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A BEM/FEM Coupling Approach for Fluid-Structure Interaction Simulation of Cell Motion

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Abstract. In this paper, accurate and efficient simulation of cell motion in a biological fluid flow is investigated. The membrane of a moving cell is represented by a thin shell composed of incompressible neo-Hookean elastic materials and the liquids around the membrane are approximated as incompressible Newtonian flows with low Reynolds numbers. The biofluid mechanics is approximated by the Stokes flow equations. A low-order BEM model is developed for the two biological fluids coupled at the membrane surface. The moving boundary problem in fluid mechanics can be effectively solved using the BEM with a GMRES solver. The FEM model based on a flat thin shell element is further developed to predict the membrane load due to the large deformation of a moving cell. Computational efficiency is greatly improved due to the one-dimensional reduction in the present BEM and FEM models. The BEM solver for the biological fluids is coupled with the FEM solver for the cell membrane at the membrane surface. The position of the membrane surface nodes is advanced in time by using the classical fourth-order Runge-Kutta method. Numerical instability is avoided by using a relatively small time step. Further numerical instabilities in the FEM solver is alleviated by using various techniques. The present method is applied to the FSI problems of cell motion in a cylindrical flow. Numerical examples can illustrate the distinct accuracy, efficiency and robustness of the present method. Furthermore, the importance of bending stiffness of a cell membrane for stable cell motion simulation is emphasized. It is suggested that the present approach be an appealing alternative for simulating the fluid-structure interaction of moving cells.

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1 Introduction

The motion of living cells in large vessels, narrow tubes, and microcapillaries is one of the most important physiological phenomena of biological systems. As a common type of living cells in the blood vessels, red blood cells, which consist of a nearly-Newtonian cytoplasm enclosed by a lipid bilayer and a supportive cytoskeleton network of proteins, are the vertebrate body's principal means of delivering oxygen from the lungs or gills to body tissues via the blood. Living cells can be generally modelled as capsules in the context of particulate microhydrodynamics [1–4], different from droplets and bubbles whose interfacial forces result from surface tension [5]. Various types of capsules exist in the fields of medicine, physiology, biotechnology, as well as in the pharmaceutical industry, with important applications in drug delivery and cell therapy [4].

In the process of cell motion, fluid-structure interaction (FSI) can be of significant importance due to the deformability of living cells [6]. The hydrodynamics inside and around the cell should be coupled with the membrane dynamics of the cell in a physiologically accurate manner. The fluid mechanics was usually approximately described by Newtonian low-Reynolds-number hydrodynamics [3–5, 7]. The structural mechanics of cell membranes can be described by either the continuum thin-shell theories [1, 4, 8–12] or discrete molecular dynamics [13, 14]. Despite less insight into the detailed molecular mechanical behaviors, the continuum approach using the thin-shell theories is easier to implement and more straightforward to use if only the biomechanical response at the cell level is needed [15]. The continuum approach can further assist in the development of more accurate molecular models since it can provide the forces to the cytoskeletal and subcellular components by appropriate distribution and transmission of the stresses induced on the cell. In this study, only the continuum approach using a thin-shell theory for the cell membrane simulation is considered. As noted in [16–19], the fluid-structure interactions are among the most important but challenging multiphysics problems with respect to both modeling and computational issues.

Tremendous research efforts have been devoted to the development of modeling and simulation approaches for the FSI problems of cell motion [4, 18]. In the early efforts by Secomb [20, 21], pellets consisting of an elastic solid were used to model the cells to illuminate some basic reviews in the context of biofluid dynamics. The fluid-structure interactions to describe the motion of individual cells were neglected. In order that the virtual incompressibility and elastic properties of the cell membrane can be taken into consideration, more accurate models using thin-shell theories were further developed [1, 4, 8–12]. Zarda et al. [8] are among the first researchers to use the finite element method (FEM) to solve the equations of low-Reynolds-number hydrodynamics around a steadily translating cell in a perfectly axisymmetric configuration. A membrane model with a finite dilation modulus and resistance to bending stresses was used, and axisymmetric flow through capillaries using the finite element method simulated. More realistic model for tightly-fitting cells based on the lubrication approximation was proposed by Secomb and co-workers [2, 22–26]. A boundary-value problem involving ordinary differential equa-