An immersed-boundary fluid-structure interaction approach for the simulation of biological flows

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ABSTRACT

Fluid-structure interaction (FSI) problems are found in many engineering areas and their computational modeling is particularly challenging. Among different FSI problems, biological applications are becoming of ever increasing interest in the scientific community. In such cases, describing the dynamics of the interaction between the body and the fluid is not a trivial task, since the numerical method needs to be able to handle in an efficient way complex and very thin geometries undergoing large deformations, while preserving accuracy.

In this work, a versatile numerical method is presented to predict the fluid-structure interaction of bodies with arbitrary thickness immersed in an incompressible fluid, with the aim of simulating different biological engineering applications. A direct-forcing immersed boundary method is adopted, based on a moving-least-squares approach to reconstruct the solution in the vicinity of the immersed surface [1]. A simple spring-network model is considered for describing the dynamics of deformable structures, so as to easily model and simulate different biological systems that not always may be described by simple continuum models, without affecting the computational time and simplicity of the overall method. The fluid and structures are coupled in a strong way, in order to avoid instabilities related to large accelerations of the bodies. The effectiveness of the method is validated by means of several test cases involving: rigid bodies, infinitely thin elastic structures with mass, flapping flags, with a very good agreement with available experimental data and numerical results obtained by different methods.

Two case studies are presented: 1) A jellyfish-inspired model swimming in a resting fluid, including the effect of active muscle contraction (bell) and passive body elasticity (appendage). Varying the strength of contraction and the material properties of the bell margin one can predict swimming performance and cost of transport in different cases, helping the design of bio-inspired water propulsion systems; 2) A bio-prosthetic aortic valve placed in a realistic geometry of the human aorta under pulsatile flow conditions. The flow and structure dynamics are reproduced accurately, giving results in good agreement with experimental data obtained for similar configurations. Blood damage is then estimated by means of a high-fidelity hemolysis model, based on a coarse-grained description of the erythrocyte membrane spectrin cytoskeleton [2], allowing for a prediction of the thrombogenicity of different valve models.

REFERENCES
