MEDINFO 2010
C. Safran et al. (Eds.)
IOS Press, 2010

doi:10.3233/978-1-60750-588-4-1268

Automatic Analysis of the Anatomy of Arteriovenous Malformations using 3D and 4D MRA Image Sequences

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Abstract

The cerebral arteriovenous malformation (AVM) is an abnormal connection between arteries and veins without capillaries in between, leading to increased blood pressure which might result in a rupture and acute bleeding. Exact knowledge about the patient's individual anatomy of the AVM is needed for improved therapy planning. This paper describes a method for automatic extraction of the AVM and automatic recognition of its feeders and draining veins and en passage vessels based on 3D and 4D MRA image sequences. After registration of the MRA datasets, the AVM is segmented using a support vector machine based on blood velocity information, a vesselness measure and the bolus arrival time. The extracted hemodynamic information is then used to detect feeders and draining veins of the AVM. The segmentation of the AVM was validated based on manual segmentations for five patient datasets, whereas a mean Dice value of 0.74 was achieved. The presented hemodynamic characterization was able to detect feeders and draining veins with an accuracy of 100%. In summary the presented approach can improve presurgical planning of AVM surgeries.

Keywords:

Intracranial arteriovenous malformations, Magnetic resonance angiography, Computer-assisted image analysis, Anatomy, Blood flow

Introduction

The cerebral arteriovenous malformation (AVM) is a disorder of cerebral vessels, represented by locally missing capillaries between the arterial and venous system [1]. The missing capillaries often lead to changes of the hemodynamic situation and especially increased blood pressure in the draining veins causing dilation, which in approx. 50% of all cases leads to a rupture and following acute bleeding [2].

The aim of AVM therapy is the disconnection of the AVM from the cerebral blood circulation coincided with rupture prevention. The therapy possibilities available include endovascular embolisation, neurosurgical resection, radiosurgery and a combination of these [2]. In any case the detection of the feeding arteries is of major interest. For risk estimation of surgical resections the Spetzler-Martin scale [3] is often used. Here the morphological parameters size and location of the AVM and its drainage patterns are used to classify the patient risk for persistent neurological deficits from neurosurgery according to five grades. Additionally the detection of en passage vessels, which are vascular structures close to the AVM but not directly connected, are important for therapy planning since impairment should be avoided during therapy.

In most cases high resolution CTA or MRA image sequences are acquired to obtain morphological information about the AVM whereas the digital subtraction angiography (DSA) remains the gold standard for evaluation of hemodynamics. Unfortunately DSA is based on ionizing radiation. Furthermore an overall complication rate of 3.89% has been reported by Warnock et al. [4]. The fact that only 2D projections of the vessel system are supplied is another drawback of this technique. Recent development of new MR image acquisition techniques, especially parallel MR and echo sharing, enables the time resolved MRA (4D) imaging of the blood flow with a high temporal resolution close to the DSA but a rather low spatial resolution. The acquisition of 4D imaging might considerably reduce the risk for the patient but due to the high number of acquired images and the complex AVM anatomy the slice wise manual visual inspection for therapy planning is very time consuming and might lead to suboptimal results. A computer based preparation and visualization of image sequences can help the clinicians to obtain improved therapy plans while at the same time reducing the temporal expenses.

Although the arteriovenous malformation is of high interest in neurosurgery and neuroradiology research the number of publications dealing with the computer based analysis is low. For visualization of the AVM Bullitt et al. [5] proposed a combined visualization of surface models of healthy vessels and a representation of the AVM using volume-rendering techniques to enable the visualization of the complicated structure of the AVM. Temporal (dynamic) information of the blood flow is not included. For the estimation of the size and location of the AVM an exact segmentation is needed. For this an approach based on dynamic CT images using factor analysis was proposed by Nyui et al. [6], as a drawback the results have not been quantitative evaluated and also previous knowledge about arterial, venous and noise signals are required.

Materials and Methods

MRA measurements

For development and evaluation of the method proposed 18 datasets of patients with an AVM were available. The MRI measurements were carried out on a 3T Trio scanner (Siemens, Erlangen, Germany) using an 8-channel phased array-head-coil.

New parallel MRA and echo sharing techniques enable the acquisition of 4D TREAT image sequences (time resolved echo-shared MR-angiography technique) after application of contrast agent and is described in detail by Fink et al [7]. These spatio-temporal image datasets serve as the basis for the analysis of the patient individual hemodynamics. The spatial quality of 4D TREAT images with a time resolution of 0.5 s and a voxel size of 1.875 × 1.875 × 5.0 mm^3 is rather low (see Figure 1 b-c).

For this reason the 3D TOF MRA (time-of-ight) image sequence with high spatial resolution (0.469 × 0.469 × 0.5 mm^3) was also acquired. Three-dimensional TOF MR angiography is one of the most commonly used non invasive method for evaluating the intracranial vasculature and offers a superior blood-to-background contrast (see Figure 1a). Therefore a detailed segmentation of the vessel system is possible.

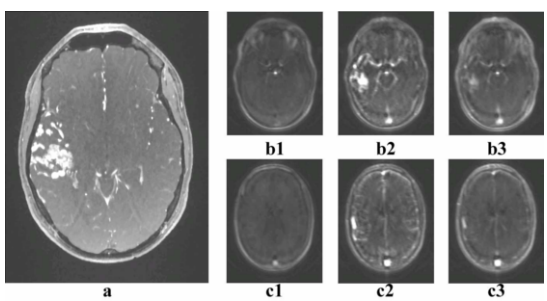

Figure 1 – Slice from TOF image sequence (a), and two slices from TREAT image sequence (b,c) at three different time-points (1-3)

Feature Generation

For segmentation of the AVM nidus several features used for the support vector machine (SVM) classification have to be extracted, which are described in the following.

Computation of the Vesselness Image

Based on the high resolution 3D TOF MRA the multi-scale vesselness filter as proposed by Sato et al. [8] is used to assign every voxel a value based on a vesselness measure based on eigenvalues of the Hessian matrix. This leads to an enhanced display of the vascular structures. Since implicitly the gray value variation of healthy vessels is used in this approach, often malformed vessels are not detected correctly (see Figure 2b).

Segmentation of the Vascular System

The cerebrovascular systems, which serve as the basis for the automatic analysis of the AVM, were automatically segmented for every dataset using an in-house developed fuzzy based method [9]. In this approach vesselness and maximum parameter images are computed first based on the TOF image. These parameter images are then combined with the TOF sequence using a fuzzy inference system. The resulting fuzzy image offers an improved enhancement of small as well as malformed vessels against the remaining brain tissues. Finally, the fuzzy-connectedness approach is used to extract the vascular system (see Figure 2c). Using the Marching Cubes algorithm a surface model of the vascular system can be generated and visualized 3D (see Figure 2d).

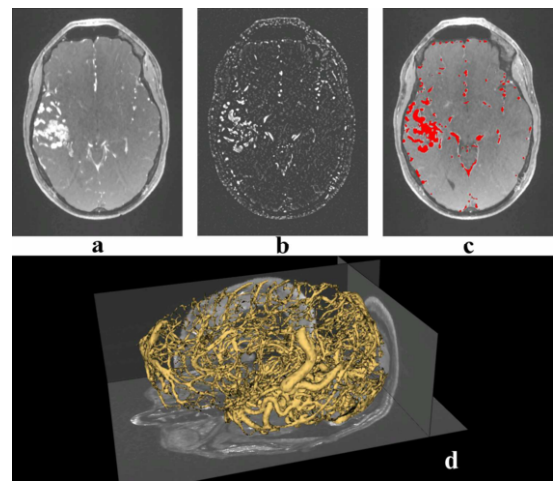

Figure 2 – Slice from TOF image sequence (a), corresponding vesselness image(b), extracted vessel segmentation (c), 3D surface model of the vascular system (d)

Bolus Arrival Time Estimation

The 4D MRA image sequences serve as the basis for the hemodynamic analysis. For every voxel a temporal signal curve representing the concentration of contrast agent at each acquired time point can be extracted from the 4D dataset.

Based on the signal curves several hemodynamic characteristics can be extracted. Whereas the bolus arrival time (BAT) of the concentration time curve is a parameter most important for the assessment of cerebral malformations. For BAT estimation the reference based linear curve fitting as proposed by Forkert et al. [10] was used.

In this approach a patient individual hemodynamic reference curve is extracted from the 4D MRA dataset by fitting and averaging a defined number of signal curves with a standard deviation higher than a given threshold σ. The threshold ensures that only signal curves which exhibit a typical signal process are used for reference curve generation. After computation of the reference curve its reference BAT (rBAT) is es-

timated using the time-to-peak criterion. Then in a following step the reference curve is linearly fitted to each signal curve of the 4D dataset such that the sum of squared differences (SSD) is minimized. Using the parameters obtained by the linear curve fit the reference BAT can be transferred to a target BAT (tBAT) (see Figure 3a).

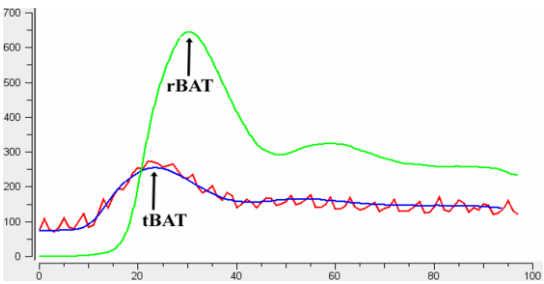

Figure 3 – Example for BAT estimation using reference based linear curve fitting: reference curve (green) signal curve (red) and fitted reference curve (blue)

Registration of 3D and 4D MRA datasets

The combined analysis of information of hemodynamics based on the voxel-wise analysis of the signal curves in the 4D TREAT dataset and anatomical vessel structures in 3D TOF dataset requires the registration of both datasets. For this purpose the method as proposed by Säring et al. [11] was used. In this approach a 3D maximum intensity projection over time (MIPt) is computed based on the 4D TREAT dataset. This projection leads to an advanced representation of the vessel system (see Figure 4a) which is helpful to improve the registration result. In a following step the resolution of the 3D MIPt is adapted to the 3D TOF MRA using a linear resampling. Finally, the transformation field between TOF MRA and MIPt is calculated using a B-spline based 3D-3D registration method with mutual information as similarity measure. The computed transformation field can then be used to transfer the BAT and MIPt datasets into the coordinate system of the 3D TOF image sequence. The transferred BAT values can then also be mapped to the surface model and visulized color coded (see Figure 4b) and dynamically over time using the method described in [12].

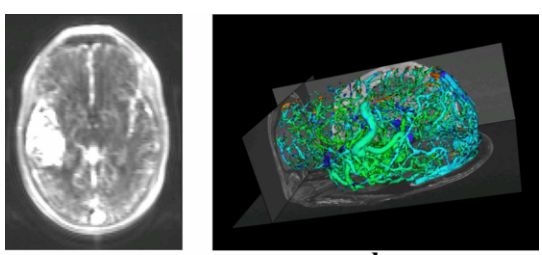

Figure 4 – Slice from the MIPt dataset (a), color coded visualization of the BAT values on the 3D surface model (b)

Support Vector Machine Based Segmentation of the AVM

Assumptions for the Method

The exact segmentation of the AVM is necessary to extract the important parameters size and location of the AVM. Furthermore it is needed for the detection of feeding arteries and draining veins. The method presented in this paper for the segmentation of the AVM is based on three assumptions:

1. The AVM does not exhibit typical vessel morphology. Therefore it can be assumed that the computed vesselness parameter image should exhibit low values for AVM structures while healthy vessels are represented by high values.
2. The missing capillaries of the AVM result in a reduced resistance in the vascular system leading to an increased blood flow velocity and early relative bolus arrival times. Since the intensities of Time-of-Flight image sequences represent the blood flow velocities it is assumed that the AVM is represented by high values in the TOF image. Due to artefacts caused by the TOF image acquisition turbulent or high flow might lead to low output values. Since the MIPt does not suffer from this problem it will be taken into account in the following step too.
3. The AVM is represented by the biggest local cluster of voxels fulfilling the previous assumptions.

These assumptions are used in the method described in the following to extract the AVM from the image sequences available.

Voxel wise Classification using Support Vector Machine

The BAT datasets are not directly comparable due to different injection and acquisition starting times. Therefore normalization of the datasets is required. For this reason the BAT dataset is masked with the vessel segmentation and the mean BAT is computed. Then in a following step the BAT dataset is normalized in terms of calculating relative differences to this mean BAT.

In the last years support vector machines (SVM) increasingly moved into the focus of supervised classification research. The aim of SVMs is to find an optimal separating hyperplane between classes based on training cases which can be used for classification. The optimal hyperplane is defined by the property of leaving the maximum margin between the classes. SVMs have been found to be a powerful recognition method. More detailed descriptions of support vector machines are for example given in [13]. In this study a linear kernel was used for training.

A total of 13 MRA datasets of patients with an arteriovenous malformation have been employed for the training of the SVM. The AVM have been manually defined based on the vessel segmentation by a neuroradiologist. The SVM was then trained voxel-wise using the four features described above, whereas only voxels, part of the vascular system, were considered for this purpose.

After training of the SVM the generated model can be used for voxel-wise classification, whereas the problem of detecting the AVM was formulated as a two-class problem. The output of the classification is a value describing the distance to the optimal hyperplane, whereas positive values represent voxels classified as belonging to the AVM. The SVM is then used to generate a distance map by classifying each voxel based on its exiting features.

After the classification dataset has been generated thresholding at distance zero is performed. Finally largest connected component analysis is used to extract the final AVM volume (see Figure 5).

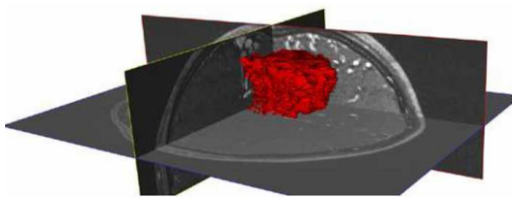

Figure 5 – Example for an automatically extracted AVM

Hemodynamic Characterization

In order to automatically detect feeders and draining veins of the AVM the mean bolus arrival time is computed based on the AVM segmentation. Then for the analysis of the vessels surrounding the AVM the segmentation is dilated. In a first step a connected component analysis is performed, whereas vessels not connected to the AVM are defined as en passage vessels. Then, the AVM segmentation is subtracted from the remaining components and a second connected component analysis is performed. For every extracted component the mean BAT is estimated. If the mean BAT is earlier than the mean BAT of the AVM segmentation the component is defined as a feeder else it is defined as a draining vein. After automatic characterization the different vascular structures can be visualized color coded (see Figure 6) based on the 3D surface model of the vascular system.

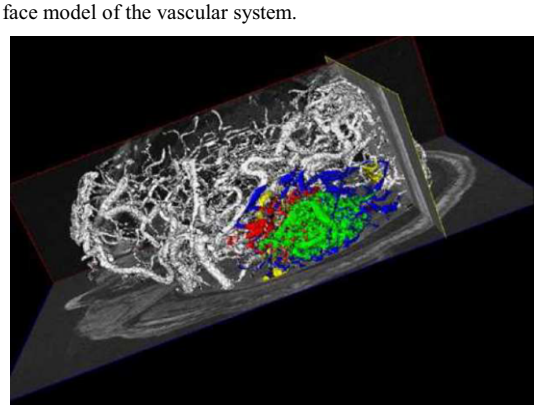

Figure 6 – Example for hemodynamic characterization

Experiments

For evaluation of the method proposed the AVM was defined for all 18 datasets by a neuroradiologist based on the vessel segmentation. 13 datasets (AVM sizes: 0.7 ml – 39.5 ml, Ø 14.1 ml) were used for the training of the support vector machine (approx. 9 mill. samples). The remaining five datasets (AVM sizes: 2 – 32 ml, Ø 13.4 ml) for quantitative evaluation of the results yielded by the AVM segmentation method. For quantitative evaluation of the segmentation results the Dice coefficient D(A,M) was used:

$$D(A,M) = (2|A \cap M|) / (|A| + |M|)$$

whereas A denotes the automatic segmentation and M the manual segmentation. Dice coefficients close to 1.0 denote a good consensus.

For evaluation of the automatic hemodynamic vessel characterization feeder and draining veins were manually defined by a neuroradiologist and compared to the results yielded by the method proposed

Results

Table 1 shows the results from the quantitative evaluation of the AVM segmentation method. A mean Dice coefficient of 0.74 and a projected volume match of 83.6% were achieved. The average time needed for the automatic segmentation procedure took approximately 5 minutes whereas the manual segmentation took between 5 – 35 minutes, depending on the size and complexity of the AVM.

Table 1 - Quantitative results of the AVM segmentation

Dataset	AVM size (in ml)	Segmented AVM size (in ml)	D(A,M)
1	32.83	25.43	0.75
2	16.95	18.99	0.74
3	9.5	11.05	0.85
4	5.71	4.66	0.71
5	3.75	4.48	0.65
Ø	13.39	13.75	0.74

The evaluation of the automatic vessel characterization revealed that feeding arteries and draining veins were detected with an accuracy of 100% for the five datasets analyzed.

Discussion and Conclusion

In this paper an automatic method for the segmentation of the AVM was presented. First quantitative results show that the AVM can be sufficiently extracted from the image data available. Ignoring dataset #3 the results suggest that bigger AVMs are easier to detect than the smaller ones. In order to achieve more significant quantitative results leave-one-out test have to

be performed. More manual segmentations from more observers are necessary in order to be able to make a statement about the inter-observer variability. Additionally it has to be evaluated how the results differ when using other kernels for the SVM, such as polynomial or radial basis function kernels.

The automatic detection and 3D visualization of the feeding arteries, draining veins and en passage vessels was rated to be very helpful for diagnosis therapy planning and can improve the therapy planning in future. Performing the mentioned leaving-one-out tests will lead to more significant results of the vessel characterization. Furthermore it has to be emphasized that the results of the hemodynamic classification rely to a great extent on the extracted vessel segmentation.

The dynamic 3D visualization of the cerebral blood flow can help the clinicians to explore the patient individual blood flow situation (see Figure 7).

A future combination with a functional atlas of the brain might enable an image guided therapy of AVM patients.

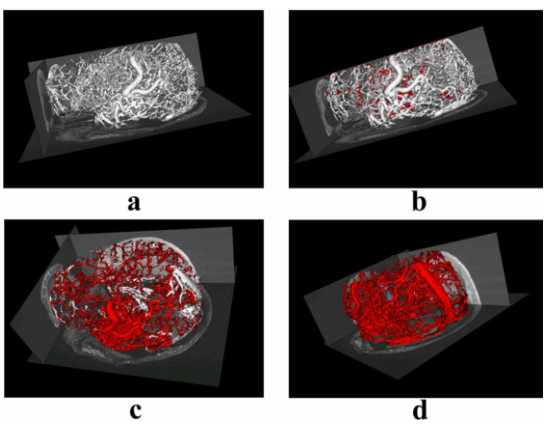

Figure 7 – Selected frames from the dynamic 3D visualization of the cerebral blood flow

Acknowledgments

The authors gratefully acknowledge the support by Prof. Dr. Jens Fiehler and Dr. Till Illies from the Department of Diagnostic and Interventional Neuroradiology, University Medical Center Hamburg-Eppendorf.

This work is supported by German Research Foundation (DFG, HA 2355/10-1)

References

[1] Choi JH and Mohr JP. Brain arteriovenous malformations in adults. Lancet Neurol 2005; 4: 299-308.

[2] Ogilvy CS, Stieg PE, Awad I, Brown RD Jr, Kondziolka D, Rosenwasser R, Young WL and Hademenos G. Recommendations for the management of intracranial arteriovenous malformations. Stroke 2001; 2(6): 1458-71.

[3] Spetzler RF and Martin NA. A proposed grading system for arteriovenous malformations. J Neurosurg. 1986; 65(4): 476-83.

[4] Warnock NG, Gandhi MR, Bergvall U and Powell T. Complications of intraarterial digital subtraction angiography in patients investigated for cerebral vascular disease. Br J Radiol 1993; 66(790): 855-8.

[5] Bullitt E, Aylward S, Bernard EJ Jr and Gerig G. Computer-assisted visualization of arteriovenous malformations on the home personal computer. Neurosurgery 2001; 48(3): 576-82.

[6] Nyui Y, Ogawa K and Kunieda E. Extraction of arteriovenous malformation with factor analysis. Image Processing, 2000 Proceedings. 2000; 2: 621-4.

[7] Fink C, Ley S, Kroeker R, Requardt M, Kauczor MU and Bock M. Timeresolved contrast-enhanced three-dimensional magnetic resonance angiography of the chest: combination of parallel imaging with view sharing (TREAT). Invest Radiol. 2005; 40(1): 40-8.

[8] Sato Y, Nakajima S, Shiraga N, Atsumi H, Yoshida S, Koller T, Gerig G and Kikinis R. Three-dimensional multi-scale line filter for segmentation and visualization of curvilinear structures in medical images. Med Image Anal. 1998; 2(2): 143-68.

[9] Forkert ND, Säring D, Wenzel K, Illies T, Fiehler J and Handels H. Fuzzy-Based Extraction of Vascular Structures from Time-of-Flight MR Images. Stud Health Technol Inform. 2009; 150: 816-20.

[10] Forkert ND, Säring D, Illies T, Fiehler J and Handels H. Comparison of Bolus Arrival Time Determination Methods for the Analysis of Cerebral Hemodynamics by Estimating the Impact of Temporal Resolution of 4D MRA Imaging. World Congress on Medical Physics and Biomedical Engineering 2009 IFMBE Proceedings 25/IV, pp. 1174–1177

[11] Säring D, Fiehler J, Forkert ND, Piening M and Handels H. Visualization and Analysis of Cerebral Arteriovenous Malformation Combining 3D and 4D MR Image Sequences. International Journal of Computer Assisted Radiology and Surgery 2007; 2, 75-79

[12] Forkert ND, Säring D, Illies T, Fiehler J, Möller D and Handels H. Analysis and dynamic 3D visualization of cerebral blood flow combining 3D and 4D MR image sequences. SPIE Medical Imaging 2009, 7261, 33.1–33.8

[13] Cortes C and Vapnik V. Support-vector networks. Mach Learn 1995; 20(3): 273-297.

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