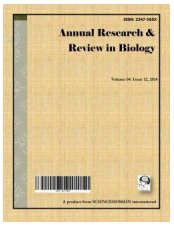

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Colon Cancer Detection Methods – A Review

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Authors' contributions

This work was carried out in collaboration between both authors. Author BS designed the study, performed the statistical analysis, wrote the protocol and wrote the first draft of the manuscript. Authors BS and ASMP managed the analyses of the study. Author ASMP managed the literature searches. Both authors read and approved the final manuscript.

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ABSTRACT

Aim: Colon is one of the major constituent of the large intestine; occurrence of cancer in it is one of the burning issues that remain unresolved. A large number of people get died every year in this problem.
Study Design: In the field of medical image processing the detection of Colon cancer is a big challenge. So far, many research works are proposed, however, no research and investigations are found to bring up the best technique to assess the disease.
Place and Duration of Study: Several strategies, in view of the spatial analysis of colon biopsy images, and serum and gene analysis of colon samples, have been proposed in such manner.
Methods: Quick advancement of colon cancer detection methods, are yet to be analyzed by the help of this particular work which ensures to coming up with best strategies.
Results: In this review, we arrange the procedures on the premise of the adopted system and basic data set, and give a detailed description of methods in every category. Also, this study gives a far extensive examination of different colon cancer detection categories, and of multiple procedures inside every category.

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Conclusions: Further, the majority of the procedures have been assessed on comparative data set to give a reasonable performance correlation. Ultimately this review can helpful for the researches to proceed their research in the field of colon cancer detection.

Keywords: Colon cancer detection; texture based analysis; object-oriented texture analysis; spectral analysis; gene analysis; blood serum analysis.

1. INTRODUCTION

Expansive running from breakage of substantial molecules to supplements digestive system performs a wide mixture of functions and water ingestion. Colon is one noteworthy constituent of an internal organ, and its cancer is a significant reason for deaths of people in the western and industrialized world [1]. There are numerous reasons of colon cancer, similar to, chain-smoking, increasing age, for example, age over 50 years, family history of colon cancer, low intake of organic products, and overwhelming intake of red meat and fats [2]. Colon cancer records for 8% of all passing by cancer, making it the fourth most normal reason for death from cancer [3]. The sickness can be averted by detection and removal of antecedent adenomatous polyps amid optical colonoscopy (OC) [4], an endoscopic examination of the colon utilizing an adaptable camcorder. Amid OC, where the endoscopist searches for anomalous developments, are commonly can be categorized as one of the two classes: hyperplastic or adenomatous polyps. Hyperplastic polyps are benevolent injuries that present minimal clinical danger of forming into cancer and don't oblige removal from the colon. Conversely, adenomatous polyps are premalignant tumors that, if left unchecked, are prone to end up cancerous and are surgically uprooted by the endoscopist amid a polypectomy [5].

The decision to evacuate or take off alone obliges aptitude past that of numerous endoscopists. Hence, it is basic to uproot every distinguished polyp for a consequent histological investigation [6]. Be that as it may, removal of hyperplastic polyps postures superfluous danger to patients (as polyp removal conveys a danger of colon aperture obliging crisis surgery) and causes pointless expenses for histological examination [7]. This work process could be fundamentally enhanced if there was an approach to perform a quick in vivo biopsy of a polyp amid OC [6]. The last diagnosis and evaluation of colorectal cancer are in light of the histopathological evaluation of biopsy tissue tests. In this assessment, pathologists settle in the vicinity of cancer in light of the presence of strange developments in a tissue and focus cancer evaluation in view of the level of the variations from the norm. As this assessment mostly depends on visual understanding, it may contain subjectivity [8]. Hence, it has been proposed to utilize computational strategies that help diminish the subjectivity level by giving quantitative measures. Along these lines, it has been proposed to utilize computational routines that help diminish the subjectivity level by giving quantitative measures.

Traditionally, colon cancer is diagnosed utilizing microscopic investigation of histopathological colon tests [9]. In such an examination, pathologists watch the colon tests under a microscope to distinguish threat and allocate cancer evaluation relying on the level of authoritative changes they see in tissues. Anyhow, the manual examination has a couple of constraints. It is subjective in light of the fact that quantitative measures, for example, cancer evaluations/stages primarily rely on upon the visual assessment of pathologists. Second, it has inter/intra observer variation in grading [10].

Automatic detection of colon cancer has two noteworthy directions: segmentation and classification. In segmentation, heterogeneous colon tests are isolated into homogenous regions in light of spatial conveyance of tissues in the images. Next, typical and harmful marks are appointed to the regions in light of specific features. In the writing, a few methodologies exist for medical image segmentation, for example, pixel-based, region based, and graph based. Pixel-based systems divide picture pixels into distinctive clusters based upon their colors utilizing different methodologies like watershed change [11], clustering [12], versatile segmentation [13], and thresholding [14]. Region-based segmentation procedures use the comparative methodology, yet they keep up a network between pixels of comparable clusters. Well understood systems of this class incorporate splitting and merging [15], and region growing [16]. Graph-based methods [17,18] assume picture pixels as nodes of a graph and

weight between them as closeness between pixels. Segmentation then includes graph partitioning into sub graphs while minimizing cost functions [19]. In classification, colon tests are separated into typical and dangerous classifications based upon specific features. Classification and segmentation may be trailed by cancer grading venture, in which quantitative cancer evaluations are allocated to the specimens relying on certain quantitative measures [20]. Automated diagnosis methods have been proposed for cancer detection in many body parts like breast [21,22], brain [23], [24], prostate [25], cervical [26], and lungs [27]. In connection to this, numerous techniques have been done for colon cancer detection.

2. REVIEW ON COLON CANCER DETECTION METHODS

Generally, there are five noteworthy classes of colon cancer detection methods relying on the underlying data set and embraced technique. These classes incorporate spectral analysis, texture analysis, gene analysis, serum analysis, and OO texture analysis. Texture, hyperspectral, and OO texture analysis-based systems work in light of images. Accordingly, these systems have alluded as image analysis-based procedures in this study. A couple of strategies, which deal with colon biopsy images yet are not settled, have been examined in the various classification. Gene and serum analysis-based methods investigate physical sample for cancer identification, thus, have been named physical sample-based colon cancer detection strategies. A wide level classification of these systems is displayed in Fig. 1, and the accompanying content clarifies these systems in detail.

2.1 Review of Texture Analysis Based Techniques

Textures are complex visual patterns made out of elements, or sub patterns, that have properties brightness, shading, slope, size, and so on. Along this texture can be viewed as a comparability gathering in an image. The local sub pattern properties offer ascent to the apparent lightness, consistency, thickness, roughness, normality, linearity, recurrence, phase, directionality, coarseness, irregularity, fineness, smoothness, granulation, and so forth., of the texture overall. There is an important variation in the texture of ordinary and malignant colon tissues. A few specialists have exploited this variation in their particular studies and accomplished great classification on colon biopsy data sets. Entropy and correlation have been usually used to quantize texture. Notwithstanding, a few different parameters are likewise practically speaking. Well, known texture analysis based colon cancer detection procedures have been compressed in the following content.

Kalkan H et al. [28] have joined texture and auxiliary features to classify colon samples into ordinary, precancerous (adenomatous and inflamed) and harmful classes. In this work, 2,000 patches every class have been utilized. A sum of 1,108 texture features is processed from every patch by assessing 32 containers color channel histograms of R, G, B, H, S, V color segments of the crude image. Further, every patch is isolated into 16 sub-patches, and the accompanying auxiliary features are calculated per sub patch: the quantity of cores every tissue zone, the individual and the pair wise proportion

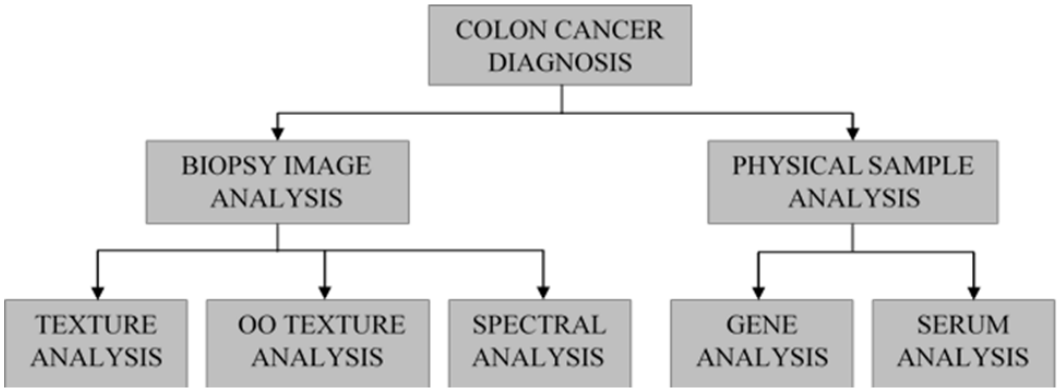

Fig. 1. Colon cancer detection techniques

of each of stroma, cell, and lumen to the tissue range. Further, forward feature selection method is connected to choose important features. Logistic regression classifier with equal class priorities is applied for classification, and 77.29, 82.25, 76.08, and 66.86 percent classification precision is accounted for adenomatous, threatening, inflamed, and typical classes.

Ng F et al. [29] have completed an exploration study with intending to focus the relationship between changes happening in the texture of malignant colon images and the survival rate of patients. In this work, texture features of standard deviation, entropy, consistency, kurtosis, and skew ness were extracted from pixel distribution histograms of contrast material-improved CT images. Kaplan-Meier examination was performed to focus the relationship between these features and 5-year survival rate. The Cox proportional risks model was utilized to survey independence of texture features from the stage. This texture investigation procedure was caught up in the same cancer patients until their death. Examination revealed that Kaplan-Meier survival plots for texture features are essentially not the same as one another. Results revealed that features are free from the cancer stage, and can be utilized to model malignancy in all the cancer stages. Further, results demonstrated that fine texture features are connected with the poorer 5-year general survival rate for the patients with colon cancer.

Xu Y et al. [30] have built a framework for colon cancer detection and classification in light of slide histopathological images. In this work, they examined huge amount of colon cancer images and found that one image contains cancer regions of multiple types. Consequently, they reformulated the task as multi-label issue. Four kinds of features like color histogram, gray level co-occurrence matrix, a histogram of arranged gradients and Euler number are acquainted with composing the discriminative feature set extracted from the dataset. The dataset consists of arbitrarily picked 230 images collected from 138 patients with colon pathology images. The entire size of the slice is around 200000×200000 pixels and they cut every slice into small images with the size of 10000×10000 pixels. The performance of the proposed multi-label model is compared with three commonly utilized multi-classification routines which are composed of this trial including one-against-all SVM (OAA), one-against-one SVM (OAO) and multi-structure SVM. The performance is accepted in light of the parameters precision, recall, and F-measure. Analysis results demonstrated that the precision, recall, and F-measure of multi-label technique as 73.7%, 68.2%, and 70.8% with all features, which are higher than the other three classifiers.

Edgar A. N et al. [31] have researched the estimation of fractal dimension in differentiating typical and cancerous images and analyzed the relationship between fractal dimension and conventional texture analysis features. Dataset comprises of 22 images of ordinary mucosa and 24 modestly separated adenocarcinoma images, each taken from an alternate lesion. A few areas of these images did not contain tissue, and smaller images were consequently chosen. It was hypothetically conceivable to acquire four images of 256×256 pixels from each original picture, nonetheless, to boost the tissue range in every 256×256 picture, generally, two and at most three images were gotten from each original picture. Therefore, an aggregate of 44 typical images and 58 cancerous images were utilized for analysis. A "leave-one-out" analysis methodology was utilized to classify the specimens into each group. A "leave-one-out" methodology was utilized to get an almost unbiased estimation of classification error rates. This system expels one observation from N observations and treats the remaining N-1 as a training set. The one left out is then classified. This procedure is then repeated for the N training observations. Fractal analysis add a little change to the outcomes obtained utilizing correlation and entropy alone. Sensitivity was enhanced from 90% to 95% and specificity from 86% to 93%.

Olgun G et al. [32] have proposed to deteriorate a tissue image into its histological parts and present a set of new texture descriptors, which is called local object patterns, to model composition of histological segments in a tissue image and the utilization of this descriptor set to characterize the visual words of the bag-of-words representation of the image. The proposed calculation develops a binary string to encode objects composition in a predefined local neighborhood. In this binary string, purple objects, which usually relate to nucleus segments, are indicated with 1 and the others with 0. Rather than this binary representation, one could consider developing ternary strings where pink and white objects are represented with different values. Also, the proposed

calculation processes the local object pattern descriptors by changing over the binary strings to their decimal reciprocals. It is additionally conceivable to get these descriptors specifically from the strings. Examinations are conducted on 3236 microscopic images of hematoxylin and eosin-re colored colon tissues of 258 patients. The training set contains 510 ordinaries, 859 low grade cancerous, and 275 high-grade cancerous images of 129 patients. The test set contains 491 typical, 844 low grade cancerous, and 257 high-grade cancerous images of the remaining 129 patients. Taking a shot at microscopic images of colon tissues, examinations revealed that the utilization of these component-level texture descriptors brings about higher classification accuracies than the past textural methodologies like local binary pattern, pixel-based algorithm, Gabor filter and so on.

Atlamazoglou V et al. [33] have evaluated the capability of texture analysis for the characterization of fluorescence images from colonic tissue areas re colored with a novel and particular fluoroprobe, Rhodamine B-phenylboronic acid. Fluorescence microscopy images of 35 colonic solid mucosa images and 35 adenocarcinomas images were digitally caught and utilized for analysis. Every procured image was converted to a grey scale format of 576 x 432 pixels and 256 grey levels and afterward subjected to textural analysis. Textural features got from the grey level co-occurrence matrix. The grey level co-occurrence part of the texture is concerned with the spatial distribution and dependence among the grey levels in a neighborhood. These systems, for the most part, have three phases of feature extraction: the first phase of handling four directional grey level co-occurrence matrices (GLCMs), the second stage computes textural features from these matrices, and the third stage averages every textural feature over the four directions. To pick an appropriate subset of textural features, a modified form of the multiple discriminant analysis measures was utilized. A base Mahalanobis distance, linear discriminant classifier, and a basic evaluation "score" technique was utilized to classify picture feature. These features contained data about such image textural attributes as local homogeneity, grey tone linear dependencies and complexity of the image. They were discovered properly to correctly classify 95% of the images in the two classes, solid and adenocarcinomatous colonic mucosa.

2.2 Review of Object-Oriented (Oo) Texture Analysis-Based Techniques

These procedures exploit foundation knowledge about the size and spatial dissemination of colon tissue segments for segmentation and classification of colon biopsy pictures. These systems have been further separated into segmentation and classification procedures.

2.2.1 Review of OO texture-based on segmentation techniques

At first, OO texture analysis was planned for segmentation of colon biopsy images. In this connection, object-oriented segmentation (OOSEG) [34] is the first segmentation strategy that consists of three well-characterized stages, to be specific, object definition, texture definition, and segmentation. In object definition stage, k means is used to divide image pixels into three clusters relying on color intensities of tissue segments, for example, purple-shaded nuclei, white shaded lumen and epithelial cells, and pink-shaded stroma. In texture definition stage, two features called object size homogeneity and object spatial distribution homogeneity are calculated for every image pixel by considering six object types, subsequently bringing about 12 features for every pixel. Segmentation procedure initializes, grows, and lastly merges seeds.

Tosun A. B et al. [35] have presented a new algorithm for the unsupervised segmentation of tissue images. It depends on using the spatial data of cytological tissue components. They introduced a new region growing algorithm, in which the growing method relies on object-to-object relations, instead of pixel connectivity. It is different than the Obj SEG algorithm that grows the regions based on pixel connectivity. They conducted their experiments on 16 arbitrarily chosen colon tissue images that comprise both normal and cancerous regions. The tissues are stained with hematoxylin-and-eosin. Working with the images of colon tissues, their experiments showed that the proposed region growing algorithm leads to improved results compared to the earlier algorithm that uses same criteria but a different region growing process.

Gunduz-Demir C et al. [36] have proposed a useful colon biopsy image segmentation method. Here purple and white clusters are utilized to find nucleus and lumen objects, separately. Next, an object-graph is developed on these objects. Edges are assigned between every lumen object

and its N nearest lumens and N nearest nucleus neighbors. For every lumen object L, features having data about regions, length of edges in the middle of L and its nucleus and lumen neighbors are extricated by considering neighbors inside a round window around L. These features are further utilized by the k-means calculation to isolate lumen objects into gland and nongland classes. Objects of gland class are dealt with as initial seeds. Region growing methodology includes another object-graph that is built on nucleus objects. Beginning from the initial lumen seeds, more lumen objects are added to the graph until an edge of the nucleus graph is experienced. Edges of the nucleus diagram are utilized to stop region growing in light of the fact that glands are normally surrounded by the nucleus objects, and experiencing a nucleus object implies that organ limit is reached. At last, false organ disposal, which has been eliminated based on the cluster information of the grown regions.

In another work, Tosun A. B et al. [37] have proposed enhanced OOSEG by utilizing graphs for measuring the spatial relationship between cytological tissue segments. In the first venture of this work, circle fitting [34], and graph generation [36] are utilized. In the second step, graph edge runs are derived. Graph edge runs are in light of the thought of grey level run-length matrices. For calculation of grey level run-length matrix (GRLM), a round window is estimated at the middle of a hub, and afterward, breadth-first search is utilized to register way for every specific edge sort that exists in the window. In feature extraction stage, four features, to be specific, short-path emphasis, long path emphasis, edge type nonuniformity, and path length nonuniformity are calculated. The last two help in deciding the impact of edge type and path length dissemination on texture, and possess minimum qualities when the runs are consistently circulated over all edge types and path lengths. Segmentation absolutely depends on objects rather than pixels and includes three stages: seed determination, region growing, and region merging. A window is fixated on a current object and gathered GRLM of the circled object is computed, which is utilized as a part of feature estimation of the current object. Objects are converged to the seeds in the event that they are nearby, and Euclidean distance between their features is littler than merge limit. At last, Voronoi outline of the objects is developed to divide final region boundaries.

Simsek A. C et al. [38] have presented co-occurrence features to evaluate spatial relationship between objects in a colon biopsy image. Round objects are situated by utilizing circle fitting calculation [34]. A co-occurrence matrix is computed for every object by putting a round window on the object, and measuring the quantity of times objects of one sort co-occur with objects of another sort at a given distance. Twenty-four co-occurrence features are extracted from the co-occurrence matrix. In this work, segmentation has been acted like a graph partitioning issue. Arbitrary objects are picked in distinctive iterations to produce graphs. Segmentation is attained to by utilizing these graphs. At long last, numerous outcomes are combined to acquire last segmentation.

2.2.2 Review of OO texture-based On classification techniques

Like segmentation, OO texture examination based strategies work just as well for classification of colon biopsy pictures.

Altunbay D et al. [39] have proposed a novel texture features-based method. In this work, previously proposed strategies for circle fitting and graph generation are utilized. A few auxiliary features, for example, degree, average clustering coefficient (CC), and diameter are processed from the object graph. Seven sorts of degrees are characterized for every node. One degree sort considers all edges while staying six-degree sorts consider edges of specific colors. Midpoints of seven degrees for all the nodes constitute seven degree-based features for a single graph. CC is a measure of the integration in the area of a node. Four CCs are registered; first CC is processed by providing food all nodes inside the area, though other three are registered by considering nodes of unique colors. Diameter is the longest of the briefest paths between any pair of nodes. Seven unique diameters are computed. The first diameter is computed by considering all edges, and the other six are computed by thinking of one as specific edge type at once. These 18 features are utilized to classify given samples by utilizing linear support vector machine.

Ozdemir Eet al. [40] have introduced are a sampling-based Markovian model for classification of colon biopsy images into normal, low grade and high-grade cancer. In this work, annoyed samples (images) are created from the original picture. First order discrete Markov

model is utilized to focus the posterior probabilities of every last one of classes for a given perturbed sample. A class having most astounding posterior probability is allocated to the perturbed sample. At long last, dominant part voting is utilized to join the classes of individual perturbed samples and to focus the class of the original test sample.

Gunduz-Demir C et al. [41] have proposed a hybrid model that utilizes both auxiliary and measurable pattern recognition methods for tissue image classification. This hybrid model depends on representing a tissue image with an attributed graph of its parts, characterizing an arrangement of smaller query graphs for typical gland description, and portraying the image with the properties of its regions whose credited sub graphs are most basically like the queried graphs. With a specific end goal to distinguish the most comparative regions, the proposed hybrid model quests every query graph over the whole graph utilizing structural pattern recognition procedures and finds the attributed sub graphs whose graph alter distance to the query graph is smaller. It then uses graph alter distances together with textural features extricated from the recognized regions to model tissue disfigurements. Clearly, the distinguished regions in cancerous tissues are required to be less like the query graphs than those in ordinary tissues. Accordingly, the proposed model installs the distance and textural features in a d-dimensional vector and classifies the picture utilizing statistical pattern recognition strategies.

2.3 Review of Hyper Spectral Analysis-Based Techniques

Hyper spectral imaging analysis measures a spectrum for every pixel in an image. There are numerous sorts of spectroscopy which are being utilized to study the spectral marks of individual cells and fundamental tissue segments. In optical spectroscopy, which measures transmission through, or reflectance from, a specimen by visible or close infrared radiation at the same wavelength as the source, classification is done basically by statistical measures. Hyper spectral analysis procedures work with respect to choose spectral bands of colon biopsy images and distinguish ordinary and malignant tissues. Hyper spectral information of colon biopsy images is gathered by utilizing hyper spectral imaging setup that comprises of tuned light source [42].

Rajpoot K et al. [43] have achieved a classification of colon biopsy images utilizing different parts of SVM. Hyper spectral image cubes having size 1024×1024×20 of colon tissues are gained from hematoxylin and eosin re colored microarray. This work consists of four stages. The first stage is preprocessing, a Flex ICA (Independent Component Analysis) variant of ICA, which was utilized to achieve dimensionality reduction. The second one is segmentation, an unsupervised nearest-centroid (k-means) clustering algorithm is used, which resulted in a 1024×1024 labeled image for each hyper spectral image cube. The third one is feature extraction, the segmented image used to extract discriminant features which were consequently utilized during the SVM classifier training stage. Multi scale morphological features (area, eccentricity, equivalent diameter, and so on) were collected to extract the structural characteristics corresponding to each distinct 16×16 size patch of the segmented image. Finally, in classification stage, Gaussian, linear, and polynomial kernels of SVM have been utilized as classifiers. Results uncover clear predominance of the Gaussian kernel with a precision of 87.5 percent.

Masood K et al. [44] have actualized GLCM and morphological features for colon tissue classification. In segmentation, the dimensionality of 3D cubes of image data is diminished by utilizing FlexICA. At that point, the data image is partitioned into four clusters of nuclei, cytoplasm, glands, and stroma by utilizing k-means algorithm. In this work, two sorts of analyses are directed. In the first, morphological features of shape, size, orientation, and other qualities are extracted from 4096 patches of four clusters. Principal Component Analysis (PCA) and Linear Discriminant Analysis (LDA) are utilized to portray images on the premise of morphological features and an accuracy of 84% is accomplished. In second, focused on 64×64 image square of every specimen. Energy, contrast, and homogeneity are obtained from GLCM of the block of exploiting every conceivable option of distance and angle. Leave one out (LOO) methodology coupled with polynomial SVM is utilized for classification. The accuracy obtained is 90%.

In another work, Masood K et al. [45] have proposed a colon biopsy classification algorithm in view of the spatial analysis of hyper spectral image data taken from colon biopsy samples. At first, a solitary spectral band is chosen from all

accessible spectral bands. At that point, spatial analysis is performed on the spectral band. The pattern in the biopsy samples is indicated by a feature vector utilizing circular local binary pattern (CLBP) algorithm. The feature selection algorithm is taking into account three measures identified with the nature of clustering. Initially, classification scatters index which gives a measure of compactness of clusters framed by a set of features. Second, Rand index which gives a measure of comparability between two unique clusters. Third, silhouette index gives a measure of every point in the clustering. The classification is accomplished by subspace projection techniques, such as PCA and LDA and additionally SVM. Classification results showed an accuracy of 90% showed that analysis in light of CLBP features had the capacity to recognize the benign and harmful patterns.

Chaddad A et al. [46] have classified multispectral images of healthy and cancerous cells in order to quicken the operations of classification between different sorts of cancerous cells. In the first stage of the work, colon biopsy image is segmented by utilizing a modified version of snake algorithm. In the second stage, Haralick features of entropy, correlation, energy, homogeneity, and contrast are extracted from segmented part of the image. At last, images are classified into ordinary and malignant classes in light of extracted features. The experimental results obtained on a few multispectral images demonstrated that the strategy was efficient for the classification of cancer cells of type Carcinoma (Ca), Intraepithelial Neoplasia (IN) and Benign Hyperplasia (BH).

Akbari H et al. [47] have proposed a method of colon cancer detection. They utilized a broad band light source to illuminate the tissue slide and a hyper spectral camera to capture wavelength bands from 450 to 950 nm. The system has been trained to classify each histologic slide based on predetermined pathology with light having a wavelength within a predetermined range of wavelengths. This technology is able to capture both the spatial and spectral data of tissue. Twelve histo-pathological slides (three slides each for normal and malignant tissues of lung and lymph node) are used in their study. SVM is used to classify the given tissues. A total of 98.3 percent specificity and 96.2 percent sensitivity was observed for colon cancer data set.

2.4 Review of Gene Expression-Based Techniques

Gene expression-based colon cancer detection is a dynamic research area. There are typically three sorts of modifications a gene could experience they are suppression, over expression, and gene mutation. Such modifications have been exploited for detection of colon cancer, and critical research studies have been committed to this field. Genes are normally analyzed by utilizing distinctive variations of microarrays, as, Oligonucleotide and DNA microarrays.

Kulkarni A et al. [48] have dealt with the prediction of colon cancer detection in view of gene expression data. In this work, they proposed an evolutionary algorithms-based technique for programmed detection of colon cancer. They utilized benchmark colon cancer dataset having expression pattern of 40 tumors and 22 ordinary colon tissue samples investigated with Affymetrix Oligonucleotide array to analyze two distinct classifiers. Here, t-statistic and mutual data are utilized for selection of discriminative genes among a given pool of genes. Genetic programming and decision trees are utilized as classifiers, and data is separated into typical and malignant samples in light of main 10 and main 20 chose genes. Result revealed that mutual data based feature selection together with genetic programming is the best solution contrasted with different blends.

Lee K et al. [49] have proposed a colon cancer detection system for the two binary bioinformatics datasets, leukemia, and colon tumor. It has been seen that the microarray gene expression samples are dealt with as time arrangement to frame the input patterns for the classification with the FIR-ELM. In this study, recently proposed a neural system based finite impulse response extreme learning machine (FIR-ELM) is utilized to assess the suitability of different FIR filter plans. The FIR-ELM algorithm performs classification taking into account single hidden layer feed forward neural system (SLFN). In SLFN, well-understood filtering techniques, as, finite length low-pass filtering, high-pass filtering, and band-pass filtering are utilized to train the input weights in the hidden layer of SLFN to extract features from the data set. These features are then used to classify the given colon samples.

Tong M et al. [50] have proposed an ensemble of SVM classifiers-based strategy for colon cancer detection. The top-scoring pair (TSP) measure is utilized as a filter feature selection system. Every chosen gene pair is dealt with as new 2-D space in this calculation. The data are projected onto diverse 2-D spaces as distinctive features of it. An advanced base SVM classifier is further built on every projected data. In this work, 50 gene expressions are chosen utilizing top scoring pair strategy, and linear SVM classifiers are trained on those pairs. GA is utilized to choose such an optimal combination of SVM base classifiers, which yields greatest conceivable execution. They explored the viability of their procedure on a few paired class and multiclass gene expression data sets including one on colon tumor. They reported classification accuracy of 90.30 percent with colon data set.

Bianchini M et al. [51] have studied the genetic mechanism of oncogenesis for human colorectal cancer and to recognize new potential tumor markers of utilization in clinical practice. They utilized cDNA microarrays to compare gene expression profiles of colorectal biopsies from 25 colorectal cancer patients and 13 typical mucosae from neighboring non-cancerous tissues. Discoveries are approved by continuous PCR: in addition, western blotting and immunochemistry investigation was done. This study additionally gives new gene candidates in the pathogenesis of human colorectal cancer infection. From the outcomes they estimate that colorectal cancer cells escape resistant reconnaissance through a particular gene expression modification; besides, over-outflow of a few survival genes appears to present a more anti-apoptotic phenotype. These genes are included in pathways not previously implicated in colorectal cancer pathogenesis and they may give new focuses to treatment.

Li L et al. [52] have extended their past work by deliberately analyzing the sensitivity, reproducibility, and stability of gene selection/sample classification to the decision of parameters of the algorithm. In past work, they presented a multivariate methodology that chooses a subset of predictive genes mutually for sample classification taking into account gene expression data. In this work, they combined genetic algorithm (GA) and the k-Nearest Neighbor (KNN) strategy to recognize genes that can jointly discriminate between distinctive classes of the sample. Results demonstrated that it can catch the correlated structure in the information. Additionally, they found that by utilizing this strategy the given dataset gene selection is exceptionally repeatable in independent runs. In general, in any case, gene selection may be less robust than classification.

Rathore S et al. [53] have proposed novel gene expressions based colon classification (GECC) plan that endeavors the variations in gene expressions for classifying colon gene samples into ordinary and malignant classes. Different feature extraction procedures like chi-square, F-score, PCA and minimum redundancy and maximum relevancy have been utilized, which select most discriminative genes amongst an arrangement of genes. The gene-based samples are ordered by majority voting based ensemble of SVM. SVM-ensemble based new approach for gene-based classification of the colon, wherein the individual SVM models are developed through the learning of different SVM kernels, like, linear, polynomial, radial basis function (RBF), and sigmoid. The anticipated consequences of individual models are combined with majority voting. Thusly, the combined choice space gets to be more discriminative. The proposed system has been tested on four colons, and a few other binary class gene expression data sets and enhanced performance has been achieved compared with already reported gene-based colon cancer identification systems.

2.5 Review of Blood Serum Analysis Based Techniques

Cancer changes the chemical mixture of various ingredients in blood serum. Thus, Raman spectrum of malignant serum intensely deviates from its typical counterpart. Procedures, in light of laser-induced fluorescence and the Raman spectroscopy, exploit such contrasts in blood serum and resultant Raman spectra for detection of colon cancer.

Li X et al. [54] have examined laser-induced fluorescence and Raman spectroscopy of serum for the detection of colon cancer. Three Raman peaks were reliably seen from ordinary blood serum emission utilizing 488.0 nm and 514.5nm excitation of an Ar-ion laser. While no Raman peak or slight Raman peaks were distinguished from colon cancer's cases. They utilized a particular parameter to recognize ordinary from colon cancers. The particular parameter is taking into account the relative intensity of Raman peak which is total intensity divided by greatest

intensity. Also, the red shift of fluorescence peak and decline of fluorescence intensity are established after samples transmitted by laser. 65 colon cancer cases are researched in this paper. Through three parameters they acquired an accuracy of 83.5% compared to the clinical determination.

Lin D et al. [55] have presented Gold nano particle based surface-enhanced Raman spectroscopy (SERS) connected to investigate the blood serum from colorectal cancer patients and wealthy volunteers. Utilizing empirical diagnostic algorithm and PCA-LDA multivariate investigation, they found themselves able to separate colorectal cancer from typical with high diagnostic sensitivity and specificity. Provisional assignments of the Raman bands in the measured SERS spectra showed interesting cancer particular bio molecular changes, incorporating an increment in the relative measures of nucleic acid, a decrease in the rate of saccharide and proteins substance in the blood serum of colorectal cancer patients when contrasted with that of healthy subjects. The empirical diagnostic algorithm in light of the ratio of the SERS peak intensities attained to a diagnostic sensitivity around 60%, while the diagnostic algorithms in view of PCA-LDA yielded a diagnostic sensitivity of 97.4% for separating cancerous specimens from ordinary specimens.

Mayingera B et al. [56] have evaluated the new, bio-optical system for light-induced auto fluorescence spectroscopy for the endoscopic in-vivo diagnosis of precancerous injuries of the colorectum, 311 endogenous fluorescence spectra were acquired from typical, adenomatous and cancerous colorectal tissue in 11 patients with cancer, six patients with familial adenomatous polyposis, and six patients with various adenomatous polyps. A light source conveyed either white or violet-blue light for excitation of tissue auto fluorescence through an adaptable endoscope. Endogenous fluorescence spectra radiated by the tissue were grabbed with a fiber optic test and examined with a spectrograph. Biopsies were taken for conclusive classification of the spectra. Rectal cancer and also adenomas with extreme dysplasia indicated particular contrasts between the transmitted fluorescence spectra as compared with typical mucosa and hyperplastic polyps. Having connected a numerical calculation to the spectra, a sensitivity of 96% and a specificity of 93% were obtained for the determination of rectal cancer. The identical qualities for the determination of dysplastic adenomas were 98% and 89%, respectively.

Roeßler M et al. [57] have studied the identification of cancer-related proteins utilizing a proteomics approach by analyzing protein expression in healthy and malignant colorectal tissues. They recognized various proteins that were expressed at markedly larger amounts in malignant tissue compared with typical colonic epithelium. Furthermore, they assessed those proteins may constitute potential serologic cancer biomarkers, they created antibodies to various proteins for immunologic assays. They demonstrate the vicinity of one protein, nicotinamide N-methyl transferase (NNMT), in the serum of patients with colorectal cancer. The sensitivity of this marker for colorectal cancer was higher than the made colorectal cancer tumor marker CEAs, in view of the measurement of 109 patients with colorectal cancer and 317 healthy controls.

Zou H. Z et al. [58] have designed to detect abnormal p16 promoter methylation in the serum of patients with colorectal cancer (CRC) and to investigate the likelihood of utilizing this assay as a part of ahead of early detection or as a prognostic marker of CRC patients. Methylation-particular PCR was utilized to detect p16 methylation in DNA extracted from 52 CRCs and coordinating serum samples and control serum samples from 34 patients with adenomatous polyps and 10 solid individuals. The relationship of p16 hyper methylation in serum DNA of CRC patients with clinicopathological attributes was then examined. P16 hyper methylation was found in 20 of 52 (38%) CRCs. Among the 20 cases with abnormal methylation in the tumor tissues, comparative changes were additionally detected in the serum of 14 (70%) cases. No methylated p16 groupings were detected in the peripheral serum of the other 32 CRC cases without these adjustments in the tumor, in 34 patients with adenomatous polyps, or in 10 healthy control subjects. This test offers a potential means for the serum-based detection and checking of CRC patients.

3. PERFORMANCE ANALYSIS

This section provides a detailed comparison and performance analysis of colon cancer detection categories, and of multiple techniques within each category. In this review, we have compared different techniques based on the parameters

like accuracy, dataset and its acquisition method, cancer detection. Accuracy is the most promising parameter to measure the effectiveness of the technique. Table 1 shows the detailed comparative analysis of various colon cancer detection methods.

Table 1. Comparative analysis of different colon cancer detection technique

Author	Dataset	Equipment	Cancer detection	Accuracy
Kalkan H et al. [28]	8000 images (patches), 36 patients	-	Yes	75.15%
Ng F et al. [29]	57 patients	proprietary software	Yes	-
Xu Y et al. [30]	230 images, 138 patients	Nano Zoomer 2.0HT digital slice scanner	Yes	73.7%
Esgiar A. N et al. [31]	44 normal, 58 malignant images	Light Microscope, JVC TK-1280E camera	Yes	94.10%
Olgun G et al. [32]	3236 images, 258 patients	Nikon Cool scope Digital Microscope	No	93.03%
Atlamazoglou V et al. [33]	70 images	Color CCD camera	No	95%
Tosun A. B et al. [34]	16 images	Nikon Cool Scope Microscope	No	94.80%
Tosun A. B et al. [35]	16 images	Nikon Cool Scope Microscope	No	86.50%
Gunduz-Demir C et al. [36]	72 images, 36 patients	Nikon Cool Scope Microscope	No	90.62%
Tosun A. B et al. [37]	150 images	Nikon Cool Scope Microscope	No	99.00%
Simsek A. C et al. [38]	200 images	Nikon Cool Scope Microscope	No	94.90%
Altunbay D et al. [39]	213 images, 58 patients	Nikon Cool Scope Microscope	Yes	82.65%
Ozdemir E et al. [40]	3236 images, 258 patients	Nikon Cool Scope Microscope	Yes	90.66%
Gunduz-Demir C et al. [41]	3236 images, 258 patients	Nikon Cool Scope Microscope	Yes	92.21%
Rajpoot K et al. [43]	32 samples	Nikon Biophot Microscope, CCD camera	Yes	87.5%
Masood K et al. [44]	2 slides	CRI Nuance Microscope, CCD camera	Yes	90%
Masood K et al. [45]	32 samples	Nikon Biophot Microscope, CCD camera	Yes	90.6%
Chaddad A et al. [46]	45 images	-	Yes	-
Akbari H et al. [47]	12 slides	Macroscopic optical histopathology	Yes	97%
Kulkarni A et al. [48]	2000 genes (22 normal, 40 malignant)	Oligonucleotide microarrays	Yes	98.33%
Lee K et al. [49]	2000 genes (22 normal, 40 malignant)	Oligonucleotide microarrays	Yes	76.85%
Tong M et al.	2000 genes (22	Oligonucleotide	Yes	90.03%

[50]	normal, 40 malignant)	microarrays		
Bianchini M et al. [51]	584 genes (25 malignant, 13 normals)	cDNA microarrays	Yes	-
Li L et al. [52]	4026 genes, 47 samples	-	No	-
Rathore S et al. [53]	Kentridge (40 malignant, 22 normal samples) BioGPS (94 malignant, 37 normal samples) Notterman (18 normal, 18 malignant) E-GOOD-40966 (463 malignant samples)	Microarrays	Yes	98.78% 98.67% 97.22% 97.71%
Li X et al. [54]	65 patients	Double Monochromator equipped with PMT	Yes	83.50%
Lin D et al. [55]	38 malignant samples, 45 normal samples	confocal Raman micro-spectrometer	Yes	Sensitivity-97.4%, Specificity-100%
Mayingera B et al. [56]	23 patients	Light-induced auto fluorescence spectroscopy	Yes	Sensitivity-98%, Specificity-89%
Roeßler M et al. [57]	109 malignant, 317 normal patients	-	Yes	Sensitivity-50.5%, Specificity-95%
Zou H. Z et al. [58]	34 malignant, 10 normal patients	-	No	-

The different types of research work and their dataset, equipment and the accuracy are shown in Table 1. The most of the techniques are implemented in the Matlab platform and each technique performs evaluation was done based on the classification accuracy. Examination exposes that simple texture and Object Oriented texture analysis-based techniques are good compared with other approaches like spectral analysis, gene analysis, blood serum analysis etc. because of their simplicity of use for histopathologists, simple access to equipment, and higher results.

4. FUTURE ENHANCEMENT

By analyzing the detailed review of the various colon cancer detection method, in the most of the papers pre-processing scheme was not used. The problems associated with the image are the changes in color and light intensity. Preprocessing improves the image information that suppresses undesired distortions or enriches image features for further processing and examination task. In most of the cases, grey level co-occurrence matrix is widely for texture analysis to extract features. In order to select the optimal set of features an artificial intelligence technique like Genetic algorithm, particle swarm optimization etc. can be used. By analyzing the review in the field of classification, Support Vector Machine (SVM) classifiers are mostly used in many of the cases. A recent classifier with a higher classification accuracy can be used for further improvement of classification of colon cancer images which helps in increase the performance of cancer detection. From this review, a complete system combined with efficient preprocessing, optimal feature extraction and better classification techniques will be encouraged in future for colon cancer detection.

5. CONCLUSION

Generally, colon cancer is diagnosed utilizing microscopic tissue analysis. Although, the methodology is subjective, and may prompt inter observer variations in grading. Further, variables like tiredness, experience, and workload of pathologist likewise influence the proper determination. These vulnerabilities in the manual process bring about the need of an automated colon cancer detection technique. In this context, a few colon cancer detection techniques have been proposed. In this paper, we have separated these techniques into five noteworthy categories: texture, OO texture, spectral, serum, and gene analysis-based techniques. A bigger subset of these techniques has been outlined in this paper. Furthermore, a far extensive comparison of different colon cancer detection categories and of various techniques inside every category has also been shown in this review.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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