance imaging [31]. These artefacts essentially corrupt the histogram of the image, making separation more difficult. For

these reasons, variations on classical thresholding have been proposed for medical image segmentation, such as for chromosome images [32] and stomach images [33].

There are two main approaches to locate the thresholds: parametric and nonparametric. In the parametric approach, a model is assumed to have the probability density function of the grey level distribution of each group. One then attempts to find an estimate of the parameters of the distributions using the given histogram. This results in a non-linear estimation problem that is computationally expensive. In the nonparametric approach, one is interested in getting the thresholds in an optimum manner according to some criterion such as within-class variance, between-class variance, total variance [34]-[35], and entropy [36]-[37]. The nonparametric approach has proved to be robust and more accurate than the parametric as long as the grey level distribution does not fit a known probability density function.

There are two kinds of thresholding methods: bilevel and multilevel thresholding methods. Bilevel thresholding method separates only two regions in the image, whereas multilevel thresholding method separates more than two regions. Some efforts on improving the bilevel thresholding methods [38]-[42] and the multilevel thresholding methods [43]-[45] have been carried out.

2.4.2 Region-based Segmentation

There are also other methods for image segmentation. These methods can be conveniently grouped into boundary-based and region-based techniques [46]. The boundary-based techniques use the assumption that pixel values change rapidly at the boundary between two regions [47]-[48]. These techniques use edge detectors to provide candidates for region boundaries. In this case, the actual region boundaries

should be closed curves [49]. Therefore, some post processing, such as edge tracking, gap filling, smoothing, and thinning, should be performed to obtain closed region boundaries. All of these post processes are very time-consuming. The time-consuming post processing can be avoided by integrating the results of boundary-based approaches and those of the region-based approaches.

Region-based techniques rely on the assumption that adjacent pixels in the same region have similar visual features such as grey level, colour values, or texture. The advantages of using region-based segmentation are: (1) there are far fewer regions than pixels in an image, thus allowing data compression; and (2) regions are connected and unique. The disadvantages of this method are: (1) assumptions are made about the uniformity of image features; (2) a region could be erroneously considered as a single surface; and (3) surface properties or reflection could produce noisy regions.

There are two principal approaches to region-based segmentation [50], namely region splitting and region merging. Region splitting has a top-down approach and it starts with the assumption that the entire image is homogeneous. If it is not true, the image is split into four sub images. This splitting procedure is repeated recursively until homogeneous image regions are encountered. This procedure produces an image representation that can be described by a tree whose nodes have four sons, each because it is recursive. Such a tree is called a quad tree and is a very convenient region representation scheme. A quad tree is shown in Figure 2.5.

Figure 2.5: (a) Original image (b) Quad tree representation

Region merging method is the opposite of region splitting. A merging procedure must be devised in order to merge adjacent regions that have similar statistical properties. The arithmetic mean μ_i and the standard deviation ν_i of a class R_i having d pixels in equations (2.1) and (2.2) can be used to decide if the merging of two regions R_1, R_2 is allowed.

$$\mu_i = \frac{1}{d} \sum_{(x,y) \in R_i} I(x,y) \quad (2.1)$$

$$\nu_i = \sqrt{\frac{1}{d} \sum_{(k,l) \in R_i} (I(x,y) - \mu_i)^2} \quad (2.2)$$

If the arithmetic means are close to each other with the constant k as stated in equation (2.3), the two regions are permitted to merge.

$$|\mu_1 - \mu_2| < k\nu_i \quad ; \quad i = 1, 2 \quad (2.3)$$

The combination of the two approaches, region splitting and region merging, is an iterative algorithm that includes both splitting and merging at each iteration.

The algorithm functions as follows:

- a. If a region R is inhomogeneous ($P(R) = FALSE$), it is split into four sub-regions.
- b. If two adjacent regions R_i, R_j are homogeneous ($P(R_i \cup R_j) = TRUE$), they are merged.
- c. Stops when no further splitting or merging is possible.

The algorithm mentioned above segments the image into regions, which have similar characteristics. The drawback of this method is that it is time-consuming since it is an iterative algorithm.

2.4.3 Texture-based Image Segmentation

Previously, methods for image segmentation based on the grey-level properties of objects were described. These methods generally work well for man-made objects, which usually have a smooth grey-level surface. A textured region is observed as being homogeneous, although the intensity across the region may be non-uniform. This leads to the intensity-based segmentation methods to produce results that do not match with the perception of the scene.

Texture refers to properties that represent the surface or structure of an object. Texture is widely used, and perhaps intuitively obvious, but has no precise definition due to its wide variability [51]. Texture can be defined as something consisting of mutually related elements; therefore while considering a group of pixels (a texture primitive or texture element), the texture described is highly dependent on the number considered.

Texture features characterise the statistical or structural relationship between pixels, and provide measures of properties such as contrast, smoothness, coarseness, randomness, regularity, linearity, directionality, periodicity, and structural complexity. A texture surface having no definite pattern is said to be stochastic, while texture with a definite array of sub patterns is said to be deterministic.

Two main texture description approaches exist: statistical and syntactic. Statistical methods compute different properties and are suitable if texture primitive sizes are comparable with the pixel sizes. Syntactic and hybrid methods are more suitable for textures where primitives can be assigned as a label, which has primitive meaning in that, primitives can be described using a larger variety of properties than just tonal properties; for example, shape description.

The simplest statistical description for texture involves the use of first-order statistics of individual pixels, such as their intensity level. Also for a set of pixels, the mean, variance, skewness and kurtosis (the first, second, third and fourth moments respectively) can be used as texture features [52].

Some texture measurements are summarized by Pitas [53]. The simplest texture descriptors are based on the image histogram. The major limitation of features derived from a histogram is that they cannot express spatial texture characteristics. Julesz observed that the human eye is also sensitive to second-order statistics [54]. The second-order statistical measurements involve the probability of a pair of pixels at different distances and rotations; these are summarised in a table called a co-occurrence matrix or the histograms of grey-level difference. Spatial texture organisation can also be revealed in terms of the run-length statistics [55], [56]. Another set of texture descriptors is based on the grey-level co-occurrence matrices [55], [57], [58].

2.4.4 Colour Image Segmentation

The colour image can provide more information than the grey level image. There are many colour spaces and the most frequently used colour space for image processing is the RGB colour space. However it is hard to visualise a colour based on R, G, B components, and impossible to evaluate the perceived differences between colours on the basis of distance in RGB colour space.

In the perception process, however, a human can easily recognise basic attributes of colour: intensity (I), hue (H), and saturation (S). Sometimes, by using HSI colour space; instead of performing a feature-based segmentation on three channels (RGB), only one feature may be used, allowing the use of much faster algorithms [59]. The hue is the attribute of colour perception denoted by red, yellow, green, blue, and so on. Saturation is used to describe how pure a colour is or how much white is added to a pure colour. The intensity is a measure of total reflectance in the visible region of the spectrum, and it is an achromatic component of colour. The colour transformation from RGB colour space to HSI colour is as follows:

$$\begin{bmatrix} I \\ V_1 \\ V_2 \end{bmatrix} = \begin{bmatrix} 1/3 & 1/3 & 1/3 \\ 0 & 1/\sqrt{2} & -1/\sqrt{2} \\ 2/\sqrt{6} & -1/\sqrt{6} & -1/\sqrt{6} \end{bmatrix} \begin{bmatrix} R \\ G \\ B \end{bmatrix}$$

$$I = 1/3(R + G + B) \quad (2.4)$$

$$Hue = \tan^{-1}\left(\frac{V_2}{V_1}\right) \quad (2.5)$$

$$S = \sqrt{V_1^2 + V_2^2} \quad (2.6)$$

The hue coordinate range is $[0, \dots, 2\pi] = [0^0, \dots, 360^0]$.

Although perceptual HSI colour spaces provide a more intuitive description of colour than, for example, RGB, they are based on simplifying assumptions and do not constitute perceptually uniform colour spaces. Equal Euclidean distances correspond to a colour space which has perceived colour differences. As perceptually uniform colour spaces, two colour spaces recommended by the CIE (Commission Internationale de l'Eclairage) are mainly used. They are the so-called CIE $L^*a^*b^*$ (for reflected light) and CIE $L^*u^*v^*$ (for emitted light). L^* stands for lightness value, the component a^* denotes relative redness-greenness, and b^* , yellowness-blueness. Similar to the case of HSI colour space, the $L^*a^*b^*$ colour space is obtained from RGB in two stages. In the first stage, XYZ colour space is obtained by using a linear transformation and in the second stage, $L^*a^*b^*$ is obtained by using a non-linear transformation on the XYZ colour space.

$$\begin{pmatrix} X \\ Y \\ Z \end{pmatrix} = \begin{pmatrix} 0.490 & 0.310 & 0.200 \\ 0.177 & 0.812 & 0.011 \\ 0.000 & 0.010 & 0.990 \end{pmatrix} \begin{pmatrix} R \\ G \\ B \end{pmatrix} \quad (2.7)$$

$$L^* = 116 \left(\sqrt[3]{\frac{Y}{Y_0}} \right) - 16 \quad (2.8)$$

$$a^* = 500 \left[\sqrt[3]{\frac{X}{X_0}} - \sqrt[3]{\frac{Y}{Y_0}} \right] \quad (2.9)$$

$$b^* = 200 \left[\sqrt[3]{\frac{Y}{Y_0}} - \sqrt[3]{\frac{Z}{Z_0}} \right] \quad (2.10)$$

where (X_0, Y_0, Z_0) are XYZ values for the standard white.

The choice of an appropriate colour space can be an important factor in determining the results of image segmentation on a colour image. In practice, there is no ideal colour space for all image processing applications. The decision as to which colour space to use depends on the processing task. An optimal decision can be very hard to find. However, knowledge of the properties of the various colour spaces makes the choice easier.

Some researchers have developed segmentation algorithms using perceptual colour space, which overcome usage of other colour spaces [60]-[70]. The image can be separated into chromatic and achromatic regions according to the region locations in the colour space.

2.4.5 Clustering Methods

Clustering methods essentially perform the same function as classifier methods without the use of training data. Thus, they are termed unsupervised methods. In order to compensate for the lack of training data, clustering methods iterate between segmenting the image and characterising the properties of each class. In a sense, clustering methods train themselves using the available data. There are two main categories of clustering methods: hierarchical and partitional clustering methods [71]. A hierarchical clustering method is a procedure for transforming a proximity matrix into a sequence of nested partitions. A partitional clustering method is a procedure that loops through the objects and assign each of the objects to the seed point to which it is the closest.

2.4.5.1 Hierarchical Clustering Method

There are two options in the hierarchical clustering method, which are

agglomerative and divisive. An agglomerative algorithm for hierarchical clustering starts with the disjoint clustering, which places each of n objects in an individual cluster. The clustering algorithm being employed dictates how the proximity matrix should be interpreted to merge two or more of these trivial clusters repeatedly until a single cluster containing all n objects, called the conjoint cluster, remains. A divisive algorithm performs the task in the reverse order. Hierarchical clustering may be represented by a two-dimensional diagram known as dendrogram, which illustrates the fusions or divisions made at each successive stage of analysis.

There are three different ways of defining inter-cluster distance in hierarchical clustering methods: single-link, complete-link, and average-link methods. In a single-link method (also called the connectedness or minimum method), the distance between one cluster and another cluster is considered to be equal to the shortest distance from any member of one cluster to any member of the other cluster. In complete-link method (also called the diameter or maximum method), the distance between one cluster and another cluster is considered to be equal to the longest distance from any member of one cluster to any member of the other cluster. In an average-link method, the distance between one cluster and another cluster is considered to be equal to the average distance from any member of one cluster to any member of the other cluster.

2.4.5.2 Partitional Clustering Method

In a partitional clustering algorithm, the k “seed” points are chosen at the start. The results obtained depend upon the selection of the seed points. The k initial seeds can arbitrarily be the first k cases, a randomly chosen k cases, k specified cases, or chosen from a k -cluster hierarchical solution.

Three commonly used partitional clustering algorithms are the K-means algorithm,

Fuzzy c-means algorithm, and the Expectation-Maximisation (EM) algorithm. The K -means algorithm clusters data by iteratively computing a mean intensity for each class and segmenting the image by classifying each pixel in the class with the nearest mean [71]. The FCM algorithm generalises the K -means algorithm [72], allowing for soft segmentations based on fuzzy set theory [73]. The EM algorithm applies the same clustering principles with the underlying assumption that the data follows a Gaussian mixture model [74], [75]. The EM algorithm iterates between computing the posterior probabilities and computing the maximum likelihood estimates of the means, covariances, and mixing coefficients of the mixture model.

The partitional clustering algorithm is simple and requires minimum computation, but the results depend on the initial cluster centre. Therefore, there is an important question that needs to be answered before applying the partitional algorithms, how many clusters are there in the data? This is not known a priori and, in fact, there might be no definite or unique answer as to what value k should be taken. In other words, k is a nuisance parameter of the clustering model. Efforts have been attempted to solve this problem. From the literatures, there are two approaches to estimate the number of clusters. One approach uses statistical methods to estimate the number of clusters for K -means and EM clustering algorithms. Another approach uses cluster validity measures to estimate the number of clusters for Fuzzy clustering algorithm.

A. Estimation of Number of Clusters using Statistical Methods

There are five common approaches to estimate the number of clusters for K -means and EM clustering algorithms: cross-validation, penalised likelihood estimation, permutation tests, resampling, and finding the knee of an error curve [76].

Cross-validation creates a model that attempts to fit the data as accurately as possible. Monte-Carlo cross-validation [77] was used to prevent over-fitting (too many clusters). In v-fold cross-validation [78], repeated (v) random samples are drawn from the data for the analysis, and the respective model or prediction method, etc. is then applied to compute predicted values, classifications, etc. Typically, summary indices of the accuracy of the prediction are computed over the v replications; thus, this technique allows the analyst to evaluate the overall accuracy of the respective prediction model or method in repeatedly drawn random samples.

Penalised likelihood estimation attempts to find a model of the data that is as accurate as possible and minimises the complexity of the model. Some methods to penalise model complexity are Bayesian Information Criterion [79], Minimum Description Length [80], and Subspace Information Criterion [81].

Permutation tests [82] analyse the possible over-fit of a model to the available data rather than uses a term for penalizing model complexity. However, permutations are computationally heavy and not necessarily suitable for time critical systems.

Resampling [83] and Consensus Clustering [84] attempt to find the correct number of clusters by clustering many samples of the data set and determining the number of clusters where clustering of the various samples are the most “stable”. Finding the knee of an error curve statistically evaluate each point in the error curve and use the point that either minimizes or maximizes some function as the number of clusters. Such methods include the Prediction Strength [85], Gap Statistic [86], and L method [76].

B. Estimation of Number of Clusters using Cluster Validity Measures

The fuzzy cluster validity is an important issue in cluster analysis because fuzzy

clustering algorithms are unsupervised in nature and the result of clustering needs to be validated in most applications. In general, cluster validation may answer questions, such as the goodness of the partitions, the possibility for better partitioning, etc. If the number of clusters is not known *a priori*, a validation index may help to find out the optimal number of clusters. This is done in three stages as follows.

- Stage one: fix all parameters of the clustering method, except for the number of clusters.
- Stage two: vary the number of clusters between 2 and an upper value c_{max} and applying a clustering algorithm for each number of clusters to find a different partition of the data.
- Stage three: apply a cluster validity measure to each partition obtained at the second stage to define a validation value. The true number of data clusters can be determined based on extrema of these validation values for all number of clusters.

The first fuzzy cluster validity functions associated with FCM clustering algorithms introduced by Bezdek are the partition coefficient (PC) [87] and the partition entropy (PE) [88]. Their main disadvantage is the lack of direct connection to the geometrical properties of the data and their monotonic evolution tendency with respect to cluster number, c . Other indexes have been proposed by taking into account the geometrical properties, such as Fukuyama-Sugeno index [89] and Xie-Beni index [90]. According to the analysis done by Pal, et al. [91], the Fukuyama-Sugeno index is sensitive to both high and low values of weighting exponent m and may be unreliable because of this. They reported that the Xie-Beni index provided the best response over a wide range of choices for 2 to 10 clusters and for weighting exponent m from 1.01 to 7. However, the

Xie-Beni index monotonically decrease as the number of clusters c becomes very large and close to the number of data points n . Kwon index [92] was developed to eliminate the monotonically decreasing tendency when the number of clusters becomes very large and close to the number of data points.

A reliable validation function for the FCM must consider both the compactness and the separation of a fuzzy c -partition. Some researchers worked on these criteria. Rezaee, et al. [93] assess the average compactness and separation of fuzzy partitions generated by FCM algorithm. Zahid, et al. [94] developed a heuristic method which is based on the combination of two functions. The first function calculates the fuzzy compactness-separation ratio by considering geometrical properties and membership degrees of data. The second function evaluates the ratio by using only the properties of membership degrees. Hou, et al. [95] proposed cluster validity criterion for the cross iterative fuzzy clustering algorithm which considers two kinds of outputs of fuzzy clustering, the ratio of fuzzy compactness to average fuzzy separation and the ratio of fuzzy union to fuzzy intersection of clusters. The minimum of the criterion is a fine indicator for a compact and well-separated partition.

The issue of finding fuzzy cluster validity is still an open problem and more developments are expected before it can be effectively used in applications. Liu, et al. [96] developed a computational algorithm based on genetic algorithms for solving clustering problem as a bilevel fuzzy criterion clustering problem. Pei, et al. [97] used fuzzy similarity to validate the number of cluster, which is found out to be simpler and robust compared to traditional cluster validity measure. Hammah, et al. [98] modified Gath-Geva validity indices [99] by deriving the fuzzy hyper-volume and sum of central members based on the geometric interpretation of their Euclidean equivalents for the fuzzy cluster analysis of orientations. Chung, et al. [100] proposed cluster

validity criterion which is suitable for hyper-plane-shaped cluster. Franco, et al. [101] extended and optimised the Fisher's Linear Discriminant so that it can be applied to measure the compactness and separation of partitions produced by any fuzzy or crisp clustering algorithm. They also proposed ICC index that evaluated correctly the number of clusters even when the overlapping among clusters is high.

Geva [102] combined hierarchical and fuzzy concepts to give a natural feasible solution to the cluster validity problem of real data. The hierarchical-fuzzy algorithm attempts to exploit the advantages of hierarchical clustering while overcoming its disadvantages by means of fuzzy clustering. But it should be noted that this algorithm's results are sensitive to the chosen cluster validity criterion. This algorithm can be realised by parallel computation where each subclustering can be made by a different processor, which can make it faster.

Some studies [91], [93] have shown that some validity indexes may fail, for example, when the numerical representation of the objects may not possess adequate information to discriminate between clusters of objects. Further, even if the data possess the desired substructure, the algorithm used may not extract it from the data. Therefore, cluster-merging methods are developed to resolve the problem of cluster validation as follows.

Bensaid, et al. [103] introduced an algorithm that uses cluster validity to mitigate two problems when clustering algorithms are applied to image segmentation. The problems are: the criterion they optimize may not be a good estimator of 'true' classification quality and they often admit many (suboptimal) solutions. Therefore, the validity-guided (re)clustering (VGC) algorithm is proposed, which uses the cluster-validity information to guide a fuzzy (re)clustering process toward better solutions. It starts with a partition generated by a soft or fuzzy clustering algorithm. Then it

iteratively alters the partition by applying (novel) split and merges operations to the clusters.

A hybrid approach for solving the cluster validity problem was proposed by Chong, et al. [104]. The proposed technique uses a cluster validity index (Fukuyama-Sugeno index) in conjunction with a merging index to find the optimal number of clusters in a set of data. The technique does not place any restriction on the fuzzy (FCM) clustering technique and the cluster validity index used. Fukuyama-Sugeno (FS) index works well when the clusters are highly separable. Therefore, when it comes to data with cluster centres close to one another, FS index produces a number greater than the desired number of clusters. Merging is needed to get the desired number of clusters.

A similarity-driven cluster merging method was proposed for unsupervised fuzzy clustering by Xiong [105]. The data is clustered initially with an over-specified number of clusters. Pairs of similar clusters are merged based on the proposed similarity-driven cluster merging criterion. The similarity between clusters is calculated by a fuzzy cluster similarity matrix, while an adaptive threshold is used for merging. Therefore, only a few iterations are needed to find the optimal number of clusters c , and more precise partitions can be obtained. In addition, a modified generalized objective function is used for prototype-based fuzzy clustering. The function includes the p -norm distance measure as well as principal components of the clusters. The number of the principal components is determined automatically from the data being clustered.

2.4.6 Feature Selection Methods

In many applications, numerous features are obtained in an attempt to ensure accurate classification of the unknown classes. Sometimes, these features must be reduced to a smaller number before classification schemes can be applied, because classifiers can become computationally and analytically unmanageable in high dimensions. Dimensionality reduction may result not only in improving the speed of data manipulation, but even in improving the classification rate by reducing the influence of noise. There are two major categories of methods of dimensionality reduction [106], which are feature selection methods and feature transform (or feature extraction) methods. Feature selection methods keep only useful features and discard others. Feature transform methods construct new features out of the original variables. Dimensionality reduction for feature selection methods are useful for selecting significant features extracted from colonoscopic images that allow a quick training of the Neural Networks; therefore these methods will be described more detail in this literature review. Feature selection techniques were classified into two basic approaches, which are filtering and wrapper approaches [107]. A brief overview of the different approaches is as follows.

2.4.6.1 Filtering Approach

The filtering approach explores various subsets of features to find an optimal subset, which preserves the classification knowledge. This approach is not dedicated to a specific type of classification method. It includes basic linear nonlinear transforms of the input variable (PCA, LDA, ICA), nonlinear transforms of the input variable (kernel PCA, kernel LDA), etc.

Principal component analysis (PCA) and linear discriminant analysis (LDA) are two popular methods used for dimensionality reduction. Both of them project the parameter vectors into a new feature space through a linear transformation matrix with different intentions. PCA is also known as Karhunen-Loève transform (KLT), uses either the correlation or covariance matrices of the data to find a linear subspace efficient for representation. Based on the correlation matrix it finds a subspace that minimizes the mean-square error between the feature vectors and their projections in this space. The principle axis then passes through the data mean. Based on the covariance matrix, the data mean is effectively shifted to the origin of the feature space. LDA is also known as Fisher's discriminant analysis, finds a linear subspace that maximizes class separability among the feature vector projections in this space. Popular separability criterion is ratio of between-class scatter and within-class scatter. LDA seeks directions efficient for discrimination.

Independent component analysis (ICA) [108] is another linear transform which transforms an N-dimensional random vector in order to minimize the statistical dependence between its components. Based on this method, an assumption of class-conditional independence was drawn to simplify the separability measure of divergence [109]. A framework which makes use of class-conditional independent component analyzers was proposed by adopting divergence and the Bayes decision scheme to the class-conditional representation.

The popularity of PCA and LDA, due to its simplicity and ease of use, has led many to overlook the fact that PCA and LDA are not the optimal method for feature dimensionality reduction in detection applications. The higher order of principal components (PC) or linear discriminant (LD) does not always guarantee retention of the discriminatory information present in the original feature space. Therefore, some

researchers developed nonlinear form for dimensionality reduction by integrating it with operator kernel functions [110]-[113].

Nonlinear component analysis as a kernel eigenvalue problem was introduced by Scholkopf, et al. [110]. Their interest was not in principal components in input space but in principal components of variables, or features, which are nonlinearly related to the input variables. They computed dot products in feature space by means of kernel functions in input space. Given any algorithm that can be expressed in terms of dot products, this kernel method has the ability to construct different nonlinear version of it. Kernel-based methods do not explicitly compute all dimensions of the feature space but work only in a relevant subspace of the feature space. The proposed method automatically chooses a subspace, which provides a means of taking advantage of lower dimensionality.

Mika, et al. [111] developed a nonlinear Fisher discriminant analysis with kernel. It computes the discriminant function in some feature space (which is non-linearly related to input space). This method uses different kernels, which allow for high flexibility due to the wide range of nonlinearities possible.

A generalized discriminant analysis (GDA) method [112] was also a method that deals with nonlinear discriminant analysis using kernel function operator. The underlying theory is close to the support vector machines (SVM) insofar as the GDA method provides a mapping of the input vectors into high-dimensional feature space. In the transformed space, linear properties make it easy to extend and generalize the classical linear discriminant analysis (LDA) to nonlinear discriminant analysis. The formulation is expressed as an eigenvalue problem resolution. Using a different kernel, one can cover a wide class of nonlinearities.

Suykens, et al. [113] developed a simple and straightforward support vector machine formulation to the problem of principal component analysis (PCA) in dual variables. By considering a mapping to a high-dimensional feature space and application of the kernel trick (Mercer theorem) kernel PCA is obtained as introduced by Scholkopf, et al. While least squares support vector machine classifiers have a natural link with kernel Fisher discriminant analysis (minimizing the within class scatter around targets $+1$ and -1), for PCA analysis one can take the interpretation of a one-class modeling problem with zero target value around which one maximizes the variance. The score variables are interpreted as error variables within the problem formulation. In this way primal-dual constrained optimization problem interpretations to linear and kernel PCA analysis are obtained in a similar style as for least square-support vector machine (LS-SVM) classifiers.

Other researchers investigated support vector machines algorithm for the application of feature selection. Rakotomamonjy, et al. [114] derived relevant criteria from SVM, Bi, et al. [115] constructed a series of sparse linear SVMs to generate linear models that can generalize well, and uses a subset of non-zero-weighted variables found by the linear models to produce a final nonlinear model, Shih, et al. [116] proposed an improved feature reduction method in input and feature spaces for classification using support vector machines (SVMs). In the input space, a subset of input features is selected by ranking their contributions to the decision function. In the feature space, features are ranked according to the weighted support vector in each dimension. By applying feature reduction in both input and feature spaces, a fast nonlinear SVM was developed without a significant loss in performance.

2.4.6.2 Wrapper Approach

The wrapper approach is a heuristic method which evaluates alternative feature sets by running some induction algorithms on the training data and using the estimated accuracy of the resulting classifiers as its metric. This approach relies on the performance of one type of classifier to evaluate the quality of a set of feature. The main disadvantage is computational expensive in running the induction algorithm repeatedly for each feature set considered. Some methods used wrapper approaches are briefly described as follows.

Attribute bagging (AB) is a wrapper method that can be used with any learning algorithm for improving the accuracy and stability of classifier ensembles induced using random subsets of features [117]. It establishes an appropriate attribute subset size and then randomly selects subsets of features, creating projections of the training set on which the ensemble classifiers are built. The induced classifiers are then used for voting.

Based on methods proposed by Figueiredo, et al. [75], Law, et al. [118] proposed the concept of feature saliency and introduced an expectation-maximization (EM) algorithm to estimate it, in the context of mixture-based clustering. Due to the introduction of a minimum message length model selection criterion, the saliency of irrelevant features is driven toward zero, which corresponds to performing feature selection. The criterion and algorithm are then extended to simultaneously estimate the feature saliencies and the number of clusters.

Dy, et al. [119] explored the issues involved in developing automated feature subset selection algorithms for unsupervised learning through FSSEM (Feature Subset Selection using Expectation-Maximization (EM) clustering) and through two different

performance criteria for evaluating candidate feature subsets: scatter separability and maximum likelihood. Proofs on the dimensionality biases of these feature criteria were presented as well as a cross-projection normalization scheme that can be applied to any criterion to ameliorate these biases.

Effort attempted to focus on a hybrid approach of feature selection was done by Sebban, et al. [120]. The analysis was begun with a filter model; exploiting the geometrical information contained in the minimum spanning tree (MST) built on the learning set. This model exploits a statistical test of relative certainty gain, used in a forward selection algorithm. It was found out that the MST can be replaced by the 1 nearest-neighbor graph without challenging the statistical framework. This leads to a feature selection algorithm belonging to a new category of hybrid models (filter-wrapper).

2.5 Colonoscopic Image Processing Algorithms

Studies on computer-based image processing and diagnosis systems for the endoscope have been cited in literature [121]-[134]. A few image processing techniques used in this thesis are derived from previous work. There have to be appropriate modification. Computer-based diagnostic systems have been developed for detecting abnormalities of the gastrointestinal tract. Some researchers used microscopic images [121]-[123] and others used colonoscopic images [124]-[128].

Microscopic images have been used for analysing and identifying features of normal and cancerous colonic mucosa. A number of quantitative techniques for the analysis of images used in the diagnosis of colonic cancer have been investigated. Features based on texture analysis were derived using the co-occurrence matrix, viz.,

angular second moment, entropy, contrast, inverse difference moment, dissimilarity, and correlation [121]. Orientational coherence metrics have been derived from neurophysiological foundations and applied to the classification of colonic cancer images [122]. Fractal analysis has also been investigated in separating normal and cancerous images [123].

Another approach is to use colonoscopic images to define features of the normal and the abnormal colon [124]-[128]. Image processing algorithms were applied to extract meaningful properties, such as chromatic and contour characteristics from the colonoscopic images [124]- [126]. Artificial intelligence algorithms such as a rule-based approach [127], a Fuzzy rule-based approach [128]-[129], and Neural Networks algorithms [130] were explored to assist the endoscopist in manoeuvring the colonoscope and to find out whether the abnormalities are present during the procedures. Methods of detecting the possible presence of abnormalities during the endoscopy of the lower gastro-intestinal system using curvature measures [131]-[132] have been developed.

Efforts for developing a shape reconstruction procedure from colonoscopic image sequences and producing global 3-D sketches of the object shape from image sequences taken by a moving endoscope [133] are undertaken to get a superior representation of the colon structure for morphological analysis of tumours on human inner organs. There are several difficulties which need to be dealt with, such as the shading problem in the case where a point light source is at the projection centre. One current development of a computer-aided diagnostic system for colonoscopy is virtual colonoscopy [134]. It is a minimally invasive technique that enables early detection of colorectal polyps and cancer. This approach collects sequences of images from Computer Tomography (CT) scans and analyses them using image processing

algorithms. If an abnormality is detected, colonoscopy should be performed to remove the cancer or polyps. Generally, the virtual colonoscopy will be in two stages, first the diagnosis and then for therapy, as opposed to the presently employed common endoscopy.

There are efforts to explore image processing techniques for colonoscopic diagnosis. However, compared with the techniques developed for the brain and cardiac image analysis, they are much less developed. Therefore, it is needed to explore more on the image processing and analysis technique for intelligent diagnostic colonoscopic instrumentation.

2.6 Problem to be solved in Diagnostic Colonoscopy

Based on literature review, attempts are made to come up with solutions to problems in diagnostic colonoscopy by developing new methods for the computer-assisted diagnosis. New approaches on image segmentation and analysis for intelligent colonoscopic instrumentation systems are proposed in this thesis. The proposed methods are: segmentation algorithm for the colonoscopic images by developing new techniques for using techniques based in texture, homogeneity index, and clustering. The extraction of the colon lumen by using modified deformable region model method, the extraction of quantitative parameters based on shape, texture, and colour information of the colonoscopic images to characterise the image, the selection of the extracted parameters by using principal component analysis for getting the significant features intelligently, and the intelligent classification of the colon state by using artificial neural network algorithm in order to help physician in doing the procedure. The proposed solution methods are described in detail in Chapter 3-Chapter 5. The

detailed linkage between chapters is shown in Appendix C.

2.7 Concluding Remarks

Significant amount of work has been done in order to improve the performance of the colonoscopic procedure to assist the physician. However, assistance to the inexperienced doctor is minimal. In this thesis, emphasis of the research is placed on the improvement of the image processing and analysis algorithms to detect abnormalities from the colonoscopic images to aid the physician performing the procedure.

Chapter 3

SEGMENTATION OF COLONOSCOPIC IMAGES

In this chapter, the newly developed methods for colonoscopic image segmentation using texture, homogeneity index, and clustering are described. The organisation of this chapter is as follows. The proposed texture-based segmentation for the colonoscopic image is presented in Section 3.2. The proposed image segmentation algorithms using homogeneity index is given in Section 3.3. The proposed clustering method for segmenting the colonoscopic image is included in Section 3.4. Some results are presented in Section 3.5 followed by the discussion. Concluding remarks are included in Section 3.6.

3.1 Introduction

Minimally invasive colonoscopic procedures are increasingly employed for diagnostic and surgical purposes in cases such as the gastrointestinal and respiratory ailments. An endoscopist performs these procedures and analyses the clinical images. Due to the

subjectivity of the image analysis by various physicians, it is preferable to develop an objective method of analysing the images. A computer-aided scheme will help considerably in the image analysis and quantitative characterisation of abnormalities, thereby improving the overall efficiency of the diagnosis. A crucial step in such an automated diagnostic scheme is the proper segmentation of the colonoscopic images. Based on this requirement, new methods have been developed in the present work for the segmentation of colonoscopic images. The following two approaches are considered while developing the new methods for segmenting the colonoscopic images.

- Identification of all the regions in a given image and then locating the regions of interest.

The given image is segmented into regions of connected pixels with predefined properties of homogeneity. After the segmentation, the region of interest in the given image is computed. In this case, the segmentation operation is always performed without *a priori* knowledge of the presence of the region of interest.

- Identification of the regions that meet the required characteristics of the region(s) of interest.

The pixel characteristics are determined from the qualitative information obtained from the domain knowledge. A quantitative measure is derived from the qualitative information to discriminate between pixels. In other words, the qualitative information from the domain knowledge provided at the macroscopic level of the image is translated to numerical values at the microscopic level of the pixels. Assigning a numerical value to the qualitative attributes is nontrivial and associated known techniques using histogram analysis, fuzzy logic, statistical

analysis, model-based techniques, etc., require extensive experimentation with the images for selection of appropriate numerical values. A new method extending the modified deformable model concept has been developed for assignment of numerical values.

The first approach described in this chapter is used for extracting multiple regions of clinical interest such as bleeding, polyps, etc. The second approach that will be described in Chapter 4 is used to extract the lumen from the colonoscopic image.

3.2 Texture-based Segmentation of Colonoscopic Image

Recently, Wang and He [135] introduced a new model of texture analysis based on the texture unit, where a texture image can be characterised by its texture spectrum.

In the study of Ojala, et. al. [136] the local binary pattern (LBP) feature performs with the lowest error rates for both the classification and pairs of complementary measures in which LBP is complemented with other measures. Hence the LBP model is the appropriate selection for this project and is implemented for the segmentation of colonoscopic image.

In the study of Wang and He, a texture unit (TU) is represented by eight elements, each of which has one of the three possible values (0, 1, 2) obtained from a neighbourhood of 3×3 pixels. In total, there are 6561 possible texture units describing spatial three-level patterns in a 3×3 neighbourhood. The distribution of texture units computed over a region is called the texture spectrum.

3.2.1 Kullback discrimination

A log-likelihood-ratio, the G statistic [137] defined in equation (3.1), is used as a pseudo-metric for comparing LBP/M (combination of LBP with the average intensity or other colour component) distributions. The value of the G statistic indicates the probability that the two sample distributions come from the same population: the higher the value, the lower the probability that the two samples are from the same population.

$$G = 2 \left[\sum_{s,m} \sum_{i=1}^n f_i \right] - \left[\sum_{s,m} \left(\sum_{i=1}^n f_i \right) \log \left(\sum_{i=1}^n f_i \right) \right] - \left[\sum_{i=1}^n \left(\sum_{s,m} f_i \right) \log \left(\sum_{s,m} f_i \right) \right] + \left[\left(\sum_{s,m} \sum_{i=1}^n f_i \right) \log \left(\sum_{s,m} \sum_{i=1}^n f_i \right) \right] \quad (3.1)$$

where s, m are the two sample histograms, n is the number of bins and f_i is the frequency at bin i . The usage of the G statistic is explained in the following section.

3.2.2 Algorithm for Texture-based Segmentation

The proposed texture-based segmentation applying the LBP model is given below:

3.2.2.1 Hierarchical splitting

Hierarchical splitting is used to divide the image into regions of roughly uniform texture. The purpose of applying the hierarchical splitting algorithm is to make the individual image regions uniform in texture. The decision whether a block is split to

four sub-blocks is based on a uniformity test.

Six pair-wise G distances between the LBP histograms of the four sub-blocks are calculated. Let the largest of the six G values be denoted as G_{max} and the smallest as G_{min} . The block is said to be non-uniform and is thus split further into four sub-blocks, if a measure of relative dissimilarity within region, R , is greater than a threshold, X , as given by

$$R = \frac{G_{max}}{G_{min}} > X \quad (3.2)$$

It is preferable to choose a smaller value for X instead of a larger one. It is better to split too much than too little, for the following agglomerative merging procedure is able to correct errors, where a uniform block of a single texture has been needlessly split.

3.2.2.2 Agglomerative merging

Agglomerative merging procedure continues to merge similar adjacent regions until a stopping criterion is met. At a particular stage of the merging, the pair of adjacent segments, which has the smallest Merger Importance (MI) value, is merged.

$$MI = p \times G \quad (3.3)$$

where p is the number of pixels in the smaller of the two regions and G is the distance measure defined in equation (3.1). At each step of the procedure, when the pair of adjacent segments with the smallest MI value has been found, the regions are merged. The two respective LBP histograms are summed to be the histogram of the

new image region. Before moving to the next step of merging, the G distances between the new region and all adjacent regions are computed. The stopping rule is given by:

$$MIR = \frac{MI_{cur}}{MI_{max}} > Y \quad (3.4)$$

where MIR is ratio of MI_{cur} , the merger importance for the current best merge, and MI_{max} , the largest merger importance of all preceding mergers, and Y is a preset threshold. When MIR is greater than Y , merging is halted.

By applying the proposed algorithm for texture-based segmentation, segmented colonoscopic images will be obtained. Testing of the proposed method and the results obtained are given in Section 3.5.1.

3.3 Homogeneity Index-based Segmentation of Colonoscopic Image

The segmentation based on homogeneity index is realised in two stages. In the first stage, the image is segmented using the homogeneity and intensity values of the pixels. In the second stage, sub-regions are obtained by differentiating the pixels on the basis of hue measure. The sub-regions obtained from the second stage with similar colour are then merged.

3.3.1 Intensity and Homogeneity Index

Suppose $I(x,y)$ is the intensity of a pixel $P(x,y)$ at the location (x,y) in an $M \times N$

image, $w_{xy}^{(1)}$ is a $d \times d$ window centred at (x, y) for computation of variation, $w_{xy}^{(2)}$ is a $t \times t$ window centred at (x, y) for the computation of discontinuity, d and t are odd integers greater than one. The windows $w_{xy}^{(1)}$ and $w_{xy}^{(2)}$ are considered as the local regions when calculating the homogeneity features.

The standard deviation of a pixel $P(x, y)$ is

$$v(x, y) = \sqrt{\frac{1}{d^2} \sum_{p=x-(d-1)/2}^{x+(d-1)/2} \sum_{q=y-(d-1)/2}^{y+(d-1)/2} (I(p, q) - \mu(x, y))^2} \quad (3.5)$$

where $0 \leq x, p \leq M-1, 0 \leq y, q \leq N-1$. $\mu(x, y)$ is the mean of the grey levels within window $w_{xy}^{(1)}$ given by

$$\mu(x, y) = \frac{1}{d^2} \sum_{p=x-(d-1)/2}^{x+(d-1)/2} \sum_{q=y-(d-1)/2}^{y+(d-1)/2} I(p, q) \quad (3.6)$$

The discontinuity for pixel $P(x, y)$ is described by the edge value. There are many different edge operators, such as Sobel, Laplace, Canny, etc. In this work, finding the exact location of the edges is not required. Therefore, the Sobel operator is employed to calculate the discontinuity due to its simplicity. The Sobel operator computes the magnitude of the gradient at location (x, y) using [138].

$$e(x, y) = \sqrt{G_x^2 + G_y^2} \quad (3.7)$$

where G_x and G_y are the components of the gradient in the x and y directions, respectively.

The standard deviation and discontinuity values are normalised in order to achieve

computational consistency.

$$V(I(x, y)) = \frac{v(x, y)}{v_{\max}} \quad (3.8)$$

$$E(I(x, y)) = \frac{e(x, y)}{e_{\max}} \quad (3.9)$$

where $v_{\max} = \max\{v(x, y)\}$, $e_{\max} = \max\{e(x, y)\}$, $0 \leq x \leq M - 1$, $0 \leq y \leq N - 1$.

The homogeneity is defined as [45] :

$$H(I(x, y)) = 1 - E(I(x, y)) \times V(I(x, y)) \quad (3.10)$$

where $0 \leq x \leq M - 1$, $0 \leq y \leq N - 1$.

The value of the homogeneity at each location of an image has a range from [0, 1].

The more uniform that the local region surrounding a pixel is, the larger the homogeneity value of the pixel is.

3.3.2 Homogeneity Histogram

A classical histogram is a statistical graph counting the frequency of occurrence of each intensity level in an image or part of an image. This idea is extended in homogeneity domain. First, homogeneity value for each pixel is calculated. Second, for each intensity value from 0 to 255, add up the homogeneity values of all the uniform pixels with this intensity. There are two issues that are of concern in computing the homogeneity for each intensity value. The first issue is how to find pixels that are uniform for a given intensity, and only uniform pixels are counted. The

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second issue is how the number of uniform pixels should be identified. Empirically, the homogeneity threshold is set to be 0.95, which means the pixels that have homogeneity equal to or greater than 0.95 are included in the computation of the homogeneity characteristics. This homogeneity histogram gives a global description of the distribution of the uniform regions across intensity levels. Each peak in this histogram represents a uniform region.

3.3.3 The Peak-Finding Algorithm

The basis of histogram analysis method is that the regions of interest tend to form modes in the corresponding histogram. A typical image segmentation method based on histogram analysis generally carries out three steps:

- a. Recognise the modes of the histogram
- b. Find the valleys between different modes
- c. Apply thresholds to the image

Locating the modes of an image is the most important and difficult task among the three steps. The key of partitioning modes in a histogram is a process of finding and removing peaks in a histogram curve. Therefore, a modified peak-finding algorithm is developed.

Suppose a homogeneity histogram of an image is represented by a function $h(i)$, where i is an integer, $0 \leq i \leq 255$. The modified peak-finding algorithm consists of three steps:

- a. *Find all peaks:* Find the set of points corresponding to the local maximums of the
-

histogram

$$P_0 = \{(i, h(i)) \mid h(i) > h(i-1) \& h(i) > h(i+1), 1 \leq i \leq 254\} \quad (3.11)$$

- b. *Find significant peaks*: The points in set P_0 form a new curve. On this new curve, repeat the operation of step 1. The result forms set P_1 .

$$P_1 = \{(p_i, h(p_i)) \mid h(p_i) > h(p_{i-1}) \& h(p_i) > h(p_{i+1}), p_i \in P_0\} \quad (3.12)$$

All the points in set P_1 are much more significant than the points in set P_0 in the determination of the peaks of the histogram.

- c. *Thresholding*: It also includes three steps.

- The first step is to remove small peaks.

If a peak is too small compared to the largest peak, then it is removed.

Suppose $i_{\max}$ is the value of the highest peak satisfying $h_{\max} = h(i_{\max})$.

For any peak j , if $\left(\frac{h(j)}{h_{\max}}\right) < 0.05$, then peak j is removed.

- The second step is to choose one peak if two peaks are too close.

For two peaks $h(p_1)$ and $h(p_2)$, $p_1 > p_2$, if $p_1 - p_2 \leq 15$, then

$h = \max\{h(p_1), h(p_2)\}$. Thus, the peak with the larger value is chosen.

- The third step is to remove a peak if the valley between two peaks is not present. The presence or absence of a valley is determined by calculating the average of the intensity values between the two peaks. The average value is computed over the pixels in the region between the peaks p_1 and p_2 as follows.

$$h_{avg} = \frac{\sum_{p_i=p_1}^{p_i=p_2} h(p_i)}{p_2 - p_1 + 1} \quad (3.13)$$

The valley between the two peaks is considered absent if the average value (h_{avg}) is too big compared to the peaks. That is if

$$h_{avg} / ((h(p_1) + h(p_2)) / 2) > 0.75 \quad (3.14)$$

The smaller of the two peaks for which the valley is absent will not be considered.

This peak-finding algorithm locates the globally significant peaks of the histogram. After the peaks are found, the valleys are determined from the minimum between any two adjacent peaks. The valleys thus obtained serve as the boundaries for the segmentation in homogeneity domain.

Let $v(k)$, $k = 1, 2, \dots, l$ be the intensity value of the valley. Using $v(k)$ as the threshold value, the image is segmented as

$$S_I(k) = \{(x, y) \mid v(k-1) \leq I(x, y) \leq v(k)\}, \quad k = 1, 2, \dots, l \quad (3.15)$$

Each segment has the same homogeneity index.

3.3.4 Sub-division based on the Colour Feature Hue

In the second stage, the regions obtained from the first stage are divided into uniform sub-regions. For the pixels in the same uniform region, another histogram of the number of pixels versus hue values is produced. The **Hue** of the pixel at (x, y) is

computed using equation (2.5) and normalised to a range of 0 to 255. After the hue histogram is plotted, the modified peak-finding algorithm is applied to identify the significant peaks. Finally, valleys between peaks are found and they are used to divide the hue range image into several segments, and each segment represents a sub-region that is similar in colour. After all the sub-regions are obtained, the average colour for each sub-region is calculated and assigned to each pixel of the region.

3.3.5 Merging the Sub-divisions

The sub-regions obtained from the second stage have similar intensity and hue values. There are possibilities for those regions with similar colour but different value of intensity and hue to be segmented into different regions. Those regions have to be merged. The measure of colour is based on the recommendation of CIE. The CIE colour system has the ability to measure even a small colour difference compared to RGB. The CIE colour values are computed using equations (2.7), (2.8), (2.9), and (2.10).

The colour differences between any two pixels in the sub-divisions i and j are computed using a Euclidean distance, given by

$$D_{ij} = \sqrt{(L_i - L_j)^2 + (a_i - a_j)^2 + (b_i - b_j)^2} \quad (3.16)$$

where $(L_i \ a_i \ b_i)$ and $(L_j \ a_j \ b_j)$ are the CIE $(L^* \ a^* \ b^*)$ colour representations for the pixels in the sub-divisions i and j , respectively. There will be total of $\frac{k(k-1)}{2}$ such colour distance measures. Note that all the pixels in the same sub-division will have the identical colour value. The above Euclidean distance measure matches the sensitivity and perceptions of a human visual system.

Based on this colour scheme, the sub-divisions with the similar colour are merged using the Euclidean distance measures given by equation (3.12). Let k be the total number of sub-divisions, which is also the total number of CIE colour values. Let μ_d and ν_d be the mean and the standard deviation respectively of the colour differences between the k sub-divisions. The mean and the standard deviation are given by

$$\mu_d = \frac{1}{n} \sum_i \sum_j D_{ij} \quad (3.17)$$

$$\nu_d = \sqrt{\frac{1}{n} \sum_i \sum_j (D_{ij} - \mu_d)^2} \quad (3.18)$$

where $n = \frac{k(k-1)}{2}$ is the total number of colour differences, μ_d is the mean of colour differences, and D_{ij} is colour difference between i and j given by the equation (3.16). The region i and region j will be merged if:

$$D_{ij} \leq Th \quad (3.19)$$

where

$$Th = \mu_d - \nu_d \quad (3.20)$$

The segments $\{S_{ij}\}$ having similar CIE colour values are merged to form the final segment.

$$S_\kappa = \bigcup_{i,j \in \kappa} S_{ij}, \kappa = 1, 2, \dots, K \quad (3.21)$$

where the index set κ is defined as $\kappa = \{i, j \mid D_{ij} \leq Th\}$.

The proposed new method integrates homogeneity index with chromatic hue feature for segmenting the colonoscopic images. The results obtained by this method are superior compared to employing the homogeneity index.

3.4 Clustering Method for Colon Image Segmentation

Given a vector of N measurements describing each pixel or group of pixels (i.e., region) in an image, a similarity of the measurement vectors and therefore their clustering in the N -dimensional measurement space implies similarity of the corresponding pixels or pixel groups [139]. The problem of image segmentation can be stated as follows. The partitioning of a given image into regions or segments such that pixels belonging to a region are more similar to each other than pixels belonging to different regions. The problem of image segmentation based on a similarity criteria for grouping the pixels into a number of segments in the image is regarded as equivalent to a clustering problem [71].

3.4.1 K-means Algorithm

K-means algorithm [140] is a non-hierarchical approach. The formation of good clusters is to specify a desired number of clusters k , then assign each pixel to one of the k clusters so as to minimise a measure of dispersion within the clusters. A very common measure is the sum of distances or sum of squared Euclidean distances from the mean of each cluster. The steps of the K-means algorithm are as follows.

1. Arbitrarily choose k samples as initial cluster centres $\mathbf{c}_1, \mathbf{c}_2, \dots, \mathbf{c}_k$ randomly from the n points

2. Assign point $\mathbf{x}_i, i=1, 2, \dots, n$ to cluster $C_j, j \in \{1, 2, \dots, k\}$ if

$$\|\mathbf{x}_i - \mathbf{c}_j\| < \|\mathbf{x}_i - \mathbf{c}_p\|, \quad p=1, 2, \dots, k, \text{ and } j \neq p. \text{ Ties are resolved arbitrarily.}$$

3. Compute new cluster centres $\mathbf{c}_1^*, \mathbf{c}_2^*, \dots, \mathbf{c}_k^*$ as follows:

$$\mathbf{c}_i^* = \frac{1}{n_i} \sum_{\mathbf{x}_j \in C_i} \mathbf{x}_j, \quad i=1, 2, \dots, k, \text{ where } n_i \text{ is the number of elements belonging to}$$

cluster C_i .

4. If $\mathbf{c}_i^* = \mathbf{c}_i, i=1, 2, \dots, k$ then terminate. Otherwise continue from step (2).

Note that in case the process does not terminate at step (4). Normally, it is executed for a maximum fixed number of iterations. It has been shown in [141] that K-means algorithm may converge to values that are not globally optimal. Initial testing with K-means algorithm yielded results which were not satisfactory. Hence effort was taken to explore application of Fuzzy C-means (FCM) algorithm.

3.4.2 Fuzzy C-Means Algorithm

Fuzzy C-means (FCM) is an unsupervised clustering algorithm that has been applied successfully to a number of problems involving feature analysis, clustering and classifier design [142]. The FCM minimises an objective function J_m , which is the weighted sum of squared errors within groups and is defined as follows.

$$J_m = \sum_{i=1}^N \sum_{j=1}^C u_{ij}^m \|\mathbf{x}_i - \mathbf{c}_j\|^2, \quad 1 \leq m < \infty \quad (3.22)$$

where m is any real number greater than 1, u_{ij} is the degree of membership of $\mathbf{x}_i$ in the

cluster j , x_i is the i th of d -dimensional data points, c_j is the d -dimension centre of the cluster, and $\|\cdot\|$ is any norm expressing the similarity between any data point and the centre.

Fuzzy partitioning is carried out through an iterative optimisation of the objective function with the updating of membership u_{ij} and the cluster centre c_j by:

$$u_{ij} = \frac{1}{\sum_{k=1}^C \left(\frac{\|x_i - c_j\|^2}{\|x_i - c_k\|^2} \right)^{\frac{2}{m-1}}} \quad (3.23)$$

$$c_j = \frac{\sum_{i=1}^N u_{ij}^m \cdot x_i}{\sum_{i=1}^N u_{ij}^m} \quad (3.24)$$

This iteration will stop when $\max_{ij} \left\{ |u_{ij}^{(k+1)} - u_{ij}^{(k)}| \right\} < \varepsilon$, where ε is a termination criterion between 0 and 1, k is the iteration step. This procedure converges to a local minimum or a saddle point of J_m .

By applying the proposed algorithm for clustering-based segmentation, segmented colonoscopic images will be obtained. Testing of the proposed method and the results obtained are given in Section 3.5.3.

3.5 Results and Discussion

New colonoscopic image segmentation methods based on texture information, homogeneity index, and clustering algorithms have been developed and implemented on a personal computer (PC) platform. The proposed methods were tested on a number

of clinical colonoscopic images from a local hospital and a model of the colon in the laboratory. This research is the pioneer in doing simulation on the model of the colon. The size of the image is 256 by 256 pixels. The format of the image is bitmap. Some selected colonoscopic images with the corresponding abnormal regions are shown in Figure 3.1.

In this section, the comparisons on segmentation results are discussed as follows. The colonoscopic image segmentation based on texture is discussed in Sub-section 3.5.1. The comparison of the proposed homogeneity index-based method and region growing method is seen in Sub-section 3.5.2. The comparison of proposed clustering methods, K-means algorithm and Fuzzy C-means algorithm, for the segmentation of colonoscopic images on three different colour spaces, namely RGB, HSI, and $L^*a^*b^*$ colour spaces, into four and five classes are given in Sub-section 3.5.3. The comparison of texture-based method, homogeneity index-based method and Fuzzy C-means method are included in Sub-section 3.5.4.

Original Image	Abnormal Region
<p>Case A02</p>	<p>Villous Polyp</p>
<p>Case A07</p>	<p>Lipoma</p>
<p>Case A29</p>	<p>Cloacogenic tumour</p>
<p>Case A32</p>	<p>Lymphoma and bleeding</p>
<p>Case 46</p>	<p>Deep excavated ulcer</p>

Figure 3.1: Selected colonoscopic images with the corresponding abnormal regions

3.5.1 Texture-Based Segmentation for Colonoscopic Images

Testing was carried out on clinical colonoscopic images by employing new texture-based segmentation method. The results are shown in Figure 3.2 for cases A02, A07, A29, A32, and A46. It is seen that the different regions are properly segmented, based on the texture characteristics of the images. The results are satisfactory. However, it is noted that chromatic information has not been considered.

Original Image	Segmentation Results
A02

A07

A29

A32

A46

Figure 3.2: Segmentation results using texture information for several cases

3.5.2 Homogeneity Index-based Method for Colonoscopic Images

The homogeneity index for each pixel is plotted in Figure 3.3. It is shown that if the region is homogeneous, the homogeneity index closes to maximum value, which is one. The proposed segmentation results based on homogeneity index are demonstrated in Figure 3.4 for cases A02, A07, A29, A32, and A46. The results using proposed homogeneity index-based method is compared with region growing method as shown in Figure 3.5. Region growing method is explained in Section 2.4.2. It is observed that the region growing method segments the image into more regions (more than twenty regions) than the homogeneity index method. The homogeneity index method is superior to region growing method in assigning homogeneous pixels to certain regions. The chromatic information is considered in the homogeneity index-based method.

Figure 3.3 : Plot of the homogeneity index

Original Image	Stage 1	Stage 2	Region Merging
A02

A07

A29

A32

A46

Figure 3.4: Segmentation results using the homogeneity index method for cases A02, A07, A29, A32, and A46

Original Image	Region Growing Method	Homogeneity Index Method
A02

A07

A32

A46

Figure 3.5: Segmentation comparison between the region growing method and the homogeneity index method for cases A02, A07, A29, A32, and A46

3.5.3 Clustering Methods for Colonoscopic Images

Clustering methods have been implemented for the segmentation of the colonoscopic images. Three colour spaces (RGB, HSI, and $L^*a^*b^*$) are used and compared to decide on which colour space gives better segmentation results. Four cluster validity measures, namely Fukuyama-Sugeno index, Xie-Beni index, Kwon index, and Rezaee index, have been applied to find the optimal number of clusters. None of these gave satisfactory segmentation results. Therefore, a feasible approach is proposed by having fixed number of clusters (4 and 5) based on prior knowledge. Experiments are carried out to decide on which fixed number of clusters giving better segmentation results.

3.5.3.1 K-means Algorithm using Three Colour

Components for Four and Five Classes

Some selected segmentation results by K-means algorithm in three different colour spaces for class (k)=4 are shown in Figure 3.6-Figure 3.10. The segmented abnormal regions are compared to those regions in Figure 3.1, which is obtained from the expert's knowledge.

It is observed that RGB colour space gives overall better segmentation compared to other colour spaces. For case A02, case A07, and case A46 in RGB colour space, the image is segmented into lumen (label 1), shading (label 2), abnormal region (label 3), and normal region (label 4). There are normal regions, which have similar properties with abnormal regions, thus they are segmented into the same label as abnormal region. Therefore, further processing is needed to put those regions into proper classes. For case A29 and case A32, images are segmented into lumen (label 1),

shading (label 2), abnormal regions (label 3), and label 4 contains partial normal and abnormal regions. Label 4 can be divided further into two classes.

Figure 3.6: Segmentation results using the K-means algorithm for case A02 (k=4)

Figure 3.7: Segmentation results using the K-means algorithm for case A07 (k=4)

Figure 3.8: Segmentation results using the K-means algorithm for case A29 ($k=4$)

(a) Original image

Label 1

Label 2

Label 3

Label 4

(b) RGB colour space

(c) WSI colour space

(d) L*a*b* colour space

Figure 3.9: Segmentation results using the K-means algorithm for case A32 ($k=4$)

Figure 3. 10: Segmentation results using the K-means algorithm for case A46 (k=4)

The segmentation results using K-means algorithm on three different colour spaces for $k=5$ are shown in Figure 3.11-Figure 3.15. It is observed that for case A32, a segment that contains both normal and abnormal regions partially shown in Figure 3.19 (b) (label 4) becomes two segments as shown in Figure 3.14 (b) (label 2 and label 3). Some cases resulted in over segmentation problem. This problem is overcome by using region-merging method.

Better segmentation results are obtained using K-means algorithm on RGB colour space for five classes. The $L^*a^*b^*$ colour space tends to segment the image into regions containing similar number of pixels. Although the results obtained are acceptable, further explorations are done on using only two components in the colour space instead of all components.

Figure 3.11: Segmentation results using the K-means algorithm for case A02 (k=5)

Figure 3.12: Segmentation results using the K-means algorithm for case A07 (k=5)

Figure 3.13: Segmentation results using the K-means algorithm for case A29 (k=5)

Figure 3.14: Segmentation results using the K-means algorithm for case A32 (k=5)

Figure 3.15: Segmentation results using the K-means algorithm for case A46 (k=5)

Experiments using only two components out of three components on each colour space have been done. The purpose of the experiment is to see whether there is a redundant colour component for the segmentation. This will increase the segmentation efficiency. The comparison of the segmentation results using three components and two components of RGB, HSI, and $L^*a^*b^*$ colour spaces for $k=4$ and $k=5$ are shown in Figure 3.16-Figure 3.21, respectively. It is observed that R and G components give better segmentation results than other combinations by looking at the segmented abnormal regions. Therefore, the results suggested that B component is a redundant component for the segmentation of the colonoscopic images.

Figure 3.16: Segmentation comparison for the K-means algorithm using different colour combinations of RGB colour space ($k=4$)

Figure 3.17: Segmentation comparison for the K-means algorithm using different colour combinations of HSI colour space (k=4)

Figure 3.18: Segmentation comparison for the K-means algorithm using different colour combinations of $L^*a^*b^*$ colour space ($k=4$)

Figure 3.19: Segmentation comparison for the K-means algorithm using different colour combinations of RGB colour space (k=5)

Figure 3.20: Segmentation comparison for the K-means algorithm using different colour combinations of HSI colour space (k=5)

Figure 3.2 1 : Segmentation comparison for the K-means algorithm using different colour combinations of $L^*a^*b^*$ colour space ($k=5$)

colour combinations of $L^*a^*b^*$ colour space ($k=5$)

3.5.3.2 Fuzzy C-Means Algorithm using Three Colour Components for Four and Five Classes

The test procedure adopted for the algorithm described in previous sections has also been applied to Fuzzy C-means algorithm. The segmentation results using Fuzzy C-means algorithm on three different colour spaces for $k=4$ are shown in Figure 3.22- Figure 3.26. It is observed that RGB colour space gives overall better segmentation compared to other colour spaces, except for case A32, where label 4 contains normal and abnormal regions. It needs to be further divided into two classes.

Figure 3.22: Segmentation results using the FCM algorithm for case A02 (k=4)

Figure 3.23: Segmentation results using the FCM algorithm for case A07 ($k=4$)

Figure 3.24: Segmentation results using the FCM algorithm for case A29 (k=4)

Figure 3.25: Segmentation results using the FCM algorithm for case A32 ($k=4$)

Figure 3.26: Segmentation results using the FCM algorithm for case A46 ($k=4$)

The segmentation results using Fuzzy C-means algorithm on three different colour spaces for $k=5$ are shown in Figure 3.27-Figure 3.31. Similar to four classes FCM, it is observed that RGB colour space gives overall better segmentation compared to other colour spaces. It is also shown that the minimum number of classes for the segmentation of colonoscopic images is five classes.

Figure 3.27: Segmentation results using the FCM algorithm for case A02 ($k=5$)

Figure 3.28: Segmentation results using the FCM algorithm for case A07 (k=5)

Figure 3.29: Segmentation results using the FCM algorithm for case A29 (k=5)

Figure 3.30: Segmentation results using the FCM algorithm for case A32 (k=5)

Figure 3.3 1: Segmentation results using the FCM algorithm for case A46 (k=5)

The comparison of the segmentation results using three and two components of RGB, HSI, and $L^*a^*b^*$ colour spaces for $k=4$ and $k=5$ are shown in Figure 3.32-Figure 3.37, respectively. It is observed as follows.

- Four classes ($k=4$)
 - R and G components give better segmentation results than using R, G, and B components.
 - H and I components give better segmentation results than using H, S, and I components.
 - L^* and a^* components give better segmentation results than using L^* , a^* , and b^* components.
- Five classes ($k=5$)
 - R and G components give better segmentation results than using R, G, and B components.
 - H and I components give better segmentation results than using H, S, and I components.
 - L^* and b^* components give better segmentation results than using L^* , a^* , and b^* components.

Overall segmentation results show that R and G components with five classes give better results compared to HI and L^*b^* . The other components are redundant and noisy so as to degrade the segmentation performance.

Figure 3.32: Segmentation comparison for the FCM algorithm using different colour combinations of RGB colour space (k=4)

Figure 3.33: Segmentation comparison for the FCM algorithm using different colour combinations of HSI colour space (k=4)

Figure 3.34: Segmentation comparison for the FCM algorithm using different colour combinations of $L^*a^*b^*$ colour space ($k=4$)

Figure 3.35: Segmentation comparison for the FCM algorithm using different four combinations of RGB colour space ($k=5$)

Figure 3.36: Segmentation comparison for the FCM algorithm using different colour combinations of HSI colour space (k=5)

Figure 3.37: Segmentation comparison of the FCM algorithm using different colour combinations of $L^*a^*b^*$ colour space ($k=5$)

Both K-means and Fuzzy C-means algorithms yield better segmentation results using R and G colour components with five classes. It is because there is a maximum of five possible homogeneous regions in the image such as lumen, bleeding, ulcers, polyps, and normal regions. Although K-means and Fuzzy C-means algorithms can be used for segmenting the colonoscopic images, Fuzzy C-means algorithm is superior to K-means algorithm, because the convergence of K-means algorithm depends on the initialisation of the cluster centres. Sometimes K-means algorithm does not converge because the initial values of the cluster centres are chosen randomly. Figure 3.38 shows the comparison of segmentation using K-means algorithm and Fuzzy C-means algorithm for case A02 and case A07.

Figure 3.38: Comparison of segmentation results for the K-means and Fuzzy C-means algorithms

The arrows show some regions, which are not included on the Fuzzy C-means algorithm result. Further post-processing operations on the Fuzzy C-means algorithm are needed to overcome the over-segmentation problem to get a fine-segmentation result.

3.5.3.3 Region Merging for FCM Algorithm in Colon

The results reported in the previous figures show the presence of over segmentation. A new colon segment region merging method is applied in order to overcome the over-segmentation problem. The colon segment region merging uses $L^*a^*b^*$ colour space which perceives colour difference. Region merging results are shown in Figure 3.39- Figure 3.43 for different cases on segmented regions using Fuzzy C-means algorithm on R and G components. It is observed that some regions are merged to the nearest colour different regions and more concise segmentation results are achieved. Each segment is well separated into different major categories such as lumen, polyp, bleeding, etc.

(a) Original image

(b) Segmented image using FCM on R, G components

(c) Region merging result

Figure 3.39: Region merging result for case A02

Figure 3.40: Region merging result for case A07

Figure 3.41 : Region merging result for case A29

Figure 3.42: Region merging result for case A32

Figure 3.43: Region merging result for case A46

3.5.4 Comparison of Texture-based Method, Homogeneity Index-based Method, and Hybrid of Fuzzy C-Means and Region Merging Algorithms

Hybrid of Fuzzy C-means and region merging algorithms for the colonoscopic image segmentation is compared to texture-based method and homogeneity index-based method, The comparison is shown in Figure 3.44.

Original Image	Texture-based Method	Homogeneity Index-based Method	Hybrid of Fuzzy C-Means and Region Merging Algorithms
Case A02

Case A07

Case A29

Case A32

Case A46

Figure 3.44:Results of three segmentation methods for colonoscopic images for cases A02, A07, A29A32, and A46

Average colour is used for representing each segmented region in the images for homogeneity index method and the hybrid of Fuzzy C-means and region merging algorithms as shown in Figure 3.44. It is seen that all the three methods yielded reasonable segmentation results.

The three methods on segmenting the abnormality regions are compared to the abnormality region which is obtained from the expert's knowledge. The comparison results of the abnormality region segmentation are shown in Figure 3.45. There are two quantitative measures to measure the goodness of the segmentation algorithm, namely normalised mean square root error (NMSRE) and accuracy as shown in Table 3.1. It is shown that the hybrid of FCM and region merging methods gives better segmentation accuracy than other methods, namely texture-based method, homogeneity index-based method, and K-means method. Over-segmentation occurs in texture-based method. Difficulty in performing the third step of the peak-finding algorithm, which is to find the threshold, is found in the homogeneity index-based method. Sometimes, the K-means algorithm does not converge due to the randomly selected initial cluster centre.

Table 3.1 : Two quantitative measures for the assessment of segmentation algorithms

Segmentation methods	NMSRE	Accuracy
Texture-based method	1.37	82.9%
Homogeneity-based method	1.19	75.12%
Hybrid of FCM and region merging methods	1.00	86.24%
<i>K</i> -means method	1.05	83.89%

Figure 3.45: Comparison results of the abnormal region segmentation using different methods for cases 5 and A09

The algorithm developed for colonoscopic image segmentation is extended for the bronchoscopic image segmentation. The bronchoscopic image segmentation results are shown in Figure 3.46. The preliminary results based on limited testing on bronchoscopic images are rather encouraging. The proposed method appears to be useful in extending the application to computer-assisted bronchoscopic image processing.

Figure 3.46: Bronchoscopic image segmentation by FCM method

3.6 Concluding Remarks

In conclusion, new methods for the segmentation of colonoscopic images based on texture, homogeneity index, and clustering methods have been proposed. Appropriate testing has been carried out with clinical colonoscopic images. The results show that segmentation based on texture and homogeneity index yields better results compared to region growing method by giving more concise regions. Two clustering algorithms are applied to segment the colonoscopic images. It is shown that Fuzzy *C*-means algorithm is more robust than *K*-means algorithm because it converges on any initial values of cluster centres chosen randomly and has better accuracy. Further post-processing operations on the image, such as region merging and filtering methods, are needed to get a fine-segmentation result.

The texture-based method, homogeneity index-based and the hybrid of Fuzzy *C*-means and region merging methods are compared to the image obtained from the knowledge of consultant endoscopist. The results obtained showed that the hybrid of FCM and region merging methods is better compared to the other two methods on segmenting the colonoscopic images. The proposed methods are able to segment the image into a number of major regions, which can be used for prompting the physician on the possible presence of abnormal regions during the colonoscopy.

Chapter 4

COLON LUMEN EXTRACTION BY MDRM

In this chapter, a new method of lumen extraction from a colonoscopic image using modified deformable region model (MDRM) method has been proposed. This method is compared with the minimum variance region growing and active contour model methods. The organisation of this chapter is as follows. Lumen extraction using two other known methods is described in Section 4.2 and Section 4.3, respectively. The proposed method on extracting the colon lumen from the colonoscopic image using modified deformable region model is presented in Section 4.4. Some results are presented in Section 4.5 followed by the discussion. Concluding remarks are given in Section 4.6.

4.1 Introduction

Lumen of the colon is one of the most important features which is used for clinical evaluation of the mucosal layer, by determining the characteristic features and

deciding on the presence or absence of abnormalities. The colon characteristic features along the lumen of the colon can be used for determining the presence of an abnormality such as a protrusion due to tumour and also facilitating safe and efficient navigation of the colonoscope inside the colon. The characteristic features are utilised to derive the diagnosis regarding colon diseases. Therefore, the extraction of lumen is very important in the implementation of a computer-assisted colonoscopic diagnostic system.

As a light source and a CCD camera are located on the tip of the colonoscope, the camera captures the image of the colon mucosal surfaces. Due to this arrangement, the part of the walls of the colon which are close to the tip of the colonoscope, appear bright and the segment covered by the mucosal contour of the colon, called lumen, typically appears as a darker region. The doctor navigates the colonoscope in the colon along the direction of the large dark region towards the central part of the region. The newly developed method to extract the lumen from the colonoscopic image based on modified deformable region model is described in the following sections. Comparative evaluation of the new method is done with two other known techniques, namely, minimum variance region growing and active contour model.

4.2 Minimum Variance Region Growing Applied to Colon Image

The minimum variance region growing algorithm uses a homogeneity criterion based on an adequate tuning between spatial neighbourhood and histogram neighbourhood [143]. The algorithm generates a region by growing a seed, which is the lumen centre extracted from the thresholding method. The region-growing algorithm mainly

consists of four operations, which are dilation, reduced dilation, extension of the reduced dilated region, and contraction of the reduced dilated region.

For a given region, the corresponding dilated area is obtained by the classical binary dilation. For example, a background pixel is added to the boundary pixel of the region. This procedure will add a layer of pixels around the circumference of the region, which causes some increase in size as shown in Figure 4. 1. A dynamic range is characterised by the maximum and minimum grey levels of the region.

pixels belonging to the dynamic range of region are kept and a new region called reduced dilation region is formed as shown in Figure 4.2.

Figure 4.2: Reduced dilation operation

The reduced dilated region is enlarged when it is homogeneous by extension of the reduced dilated region procedure as shown in Figure 4.3. It is achieved by increasing the histogram's dynamic range of reduced dilated region. There are two kinds of extension: the left extension and the right extension. The extension is defined as follows. The pixels of the extension region consist of both the pixels of the reduced dilated region and the pixels whose grey levels belong to the first non-void bin to the

extension. The resulting region of the extension operation must be homogeneous. If the left extension and the right extension are not homogeneous, then the original reduced dilated region is retained. If both the left and the right extensions are homogeneous, then the most homogeneous region is retained.

Left extension of (E - R):

- (a) Region for $E_{left}(R)$
- (b) Histogram of region $E_{left}(R)$

Right extension of (E - R):

- (a) Region for $E_{right}(R)$
- (b) Histogram of region $E_{right}(R)$

Figure 4.3:Extension operation (Left or right)

The last procedure is the contraction of the reduced dilated region as shown in Figure 4.4. During this procedure, some pixels belonging to the homogeneous region are eliminated. This modifying operation is achieved by narrowing the dynamic range

of the reduced dilated region, which also reduces the dynamic range of the region. There are three types of contraction, namely left contraction, right contraction and bilateral contraction. Left contraction is obtained by removing all the pixels which belong to the two extreme bins on the left side of the histogram. Similar operation is performed for the right contraction with two extreme bins on the right side of the histogram. The bilateral contraction is obtained by removing all the pixels which belong to one extreme bin on the left and the right side of the histogram.

This method reconsiders the assignment of a pixel at any step. Hence, it does not guarantee the absence of holes in the segmented region. The holes in the lumen are found and filled. An approximate surrounding outline of the lumen region in the binary image is produced by 4-neighbourhood dilation and EX-OR operation with the original image.

The above minimum variance region growing technique is applied to the colonoscopic image for detection of the lumen. The results show that this technique can extract the lumen of the colon. However, there is problem encountered which is in extracting the dark background region to get proper lumen contour. To alleviate this problem, a new technique has been developed based on modified deformable region model (MDRM). The results of the minimum variance region growing technique are evaluated against the results obtained using a newly developed technique MDRM as shown in Figure 4.12.

(a) Left contraction operation: two at left

(b) Bilateral contraction operation: one at right, the other at left

(c) Right contraction operation: two at right

Figure 4.4: Contraction operation

4.3 Active Contour Model Applied to Colon Image

A snake is an energy minimising spline guided by extended constraint forces and influenced by image forces that pull it towards features such as lines and edges [144]. Snakes are active contour models. They lock onto nearby edges, localising them accurately. Scale-space continuation is used to enlarge the captured region surrounding a feature. Snakes provide a unified account of a number of visual problems.

The basic snake model is a controlled continuity spline under the influence of image forces and external constraint forces. The internal spline forces serve to impose a piecewise smoothness constraint. The image forces push the snake toward salient image features like lines, edges, and subjective contours. The external constraint forces are responsible for putting the snake near the desired local minimum.

Given a parametric curve $\nu(s) = (x(s), y(s))$, the potential energy function of the snake model can be written as

$$\begin{aligned} E_{snake}^* &= \int_0^1 E_{snake}(\nu(s)) ds \\ &= \int_0^1 (E_{internal}(\nu(s)) + E_{image}(\nu(s)) + E_{constraint}(\nu(s))) ds \end{aligned} \quad (4.1)$$

where E_{snake} is the total energy, $E_{internal}$ represents the internal energy, E_{image} is the image energy, and $E_{constraint}$ is the external constraint energy. The curve is found when the energy E_{snake}^* is minimised.

The internal energy has two parts given as

$$E_{internal} = w_{int1} \|\nu'(s)\|^2 + w_{int2} \|\nu''(s)\|^2 \quad (4.2)$$

where ν' and ν'' are the first and second derivatives at a point on the contour, w_{int1}

controls the tension of the snake, w_{int2} controls the rigidity of the snake. The spatial discretisation is done by sampling the active contour $\mathbf{v}$ into N points ($\mathbf{v}_i, i = 1, 2, \dots, N$), which are chosen to be evenly spaced on the contour. The discretisation of the internal energy is done by approximating the first and second derivatives $\mathbf{v}'$ and $\mathbf{v}''$ by finite difference [145] as follows:

$$\left| \frac{d\mathbf{v}_i}{ds} \right|^2 = |\mathbf{v}_i - \mathbf{v}_{i-1}|^2 = (x_i - x_{i-1})^2 + (y_i - y_{i-1})^2 \quad (4.3)$$

and

$$\begin{aligned} \left| \frac{d^2\mathbf{v}_i}{ds^2} \right|^2 &= |\mathbf{v}_{i-1} - 2\mathbf{v}_i + \mathbf{v}_{i+1}|^2 \\ &= (x_{i-1} - 2x_i + x_{i+1})^2 + (y_{i-1} - 2y_i + y_{i+1})^2 \end{aligned} \quad (4.4)$$

where x_i and y_i are the x and y coordinates of the $\mathbf{v}_i$ th contour point, respectively.

The image energy is defined as the negative gradient magnitude of each contour point in the image, which can be expressed as

$$E_{image} = -|\nabla(G_\sigma * I(x, y))|^2 \quad (4.5)$$

where G_σ denotes a Gaussian smoothing filter of standard deviation σ , $I(x, y)$ is the intensity value of the pixel at (x, y) coordinate.

In this study, the initial contour is set to be a small circle at the lumen centre. In order to make it deform to the mucosal contours, the pushing force is defined as the external constraint energy. Let the snake point be $\mathbf{v}_i$, the lumen centre be (X_{ctr}, Y_{ctr}) , then the pushing force E_{push} can be expressed as:

$$E_{push} = -[v_i - (X_{cntr}, Y_{cntr})]^2 \quad (4.6)$$

The contour optimisation is the step to achieve all the significant solutions which satisfy the constraints. Optimisation principles are used to find the solution which is the best one under some criteria of goodness from the general solutions. One such method uses Greedy algorithm [146]. In the Greedy algorithm, the energy function is computed iteratively. During each iteration, a neighbourhood giving the smallest value for the energy term is chosen as the new location of the point.

The above active contour model approach is applied to the colonoscopic image for detection of the lumen. The results of this technique are evaluated against the results obtained using a newly developed technique, as shown in Figure 4.12.

4.4 Modified Deformable Region Model for Colonoscopic Image

A newly developed method on extracting lumen of the colon has been proposed based on modified deformable region model (MDRM). Accurate extraction of the lumen and its boundary in a short time are essential for the detection of abnormality. The modified deformable region model has been used for locating the boundary of the brain tumour [147], [148]. The modified deformable region model determines the lumen from the colonoscopic images by giving an approximate boundary plan of the lumen, and then deforms this plan to the real boundary automatically. The complexities of the segmentation problem are somewhat alleviated, thus rendering the proposed scheme to be attractive to clinicians.

4.4.1 Initial Colon Lumen Boundary Estimation

Initially, the background of the image is eliminated using template-matching method. The first initial boundary plan (lumen) is then estimated using thresholding method before the region deformation. Thresholding method is a simple yet often effective means for obtaining segmentation in images where different structures have contrasting intensities of other quantifiable features. In this work, two thresholding methods are described and compared. The coarse colon lumen is extracted using minimum cross-entropy thresholding method.

4.4.1.1 Otsu Thresholding

A method for segmentation suggested by Otsu is based on discriminant analysis, which partitions the image into two classes G_0 and G_1 at grey level ' t ' such that $G_0 = \{0, 1, 2, \dots, t\}$ and $G_1 = \{t+1, t+2, \dots, L-1\}$, where L is the total number of grey levels in the image [34].

Let σ_B^2 and σ_T^2 be between-class variance and total variance, respectively. The optimum threshold t^* is obtained by maximising the between-class variance. Hence,

$$t^* = \text{Arg Max}_{0 \leq t < L} \{\eta\} \quad (4.7)$$

where $\eta = \frac{\sigma_B^2}{\sigma_T^2}$, $\sigma_B^2 = w_0 w_1 (\mu_1 - \mu_0)^2$, and $\sigma_T^2 = \sum_{i=0}^{L-1} (i - \mu_T)^2 P_i$.

The w_0 and w_1 denote the fraction of pixels lying in G_0 and G_1 class respectively and are represented by,

$$w_0 = \sum_{i=0}^t P_i \text{ and } w_1 = 1 - w_0 \quad (4.8)$$

where $P_i = \frac{n_i}{N}$ and $N = \sum_{i=0}^{L-1} n_i$.

The n_i is the number of pixels on i^{th} grey level and N is total number of pixels in the image. μ_0 and μ_1 represent the class means for G_0 and G_1 respectively and are calculated by using,

$$\mu_0 = \frac{\mu_t}{w_0} \text{ and } \mu_1 = \frac{\mu_T - \mu_0}{1 - w_0} \quad (4.9)$$

where $\mu_t = \sum_{i=0}^t iP_i$ and $\mu_T = \sum_{i=0}^{L-1} iP_i$.

Iterative computation was required to find the best threshold for a given image. In the case of images where the colour information can be used to separate the image into two distinct classes, Otsu's method is efficient in thresholding these images.

The property of distinct class separation describes that an object in the image can be easily identified out from the background due to the distinct difference between the object and its background. From the technical point of view, the histogram of the image has the property of distinct class separation which is shown in Figure 4.5.

Figure 4.5: Histogram of an image which displays distinct class separation properties

In the histogram above, there are two distinctive peaks whereby one represents the object of interest and the other represents the background. Based on this principle, by

performing a simple thresholding at the valley between the two peaks, the object of interest will be segregated out from the background. In such cases, Otsu's method works well.

However, in the colonoscopic image, what the image represents is the illumination of the colon wall from a light source. As the distance from the light source increases, the illumination decreases. The histogram of a typical colonoscopic image is shown in Figure 4.6. It may be observed that it has many peaks and valleys.

Figure 4.6: Histogram of a typical colonoscopic image

Basically, the image displays the information of the wall, which is having the same property, and the only difference is the amount of intensity of the light that is reflected on the wall. Hence the colonoscopic images do not exhibit distinct class separation property. Therefore the Otsu's method of thresholding does not work well in the processing of the colonoscopic images.

4.4.1.2 Minimum Cross-Entropy Thresholding

The histogram thresholding technique is conceptually a simple method to separate an object of interest from its background. The pixels in the dark region have low intensity

values. Therefore, it is important to find the threshold, which will separate the dark region from the other parts of the colon on the image.

Many techniques for the automatic selection of grey-level thresholds have been developed [149], [150]. These methods involve the optimisation of a criterion function based on some property of the image or its histogram, for example, the maximum entropy method [35] and maximum correlation method [151], [152].

The principal of cross-entropy minimisation due to Kullback [153] can also be used in this way. The threshold selection processed is based on the cross-entropies of the images themselves, as opposed to measures based on the histogram [154]. For the purpose of threshold selection, the original grey-scale image is regarded as the prior distribution with each grey-level g representing a frequency. The means of the below threshold and the above threshold, $\mu_0(T)$ and $\mu_1(T)$, of the image can be used as the two grey-levels of the binary thresholded image. These levels are given by:

$$\mu_0(T) = \sum_{I=a}^T \left(I \frac{f_I}{\sum_{I=a}^T f_I} \right) \quad (4.10)$$

$$\mu_1(T) = \sum_{I=T+1}^b \left(I \frac{f_I}{\sum_{I=T+1}^b f_I} \right) \quad (4.11)$$

where a and b are, respectively, the smallest and largest grey-levels present in the original images, T is the threshold level and f_I is the number of pixels having grey-level I . The cross-entropy value for each level is defined as follows.

$$H_{CE}(T) = \sum_{I=a}^T f_I \mu_0(T) \log \frac{\mu_0(T)}{I} + \sum_{I=T+1}^b f_I \mu_1(T) \log \frac{\mu_1(T)}{I} \quad (4.12)$$

The simplest and most direct scheme for threshold selection would be to iterate through all possible threshold values, T , and to select the threshold, τ_{CE} , corresponding to the minimum of the cross-entropy equation (4.17) as shown in equation (4.18).

$$\tau_{CE} = \arg\left\{\min_{a \leq T < b} \{H_{CE}(T)\}\right\} \quad (4.13)$$

The procedure on getting the threshold is repeated until the third epoch. τ_{CE} is substituting b at every epoch. The thresholding results are the regions, which have pixels with intensity level less than τ_{CE} . A big region considered as lumen. There are other small regions, which do not belong to the lumen. The morphological opening operation is used to remove these regions.

4.4.1.3 The Estimation of Lumen Centre

The result of thresholding determines the lumen of the colon. The estimation of the lumen centre is determined by the centroid of the large dark region with the computed lumen. The centroid is calculated by the following formula:

$$X_{ctr} = \frac{\sum_{y=1}^N \sum_{x=1}^M xyI(x, y)}{\sum_{y=1}^N \sum_{x=1}^M yI(x, y)} \quad (4.14)$$

$$Y_{ctr} = \frac{\sum_{y=1}^N \sum_{x=1}^M xyI(x, y)}{\sum_{y=1}^N \sum_{x=1}^M xI(x, y)} \quad (4.15)$$

where M and N are the length and the width of the image, $I(x,y)$ is the intensity value

for the binary image. For the object $I(x,y)=1$ and the background $I(x,y)=0$.

4.4.2 Region Description of a Lumen

Let S be the pixel set of an image, $s \in S$ be a pixel. g_s is the grey level of s , $0 \leq g_s \leq G$. An object in an image can be described as a homogenous region I_O . The boundary of the region I_B is a simple closed curve (Figure 4.7). L_S is a binary label image related to the original image, in which l_s is the label of s , $l_s=1$ inside I_O , $l_s=0$ outside I_O . So $I_O = \{s | l_s=1\}$, and $I_B = \{s | l_s=1, \text{ and } \exists s \in N_s, l_s=0\}$, where N_s corresponds to the eight neighbours of s .

Figure 4.7: Lumen description as a region with a closed curve as its boundary

Let H_O and H_B represent the grey level frequency distribution functions of I_O and I_B , and F_O and F_B be the grey level cumulative frequency distribution functions of I_O and I_B respectively, then

$$H_O(g_s^*) = \frac{1}{A} \sum_{s \in I_O, g_s = g_s^*} l_s \quad (4.16)$$

$$H_B(g_s^*) = \frac{1}{\ell} \sum_{s \in I_B, g_s = g_s^*} l_s \quad (4.17)$$

$$F_O(g_s^*) = \sum_{g_s \leq g_s^*} H_O(g_s) \quad (4.18)$$

$$F_B(g_s^*) = \sum_{g_s \leq g_s^*} H_B(g_s) \quad (4.19)$$

A is the area of the object and ℓ is the length of the boundary given the condition $0 \leq g_s \leq G$.

$$A = \sum_{s \in I_O} l_s \quad (4.20)$$

$$\ell = \sum_{s \in I_B} l_s \quad (4.21)$$

The grey level cumulative frequency distribution functions of I_O and I_B are then used for Kolmogorov-Smirnov (KS) test as stated in the following section.

4.4.3 Grey Level Distribution Disparity of the Lumen

Boundary

The KS test method [155] from nonparametric statistics is used to test if two sets of probability distributions belong to the same particular probability distribution. In the proposed method, it is used to test whether or not the lumen boundary pixel set and the lumen pixel set have the same grey level distribution.

The KS distance between F_O and F_B is defined as follows.

$$D = \max_{0 \leq g_s \leq G} |F_B(g_s) - F_O(g_s)| \quad (4.22)$$

and it is the maximum distance between F_O and F_B . The hypothesis $F_O = F_B$ is accepted when $D < \psi$, and ψ only depends on the pixel amounts of F_O and F_B , and on the significance level of the test.

$$\psi = \frac{c}{\sqrt{n}} \quad (4.23)$$

where $n = \frac{A\ell}{A + \ell}$ and c is related to the test significance level.

When $D < \psi$, the region plan covers a region inside the lumen, growing algorithm is performed to obtain the maximum area. When $D > \psi$, the region plan covers a region outside the lumen, shrinking algorithm is executed to deform the region to meet $D < \psi$.

4.4.4 Growing and Shrinking for Region Deformation

The aim of region deforming is to find a maximum area region with the grey level distribution in the same band using a growing-shrinking method [156].

Region growing is a method used commonly in region-based image segmentation. It starts with a seed and grows the seed under some homogeneity rules until the entire image is covered. These homogeneity rules are always application-dependent. It is difficult to give the rules first if segmentation method has to be used to segment various objects [147]. In the present method, instead of testing if the region can meet some particular rules, the testing is done based on whether the object and its boundary have the same properties. A growing-shrinking method is developed with two basic operations, growing and shrinking.

The initial lumen boundary is a small circle inside the lumen. In this case, $D < \psi$,

growing is performed to obtain the maximum area. The growing operation is the dilation operation in mathematical morphology. It grows the region boundary elements from the region in the label image. In this case, not all boundary elements grow. Only those elements, which have the same property within the region, are considered. Let the pixel be s . A small window Ws is set with s being the centre as shown in Figure 4.7. μ_{Ws} is the mean of the grey level in window Ws . If $\mu_{Ws} = \mu_O$, s is grown; otherwise, s is kept.

Shrinking algorithm is executed after the growing procedure because there are some of the boundary pixels outside the lumen. A normal shrinking algorithm is the erosion operation in mathematical morphology. If $\mu_{Ws} = \mu_O$, s is kept; otherwise, s is deleted.

After each growing or shrinking operation, the area of the region from current operation is compared to the area from the previous operation to decide if the operations should continue. The process stops when the area of the region from the current operation is same as the area from the previous operation.

4.4.5 Morphological Filtering, Region Labelling and Filling

After finishing the deformation of the lumen, there are small regions outside and/or inside the lumen, referred to as holes. Very small regions outside and/or inside the lumen are filtered using morphological filtering, thus performing the opening operation.

Connected components labelling method [53] is used to eliminate bigger regions outside the lumen. The algorithm uses a modified version of grassfire concept implemented recursively. The component with maximum area is considered the

lumen, and it is retained.

The holes inside the lumen are eliminated by a similar method. The connected component labelling is applied to the inverted image. The component with maximum area is considered as the background. Other components are given the same label as the lumen.

4.5 Results and Discussion

A new method on extracting lumen boundary has been developed by modified deformable region model algorithm. This newly developed method is compared to other methods previously developed, viz., minimum variance region growing method and the active contour model method. The results of minimum variance region growing method are shown in Figure 4.8. The active contour model results are shown in Figure 4.9.

The newly proposed modified deformable region model method starts with the initial lumen boundary which is obtained from a thresholding method. Thresholding methods yielded coarse lumen boundary. The two thresholding methods adopted in this work are modified Otsu and minimum cross entropy methods.

The pixels in the colonoscopic image have grey levels of 0 to 255. However, the region of interest, which is the lumen of the colon, has low grey levels in the range of 0 to 35. The maximum range for threshold searching is limited to the value of 35 in order to decrease the computation time and increase the accuracy percentage.

Original Image	Lumen Contour Extraction	Original Image	Lumen Contour Extraction
A07		A32

A10		A46

Figure 4.8:Lumen contour extraction by minimum variance region growing algorithm

Original Image	Initial Lumen	Final Lumen Contour using Snake Method
A02

A46

Figure 4.9: Lumen contour extraction by active contour model

Original Image	Grey Image	Modified Otsu Method	Minimum Cross-Entropy Method
A02		Th=11	Th=19
A07		Th=8	Th=9
A29		Th=12	Th=16
A46		Th=9	Th=9

Figure 4.10: Comparison results of the modified Otsu thresholding method and the Minimum Cross Entropy method

Figure 4.11: Lumen contour extraction using the modified deformable region model

The results of modified Otsu and minimum cross-entropy methods on extracting the coarse lumen are shown in Figure 4.10. The background of the image is first eliminated. The modified Otsu and Minimum Cross Entropy methods can extract the coarse lumen but the former thresholding method has a threshold value less than or equal to that corresponding to Minimum Cross Entropy method. The Minimum Cross Entropy method extracts more precise lumen region. Morphological opening is applied to the coarse lumen to fill in the small holes. The lumen centre is then extrv small circle is drawn around the centre as initial lumen. The lumen contour is extracted using modified deformable region model as shown in Figure 4.1 1.

In the snake method, it is needed to adjust the energy parameters in order to detect the lumen from different colonoscopic images. In the minimum variance region-growing algorithm, it is important to extract the dark background region properly in order **to** detect the lumen contour. The modified deformable region model method yields better results compared to the active contour model and minimum variance region growing algorithms as shown in Figure 4.12. The proposed method overcomes the constraints posed by the other methods.

The proposed modified deformable region model method is compared with the other segmentation algorithm which is described in Chapter 3, namely FCM, to extract the lumen of the colon. The results obtained are compared to the lumen extracted from the expert's knowledge. The comparison results of the lumen extraction are shown in Figure 4.13. The same quantitative measures are used to measure the goodness of the lumen extraction algorithm, namely normalised mean square root error (NMSRE) and accuracy as shown in Table 4.1. The smaller the NMSRE value, the better the lumen extraction algorithm is.

Table 4.1 : Two quantitative measures for assessment of the colon lumen extraction algorithms

Lumen extraction algorithm	NMSRE	Accuracy
Modified deformable region model method	1.00	98.21%
FCM method	1.27	96.74%

It is shown in Table 4.1 that those two methods give comparable results on extracting the lumen of the colon from the colonoscopic image. The first method is concentrating on directly finding the lumen so as to speed up the lumen extraction process. This will assist the physician on manoeuvring the tip of the colonoscope along the centre of the colon to avoid perforation during the procedure. Those methods are applied to each individual image frame of the video endoscope. Lumen centre for each image frame is detected and a three dimensional reconstruction method [157] is used to reconstruct the path to navigate the colonoscope.

The colon lumen detection algorithm application is extended to the bronchoscopic lumen boundary detection. The results are shown in Figure 4.14. It is shown that it is viable to extend the proposed algorithm for other type of images.

Minimum Variance Region-Growing Method	Active Contour Model Method	Modified deformable Region Model Method
Case A07

Case A08

Case A10

Case 14

Figure 4.12:Lumen boundary extraction using three different methods for cases
A08, A10, 14

Figure 4.13: Comparison results of lumen extraction using two approaches for cases

A04, A35

Figure 4.14:Bronchoscopic lumen detection by MDRM

4.6 Concluding Remarks

In conclusion, a new colonoscopic image analysis method using modified deformable region model has been proposed for clinical diagnosis. The feasibility of automatically generating the initial lumen boundary (initial region plan) and extracting the lumen contour has been shown. It has been shown that the proposed modified deformable region model method detects the lumen contour faster and more accurately than the snake and minimum variance region growing methods. The modified Otsu and minimum cross entropy thresholding methods are applied on an image histogram at a certain level of interest to obtain the lumen centre. The newly proposed modified deformable region model results are comparable to the results obtained by Fuzzy C -means algorithm.

The derived information regarding the lumen of the colon gives guidance to the physician on the mucosal abnormalities, if present. The central part (centroid) of the colon cross section can be estimated and by manoeuvring, the endoscope can be directed towards the centroid of colon section. This could lead to a safety-enhanced procedure. It is possible to extend the proposed method for the extraction of lumen from other type of images such as bronchoscopic images and upper gastro-intestinal images.

Chapter 5

FEATURE EXTRACTION AND CLASSIFICATION OF COLONOSCOPIC IMAGES

In the initial part of the intelligent colonoscopic instrumentation system, image processing is carried out on clinical colonoscopic images to achieve segmentation. This work is described in earlier Chapter 3 and Chapter 4. In this chapter, new methods have been proposed for feature extraction and classification of abnormalities from the colonoscopic images. The organisation of this chapter is as follows: Different types of features extracted from the colonoscopic image are described in Section 5.2. The evaluations based on the features, singly or in association, are described in Section 5.3. Some results are presented in Section 5.4 followed by the discussion. This chapter is closed by concluding remarks as stated in Section 5.5.

5.1 Introduction

Computer-assisted diagnosis in intelligent colonoscopic instrumentation system consists of colonoscopic image acquisition, image processing, parametric feature extraction, and classification. In the present work, a number of techniques have been developed for computer-assisted diagnosis for the detection of colonic cancer images. Segmentation and extraction of lumen of the colon have been described in Chapter 3 and Chapter 4. The segmentation results for the colonoscopic images are shown in Figure 5.1. New image analysis method is performed with newly defined parameters derived from colonoscopic images.

Figure 5.1 : The segmentation results for colonoscopic images

5.2 Quantitative Characterisation of Colon

In this innovative effort, quantitative characterisation of the colon is achieved by formulating and defining new parameters extracted from the images. Colonoscopic images are rich in texture and colour information. Therefore, the additional texture and colour information can provide better results for the image analysis than the methods

which use merely intensity information. In this research work, the definition and extraction of quantitative parameters from colonoscopic images based on shape, texture and colour information have been proposed. The preliminary test results obtained by using the proposed method are encouraging.

5.2.1 Basics Aspects of Colonoscopic Feature Extraction

Colonoscopic imaging methods have been used to examine the condition of the colon. The development of an intelligent method for the identification of the colon status is being explored as a computer-aided tool for the early detection of colorectal cancer. It is important to extract the quantitative parameters representing the characteristic properties of the colon from a colonoscopic image. The quantitative features are used for detecting the normal or abnormal condition of the colon from the colonoscopic images. Colonoscopic images contain texture and colour information. Features from texture and colour are extracted from the colonoscopic image to identify a normal colon from an abnormal colon. Krishnan, et al. extracted features from the histogram of the image in the chromatic domain and the shape of the lumen in the spatial domain, and then fed them into a feed-forward Neural Network [128]. Four statistical measures derived from the co-occurrence matrix in four different angles, namely angular second moment, correlation, inverse difference moment, and entropy, have been extracted by Karkanis [158].

5.2.2 Shape-based Feature Extraction

A set of new features associated with the shape of the object of interest extracted from

colonoscopic images and a new matrix combining the parameters are defined as described follows.

a. Lumen Contour Length (L_{CL})

Lumen contour length is the length of the boundary, which surrounds the object of interest.

$$L_{CL} = \sum_{i=1}^M \left[\sqrt{(x_{i+1} - x_i)^2 + (y_{i+1} - y_i)^2} \right] \quad (5.1)$$

where (x_i, y_i) is the coordinate of the image pixel i , (x_{i+1}, y_{i+1}) is the coordinate of the image pixel $i+1$, and M is the number of pixels in the object boundary. In the present case, L_{CL} corresponds to lumen contour for the mucosal layer control.

b. Lumen Cross Sectional Planar Projection (LC_{int})

The lumen cross sectional planar projection refers to the area of the object of interest, is measured in pixels and indicates the relative size of the object. The accuracy of lumen cross sectional planar projection increases with the number of boundary pixels considered.

$$LC_{int} = \sum_{x=1}^M \sum_{y=1}^N I(x, y) \quad (5.2)$$

where $I(x, y)$ is the intensity value for the binary image. For the object $I(x, y)=1$ and the background $I(x, y)=0$.

Figure 5.2: Illustration of L_{CL} and LC_{int} c. Lumen Shape Index (ϕ)

Lumen shape index is a parameter to describe the irregularity of the object. A lumen shape index of 1 is a perfect circle. The more irregular the shape of the object, the smaller the value of the lumen shape index. A colon affected with growth abnormalities having a very irregular and distorted object has significantly low lumen shape index as the lumen cross sectional planar projection is increased and the lumen contour length is decreased when compared to an identical healthy colon.

$$\phi = \frac{4\pi \times LC_{int}}{L_{CL}} \quad (5.3)$$

It is possible to relate the muscle contraction with the diameter.

d. Colon Shape Matrix [S]

The colon shape matrix elements are utilised to assess the diseased state of the colon by applying decision making or a neural network technique. The newly developed technique is described in Sub-section 5.3.3.

Lumen contour length, lumen cross sectional planar projection, lumen shape index,

and colon shape matrix are measures of deviation of the shape of the given object (lumen of the colon) from that of an equivalent circle. The shape-based features determine whether there are any obstructions or blockages in the colon. These blockages are normally caused by the presence of polyps or growth.

5.2.3 Texture-based Feature Extraction

Texture is one of the most important features used in image processing and pattern recognition. It can give information about the arrangement and spatial properties of fundamental image elements. Many methods have been proposed to extract texture features, e.g. the co-occurrence matrix [159], and the texture spectrum in the achromatic component of the image [160]. In this research, a new method of obtaining quantitative parameters from the texture spectra is proposed both in the chromatic and achromatic domains of the image. These features are evaluated to demonstrate their usefulness and potential for classifying the colon status.

The definition of texture spectrum employs the determination of the texture unit (TU) and texture unit number (N_{TU}) values. Texture units characterise the local texture information for a given pixel and its neighbourhood, and the statistics of all the texture units over the whole image reveal the global texture aspects.

Given a neighbourhood of $\delta \times \delta$ pixels, which are denoted by a set containing $\delta \times \delta$ elements, $P = \{P_0, P_1, \dots, P_{(\delta \times \delta) - 1}\}$, where P_0 represents the chromatic or achromatic value of the central pixel and P_i $\{i = 1, 2, \dots, (\delta \times \delta) - 1\}$ is the chromatic or achromatic value of the neighbouring pixel i , the $TU = \{E_1, E_2, \dots, E_{(\delta \times \delta) - 1}\}$, where E_i $\{i = 1, 2, \dots, (\delta \times \delta) - 1\}$ determined as follows:

$$E_i = \begin{cases} 0 & \text{if } P_i < P_0 \\ 1 & \text{if } P_i = P_0 \\ 2 & \text{if } P_i > P_0 \end{cases} \quad (5.4)$$

The element E_i occupies the same position as the i -th pixel.

Each element of the TU has one of three possible values; therefore the combination of all the eight elements results in 6561 possible TU 's in total. The texture unit number (N_{TU}) is the label of the texture unit and is defined using the following equation:

$$N_{TU} = \sum_{i=1}^{(\delta \times \delta)-1} E_i \times \delta^{i-1} \quad (5.5)$$

The texture spectrum histogram h_i is obtained as the frequency distribution of all the texture units, with the abscissa showing the N_{TU} and the ordinate representing its occurrence frequency.

The texture spectra of various image components $C = \{R, G, B, H, S, I\}$ are obtained from their texture unit numbers. Six statistical measures are used to extract new features from each texture spectrum of the colonoscopic image. The statistical measures are energy (α), mean (μ), standard deviation (ν), symmetrical distribution (ϕ), peakedness index (κ), and orderly index (θ) described as follows.

- a. Energy (α_c) measures the homogeneity of the image or region. The more homogeneous the image or region, the larger the energy value is.

$$\alpha_c = \sum_{i=0}^{(\delta^{(\delta \times \delta)-1})-1} h_c(i)^2 \quad (5.6)$$

where $h_c(i)$ is the number of pixel at i -th level.

- b. Mean (μ_c) measures the central tendency of the pixels distribution in the image. The larger the sample size, the more reliable it's mean. The larger the variation of data values, the less reliable its mean.

$$\mu_c = \frac{1}{(\delta^{(\delta \times \delta)} - 1)} \sum_{i=0}^{(\delta^{(\delta \times \delta)} - 1) - 1} h_c(i) \quad (5.7)$$

- c. Standard deviation (ν_c) is one of several indices of variability to characterise the dispersion among the measures in a given pixels distribution.

$$\nu_c = \sqrt{\frac{1}{(\delta^{(\delta \times \delta)} - 1)} \sum_{i=0}^{(\delta^{(\delta \times \delta)} - 1) - 1} (h_c(i) - \mu_c)^2} \quad (5.8)$$

- d. Symmetrical distribution (ϕ_c) measures the deviation of the distribution from symmetry. If the ϕ_c is clearly different from 0, then that distribution is asymmetrical, while normal distributions are perfectly symmetrical.

$$\phi_c = \frac{1}{\nu_c^{1.5}} \sum_{i=0}^{(\delta^{(\delta \delta \delta - 1)} - 1) - 1} ((i + 1) - \mu_c)^3 \times h_c(i) \quad (5.9)$$

As general rule,

- If the mean is larger than the median then the distribution will have positive ϕ_c .
 - If the mean is less than the median then the distribution will have negative ϕ_c .
 - If the mean and the median are equal then the distribution will have zero ϕ_c .
-

- e. Peakedness index (κ_C) measures the "peakedness" of a distribution. If the κ_C is clearly different than 0, then the distribution is either flatter or more peaked than normal; the κ_C of the normal distribution is 0.

$$\kappa_C = \frac{1}{4} \left(\sum_{i=0}^{(\delta(\delta \times \delta)-1)-1} ((i+1) - \mu_C)^4 \times h_C(i) \right) - 3 \quad (5.10)$$

- f. Orderly index (θ_C) measures the degree of disorder of pixels distribution.

$$\theta_C = - \sum_{i=0}^{(\delta(\delta \times \delta)-1)-1} h_C(i) \times \log(h_C(i)) \quad (5.11)$$

- g. The colon texture matrix [T] is defined as the texture index matrix of the colon which is used to utilise the assessment of colon state.

These extracted features are used as input for the classification part.

5.2.4 Colour-based Feature Extraction

Colour colonoscopic images exhibited the same colour features for the same colon status [22]. Malignant tumours are usually inflated and inflamed. The inflammation is usually reddish and more severe in colour than the surrounding tissues. Benign tumours exhibit less intense hues. Red may specify bleeding and black may be treated as deposits due to laxatives. Green may be the presence of faecal materials, which are not cleared during the pre-operative preparation, and yellow relates to pus formation. Based on these properties, some features are extracted from the chromatic and achromatic histograms of the image. In the histograms of each image, certain lower and upper threshold values of the regions of interest are selected for the extraction of the quantitative parameters. The colour feature, namely Colour of Interest

Concentration (CLIC), is defined as follows:

$$CLIC = \frac{\sum_{i=L_1}^{L_2} h_c(i)}{\sum_{i=0}^{L-1} h_c(i)} \quad (5.12)$$

where CLIC are the colour features for various image components $C = \{R, G, B, H, S, I\}$, $h_c(i)$ is the histogram amplitude at level i of a particular colour component C , L is the number of grey levels, and L_1 and L_2 are the lower and upper threshold values of the histogram of the region of interest (ROI).

5.3 Feature Evaluation and Classification of Colonoscopic Images

A simplistic approach using lower and upper bounds of the quantitative parameters or a set of relatively straight-forward 'if-then' rules will not result in accurate classification of the state of the patient's colon. Detection of colon abnormalities can be quite complex in most instances. Thus, these colonoscopic features are evaluated using BPNN in conjunction with various training algorithms, viz., resilient propagation (RPROP) algorithm [161], scaled conjugate gradient (SCG) algorithm [162], and the Marquardt algorithm [163]. The various training algorithms were originally developed in order to speed up the training phase of the BPNN. Another method to decrease the training time is to use a principal component analysis (PCA) algorithm [164] to substitute the high-dimensional original features set with a low-dimensional set. This algorithm does not only decrease the dimensionality of feature

set but also forms a dominant feature set.

5.3.1 Principal Component Analysis of Colonoscopic

Quantitative Parameters

Some of the features extracted from the colonoscopic image have meaningful information for the colon state classification while some do not. Therefore, it is important to extract the significant information to facilitate efficient diagnosis. Principal component analysis (PCA) is a feature reduction technique, which can extract the significant information for a set of features. It is an orthogonal decomposition, which projects data onto the eigenvectors of the covariance matrix of the data. By sorting the eigenvectors by eigenvalue, the projected dimensions can be ranked by variance (which is proportional to eigenvalue). The highest eigenvalues correspond to the dimensions of highest variance and class separability. By eliminating dimensions with very small eigenvalues, the dimensionality of the projected space is reduced without losing much information.

The principal component analysis (PCA) algorithm is as follows:

- Get a set of colon features and subtract the mean

For PCA to work properly, the mean from each of the data dimensions have to be subtracted. The mean subtracted is the average across each dimension. The adjusted data set has zero mean.

- Calculate the covariance matrix

Covariance matrix is a matrix whose elements are the possible covariance values between all the different dimensions. So, the definition for the covariance matrix for a set of data with n dimensions is:

$$C^{n \times n} = (c_{i,j}, c_{i,j} = \text{cov}(Dim_i, Dim_j)) \quad (5.13)$$

where $C^{n \times n}$ is a matrix with n rows and n columns, Dim_x is the x th dimension.

- Calculate the eigenvectors and eigenvalues of the covariance matrix

The eigenvalues and eigenvectors [165] are calculated as follows. Let $C^{n \times n}$ is a matrix with n rows and n columns.

- o Form the characteristics equation $|\lambda I - C^{n \times n}| = 0$. It will be a polynomial equation of degree n in the variable $C^{n \times n}$.
- o Find the real roots of the characteristic equation. These are the eigenvalues of $C^{n \times n}$.
- o For each eigenvalue λ_i , find the eigenvectors corresponding to λ_i by solving the homogeneous system $(\lambda I - C^{n \times n})\mathbf{x} = \mathbf{0}$. This requires row-reducing $n \times n$ matrix. The resulting reduced row-echelon form must have at least one row of zeros.

It is important to notice that these eigenvectors are all unit vectors. The eigenvectors of the covariance matrix provide information on the patterns in the data.

- Choosing components and forming a colon feature vector

The eigenvector with the highest eigenvalue is the principal component of the set of colon features. Therefore, once eigenvectors are found from the covariance matrix, the next step is to order them by eigenvalue, from highest to lowest. This will order the components according to their significance. Some components can be ignored if they have lesser significance (eigenvalues are small). Then a colon feature vector can be formed. This colon feature vector is

constructed by taking the significant eigenvectors.

$$\text{FeatureVector} = (eig_1 \quad eig_2 \quad eig_3 \cdots eig_n) \quad (5.14)$$

- Deriving the new data set

Once the components (eigenvectors) formed a colon feature vector, the final data is taken from the transpose of the vector and multiplied on the left of the transposed original colon feature set:

$$\text{FinalData} = \text{RowFeatureVector} \times \text{RowDataAdjust} \quad (5.15)$$

where *RowFeatureVector* is the matrix with the eigenvectors in the columns *transposed* so that the eigenvectors are now in the rows, with the most significant eigenvector at the top, and *RowDataAdjust* is the mean-adjusted data *transposed*, ie. the data items are in each column, with each row holding a separate dimension. *FinalData* is the final colon feature set, with data items in columns, and dimensions along rows.

This algorithm has been implemented to the colon feature set. It forms a significant colon feature set for the colon state classification.

5.3.2 Artificial Neural Network for Colon State Classification

Colon state classification is obtained from the colon feature set through artificial neural network (ANN-CSC). An artificial neural network is an information-processing paradigm inspired by the way the densely interconnected, parallel structure of the mammalian brain processes information. Artificial neural networks are collections of mathematical models that emulate some of the observed properties of biological

nervous systems and draw on the analogies of adaptive biological learning. The key element of the ANN-CSC paradigm is the novel structure of the colon feature processing system. It is composed of a large number of highly interconnected processing elements that are analogous to neurons and are tied together with weighted connections that are analogous to synapses.

Learning in biological systems involves adjustments to the synaptic connections that exist between the neurons. The learning process typically occurs by training through examples, or exposure to a set of input/output data where the training algorithm iteratively adjusts the connection weights (synapses). These connection weights store the knowledge necessary to solve specific problems.

There are multitudes of different types of artificial neural networks. Some of the more popular include the multilayer perceptron, which is generally trained with the back propagation algorithm, learning vector quantisation, radial basis function, Hopfield, and Kohonen, to name a few. Some of artificial neural networks are classified as feed forward while others are recurrent (i.e., implement feedback) depending on how data is processed through the network. Another way of classifying ANN types is by their method of learning (or training), as some of artificial neural networks employ supervised training while others are referred to as unsupervised or self-organising. Supervised training is analogous to a student guided by an instructor. Unsupervised algorithms essentially perform clustering of the data into similar groups based on the measured attributes or features serving as inputs to the algorithms. This is analogous to a student who derives the lesson totally on his or her own.

The multilayer neural network algorithm is applied to the colon state classification and is described in Sub-section 5.3.3. This artificial neural network algorithm classifies the colon state automatically. In addition, work was undertaken to explore

the application of Self Organising Maps (SOM) for the colon state classification. The details are described in Sub-section 5.3.4.

5.3.3 Back Propagation Neural Network Applied to

Characteristic Parameters for Colonoscopic Images

Back propagation (BP) is an algorithm for supervised learning with multi-layered feed-forward networks. This algorithm is applied to the characteristic parameters of colonoscopic images. The block diagram of multilayer neural network for colon disease state classification is shown in Figure 5.3. The input for the BP is a colon feature set as defined in Section 5.2. The output of the BP is the colon state.

The basic idea of the BP learning algorithm is the repeated application of the chain rule to compute the influence of each weight in the network with respect to an arbitrary error function E :

$$\frac{\partial E}{\partial \omega_{ij}} = \frac{\partial E}{\partial o_i} \frac{\partial o_i}{\partial net_i} \frac{\partial net_i}{\partial \omega_{ij}} \quad (5.16)$$

where ω_{ij} is the weight from neuron j to neuron i , o_i is the output, and net_i is the weighted sum of the inputs of neuron i . Once the partial derivative for each weight is known, the aim of minimising the error function is achieved by performing a simple gradient descent:

$$\omega_{ij}(t+1) = \omega_{ij}(t) - \varepsilon \frac{\partial E}{\partial \omega_{ij}}(t) \quad (5.17)$$

Figure 5.3: Multilayer neural network for colon disease state classification

The choice of the learning rate ε which scales the derivative has an important effect in the time needed until convergence is reached. If it is too small, too many steps are needed to reach an acceptable solution; but a large learning rate will possibly lead to oscillation, preventing the error to fall below a certain value. A momentum-term was introduced to solve the above problem:

$$\Delta\omega_{ij}(t) = -\varepsilon \frac{\partial E}{\partial \omega_{ij}}(t) + \chi \Delta\omega_{ij}(t-1) \quad (5.18)$$

where the momentum parameter χ scales the influence of the previous step on the current. The momentum-term is believed to render the learning procedure more stable and to accelerate convergence in shallow regions of the error function.

However, this is not always true in practice. It turns out, that the optimal value of the momentum parameter χ is equally problem dependent as the learning rate ε , and

thus no general improvement can be accomplished. Many algorithms have been proposed to deal with the problem of appropriate weight-update by doing some sort of parameter adaptation during learning.

In this thesis, three learning methods, namely Resilient Propagation (RPROP), Scaled Conjugate Gradient (SCG), and Levenberg-Marquardt (LM) algorithms, are investigated and compared in order to accelerate the speed of convergence considerably and get better classification result. Each algorithm is described briefly as follows.

- **Resilient Propagation algorithm applied to colon state training**

Resilient propagation (RPROP) algorithm performs a direct adaptation of the weight step based on local gradient information. Its individual update-value Δ_{ij} is introduced to each weight which solely determines the size of the weight-update. This adaptive update-value evolves during the learning process based on its local sight on the error function E , according to the following learning-rule:

$$\Delta_{ij}(t) = \begin{cases} \eta^+ \times \Delta_{ij}(t) & , \text{ if } \frac{\partial E}{\partial \omega_{ij}}(t-1) \times \frac{\partial E}{\partial \omega_{ij}}(t) > 0 \\ \eta^- \times \Delta_{ij}(t) & , \text{ if } \frac{\partial E}{\partial \omega_{ij}}(t-1) \times \frac{\partial E}{\partial \omega_{ij}}(t) < 0 \\ \Delta_{ij}(t) & , \text{ else} \end{cases} \quad (5.19)$$

where $0 < \eta^- < 1 < \eta^+$.

Every time the partial derivative of the corresponding weight ω_{ij} changes its sign, which indicates that the last update was too big and the

algorithm has jumped over a local minimum, the update-value Δ_{ij} is decreased by the factor η^- . If the derivative retains its sign, the update-value is slightly increased in order to accelerate convergence in shallow regions.

Once the update-value for each weight is adapted, the weight-update itself follows a very simple rule: if the derivative is positive (increasing error), the weight is decreased by its update-value, if the derivative is negative, the update-value is added:

$$\Delta\omega_{ij}(t) = \begin{cases} -\Delta_{ij}(t) & , \text{ if } \frac{\partial E}{\partial \omega_{ij}}(t) > 0 \\ +\Delta_{ij}(t) & , \text{ if } \frac{\partial E}{\partial \omega_{ij}}(t) < 0 \\ 0 & ,, \text{ else} \end{cases} \quad (5.20)$$

$$\omega_{ij}(t+1) = \omega_{ij}(t) + \Delta\omega_{ij}(t) \quad (5.21)$$

However, there is one exception: if the partial derivative changes sign, i.e. the previous step was too large and the minimum was missed, the previous weight-update is reverted:

$$\Delta\omega_{ij}(t) = \Delta\omega_{ij}(t-1) \quad , \quad \text{if} \quad \frac{\partial E}{\partial \omega_{ij}}(t-1) \times \frac{\partial E}{\partial \omega_{ij}}(t) < 0 \quad (5.22)$$

Due to the step of 'backtracking' of the weight, the derivative is supposed to change its sign once again in the following step. In order to avoid a double punishment of the update-value, there should be no adaptation of the update-value in the succeeding step. In practice this can be done by setting

$\frac{\partial E}{\partial \omega_{ij}}(t-1) := 0$ in the Δ_{ij} adaptation-rule above. The update-value and the

weights are changed every time the whole pattern set has been presented once to the network (learning by epoch).

- **Scaled Conjugate Gradient algorithm applied to colon state training**

Scaled conjugate gradient (SCG) algorithm is a new variation of the conjugate gradient method, which avoids the line search per learning iteration by using a Levenberg-Marquardt method [166]-[167] to scale the step size. Its advantages are the increased learning speed and the fact that it eliminates the dependence on critical user-selected parameters. Let $\omega_{ij}(k) = \mathbf{W}(t)$ denotes the weight vector and $-\frac{\partial E}{\partial \omega_{ij}}(t) = -\nabla f(\mathbf{W}(t)) = \mathbf{D}(t)$ denotes the direction vector at

iteration t of the algorithm. Equation (5.17) can be rewritten as

$$\mathbf{W}(t+1) = \mathbf{W}(t) + \varepsilon(t)\mathbf{D}(t) \quad (5.23)$$

where the step size or learning rate $\varepsilon(t)$ is computed for each iteration t . The algorithm starts at $t=0$ with an initial direction vector set to the negative gradient vector $\mathbf{D}(0) = -\nabla f(\mathbf{W}(0))$. Each successive direction vector is evaluated as

$$\mathbf{D}(t+1) = -\nabla f(\mathbf{W}(t+1)) + \gamma(t)\mathbf{D}(t) \quad (5.24)$$

where the iteration-varying parameter $\gamma(t)$ can be determined with various formulas presented in the optimisation literature. A summary of the algorithm is given below.

1. Initialisation:

At $t=0$, choose an initial weight vector $\mathbf{W}(0)$, and set the initial direction vector $\mathbf{D}(0) = \mathbf{G}(0) = -\nabla f(\mathbf{W}(0))$. Set the scalars $0 < \sigma \leq 10^{-4}$, $0 < \rho(0) \leq 10^{-6}$, $\bar{\rho}(0) = 0$, success=true.

2. If success=true then calculate second order information:

$$\sigma(t) = \sigma / \|\mathbf{D}(t)\|, \mathbf{S}(t) = (\nabla f(\mathbf{W}(t) + \sigma(t)\mathbf{D}(t)) - \nabla f(\mathbf{W}(t))) / \sigma(t),$$

$$\delta(t) = \mathbf{D}(t)^T \mathbf{S}(t)$$

3. Scale $\delta(t)$:

$$\delta(t) = \delta(t) + (\rho(t) - \bar{\rho}(t)) \|\mathbf{D}(t)\|^2$$

4. If $\delta(t) \leq 0$ then make the Hessian positive definite:

$$\bar{\rho}(t) = 2(\rho(t) - \delta(t) / \|\mathbf{D}(t)\|^2), \delta(t) = -\delta(t) + \rho(t) \|\mathbf{D}(t)\|^2, \rho(t) = \bar{\rho}(t)$$

5. Calculate the step size:

$$\xi(t) = \mathbf{D}(t)^T \mathbf{G}(t), \varepsilon(t) = \xi(t) / \delta(t)$$

6. Calculate the comparison parameter, $c(t)$

$$c(t) = 2\delta(t) [f(\mathbf{W}(t)) - f(\mathbf{W}(t) + \varepsilon(t)\mathbf{D}(t))] / \xi(t)^2$$

7. Weight and direction update:

If $c(t) \geq 0$ then a successful update can be made:

$$\mathbf{W}(t+1) = \mathbf{W}(t) + \varepsilon(t)\mathbf{D}(t)$$

$$\mathbf{G}(t+1) = -\nabla f(\mathbf{W}(t+1))$$

$$\bar{\rho}(t) = 0, \text{ success=true}$$

If $t \bmod N = 0$ then restart the algorithm with:

$$\mathbf{D}(t+1) = \mathbf{G}(t+1)$$

else

$$\gamma(t) = \left(\|\mathbf{G}(t+1)\|^2 - \mathbf{G}(t+1)^T \mathbf{G}(t) \right) / \xi(t)$$

$$\mathbf{D}(t+1) = \mathbf{G}(t+1) + \beta(t)\mathbf{D}(t)$$

If $c(t) \geq 0.75$ then reduce the scale parameter:

$$\rho(t) = \frac{1}{4}\rho(t)$$

else

$$\bar{\rho}(t) = \rho(t), \text{ success=false}$$

8. If $c(t) < 0.25$ then increase the scale parameter:

$$\rho(t) = \rho(t) + \delta(t)(1 - c(t)) / \|\mathbf{D}(t)\|^2$$

9. Repetition:

If the steepest descent direction $\mathbf{G}(t) \neq 0$, set $t=t+1$ and go back to step (2)

else terminate and return $\mathbf{W}(t+1)$ as the desired minimum.

The scaled conjugate gradient can be viewed as a generalised BP, with $\varepsilon(t)$ recalculated in every iteration, and the usual “momentum” term replaced by $\gamma(t)$.

- **Levenberg-Marquardt algorithm applied to colon state training**

Levenberg-marquardt (LM) algorithm is an approximation to Newton's method [168], while BP is a steepest descent algorithm. This algorithm gives a good compromise between the speed of the Newton algorithm and the stability of the steepest descent method, and consequently it constitutes a good transition between these methods [169]. The performance index for LM algorithm is optimised and defined as

$$F(\mathbf{W}) = \sum_{j=1}^P \left[\sum_{i=1}^K (d_{ij} - o_{ij})^2 \right] \quad (5.25)$$

where $\mathbf{W} = [w_1 \ w_2 \ \dots \ w_N]^T$ consists of all weights of the network, d_{ij} is the desired value of the i^{th} output and the j^{th} input pattern, o_{ij} is the actual value of the i^{th} output and the j^{th} input pattern, N is the number of the weights, P is the number of input patterns, and K is the number of the network outputs. Equation (5.24) can be written as

$$F(\mathbf{W}) = \mathbf{E}^T \mathbf{E} \quad (5.26)$$

where $\mathbf{E} = [e_{11} \ \dots \ e_{K1} \ e_{12} \ \dots \ e_{K2} \ \dots \ e_{1P} \ \dots \ e_{KP}]^T$ is the cumulative error vector (for all input patterns), $e_{ij} = d_{ij} - o_{ij}$, $i = 1, \dots, K$, and $j = 1, \dots, P$.

From equation (5.25), the Jacobian matrix is defined as

$$\mathbf{J} = \begin{bmatrix} \frac{\partial e_{11}}{\partial w_1} & \frac{\partial e_{11}}{\partial w_2} & \dots & \frac{\partial e_{11}}{\partial w_N} \\ \frac{\partial e_{21}}{\partial w_1} & \frac{\partial e_{21}}{\partial w_2} & \dots & \frac{\partial e_{21}}{\partial w_N} \\ \vdots & \vdots & & \vdots \\ \frac{\partial e_{K1}}{\partial w_1} & \frac{\partial e_{K1}}{\partial w_2} & \dots & \frac{\partial e_{K1}}{\partial w_N} \\ \vdots & \vdots & & \vdots \\ \frac{\partial e_{1P}}{\partial w_1} & \frac{\partial e_{1P}}{\partial w_2} & \dots & \frac{\partial e_{1P}}{\partial w_N} \\ \frac{\partial e_{2P}}{\partial w_1} & \frac{\partial e_{2P}}{\partial w_2} & \dots & \frac{\partial e_{2P}}{\partial w_N} \\ \vdots & \vdots & & \vdots \\ \frac{\partial e_{KP}}{\partial w_1} & \frac{\partial e_{KP}}{\partial w_2} & \dots & \frac{\partial e_{KP}}{\partial w_N} \end{bmatrix} \quad (5.27)$$

The weights are calculated using the following equation:

$$\mathbf{W}(t+1) = \mathbf{W}(t) - (\mathbf{J}(t)^T \mathbf{J}(t) + \varepsilon(t) \mathbf{I})^{-1} \mathbf{J}(t)^T \mathbf{E}(t) \quad (5.28)$$

where $\mathbf{I}$ is identity unit matrix, ε is a learning parameter and $\mathbf{J}$ is Jacobian of m output errors with respect to n weights of the neural network. For $\varepsilon=0$ it becomes the Gauss-Newton method. For very large ε the LM algorithm becomes the steepest decent method. The parameter is automatically adjusted at each iteration in order to secure convergence.

The three learning algorithms mentioned above are implemented and observed for training the BPNN. They have the ability to speed up the training process, hence increase the training efficiency. The BPNN algorithm is compared to Self-Organising Map algorithm for the colon state classification.

5.3.4 Self-Organising Map Applied to Colon State

Classification

In addition to the BPNN, another neural network technique based in Self-Organising Map is attempted. This algorithm alleviates the difficulties with the supervisory mode in learning. Self-organising neural network is based on competitive learning; the output neurons of the network compete among themselves to be activated or fired, with the result that only one output neuron, or one neuron per group, is on at any one time. A self-organising map is therefore characterised by the formation of a topographic map of the input patterns in which the spatial locations of the neurons in the lattice are indicative of intrinsic statistical features contained in the input patterns.

The self-organising map algorithm introduced by Kohonen implements the properties of a vector quantisation and a topology of preserving mapping [170]. Neighbouring cells in a self-organising neural network compete in their activities by

means of mutual lateral interactions and develop adaptively into specific detectors of different signal patterns. The layout of Kohonen model is displayed in Figure 5.4.

Figure 5.4: Self-organised feature map of Kohonen model

In the case shown in Figure 5.4, the output neurons are arranged in a two-dimensional lattice. This type of topology ensures that each neuron has a set of neighbours. The algorithm responsible for the formation of the self-organising map proceeds first by initialising the synaptic weights in the network. In order to perform this process, small values picked from a random generator are assigned to the synaptic weights. No prior order is imposed on the feature map. Once the network has been properly initialised, there are five essential processes involved in the formation of the self-organising map, namely competition, cooperation, synaptic adaptation, self-organising or ordering phase and convergence phase.

Once the SOM has converged, the feature map displays important statistical characteristics of the input space. Let $\mathcal{X}$ denote a spatially continuous input data space, the topology of which is defined by the metric relationship of the vectors $\mathbf{x} \in \mathcal{X}$. Let

ψ denote a spatially discrete output space, the topology of which is endowed by arranging a set of neurons as the computation nodes of a lattice. Let Φ denote a non-linear transformation called a feature map, which maps the input space χ onto the output space ψ as shown by

Figure 5.5: Relationship between feature map Φ and weight vector $\mathbf{w}_i$ of winning neuron i

For a given input vector $\mathbf{x}$, the SOM algorithm proceeds by first identifying a winning or best matching neuron $i_{(\mathbf{x})}$ in the output space ψ , in accordance with the feature map Φ . The synaptic weight vector $\mathbf{w}_{(i)}$ of neuron $i_{(\mathbf{x})}$ is then viewed as a pointer for that neuron into the input space χ . The synaptic elements of vector $\mathbf{w}_{(i)}$ can be viewed as the coordinates of the image of neuron i projected in the input space. These two operations are depicted in Figure 5.5.

The SOM algorithm substitutes a simple geometric computation for the more detailed properties of the Hebbian-like rule and lateral interactions. The essential parameters of the algorithm are:

- A continuous input space of activation patterns that are generated in accordance

with a certain probability distribution.

- A topology of the network in the form of a lattice of neurons, which defines a discrete output space.
- A time-varying neighbourhood function $h_{j,i(\mathbf{x})}(n)$ that is defined around a winning neuron $i(\mathbf{x})$.

A learning-rate parameter $\eta(n)$ that starts at an initial value η_0 and then decreases gradually with time, n , but never goes to zero.

For the neighbourhood function and learning-rate parameter the following functions may be used:

$$h_{j,i(\mathbf{x})}(n) = \exp\left(-\frac{d_{j,i}^2}{2\sigma^2(n)}\right), \quad n = 0, 1, 2, \dots \quad (5.30)$$

and

$$\eta(n) = \eta_0 \exp\left(-\frac{n}{\tau^2}\right), \quad n = 0, 1, 2, \dots \quad (5.31)$$

where $d_{j,i}$ is distance measure of neuron j and i , $\sigma(n)$ is a time varying factor and τ is a constant factor, for the ordering phase.

The steps involved in the application of the algorithm after initialisation is sampling, similarity matching, and updating. These three steps are repeated until the formation of the feature map is complete. The algorithm is summarised as follows:

1. *Initialisation.* Choose random values for the initial weight vectors $\mathbf{w}_j(0)$. The

only restriction here is that the $\mathbf{w}_j(0)$ be different for $j = 1, 2, \dots, l$, where l is the number of neurons in the lattice. Generally, it may be desirable to keep the magnitude of the weights small. A different way of initialising the algorithm is to select the weight vectors $\{\mathbf{w}_j(0)\}_{j=1}^l$ from the available set of input vectors $\{\mathbf{x}_i\}_{i=1}^n$ in a random manner.

2. **Sampling:** Draw a sample x from the input space with a certain probability. The vector $\mathbf{x}$ represents the activation pattern that is applied to the lattice. The dimension of vector $\mathbf{x}$ is equal to m .
3. **Similarity Matching:** Find the winning or the best-matching neuron $i(\mathbf{x})$ at time step n by using the minimum-distance Euclidean criterion:

$$i(\mathbf{x}) = \arg \min_i \|\mathbf{x}(n) - \mathbf{w}_i\|, \quad j = 1, 2, \dots, l \quad (5.32)$$

4. **Updating:** Adjust the synaptic weight vectors of all neurons by using the update formula

$$\mathbf{w}_j(n+1) = \mathbf{w}_j(n) + \eta(n) h_{j,i(\mathbf{x})}(n) (\mathbf{x}(n) - \mathbf{w}_j(n)) \quad (5.33)$$

where $\eta(n)$ is the learning-rate parameter, and $h_{j,i(\mathbf{x})}(n)$ is the neighbourhood function centred around the winning neuron $i(\mathbf{x})$; both $\eta(n)$ and $h_{j,i(\mathbf{x})}(n)$ are varied dynamically during learning for best results.

5. **Continuation:** Continue with step (2) until no noticeable changes in the feature map are observed.

The Self-Organising Map is applied for the colon state classification process. The

principal goal of the SOM is to transform an incoming colon feature vector of arbitrary dimension into a one-dimensional or two-dimensional discrete map, and to perform this transformation adaptively in a topologically ordered fashion. It is generally held that the SOM is formed in an unsupervised process, which means there is no external teacher or critic to oversee the learning process. Due to the complexity of colonoscopic images, it is sometimes difficult to determine the class to which the individual regions belong. Therefore SOM can be applied because of its unsupervised nature.

Figure 5.6: The array of neurons in a two-dimensional SOM array

As shown in Figure 5.6, the SOM defines a mapping from the input data space R^n onto a two-dimensional array of nodes. Here R^n is defined upon the N-dimensional colon feature vector. The lattice type of the array is defined to be rectangular with the size of 4×4 . When training the SOM, normal and abnormal features of both normal and abnormal images are used as input vectors. When the training process is completed, the feature vectors of neurons will reflect the characteristics of the images. Some neurons can be observed to associate with the normal images and the other with the abnormal. In testing procedure, an arbitrary image is given as input and the diagnosis can be obtained based on the property of its winning neuron. The classification results

obtained by using SOM are seen in the following section.

5.4 Results and Discussion

The proposed methods were evaluated using clinically obtained colonoscopic images. A set of selected colonoscopic images of normal and abnormal cases is shown in Figure 5.7. New features based on texture and colour are defined and extracted from the colonoscopic images for diagnosis of the colon's status. There were efforts attempted to evaluate and classify the features extracted from the segmented colonoscopic.

Figure 5.7: Selected colonoscopic images of normal and abnormal states

The first effort attempted was to evaluate and classify the features extracted from the segmented colonoscopic images for the colon state classification using unsupervised self-organising map algorithm. It is due to the complexity of

colonoscopic images, which sometimes cause difficulty in determining the class to which the individual regions belong. Therefore, it is convenient to select the SOM for its unsupervised nature.

The classification statistics for colon state are obtained on the mutually exclusive categories of true positives colon state (*TPCS*), false positive colon state (*FPCS*), true negatives colon state (*TNCS*), and false negative colon state (*FNCS*). The *TPCS*, *FPCS*, *TNCS*, and *FNCS* are defined approximately as listed in Table 5.1 since it is more important that the abnormal colon can be recognised from normal colon.

Table 5.1: Definition of classification colon state categories

<i>TNCS</i>	Known normal colon regions are classified as normal ones
<i>TPCS</i>	Known abnormal colon regions are classified as abnormal ones
<i>FPCS</i>	Known normal colon regions are classified as abnormal ones
<i>FNCS</i>	Known abnormal colon regions are classified as normal ones

Three statistical parameters, namely *Sensitivity* (ϖ), *Specificity* (o) and *Accuracy* (ϑ), are used to measure the performance of classification results. *Sensitivity* is the fraction of real events that are correctly classified among all real events; *Specificity* is the fraction of non-events that have been correctly rejected; and *Accuracy* is the fraction of real events that are correctly detected and non-events that are correctly rejected among all testing events. They are given by:

$$\varpi = \frac{TPCS}{TPCS + FNCS} \quad (5.34)$$

$$o = \frac{TNCS}{TNCS + FPCS} \quad (5.35)$$

$$\mathcal{J} = \frac{TPCS + TNCS}{TPCS + FNCS + TNCS + FPCS} \quad (5.36)$$

The colon state classification using self-organising map results are as follows: for shape feature, ϖ is in the range of 50% to 60%, $\circ$ is in the range of 60% to 70 %, $\mathcal{J}$ is in the range of 55% to 60%; for texture feature, ϖ is in the range of 55% to 65%, $\circ$ is in the range of 60% to 70 %, $\mathcal{J}$ is in the range of 60% to 70%; for colour feature, ϖ is in the range of 80% to 90%, $\circ$ is in the range of 60% to 70 % $\mathcal{J}$ is in the range of 70% to 80%; for texture and colour features, ϖ is in the range of 60% to 70%, $\circ$ is in the range of 40% to 50 %, $\mathcal{J}$ is in the range of 55% to 60%;.and for shape, colour and texture features, ϖ is in the range of 65% to 75%, $\circ$ is in the range of 60% to 70 %, $\mathcal{J}$ is in the range of 60% to 70%;.

From the results shown above, the colour feature set gives better results than other feature sets. The reason for that is the characteristics of the data set available contain more distinguishes colour information. The shape feature only can be extracted from the lumen of the colon in order to detect whether there is growth or polyp which protrude the colon.

The second effort attempted was to classify the extracted feature using supervised classification method, which is back propagation neural network (BPNN). These features were evaluated using BPNN with various training algorithms, viz., resilient propagation (RPROP), scaled conjugate gradient (SCG), and Levenberg-Marquardt (LM) algorithms.

For training the BPNN, half of the sample sets of images were used. The training and testing procedures were carried out with different sets of colour components {C} and different numbers of neurons in the hidden layer. The number of input neurons of the BPNN depends on the sets of colour components {C}. The BPNN has a boolean output, which tells whether the colon’s status is normal or abnormal. Table 5.2 shows a number of features having various colour component combinations {C}.

Table 5.2: The numbers of colon features with various colour component combinations

{C}	Number of Features
{I, R, G, B, H, S}	36
{I, R, G, B}	24
{H, S, I}	18
{H, S}	12

The graphs of training time comparison for different training algorithms with various numbers of hidden neurons is shown in Figure 5.8.

Figure 5.8: Graphs of training time comparison for various training algorithms with different number of hidden neurons in colonoscopic abnormality detection scheme

Table 5.3: The number of training epochs for the different algorithms in colonoscopic abnormality detection scheme

C={I, R, G, B, H, S}			
Number of Hidden Neurons	Training Epochs		
	Marquardt Algorithm	SCG Algorithm	RPROP Algorithm
5	33	3294	11102
10	28	1583	2435
15	17	1798	2090
20	27	1256	1093
25	19	922	524
C={I, R, G, B}			
5	20	2281	100000
10	23	2795	36776
15	37	1380	5294
20	27	1184	1579
25	37	1019	1362
C={H, S, I}			
5	30	1293	100000
10	23	2647	28238
15	22	1601	2337
20	21	976	9683
25	26	961	2480
C={H, S}			
5	17	2256	75574
10	22	3728	12624
15	35	1948	27195
20	58	2012	6269
25	34	2396	4403

The LM algorithm needs lesser time to converge during training than SCG and RPROP algorithms. It is shown in Table 5.3 that the number of epochs needed for BPNN to converge to the minimum mean-squared error of the system in the training using LM training algorithm is fewer than SCG and RPROP algorithms.

The sensitivity and accuracy are shown in Table 5.4 and Table 5.5, respectively, for various feature sets and different training algorithms, viz., LM, SCG and RPROP training algorithms with different numbers of hidden neurons. The average specificity obtained from the experiment is around 99% for all training algorithms. It is seen on Table 5.4 and Table 5.5 that the RPROP training algorithm gives better sensitivity and accuracy percentages than SCG and LM training algorithms. Although it gives better results, the training time is longer than the LM algorithm. The LM algorithm yielded reasonable results. Therefore, LM training algorithm is used in the current work.

It is also observed that the classification sensitivity and accuracy percentages for {H, S, I} feature set is better than other data sets {C}. The average classification sensitivity and accuracy percentages are 91.48% and 93.02%, respectively. Therefore, {H, S, I} feature set is extracted for further analysis for the current work.

Table 5.4: Sensitivity ϖ (%) of colon status classification

Number of hidden neuron	C={I, R, G, B, H, S}	C={I, R, G, B}	C={H, S, I}	C={H, S}
LM training algorithm				
5	87.04	81.48	92.59	85.19
10	90.74	81.48	90.74	81.48
15	88.89	94.44	94.44	88.89
20	94.44	90.74	90.74	87.04
25	94.44	90.74	88.89	96.30
Average	91.11	87.78	91.48	87.78
SCG training algorithm				
5	83.33	83.33	85.19	88.89
10	81.48	77.78	83.33	85.19
15	92.59	94.44	94.44	83.33
20	90.74	92.59	85.19	85.19
25	92.59	94.44	96.30	92.59
Average	88.15	88.52	88.89	87.04
RPROP training algorithm				
5	94.44	94.44	88.89	94.44
10	90.74	94.44	92.59	94.44
15	88.89	90.74	90.74	96.23
20	94.44	87.04	88.89	94.44
25	98.15	94.44	90.74	100.00
Average	93.33	92.22	90.37	95.91

Table 5.5: Accuracy & (%) of colon status classification

Number of hidden neuron	C={I, R, G, B, H, S}	C={I, R, G, B}	C={H, S, I}	C={H, S}
LM training algorithm				
5	89.39	84.84	93.93	87.87
10	92.42	84.84	92.42	84.84
15	90.90	95.45	95.45	90.90
20	95.45	92.42	92.42	89.39
25	95.45	92.42	90.90	96.96
Average	92.72	89.99	93.02	89.99
SCG training algorithm				
5	86.36	86.36	87.87	90.90
10	84.84	81.81	86.36	87.87
15	93.93	95.45	95.45	86.36
20	92.42	93.93	87.87	87.87
25	93.93	95.45	96.96	93.93
Average	90.30	90.60	90.90	89.39
RPROP training algorithm				
5	95.45	95.45	90.90	95.45
10	92.42	95.45	93.93	95.45
15	90.90	92.42	92.42	96.96
20	95.45	89.39	90.90	95.45
25	98.48	95.45	92.42	100
Average	94.54	93.63	92.11	96.66

Based on the classification results obtained using unsupervised SOM algorithm and supervised BPNN, the unsupervised SOM failed to yield on better classification sensitivity, specificity, and accuracy compared to supervised BPNN. Therefore, further

research is carried out to improve the performance of the classification using BPNN. New approach using principal component analysis and BPNN was developed. This approach is also another way to help speed up the training time is to choose a significant feature vector. Principal component analysis reduced the dimension of the features and was applied before using BPNN for classification of the colon status. The BPNN that is used to classify the PCA features has a Boolean output assigned for normal or abnormal colon status. Table 5.6 shows the number of features after applying PCA with different threshold values, τ , and without applying PCA. For example, $\tau=5\%$ means that those principal components whose contribution is less than 5% to the total variance in the feature set are eliminated.

Table 5.6: The number of features with and without PCA

{C}	Number of Features				
	Without PCA	With PCA			
		$\tau=5\%$	$\tau=2\%$	$\tau=1\%$	$\tau=0.1\%$
{I, R, G, B, H, S}	36	3	5	9	15
{I, R, G, B}	24	3	6	8	13
{H, S, I}	18	4	7	8	11
{H, S}	12	4	6	7	9

The graphs of the LM training time comparison using PCA with different τ (5%, 2%, 1%, 0.1%) and various numbers of hidden neurons are shown in Figure 5.9. The LM training time comparison between BPNN which is using PCA ($\tau=1\%$) and without using PCA is shown in Figure 5.10. It shows that by using PCA, the overall training time is decreased thereby increasing the performance of BPNN.

Figure 5.9: Graphs of Marquardt training time comparison using PCA with different τ (5%, 2%, 1%, 0.1%) and various numbers of hidden neurons in colonoscopic abnormalities detection scheme

Figure 5.10: Graphs of Marquardt training time comparison on the usage of PCA with various numbers of hidden neurons ($\tau = 1\%$) in colonoscopic abnormalities detection scheme

The classification sensitivity and accuracy are calculated for {H, S, I} feature set as shown in Table 5.7-Table 5.8. The classification specificity for all training algorithm is about 99%. It is seen in Table 5.7-Table 5.8 that the average classification sensitivity and accuracy percentages are increased after employing PCA in conjunction with BPNN and $\tau=1\%$ gives better accuracy rates than other values of τ . The average classification sensitivity and accuracy are 96.26% and 96.96% with $\tau=1\%$.

Table 5.7: Sensitivity (%) of the colon status classification using the Marquardt algorithm with and without PCA for {H, S, I} feature set

Number of hidden neurons	Without PCA	With PCA			
		$\tau=5\%$	$\tau=2\%$	$\tau=1\%$	$\tau=0.1\%$
10	90.74	90.74	94.44	98.15	98.15
15	94.44	90.74	94.44	94.44	94.44
20	90.74	87.04	92.59	96.23	90.74
25	88.89	90.74	96.23	96.23	96.23
Average	91.20	89.82	94.43	96.26	94.89

Table 5.8: Accuracy (%) of the colon status classification using the Marquardt algorithm with and without PCA for {H, S, I} feature set

Number of hidden neurons	Without PCA	With PCA			
		$\tau=5\%$	$\tau=2\%$	$\tau=1\%$	$\tau=0.1\%$
10	92.42	93.94	95.45	98.48	98.48
15	95.45	86.36	95.45	95.45	95.45
20	92.42	95.45	93.94	96.96	92.42
25	90.90	84.85	96.96	96.96	96.96
Average	92.80	90.15	95.45	96.96	95.83

Colour features extracted from the histogram of the colonoscopic images were also defined. Certain lower and upper threshold values of the region of interest (ROI) were selected for the histograms of each image. Certain patterns from R, G, B, H, S, and I histograms were identified which could distinguish between normal and abnormal colon conditions. The histograms are plotted in Figure 5.11-Figure 5.16. The selection of the ROI is rather subjective.

Based on the histograms of the images, the ROI for each type of histogram is selected as an input for the NN classification. The ROI is chosen such that patterns are seen in the ROI for both normal and abnormal cases. A histogram for both normal and abnormal colonoscopic images is shown in Figure 5.11. It is observed that for normal and abnormal conditions, the redness is concentrated around the 200 to 255 levels (where 0 is the lowest intensity value and 255 is the highest intensity value). Another histogram of both normal and abnormal colonoscopic images is shown in Figure 5.12. It is observed that the histogram has a bell shape pattern for the normal condition and very little pattern is observed for the abnormal condition. The green parameter can be extracted in the ROI from 100 to 255 of the green level. From a similar histogram in Figure 5.13, the abnormal condition exhibits certain patterns, but the same pattern is not observed in the normal condition.

This does not pose a problem to the feature extraction module, as the main objective behind the parameter extraction was to differentiate the normal condition from the abnormal condition. As long as there are some patterns observed in one of the conditions, the parameter extracted from this colour space can be considered useful in classification. The selected ROI in the blue level histogram is in the range of 0 to 50.

Figure 5.1 1 : Histograms of the red component of selected coloscopic images

Figure 5.12: Histograms of the green component of selected colonoscopic images

Figure 5.13: Histograms of the blue component of selected cdonoscopic images

Very similar patterns are observed for the normal and abnormal conditions for the hue component shown in Figure 5.14. Its ROI is determined to be in the range of 10 to 50 for both normal and abnormal cases. In the saturation domain shown in Figure 5.15, the shapes of the histograms for the normal and abnormal cases are also very similar. However, the tail for the normal case has a higher value. The ROI for the extraction of the saturation parameter is then set in the range of 100 to 150. In the intensity histogram shown in Figure 5.16, the pattern observed is very similar to that of the

green histograms. In this case, the range is 150 to 255 of the intensity level.

(a) Normal Cases

(b) Abnormal Cases

Figure 5.14: Histograms of the hue component of Selected Colonoscopic Images

Figure 5.15: Histograms of the saturation component of selected colonoscopic images

Figure 5.16: Histograms of the intensity component of selected colonoscopic images

The classification results for detecting the colon status using colour features (CLIC) are shown in Table 5.9. The same procedures for the classification using texture feature are applied for colour features. The training was done by using the Marquardt algorithm. It was found that the average accuracy using PCA with $\tau = 0.1\%$ is higher than the classification using PCA, with $\tau=5\%$, 2% , or 1% or without PCA. At $\tau = 0.1\%$, PCA does not change the dimension of the features. The number of features will be the same as the number we would have if we were not using PCA at all. The fewer the number of features used, the worse the average classification rate becomes. This shows that all of the extracted colour features (CLIC) are significant.

The images are rich with texture and colour information. Therefore, it is important to utilise the extracted texture and colour features. Experiments on the hybrid of the texture and colour features for colon status classification have been done. It is shown in Table 5.10 that the average classification accuracy with a hybrid of texture and colour features for the classification using PCA with $\tau=1\%$ is higher than the classification with other τ value and without PCA.

Table 5.9: Accuracy (%) of the colon status classification using colour features

Number of Hidden Neurons	Without PCA	With PCA			
		$\tau=5\%$	$\tau=2\%$	$\tau=1\%$	$\tau=0.1\%$
10	96.96	96.96	92.42	84.84	92.42
15	87.87	95.45	87.87	96.96	98.48
20	93.93	90.9	92.42	86.36	96.96
25	98.48	93.93	86.36	93.93	93.93

Table 5.10: Accuracy (%) of the colon status classification using hybrid texture and colour features

Number of Hidden Neurons	Without PCA	With PCA			
		$\tau=5\%$	$\tau=2\%$	$\tau=1\%$	$\tau=0.1\%$
10	95.45	93.93	90.9	98.48	92.42
15	90.9	93.93	95.45	96.96	98.48
20	93.93	89.39	92.42	98.48	93.93
25	95.45	90.9	96.96	96.96	96.96

Table 5.1 1: Average accuracy (%) of the colon status classification

Features	Without PCA	With PCA			
		$\tau=5\%$	$\tau=2\%$	$\tau=1\%$	$\tau=0.1\%$
Texture	93.02	90.15	95.45	96.96	95.83
Colour	94.31	94.31	89.77	90.52	95.45
Hybrid	93.93	92.04	93.93	97.72	95.45

Colonoscopic images are complex. With the present technique, the defined parameters coupled with PCA forcing the principal components, images with the abnormalities can be differentiated from the images which are normal.

The accuracy obtained for the innovative effort is considered to be encouraging. Extensive testing must be done with formulation of new parameters which will be the characteristic of different types of abnormalities in order to have a better comprehension computer-assisted analysis and diagnosis solution.

At the present time, there is a very high incidence of colorectal cancer. Fatalities are also very high. One of the reasons is the detection of cancer at the later stage. Therefore, screening is needed to detect the cancer at the early stage. The computer-assisted colonoscopic system which can pick abnormal regions through image processing algorithm can prompt the physicians on the presence of different regions in

the image

The proposed technique can be extended to determine other diseased states of the colon to facilitate the type of abnormality with additional intelligence, the occurrence of multiple abnormalities can be detected thus can prove to be an invaluable tool for physicians in training.

5.5 Concluding Remarks

In conclusion, new methods for extracting new shape-based features, texture-based features and colour-based features from colonoscopic images for the analysis of the colon status have been developed. The quantitative parameters are important to characterise the colon to facilitate the comparative evaluation and quantitative documentation. Study can be done to assess the extension of polyp or tumour and the speed of recovery when the patient is treated with a certain treatment. However, not all extracted features are useful. Therefore, feature selection method is employed.

Principal component analysis is a powerful tool for analysing these features. It provides a way of identifying patterns in features, and expressing the features in such a way so as to highlight their similarities and differences. The performance of back propagation neural network increases by associating it with principal component analysis. The results obtained verified the effectiveness of the proposed methods. It can be seen that the quantitative characteristics are related to certain conditions, and the meaningful mathematical relationships are derived based on individual parameters as a combination of them to correlate to a certain colon diseases condition.

The present work forms part of an innovative effort in having new approaches of image processing, image segmentation and extraction of meaningful parameters, thus

formulating a new paradigm of quantitative characterisation of the colon, leading to intelligent technique of analysis and decision making for determining the presence of abnormalities. It is envisioned that the proposed technique will pave the way for new methods of intelligent endoscopy which will facilitate the physicians in clinical diagnosis particularly in a screening mode. It is therefore considered that the present work can be the key to aiding the clinicians by computer-assisted endoscopy for cancer screening.

Chapter 6

EXTENDED APPLICATIONS FOR THE INTELLIGENT COLONOSCOPIC INSTRUMENTATION SYSTEM

In this chapter, some extended applications for the intelligent diagnostic colonoscopic instrumentation system are described. The diagnostic endoscopy coupled with laser induced autofluorescence is described in Section 6.4. The application of tele-endoscopy is shown in Section 6.3. The extended application to the pseudo real-time image analysis is given in Section 6.2.

6.1 Introduction

In order to work with physicians in clinical setting, it is essential that real-time image capture has to be carried out. Pseudo real-time intelligent diagnostic colonoscopic

instrumentation system has been designed and implemented. In order to work with physicians in clinical setting, it is essential that real-time image capture, processing, and analysis have to be carried out. A new method was developed to achieve the real-time image capture coupled with intelligent image processing leading to pseudo real-time colonoscopic image processing and analysis. This method facilitates computer-assisted decision making by the physician. It is expected that the proposed technique would be of great value in medical training where different types of abnormalities can be detected if a series of images is presented and corresponding analysis is made available.

6.2 Pseudo Real-Time Colonoscopic Image Analysis

Real-time image processing is image information processing where the output is generated nearly simultaneously with the corresponding input. It is used usually where the results of the computation are used to influence a process while it is occurring. Real time image capture is the retrieving of image at the current time of operation. These images have to be segmented and classified fast enough to be termed real time.

The general flow of real time navigation and diagnosis of endoscope images begins with the capture of an image from a source such as a video or directly from a hardware camera. The captured image will be sent through a pre-processing module to remove noise. The 'clean' image will go through image segmentation for the isolation of the various regions, such as the lumen. Features are extracted and calculated through feature extraction. The back propagation neural network is then employed in the computer-assisted diagnosis of colonoscopic images to assist the physician in detecting the colon status.

As colonoscope is manoeuvred and stopped at critical site in the colon, an analysis of the corresponding colon image is made and an intelligent documentation of the specific site can be maintained in the patient record if an abnormality is detected at that site.

Figure 6.1 : Flowchart of real-time colonoscopic image analysis

6.2.1 Fast Image Capture

In capturing of real-time endoscopic images, live images are obtained from the hardware camera, such as a CCD, at the tip of the endoscope. The block diagram of the real-time colonoscopic image acquisition is shown in Figure 6.2. The image is decoded using NTSC/PAL format. Through a pixel converter, the ‘live’ image is transformed into a digital image which is stored in the buffer of the frame grabber card. Using software control via the AGP/PCI bus found in the PC, these digital images could be captured from the buffer of the frame grabber card and stored as a bitmap or to be viewed ‘live’ on a PC monitor screen.

Figure 6.2: Block diagram of the real-time colonoscopic image acquisition

6.2.2 Colonoscopic Image Processing

The captured image is then processed by the image processing algorithms. There are many image processing methods used in this field, such as image segmentation algorithms for the colon lumen extraction and the segmentation of regions of interest in the lumen for the detection of abnormalities. The flowchart of a fast lumen extraction is shown in Figure 6.3. The lumen is segmented from the rest of the image and through centroid determination method, the centre location is identified. Other segmentation methods are described in Chapter 3. Based on the fast lumen detection algorithm, lumen centre from clinical colonoscopic image is accurately indicated as shown in Figure 6.4 for normal and abnormal images.

Figure 6.3: Flowchart of fast detection algorithm for the colon lumen using thresholding method

(a) Normal case

(b) Abnormal case

Figure 6.4: Pseudo real-time colon lumen centre extraction

The similar procedure is applied to the model of the colon, which is available in the laboratory. This work is the pioneer on doing image processing and analysis simulation for the model of the colon. The image of the model of the colon has different properties compared to clinical colonoscopic image. The fast lumen detection

algorithm is modified for the extraction of the lumen from the model of the colon. Instead of using the intensity value, the saturation of the image is employed to obtain the lumen. The cross indicates the lumen centre location as shown in Figure 6.5.

Figure 6.5: Lumen extraction from the model of the colon

In case of polyp or growth existing in the image, the algorithm can also detect the presence of the polyp by marking the polyp with a cross indication as shown in Figure 6.6. The fast lumen extraction algorithm is also applied to the playback video obtained from the video endoscope. The image is captured when the video stream is paused and immediately analysed.

Figure 6.6:Lumen and polyp detection fromthe model ofthe colon

(a) Paused event

(b) Lumen detected

Figure 6.7: Lumen extraction from playback video obtained of the video endoscope

The lumen centre is marked out almost instantly as shown in Figure 6.7. The next step is to extract quantitative parameters from the lumen and regions of interest obtained from segmentation algorithm.

6.2.3 Colonoscopic Feature Extraction

Features are extracted from the segmented image and are used as input to the BPNN for the classification of colon state. Selected segmentation results are shown in Figure 6.8. The features extracted from those segmented images are shown in Figure 6.9.

Figure 6.8: The segmentation result for colon bleeding images

The features are extracted from the histogram of the image in different colour spaces. Red, green, and blue colour features are calculated using the mean of each colour component histogram. Upon obtaining the colour feature of red, green, and blue

component of the colonoscopic image, hue, saturation and intensity features are easily computed by applying simple algebraic and trigonometric equations. Other features are skewness, which characterises the degree of asymmetry of intensity histogram around its mean and kurtosis that characterises the relative peakedness or flatness of a distribution compared to the normal distribution. Standard deviation is obtained by taking the square root of the variance.

Figure 6.9: Features extracted from colon bleeding images

By analysing the bleeding data file, we can conclude that the red component of the bleeding category is ranging from 0.6 to 0.8 while the blue component is relatively small only from 0.001 to 0.04. It is obvious as the red component should dominate in bleeding region. The saturation features for colon bleeding is very close to 1 and its intensity is around 0.2. However, kurtosis of the images varies quite significantly while the other features are quite close in value with one another.

Features from other types of abnormalities, such as polyp, ulcers, are also extracted and interpreted. Half of the features are fed into BPNN for the training of the neural network, and the other half are used for testing the BPNN.

6.2.4 Classification of Colonoscopic Images

The classification of the colon state is performed by BPNN. Before using the BPNN to do classification, training to the neural network is performed. The training of the network consists of three stages: feed-forward of the input training pattern, the calculation and back-propagation of the computed error, and the adjustment of the weights. The application of the network only involves the computations of the feed-forward stage. Although the training may take a very long time, a trained network can produce its output very rapidly during the testing.

A good back-propagation net requires more than the core of the learning algorithms. The parameters must be Carefully selected to ensure good performance. The input layer of our BPNN consists of 12 neurons. Each neuron represents one input feature in a 1-to-1 mapping. All 12 input variables are normalised to values less than 1 or near to 1. These 12 features vector are area, perimeter, form factor, red component, green component, blue component, hue, saturation, intensity, skew, kurtosis and standard deviation of each colonoscopy medical image.

The classification phase is represented by the output layer. In the present work, the output layer consists of 3 neurons. Since supervised back-propagation learning algorithms are applied, the neural network is trained with features that are predefined with a known category. There are 5 categories used for training purpose namely “Bleeding”, “Polyps”, “Ulcer”, “Abnormal” and “Normal” to classify different colorectal cancer. Each category is accompanied with 3 predefined binary values “1” or “0” as shown in Table 6.1. In another word, these binary values act as the target values for each category. The Table 6.1 shows the output interpretation of each category.

Table 6.1 : Output Interpretation

No	Category	Output target vector
1	Bleeding	1 0 0
2	Polyp	0 1 0
3	Abnormal	0 0 1
4	Ulcer	1 1 0
5	Normal	1 0 1

For example, if the output layer neurons produce “1 0 0” during testing phase, the network will classify the colonoscopy image as a bleeding colon. The assumption here is that the feed-forward phase of the network using the trained weights produces a neuron value greater than 0.5 will be considered as “1” while less than 0.5 will be considered as “0”. This assumption only applies to the testing of the network. However, for training part, the values of the output neurons after training must be very close to the target value. For example, for bleeding colon, the output value vector must have the first value close to “1” (0.98) and the other two values close to “0” (0.01) to be counted as convergence of a particular input pattern.

The classification results are shown in Figure 6.10 for bleeding and normal regions from abnormal image. Normal region is detected from a normal image as shown in Figure 6.11.

(a) Original colonoscopic image

(b) Bleeding detected in the colon

(c) Normal colon detected

Figure 6.10: Classification results for bleeding and normal regions of abnormal image

(a) Original colonoscopic image

(b) Normal colon detected

Figure 6.11 : Classification results for normal image

The classification accuracy for colon abnormalities detection using 15 and 25 hidden neurons are shown in Figure 6.12. The accuracy for ulcer detection is the lowest due to the fact that it possesses the lowest training data sets in the training file. In other words, accuracy of ulcer detection can be increased by adding more data sets featuring ulcer category to the training process. On the contrary, the accuracy for classifying bleeding and abnormal images is satisfactory. The reason for this is due to high number of training data sets available for these two categories. The constraint here is because of the lack of ulcer images in the colonoscopy images database used in this

project. Among 60 images, only 7 images are characterised under ulcer abnormality.

Figure 6.12: Classification accuracy for the colon abnormalities detection

The average accuracy of the network is about 76.5%. Possible reasons could be due to insufficient or inadequate training data sets available and choosing the image of wrong abnormal category for training as some of the images is assessed by visual inspection. In order to increase the accuracy, the overall weight values may need to be fine-tuned by inputting more data sets before the testing is carried out.

The proposed methods for the extended application towards the real-time colonoscopic image analysis have been developed. The results obtained show the

visibility of the proposed method. Further refinement on the methods will increase the efficiency of the computer-assisted diagnostic for helping physician during the colonoscopy.

6.3 Tele-Endoscopy

Tele-endoscopy is part of telemedicine services. Tele-endoscopy refers to the transmission of real-time compressed endoscopic video images over a distance. This technology offers the potential to provide consultative support for isolated rural practitioners and may reduce costs by avoiding patient transfers or duplicate invasive testing. Tele-endoscopy requires the transmission of high resolution motion images with the highest degree of colour depths. Methods of recording and retrieving data, as well as mechanisms for transmitting and coding in tele-endoscopy are very crucial to ensure quality outcome of transmitted endoscopic images.

Tele-endoscopy is designed for rapid diagnosis and consultation by imaging specialists among one hospital to another hospital or physicians' homes or clinics by means of telephone lines, digital networks, microwave or satellite transmission. The tele-endoscopy consists of an image capture station and a receiving station. The image capture station includes a personal computer (PC) with a high-speed modem, a high-resolution display card, a viewing monitor and an image capture device. Before it can be stored or transmitted, the image must be digitised by the capture device, which electronically divides the image into rectangular areas called picture elements (pixels); the sequence of pixel values representing the image can then be stored, processed and transmitted digitally.

As part of the present project, a video-conferencing system for medical tele-

consultation is developed. The system included an endoscope with the patient and a clinician and one or more remote sites for tele-endoscopy connected with a suitable links.

The block diagram of tele-endoscopy is shown in Figure 6.13. Because of the amount of information that must be transmitted for each pixel, digital transmission is almost always slower than analog transmission. Digital systems usually use sophisticated high-speed modems, resulting in a slightly higher cost to compensate that problem.

Figure 6.13: Block diagram of tele-colonoscopy

The modem converts the digital data from the PC into an analog signal for transmission over standard telephone lines. Another modem at the receiving station then converts the incoming analog signal into digital data for the display computer. Modem speed is measured in bits per second (bps) of data transmitted or received, and speeds can range from 13,000 to 28,800 bps. Speeds greater than 28,800 bps can be

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achieved over leased lines dedicated to data transmission. Unlike analog transmission, digital transmission is not affected by background noise or other audio interference because there is a sufficiently wide difference between the frequencies of the digital signal to avoid encoding errors.

Images are stored in the computer memory, hard disks or optical disks. After image capture and conversion, the images are then transmitted to a remote location for viewing. The computer system in tele-endoscopy controls the acquisition, display, manipulation, and transmission of image data. Workstations at each site are used for interactively reviewing digitised endoscopic images before and after transmission, for archiving digital images, and for controlling the capture devices and printers.

Several image enhancement features are available with the proposed tele-endoscopy system. Software can be used to enhance contrast, improve edge delineation, or magnify an area of interest. Continued improvements in ISDN technology, microcomputers, compression algorithms, interactive workstations, and digitising technology, as well as the demand for faster and more convenient information transfer within the medical community coupled with a refined model of the proposed intelligent colonoscopic instrumentation system will increase the demand for tele-endoscopy systems and digital data transmission. The growth of a national and international telecommunications infrastructure will also facilitate the installation and the use of tele-endoscopy systems. Image and data transmission via cable modem is currently under development as a faster and more cost-effective alternative to ISDN and T-1 lines. With transmission rates of 1.5 Mbps, this cable service will use coaxial networks rather than phone lines.

The proposed tele-endoscopy system can be used for subspecialty consultations and for off-site reading of images by on-call clinicians. The emphasis on managed

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care, integrated healthcare delivery networks, and the computer-based patient record has increased the interest in expanding tele-endoscopy applications. These networks which are rapidly growing in response to managed care typically consist of multiple remote sites that transmit images to clinician groups.

Tele-endoscopy can be used as delivering tool for medical care to patients worldwide through telecommunications technologies and multimedia applications. By combining teleconferencing, telephone consultations, tele-pathology, and other technologies and applications, tele-endoscopy may become practical and cost-effective alternative to in-hospital procedures and care.

The image quality will have to be improved in order to make a clinical decision by using tele-endoscopy system. Finally, the transmission speed of the image and/or sound appropriate to the application used in different location should be considered. Tele-endoscopy has a lot of benefits such as faster delivery of medical support, cheaper, comfortable for the patients and enhanced quality of support.

6.4 Diagnostic Endoscopy Coupled with Laser-Induced Autofluorescence

A new attempt is made to integrate the proposed intelligent endoscopic instrumentation system with laser-induced autofluorescence (LIAF) for mucosal tissue characterisation and early stage detection of malignancy in the colon. LIAF diagnostics is a spectroscopic method, which can provide information on the biochemistry and indirectly on the pathology of the tissue.

The conventional methods for morphological characterization of lesions are mainly based on histopathology. Small pieces of tissue or in some cases whole lesions

are excised and analysed by microscopy after thorough preparation. Histopathology is fairly reliable but it has risks of sampling errors, as the doctor may not be able to get the correct diseased tissue specimens during sampling. It also has disadvantage in cost and time required for histopathological diagnosis. Among the various alternatives or complementary techniques that are capable of providing diagnostic information in real-time during examination, autofluorescence is a complementary method to yield cheap information noninvasively.

Neoplastic polyps harbour some malignant potential and may develop into carcinomas if left untreated. There is strong evidence that most invasive colorectal adenocarcinomas arise in adenomatous polyps which is a kind of neoplastic polyps. It is sometimes difficult to distinguish between non-neoplastic and neoplastic polyps by conventional endoscopy, especially if they are small and flat. Autofluorescence method might provide the necessary information to assist the examining physician to classify polyps during the endoscopic procedure and it is expected to improve the accuracy of abnormal-suspected position of mucosa colon in real-time since the LIAF spectra technique can detect small flat abnormal spot earlier than traditional endoscopy.

During colonoscopy or endoscopy, the colon and rectum mucosa autofluorescence of a patient are excited by continuous wavelength laser with a certain range of intensity [171], [172]. The detection fibre bundle tip is delivered to the large intestine inter-surface through biopsy channel of the colonoscope. While collecting the autofluorescence signal, the diagnostic endoscope will use the features from detected signal to identify the abnormal-suspected position.

The LIAF method generates autofluorescence spectra intensity of a mucosa colon from colonoscopy. The autofluorescence spectra intensity of cancer or diseased

colorectal mucosa is significantly different from those of normal area. This fact helps physicians to examine the results of colonoscopy. The feature classification of the LIAF method coupled with the proposed instrumentation system can contribute to coming up with a new method for cancer detection and staging.

6.5 Concluding Remarks

It is noted that the real-time colonoscopic data capture makes the proposed intelligent colonoscopic instrumentation system attractive for clinical use. Due to computational limitations, at the present time the proposed instrumentation system tends to be pseudo real-time.

A tele-endoscopy system greatly enhances the usability of the proposed intelligent instrumentation system with tele-consultation available on a real-time, the diagnosis will improve significantly. This technique will be particularly useful in cancer screening.

The diagnostic endoscope system in this thesis will be improved by coupling the autofluorescence spectra intensity feature to its decision vectors as well as in identifying early-stage cancer.

Chapter 7

CONCLUSIONS AND RECOMMENDATIONS

7.1 Conclusions

This thesis presents research on an intelligent diagnostic colonoscopic instrumentation system. The major objectives of the research effort reported in this thesis are: to develop new segmentation methods for the colour colonoscopic images in order to extract new sets of quantitative parameters from the images, which are essential for further analysis on detecting abnormalities from the colonoscopic images. The research work comprises four parts: colonoscopic image segmentation, colon lumen extraction, feature extraction of colonoscopic image, and classification of colonoscopic images. The following are the distinct techniques.

1. A texture-based segmentation method has been proposed for the colonoscopic images. The texture information was measured with a method based on linear binary pattern and magnitude. The main advantages of the proposed method are
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absence of any requirement of prior knowledge of the image to be processed and parameter values not being sensitive for different images.

2. A homogeneity index-based segmentation technique has been developed for the segmentation of the colour colonoscopic images. The image segmentation based on homogeneity index is carried out in two stages. In the first stage, the image is segmented using the homogeneity and intensity values of the pixels. In the second stage, sub-regions are obtained by differentiating the pixels on the basis of hue measure. The sub-regions obtained from the second stage with similar colour are then merged. This method is superior to the region merging and splitting method.
 3. A clustering method has been established for the image segmentation of the colour colonoscopic images. Clustering method is closely related to image segmentation because of the similarity criteria for grouping the pixels and number of segments in the image. Two clustering algorithms were explored, namely fuzzy C-means and K-means algorithms. Fuzzy C-means algorithm was found to give better segmentation results and more stable than K-means algorithm.
 4. A modified deformable region model method has been elaborated for the extraction of the colon lumen from the colonoscopic image. The modified deformable region model determines the lumen boundary from the colonoscopic images by giving an approximate boundary plan of the lumen, and then deforms this plan to the real boundary automatically. The complexities of the segmentation problem are somewhat alleviated, thus rendering the proposed scheme to be attractive to clinicians. It has been proved that the modified deformable region model method detects the lumen contour faster and more accurately than the snake
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and minimum variance region growing methods.

5. Quantitative parameters have been extracted from the colonoscopic images based on the shape, texture and colour information to characterise the colon quantitatively. The quantitative parameters are used to facilitate the analysis of the colon status.
6. The selections of the extracted quantitative parameters are employed by using principal component analysis to evaluate features which are significant in distinguishing the normal and abnormal colon. The artificial intelligent classification algorithm is applied for the classification of colon state.
7. Pseudo real-time colonoscopic image analysis system has been designed and implemented to assist the physician in the detection of colon abnormalities.

7.2 Major Contributions

In the present work, an in-depth study of three main problems has been carried out for the development of an intelligent diagnostic colonoscopic instrumentation system. This includes colonoscopic image segmentation, colon lumen extraction, and feature extraction, and classification of the colonoscopic images. They form the distinguished contributions of this thesis.

In author's opinion, the most distinguished aspects of the contributions in the presented research are listed below:

1. New methods for the segmentation of the colonoscopic images which automatically segment the image into several meaningful regions for supporting
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decision making.

2. New colon lumen boundary extraction method to facilitate the physicians in manoeuvring the endoscope during endoscopy.
3. New quantitative parameters obtained from colonoscopic image which characterise the colonoscopic image quantitatively for objectivity of the diagnosis, doing the study of the extension of the polyps or tumour and the speed of recovery when the patient is under certain treatment.
4. Intelligent method for the selection of the extracted feature from the colonoscopic images to facilitate fast, accurate and intelligent colon state classification using artificial intelligent algorithm.
5. A new pseudo real-time intelligent colonoscopic instrumentation system for assisting the physician in the detection of colon abnormalities.

It is pointed out that the research work on the development of intelligent colonoscopy has significant breadth in terms of explaining new approaches of segmentation, feature extraction, and decision making as well as depth in terms of quantitative characterisation and assistance to clinical diagnosis.

Extending the techniques developed in the present work on lower gastro-intestinal system to upper gastro-intestinal system (oesophagus) and to bronchoscopic images appeared to be feasible based on limited testing with clinical data. This lends support to the presently proposed intelligent endoscopic instrumentation system.

7.3 Recommendations for Future Work

The task of intelligent diagnostic colonoscopic instrumentation system can be divided into three steps: image segmentation, feature extraction and feature clustering or classification. High qualities of image segmentation and suitable feature set are undoubtedly the most important factors for good performance of colonoscopic image analysis algorithms. Based on these and other factors, recommendations for further research are listed below.

1. New visualisation techniques to display the sequence of images in 3-D form to give better visualisation for colon diagnosis from the colonoscopic image and for the colonoscope navigation as well as new techniques to solve colonoscopic image processing and analysis as a 4D problem.
 2. The feature definition and extraction based on information obtained from the colonoscopic image to provide meaningful determination of many types of abnormalities such as polyps, tumours, ulcers, etc., especially at an early stage.
 3. It is expected that in order to get real-time analysis and diagnosis, the computational aspect can be addressed by using faster processors, faster algorithms, and also prudent parallel processing. Initial attempts were made in parallel processing for successive image on four-processor system to reduce the diagnosis time during the procedure.
 4. It is envisioned that the presently developed intelligent colonoscopic instrumentation system will be coupled with laser-induced fluorescence to obtain fluoroscopic patterns, which may be characteristic of normal and abnormal
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mucosal layers. It is conceivable that the information available from this technique can be applied for detection of early stage or onset of malignant growth. Necessary animal testing and subsequent clinical trial can be carried out in the future.

5. It is encouraging to extend the proposed method for the application of upper gastro-intestinal images and bronchoscopic images.
6. Other artificial intelligent algorithm including fuzzy approach can be attempted to improve the overall accuracy.

7.4 Closing Remarks

In closing, research efforts were undertaken on applying engineering methods and technologies to solve challenging medical problems, particularly for the detection of abnormality of the colon from the colonoscopic images. It is believed that the significant contributions in the present research work have been made paving the way for intelligent and quantitative diagnosis for the colorectal cancer screening which could aid in early detection, proper treatment, and improved quality of life as well as containment of associated cost.

Based on the evaluation of the results obtained, the proposed method is found to be of great interest and potential diagnostic value to the clinicians. After extensive clinical testing and appropriate refinements, it is strongly believed the proposed solution can be implemented in clinical endoscopy for intelligent computer-assisted diagnostic colonoscopy.

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APPENDIX A

NOMENCLATURE

a^*	Relative redness-greenness value of pixel on L*a*b* colour space
A	The area of the object
A_{encl}	The enclosed boundary area
b^*	Relative yellowness-blueness value of pixel on L*a*b* colour space
c_j	The d-dimension centre of the cluster
$C^{n \times n}$	The covariance matrix for a set of data with n dimensions
$CLIC$	The colour feature
D_{ij}	The colour difference between region i and region j
$D(t)$	The direction vector at iteration t
$e(x,y)$	The edge value at (x,y)
E	The error function

Appendix A

A-2

E_{snake}^*	The total energy
$E_{internal}$	The internal energy
E_{image}	The image energy
$E_{constraint}$	The external constraint energy
E_{push}	The pushing force
f_I	The number of pixels having intensity level I
$F_o(g_s^*)$	The grey level cumulative frequency distribution function of object in an image
$F_B(g_s^*)$	The grey level cumulative frequency distribution function of boundary of an object
$F(W)$	The performance index
FP	False positive
FN	False negative
g_s	The grey level of pixel set s
G	G statistic
Hue	Hue value of pixel on HSI colour space
$H(I(x,y))$	Homogeneity value in intensity level domain at (x,y)
$H_{CE}(T)$	The cross-entropy value for each level T
$H_o(g_s^*)$	The grey level frequency distribution function of object in an image
$H_B(g_s^*)$	The grey level frequency distribution function of boundary of an object

h_C	The histogram of various texture spectra c
$h_{j,i(x)}$	The neighbouring function for SOM
$I(x,y)$	The intensity level of pixel at (x,y)
I_O	An object in an image as a homogeneous region
I_B	The boundary of an object
I	Identity matrix
J_m	The objective function
J	Jacobian matrix
L^*	Lightness value of pixel on $L^*a^*b^*$ colour space
L_S	A binary label image related to original image
L_{CL}	Lumen contour length
LC_{int}	Lumen cross sectional planar projection
MI	Merger Importance value
MIR	The ratio of the current merger importance and the largest merger importance of all preceding mergers
n_i	The number of pixels on i th grey level
N	Total number of pixels in the image
net_i	The weighted sum of the inputs of neuron i
N_{TU}	The texture unit number
o_i	The output of neural network
P	Perimeter

R	The ration between largest and smallest G statistics
S	Saturation value of pixel on HSI colour space
$[S]$	Colon shape matrix
t^*	Optimal threshold for modified OTSU algorithm
Th, T	The threshold value
TU	The texture unit
$[T]$	Colon texture matrix
TP	True positive
TN	True negative
u_{ij}	The degree of membership of x_i in the cluster j
W_{xy}	A size $d \times d$ window centred at (x,y)
w_{int1}	The weight to control the tension of the snake
w_{int2}	The weight to control the rigidity of the snake
x_i	The i^{th} of d-dimensional data points
$\mathbf{x}$	The eigenvector
X_{ctr}	The centroid at x-axis
Y_{ctr}	The centroid at y-axis
Y	Preset threshold for <i>MIR</i>
α_c	The energy value
Δ_{ij}	The individual update-value which introduce to each weight

$\nabla f(\mathbf{W}(t))$	The direction vector at iteration t
ε	The learning rate for BPNN
η	The learning rate for SOM
κ_C	The peakedness index of texture feature
ℓ	The length of the boundary
λ	The eigenvalue
$\gamma(t)$	The iteration-varying parameter at iteration t
ω_{ij}	The weight from neuron j to neuron i
ϖ	Sensitivity measure
σ	Specificity measure
φ	The lumen shape index
Φ	Non-linear transformation (feature map)
ϕ_C	The symmetrical distribution of the texture feature
ψ	The significance level of the Kolmogorov-Smirnov (KS) test
θ_C	The orderly index of texture feature
σ_B^2	Between class variance
σ_T^2	Total variance
μ_i	Mean value of the region i
μ_C	The mean value of various colour combination C

$\mu(x, y)$	Mean value of the grey level within window W_{xy}
ν_i	The standard deviation of region i
ν_C	The standard deviation value of various colour combination C
$\nu(x, y)$	The standard deviation of the grey level within window W_{xy}
ϑ	Accuracy measure
τ_{CE}	Threshold corresponds to the minimum of the cross entropy
χ	The momentum parameter (in Sub-section 5.3.3)
$\mathcal{X}$	A spatially continuous input data space (in Sub-section 5.3.4)
$\ \cdot\ _*$	Any norm expressing the similarity between any data point and the centre

APPENDIX B

CLINICAL COLONOSCOPIC

INSTRUMENTATION

Endoscope is a thin, flexible or rigid instrument used to view the inside of an organ or body cavity. It has a light and an optical system, as well as the capacity to take images. It is inserted through a body opening (the mouth or anus) or through a small surgical incision to view the interior of the body. Small amounts of tissue can be removed for biopsy.

Endoscopes range in diameter from about $\frac{1}{4}$ inch to about $\frac{1}{2}$ inch and range in length from about 1 foot to about 5 feet. Fibber-optic video systems allow the endoscope to be flexible while providing both a lighting source and a viewing system. Many endoscopes also are equipped with a small clipper to remove tissue samples and an electric probe to destroy abnormal tissue.

When passed through the mouth, an endoscope can be used to examine the oesophagus (oesophagoscopy), the stomach (gastroscopy), and the small intestine

(upper gastrointestinal endoscopy). When passed through the anus, an endoscope can be used to examine the rectum and the lower portion of the large intestine (sigmoidoscopy) and the entire large intestine (colonoscopy).

The instrument enables the doctor to look directly at the oesophagus, colon and rectum through a thin flexible tube called an oesophagoscope, colonoscope and anoscope, respectively.

Figure B.1: Video endoscopy system

A clinical video endoscopy system consists of:

- An endoscope which is a device that consists of a thin flexible tube, which has a tiny charged couple device (CCD) camera, a light at the end of the tube, and an air and water supply channel. This device is able to take small sample for biopsy.
 - The movement controller.
 - Display monitor which is directly connected to CCD camera and the processing device which reproduce the high-clarity images.
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APPENDIX C

DESIGN OF SOFTWARE MODULES

The overall block diagram of the intelligent diagnostic colonoscopic instrumentation system is shown in Figure C. 1. The image captured by the endoscope is shown on the monitor and then converted into digital image by the frame grabber in the computer. The image processing methods, which include image pre-processing (A) and image segmentation (B), are used to get the quantitative parameters (C) as extracted features. The extracted features are then used to diagnose the abnormalities in the colon (D) and provide navigational guidance as the input for the physician while doing the colonoscopic procedures. Final diagnosis is given based on combined information acquired from the physician's knowledge and diagnosis of abnormalities from the system. The block diagram of the overall algorithms of intelligent system of the endoscope is shown in Figure C. 2. The intelligent diagnostic colonoscopic instrumentation system consists of two major parts, which are image segmentation (shown in Figure C. 3) and feature extraction and classification (shown in Figure C. 4). Block diagram of newly proposed approaches/methods of intelligent diagnostic

colonoscopic system is shown in Figure C. 5.

Figure C. 1: Overall block diagram of the intelligent diagnostic colonoscopic instrumentation system

Figure C. 2: Overall block diagram of the algorithms of intelligent diagnostic colonoscopic instrumentation system

Figure C. 3: Block diagram of colonoscopic image segmentation approaches

Figure C. 4: Block diagram of feature extraction and classification of colonoscopic image

Figure C. 5: Block diagram of newly proposed approaches/methods of intelligent diagnostic colonoscopic instrumentation system