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Removal of bone in CT angiography of the cervical arteries by piecewise matched mask bone elimination

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In maximum intensity projection (MIP) images of CT angiography (CTA) scans, the arteries are often obscured by bone. A bone removal method is presented that uses an additional, nonenhanced scan to create a mask of the bone by thresholding and dilation. After registration of the CTA scan and the additional scan, the bone in the CTA scan is masked. As the cervical area contains bones that can move with respect to each other, these bones are separated first using a watershed algorithm, and then registered individually. A phantom study was performed to evaluate and quantify the tradeoff between the removal of the bone and the preservation of the arteries contiguous to the bone. The influence of algorithm parameters and scan parameters was studied. The method was clinically evaluated with data sets of 35 patients. Best results were obtained with a threshold of 150 HU and a dilation of 8 in-plane voxels and two out-of-plane voxels. The mean width of the soft tissue layer, which is also masked, was approximately 1 mm. The mAs value of the nonenhanced scan could be reduced from 250 mAs to 65 mAs without a loss of quality. In 32 cases the bones were registered correctly and removed completely. In three cases the bone separation was not completely successful, and consequently the bone was not completely removed. The piecewise matched mask bone elimination method proved to be able to obtain MIP images of the cervical arteries free from overprojecting bone in a fully automatic way and with only a slight increase of radiation dose. © 2004 American Association of Physicists in Medicine.

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I. INTRODUCTION

Arteries and veins can be visualized in a minimally invasive way with CT angiography (CTA). Resulting data sets are often visualized by means of maximum intensity projection (MIP) images. In a CTA data set, however, the maximum value along a line in the direction of projection is often that of bone, which obscures the vessels; therefore, the voxels that represent bone have to be removed from the data set, prior to the generation of the MIP image.¹⁻³ We present a method to remove the bone in a fully automatic way.

Because arteries are often in close proximity of the bone, for example, in the skull base and near the vertebrae, manual removal of bone can be time consuming or virtually impossible. Methods that use image processing techniques such as thresholding and region growing to identify the bone, have been reported as an alternative.⁴⁻⁹ As CT values of the edges

of the bones are in the same range as the CT values of the contrast-enhanced arteries, these techniques are prone to the choice of parameters. Thresholding images that contain contrast-enhanced arteries implies the use of a rather high threshold. Therefore, several post-processing steps (e.g., dilation) may have to be used in order to remove the bone sufficiently. This may also affect the contrast-enhanced structures. Even then the quality of the bone removal may be mediocre, especially in regions with thin bone structures that have not been included in the initial mask.

Our approach is to use an additional scan to make a mask. This scan is made prior to the injection of contrast agent; therefore, a relatively low and constant threshold can be used to acquire the mask. This initial mask is already of good quality, so that only one dilation step has to be used. This approach, called matched mask bone elimination (MMBE), has been introduced for CTA examinations of the Circle of

Willis.¹⁰ Alternatively, subtraction of the nonenhanced scan has been reported.^{11,12} A disadvantage of subtraction of two scans is that the noise of the two scans is added. With MMBE, the original quality of the CTA images is retained.

Due to inevitable motion of the patient in between the two scans, the CTA data set and the additional data set have to be registered. A restriction of the original MMBE method is that it is only applicable to volumes containing a single rigid bone structure. This is a considerable limitation, since a volume may contain multiple bones that can move with respect to each other (e.g., in the neck region). In this paper, an improved method is introduced to be able to register volumes containing multiple bones. In this method, called piecewise MMBE, the bones are separated first and then registered individually.

The internal carotid arteries and the vertebral arteries are often very close to bone; therefore, it is essential to find the correct balance between the removal of the bone and the preservation of these arteries. We evaluated the influence of the parameters of the CT scans and the parameters of the piecewise MMBE method on the quality of the removal of the bone in the MIP images and the integrity of the arteries in the CTA images. Finally, the performance of the piecewise MMBE method was evaluated in a clinical setting with CTA examinations of the cervical arteries of 35 patients.

II. PIECEWISE MMBE METHOD

A. Overview

The piecewise MMBE method uses two CT data sets. The first data set $B(\mathbf{x})$ is made prior to the injection of contrast agent. The second data set $C(\mathbf{x})$ is the contrast-enhanced CTA data set. In $B(\mathbf{x})$ and $C(\mathbf{x})$, $\mathbf{x}=(x,y,z)$ is the discrete coordinate of a voxel in the depicted volume.

The method consists of three steps (see Fig. 1). The first step is a registration step to compensate for movements of the patient between the scans. For this purpose the bones in the nonenhanced data set $B(\mathbf{x})$ are identified, separated and registered individually with the corresponding bones in the contrast-enhanced data set $C(\mathbf{x})$. Next, the bone voxels in the registered nonenhanced data set are converted to a mask. Finally, the corresponding voxels in the contrast-enhanced data set that belong to the mask are given an arbitrary low value. The masked data set is used to make MIP images of the arteries. In the following we describe the piecewise MMBE method in more detail.

B. Identification and separation of the bones

Each bone in the nonenhanced data set is surrounded by soft tissue with relatively low CT values. However, at a considerable number of locations, only a small distance between the bones is present. Because of the spatial blurring of the CT imaging process, the voxels that represent soft tissue have relatively high CT values at these locations. In Fig. 2 this is illustrated for a small region of the skull base and the adjoining vertebra.

The separation of the individual bones is done by using a watershed algorithm.¹³ The implementation of the algorithm by the National Library of Medicine Insight Segmentation and Registration Toolkit is used. It is applied to the inverted three-dimensional (3D) CT data set [Fig. 2(c), bottom curve]. The algorithm separates the volume into so-called catchment basins. A catchment basin is defined as a set of voxels whose paths of steepest descent terminate at the same local minimum of the input data. In order to speed up the watershed algorithm, the nonenhanced data set is clipped first, so that the initial number of catchment basins is significantly reduced. Voxels with CT values lower than $b_{\min}$ are set to $b_{\min}$. Voxels with CT values higher than $b_{\max}$ are set to $b_{\max}$. The value of $b_{\min}$ should assure that both the transition region from bone to tissue is not affected and that all soft tissues are set to a constant value. In order to avoid that contiguous bones are merged, the upper boundary $b_{\max}$ should be considerably higher than the highest CT value of soft tissue between these bones. The depth of a catchment basin is defined as the difference between the value of the local minimum and the lowest value at the boundary of the basin. The number of basins is reduced by merging relatively shallow basins. The amount of merging m determines the minimal depth of a catchment basin. It can be set between 0% and 100% of the difference $b_{\max} - b_{\min}$.

The output of the watershed algorithm consists of a volume with N labeled regions of connected voxels. We will refer to these regions by R_i , with $i=1,2,\dots,N$. In Fig. 2(b) an example of two separated bones is shown. In Fig. 2(c) the positions of the boundaries between the regions are given by the dashed vertical lines. Ideally, the number of regions N equals the number of bones.

C. Registration of the bones

For an accurate determination of the mask, both the bones and the transition zone from bone to surrounding tissue, has to be available in the registered nonenhanced data set. Therefore, the whole region R_i containing each bone and the surrounding soft tissue is registered.

In the registration procedure, voxels are used that lie at the edges of the bones. These voxels are obtained by selecting all voxels with CT values in a certain interval $[s_{\min}, s_{\max}]$ in both images. The collection of selected voxels in the non-enhanced data set $B(\mathbf{x})$ and contrast-enhanced data set $C(\mathbf{x})$ is denoted by S_B and S_C , respectively.

The registration is performed in three steps. In each step a transformation, consisting of translation in three directions and rotation around three axes, is determined by minimization of a cost function that depends on the six parameters of the transformation. For the minimization of these cost functions, the downhill simplex method is used.¹⁴ In the first two steps, the chamfer matching method is used.¹⁵ For that purpose a template $D(\mathbf{x})$ is made of the contrast-enhanced data set. $D(\mathbf{x})$ is the distance between a voxel coordinate $\mathbf{x}$ and the closest selected bone voxel in S_C . To reduce computation time the city-block distance is used.¹⁵

FIG. 1. The piecewise MMBE method illustrated with coronal images of the neck region of a patient. The method uses two CT scans: (a) a nonenhanced and (b) a contrast-enhanced scan. First, the bones in the nonenhanced data set are registered with those in the contrast-enhanced data set, resulting in (c) a registered nonenhanced data set. Next, the bone in the registered nonenhanced data set is converted to (d) a mask. Finally, the corresponding voxels in the contrast-enhanced data set are given (e) an arbitrary low value and (f) a MIP image can be made.

In the first step, the transform T_1 is determined that describes the overall motion of all bones between the two scans by minimizing the cost function

$$F_1(T_1) = \sum_{x \in S_B} D(T_1 \mathbf{x}), \quad (1)$$

which represents the mean distance between the transformed bone voxels in the nonenhanced data set and those in the contrast-enhanced data set. Next, each bone i is registered individually by an additional transform $T_{2,i}$, which is concat-

enated with T_1 . The cost function of the second step is given by

$$F_{2,i}(T_{2,i}) = \sum_{x \in S_{B,i}} D(T_{2,i} T_1 \mathbf{x}), \quad (2)$$

with $S_{B,i} = S_B \cap R_i$. In the third and final step, an additional transformation $T_{3,i}$ is determined for each bone, which registers the bone with a higher accuracy. In this step, the sum of squared differences of the CT values, given by

FIG. 2. Separation of bones by the watershed algorithm. (a) Sagittal image of a detail of the skull base and the upper vertebra. (b) Separated bones. Each gray value represents a region R_i . (c) CT values along the vertical line depicted in (a). The voxels that represent soft tissue have a relatively high CT value at locations between the bones (arrow). The bottom profile depicts the input for the watershed algorithm. The dashed vertical lines give the locations of the transition from one region to the other.

$$F_{3,i}(T_{3,i}) = \sum_{x \in S_{B,i}} [B(x) - C(T_{3,i}T_{2,i}T_1x)]^2, \quad (3)$$

is used as cost function. Trilinear interpolation is used in the matching method.

D. Conversion of bone to a mask

The mask is constructed by thresholding the registered nonenhanced data set, followed by dilation. Due to the spatial blurring of the CT imaging process, soft tissue voxels directly adjacent to bone have relatively high CT values. Since these CT values are in the range of the CT values of contrast-enhanced blood, they hinder the visualization of the arteries on a MIP image. For the determination of the mask, the threshold should preferably be only marginally above the CT value of tissue. However, tissue has varying CT values and noise is present in the measured CT values. Consequently, the use of a threshold value that is too low leads to masking of voxels in isolated tissue areas that may include arteries. Therefore, the threshold level should exceed a minimum value. After thresholding, some of these small isolated

regions may still be present. Therefore, the volume of each isolated region should exceed a lower limit $V_{\min}$, before it is included in the mask. The results are not expected to be sensitive for the precise value of $V_{\min}$ because the volume of a bone is a few orders of magnitude larger, and the volume of a noise cluster is an order of magnitude smaller. Finally, a binary dilation is applied to mask adjacent voxels with CT values that are lower than τ , but still may hinder the visualization of the arteries.¹⁶ The amount of dilation is denoted by the number of voxels d that is added to each voxel of the initial mask obtained by thresholding. The values of τ and d are chosen with the aid of a phantom study (see Sec. III B).

III. EXPERIMENTS

A. Overview

A phantom study was performed to evaluate and quantify the tradeoff between the removal of the bone and the preservation of the arteries contiguous to the bone. This study allowed us to make a clear choice for the threshold level τ and the amount of dilation d .

In a patient study, the performance of the complete piecewise MMBE method was evaluated, both with respect to the robustness of the procedure and the quality of the MIP images that were obtained.

All scans were made with a multislice CT scanner (Mx8000 Quad; Philips Medical Systems, Best, Netherlands). Scans were made with a tube voltage of 120 kV and a rotation time of 0.75 s. Reconstructions were made with a 180° interpolation algorithm¹⁷ and a voxel size of $0.29 \times 0.29 \times 0.50$ mm³. The remaining scan and reconstruction parameters for both the phantom study and patient study are listed in Table I. In the following we describe the scans and studies in more detail.

B. Phantom study

A phantom consisting of a human skull embedded in a synthetic material was used. The CT value of the synthetic material is approximately 150 HU, which is roughly 100 HU higher than the soft tissue *in vivo*. The phantom did not contain any arteries or contrast agent. This did not affect the relevance of the study because the purpose was not to test the visualization of arteries but to quantify the quality of the removal of bone. For the sake of clarity we still use the terms nonenhanced and contrast-enhanced to describe the CT scans of the phantom.

A number of scans were made that were evaluated pairwise. Each pair of scans mimicked the clinical situation of a nonenhanced and contrast-enhanced CT scan. Between the nonenhanced and contrast-enhanced scans, the phantom was slightly displaced in a random way to mimic the clinical situation, in which small motions of the patient between scans are often present. We studied the influence of the mAs value of the nonenhanced CT scan and the pitch value of both scans on the quality of the mask (see Table I).

From each of the nonenhanced scans a mask was calculated for different threshold levels τ and amounts of dilation

TABLE I. List of the scan and reconstruction parameters used for the phantom study and patient study.

Parameter (unit)	Phantom study		Patient study
	True bone voxels	Optimization	
Scan mode	Ultrahigh ^a	High	High
Number of detector rows $\times$ collimation per row (mm)	2×0.5	4×1	4×1
Pitch	0.375	0.375/0.875	0.875
Tube charge nonenhanced scan (mAs)	not applicable	35/70/140/280	65
Tube charge contrast-enhanced scan (mAs)	2000 ^b	280	250
Full width at half-maximum of in-plane point spread function (mm)	0.6	1.3	1.3

^aSmall focal spot and additional collimation between the detectors.^bFour consecutive scan of 500 mAs were averaged.

d. The threshold level τ was varied between 190 and 300 HU, with increments of 10 HU. Threshold levels below 190 HU produced unsatisfactory results for nonenhanced scans made with 280 mAs, because regions of soft tissue, connected to the bone region, were included in the mask. The lowest threshold that produced acceptable quality of the mask increased somewhat with decreasing mAs level. Therefore at 140, 70, and 35 mAs, minimum thresholds of 200, 210, and 220, respectively, were used. The following values for the amount of dilation d were investigated: 0 (no dilation), 4 (adjacent voxels in the scan plane), 6 (all adjacent voxels), 10 (8 in the scan plane plus 2 adjacent out of plane), 18 (8 in the scan plane plus 10 out of plane) and 26 (all surrounding voxels). The bone in the contrast enhanced data sets was masked and MIP images were made on the coronal plane.

The quality of a mask depends both on the amount of removed soft tissue in the vicinity of the bone and on the quality of the MIP images. For the quantification of the quality of the mask both the collection of true bone voxels and the ground truth of the MIP image had to be known. Because there was now way to separate the bone and synthetic material of the phantom exactly, the determination of true bone voxels could only be done approximately. A reasonable approximation was obtained by scanning the phantom with ultra high spatial resolution. The parameters for this scan are

listed in Table I. A region of interest (ROI) was chosen and investigated further [see Fig. 3(a)]. The true bone voxels in this ROI were determined by thresholding with a threshold of 860 HU, which is halfway between the maximum CT value of bone in the ROI and the mean CT value of the synthetic material.¹⁸

We determined the ground truth of the MIP image by masking the bone in the contrast-enhanced data set thoroughly. The mask was obtained by thresholding the ultrahigh resolution data set at 230 HU and binary dilation of the result with a spherical kernel with a radius of 3 mm. The resulting ground truth MIP image is an almost uniform image with an intensity slightly above the mean CT value of the synthetic material.

For each voxel at the edge of the mask, the minimal euclidian distance w between this voxel and the edge of the bone was determined in order to quantify the thickness of the soft tissue layer contiguous to the bone removed by the mask. The mean value of w for all edge-voxels in the region of interest is denoted by $\bar{w}$. For each pixel in the coronal MIP image, the difference v between the CT value in this MIP image and the CT value in the ground truth MIP image was determined. The quality of the MIP image was quantified by calculating the mean value $\bar{v}$ over all pixels. The definitions of these parameters are listed in Table II.

C. Patient study

For the clinical evaluation of the piecewise MMBE method CTA scans of 35 patients were used. Scans were made because of the suspicion of either carotid stenosis, oc-

FIG. 3. Images of the region of interest of $23 \times 23 \text{ mm}^2$, which is investigated in the phantom study. Window center: 100 HU. Window width: 650 HU. (a) Image of the contrast-enhanced scan (280 mAs, pitch 0.875). (b) As (a), with the true bone voxels indicated with dark gray. The remaining white voxels represent synthetic material, but have a high CT value due to the spatial blurring of the CT imaging process. (c) As (a), with a mask with $\tau=235$ HU and $d=10$ voxels using 280 mAs for the nonenhanced scan. The mask voxels included by thresholding are light gray; the mask voxels included by dilation are black.

TABLE II. List of the parameters that were used to quantify the quality of the mask.

Parameter	Symbol (unit)
Difference in pixel value in MIP and value of corresponding pixel in ground truth MIP	v (mm)
Mean value of v in coronal MIP image	$\bar{v}$ (mm)
Minimal distance from voxel at edge of the mask to edge of the bone	w (mm)
Mean value of w in ROI	$\bar{w}$ (mm)

TABLE III. List of the values of the piecewise MMBE parameters that were used in the patient study. The values for τ and d were chosen with the aid of a phantom study (see Sec. IV A).

Part of method	Parameter	Symbol	Value used (unit)
Separation of the bones	Lower clipping level	$b_{\min}$	100 (HU)
Upper clipping level	$b_{\max}$	1600 (HU)	
Merging level	m	70 (%)	
Registration of the bones	Lower boundary	$s_{\min}$	600 (HU)
Upper boundary	$s_{\max}$	800 (HU)	
Conversion of bone to a mask	Lower boundary for inclusion in mask	τ	150 (HU)
Minimal volume of included region	$V_{\min}$	40 (mm ³)	
Amount of dilation of the mask	d	10 (adjacent voxels)	

clusion, or dissection of the carotid or vertebral arteries. Scanning is started at the level of the disk space between the sixth and seventh cervical vertebra and continues cranially including the skull base. Patients were instructed to breathe quietly without swallowing during scanning. Nonionic contrast material containing either 300 mg of iodine per milliliter (Iohexol; Omnipaque; Nycomed, Oslo, Norway) or 320 mg of iodine per milliliter (Iodixanol; Visipaque; Amersham Health) was injected in a cubital vein at 4 ml/s. First, the delay between contrast injection and enhancement of the arteries of interest was measured by injecting a small amount of contrast agent and measuring the time to peak for the mean CT value of blood at a fixed location in the patient. Next, a total of 120 ml contrast agent was injected and scanning was started after the measured delay.

The values of the parameters of the MMBE method that were used in the patient study are listed in Table III. In the original MMBE method good registration results were obtained with $s_{\min}=600$ HU and $s_{\max}=800$ HU; therefore, these values were used in the piecewise MMBE method as well. For relatively large structures the number of selected voxels in S_B and $S_{B,i}$ easily exceeded one million. To reduce the computation time, a random sample of 50 000 voxels of S_B and $S_{B,i}$ was used when evaluating the cost functions in Eqs. (1)–(3). This did not affect the registration results.

To be able to assess the advantages of the piecewise method over the original MMBE method, the latter was applied here as well. The completeness of the identification and separation of the bones was visually inspected and the quality of the bone removal was judged from MIP images on the coronal plane.

IV. RESULTS

A. Phantom study

In Fig. 4 MIP images on the coronal plane are shown for the ground truth and for eight masks obtained with different combinations of threshold value τ and amount of dilation d . Furthermore, the corresponding values for $\bar{v}$ and $\bar{w}$ are given. For lower thresholds and more dilation the difference $\bar{v}$ is smaller. From Fig. 4 we conclude that the quality of MIP images with $\bar{v}$ values of approximately 40 HU or more are unacceptable. For these values large amounts of bone remain. Preferably, $\bar{v}$ has to be in the order of 20 HU or less.

In Fig. 5 the relation between $\bar{v}$ and $\bar{w}$ is shown for different combinations of τ (threshold value) and d (number of voxels dilation). The nonenhanced scans were made with 280 mAs. For pitch 0.375, data are shown for $d=0$ voxels only (filled triangles). For pitch 0.875, data are shown for $d=0, 4, 6, 10, 18$, and 26 voxels. In case no dilation is applied, the quality of the mask for pitch 0.375 is slightly better than for pitch 0.875 (smaller values of both $\bar{v}$ and $\bar{w}$). For masks with dilation $d>0$, the quality is approximately equal for pitch 0.375 and pitch 0.875 (not shown). If the threshold value τ is lowered for a fixed amount of dilation d , the value of $\bar{v}$ decreases (better MIP quality) and the mean width $\bar{w}$ of the masked soft tissue layer increases. If the amount of dilation d is lowered for a fixed threshold value τ , again the value of $\bar{v}$ decreases and the mean width $\bar{w}$ increases. From Fig. 5 it is clear that for a fixed quality of the MIP image $\bar{v}$, the width of the masked tissue layer $\bar{w}$ depends on τ and d . In the region of acceptable MIP images (i.e., $\bar{v}<40$ HU) minimal values for $\bar{w}$ are obtained using dilations d of 10, 6, or 4 voxels. Any of the combinations $(\tau, d)=(205, 4)$, $(225, 6)$, and $(235, 10)$ will produce MIP images with $\bar{v}\approx 20$ HU and a minimal value for $\bar{w}$. A higher threshold value τ , how-

FIG. 4. MIP images after masking for different combinations of threshold τ and amount of dilation d . Top: ground truth MIP image. The numbers on the right represent τ (HU), d (voxels), $\bar{v}$ (HU), and $\bar{w}$ (mm). Images are ordered according to the value of $\bar{v}$. Window center: 180 HU. Window width: 200 HU.

FIG. 5. Relation between $\bar{v}$ and $\bar{w}$ for different combinations of threshold τ , amount of dilation d , and pitch. The symbols represent different amounts of dilation. Pitch 0.875: $\blacktriangleright$ 0 voxels. Pitch 0.875: $\triangleright$ 4 voxels; $+$ 6 voxels; $\square$ 10 voxels; $\triangleleft$ 18 voxels; $\times$ 26 voxels. For each amount of dilation data are given for $\tau=190, 200, \dots, 300$ HU (see numbers in graph). The nonenhanced scans were made with 280 mAs.

ever, produces less isolated noise regions (see Sec. II D); therefore, we had a preference for $d=10$ voxels.

In Fig. 6 the influence of the mAs value on the quality of the mask is shown for pitch 0.875 and $d=10$ voxels. The quality of the mask was approximately equal for all mAs values. Consequently, the nonenhanced CT scan can be made with a lower mAs value without a loss of quality.

B. Patient study

A final choice had to be made on the desired quality of the MIP images and, consequently, the width of the masked soft tissue layer. The CT scans of the phantom lacked the contrast-enhanced vessels; therefore, the desired quality of

FIG. 6. Value of $\bar{v}$ and $\bar{w}$ for different mAs values of the nonenhanced scan: $\triangleright$ 280 mAs; $+$ 140 mAs; $\square$ 70 mAs; $\circ$ 35 mAs. Threshold value $\tau=190, 200, \dots, 300$ HU. Amount of dilation $d=10$ voxels. Pitch 0.875. The dashed lines depict the combination of $\bar{v} \approx 20$ HU and $\bar{w} \approx 1$ mm at $\tau=235$ HU.

FIG. 7. Histogram of the CT values of soft tissue in the head and neck region of a patient and of the CT values of the synthetic material in phantom data. The dashed line represents the scaled histogram for the phantom shifted to the left by 85 HU. The patient and phantom were scanned with 65 and 70 mAs, respectively.

the MIP images was determined with the clinical CTA scans. As the amount of dilation of $d=10$ voxels was most favorable (see Sec. IV A), the choice came down to a choice for the value of τ . After discussion with the radiologists it appeared that a suitable quality of the MIP images was obtained with $\tau_{in vivo}=150$ HU.

Because the CT values of the synthetic material in the phantom study were higher than the CT values of soft tissue *in vivo*, the value $\tau_{in vivo}$ had to be increased accordingly when used in the phantom study. In Fig. 7 the histograms of the CT values of the synthetic material of the phantom and the CT values of soft tissue in a clinical CT scan are shown. For the thresholding step, the right tails of these distributions are of decisive importance. A shift to the left of 85 HU of the distribution of the synthetic material appeared to let the right tail of this distribution coincide with the right tail of the distribution of the soft tissue *in vivo*. Thus, the choice of $\tau_{in vivo}=150$ HU can be converted to a choice of $\tau=235$ HU in the phantom study. From Fig. 6 it appears that $\tau=235$ HU (and $d=10$ voxels) corresponds with a value of $\bar{v}$ of approximately 20 HU and a mean width of the masked soft tissue layer $\bar{w}$ of approximately 1 mm.

In the watershed algorithm, the number of regions N varied from 11 to 50 regions for the 35 patients (mean value was 23 regions). The mean number of separate bones in the 35 data sets was in the order of 15 (skull, mandible, hyoid bone, five vertebrae, calcifications, and parts of the collarbones and scapula), which means that often there were more regions than bones. The additional regions were caused mainly by bones that were split up in two or more regions.

The hyoid bone and arterial wall calcifications (if present) were separated from the other bones in all cases. In Table IV a list is given of the success rates for the separation of the other bones. In 17 patients (49%) there were artifacts present in the images due to metal fillings in the teeth. An example is given in Fig. 8(a). These streak artifacts did not influence the

TABLE IV. Success rates of the separation of bones for 35 data sets.

Bones	Times successfully separated ^a
Skull-mandible	28 ^b (80)
Skull-upper vertebra	33 (94)
Vertebrae mutually	
All	4 (11)
Partly	19 (54)
None	12 (34)

^aData in parentheses are percentages.^bRemaining seven cases not separated due to metal fillings.

performance of the separation of the bones by the watershed algorithm. In 7 patients (19%), however, the mandible was connected to the maxilla via the hyperdense fillings and was not separated by the watershed algorithm [see Fig. 8(b)]. The upper vertebra was separated from the skull base in 33 patients (94%). A complete separation of all vertebrae was obtained in 4 patients (15%), and in 19 patients (54%) they were separated partially.

In comparison with the original MMBE method, the piecewise MMBE method resulted in MIP images with fewer remnants of bone, which obscure the arteries, in 17 cases (49%). In Fig. 9 an example is given of the difference between the original method and the piecewise MMBE method. This patient had moved his mandible in between the two scans. With the original method registration errors were present. With the piecewise method, which registered the mandible and vertebrae separately, a correct masking was obtained. For 15 patients (43%) the MIP images of the original MMBE method had virtually the same quality as the MIP images of the piecewise MMBE method. For these patients the bones evidently had not moved with respect to each other between the scans. For the remaining three patients (9%) the piecewise MMBE method did not mask all the bones correctly. In these cases two or more vertebrae had moved with respect to each other in between the scans and were not separated by the watershed algorithm. In Fig. 10 this is illus-

trated with a vertebra that was connected to three other vertebrae, causing a suboptimal registration of the bones with the piecewise MMBE method.

V. DISCUSSION

In this paper we described and evaluated the piecewise MMBE method for the removal of bone from CTA scans. The method is an extension of a method described earlier.¹⁰ It can cope with situations in which the data set contains bones that can move with respect to each other.

We performed a phantom study to optimize the mask parameters for each scan protocol. The quality of the mask increases when more bone is removed from the MIP image (smaller value of $\bar{v}$) and less soft tissue contiguous to the bone is removed (smaller value of $\bar{w}$). These requirements are conflicting. The value of $\bar{v}$ can be decreased at the cost of an increase of $\bar{w}$ and vice versa.

For the chosen clinical settings with a threshold of 150 HU and a dilation of 10 voxels, the mean width of the masked soft tissue layer was approximately 1 mm. Parts of arteries that were contiguous to the bone (e.g., the vertebral-lis) were therefore also masked. If an artery was affected, a large part of the lumen was preserved because the arteries were relatively large. However, if accurate measurement of a stenosis is desired, the CTA source images should be used.

When no dilation was applied ($d=0$ voxels) the quality of the mask appeared to be better for pitch 0.375 than for pitch 0.875. This can be explained by the influence of spiral reconstruction artifacts, which are more pronounced at pitch 0.875. We have shown that such artifacts are in general not equal in two otherwise identical scans that are made of the same object.¹⁹ Consequently, the mask obtained with the nonenhanced scan may have a slightly different shape compared to the shape of the bone in the contrast-enhanced scan. When dilation was applied, the differences in quality between both pitch values practically disappeared. Apparently, the dilation of the mask minimized the effects of these slight amounts of mismatch.

FIG. 8. Influence of artifacts induced by metal fillings on the separation of bones. (a) Axial image of the non-enhanced CT scan. The vertebra in the same axial plane as the metal is not connected to the mandible and/or the skull via the hyperdense streak artifacts. (b) Coronal image of the non-enhanced CT scan. The hyperdense metal fillings connect the mandible to the maxilla.

FIG. 9. MMBE results for different registration methods. (a) Cross-sectional MMBE image with the original method. (b) Cross-sectional MMBE image with the piecewise method. (c) Coronal MIP image with the original method. (d) Coronal MIP image with the piecewise method. With piecewise rigid registration the mandible and vertebrae are all registered correctly.

Apart from the values for the threshold level τ and amount of dilation d , which determined the amount of bone and contiguous tissue removed, the performance of the MMBE method was strongly influenced by the quality of the separation and registration of the bones. The parameters of the separation step and registration step (see Table III) were determined experimentally. It appeared that the quality of the separation and registration was not very sensitive for the exact value of the parameters. The exact value mainly influenced the computation time.

In this study the separation was performed by a watershed algorithm. The degree of separation could be chosen by set-

FIG. 10. MMBE results for different registration methods. (a) Coronal MIP image with the original method. (b) Coronal MIP image with the piecewise method. (c) Sagittal contrast-enhanced image after application of piecewise MMBE, showing slight mismatch because not all vertebrae were separated by the watershed algorithm.

ting the merging level m . After some experiments it appeared that a merging level of $m=70\%$ gave satisfactory results. In general, the algorithm successfully separated the bones that often move with respect to each other in between the two scans (e.g., the mandible and the skull or the upper vertebra and the skull). The vertebrae, however, could not be separated completely in 31 out of the 35 cases. Even if the merging level of the watershed algorithm was decreased considerably, the vertebrae remained connected. Luckily, the upper vertebrae appeared to be relative immobile with respect to each other and the registration of two or more vertebrae as one rigid structure generally did not have consequences for the quality of the match. In only 4 out of 35 patients (9%) the registration of the vertebrae was suboptimal. Somewhat unexpectedly, the original MMBE method did register the vertebrae in these cases correctly. In the original MMBE method each two-dimensional slice of the contrast-enhanced data set was registered separately with the 3D nonenhanced data set.¹⁰ Due to this approach the original registration method was, in a small number of cases, better able to cope with the relative movements of the vertebrae than the piecewise MMBE method was.

In 7 out of 35 cases the maxilla and mandible remained connected due to the presence of metal fillings. In case the mandible would have moved relatively to the other bones,

the registration would have been suboptimal. Luckily this was not the case. This problem can be remedied by automatically removing the metal and its direct surroundings prior to the separation of the bones. As no vascular structures of clinical interest are in close proximity to the metal fillings, this can be done without problems. The metal fillings, which have higher CT values than bone, can easily be identified by thresholding.

Besides bone, other high-attenuation structures such as calcifications, which may be present in the arterial wall, are removed in the masking method as well. We are aware of the fact that masking of calcifications may lead to an overestimation of the degree of stenosis. We previously described a method to remove calcifications from CTA data sets.²⁰ This method could be combined with the piecewise MMBE method to remove both bone and calcifications from CTA data in a correct way.

In this article the results of the MMBE method were presented with the aid of MIP images of the cervical arteries. The method can also be used in combination with other visualization techniques, such as shaded surface display and volume rendering. These techniques have in common with the MIP technique that the bone may hinder the visualization of the arteries.²¹ Furthermore, the method can be extended to CTA examinations in other parts of the body. As the parameters of the MMBE method have been optimized for CTA scans of the head and neck region, they should then be reconsidered.

We conclude that the piecewise MMBE method is a powerful tool to obtain MIP images of the cervical arteries free from overprojecting bone in a fully automatic way and with only a slight increase of the total radiation dose.

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