Parallel and Adaptive Infrastructure for Biological Fluid-Structure Interaction

Coupled fluid-structure systems are ubiquitous in biology. The immersed boundary (IB) method is both a mathematical formulation and a numerical approach to such problems, treating the case in which an elastic structure is immersed in a viscous incompressible fluid. The IB method was introduced to describe the fluid dynamics of heart valves and cardiac fluid dynamics, but this methodology has also been applied to a wide range of problems in biological fluid dynamics and, more generally, to a variety of problems in which an incompressible flow interacts with an immersed structure.

Although the IB method is a broadly useful approach to biofluid mechanics, high spatial resolution is generally required to resolve viscous boundary layers at fluid-structure interfaces and, especially at higher Reynolds numbers, to resolve vortices shed from such interfaces. Increased resolution with a uniform computational grid can lead to problem sizes which are computationally infeasible. To improve the efficiency of the IB method, we have developed an adaptive version of the IB method that employs block-structured adaptive mesh refinement (AMR) to deploy high spatial resolution only where it is needed, such as in the vicinity of fluid-structure interfaces, or near localized regions of high vorticity in the flow field. The IBAMR software is a distributed-memory parallel implementation of this adaptive scheme. This code is being actively used within several independent research projects that aim to model different aspects of cardiovascular dynamics, such as platelet aggregation and the fluid dynamics of natural and prosthetic heart valves, as well as within projects that study other problems in biofluid mechanics, including insect flight, aquatic locomotion, and the dynamics of phytoplankton.

For more information about IBAMR, visit: http://code.google.com/p/ibamr/