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Computer-Aided Design AND APPLICATIONS

Automatic Colorectal Segmentation with Convolutional Neural Network

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ABSTRACT

This paper presents a new method for colon tissues segmentation on Computed Tomography images which takes advantages of using deep and hierarchical learning about colon features through Convolutional Neural Networks (CNN). The proposed method works robustly reducing misclassified colon tissues pixels that are introduced by the presence of noise, artifacts, unclear edges, and other organs or different areas characterized by the same intensity value as the colon. Patch analysis is exploited for allowing the classification of each center pixel as colon tissue or background pixel. Experimental results demonstrate the proposed method achieves a higher effectiveness in terms of sensitivity and specificity with respect to three state-of the art methods.

Keywords: Colon Segmentation, Convolutional Neural Network, Tissues Segmentation.
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1 INTRODUCTION

Segmentation techniques are relevant in many fields of applications from artificial vision systems to medical applications and mechanical engineering. In particular in this field it is successfully applied in microstructure analysis of materials [5],[8],[22-23] and it also has peculiar applications related to reverse engineering of components where it is applied for mechanical feature recognition and modeling or measuring [11],[15]. In particular in [2] starting from a voxel subdivision of the digitized shape, some image analysis techniques are used to classify the 3D feature from the edges of the part.

Concerning medical applications, soft tissue segmentation is a fundamental issue for the development of Computer Aided Diagnosis System (CAD) based on Computed Tomography (CT). In the recent years, soft tissues segmentation, such as colon segmentation has increased its applications in modern medicine fields, which use CAD in order to overview the 3D model of the organ and reduce the dependence of diagnosis by doctors' knowledge and experience to locate the prior tissue lesions timely and effectively [15].

In this way, the colon 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 polyp detection, which can reduce the incidence of colon cancer [11],[15],[24]. Moreover, the colon segmentation also may be introduced to make preoperative planning and simulations of general surgery [13],[21]. For reliably differentiating the colon (foreground) and the no colon (background) pixels, an accurate process is required to avoid erroneous classification. In these cases, colon pixels may be wrongly recognised instead of noise, artifacts, limitations, unclear edges [17], and other organs (such as the lung, stomach, and small intestine), or different areas with the same intensity values as the colon.

Some works related to colon segmentation have been introduced in literature, each one has its own model, computational complexity, and overall quality. Such as region-based statistics analysis [9], [15], [27-28], which builds local models of the tissue of interest, instead of a global model. Therefore, a segmented image consists of homogeneous regions characterized by some statistical properties. In [28], an isotropic volume, reconstructed from the CT images, is used to extract a thick region encompassing the entire colon, where the mean curvature, dimensionless ratio sphericity and minimum polyp size are used as parameters to filter anomalies and reduce false positives. Other approaches have adopted probabilistic techniques [1],[26]. Authors in [26], used probabilistic boosting tree for learning discriminative models for the appearance of patterns/objects of interest. Probabilistic Markov Random Field was introduced in [1], in order to handle the problem of accurately un-supervised segmentation.

On the other hand, recently, deep learning technique (particularly Convolutional Neural Network, CNN), has found applications for medical image analysis focused on medical pattern recognition [20], abnormal tissue detection [14-15], and tissues classification [10] to cover a broad range of problems related to ophthalmology, pathology, radiology and disease monitoring to personalised treatment suggestions [25]. Consequently, authors in [14] has used CNN in a set of colorectal tissues samples to classify regions corresponding to pathological tissues.

Some works presented in literature have demonstrated how CNN provides effective results to analyse colon images, those are based on the segmentation of image regions that contain pathological colorectal tissues [14],[16], and glandular colon structure [19], where particularly the segmentation process is performed on histology images [16],[19], and biopsy images [14]. Hence, the analysis of colon tissues as pre-processing task for applications, such as preoperative planning and simulations of tissues on general surgery, is our motivation to challenge the colon segmentation through the use of a deep and hierarchical learning about colon features on CT images with CNN. Differently from state-of-the arte CNN-based methods, this work is focused on CT image analysis, the network architecture ends with two full connected layers, as also as a reduced input patch size of 28 x 28 is used, to demonstrate that smaller patch size provides enough information to classify the center pixel and achieve a high effectiveness with an expected reduction of filtering operations.

In order to overcome the problem of misclassifying colon tissue pixels, in this paper, we propose a new method for automatic colon tissues segmentation based on spatial features learned with by using CNN. The proposed method is tested with a set of input image patches from CT slices. The rest of this paper is organized as follows: Section 2 describes the proposed method. Section 3 presents the experiments and the results. Finally, Section 4 deals with the concluding remarks.

2 PROPOSED METHOD

In order to predict the probability that a pixel could be part of the colon tissues or background, we propose a colon tissues segmentation method based on binary classification by using LeNet-5

network for handwritten digit classification [18] with the aim of learning colon features in a deep and hierarchical way. CNN is trained with patches dataset built from CT images with hundreds of slices to identify colon tissues for each centered pixel location. Only in the training patches dataset, each patch provides labeled information to show whether a centered pixel value is part of the colon tissues pixels or background. Each training patch passes through a sequence of convolution layers, layers of ReLU (rectified linear unit) activation functions (It is used throughout each layer), pooling layers, and full connected layers to output the binary classification label. During this phase, lower level features (such as lines, edges, curves) are learned in the first hidden layers, which are compounded in higher level ones in the subsequent hidden layers. The workflow of the proposed method is schematized in Fig.1. In the following sub-sections, the main steps are described.

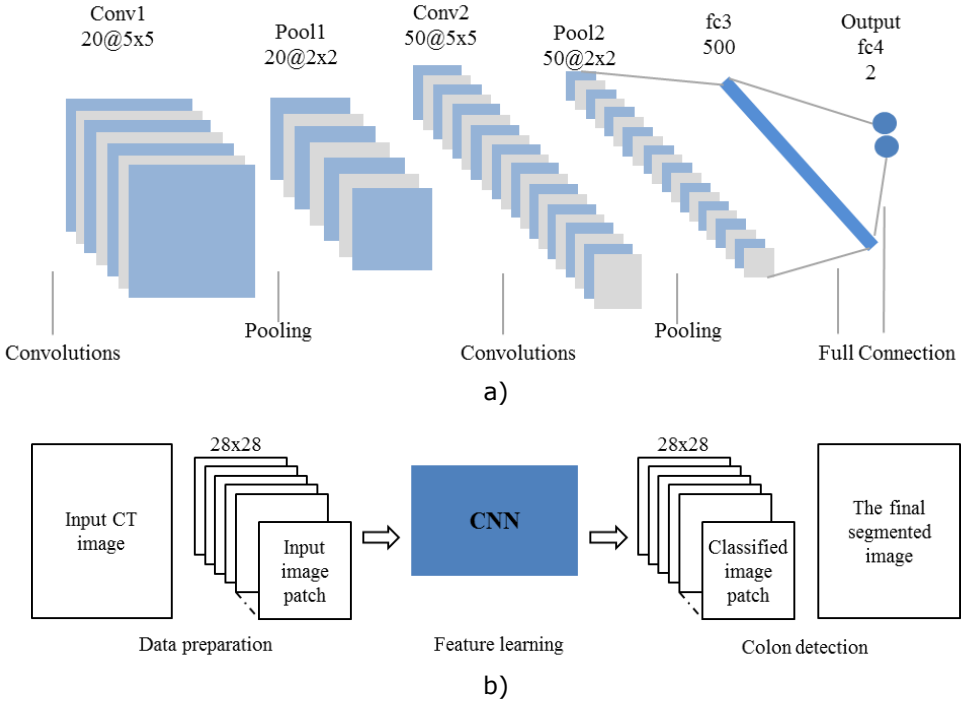

Figure 1: Workflow of the colon segmentation method: a) CNN architecture; b) Overview of the proposed method.

2.1 CNN architecture

CNN architecture depicted in Fig.1.a) is particularly structured as a sequence of stages composed of repeating types of convolutional layers and pooling layers; followed by a series of fully connected layers, and ending with classifier layers in order to perform operations on the input patches for feature learning and classification purposes.

2.1.1 Convolutional layers

They convolve the input data with an established number of (k) linear convolution filters with a defined size. This layer slides the filters over the input, computing dot product between the input data and the entries of the filters to detect and learn local conjunctions of features from the previous layer. Eqn. (2.1).

$$(f_k)_{ij} = (W_k * x)_{ij} + b_k \tag{2.1}$$

where *k=1,…, K* is the index of the *k-th* feature map, (i,j) is the index of neuron in the *k-th* feature map, and x is the input data. W_k and b_k are trainable parameter weights and biases from the visible units to the hidden units. $(f_k)_{ij}$ is the learning *k-th* feature map.

2.1.2 Pooling layers

They are non-linear down-sampling layers for progressively reduce the spatial size after obtaining features using convolutional layers, to reduce the amount of parameters and computation in the network. Its purposes is to merge semantically similar features into one.

Pooling layers establish the size of the regions $s_p = m \times n$ to pool the convolved features over, then, divide convolved features into disjoint $m \times n$ regions, and take the mean or maximum feature activation over disjoint regions to obtain pooled convolved features, which can then be used for classification.

Summary statistics based on mean "mean pooling" or max "max pooling" value of a particular feature over a region of the input data are likely computed to obtain much lower dimension respect to using all of the extracted features, which can also control overfitting (the production of an analysis that corresponds too closely or exactly to a particular set of data).

2.1.3 Fully-connected layers

They are a linear combination where each node is connected to all nodes of the previous layer. Eqn. (2.2).

$$y_k = \sum_l^{sl} W_{kl}\, x_l + b_k \tag{2.2}$$

where y_k is the *k-th* output neuron and W_{kl} is the *kl-th* weight between x_l and y_k.

2.1.4 Activation functions

They often follow a pooling layer or fully-connected layer and apply a non-linear activation operation to encode complex patterns of the input, through a transformations of the weights sum of inputs that goes into the artificial neurons. There are some activation functions such as sigmoid, hyperbolic tangent, and rectified linear unit (ReLU). However, ReLU activation function is used in practice for deep neural networks, which is different from others functions due to it is not continuously differentiable and does not vanish for high activations. ReLU is given by Eqn. (2.3).

$$f(z) = \max(0, x) \tag{2.3}$$

2.1.5 Output layer

It is the last layer in the network and holds the name of the loss function used for training the network for multiclass classification, the size of the output (number of output units), and the class labels.

2.1.5.1 Classifier layer

It computes a class label probability of the input data. Softmax classification layer is the most extensively used in CNNs. Its purpose is to transform all the net activations in the final output layer to a series of values which can be interpreted as probability vector values between 0 and 1 (which has to be positive, smaller than 1, and sum up to 1). Softmax classification layer applies a categorical probability distribution based on exponential function as denotes Eqn. (2.4). for the k-th class and an input X.

$$P(y = j|X; W, b) = e^{X^T W_j} / \sum_{k=1}^{K} e^{X^T W_j} \tag{2.4}$$

2.1.5.2 Loss layer

It computes the difference between true class labels and its corresponding predicted class labels to determine the goal of learning by matching parameter settings as current network weights to a scalar value establishing the "badness" of the settings. Thus, the learning purpose is to find a weights setting that minimizes the loss (called also error, cost, or objective) function. The most widely loss layer for CNNs is the cross-entropy loss given by Eqn. (2.5).

$$E = -\sum_n (t_n \ln(y_n) + (1 - t_n) \ln(1 - y_n)) \tag{2.5}$$

where $t_n = t(x)$ and $y_n = p(T_c|x_n)$ is the probability that the indexed sample $\mathrm{x_n}$ belongs to a given class.

2.2 Data Preparation

Prior to colon tissues segmentation, 75% of the gray scale slices of CT colon images [7] (each CT image has approximately 1600 slices) are preprocessing to generate a patches dataset that learns the CNN.

Based on the sample size expected by the network [18], the size of each training patch is 28 x 28 centered on each pixel for the colon pixel identification. Dataset generation 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).

Deep learning framework CAFFE allows to process data that comes from in normal image format (.jpg, .png, and so on) and LMDB format. Thus, after obtaining the set of patches, LMDB dataset file is generated to be used as input to the CNN, taking into account that LMDB is a compressed format for working with large dataset.

2.3 Feature Learning

The feature learning is performed in the CNN training, which is done through the entire model from input data to loss layer without disjoin the feature extraction and the classification step. CNN receives raw input data in LMDB format to produce classification output.

CNN training allows learn the hidden patterns from the input data by using a training dataset. It starts with the first convolutional layer (conv1), where each input image patch $P(x)$ from the patch LMDB dataset is convolved with 50 learnable filters of size 5 x 5. After that, a down-sampling is performed through the pooling layer (pool1) of size 2x2 with stride of 2, to reduce the spatial size of representation to a ¼ of its previous size, and so reduce the amount of parameters and computation in the network (Similar settings have 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.

Differently to original LeNet5 [18] that uses a layer with sigmoid activation function after each full connected layer, all layers in the proposed method are followed by one layer of ReLU activation function to cause sparsity in the features.

The output from the convolutional and pooling layers represent high-level features of the input image patches (feature extractors). While, the purpose of the full connected layers is to use these features for classifying the input image into various classes/labels based on the training dataset. Therefore, fc3 and fc4 layers encode the details of patterns of the input patches. The sum of output probabilities of fc4 is 1. This is ensured by using the softmax as the activation function that takes the output of fc4 as source, to provide the center pixel's probability distribution over the labels. The softmax function takes a vector of arbitrary real-valued scores and forces it into a vector of values between zero and one that sum to one.

In the training stage, the deep learning framework CAFFE was used to learn the weights of convolutional and full connected layers, which are learned by back-propagation with a cross-entropy loss function. Eqn. (2.5)., where particularly for the proposed method $y_n = p(T_c|x_n)$ is the probability that the indexed sample $\mathrm{x_n}$ belongs to the colon tissue. The loss function E measures how far the predicted output of the CNN from the correct output is, while back-propagation process propagates

the loss function gradient to previous layers. The gradient descent is carried out based on loss function gradient $\triangle E/\triangle w_{i,j}$ to adapt the weights in order to decrease the loss function output by changing into the direction contrary to the direction of increasing gradient with a learning rate of 0.001.

CNN used a patch training set of 282 x 10^6 colon image patches, where patches were sampled at random from the available samples of training. The bias was initialized with a value of 0.1. The optimization strategy uses a mini-batch size of 1,000 training sample patches. The training stage was performed in 45 x 10^3 iterations, where we can see a training error of 0.041 and a test error of 0.0485 (based on loss function). Differently to the mentioned work [4], 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],[28].

2.4 Colon Detection

This stage uses the trained CNN, where achieved probability ($p(T_c|x_n)$) by each output patch allows to classify each center pixel as colon tissue pixel or nor colorectal pixel. At the end, it composes all patches in order to obtain each corresponding final segmented image.

3 EXPERIMENTAL RESULTS

As a preliminary result, the proposed colorectal segmentation method has been qualitatively validated on the last 407 slides of CT colonography images [7] (Similarly to training stage, input slide images were divided into input patches of size 28 x 28). Some resulting segmented images obtained in colon detection stage are depicted in Fig.2. Respect to ground truth images, it can be observed that the proposed method identifies a sufficient number of pixels of the colon tissues leading to less misclassified pixels produced by close tissues or organs with similar texture or color, which can be erroneously classified as colon tissue.

For purposes of numerical comparisons, the accuracy metrics reported in [11], about approaches introduced in [1],[9],[11], were also compared to the proposed method. Results summarized in Tab. 1., depict the average values of the sensitivity (Se), specificity (Sp), and accuracy (Ac) using Eqn. (3.1), Eqn. (3.2), and Eqn. (3.3), respectively.

$$Se = \frac{TP}{FN + TP} \tag{3.1}$$

$$Sp = \frac{TN}{FP + TN} \tag{3.2}$$

$$Ac = \frac{TP + TN}{FP+FN+TP+TN} \tag{3.3}$$

Axial

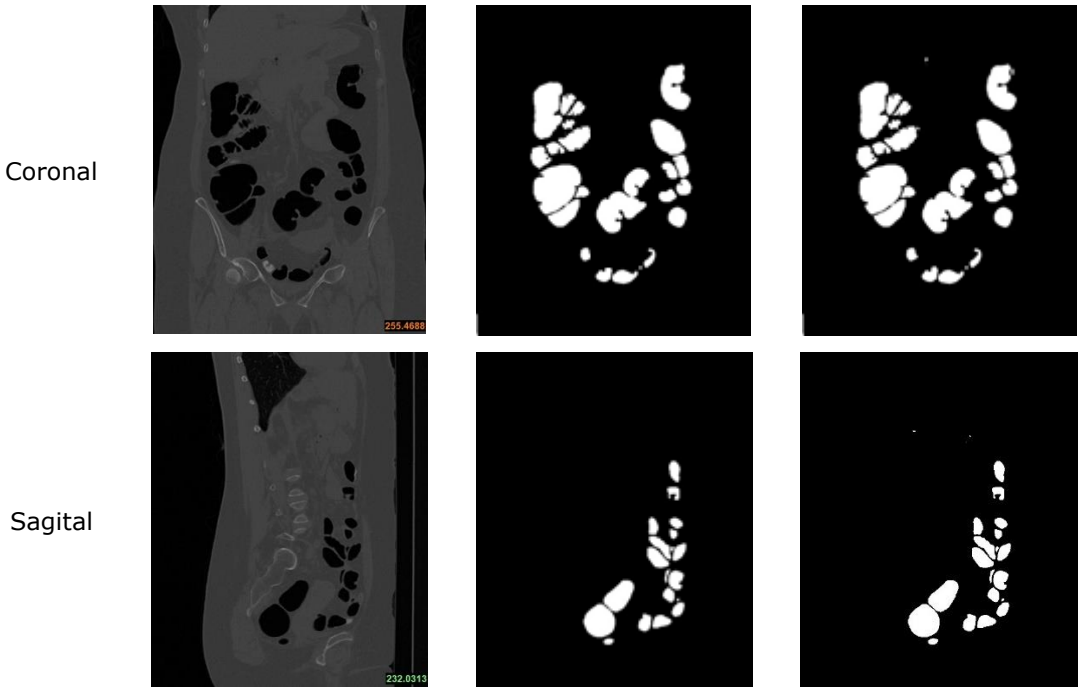

Figure 2: Some qualitative results: a) CT abdominal image; b) Ground truths; c) Segmented Image.

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 method performs better on evaluated datasets in terms of sensitivity and specificity with respect to compared methods, maintaining a very close accuracy value to the highest one. Averaging all Se, Sp, and Ac measures, it can be seen that the proposed method reaches the highest overall score. As also shown the closets average score (Avg) is represented by existing method [11] based on neural network trained with Bayesian regulation algorithm. The high rates of true positive show, as expected, a patch size of 28 x 28 provides sufficient tissue information to classify the center pixel as colon tissue or background pixel. The relationship between sensitivity and specificity depicted in Fig.3., shows that presented approach provides better ability to identify correctly colon tissues pixels and background pixels.

Method	*Se*	*Sp*	*Ac*	*Avg*
[1]	94.1%	94.3%	90.8%	93.07%
[9]	96.02%	96.08%	97.6%	96.57%
[11]	96.75%	97%	**98%**	97.25%
Proposed method	**96.9%**	**98.7%**	97.9%	**97.83%**

Table 1: Average sensitivity, specificity, and accurate values.

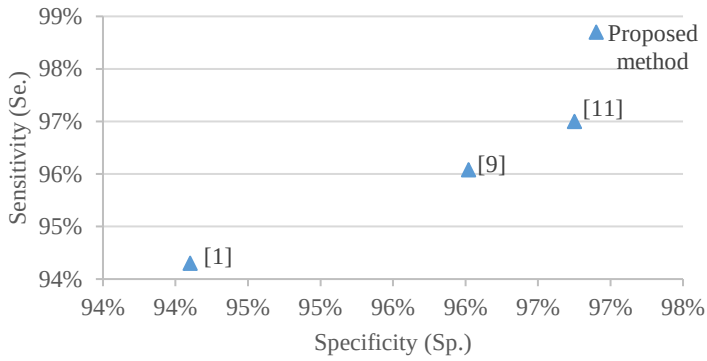

Figure 3: Plot of sensitivity vs. specificity.

4 CONCLUSIONS

In this work, a new approach has been proposed for colon tissues segmentation. The proposed method deals with pixel classification on CT images through the use of a deep and hierarchical learning about colon features with CNN, which learns features on image patches to directly classify a pixel as colon tissue pixel or no colon tissue pixel. Convolution layers in CNN are specialised image feature detectors that have shown impressive results in image analysis for medical applications. However, it is still a challenge for colon tissues segmentation. 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), maintaining the same level of Accuracy.

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, a greater time for preparing data and network training will be required. That could be improved with the use of transfer learning (reuse already trained Neural Networks) to decrease the training time with great scale.

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