

Partially Rigid Bone Registration in CT Angiography

Martin Urschler¹, Hendrik Ditt², and Horst Bischof¹

¹Institute for Computer Graphics and Vision, Graz University of Technology, Austria
urschler@icg.tu-graz.ac.at, bischof@icg.tu-graz.ac.at

²Siemens Medical Solutions, CTE PA, Forchheim, Germany
hendrik.ditt@siemens.com

Abstract *Maximum intensity projection (MIP) studies of CT angiography (CTA) images are a widely used tool for artery and vein visualization especially in the brain. Due to their high CT intensity bone structures lead to visualization artifacts in MIP studies, therefore they have to be removed to get an undistorted view of the vessel structures. Often this removal is possible by a rigid registration step of an additional native scan to the contrast-enhanced CTA scan followed by a bone mask subtraction. This technique is also referred to as "Matched Mask Bone Elimination" [14]. However, sometimes several unrelated patient movements occur during and between contrast-enhanced and native scans. These intra- and inter-scan motion artifacts cannot be removed by a single rigid registration step. To address these problems in an efficient and general way we have developed a refinement of the "Matched Mask Bone Elimination" technique that incorporates a joint segmentation and registration method in an iterative fashion. We describe our experiments and show our qualitative and quantitative results in terms of decreasing numbers of misregistration voxels and sum of squared intensity differences on several large volume data sets of the head, where independent rigid movements have been successfully removed.*

1 Introduction

A maximum intensity projection (MIP) study of computed tomographic angiography (CTA) scans is a widely used imaging tool for artery and vein visualization especially in the brain. This method allows the detection of cerebral aneurysms, arterial stenosis, and other vascular brain anomalies. CTA studies are CT scans where a contrast agent is applied via intravenous injection. Often the contrast-enhanced scan is accompanied by a native scan to be able to support vessel visualization by subtraction techniques. More specifically, if one ignores intra- and inter-scan patient movement, CTA is performed by a subtraction of the native from the contrast-enhanced scan, leaving solely the vascular structures. The resulting data set is visualized in 3D using a MIP, where the maximum value in the CT volume data set is displayed along each ray through a pixel in the direction of the viewpoint projection (see Figure 1 for MIP examples).

In practice patient movement between native and contrast-enhanced scans often is inevitable. Therefore, a

subtraction algorithm has to deal with misregistered areas. Due to their high CT intensity especially misregistered bone structures lead to considerable visualization artifacts in MIP studies (see Figure 1 for examples). These artifacts have to be removed to get an undistorted view of the otherwise obstructed vascular structures. In many cases this removal is possible by a rigid registration of native to contrast-enhanced scan followed by a subtraction of a bone mask generated from the registered native scan. This technique is also referred to as "Matched Mask Bone Elimination" [14].

However, sometimes several independent patient movements occur during contrast-enhanced and native scans. Although each of the independent movements can be regarded as being rigid, the combination of these inter- and intra-scan motion artifacts cannot be effectively removed by a single rigid registration step. In the remainder of this paper we will refer to the problem of independently moving bone structures as a "partially rigid registration" problem. An example of independent movements is a slight head rotation combined with a different position of the jawbone due to swallowing or yawning between scans. Further, one can easily imagine that the problem of independently moving bone structures becomes even more important as soon as not only the head is involved in the CTA study but the vascular structures of interest are extended into the neck and shoulder region [7]. Independent shoulder movements due to e.g. an uncomfortable resting position of a patient additionally pose registration problems.

To address these problems we have developed a refinement of the "Matched Mask Bone Elimination" technique that incorporates a joint segmentation and registration method in an iterative fashion. Moreover our novel approach takes the large size of current routinely acquired CT scans into account. With volume data sets that consist of several hundred slices and an x-y resolution of 512 by 512 voxels memory and run-time issues are a challenge in the development of medical imaging algorithms.

The following section gives a literature review on existing techniques for bone removal in CTA applications. Next we describe our approach in more detail. Section 4 explains our experimental setup and shows the results of evaluating our algorithm on clinical data. The final section concludes the paper and gives an outlook on possible improvements.

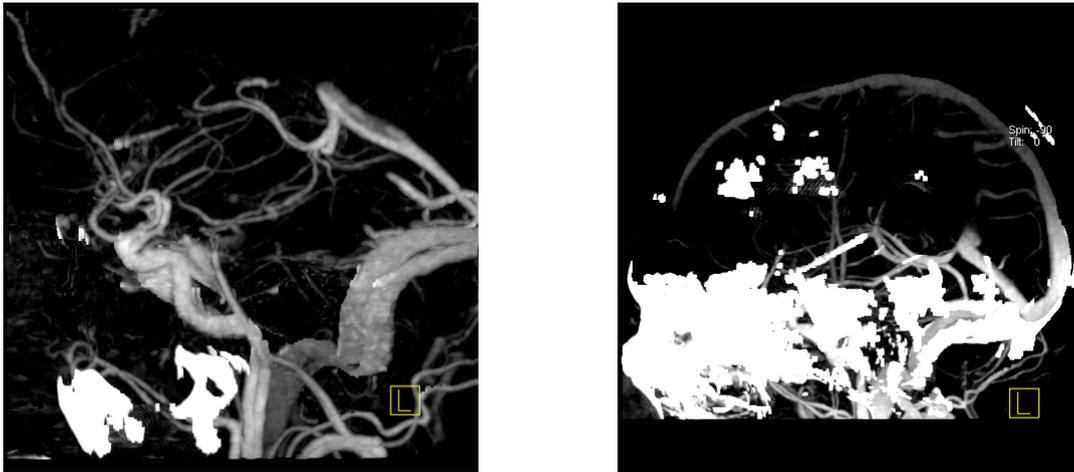


Figure 1: Maximum intensity projections of two different CTA data sets with bone artifacts obstructing vascular structures. Left image shows data set A with an independently moving jawbone. Right image shows data set D with intra-scan artifacts in the skull region.

2 Related Work

In the literature there are mainly three directions to solve the problems in CTA studies where the accurate removal of bone structures is necessary to get rid of obstructed vessels.

First, many publications make use of a rigid registration step with or without a subsequent nonlinear refinement stage. The approaches without refinement are of course not able to adapt to independently moving bone structures. The original "Matched Mask Bone Elimination" (MMBE) technique was proposed by Venema et al. [14] in 2001. The MMBE method finds in the native data set those bone voxels that correspond to bone voxels in the contrast-enhanced data set. Therefore, the two data sets are matched by a single automatic registration step involving a gray-value correlation similarity function and using a downhill simplex optimizer on the rigid transformation parameters. The registered images are combined to form a mask image which represents the bone voxels that have to be masked from the contrast-enhanced scan. In 2004 the same group published an extension of the MMBE method to deal with independently moving bone structures [13]. Their extended approach incorporates a watershed segmentation after the registration to separate the regions that can move independently with respect to each other. Finally the separated regions are registered individually to achieve a piecewise MMBE. They show that their method is able to improve bone removal results on several clinical data sets, however, there still remain problems due to its dependence on the success of the fragile segmentation step. Luboldt et al. [9] describe an "elastic" subtraction algorithm for CTA studies where a rigid registration step is followed by a nonlinear registration, however, few details are given in this paper. Two more bone removal techniques based on rigid registration may be found in Yeung et al. [15] who develop a combination of feature-extraction and optical flow method to estimate the rigid transformation and in Kwon et al. [6] who present a registration technique based on normalized mutual information. Both of them neglect the issue of independently moving bone structures.

Second, there are some publications that deal with the

partially rigid registration problem by using nonlinear (elastic) registration schemes with deformation constraints at rigid regions. Little et al. [8] locate rigid structures and treat them as being rigid for the registration while all other structures are treated as nonlinearly deformable. The nonlinear registration is performed by using manually selected landmarks and radial basis functions for displacement interpolation. The nonlinear registration model is weighted by using a distance map that specifies the distance to the rigid anatomical structures. Separation of rigidly and nonlinearly transformable parts is performed by a pre-segmentation of the rigid structures of interest. Disadvantages of the method are the need for manual selection of corresponding landmark points, the need for manual segmentation of the rigid structures and the choice of the elastic model that interpolates the displacements between landmarks. An extension of this approach has been published by Pitiot et al. [10] who remove the needs for manual segmentation and landmark selection by a block matching technique and a hierarchical clustering to extract independent pairs of subimages which are rigidly registered. Their approach was only shown on 2D images and would require a high computational effort for 3D volumes. Bentoutou et al. [2] have presented a feature-based matching and registration approach using a thin-plate spline elastic control point interpolation. Their algorithm works well on coronary DSA images. However, the capability to model large deformations like jawbone movement remains an open question. Another interesting approach based on deformable registration can be found in [11] but in this work the rigidity constraint is too weak for our purpose.

The final group of publications found in the literature uses segmentation techniques solely in the contrast-enhanced CTA scan. An overview of vessel tracking algorithms used for segmentation of vascular structures can be found in Felkel et al. [3]. Alyassin et al. [1] propose a semi-automatic bone segmentation involving thresholding, region growing and morphological operations. Kang et al. [5] also show a bone segmentation involving region growing based on local adaptive thresholds and morphological operations followed by a boundary refinement. All of

these approaches are prone to typical segmentation problems like leaking, unstable threshold selection procedures and the need for parameter tuning. Semi-automatic methods somehow overcome these problems but they add a lot of expert effort to each investigation. For these reasons we decided not to follow this direction any further.

3 Methods

This work presents a novel algorithm to prepare native and contrast-enhanced CTA images for MMBE. As mentioned in the previous sections, the algorithm has to deal with several problems which may be summarized as follows:

- Accurate registration of native and contrast-enhanced scans taking independently moving bone structures like e.g. inter-scan skull and jawbone movement into account.
- Accurate registration despite local intra-scan errors like rapid skull movements during a single acquisition.
- Memory- and runtime-efficiency due to large volume data sets of several hundred slices.

We decided to follow a similar direction like vanStraten et al. [13]. However, our approach replaces the error-prone watershed segmentation step by a more robust approach that uses joint segmentation and registration in an iterative fashion. Therefore, no high-level or semi-automatic segmentation step is necessary, the algorithm is based on the combination of low-level segmentations and rigid registrations. Our method guarantees that nonlinear deformations never occur at the bone structures but are solely used for tissue structures by a registration matrix interpolation step. The only important assumption that we have to make is that it is possible to rigidly register and remove independently moving bone structures in sequential steps, i.e. each registration step in the iterative loop has to remove a certain area of misregistration. If this assumption does not hold anymore the algorithm will terminate too soon. This situation might happen if two independent misregistration areas cancel each other out in terms of the registration metric.

The basic idea of the proposed algorithm is to iteratively perform rigid registration on areas where large misregistrations occur. The algorithm takes a native and a contrast-enhanced volume as input and starts with an initial mutual information based rigid registration that is restricted to bone structures segmented by a bone threshold. Calculating the misregistration error identifies areas where the registration has to be refined. This refinement is performed in an iterative manner as long as the number of misregistration errors is too large. Each iteration consists of calculating the misregistration area, a rigid registration step restricted to the current misregistered area and an interpolation step that combines the different registration results. Algorithm 1 shows this algorithm in pseudo-code, while the following subsections explain its behaviour in more detail.

3.1 Single Rigid Registration Step

Our technique consists of several rigid registration steps always using the same mutual information based matching

Algorithm 1 Partially Rigid Registration

- 1: Mutual information based rigid registration of native and contrast-enhanced scan
 - 2: Initialize data structure of resulting registration matrices with initial transform
 - 3: Calculate the misregistration area
 - 4: **while** size of misregistration area larger threshold **do**
 - 5: Derive a bone mask from the misreg. error area
 - 6: Mutual information based registration restricted to bone mask
 - 7: Update registration matrix data structure by checking if the new transform improves the error
 - 8: Smooth and interpolate registration matrices
 - 9: Update misregistration area
 - 10: **end while**
-

method. Mutual information based registration has become a standard method for rigid registration problems over the last decade [4]. It uses a measure from information theory, which is derived from the Shannon entropy measure $H(A)$ if an image A is regarded as consisting of a string of symbols, with each symbol having a certain probability of appearance. The expected amount of information $H(A)$ one can obtain from image A by probing the gray value of one (random) pixel is given by

$$H(A) = - \sum_{i=1}^N p_i \log(p_i).$$

Given two images A and B , the joint entropy $H(A, B)$ is defined as

$$H(A, B) = - \sum_{a=1}^N \sum_{b=1}^N p_{ab} \log(p_{ab})$$

and resembles the amount of information obtained from both images when probing pairs of gray values from the two images. If images A and B are totally unrelated, the joint entropy $H(A, B)$ is the sum of the individual entropies. Otherwise, the joint entropy is smaller than $H(A) + H(B)$. Joint entropy cannot be directly taken as a measure for image similarity in registration, since the estimated probabilities depend on the overlap of volumes which changes during registration. Therefore, joint probability has to be measured in relation to the individual entropies. The mutual information (MI) measure $I(A, B) = H(A) + H(B) - H(A, B)$ overcomes this problem. MI can qualitatively be thought of as measuring how well one image explains the other, it is maximized at optimal alignment. However, the classic MI measure does not fully solve all overlap problems during registration. In our algorithm we use the normalized MI measure

$$I(A, B) = \frac{H(A) + H(B)}{H(A, B)}$$

proposed by Studholme et al. [12] which is currently regarded as the state of the art MI measure for registration. Besides the normalized MI as image similarity metric a registration algorithm also needs an optimization strategy, an interpolation method and a transformation representation

that provides the parameters to be optimized. Our optimizer is a regular step gradient descent optimizer that takes larger steps at the beginning of optimization and consecutively reduces its step size until a local minimum is reached. The interpolation method is trilinear due to performance reasons. Finally our transformation is composed of six parameters, three representing 3D translation and the other three representing 3D rotation encoded as a unit quaternion.

3.2 Partially Rigid Registration - Initial Stage

The partially rigid registration algorithm starts with a threshold based bone segmentation of the contrast-enhanced CTA image. This bone segmentation is used as a mask restricting the following initial mutual information based registration procedure to bone structures. The result is a transformation which is stored as the initial transformation in the result data structure at bone voxel locations only. With this initial transformation it is possible to calculate a misregistration area by subtracting the accordingly warped native image from the contrast-enhanced image. Now the iterative stage is entered.

3.3 Partially Rigid Registration - Iterative Stage

The iterative stage terminates if the misregistration area is smaller than a certain threshold. The first step in this loop is the creation of another bone segmentation mask to restrict the subsequent mutual information registration. The bone segmentation mask is derived from the misregistration area, which is located at the edges of misregistered bone structures, by a dilation into the bones nearby using a distance-constrained region growing method. This dilation step can be seen as a bone segmentation procedure, however this bone segmentation is only used to focus the following registration step on misregistered areas. The restricted registration step results in another transformation which overwrites the result data structure after checking if the current transformation is able to reduce the misregistration at each bone voxel location. Now the transformation results have to be smoothed in local neighborhoods to remove some noise and to prepare the following transformation interpolation. Since the rigid transformations are only stored at bone voxel locations, it is necessary to find transformation parameters for tissue voxels. This can be performed by a linear or a nearest-neighbor interpolation. Although a linear interpolation would be more accurate, we decided to use nearest-neighbor interpolation due to reasons of reduced computation time and its low memory consumption. The evaluation section will show that the accuracy of nearest-neighbor interpolation is sufficient for our application. The final step in the iterative stage is the warping of the native to the contrast-enhanced image according to the transformation result data structure. The result can be used to calculate another misregistration which gets checked if it is larger than a threshold by the loop termination condition. After the loop has terminated the MMBE method is used to remove bone structures from the contrast-enhanced image.

3.4 Memory and Runtime Efficiency Issues

As already mentioned above the large size of current routinely acquired volume data sets always poses restrictions on practically useful algorithms due to runtime and memory

consumption issues. CT data sets the proposed algorithm is intended for easily have several hundred slices with x-y resolutions of 512 by 512 voxels respectively, thereby requiring around 250 MB in memory due to a 12 bit gray level resolution. Runtime efficiency requires the data sets to be fully held in memory, therefore it is important to reduce the need for intermediate data structures. The partially rigid registration algorithm only requires one additional volume data set of the same size as the two input images to store intermediate results. This can be achieved by representing bone segmentation results and registration error regions as single bits and by using indices into a list of possible transformation parameters to store the different registration results of the iterative algorithm. Since memory and time consumption always imposes some trade-off, we will show in the evaluation section that our runtime results are nevertheless acceptable.

4 Experiments & Results

The presented approach was evaluated on several CT data sets showing problems of state-of-the-art bone removal techniques for CTA images based on maximum intensity projections. All of these data sets still have problems after one single registration step for Matched Mask Bone Elimination (compare first row of Figure 3). More specifically we used 5 clinical data sets whose characteristics are shown in Table 1.

DS	Size	Problem Characteristics
A	512,512,231	independent head & jaw movement
B	512,512,344	independent head & jaw movement
C	512,512,429	head movement & teeth artifacts
D	512,512,233	intra- and inter-scan movements
E	512,512,269	swallowing and teeth artifacts

Table 1: Evaluation data set characteristics

Most of the data sets show several independent movements typical for CTA acquisitions. Data sets C and E also show some artifacts in the tooth regions due to implanted gold teeth disturbing the CT scans. In our experiments we calculate two measures from the data sets. The first one is the progression of the number of misregistration voxels during our algorithm. The number of misregistration voxels is calculated as the number of voxels which is larger than a threshold from the difference between contrast-enhanced and (partially) rigidly warped native image. Table 2 depicts this measure, note that data sets A and E finished earlier due to additional termination conditions in the main loop. The first column specifies this measure before registration. To restrict runtime the loop was terminated after four iterations.

DS	0	1	2	3	4
A	306 705	37 078	26		
B	208 846	94 601	991	926	801
C	53 443	9 007	6 529	6 514	5 755
D	164 939	136 603	19 165	14 347	14 189
E	26 868	9 036	5 387		

Table 2: Decrease of misregistration error voxels for evaluation data sets A-E

The second measure is the progression of the sum of squared

intensity differences (SSD) between the contrast-enhanced image CE and the warped native image N' according to the partially rigid registration transformations. The sum of squared intensity difference is calculated as

$$SSD = \frac{1}{|\Omega|} \sum_{\Omega} (CE(x, y, z) - N'(x, y, z))^2$$

where Ω is the domain of the overlapping part of the images. One should note that the SSD will never decrease to zero, since there are always contrast differences in the images due to contrast agent injection. Figure 2 shows the decrease of the SSD for the five data sets.

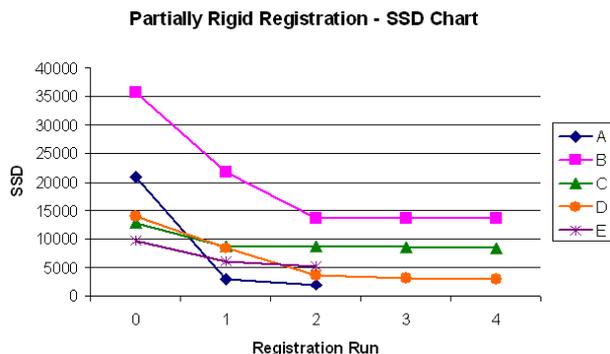


Figure 2: Decrease of sum of squared difference measure for evaluation data sets A-E

The execution times of the algorithm for data sets A,B,C,D and E were 93.25s, 233.95s, 276.02s, 205.67s and 93.27s, respectively. The algorithm implementation was performed under Windows in C++ and evaluation was executed on a Pentium M with 2.0 GHz and 1.5 GB RAM.

In Figure 3 the three data sets A,B and D are shown to give qualitative results as well. The first row is the MIP of each data set after a MMBE with a single rigid registration to take patient movement into account. One can clearly see the bright bone structures that obstruct several portions of the vascular structures. The second row shows the resulting MIP after a MMBE using the novel partially rigid registration procedure.

4.1 Discussion

Our experiments show very clearly that our proposed algorithm is capable to improve the MMBE method in those cases where several independent rigid movements occur during two scans in CTA studies. In all clinical test cases the sum of squared intensity differences and the number of registration error voxels is significantly reduced after one or two additional registration steps in our iterative algorithm. We observe that both measures are going into a converged state after a few iterations, therefore we decided to restrict the additional registration steps to at most three. Data sets A and B show the algorithms excellent behavior in the presence of independent head and jawbone movement. In data set A the obstructing structures have been completely removed, while data set B has improved a lot, although some very small regions still remain. Data sets C and E show the algorithms behavior in the presence of artifacts due to CT scan errors from gold teeth or due to a patient swallowing

during scans. Both effects do not have a great impact on the result, all obstructions are successfully removed. Finally data set D has inter- and intra-slice scanning errors which are also removed, however in this case a larger number of obstructing bone structures remains. An important property of the algorithm is that it never worsens a result if the registration is already accurate enough after a single registration step. So it is very suitable as an additional refinement step if the classical MMBE method does not succeed. The fact that the algorithm runtime lies between two and five minutes on a standard notebook computer underlines that the additional computational effort is acceptable.

5 Conclusion & Outlook

In a number of medical applications the removal of bone structures is of crucial importance for a high-quality CTA visualization using MIPs. This paper shows a novel algorithm for bone removal that addresses the problems of independent inter- and intra scan movements. It extends the classical MMBE algorithm by a joint segmentation and registration stage. The presented experimental results on clinical data sets show examples of intra- and inter-scan patient movements which were successfully registered with the proposed algorithm. The improved MIP visualization quality underlines the usefulness of our novel method, while the quantitative evaluation of the number of registration voxels and the progression of the sum of squared intensity differences proves the algorithms correct behavior.

After this first prototypical evaluation it will be necessary to perform a more thorough evaluation on a larger number of clinical data sets to show the relevance of our refinement algorithm. Another possible direction for future work is to look into more sophisticated algorithms for joint segmentation and registration like techniques working in a variational framework [16] or compare it to the elastic registration scheme in Bentoutou et al. [2].

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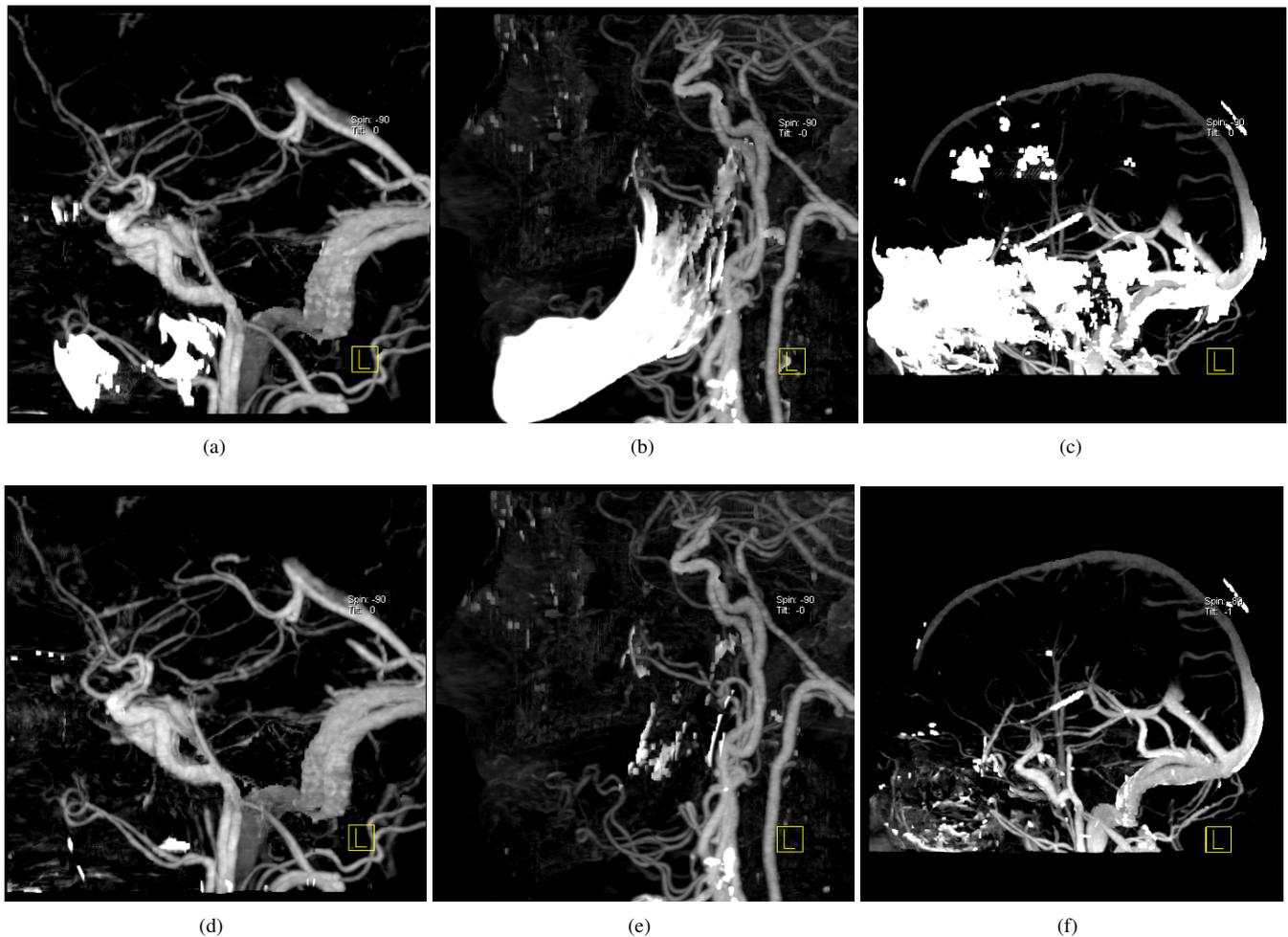


Figure 3: Selected results comparing the classical MMBE method (first row) with the improved MMBE method (second row) (a) data set A after original MMBE, (b) data set B after original MMBE, (c) data set D after original MMBE, (d) data set A after partially rigid registration MMBE, (e) data set B after partially rigid registration MMBE, (f) data set D after partially rigid registration MMBE

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