A New Electronic Colon Cleansing Method for Virtual Colonoscopy

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ABSTRACT

Virtual colonoscopy has been developed as a non-invasive, safe, and low-cost method to evaluate colon polyps. Implementation and efficiency of virtual colonoscopy requires rigorous cleansing of colon prior to the examination. Electronic colon cleansing is a new technology that virtually clean stool residues tagged with contrast agents from the obtained computed tomography (CT) images. From our previous studies on electronic colon cleansing, we found that residual stool and fluid are often problematic for optimal viewing of colon. In this paper, we focus on developing a model-based approach to correct both non-uniformity and partial volume effects appearing in regions of bone and tagged stool residues. A statistical method for maximum a posterior probability (MAP) was developed to identify and virtually clean the tagged stool residuals. In calculating the solution, the well-known expectation maximization (EM) algorithm is employed. Experimental results of electronic colon cleansing are promising.

Keywords: virtual colonoscopy, electronic colon cleansing, non-uniformity, expectation maximization.

1. INTRODUCTION

Colorectal cancer has a high prevalence in the United States. The overall risk of developing the disease is approximately 5% over a lifetime [1]. It is the second leading cause of death from cancer in the United States. Early detection and removal of polyps is the key to prevent colon cancer. Most colon cancer arises from polyps, which may take 5 to 15 years for malignant transformation [2]. The American Cancer Society has recommended a colon exam every 3 to 5 years for people with age over 50. Fiber optical colonoscopy is the most commonly used diagnostic procedure. However, patients are usually reluctant to take the optical colonoscopy procedure because it is expensive, invasive, time consuming, and carries a small risk of perforation and death.

Virtual colonoscopy has been developed as a non-invasive, safe, and low-cost method to evaluate colon polyps [3-5]. It is a new procedure in which computed tomographic (CT) images of the patient's abdomen are taken and a computer visualization system is used to virtually navigate within a reconstructed three-dimensional (3D) model of the colon, looking for polyps. An accurate diagnosis by virtual colonoscopy requires a clean view of the colon lumen during the virtual fly-through. One way to achieve a clean colon lumen is to perform physical bowel cleansing prior to the image scan. This method, although effective, is highly uncomfortable for the patient. As a result, electronic colon cleansing technologies have been developed as an alternative solution by virtually removing the stool and residual materials from the scanned dataset [6-11].

From our previous studies on electronic colon cleansing, we found that residual stool and fluid are often problematic for virtual colonoscopy. In this paper, we are developing a model-based approach to correct both non-uniformity and partial volume effects appearing in the regions of stool residue and bone. A statistical method for maximum a posterior probability (MAP) was developed to identify and virtually clean the tagged stool residuals. In calculating the solution, the well-known expectation maximization (EM) algorithm is employed. Experimental results of electronic colon cleansing are promising.

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2. METHOD

Prior to obtaining CT images for virtual colonoscopy, the patient undergoes a one-day bowel preparation of mild laxatives and a low residue diet. The purpose of bowel preparation is to enhance the stool and residue fluid so that they can be distinguished from other tissues. Figure 1 shows one transverse slice of CT images with tagged stool and residue fluid. Non-uniformity can be observed in regions of bone and tagged stool residues. In addition, there exist partial volume effects around the mucosa layer of colon wall.

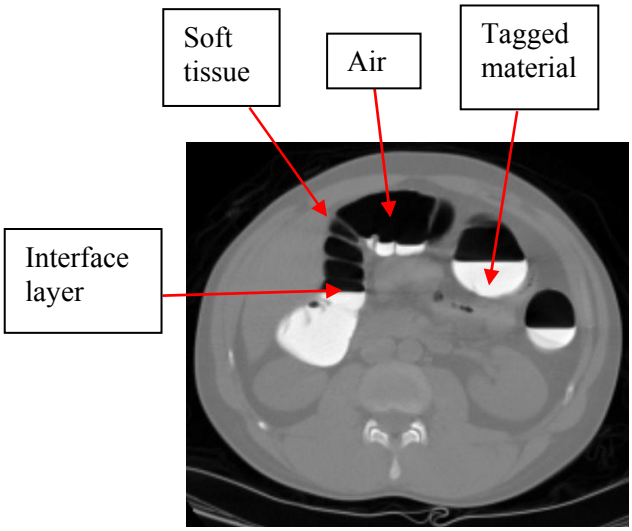


Figure 1 shows one transverse slice of CT images.

In order to minimize the partial volume effect, we allow each voxel to contain a mixture of multiple tissues [12-15]. We apply a new unifying mixture model-based tissue classification of CT images for electronic cleansing. Our method models a mixture to estimate the partial volume effects of multiple tissue types within a voxel. It also simultaneously takes into account the inhomogeneity effect that commonly appears in regions of bone and tagged stool residuals. The following is a brief description of the model selection for integrating inhomogeneity correction and partial volume segmentation.

2.1. Image Model

Let Γ and S be two sets: $\Gamma = \{1,2,...,K\}$, and $S = \{1,2,...,N\}$, where K is the total number of tissue classes and N is the total number of voxels in the acquired image. Let image density $\boldsymbol{Y}$ be a set of random viable $\{y_1,...,y_i,...,y_N \mid i \in N\}$. Assume $\{ y_i \}$ contains K tissue types, where each tissue type has a contribution of x_{ik} to the observed density value y_i at that voxel.

Let M be a set of vector $\{m_1,...,m_i,...,m_N \mid i \in N\}$ with $m_i = \{m_{i1}, m_{i2},...,m_{iK}\}$, where m_{ik} reflects the fraction of tissue type k inside voxel i. Each voxel value y_i in the observed image is considered as a random process: $y_i = \rho_i \sum_{k=1}^{K} m_{ik} \mu_k + \varepsilon_i$, where μ_k is the observed mean value of tissue type of class k when it fully fills in a voxel, ε_i is a Gaussian noise associated with the observation y_i at voxel i with its mean being zero and variance of

σ_k^2, and ρ_i reflects the inhomogeneity effect at voxel *i*. We further assume that $\{ y_i \}$ are statistically independent from each other, i.e.

$$\Pr(Y \mid M , \rho , \mu , \sigma) = \prod_{i=1}^{N} \frac{1}{\sqrt{2\pi \sum_{k=1}^{K} m_{ik} \sigma_k^2}} \exp[- \frac{(y_i - \rho_i \sum_{k=1}^{K} m_{ik} \mu_k)^2}{2 \sum_{k=1}^{K} m_{ik} \sigma_k^2}] \quad (1)$$

The probability distribution of sampling $\{ x_{ik} \}$, given the tissue model parameters $\{ m_{ik} , \rho_i , \mu_k , \sigma_k^2 \}$, is:

$$\Pr(X \mid M , \rho, \mu, \sigma) = \prod_{i,k=1}^{N,K} \frac{1}{\sqrt{2\pi\, m_{ik} \sigma_k^2}} \exp[-\frac{(x_{ik} - \rho_i m_{ik} \mu_k)^2}{2 m_{ik} \sigma_k^2}] \quad (2)$$

Estimating the model parameters $\{ m_{ik} , \rho_i , \mu_k , \sigma_k^2 \}$ through MAP criteria requires the prior information for both $\{ m_{ik} \}$ and $\{ \rho_i \}$ [16-17].

A Markov random field (MRF) *prior* is designed for the mixture m_i as

$$\Pr(m_i \mid N_i) = \frac{1}{Z} \exp(-\beta \sum_{k=1, j \in N_i}^{K} \alpha_{ij} (m_{ik} - m_{jk})^2 \quad (3)$$

where N_i denotes the neighborhood of voxel *i*, β is a parameter controlling the degree of the penalty on mixtures $\{ m_{ik} \}$, α_{ij} is a scale factor reflecting the difference among different orders of the neighbors, and *Z* is the normalization factor for the MRF model.

The MRF prior for $\{ \rho_i \}$ is defined as

$$\Pr(\rho_i \mid N_i) = \frac{1}{Z} \exp[-\gamma_1 \sum_{j=1}^{R} (D_j * \rho)_i^2 - \gamma_2 \sum_{j,l=1}^{R} (D_j * D_l * \rho)_i^2] \quad (4)$$

where *R* equals 2 for two-dimensional (2D) slice images and 3 for 3D volume images [18-20]. Notation *D* is the standard forward finite difference operator along the corresponding directions. Symbol * denotes the 1D discrete convolution operator. The first-order regularization term (associated with γ_1) penalizes a large variation in the bias field and the second-order regularization term (associated with γ_2) penalizes the discontinuities in the bias field.

2.2. Parameter Estimation

By the well-established EM algorithm [21-22], we have

$$\mu_k^{(n+1)} = \frac{\sum_{i=1}^{N} x_{ik}^{(n)}}{\sum_{i=1}^{N} \rho_i^{(n)} m_{ik}^{(n)}} . \quad (5)$$

and

$$\sigma_k^{2(n+1)} = \frac{1}{N} \sum_{i=1}^{N} \frac{x_{ik}^{2(n)} - 2\rho_i^{(n)} m_{ik}^{(n)} \mu_k^{(n)} x_{ik}^{(n)} + \rho_i^{(n)} m_{ik}^{2(n)} \mu_k^{2(n)}}{m_{ik}^{(n)}} \quad (6)$$

For the bias field parameter $\{\rho_i\}$, we have:

$$\sum_{k=1}^{K}\frac{\mu_k^{(n)}x_{ik}^{(n)}}{\sigma_k^{2(n)}}=\rho_i\cdot\sum_{k=1}^{K}\frac{m_{ik}^{(n)}\mu_k^{2(n)}}{\sigma_k^{2(n)}}m_{ik}^{(n)}\mu_k^{2(n)}+\gamma_1(H_1*\rho)_i+\gamma_2(H_2*\rho)_i \quad (7)$$

where

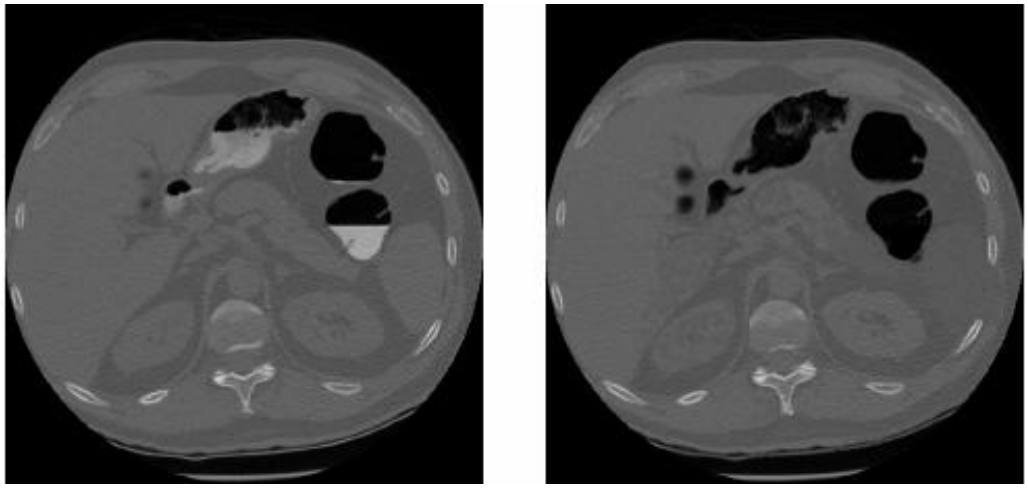
$$H_1=\begin{bmatrix}0&-1&0\\-1&4&-1\\0&-1&0\end{bmatrix} \qquad H_2=\begin{bmatrix}0&0&1&0&0\\0&2&-8&2&0\\1&-8&20&-8&1\\0&2&-8&2&0\\0&0&1&0&0\end{bmatrix}.$$

3. RESULTS

In this study, a two-day bowel preparation is used. On day 1, patients follow a list of suggested foods, and take a low-residue food kit on day 2. At dinner on day 1 and with each meal on day 2, patients take 250cc of barium sulfate (2.1%, E-Z-EM Inc.). In the evening prior to virtual conlonsocopy, patients take 16.4g magnesium citrate, 5mg bisacodyl tablets, and 60ml Gastroview (Malinckrodt). In the morning before the CT scan, patients take another 60ml Gastroview and enema suppository.

Prior to acquiring CT images, approximately 1-2 liters of CO_2 is introduced through a small bore rectal tube to inflate the colon. CT images are acquired in less than 40s during a single breath hold. Scan parameters are 5mm collimation, pitch 1.6-2.1, 120 kVp, FOV 36-50 cm, and 100mA. Both supine and prone CT images are obtained. The acquired data is subsequently reconstructed at the 1mm intervals with a 512x512 array, resulting in 300-520 slices for each dataset.

The new electronic cleansing method has been tested by the patient datasets. Figure 2 shows a transverse slice of the colon image before (left) and after (right) electronic cleansing.



. Figure 2 shows a transverse slice of the colon image before (left) and after (right) electronic cleansing.

4. DISCUSSION AND CONCLUSIONS

We have applied a new unifying electronic cleansing method to virtually clean tagged residual materials. The presented method requires less-stressful bowel preparation, therefore eliminating conventional physical bowel washing. The model-based algorithm further overcomes the non-uniformity and partial volume effects appearing in regions of bone and tagged stool residues. Experiment results are promising. Further evaluation of the method through a large number of datasets is under progress.

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