Blood flow modeling in a synthetic cylindrical vessel for validating methods of vessel segmentation in MRA images

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Abstract The paper presents new concept of validating blood segmentation methods. The idea is to create a Magnetic Resonance Angiography simulator which can generate synthetic MRA images based on pattern objects. In order to reproduce angiographic sequences such as Time of Flight or Susceptibility Weighted Imaging, laminar flow in digital phantoms was modeled. Results were presented and discussed. Comparison of the new concept with existing validation methods was carried out.

1 Introduction

Magnetic Resonance Imaging (MRI) is one of the most popular radiology techniques used to obtain anatomical images of the human body [4]. Modern MRI scanners can receive high resolution 3D images with good contrast between different tissues. In comparison to traditional X-rays or Computer Tomography, MRI is noninvasive because it does not use ionizing radiation. Another advantage is the number of different sequences. Using angiographic techniques such as Time of Flight [3] and Susceptibility Weighted Imaging [18] methods combined together, results in a full map of veins and arteries [9]. Such a map carries important information about patient health and can be used in diagnosis and planning surgical operations.

Image segmentation methods are created in order to help physicians in analyzing those complex images [6]. Separating vessels from other tissues can result in revealing important information. Reconstructing vessel walls may lead to detecting clots, narrowings or other anomalies much faster than without image processing techniques [21]. Although results of blood segmentation algorithms can increase the scope of knowledge about patient health, they are

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Fig. 1 Comparison of standard MRI imaging sequence with described concept.

rarely used in clinics. Diagnosticians cannot rely on segmented images and must make diagnoses based on their knowledge and medical experience. This is mainly due to problems with validating results of blood segmentation methods [13]. Their results cannot be compared with some ground truth pattern. Firstly, after transformation and rasterization of input data during the imaging sequence, a significant part of information is lost irrevocably. Secondly, there is no method to get precise dimensions of a patient vessel network. It is not possible to measure such complex structures inside a human body.

In order to use image processing methods for medical purposes there is a need of creating a reliable validation method. A method which not only allows to evaluate the correctness of reconstructed structures but also helps in the process of developing segmentation algorithms. To meet these requirements we propose a new method of validation. We want to simulate angiographic imaging sequences using a computer unit (cf. Fig. 1). This allows us to replace real image data with a 3D digital model of human vessels. A properly implemented simulator working on known patterns will create an effective and objective criterion of validation for image segmentation methods.

In standard MRI imaging, contrast is acquired thanks to chemical and physical differences between tissues. However, in magnetic resonance angiography (MRA) sequences voxel brightness is also dependent on the position of proton particles in time. Here, the phenomenon of blood flow is utilized. During the imaging process blood is moving in vessels while other tissues are stationary. Therefore, an appropriate simulation of this phenomenon is crucial for the postulated approach to succeed.

At an early stage of this project development laminar flow was modeled and applied in a simple digital tubular phantom vessel. The reason for this is the existence of real test objects with exactly the same parameters. After performing blood flow simulation for digital phantom there is a possibility to

measure values obtained in a physical model and to compare the results. This phantom can be used not only to test the correctness of blood flow simulation but also to validate results of MRA sequences. If successful this could lead to using more complex vessel models, similar to the ones in a human body.

2 Blood vessel segmentation

Image segmentation techniques are used to divide data into regions with common characteristics. In case of MRA images the purpose is to separate blood vessels from other tissues. As mentioned earlier, it allows to portray arteries and veins as a 3D model. Data in that form is much easier to be analyzed than 2D cross-sections. Additionally, segmentation allows to automatically search for risk regions based on vessel diameter.

There are plenty of segmentation algorithms to choose from [15]. Depending on which part of the body has been imaged and what types of vessels need to be detected different methods should be applied. We can divide vessel segmentation techniques into two main categories: the mathematical morphology approach and geometrical methods [10]. Algorithms from the first group are considered to be fast but not very effective. The best example is image thresholding or a more advanced technique known as region growing. Output images are obtained almost instantly, but—e.g in cerebrovascular imaging it is impossible to separate small veins from white matter or even from the bone. There are more advanced morphology methods such as watershed segmentation or top-hat.

Algorithms from the second group not only use the voxel brightness level but also the relative position of neighboring points. Deformable models or generalized cylinders approach are thought to give accurate results. However, the time needed to process a high resolution MRA 3D image is very long and the reconstruction of veins with small diameters (compared to the size of the voxel) is impossible. Base on experiments, low level geometric methods seem to be more appropriate. Usage of Hessian matrix to find local direction of white tubular objects is one of these methods [11].

In order to test various attempts and develop new ones, an image segmentation application was created. Using implemented image functions and filters there is a possibility to build and run complex algorithms in a short time. Additionally, thanks to an intuitive graphic user interface (see Fig. 2) and advanced task tracking system, changing used parameters or adding new methods to existing process posses no problem.



Fig. 2 Graphical user interface of created segmentation software.

3 Validation of biomedical image processing methods

Although some segmentation algorithms results looks promising it is difficult to perform an objective assessment of their correctness [8]. The Most common method of validation is relying on medical knowledge and subjective assessment made by physicians [5]. However, gathered information cannot be used as a reliable pattern due to uncertainty and poor reproducibility.

The Second group of validation methods is based on physical phantoms. These artificial structures are mainly used to calibrate MRI scanners, but can also be used to test results of segmentation methods. This time, the pattern is familiar and comparison can be made. This method of validation is much more accurate, but has its drawbacks. Physical phantoms are expensive and, so far, there is no structure similar to the real blood network. This is a result of complicated topology and small vessel diameters.

The third group consists of digital phantoms. Similarly to physical structures they provide a priori known and measurable reference pattern [1]. A complex geometrical shape is much easier to create using computer 3D graphics. What is more, they are much faster and cheaper to create. They can be duplicated with different parameters and can be used to create large sets of test objects. The only disadvantage is that it is not possible to use these phantoms in a real MRI scanner.

All three methods have their drawbacks and potentials. An ideal solution seems to be a combination of all methods. As a pattern we would like to use easy to create digital objects, with known dimensions and blood flow inside it.

4 MRA Simulation

Problems with validating segmentation results can be solved by an MRA simulator. Simulating movement of blood in vessels allows implementing angiographic sequences and obtaining images similar to those from a real scanner (with noise and distortion caused by imaging sequence). Contrary to image acquisition using real MRI apparatus, the input object is known and can be used as a reference source.

Simulating the physical phenomena of an MRI scanner is a complex problem. Only a few attempts to this issue can be found in literature [17, 16, 14, 2], but they work only for static objects. In case of angiographic imaging, these methods cannot be used because sequences such as Time of Flight (ToF) and Susceptibility Weighted Imaging (SWI) are based on blood flow in arteries and veins. In ToF, image contrast is acquired by unsaturated molecules of blood which flows through acquisition volume in a given time moment. SWI depends on blood oxygenation and uses amplitude and phase gradient echo, with compensated blood flow effect.

5 Blood flow modeling

Simulation of laminar flow is performed in COMSOL Multiphysics software by solving incompressible Navier-Stokes equations. This type of blood movement, known also as stratified flow, assumes that fluid moves in parallel layers [12] . Each layer has its own speed and slides past one another so there is no lateral mixing. Blood flows in one direction. Velocity is greatest in the middle of the cylinder. The value decreases as we approach the vessel wall. For simulating blood flow in a pipe this model is sufficient. For more complex structures with many branches and bifurcation there is a need to use turbulent model of flow.

To solve flow equations there is a need to set viscosity and density of the liquid. Based on literature these values for blood were adjusted to 1060 Kg/m³ (density) and 0.005 Ns/m² (dynamic viscosity).

The goal of this part of the project is to simulate blood flow in a complex artificial model of a vessel tree. It cannot be done until it is certain that the simulation is consistent with the real flow. That is the reason why the geometric shape of a digital pattern should be uncomplicated and identical to the physical phantom. If successful this could lead to using vessel models, similar to these in a human body.

Firstly, Geometry objects are created on the model of the Flow Phantom Set produced by Shelley Medical Imaging Technologies [20]. This Model is compatible with the high class CompuFlow 1000 MR pump which allows to force and precisely control the flow in test objects [19]. This Phantom Set consists of 4 straight (Fig. 3a) and 1 U-bend tubes (Fig. 3b). The geometrical parameters of the tubes are as follows:

- Straight tubes phantom QA-STV (all tubes are 207 mm long)
 - $\circ~8~\mathrm{mm}$ diameter vessel with 75% sinusoidal stenosis by diameter
 - \circ 8 mm diameter vessel
 - $\circ~~8~\mathrm{mm}$ diameter vessel with 50% sinusoidal stenosis by diameter
 - $\circ~5~\mathrm{mm}$ diameter vessel
- U-bend phantom QA-USV
 - $\circ~~8~\mathrm{mm}$ diameter, 44 mm midline radius-of-curvature

There is no fluid leek through the walls and no deformation caused by flow. This simplification makes the model easier to implement. Created digital models are an exact copy of their real equivalents, including details such valves and silicone control drillings (cf. Fig. 4).



Fig. 3 Physical silicon phantoms: a) straight cylinders with stenosis, b) U-bend tube.



Fig. 4 Digital phantoms based on respective real models illustrated in Fig. 3.



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Fig. 5 Pressure distribution in 4 tubular phantoms. Value range is 11136–11208 Pa.



Fig. 6 Velocity magnitude in 4 tubular phantoms. Value range is 0–0.18 m/s.

6 Results

Blood flow simulation was performed for both phantom sets. Fluid flow is forced by setting pressure difference between input (11208 Pa) and output (11148 Pa) boundaries [7]. There is no slip allowed through phantom walls. Distribution of pressure and velocity of particles inside straight vessels are depicted in Fig. 5 and 6. In a vessel with a 5 mm diameter pressure distribution is linear. According to the theory of laminar flow, highest velocity is obtained in the center of the tube. Moving towards the wall this value decreases. Based on the laminar flow solution, particle tracing was performed. The Number of molecules was set to 32. All of them were defined by density and diameter. At the beginning, all particles are located at input boundary. With time, each element moves towards the exit. All trajectories are straight lines parallel to the main axis of the vessel. The fastest particles reach its goal in about 2.5 second; ones next to the wall are over five times slower. Results from this study are relevant to values obtained in laminar flow simulation.

Similar situation can be observed for a second straight tube of 8 mm. The main difference is time of flight of particles in the middle of the tube which equals 1.19 seconds. These values are relevant to the theory where local velocity depends on distance from the edge of the vessel.

Next two phantoms contain sinusoidal stenossis. Parameters of the flow are still the same. Due to narrowing, pressure distribution is no longer a linear function. Although in a phantom with 75% stenosis values of magnitude velocity are similar to those in a straight tube, small acceleration is visible in the narrowing region. The fastest particle reaches a distance of 207 mm in 1.25 s which is 0.06 slower than in previous test. In the case of a vessel with 50%narrowing (Fig. 7), pressure applied on the particles before reaching stenosis is almost constant and equals the input parameter. Velocity magnitude is no longer a constant value. It changes from 0.2 m/s in the input section to about 0.4 m/s in the middle of stenosis. Time of the flow is much longer and equals 1.79 s. After the narrowing, the density of particles is higher because they do not return to their previous positions. The final U-bend phantom is different from previous 4 tubes. It is much longer and bent to an angle of 180 degrees. Because of the lack of narrowings, pressure is a linear function. Time of flight for the particles in the middle equals 3.55 s. In the curve section small deviations from the central axis can be observed in the molecules trajectory (cf. Fig. 8).



Fig. 7 Particle trajectories in vessel with 50% stenosis by diameter.



Fig. 8 Velocity magnitude in U-bend phantom. Value range is 0–0.12.

7 Conclusion

A new concept of validating blood segmentation methods was presented. The idea was compared with existing methods. For the purpose of implementing angiographic sequences blood, flow was simulated in digital phantoms specially created for this project. Expected values and 3D coordinates were gathered and will be used in future validation process. Although much work still needs to be done, this report brings us closer to the final goal of a project—an MRA Simulator

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