

Title:

**Automatic Colorectal Segmentation with Convolutional Neural Network**

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Introduction:

In the recent years, modern medicine uses image processing technique, such as image segmentation in Computer Aided Diagnosis System (CAD) in order to reduce the dependence of diagnosis by doctors' knowledge and experience, as well as to locate the prior tissue lesions timely and effectively [6]. Medical image segmentation uses several imaging modalities (MRI, Computed Tomography (CT), Positron Emission Tomography (PET), X-RAY, Ultrasound). However, it is a challenge yet, due to added noise, artifacts, limitations, and unclear edges [8]. In this way, colon tissues segmentation in human abdominal CT images is the base of analysis and identification of cancer nidus, providing powerful information in a CAD, such as early polyps detection, which can reduce the incidence of colon cancer [3],[6],[14]. Colon segmentation techniques can also be used in colorectal tissues simulations to make preoperative plans and simulations of surgery [4].

Some colon segmentation algorithms are introduced in literature, each one having its own model, computational complexity, and overall quality. Such as Local region based active contours [6], which is based on local statistics of tissue of interest and background, instead of global statistics. In [15], an isotropic volume reconstructed from the CT images is used to extract a thick region encompassing the entire colon, where mean curvature, dimensionless ratio sphericity and minimum polyp size are used as parameters to filter anomalies and reduce false positives. Classifications of multispectral colorectal cancer tissues [5], classify tissues samples using convolutional neural network (CNN) and uses active contours technique to extract colorectal regions corresponding to pathological tissues.

Although some works presented in literature have demonstrated how CNN provides effective results to analyze colon images, those works are based on the segmentation image regions containing pathological colorectal tissues [5],[7], and glandular colon structure [10]. On the contrary, the analysis of colon tissues as pre-processing task for applications, as tissues simulations, is our motivation to challenge the use of pixel-wise segmentation with CNN.

In order to overcome the problem of misclassifying colon tissue pixels, in this paper, we propose a method for automatic colon tissues segmentation based on spatial features learned with CNN. The proposed method has been compared to three state-of-the-art methods. Preliminary experimental results demonstrate the proposed method achieves a higher robustness in terms of sensitivity and similarity, and reduces the number of misclassified colon tissue pixels.

Proposed method:

Recently in state of the art, CNN models have shown efficient performance in various computer vision challenges such as object recognition, scene labeling, document analysis, large-scale object classification [1],[5]. In medical image analysis, CNNs have shown impressive results for applications as medical image pattern recognition [11], abnormal tissue detection [5-6], and tissue classification [2]. Therefore, herein

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we propose a colon tissue segmentation method based on LeNet-5 network architecture for handwritten digit classification [9], as shown in Fig. 1. The proposed method here presented is compounded by three general blocks: data preparation, feature learning, and colon detection.

- **Data preparation.** It extracts  $W_p \times H_p$  image patches from 1221 input CT colon images [13]. Where 814 images are used in the training phase for feature learning, and 407 images are used in the test phase. Data preparation uses ground truth images manually labeled by human in order to assign the corresponding label value to input image patches (1 if the center pixel belongs to the colon tissues, otherwise 0).

According to the sample size expected by CNN network [9], input CT colon images are divided into patches with a size of  $W_p = 28 = H_p$ , after obtaining the set of input image patches, LMDB dataset file is generated to be used as training source to the CNN.

- **Feature learning.** Spatial features are learnt in the network training phase, which is performed through a sequence of convolutional and pooling layers, and ends with two full-connected layers. In the first convolutional layer (conv1), each input image patch  $P(x)$  from the patch LMDB dataset is convolved with 50 learnable filters of size  $5 \times 5$ . After that, a down-sampling is performed through the pooling layer (pool1) of size  $2 \times 2$  with stride of 2, to reduce the spatial size of representation to a  $\frac{1}{4}$  of its previous size, and so reduce the amount of parameters and computation in the network (Similar settings has been used for the second convolutional and pooling layers). At the end, the full connected layers (fc3 and fc4) act as classifier and contain 500 and 2 output units, respectively. The output of fc4 is the source into a softmax function, to provide the center pixel's probability distribution over the labels.

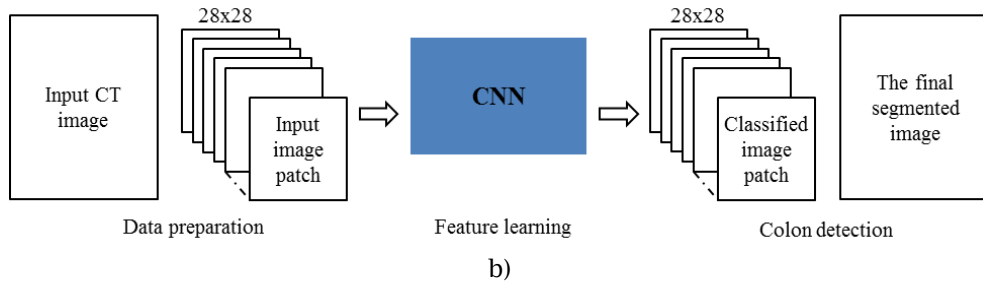
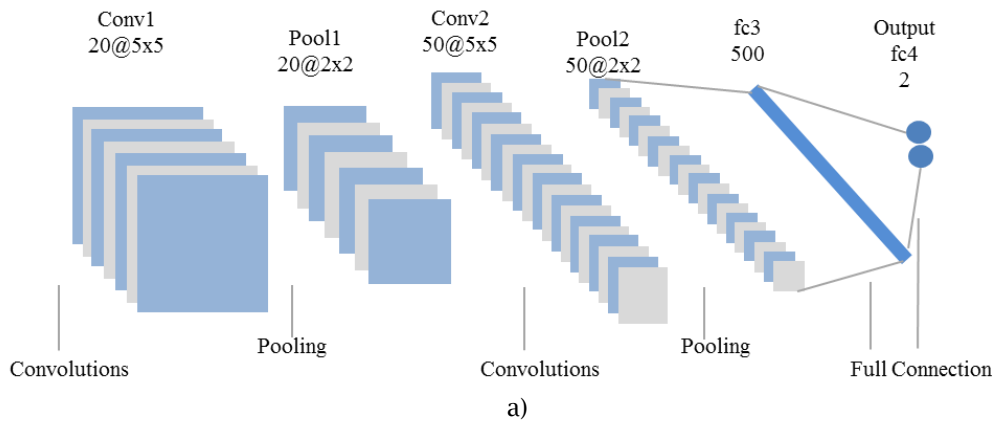


Fig. 1: Workflow of the colon segmentation method: a) CNN architecture; b) Overview of the proposed method.

Network training is performed using the deep learning framework Caffe to learn the weights by back-propagation with a cross-entropy error function. Eqn. (2.1).

$$E = -\sum_n(t_n \ln(y_n) + (1 - t_n) \ln(1 - y_n)) \quad (2.1)$$

where  $t_n = t(x)$ ,  $y_n = p(T_c|x_n)$  is the probability that the indexed sample  $x_n$  belongs to the colon tissue. The bias was initialized with a value of 0.1. The optimization strategy uses a mini-batch size of 1,000 training sample patches, and a learning rate of 0.001. The training block is performed in 10,000 iterations. Differently to the mentioned work [1], weights were initialized randomly with a Gaussian distribution, in order to preserve local structures in the original collection of data, and perform a stable introduction of the data, throughout an association between the dimension of the features produced by the network that still keep the metric information of the original data, and its complexity [12].

- Colon detection. This block uses the output of softmax function, where achieved probability ( $p(T_c|x_n)$ ) by each output patch allows to classify each center pixel as colon tissue pixel or non-colorectal pixel. After pass all patches throughout trained CNN, a composition step is performed to assemble all classified patches, and to obtaining the corresponding final segmented image.

#### Experimental results:

The proposed colorectal segmentation method has been first tested on the last 407 CT colonography images [13]. Some resulting segmented images are depicted in Fig.2.

From a qualitative analysis, it may be observed that, the proposed method leads to less misclassified pixels produced by added noise and close tissues or organs with similar texture or color, which can be erroneously classified as colon tissue.

For numerical comparison purposes, sensitivity and specificity metrics reported in [3] of the three state-of-the-art methods were also compared to the proposed method. Results summarized in Tab. 1., depict the average values of the sensitivity (Se) and specificity (Sp) using Eqn. (3.1) and Eqn. (3.2) respectively.

$$Se = \frac{TP}{FN + TP} \quad (3.1)$$

$$Sp = \frac{TN}{FP + TN} \quad (3.2)$$

where TP is the number of pixels correctly detected as colon tissue; TN is the number of pixels correctly detected as background; FP is the number of pixels wrongly detected as colon tissue; FN is the number of pixels wrongly detected as background.

Tab. 1. demonstrates that the proposed algorithm performs better on evaluated dataset in terms of sensitivity and specificity. The high rates of true positive shows that, as expected, a patch size of 28 x28 provides sufficient tissue information to classify the center pixel as colon tissue or background pixel.

<i>Algorithm</i>	<i>Se</i>	<i>Sp</i>
[1]	94.1%	94.3%
[9]	96.02%	96.08%
[11]	96.75%	97%
Proposed method	96.9%	98.7%

Tab. 1: Average sensitivity and values.

#### Conclusions:

Based on literature review, CNNs have shown impressive results in image analysis for medical applications. However, CNNs for colon tissues segmentation is still a challenge. The proposed method deals with pixel-wise segmentation, which learns features on image patches to directly classify a pixel as colon tissue pixel or no colon tissue pixel. The CNN is trained by the deep learning framework CAFFE. As its main advantage, the proposed solution reduces the misclassified colon tissue pixels in comparison with three state-of-the-art methods. In particular we found an increase in terms of Sensitivity and Specificity (from 1% to 4% in respect to other methods).

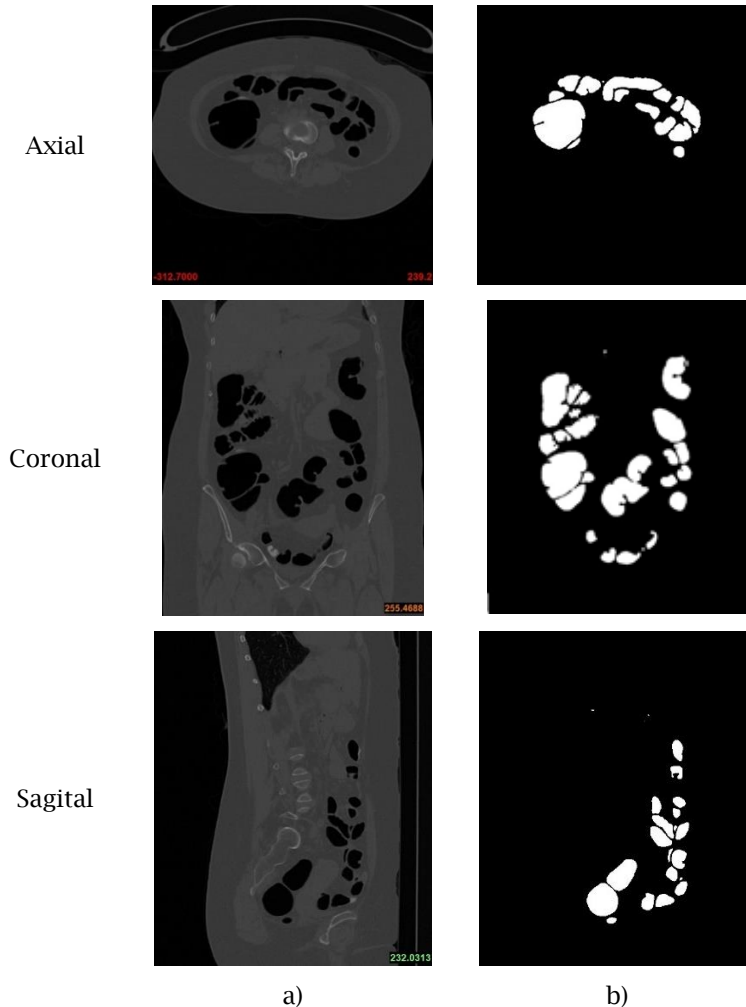


Fig. 2: Some qualitative results. a) CT abdominal image. b) Segmented Image.

A disadvantage of using feature learning based on image patches centered on each pixel is that depending on the image size, patch size, number of filters, and kernel size, while those are bigger, in the same time greatly preparing data and training time are required.

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