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Exact Singularity Subtraction from Boundary Integral Equations in Modeling Vesicles and Red Blood Cells

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Abstract. The study of vesicles, capsules and red blood cells (RBCs) under flow is a field of active research, belonging to the general problematic of fluid/structure interactions. Here, we are interested in modeling vesicles, capsules and RBCs using a boundary integral formulation, and focus on exact singularity subtractions of the kernel of the integral equations in 3D. In order to increase the precision of singular and near-singular integration, we propose here a refinement procedure in the vicinity of the pole of the Green-Oseen kernel. The refinement is performed homogeneously everywhere on the source surface in order to reuse the additional quadrature nodes when calculating boundary integrals in multiple target points. We also introduce a multi-level look-up algorithm in order to select the additional quadrature nodes in vicinity of the pole of the Green-Oseen kernel. The expected convergence rate of the proposed algorithm is of order $\mathcal{O}(1/N^2)$ while the computational complexity is of order $\mathcal{O}(N^2 \ln N)$, where N is the number of degrees of freedom used for surface discretization. Several numerical tests are presented to demonstrate the convergence and the efficiency of the method.

AMS subject classifications: 64N38, 65N80, 74F10, 76Z05

Key words: Stokes flow, fluid structure interaction, boundary integral method, red blood cells, singularity subtraction.

1. Introduction

Blood is a complex fluid that is primarily composed of red blood cells (RBCs), which occupy (in a healthy human body) about 45% of the blood volume. The rest consists of plasma, while the other blood elements (white blood cells, platelets, etc.) take up less than 1% of the total blood volume.

The complex character of blood flow results from an intimate coupling between the shape of RBCs and the fluid dynamics of the ambient plasma, which leads to a rich

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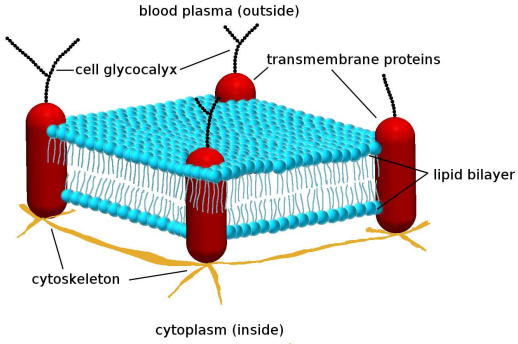

Figure 1: A schematic view of the RBC membrane showing the phospholipid bilayer, the spectrin network (called cytoskeleton) beneath and several membrane and transmembrane proteins.

set of RBC morphologies in the blood circulatory system. Understanding the selection of shapes and dynamics among a large manifold of possibilities, the collective effects, the spatiotemporal organizations is a challenging problem. This type of complexity is a characteristic property of non-equilibrium dissipative systems for which general thermodynamic principles, such as minimization of energy, maximization of entropy, etc., cannot be applied.

Due to the predominance of the concentration of RBCs in blood, blood flow is dictated primarily by RBCs. A RBC is made of a bilayer of phospholipid (see Fig. 1). In addition, several proteins are anchored on this membrane (like ion channels), while beneath the membrane there is a cytoskeleton, a network of proteins, called spectrin, that confers to the cell viscoelastic properties. Healthy human RBC has a biconcave shape at rest. Its size is about few μm. The interior of the RBC is made of an aqueous solution containing hemoglobin (and other species, like ATP-adenosine triphosphate). Hemoglobin is responsible for oxygen transport from lungs towards the microvasculature (arterioles, veinules and capillaries), where gas exchange takes place for tissue metabolism. ATP is, among other functions, responsible for vasodilation. The hemoglobin solution is believed to be a newtonian fluid. It has a viscosity which is of about 5 times that of the plasma (whose viscosity is close to that of water).

In this paper, we shall present modeling of these systems based on the boundary integral(BI) formulation. We propose a method for calculation of BIs in flows of complex geometry. The method combines the singularity subtraction (SS) technique with the refinement in vicinity of the pole of the Green kernels in order to achieve good precision of singular and near-singular integration without excessive increase of computation time with respect to traditional integration techniques.

2. Modeling of blood flow

2.1. Modeling of red blood cells

Due to the complexity of the RBC modeling, especially because of its cytoskeleton, two model systems have been considered as alternative systems serving as a basis for