

Identification of Polyp from Colonoscopy Images by Deep Belief Network based Polyp Detector Integration Model

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Abstract

Cancer is a disease involving unusual cell growth likely to spread to other parts of the body. According to WHO 2020 report, colorectal malignancy is the globally accepted second leading cause of cancer related deaths. Colorectal malignancy arises when malignant cells often called polyp, grow inside the tissues of the colon or rectum of the large intestine. Colonoscopy, CT scan, Histopathological analysis are some manual approaches of malignancy detection that are time consuming and lead to diagnostic errors. Supervised CNN data model requires a large number of labeled training samples to learn parameters from images. In this study we propose an expert system that can detect the colorectal malignancy and identify the exact polyp area from complex images. In this approach an unsupervised Deep Belief Network (DBN) is applied for effective feature extraction and classification of images. The classified image output of DBN is utilized by Polyp Detector. Residual network and feature extractor components of Polyp Detector helps polyp inspector in pixel wise learning. Two stage polyp network (PLPNet) is a R-CNN architecture with two stage advantage. The first stage is the extension of R-CNN to detect the polyp lesion area through a location box also called Polyp Inspector. Second Stage performs polyp segmentation. Polyp Inspector transfers the learned semantics to the polyp segmentation stage. It helps to enhance the ability to detect polyp with improved accuracy and guide the learning process. Skip schemes enrich the feature scale. Publicly available CVC-Clinical DB and CVC Colon DB datasets are used for experiment purposes to achieve a better prediction capability for clinical practices.

Keywords: DBN, Deep Residual Network (Resnet-50), Polyp Detector, Two Stage Model, Polyp Network

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1. Introduction

High mortality rates are largely attributed to cancer as the primary cause. According to the National Cancer Institute (NCI), when abnormal cells grow and multiply by the cell division process, they form tumors that may be benign or malignant [1]. Benign tumors are large in size but not dangerous which can be often removed. Malignant tumors are small in size and grow uncontrollably and irregularly to different parts of the body by a process called metastasis [2]. According to WHO 2020 report, colorectal malignancy is the globally accepted second leading cause of death which is recorded to be about 916000 in numbers. According to GLOBOCAN, from 19.3 million cancer cases, 10% of cases are related to colon and rectal [3]. In this regard, development of an expert system that can identify colorectal malignancy at its early stage in order to reduce the mortality rate is highly desirable. Colorectal cancer begins as a growth of polyp inside the colon (large bowel of large intestine) or rectum (opening of the large intestine near anus) that gradually damages the whole digestive system. Change in bowel habits, constipation, frequent gas pain, blood in stool and bloating are some common symptoms of colorectal cancer. Sigmoidoscopy, colonoscopy, Biopsy, Digital rectal exam, DNA stool test and Fecal Occult Blood Test (FOBT) are some common steps taken to examine colorectal malignancy. Colonoscopy is one of the most popular ways to identify polyps in a rectum or colon. Like a sigmoidoscope it is also an instrument containing lens and light to view polyps [4-6]. It can be used as a polyp removal tool from tissue samples. However, it is very difficult to identify CRC at the early stage which begins as an adenomatous polyp only through colonoscopy. Identification of exact polyp areas from complex images is a challenging task.

Automatic detection of polyp from colonoscopy images is a challenging task because in stage 0, abnormal cells are available in the innermost layer (Mucosa) of the colon wall, popularly known as Carcinoma in Situ. In stage 1, malignancy has formed in the mucosa and affects sub mucosa (colon wall's muscle layer) and it is very difficult to discriminate intraclass variations of polyps. Stage II is divided into three parts: Stage- IIA spreads through the colon muscle layer to the outermost colon wall (Serosa). Stage-IIB spreads through the serosa to the Visceral Peritoneum tissue that helps for lining the organs in the abdomen. Stage-IIC spreads to nearby organs by serosa. Low contrast colonial images of obscure boundaries is another difficult challenge. Stage-III is further divided into three parts: stage-IIIA spreads through the mucosa to the muscle layer. Often it spreads to four to six nearby lymph nodes. Stage-IIIB spreads through submucosa to the outermost colon layer. It can be spread to more than seven lymph nodes. Stage-IIIC spreads by serosa to the tissues that help to line the organs of the abdomen. In this stage generation of intestinal bubbles and fecal particles enhance the difficulty level. Stage IV is of three types. Stage-IVA spreads to a remote organ of the colon. Stage-IVB spreads to multiple remote organs. Stage-IVC spreads to the tissues that line the wall of the abdomen and other areas of the organ. To identify CRC from remote organs is another difficult challenge.

Polyps play a significant role in early

diagnosis of malignancy. It is a visual detection of diseases by analyzing a huge amount of image data, processing and interpreting them to understand the structural changes of the lesion sites of patients. Machine learning [7-10] is a widely used technique for processing medical images for malignancy detection, segmentation, classification, diagnosis. Computer-aided detection (CAD) algorithm, Computed Tomography (CT), MRI and Ultrasound methods are used for feature extraction with various data driven approaches of deep learning algorithms. CNN is very efficient in image analysis of biomedical applications such as cell classification, gland segmentation etc. Deep Belief Network (DBN) is an unsupervised learning model used to perform image classification, feature extraction and dimension reduction tasks.

Therefore, in this study, patients with colorectal cancer are selected as the research object. We propose an integrated DBN based deep polyp detection system which extracts features from DBN for image classification and achieves accuracy from deep CNN architecture by analyzing colonoscopy images.

This paper makes the following contributions: Section 2 discusses literature survey, section 3 explains about the proposed approach, Section 4 discusses about the experimental setup, Section 5 discusses concludes.

2. Literature Survey

Figure Segmentation of image from the MRI is a significant and complex task for recognition of tumor tissues. Medical images mostly contain complex uncertain structures. By implementing segmentation their accurate clinical diagnosis can be performed. To overcome the limitations of data availability and reduce model variance in rectal cancer networks, Lee et al. (2019) proposed a novel method [24]. In order to decrease model variance in segment networks, a bias variance analysis is conducted on a designated region of interest (ROI), resulting in a reduction of the variance factor by 0.90. Additionally, data augmentation is employed to further reduce the variance factor by 0.89. Rectal cancer segmentation and rectum segmentation techniques are utilized to get an improved accuracy in the proposed model. Geometric correlation is established between rectal cancer and rectum to reduce the model variance. It can be further improved by using a large dataset [24]. Jia, Xiao, et al. (2020) focused on the recognition of polyps, from pixels of colonoscopy images, that is achieved through the development of a two-stage framework, named PLPNet, which is effective in its approach [18]. CNN architecture helps to gain accuracy from Deep residual network (ResNet) with feature extractor to get hidden semantics at all network levels. YOLO is helpful for polyp region identification in colonoscopy images. Multilevel feature learning via ResNet, Representing Multi scale feature via feature extractor Network (FENet), Polyp region proposal, pixel wise Polyp segmentation are some of the methods used here for colorectal cancer recognition. CVC-ColonDB, CVC-ClinicDB datasets are used for this research paper and CVC-300 database is used for model training. C++ and python with the GTX TITAN Xp and Caffe framework on single NVIDIA GeForce are utilized for model implementation

[18]. PLP Net get accuracy up to 81.7 in Recall criterion. However, PLP net can be improved by using stage integration techniques such as SSDs, RetinaNet and YOLO-V3 for multiclass classification with depth estimation. In their paper, Yang et al. (2020) introduced the Mask Regions Convolutional Neural Network (MRCNN) for the precise detection and segmentation of colon polyps, which utilizes a Pr.ROI pooling layer [19][26]. Datasets are collected from a Chinese Hospital and from an open challenge. The evaluation of the system demonstrated an average precision of 76% and successful segmentation of polyps with an intersection over union (IOU) of 86.87%. An identified limitation of this manuscript is the disorderly convergence rate of each function branch within the model. Dataset problems can be further improved by using an effective model [19]. To identify areas of tumor histology slides of colorectal cancer Shen, Y., & Ke, J. et al. (2021) suggested a high throughput system based on deep learning techniques [16]. The Monte Carlo (MC) adaptive sampling method is used to train a deep convolutional neural network (CNN) model for estimating patches in a whole slide image (WSI). Spatial dependencies of patches are incorporated by integrating conditional random field models. The system performance is evaluated using three datasets of colorectal cancer obtained from The Cancer Genome Atlas (TCGA). The improved classification accuracy leads to an overall time reduction of 56.7% to 71.7% on different tumor slides. A deep learning-based technique for monocular depth estimation (MDE) proposed by Sasmal et al. (2021) is utilized to identify the most informative frames in endoscopic videos for the detection of colorectal cancer [17]. Zero-shot learning method is useful to get unseen classes of endoscopic images. Transfer learning is utilized to get the depth of polyps. 3D reconstruction of polyps is done from the extracted key frames. Depth estimation by using modified loss function and regularization methods, Key frame selection by considering color space conversion, image moment, edge density, key point detection are some techniques that are utilized to get optimized results [17][27]. A deep learning-based model, introduced by KMA Adweb et al. (2021), is proposed for the screening of transformation zones in three types of cervical precancerous stages that have the potential to transform into cancer [21]. Similar structured three Residual networks (ResNet) are constructed with different activation functions. The colonoscopy cervical image dataset is used for training and testing the proposed model. The experimental results of Parametric-RELU (PRELU) and Leaky-RELU activation functions performed with approximately 100% accuracy and 90.2% accuracy respectively. It can be used for the screening of some other types of cervical cancer. Furthermore, RELU structure can be modified to improve the ResNet model. In their recent research, Kiehl et al. (2021) explore the potential of using image features extracted from histological slides and/or clinical data through a deep learning model for predicting lymph node metastasis (LNM) in colorectal cancer (CRC)[22]. The convolutional neural network is trained using tumor data from 2431 patients in histological whole slide images (WSIs) to predict lymph node metastasis (LNM).

An external test set consisting of histological whole slide images (WSIs) and data from 582 patients of the TCGA cohort was utilized. The SBAIP achieved an AUROC of 71.0% on the internal test set, while the clinical classifier obtained a score of 67.0%. When the two classifiers were combined, the AUROC improved to 74.1%. While the clinical classifier's performance remained consistent on the TCGA set, the SBAIP's performance dropped to an AUROC of 61.2%. Clinical classifiers depended strongly on the T stage. However, it can be further improved to enhance the performance of SBAIP which is dropped due to the combination of two classifiers. To overcome the limitations of deep learning methods in detecting colorectal cancer arising from dimensionality, sparsity, and feature dominance due to microbiome data, Mulenga, Mwenge, et al. (2021) suggested the use of stacking and chaining of normalization techniques [23]. By incorporating the chaining approach as an alternative to data normalization, stacking offers an interpretable method for enhancing microbiome and other tabular data accuracy. This research employs three publicly available datasets, with the first dataset consisting of 884 samples and 2031 features derived from curated samples of shotgun sequence data. The second data is based on 16S rRNA sequence data having 490 samples and 336 features. In this research the third data comprises a 16S rDNA dataset obtained from the Machine Learning Repository (MLrepo), which comprises 95 CRC and 95 non-CRC samples. To implement the proposed method and DNN architecture, the Python 3 Keras framework with Tensor Flow is utilized, along with the Graphical Processing Unit and Google Colaboratory for program execution. The proposed model's performance is enhanced using feature selection and rank transformation techniques, resulting in Area Under Curve (AUC) values ranging from 0.857 to 0.987. This combination of staking and chaining techniques with other state-of-the-art methods can be very helpful to improve this model for further investigation. The study by Wulczyn, Ellery, et al. (2021) was centered on developing a deep learning-based system for predicting the survival rates of patients with stage II and stage III colorectal cancer [25][28]. Dataset used for evaluation contains 3652 cases (27,300slides) in total. The disease-specific survival AUC of 0.70 and 0.69 is achieved using two separate validation datasets. For validation two datasets contain 1239 cases or 9430 slides and 738 cases or 7140 slides respectively. Prognostic model of neural network is used to predict the survival loss due to colorectal malignancy. Tavanapong, Wallapak, et al. (2022) proposed two varieties of Artificial Intelligence (AI) methods for clinical trials [20]. First variety talks about the analysis and feedback for improving the quality of colonoscopy and the second one detects the abnormalities. Various methods such as informative frame analysis, Bowel preparation and cleaning, analysis of navigation quality, Polyp detection and segmentation for abnormality detection are used in this proposal. Real time AI assisted colonoscopy includes some techniques of deep learning for this diagnosis. However, complications of matters due to medical data privacy are always present as a limitation. Furthermore, a perfect AI score for cleaning is not the same as circumferential inspection of the colon and endoscopies need AI based classifiers [29].

From the above observation, we conclude that a lot of research work has already been done by the researchers to detect and analyze the colorectal malignancy. However, these methods are still incapable of identifying the exact polyp area due to the complexity in the image. In this study we propose a DBN model to reduce this image complexity by image classification and feature selection. Those classified images are fed to the two-stage polyp Detector model to identify the exact area of polyp by using a location box in the first stage and polyp segmentation with masking is used to effectively recognize the polyp in the second stage.

3. Structure of the Control Circuit

According to the present scenario, the analysis of colorectal malignancy is done through more advanced techniques. Here our approach is to develop a Deep learning-based CNN architecture with Deep Belief Network integration to get optimized solutions for detecting malignant polyp. The proposed approach of DBN-Polyp Detector integration model is represented in Fig. 1. CVC-Colon DB and CVC-Clinical DB datasets are used for this experimental setup.

The Deep Belief Network improves the model capability by learning essential features from unlabelled samples and also helps in classifying those image samples. for further processing. Polyp Detector model includes CNN architecture with two stage benefits for identifying polyp area through bounding box and polyp segmentation is performed with mask prediction.

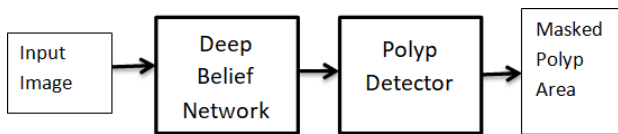


Figure 1. Deep Belief Network-Polyp Network integration mode

3.1 Deep Belief Network (DBN) Approach

A generative model, also known as DBN, is composed of multiple layers with stochastic nodes and latent variables. The hidden units, also referred to as binary values, are contained within the latent variables of the model. It comprises a stack of Boltzmann Machines with connected layers where each Restricted Boltzmann Machine (RBM) layer interacts with both previous and next layers to detect the image accurately. Multi-Layer RBN architecture helps to reduce the dimensionality of data to provide easy feature learning benefits. Figure 2 provides an illustration of the DBN architecture.

DBN performs unsupervised pertaining over the unlabelled samples for getting useful features and other important information from those samples. Then supervised fine-tuning is performed with pretrained DBN over the small number of labeled samples. Hierarchical series of RBM constructs the DBN model. First hidden layer captures the input information from the images. Subsequent hidden layers extract further detailed features from the input data.

Softmax layer is included as the last layer of DBN to classify the extracted features collected from RBM.

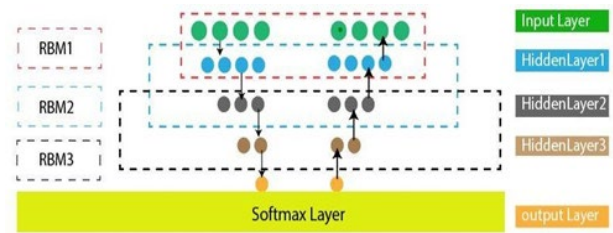


Figure 2. Deep Belief Network architecture

3.2 Polyp Detector Model

We suggest a two-step methodology, named Polyp Detector that employs a Deep CNN model to precisely detect polyps from image pixels. To improve the model performance residual networks and feature extractors are included to get hidden features to enhance the capability at all network levels of the polyp detector model. The model includes the following:

- I. Our strategy involves integrating a region-level polyp inspector into the feature extractor components of a ResNet-50 model. This strategy is very beneficial for pixel wise polyp recognition.
- II. We employ feature sharing to transfer the learned semantics of the polyp inspector. That can be utilized further to guide polyp segmentation for training purposes.
- III. The skipping techniques are used to emerge the semantic information from multi scale feature extractor levels to get the details of mask predictions.
- IV. Our proposed framework uses a publicly available dataset of CVC-Clinic DB. This approach will be applicable for clinical practices.

4. Experimental Setup

In the proposed experimental setup, the Polyp Detector architecture is shown in Fig. 3. Polyp Detector contains two parts: Polyp inspector and polyp segmentation. The two-part framework reduces the complexity of colon wall pixel wise training performance on the CNN model. Polyp inspector inspects the pixels and in the polyp segmentation it helps to guide the pixel-level learning. ResNet-50 and feature extractor components are used to extract hidden semantics from polyp images at each frame. Sharing features and skipping techniques provide transfer learning with multi scale capability between stage I and stage II. For the detection of accurate polyp area masking technique is utilized to obtain multilevel distinct features from raw data. The architecture of Polyp Detector relies on ResNet-50 as its backbone, as depicted in Figure 3. Polyp Detector contains residual four layers as {Res 2, 3, 4,5} having multiple residual blocks.

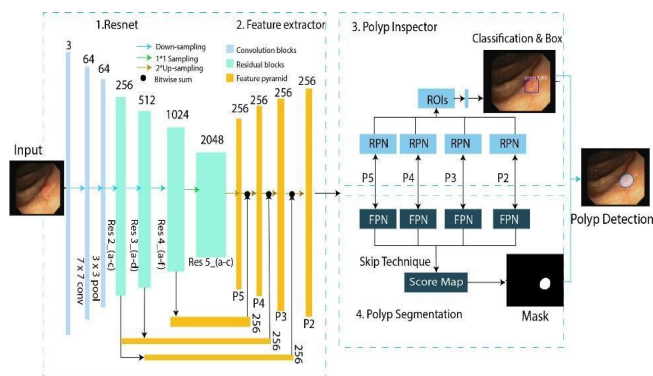


Figure 3. Deep Belief Network architecture

Convolution layer 7×7 is followed by a 3×3 max pooling layers used to perform downsampling for initialization of the network. The height and width of residual networks have spatial scale of the input image. The residual layer terminations in each section are linked to the feature extractor modules in Section II-B, enabling multi-scale feature extraction.

Polyp inspector includes two stages. First stage inspects the polyp area through a bounding box and in the second stage polyp segmentation is performed by extracting features by the help of region polyp network (RPN) and fully connected network (FCN). Region polyp network (RPN) and region of interest (ROI) are parallelly perform bounding box regression and image classification. Each RPN block is attached with a pyramid component represented by P1, P2, P3, P4 which is useful for multiscale feature mapping. Each RPN block is associated with a single scale feature map (Res-4). ROI is a max pooling layer that helps in down sampling the arbitrary sized features of polyp regions mapped into a fixed small spatial size (7×7) by default. RPN batch size is taken as 256 and ROI output size is taken as 128 [10]. All the pyramid components are concatenated and fed to a fully connected network (FCN) layer to perform feature extraction tasks. FCN layer increases the spatial dimension by up sampling to reduce the resolution gap between feature map and prediction output. The output of FCN layer is further used in polyp segmentation where skipping scheme is utilized for mask prediction in detail.

Fig. 4 illustrates the graphical representation of the training dataset representing the relative polyp size, that calculates the size ratio between the bounding box around the polyp area and the original image size. Here the height ratio ranges between 0.068 to 0.82 and width ratio ranges between 0.063 to 0.069. It indicates the large variation in the polyp size. Therefore, size representation is challenging.

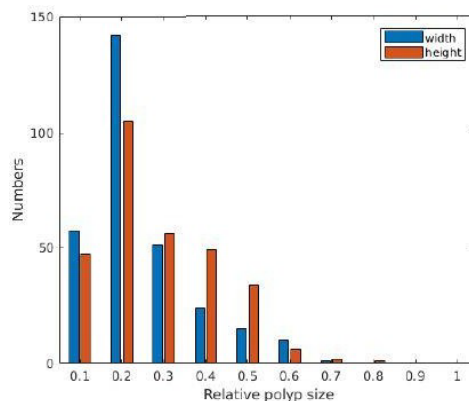


Figure 3. Training data set and Relative Polyp size

- It works well to identify the exact polyp lesion area from complex colonoscopy image samples.
- During experiment it is realized that ResNet-50 is more convenient as compare to VGG-16
- DBN architecture is helpful to capture essential features and classify unlabeled samples.

5. Conclusion

We propose an efficient DBN-Polyp Detector integration model for polyp detection from colon images. The CNN model achieves accuracy by residual learning and feature extractor. Furthermore, Polyp proposal stage guides the pixel accurate training to get lesion regions and polyp segmentation stage helps the model to predict the masked classification and box areas with the polyp identification. Our proposed model is applicable for clinical practices.

In recent days, there have been significant advancements in cancer in various areas of the human body. The CNN architecture nowadays has been implemented in most areas of science for complex analytical predictions. the field of medical science for diagnosing and treating

This paper depicts an approach to detect and identify the polyp. DBN-PLPNet can be further integrated with YOLO-V3 to enhance its capability. In the near future, many hybridized CNN models can be implemented in image guided surgeries. It can be extended for grade detection. Polyp endoscopic experiments can utilize it for accurate results. It will be a technique which will help the doctors to identify the affected areas of malignant colon and rectum more effectively with remarkable accuracy.

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