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Effects of Filtering on Colorectal Polyp Detection in Ultra Low Dose CT

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ABSTRACT

We have evaluated the feasibility of polyp detection on simulated ultra low dose CT Colonography data by a computer aided polyp detection (CAD) algorithm. We compared the results of ultra low dose to normal dose data. Twenty-three extensively prepared patients were scanned in prone and supine position at 25 to 100 mAs (average 70 mAs) depending on their waist circumference. Noise was added and the scans were reconstructed at 6.25 and 1.39 mAs with a validated simulation technique. To evaluate the performance of the CAD system, polyps detected by an experienced reviewer and confirmed at colonoscopy were used as ground truth. Curvature, concavity and sphericity of the colon surface were used to detect polyp candidates. In order to reduce noise, Bilateral filtering was used. We present the results for 40 polyps of 6 mm or larger as measured during colonoscopy. The by-polyp sensitivity was 80% for medium size polyps (6-9 mm) and 97% for large polyps (10 mm or larger) at an average value of 5 false-positives per scan for normal dose data. The by-polyp sensitivity was 81% for medium size polyps and 85% for large size polyps at an average value of 5 false-positives per scan for low dose data (6.25 mAs). Finally for the ultra low dose data (1.39 mAs) we achieved a by-polyp sensitivity of 75% for medium size polyps and 97% for large polyps at an average value of 5 false-positives per scan. These results were obtained when using a CAD system with optimal features per dose level. When using one CAD system for all dose levels the performance decreases slightly. The conclusion of our study is that CAD for polyp detection is feasible on ultra low dose CT colonography data.

Keywords: Virtual colonoscopy, CT colonography, computer aided detection, ultra low dose CT, colorectal cancer, colorectal polyps.

1. INTRODUCTION

Colorectal cancer is the second leading cause of cancer-related deaths in the industrialized countries, accounting for approximately 10% of all cancer mortality[1]. Colorectal cancer has a high prevalence and a long asymptomatic premalignant phase and is well treatable when detected early; it is, therefore, an inherently suitable disease for screening[2]. The American Cancer Society recommends the fecult occult blood test (FOBT), flexible sigmoidoscopy, double contrast barium enema (DCBE) or colonoscopy for the early detection of colorectal cancer[3]. However, these methods all have shortcomings. FOBT and DCBE have medium sensitivity and specificity. The endoscopic examinations are invasive and burdensome for the patient. A future screening candidate is Computed Tomography Colonography (CTC), however it also has some shortcomings. First, the time a radiologist needs to evaluate the data, as well as the performance of the radiologist. Thirdly, the radiation dose is a drawback, especially for population screening. Also the extensive patient preparation is a shortcoming, however this accounts for multiple methods such as colonoscopy and in a lesser extend for flexible sigmoidoscopy. New technology might overcome the shortcomings of CTC and turn it into a low risk screening test patients prefer. Computer aided detection (CAD) can assist the radiologist and increase observer sensitivity and decrease observer variation[4]. The latest CT scanners can scan the abdomen using less radiation. Even the feasibility of electronic cleansing of the colon is investigated[5] to diminish the patient reluctance to undergo bowel preparation. In this paper a CAD system will be tested using simulated low dose CT data in an attempt to tackle some of the shortcomings of CTC as a screening method for colorectal cancer.

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During the last decade, various groups investigated the use of computer aided polyp detection in CTC to increase reading sensitivity and specificity and decrease interpretation time[6-13]. Also the use of low dose CT colonography was investigated[14,15,16]. In general the results are promising. The last few years the combination of low dose CT colonography with CAD is under investigation[17, 18]. This tackles a few problems, namely radiation dose, radiologic performance and maybe in the future interpretation time if CAD is used as first reader. Lowering the dose in CT colonography results in more noisy data, which is a challenge for radiologists interpreting the data, as well as fully automatic polyp detection algorithms.

2. METHOD

In order to reduce the noise present in low dose CT datasets filtering is applied first. In a study by van Gelder *et al.*[14] the feasibility of polyp detection with low dose CTC data was evaluated with simulated low dose data. They already stated that application of a noise reduction filter is essential for detection of polyps in very low dose data. The images they used (image resolution 0.74 x 0.74 x 1.6 mm) were filtered with a Gaussian kernel with a width of 1.2 mm. This filtering operation results in smoother images. This smoothing effect does not just remove noise, but also anatomical structures that can be of importance. The Bilateral filter proposed by Tomasi and Manducci[19] is similar to Gaussian filtering, but partially avoids smoothing of anatomical structures by reducing the blurring of high contrast regions.

2.1. Noise reduction filters

Filtering can take place on continuous signals and discrete signals. The CT colonography datasets used in this study are discrete datasets. The Gaussian and Bilateral filters will therefore be presented as discrete filters.

2.1.1. Gaussian filtering

The three-dimensional isotropic Gaussian filter kernel is defined as follows:

$$G[\vec{n}] = \frac{1}{\left(\sqrt{2\pi}\sigma\right)^3} e^{-\frac{|n|^2}{2\sigma^2}} \tag{2.1}$$

The σ is the scale of the Gaussian filter and $\vec{n}$ the voxel position in the kernel. $G[\vec{n}]$ is the value of the kernel at $\vec{n}$. This filter is symmetric around the origin. The voxel weights $G[\vec{n}]$ in an isotropic Gaussian kernel depend only on the distance to the origin and the scale.

A Gaussian kernel can be used to filter a 3D image *I*, e.g. a CT dataset. The voxel value at position $\vec{k}$ is $I[k]$. Filtering the data set *I* with the Gaussian kernel *G* can be done with a discrete convolution. Convolving *I* with *G* is defined as:

$$I_{Gaussianfiltered}\left[\vec{k}\right] = I\left[\vec{k}\right] * G\left[\vec{k}\right] = \sum_{\vec{n}\in \text{kernel}} I[\vec{n}]G\left[\vec{k}-\vec{n}\right] \tag{2.2}$$

2.1.2. Bilateral filtering

The voxel weights in a Gaussian kernel only depend on the distance to the origin of the kernel. In the Bilateral filter not only the distance between voxels is taken into account, but also the grey-level intensity difference between voxels in the 3D image. When voxels are located closer to the origin of the kernel, or differ less in intensity, the weight is higher.

To compute the distance and intensity weights $\left(W_{dis}, W_{\text{int}}\right)$ of the Bilateral filter for a voxel position $\vec{k}$ in the original image and a voxel position $\vec{n}$ in the Bilateral kernel the following formula apply:

$$W_{dis}[\vec{n}] = \frac{1}{\left(\sqrt{2\pi}\sigma_{dis}\right)^3} e^{-\frac{|\vec{n}|^2}{2\sigma_{dis}^2}} \tag{2.3}$$

$$W_{\text{int}}\left[\vec{k},\vec{n}\right]=\frac{1}{\sqrt{2\pi}\sigma_{\text{int}}}e^{-\frac{\left(I\left[\vec{k}\right]-I\left[\vec{k}+\vec{n}\right]\right)^2}{2\sigma_{\text{int}}^2}} \tag{2.4}$$

The final Bilateral filter weight for a given voxel position is defined as the product of the corresponding two weights:

$$B\left[\vec{k},\vec{n}\right]=W_{dis}\left[\vec{n}\right]\cdot W_{\text{int}}\left[\vec{k},\vec{n}\right] \tag{2.5}$$

The Bilateral filtered voxel value at position $\vec{k}$ for a 3-dimensional volume can be calculated as follows:

$$I_{Bilateralfiltered}\left[\vec{k}\right]=\frac{\sum_{\vec{n}\in\text{kernel}}B\left[\vec{k},\vec{n}\right]\cdot I\left[\vec{k}+\vec{n}\right]}{\sum_{\vec{n}\in\text{kernel}}B\left[\vec{k},\vec{n}\right]} \tag{2.6}$$

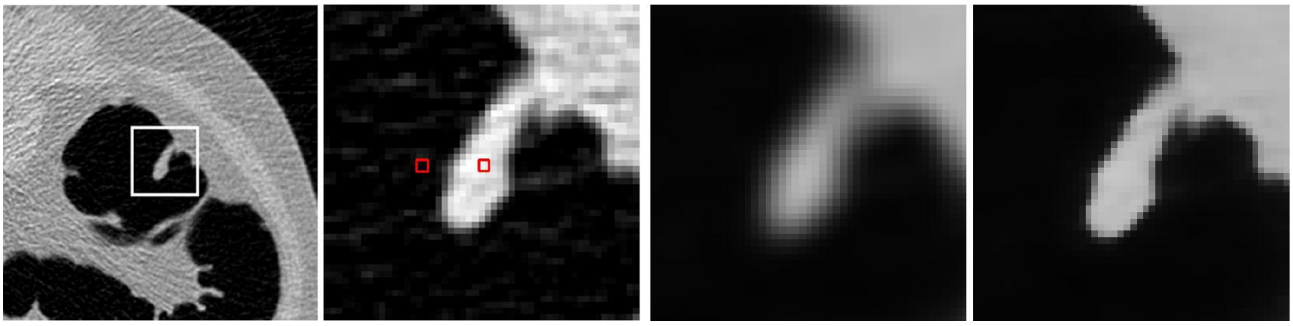

Figure 1: From left to right: Axial slice with boxed polyp; enlarged polyp, squares denote two locations, the left one is in air and the right one inside the polyp; Gaussian filtered result (σ =2.0 mm); Bilateral filtered result (σ_{dis} = 3.0 mm and σ_{int} = 250 HU).

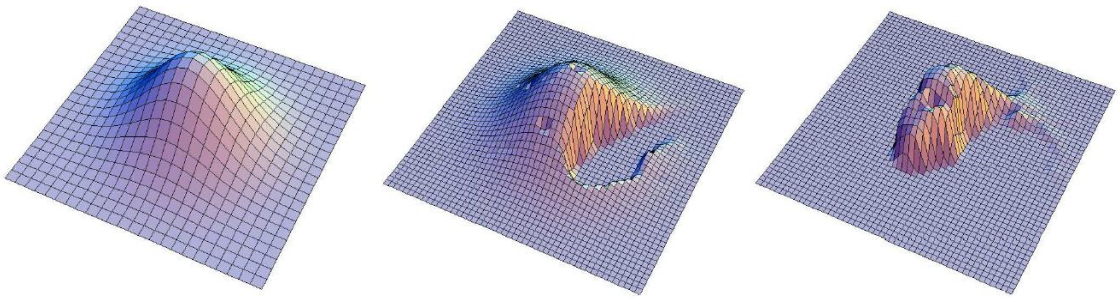

Figure 2: From left to right: Gaussian kernel for air and polyp voxel; Bilateral kernel for air voxel; Bilateral kernel for polyp voxel.

2.1.3. Gaussian versus Bilateral filtering

The three-dimensional convolution with the Gaussian filter is separable. This means that the convolution can be done by 3 individual one-dimensional convolutions, which is faster than one three-dimensional convolution. In case of Gaussian filtering, the kernel looks the same for all voxels in *I* and is not dependent on *I*. However in the Bilateral filter the weights of W_{int} are dependent on *I*. For each voxel in *I* the filter kernel is different and convolution cannot be used.

Equation 2.4 shows that the filter kernel is dependent on input image *I*. The Gaussian filter is unable to adapt to the local image structure, but the Bilateral filter is. In Figure 1 an axial slice is shown, denoted are two different voxels. The left voxel is an air voxel and the right voxel a polyp voxel. The Gaussian kernels for these voxels are identical as expected and the kernel is shown in Figure 2. This figure also shows the Bilateral kernels for these two voxels. It is clear that when filtering an air voxel, only other air voxels should contribute in the filtering process, whereas in the polyp voxel only polyp voxels should contribute. The adaptation of the Bilateral filter to the local image structure reduces smoothing of the high contrast air to tissue boundary. It thus reduces smoothing of the anatomical shape of the colon wall, as shown in Figure 1.

The σ of the Gaussian filter determines the extent of the filter. Also in the Bilateral filter the σ_{dis} determines the extend of the filter. The σ_{int} determines which edges should not be blurred. In case of colon applications, the difference in intensity between air and colon is about 800 HU. Therefore $2 \cdot \sigma_{\text{int}} < 800$ is used to overcome blurring of tissue and air.

2.2. Computer aided polyp detection

The proprietary algorithm (patents pending) to detect colonic polyps includes three main steps: colon wall segmentation, identification and segmentation of polyp candidates, and false candidate reduction. These three steps will be described briefly.

2.2.1. CAD input

The minimum input for a computer aided polyp detection algorithm is a specially prepared CT scan of the abdomen. The colon has to be emptied and distented with air. Normally prone are supine scans are used in order to reveal polyps that are hidden under intraluminal remains or hidden in segments that are not well distented and to distinguish polyps from intraluminal remains. The intraluminal remains will be at different positions in both scans due to gravity. A path through the colon defined by a radiologist or a fully automatic tracked colon path [19] is additional input.

2.2.2. Step 1: Segment the colon wall

The first step in a CAD system is the segmentation of the colon wall. This can be done fully automatic by combining a priori known information such as the differences in CT values and anatomy of the human body, or by using a predefined path. Our algorithm uses a predefined path. The purpose of segmenting the colon wall is to reduce the search area in which polyps need to be detected. It reduces processing times and, in case of good segmentation, overcomes extracolonic findings.

2.2.3. Step 2: Identify and segment polyps

The following step is the actual detection of polyps. The colon wall is reduced to polyp-like regions. The most important issue is achieve a high sensitivity, once a polyp is missed it cannot be detected in a next step. A secondary issue is the detection of non-polyp structures, these should be minimized. These unwanted structures can be folds, stool due to incomplete bowel cleansing, noise or other objects. Polyps protrude inward from the colon wall toward the air filled lumen and have a cap like structure. Useful features to initially identify polyps are surface shape and CT values of the colon wall.

2.2.4. Step 3: Reduce false positives based on feature values

The last step serves to limit the number of false positive detections. In general this is necessary due to the large number of detections in the previous step. For all segmented candidate polyps a set of feature values can be calculated. These features are more specific to polyps than the features used in the detection step. Examples of such features are curvature, concavity and sphericity of the colon surface. A system has to differentiate polyps from non-polyps based upon the calculated features. The purpose is to eliminate false positives without eliminating true positives.

2.2.5. CAD output

The final result of the CAD algorithm is a set of detections that are classified as polyps. A polyp likelihood can be additional output for a detection.

3. PATIENT DATA AND RESULTS

3.1. Patient data

Twenty-three patients were scanned with a 4-detector CT scanner in prone and supine position. The scanner parameters are listed in Table 1. To create lower dose data, noise wais added to the normal dose scans before they are reconstructed[21]. The estimated effective dose values and mAs levels are listed in Table 2. The reference standard to verify if polyps detected by the CAD system were real polyps was created on basis of the colonoscopy findings. All 46 CTC datasets were viewed by a radiologist. A research fellow marked all polyps and linked them with colonoscopy findings. The linking was possible by simultaneously viewing the CTC data, the readings of the CTC and viewing the video that was acquired during colonoscopy. The linking was done based on three criteria: morphology (shape), segment (location) and size. The annotations of the radiologist consisted of the position, size and morphology of the polyp. Table 3 shows how many polyps of a certain size were identified in the CT scans, Table 4 shows the morphology of the polyps of various sizes and Table 5 shows the location of the polyps of various sizes. The morphology, location and sizes measured are based on the colonoscopy findings and not influenced by the CT findings.

Table 1: Scanner parameters.

Scan parameter	**Value**
Scanner	Philips Mx8000 – CT: 4 detectors
Tube current	18.75, 30, 48, 52.5 or 75 mA
Gantry rotation time	0.75 s
mAs level	25, 40, 64, 70 or 100 mAs
Voltage	120 kVp
Pitch	1.25
Collimation	4 x 2.5 mm
Reconstruction interval	1.6 mm
Section thickness	3.2 mm
Image resolution	0.74 x 0.74 x 1.6 mm

Table 2: Overview of normal dose and simulated low and ultra low dose data.

Label	**Tube current x rotation time (mAs)**	**Effective dose (mSv)**	**Dose reduction compared to normal dose**
Normal dose	69 (average)	8.4	-
Low dose	6.25	0.75	11-fold
Ultra low dose	1.39	0.17	50-fold

Table 3: Polyps found at colonoscopy and corresponding findings in the CT scans.

Findings at colonoscopy			**Identified at CT**			
Polyp category	*Diameter*	*Nr. Of polyps*	*Neither of the scans*	*Prone scan only*	*Supine scan only*	*Both scans*
Medium	6-9 mm	27	6	4	8	9
Large	10-19 mm	20	5	3	3	9
Masses	≥20 mm	4	0	0	1	3

Table 4: Morphology of the polyps found at colonoscopy.

Polyp size			**Morphology**			
Polyp category	*Diameter*	*Nr. Of polyps*	*Sessile*	*Flat*	*Pedunculated*	*Unknown*
Medium	6-9 mm	27	17	2	4	4
Large	10-19 mm	20	8	5	5	2
Masses	≥20 mm	4	2	0	1	1

Table 5: Location of the polyps found at colonoscopy.

Polyp size			Location						
Polyp category	*Diameter*	*Nr. Of polyps*	*Cecum*	*Asc. colon*	*Trans. colon*	*Desc. colon*	*Sigmoid colon*	*Rectum*	*Unknown*
Medium	6-9 mm	27	0	4	4	1	5	5	8
Large	10-19 mm	20	1	5	3	0	6	2	3
Masses	$\geq$20 mm	4	0	3	0	0	1	0	0

3.2. Validating the algorithm

The leave-one-patient-out method is used to keep the training and test data separate. During the training a subset of features was chosen that distinguishes the polyp candidates best from the non-polyp candidates. The polyps that are found at colonoscopy and confirmed by CT are used as reference standard for testing and training. Matching detected polyps with the reference standard can be done in various ways and thus the TP definition can vary due to this matching. The method we used is that the CT annotated location lies within or directly against the segmentation of the polyp candidate. The physician annotates at the surface of a polyp or in the center of a polyp; as a result the detection will always be the annotated polyp. If the colon is badly segmented, detections can occur outside the colon. The segmentation process is part of the CAD system and detections outside the colon are therefore classified as false positives. Sensitivity levels can be reported at patient level, polyp level or CT-polyp level [18]. In this paper reported sensitivities are mainly at CT-polyp level. All scans and polyp occurrences are treated independently. A true positive is defined as a detection that is really a polyp. A false positive is a detection that is not a real polyp. A false negative is a polyp (proven by colonoscopy) that is not found in the scan by the CAD algorithm. Due to the setup of this study true negatives are undefined. To achieve 100% by-CT-polyp sensitivity all polyp occurrences need to be detected in all scans. The sensitivity at polyp level is usually higher, because the prone and supine scan are not treated independently. A false negative is then a polyp (proven by colonoscopy) that is not found in both scans.

3.3. Experiments

Two experiments are performed to investigate the feasibility of computer aided polyp detection on low and ultra low dose data. The goal of the first experiment is to tune the CAD algorithm for each dose level individually to investigate the optimal performance. The goal of the second experiment is to create one CAD algorithm for all dose levels ranging from 1.39 to 100 mAs. This will give us an estimate of the performance of a CAD algorithm robust to dose changes. In the first experiment features are chosen on each dose level separately and trained on each dose level separately. In the second experiment robust features are chosen and always trained on normal dose data and tested on all dose levels. All experiments are done with and without Bilateral filtering.

3.4. Results

Table 6 shows the results of the detection step for the various dose levels. Bilateral filtering reduces false positives with 33% on all dose levels, with only a small decrease in by-CT-polyp sensitivity (2% for polyps larger than 6 mm) of mainly the small polyps.

Table 6: Results for the detection step. In parenthesis the total number of polyps found at colonoscopy and confirmed by CT are given.

Dose level	Filtering	Polyps 1-5 mm	Polyps 6-9 mm	Polyps 10-19 mm	Polyps > 20 mm	Amount of false positives
Normal	None	36 (38)	26 (29)	24 (24)	7 (7)	134
Low	None	35 (38)	26 (29)	24 (24)	7 (7)	163
Ultra low	None	36 (38)	26 (29)	24 (24)	7 (7)	312
Normal	Bilateral	34 (38)	25 (29)	24 (24)	7 (7)	97
Low	Bilateral	32 (38)	25 (29)	24 (24)	6 (7)	109
Ultra low	Bilateral	32 (38)	25 (29)	24 (24)	7 (7)	201

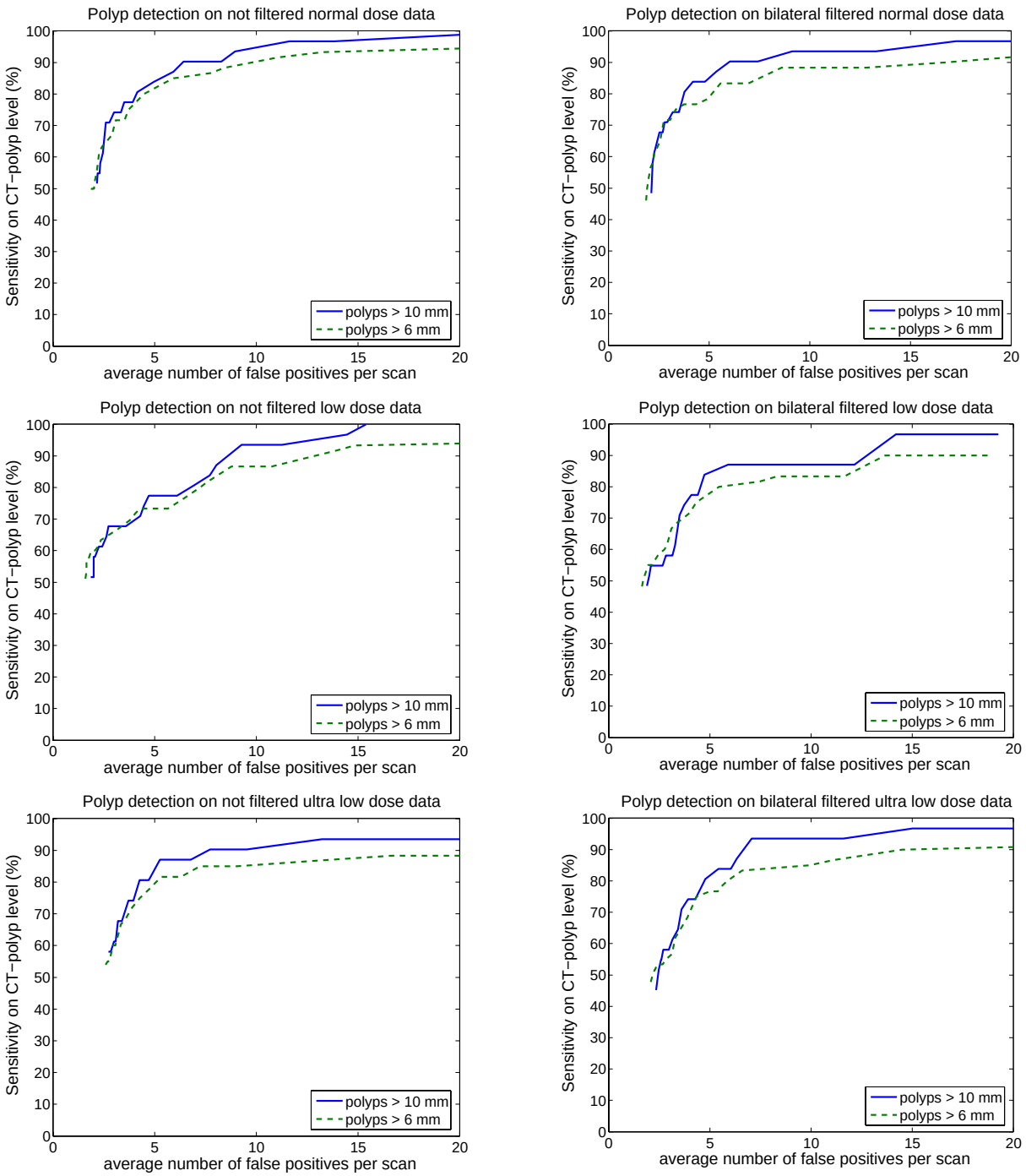

Figure 3: Free-response Receiver Operating Characteristic curves (FROC curves) show the results of the polyp detection algorithm using an optimal feature set per dose level. Left column: not filtered data. Right column: Bilateral filtered data. From top to bottom: normal dose (average 70 mAs), low dose (6,25 mAs) and ultra low dose (1.39 mAs).

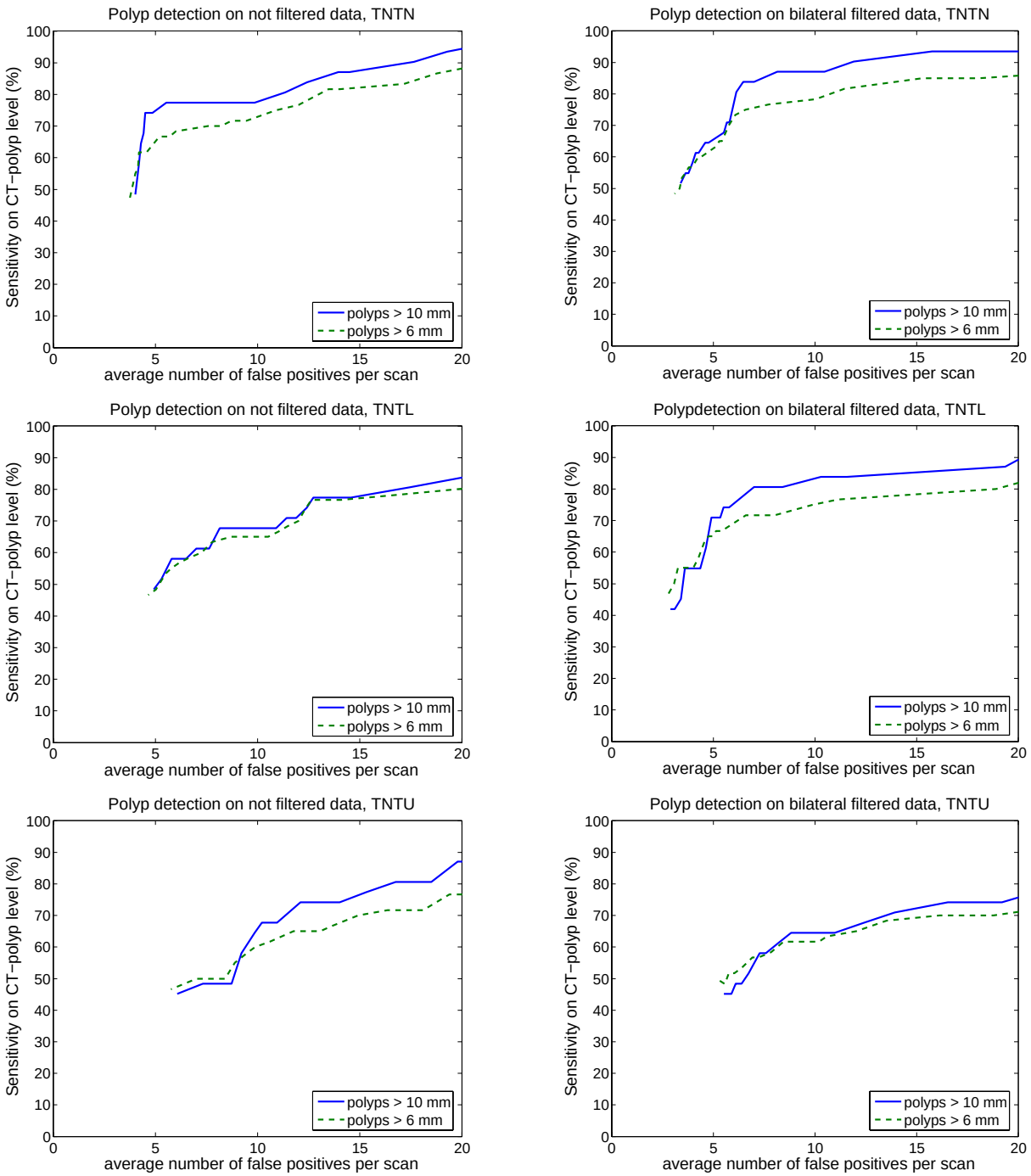

Figure 4: Free-response Receiver Operating Characteristic curves (FROC curves) show the results of the polyp detection algorithm using one robust feature set for all dose levels. Left column: not filtered data. Right column: Bilateral filtered data. From top to bottom: normal dose (average 70 mAs), low dose (6,25 mAs) and ultra low dose (1.39 mAs). TNTN means train on normal dose, test on normal dose; TNTL means train on normal dose test on low dose; TNTU means train on normal dose test on ultra low dose.

Figures 3 and 4 show Free-response Receiver Operating Characteristic curves (FROC-curves) for both experiments on all dose levels and with and without Bilateral filtering. The difference between the results in Table 6 and Figures 3 and 4 is the linear classifier that was used to further eliminate false positives. The decision point between polyp class and non-polyp class is variable and can be changed to make the algorithm more or less conservative. This gives us multiple working points with a sensitivity and corresponding number of false positives, these are plotted in the FROC-curves and linear interpolated.

Features calculated on Bilateral filtered data show less deviation when decreasing the dose than the unfiltered data, which enables more features to be used to reduce false positives. In these experiments the amount of features in the false reduction step was kept constant at 4 features for Bilateral and not filtered data. However for the Bilateral filtered data more features could be used. The results for Bilateral filtered data appear slightly better than for not filtered data. Table 7 summarizes the *by-polyp* sensitivities for the two experiments using Bilateral filtering.

Table 7: Results CAD algorithm when using Bilateral filtered data of varing dose levels. By-polyp sensitivity for various polyps sizes is given. Training was done on normal dose Bilateral filtered data.

Data	Polyps < 6 mm	Polyps 6-9 mm	Polyps > 9 mm	FP/scan
Normal dose, optimal CAD	61%	80%	97%	5
Low dose, optimal CAD	64%	81%	85%	5
Ultra low dose, optimal CAD	64%	75%	97%	5
Normal dose, robust CAD	68%	75%	95%	7
Low dose, robust CAD	64%	75%	84%	7
Ultra low dose, robust CAD	60%	65%	78%	8

4. CONCLUSION AND DISCUSSION

Computer-aided polyp detections gives acceptable performance (at least 80% by-CT-polyp sensitivity for polyps larger than 10 mm at 5 false positives per scan) on all dose levels tested in this report, ranging from 1.39 to 100 mAs. Using bilateral filtering has advantages. First of all Bilateral filtering reduces initial candidate polyps with 33% with only a small decrease in by-CT-polyp sensitivity (2% for polyps larger than 6 mm) of mainly the small polyps. Second, features calculated on Bilateral filtered data are more robust to dose. Third, using Bilateral filtered data the results for one CAD system for all dose levels performs better than when using not filtered data.

Optimizing the computer-aided polyp detection algorithm for a specific dose level results in good performance on all dose levels. Good performance means in this case almost 100% by-polyp sensitivity at 5 false positives per scan for polyps larger than 9 mm.

Building one computer aided polyp detection algorithm for all dose levels results in good performance on all dose levels. Compared to the optimal features the sensitivity is lower and the average number of false positives per scan is slightly higher.

Large multi-site studies should still confirm the use of computer aided polyp detection in combination with ultra low dose CT colonography for the early detection of colorectal cancer.

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