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MODEL AND METHOD HIERARCHIES FOR BIOMEDICAL FLOW SIMULATION

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Computational analysis and design has achieved a widespread application across all engineering and scientific disciplines. Yet, as the systems being analyzed gain in complexity, the simulation process itself has become complex and fraught with ad hoc solutions and intuition. Continued impact may depend on systematizing the computational practice.

The simulation process may be divided into model, method, and data aspects. Each of the components of this tripod can be seen as a hierarchy of available options, each with certain predictivity (or fidelity) and a certain cost. A rational simulation process should involve selection of a model or models, discretization and numerical methods, and data sets or parameters, with a matched and sufficient predictivity at a minimal cost.

For this vision to become possible, progress needs to be made towards both establishing model and method hierarchies, and gaining insights into their predictivity and cost. On the modeling side, a hierarchy may represent a description of physical phenomena at different levels of abstraction. Examples of biomedical applications relying on varying description of blood constitutive behavior and geometric details are given. The issue of model adaptation, whether global or local, is also discussed [1].

On the method side of the tripod, certain hierarchies in the sense of varying and even adaptive refinement are well known. But this flexibility is not matched for problems involving deforming fluid domains or moving components. A universal treatment appears to be elusive. A concept of unstructured space-time meshing provides one way out of this dilemma. Flows around moving valves are given as an example [2].

This is joint work with Anna Ranno, Max Schuster, Fabio Guglietta, Max von Danwitz, Norbert Hosters, and Christoph Susen.

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