# Robust Colon Residue Detection Using Vector Quantization Based Classification for Virtual Colonoscopy

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## ABSTRACT

We present an automatic and robust tagged-residue detection technique using vector quantization based classification. This technique enables electronic cleansing even on poorly tagged datasets, leading to more effective virtual colonoscopy. In order to reduce the sensitivity towards intensity variation among the tagged residual material, we use a multi-step technique. First, we apply classification using an unsupervised and self-adapting vector quantization algorithm. Then, we sort the resultant classes by their average intensities. We apply thresholding on these classes based on a conservative threshold. This helps us in differentiating soft tissue inside tagged material from poorly tagged region or noise.

**Keywords:** Virtual Colonoscopy, Vector Quantization, Segmentation, Electronic Cleansing

## 1. INTRODUCTION

Colon cancer is the third most commonly diagnosed and the second leading cause of cancer deaths in the United States. Often it is diagnosed at an advanced stage, after the patient has developed symptoms, explaining its high mortality rate. This mortality could be reduced if cancerous colon polyps were detected and removed before turning into malignant cancers[1] . Various health organizations such as the American Cancer Society, the American College of Physicians and the World Health Organization have thus recommended colon screening every 1 to 10 years depending on the specific examination needed. Optical colonoscopy is currently the best method of polyp detection. Unfortunately, most patients do not follow their physician's advice to undergo such a procedure because of the associated pain, risk, discomfort and high cost. Consequently, considerable interest has arisen in developing a computer-based screening modality as an alternative to optical colonoscopy, by employing advanced computer graphics and visualization techniques[2] .

At Stony Brook University we have developed a system called the *3D Virtual Colonoscopy*[3–5] . This system allows interactive navigation inside the virtual colon lumen extracted from the CT scan of a patient's abdomen. This enables radiologists to view and explore the colon surface non-invasively. To enable the virtual navigation and exploration of the colon lumen, several pre-processing steps are needed[6] . Before the data acquisition by a CT scan, the patient's colon is cleansed and inflated with $CO_2$. Then a helical CT scan of the patient's abdomen is taken such that it covers the entire colon. This takes about 30-40 seconds and can be done in a single breath hold. The scan produces several hundred slices of 512x512 resolution which are later reconstructed into a 3D volume of 100-250 MB. This volumetric data then undergoes a series of pre-processing stages which are required for the virtual navigation. The most important of these stages is the accurate segmentation of the colon lumen, which is the interior of the colon, from the original CT images. In the final step, we use accurate volume rendering for virtual navigation through the inside of the colon, to locate polyps.

All current colonoscopy techniques, including virtual colonoscopy, require a clean colon lumen for accurate detection of the polyps. Residual materials inside the colon can hinder the view of the colon surface. Some

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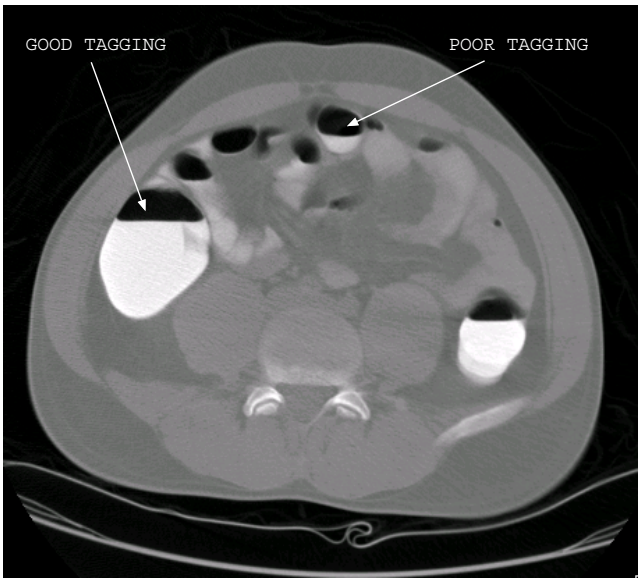


**Figure 1**. A traverse slice showing poor tagging (top) and good tagging (bottom) of residual material.

residual material could also be erroneously interpreted as polyps, leading to false positive results. As a result, patients must undergo physical bowel cleansing prior to optical colonoscopy. This can include washing the colon with large amounts of liquids and administrating medications and enemas to induce bowel movements which is often more uncomfortable and unpleasant than the examination itself.

An alternative technique which does not require this uncomfortable cleansing would be beneficial to patients. As a result, we have developed a new bowel preparation scheme for virtual colonoscopy[7,8] which makes the entire procedure more comfortable for patients. The basic idea of the new bowel preparation scheme is to enhance the CT intensity of the residual material and then digitally remove them from the dataset. Once removed, the virtual navigation of the colon will provide the radiologist with a better view of the surface of the colon.

In order to enhance the stool and fluid, the patient is asked to remain on a soft-food diet (yogurt, cereals, mashed potatoes, etc.) for an entire day before the CT scan. Barium sulfate and iodine bases contrast agents are taken during the day prior to and the day the CT study is performed. Some additional solutions are also taken by the patient for the purpose of liquidizing and enhancing the stool. After following this preparation, the patient undergoes the CT scan. The acquired data now contains enhanced residual stool and fluid.

The next step is to remove the enhanced residual material. For this, we have developed a technique called *Electronic Cleansing*[9,10] . This technique segments and removes the residual material from the colon. However, for this technique to be effective, it needs good and uniform tagging (enhancement) of the residual material. It is possible to get good tagging using a perfectly controlled diet. However, in reality, patients have a huge variety in their diet, digestive system and age which makes it almost impossible to perfect a uniform dietary preparation, which commonly leads to tagging that is poor and non-uniform.

In Figure 1, we show a slice from an example dataset. In this dataset, two areas of the colon contain a large amount of residual material that is tagged well. However, a small region of the colon on the top has residual material that is not tagged well. the goal of this work is to make the residual material detection more robust enabling electronic cleansing to be effective even in such cases. In the following sections, we present out algorithm.

## 2. SEGMENTATION

Figure 2 shows the histogram of a typical dataset that we obtain from the CT scan. In the first step of our algorithm, we analyze this histogram for peaks and approximately divide the histogram into different regions.

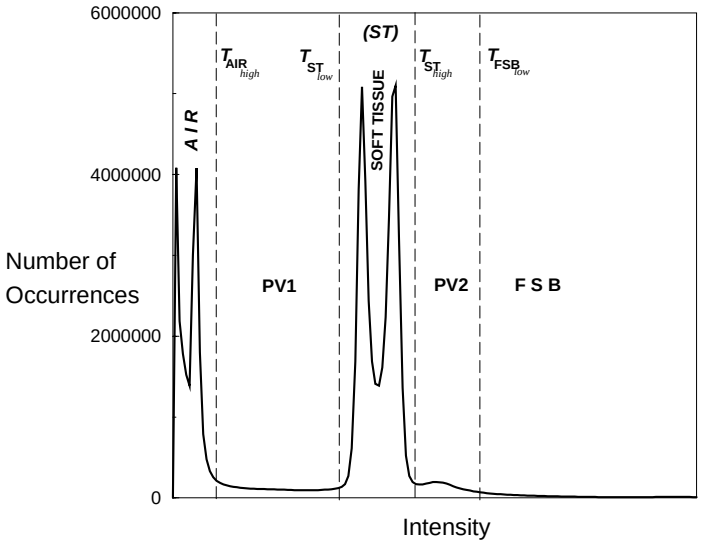


**Figure 2**. Histogram of a typical CT dataset for virtual colonoscopy.

Each region is characterized by thresholds which are flexible and approximate (shown by vertical dashed lines). The first region from the left ($AIR$) is the air region. The peaks in the center represent the soft-tissues which we mark by two thresholds, $T_{STlow}$ and $T_{SThigh}$. To the extreme right of the histogram is the region ($FSB$) which belongs to bones and very well tagged residual fluid and stool. The areas between these three regions represent the partial volume voxels ($PV1$, $PV2$).

From the histogram we can see that it is difficult to distinguish between well tagged region and soft-tissue as there is no peak in the well-tagged intensity range. This happens mainly due to poor tagging of the residual material. The partial volume region between the soft-tissues and the higher end contains voxels of two types: voxels which are actually soft-tissues but their intensity is enhanced due to neighboring high intensity voxels, and voxels which belong to poorly tagged residual material. Our goal is to separate these two types of voxels effectively. It is impossible to separate them by simple thresholding because there is no intensity value that separates the two types of voxels.

Before we move to the next step of our algorithm to separate the voxels, we find a liberal threshold such that we have all the voxels that belong to the residual material and the partial volume voxels between the soft-tissue range and the higher range. We select the $T_{SThigh}$ threshold. We then apply thresholding on the dataset based on this threshold and mark the voxels whose intensities are above our threshold. Henceforth, we deal only with these voxels. The count of these voxels is really small compared to the total voxels in the dataset. This helps in reducing the computation cost of our algorithm.

## 3. VECTOR QUANTIZATION BASED CLASSIFICATION

In the next step of our algorithm, we perform classification. Similar to Markov random field (MRF) models, we assume that a three-dimensional (3-D) object of a similar tissue type in a CT image should be in a contiguous 3-D volume, including partial volume effect. It is reasonable to classify the body voxels based on the intensity similarity within certain spatial range. The diameter of the local range for a given voxel should be less than 5mm considering the partial volume effect and the 5mm thick collimation. By the acquisition protocol used for our datasets, each voxel was 1mm thick with size in the $x$-$y$ axial plane varying from 0.64 to 0.94 mm depending on the field of view. The chosen local neighborhood is depicted in Figure 3. Its diameter is less than 4.6 mm in all directions. The intensities of those 23 voxels in the local neighborhood form a 23 dimensional local intensity vector. The goal is to classify the residual material voxels based on their local intensity vectors.

Each dataset consists of millions of voxels which belong to the residual material. This requires intensive computational effort to manipulate such a large quantity of vectors. To reduce the computing burden a feature

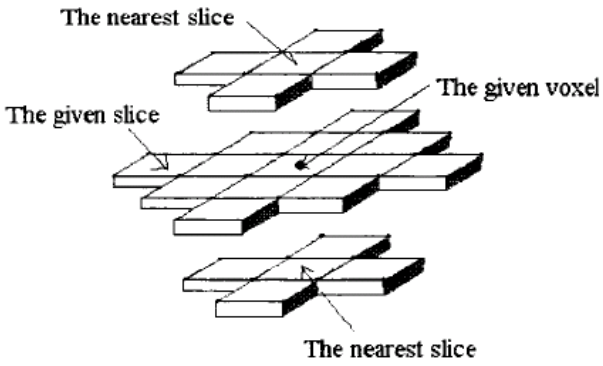


**Figure 3**. Local neighborhood of a voxel that is used in classification.

analysis of the local vector series is necessary[11] . The principle component analysis (PCA)[12] was then applied to the local vector series to determine the dimension of the feature vectors and the associated orthogonal transformation matrix (i.e., the Karhunen-Loeve (K-L) transformation matrix). The PCA on the datasets of the training samples showed that a reasonable dimension of the feature vectors was 5, where the summation of the first five principal components' variances was more than 92% of the total variance. It is computationally costly to determine the K-L matrix for each dataset. A general K-L matrix was then determined by training samples and was used for segmenting all datasets[13] .

For the low-level classification, the K-L transformation was first applied to the local vector series. In the K-L domain, the feature vectors were formed by the first five principal components from the transformed vector series. Then, the feature vectors were classified into several classes. There are several approaches to classify the vectors[14] . In general, an automated algorithm is desired, i.e., an unsupervised self-adaptive vector quantization (VQ) algorithm is a candidate. A self-adaptive on-line VQ algorithm was developed[13] . Using the algorithm, the class number and the representative vector for each class can be obtained in a single scan on all feature vectors. This reduces greatly the computing time as compared to iterative VQ algorithms, such as the LBG algorithm[15] . The representative vector of each class is an estimation of the mean vector of that class. From the central limit theorem[16] , the larger the number in a class is, the more accurate the representative vector estimates the mean vector of that class. In our case, there are millions of voxels. Hence, the representative vector is a good estimation of the mean of that class.

The algorithm is similar to an unsupervised clustering algorithm. The number of classes and the representative vectors are updated continuously when more vectors are included in the calculation. From this point, the algorithm can be regarded as a learning procedure. It depends only on two parameters: $K$, the upper bound of possible classes and $T$, the vector similarity threshold. The value of $T$ is more crucial than the value of $K$ for the classification. If it is too large, only one class can be obtained. Or if it is too small, redundant classes may occur. According to our numerical experiments, $T$ was set to be the square root of the maximum component variance of the feature vector series. This allows the VQ algorithm to achieve the minimum class number with the maximum variance. Since $T$ is estimated from the data, the algorithm is self-adaptive.

## 4. THRESHOLDING THE CLASSES

Figure 4 shows the results of applying the previous classification step on an example dataset. The left image shows a slice from the input dataset, and the right image shows the different classes for the same slice. It can be noted that the good tagged residual material (bottom left) as well as poorly tagged residual material (top right) both are part of some class in the classification results.

In this final stage of our algorithm, we aim to eliminate the classified voxels which do not belong to the poorly tagged residual material. In order to do that, we first find the average intensity for each class. The

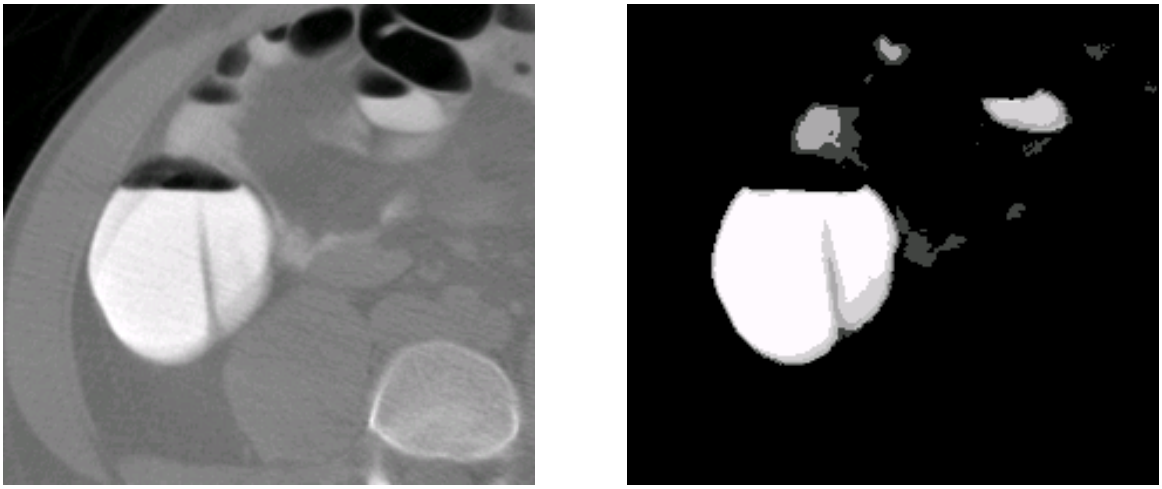

**Figure 4**. Original dataset (left) and the results after applying classification (right).

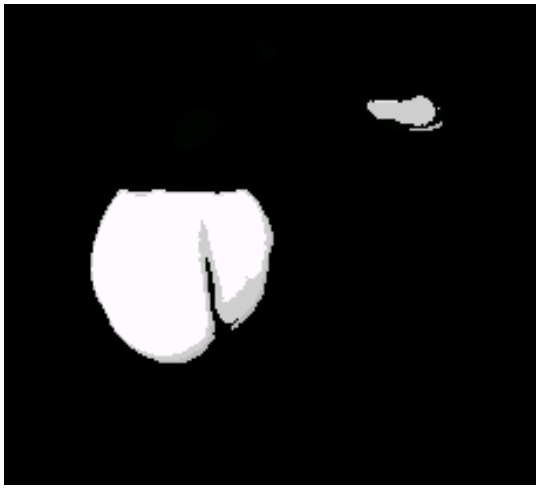

**Figure 5**. Result after removing classes with average intensity below threshold.

average intensity is computed by adding the voxel intensities of all the voxels in each class and dividing that by the number of voxels in the class. We then select a reasonable threshold which will define *sufficient* tagging. By sufficient tagging we mean the minimum difference between the average intensity of a tagged region and soft tissue required to separate the regions.

The classes are sorted in ascending order of their average intensities. In Figure 4 we show this order (brightest means highest average intensity). The classes whose average intensity is lower than our selected threshold are removed, while the others are retained. The voxels which are part of the retained classes belong to the poorly tagged residual material. In Figure 5 we show the result after removing classes with low average intensities.

## 5. RESULTS

We tested our algorithm on a variety of volunteer datasets. The residual material detection was found to be more effective than earlier approaches using thresholding based on a single threshold. With our algorithm, we were able to decrease the tagging requirement (the intensity difference between tagged voxels and soft-tissue voxels) for a successful electronic cleansing from around 500 Hu to 250 Hu by using our algorithm. With this improvement, it was possible to successfully remove residual material with lower tagged values.

## 6. CONCLUSION

We presented an automatic and robust tagged-residue detection technique using vector quantization based classification. We used a multi-step technique to reduce sensitivity towards intensity variation among the tagged residual material. The use of vector quantization has helped us detect poorly tagged material which was not possible before. The grouping of classes by their average intensity and then applying thresholding based on a conservative threshold helps us in differentiating soft tissue inside tagged material from poorly tagged region or noise.

## ACKNOWLEDGMENTS

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