



On locating the obstruction in the upper airway via numerical simulation



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ABSTRACT

The fluid dynamical properties of the air flow in the upper airway (UA) are not fully understood at present due to the three-dimensional (3D) patient-specific complex geometry of the airway, flow transition from laminar to turbulent and flow-structure interaction during the breathing cycle. It is quite difficult at present to experimentally measure the instantaneous velocity and pressure at specific points in the human airway. On the other hand, direct numerical simulation (DNS) can predict all the flow properties and resolve all its relevant length- and time-scales. We developed a DNS solver with the state-of-the-art lattice Boltzmann method (LBM), and used it to investigate the flow in two patient-specific UAs reconstructed from CT scan data. Inspiration and expiration flows through these two airways are studied. The time-averaged first spatial derivative of pressure (pressure gradient), $\partial p/\partial z$, is used to locate the region of the UA obstruction. But the time-averaged second spatial derivative, $\partial^2 p/\partial z^2$, is used to pinpoint the exact location of the obstruction. The present results show that the DNS-LBM solver can be used to obtain accurate flow details in the UA and is a powerful tool to locate its obstruction.

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1. Introduction

The human upper airway, UA, includes the parts of the respiratory tract above the thorax, i.e. the nasal cavity, the pharynx, the larynx and the upper part of the trachea. Common surgeries for correcting the UA obstruction include septoplasty, tonsillectomy and adenoidectomy. In the United States, about 600,000 children undergo adenotonsillectomy operation each year. However, the success rate of these operations is only about 50% due to lack of information on where the flow is constricted and where the UA dynamically collapses. Thus, understanding the UA flow properties and accurately locating the obstruction are of practical importance.

Several experimental studies have been carried out to measure the flow properties in laboratory models of the airway. However, the lack of complete fidelity of hot-wire and particle image velocimetry has been demonstrated by [Johnstone et al. \(2004\)](#) and [Pollard et al. \(2012\)](#). On the other hand, computational fluid dynamics (CFD) methods have become increasingly capable of simulating the biofluid flows ([Yoganathan et al., 2004](#); [Kleinstreuer and Zhang, 2010](#); [Calay et al., 2002](#); [Doorly et al., 2008](#); [Wen et al., 2008](#); [Choi et al., 2009](#); [Zhu et al., 2011](#); [Na et al., 2012](#); [Deng et al., 2013](#); [Gambaruto et al., 2012](#); [Xi et al., 2012](#)), and providing quantitative

information about the flow properties that can minimize the guess work in corrective surgeries.

The flow in the UA is 3D, time-dependent, undergoes transition from laminar to turbulent, and reverses its main direction about every two seconds. The complex geometry of the UA results in curved streamlines, recirculation regions, secondary and jet flows. For example, the minimum cross-sectional area in the overlap region between the nasopharynx and oropharynx usually generates a turbulent jet downstream of the restriction in the apnea cases. Therefore, in order to predict this flow accurately, the numerical method should be able to simulate low Reynolds number turbulent flow in complex geometry efficiently and with minimum empiricism.

In order to investigate the laminar–transitional–turbulent flow in the airway, three approaches with different accuracies have been adopted in the literature: the Reynolds-averaged Navier–Stokes (RANS), large eddy simulation (LES) and direct numerical simulation (DNS). In RANS approach, Reynolds-averaged Navier–Stokes (NS) equation generates a number of statistical correlations between all the dependent variables and thus creates more unknowns than the available equations, leading to the closure problem. The closure is achieved via mathematical models (such as $k-\omega$ and $k-\varepsilon$) with additional transport equations that usually require fine-tuning for different turbulent flows. Although the accuracy of RANS is acceptable in simple turbulent flows such as straight pipes and channels, it is questionable in turbulent flows with strong streamline curvature, flows in transition from laminar to turbulent

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and low Reynolds number turbulent flows. All these challenging flows exist in the UA. LES is more accurate than RANS, as large scale turbulent structures (eddies) are numerically resolved and only small (sub-grid scale) structures are modeled by methods similar to RANS. However, LES is not as accurate as DNS due to the empiricism of sub-grid scale models. In DNS, all relevant length- and time-scales are resolved numerically. Thus DNS produces the most accurate information about turbulent flows and is the gold standard for evaluating the accuracy of other methods.

Mihaescu et al. (2008) used both RANS and LES to simulate the flow in a pharyngeal airway model. Large differences were observed between the RANS and LES results of the axial velocity downstream of the maximum narrowing. The authors stated that RANS is not suitable for the UA whereas LES is. Mylavarapu et al. (2009) performed both simulations and experiments for a human UA. The RANS with two-equation turbulence models ($k-\varepsilon$, $k-\omega$, and $k-\omega$ -shear stress transport (SST)) as well as one-equation Spalart–Allmaras model, and LES were used. Mylavarapu et al. stated that the $k-\omega$ model resulted in the best agreement with the experimental data. Zhang and Kleinstreuer (2011) performed simulations for an idealized UA laboratory model with RANS and LES. They found that the RANS with SST transition model produced a better prediction of the turbulence kinetic energy profiles in some cases, while the $k-\omega$ model amplified the flow instabilities after the constriction, and suggested that more accurate turbulence models are still needed for the turbulence-onset prediction in complex geometries. It is clear from the above review that neither RANS nor LES is capable of accurately predicting the flow in the human UA.

The conventional approach for DNS is DNS-NS which solves the three-dimensional Navier–Stokes equations numerically in simple geometries at moderate Reynolds numbers. However, in complex geometries such as that of UA, it becomes computationally prohibitive for DNS-NS to resolve the flow in the near-wall regions. Lin and Tawhai (2007) employed DNS with second-order characteristic Galerkin fractional four-step finite element method to simulate the airflow in human intra-thoracic airways, and concluded that the simulation should consider both the UA and the intra-thoracic airway. An alternative DNS approach is the DNS-LBM which solves the discretized lattice Boltzmann equations (Succi, 2001; Sukop and Thorne, 2005) and is well-suited for resolving all the relevant length- and time-scales of flows confined by walls with complex geometries which are typical of the UA. Compared to the conventional DNS-NS, DNS-LBM has several advantages as will be discussed at the end of Section 2.1.

LBM has been introduced twenty years ago and developed rapidly in the past 10 years. It has been used in simulating biomedical flows, such as flows in the respiratory system (Ball et al., 2008; Finck et al., 2007; Hörschler et al., 2010; Eitel et al., 2010; Lintermann et al., 2012) and cardiovascular system (Munn and Dupin, 2008; Boyd and Buick, 2008; Kim et al., 2010). The published LBM studies related to the UA are mostly concerned with the laminar flow in the nasal cavity (Finck et al., 2007; Eitel et al., 2010). These studies demonstrated the capability of the LBM for predicting the complex flow in the UA. Recently, the DNS-LBM has been used to simulate the laminar–transitional–turbulent flows in an idealized laboratory model of the airway (Ball et al., 2008). The results of Ball et al. showed that the DNS-LBM was superior to RANS as it reproduced the critical flow features observed in the experiment. Some other DNS-LBM studies for the flows in patient-specific nasal cavities can be found in Hörschler et al. (2010) and Lintermann et al. (2012).

The objective of the present study is to numerically investigate the flow in real UA (including the nasal cavity, pharynx, larynx and trachea) via DNS-LBM, and develop a method for locating the obstruction based on the fluid dynamic properties of the flow. The DNS-LBM is described in Section 2. Validation of the

DNS-LBM is discussed in Section 3. The computational details are described in Section 4. Results of the UA simulations and discussion are presented in Section 5. The proposed method for locating the obstruction is discussed in Section 6. The conclusions are summarized in Section 7.

2. Numerical method

2.1. Lattice Boltzmann method

In order to understand the complex flow in the human UA and produce accurate flow properties for pre-surgery decisions and virtual surgery, the state-of-the-art LBM is selected as the DNS method. We developed a 3D solver based on the standard LBM with stream-collision procedures (Succi, 2001; Sukop and Thorne, 2005). Our DNS-LBM solver uses massively parallel computers efficiently due to the natural parallel characteristics of the LBM.

Both single-relaxation time, SRT (also known as BGK) (Qian et al., 1992), and multi-relaxation time (MRT) (d’Humières et al., 2002) collision operators are considered in our DNS-LBM solver. In the LBM with BGK collision operator, the fluid particle probability density distribution function f_α obeys a set of lattice BGK equations:

$$f_\alpha(\mathbf{x} + \mathbf{c}_\alpha \delta t, t + \delta t) - f_\alpha(\mathbf{x}, t) = \frac{f_\alpha^{\text{eq}}(\mathbf{x}, t) - f_\alpha(\mathbf{x}, t)}{\tau}, \quad (1)$$

where \mathbf{x} is the spatial coordinate of fluid particle; δx and δt are the lattice spacing and time increment, respectively; f_α^{eq} is the local equilibrium distribution function; $\tau = \tau'/\delta t$ is the non-dimensional relaxation time, which is a function of the kinematic viscosity ν , δt and sound speed c_s according to $\nu = c_s^2(\tau - 0.5)\delta t$; α is the directional index of the discrete velocity vector \mathbf{c}_α . The arrangement of \mathbf{c}_α in the velocity space is called lattice. One of the most popular lattices for 3D flow is the D3Q19 lattice which we used in our simulations.

The left-hand side of Eq. (1) represents the streaming motion of the fluid particles, whereas the right-hand side describes their collision. The macroscopic fluid density ρ and velocity \mathbf{u} are functions of f_α , while the pressure is calculated from $p = c_s^2 \rho$. It should be noted that the incompressible Navier–Stokes equations can be obtained from Eq. (1) using Chapman–Enskog expansion (Succi, 2001). In our simulation, the 3D computational domain is divided into a number of uniform 3D cells which coincide with the lattice if $\delta x = \delta t = c$. The node at the center of each lattice is connected to the neighboring by the velocity vectors \mathbf{c}_α .

When the MRT collision operator is used instead of the BGK operator, the relaxation coefficient $1/\tau$ on the right-hand side of Eq. (1) is replaced by a collision matrix $\Lambda_{\alpha\beta}$

$$f_\alpha(\mathbf{x} + \mathbf{c}_\alpha \delta t, t + \delta t) - f_\alpha(\mathbf{x}, t) = \Lambda_{\alpha\beta} (f_\beta^{\text{eq}}(\mathbf{x}, t) - f_\beta(\mathbf{x}, t)), \quad (2)$$

where $\Lambda_{\alpha\beta} = \mathbf{M}^{-1} \mathbf{S} \mathbf{M}$; \mathbf{M} is a given $m \times m$ transformation matrix for the DnQm lattice; $\mathbf{S} = \text{diag}(s_1, s_2, \dots, s_m)$ and s_α can be determined by linear analysis and some physical parameters such as viscosity (d’Humières et al., 2002). The MRT operator allows the solution of Eq. (2) to be more stable than that of Eq. (1), at the cost of slightly more computational time. It is noted that most of the published LBM studies on the respiratory system used the BGK operator (Finck et al., 2007; Hörschler et al., 2010; Eitel et al., 2010; Lintermann et al., 2012).

It is clear that the linear LBM Eqs. (1) and (2) are simpler than the nonlinear NS equations and are readily parallelizable. Moreover, the pressure is a local property in the DNS-LBM, whereas in DNS-NS the pressure is obtained by solving the elliptic Poisson equation at a considerable computer cost. Thus the DNS-LBM is certainly more computationally efficient than the conventional DNS-NS methods.

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