Magnetic Resonance Imaging 31 (2013) 1163–1173

Contents lists available at SciVerse ScienceDirect

Magnetic Resonance Imaging

journal homepage: www.mrijournal.com

Computational modeling of MR flow imaging by the lattice Boltzmann method and Bloch equation

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ARTICLE INFO

Article history:
Received 30 October 2012
Revised 4 December 2012
Accepted 14 January 2013

Keywords:
Magnetic resonance imaging (MRI)
Fluid flow
Computer modeling and simulation
Bloch equation
Lattice Boltzmann method (LBM)

ABSTRACT

In this work, a computational model of magnetic resonance (MR) flow imaging is proposed. The first model component provides fluid dynamics maps by applying the lattice Boltzmann method. The second one uses the flow maps and couples MR imaging (MRI) modeling with a new magnetization transport algorithm based on the Eulerian coordinate approach. MRI modeling is based on the discrete time solution of the Bloch equation by analytical local magnetization transformations (exponential scaling and rotations).
Model is validated by comparison of experimental and simulated MR images in two three-dimensional geometries (straight and U-bend tubes) with steady flow under comparable conditions. Two-dimensional geometries, presented in literature, were also tested. In both cases, a good agreement is observed. Quantitative analysis shows in detail the model accuracy. Computational time is noticeably lower to prior works.
These results demonstrate that the discrete time solution of Bloch equation coupled with the new magnetization transport algorithm naturally incorporates flow influence in MRI modeling. As a result, in the proposed model, no additional mechanism (unlike in prior works) is needed to consider flow artifacts, which implies its easy extensibility. In combination with its low computational complexity and efficient implementation, the model could have a potential application in study of flow disturbances (in MRI) in various conditions and in different geometries.

1. Introduction

Magnetic resonance (MR) images of vascular structures play a very important role in clinical angiography [1]. Many diseases are directly related to changes in vessel structures, and a lot of these modifications can appear in medical images. Signal intensity enhancements may indicate hypervascularized areas of tumoral lesions (e.g., hepatocellular carcinoma) [2]. In contrast, flow-related signal voids can appear in the place of serious vessel shape perturbations (e.g., aneurysm, stenosis) [3,4]. Hence, the ability to understand MR flow images and to predict consequences of changes in vascular geometries is crucial.

Although MR imaging (MRI) is known as a highly detailed three-dimensional (3D) imaging modality, there are still a lot of difficulties in vascular image interpretation. This is mainly due to flow-induced disturbances appearing in such areas, caused by intravoxel phase dispersion (IVPD) [5], misregistration [6,7] or inflow/outflow effects [8]. Moreover, imperfections and limitations of hardware continue to reduce the effectiveness and accuracy of fluid motion characterization and visualization. This motivates the creation of computational models of MR flow imaging as a tool to enhance understanding of involved processes. For instance, they can help to study the relationship between vascular geometry changes and hemodynamic factors in silico [9]. The connection between fluid flow and image appearance can also be investigated [4]. Turning on/off particular physical phenomena and evaluation of various combinations of MRI equipment parameters are often time consuming or even impossible. On the other hand, in computational models, it is far easier to switch on/off their components and to study contribution of each factor alone or together. Therefore, such modeling can certainly contribute to increase our understanding of pathological processes and to improve MRI sequence design. Finally, controlled simulation experiments are also a valuable way of education [10].

There were many studies on flow influence on MRI, both experimental and by simulations, e.g., [4–9,11–20]. Most of them are focused on a chosen imaging sequence/technique and chosen

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http://dx.doi.org/10.1016/j.mri.2013.01.005

geometry and flow pattern, e.g., on balanced steady-state free precession (b-SSFP) in simple geometry [8], spiral imaging [7], phase contrast imaging in a carotid bifurcation [19] or slice selection process [11,17]. In contrast to them, in this paper, we propose a more general approach in computational modeling of MR flow imaging with a computer program allowing fast simulations of the effect of complex flow geometries in arbitrary imaging procedure. Our goal is not to concentrate on one particular geometry but to provide extensible solution that integrates geometry, flow and MRI managing modules to increase understanding and unravel their interactions by efficient tests of many scenarios (parameters).

The proposed computational model consists of two connected components: a fluid dynamics component and an MRI one. The first one is responsible for flow modeling by the lattice Boltzmann method (LBM) [21] in given geometries. It provides flow maps which are then used in the second component of the model. This second component reproduces the MRI process. During the imaging simulation, a newly proposed magnetization transport algorithm is used to model the flow influence. The algorithm is based on the Eulerian coordinates approach (i.e., stationary frame [22]). MRI processes are modeled with the use of the discrete time solution of the Bloch equation [23] by means of local magnetization rotations and exponential scaling [24]. These analytical magnetization transformations closely follow the physical process of MRI and in combination with the magnetization transport algorithm naturally incorporate flow-related artifacts. As a result, no additional mechanism is needed to consider the flow influence during most MRI processes (including excitation, relaxation, precession as well as space encoding and signal sampling in 3D objects), in contrast to the one of the most advanced prior works [4,19]. This also implies that the whole imaging procedure for various sequences (e.g., spoiled gradient echo or b-SSFP) with different view ordering (e.g., linear, centric or cyclic) or with different *k*-space trajectory (e.g., radial or spiral) is straightforward to model, unlike in previous studies [7,8]. Another advantage of the proposed solution is its implementation (computer program) that allows to easily control modeling parameters starting from geometry specification, through flow and MRI, and ending on image processing. These features render the solution as a tool that is user friendly and manageable at different levels, which facilitates running series of simulations with different physiological and imaging parameters. In this study, as a first step, we focus on magnitude images acquired in the spoiled gradient echo sequence. Our initial efforts to create the presented solution are described in the conference paper [25].

In the second section of the paper, the proposed computational model and its implementation (integrated simulation environment) are described. Simulation and experimental setups, used in model validation, are also presented. In the Results section, the validation of the model is performed by comparison between experimental and simulated images as well as by quantitative analysis. The computational performance is also investigated. Finally, in the Discussion section, the model is confronted with prior works, its limitations and advantages are described, and also future works are sketched.

2. Methods

At the beginning, the two parts of the model are described. Then, the way of flow influence incorporation in MRI modeling is presented. Next, the integrated simulation environment (computer program implementing the model with additional supporting modules) is briefly described. Finally, the simulation and experiment setups, used to validate the model, are presented.

2.1. Fluid flow modeling

In the proposed solution, LBM [21] is applied to model fluid flow. This method has been intensely developed over the last two decades, becoming a powerful alternative to the numerical solving of Navier–Stokes equations known as the conventional computational fluid dynamics mechanism [26]. Many theoretical analysis [27] and numerical investigations [28,29] have shown that LBM is commonly recognized as a method able to simulate realistic fluid flows obeying the Navier–Stokes equations with high accuracy.

LBM is a mesoscopic method placed in between microscopic molecular dynamics and continuous macroscopic approaches [30]. It does not consider each elementary particle alone but treats the behavior of a collection of particles as a unit whose properties are represented by a particles distribution function. Therefore, LBM preserves most of the advantages of both micro- and macroscopic approaches. Its clear physical insight into molecular processes provides easy treatment of boundary conditions and, consequently, high applicability for complex geometries [31]. At the same time, the relevant quantities (e.g., mass, energy, etc.) are conserved at the macrocontinuous regime, like in the Navier–Stokes equations. Moreover, it shows numerous computational advantages, e.g., good stability properties or simple arithmetic calculations. Finally, owing to the intrinsic space–time locality of LBM (i.e., in each time step, only data from neighboring lattice nodes are needed), it is ideal for parallel computing [32].

In LBM, fluids consist of a set of discrete nodes creating regular lattices. At each lattice node, the virtual particles (represented by their distribution function) reside. At discrete time moments, these particles can move along specified directions to the neighboring nodes (propagation step). When the particles meet, they collide (collision step), but they always stay on the lattice nodes. The collision rules are set according to the conservation laws of mass (i.e., number of particles), momentum and energy. The exact conservation laws are fulfilled, not only their numerical approximations. These two steps are expressed by a mathematical formula known as the lattice Boltzmann equation:

$$f_i(\mathbf{r}+\mathbf{e}_i\Delta t, t+\Delta t)-f_i(\mathbf{r},t)=\Omega(\mathbf{r},t), \tag{1}$$

where $f_i(\mathbf{r}, t)$ is the particle distribution function in the grid node located at position $\mathbf{r}$ at the time t and streaming in the next time step Δt in the direction i with the velocity $\mathbf{e}_i$. Ω is the collision operator standing for collision rules of the simulated physical phenomenon.

Using the Bhatnager–Gross–Krook (BGK) model [33], the collision operator (complex integro-differential expression) is simplified by the widely used, single-time relaxation approximation [31]:

$$\Omega_i(\mathbf{r},t)=1/\tau\left(f_i^{\mathrm{eq}}(\mathbf{r},t)-f_i(\mathbf{r},t)\right), \tag{2}$$

where τ is the dimensionless relaxation time related to fluid viscosity. The local equilibrium distribution function f_i^{eq} is given by [34]:

$$f_i^{\mathrm{eq}}=\rho\omega_i\left[1+\frac{3}{c^2}\mathbf{e}_i\cdot\mathbf{u}+\frac{9}{2c^4}(\mathbf{e}_i\cdot\mathbf{u})^2-\frac{3}{2c^2}\mathbf{u}\cdot\mathbf{u}\right], \tag{3}$$

where $\mathbf{u}=\frac{1}{\rho}\sum_{i=0}^{n-1}\mathbf{e}_i f_i$ is the macroscopic lattice velocity, $\rho=\sum_{i=0}^{n-1} f_i$ is the dimensionless lattice density, ω_i is the weighting factor of a lattice topology and c is the lattice constant related to a propagation factor on the lattice and is set to unity in most cases [34]. Lattice velocity is a fraction of distance between neighboring nodes traveled by fluid per time step (e.g., lattice velocity of 0.5 means that the fluid moves 0.5 lattice cell in time step Δt). To obtain the physical macroscopic velocity, the lattice velocity is multiplied by $\Delta d/\Delta t$, where Δd is the lattice cell size (distance between neighboring lattice nodes).

In two-dimensional (2D) fluid flows, we use the model with $n=9$ discrete velocities (D2Q9) (Fig. 1A) where

$$\begin{array}{rl} e_0=[0,0]c & \omega_0=4/9 \\ e_{1,2},e_{3,4}=[\pm1,0]c,[0,\pm1]c & \omega_{1..4}=1/9 \\ e_{5,\ldots,8}=[\pm1,\pm1]c & \omega_{5..8}=1/36 \end{array},$$