

Monolithic and partitioned numerical models for coupled problems in biological applications

Scientific area: Computational Applied Mathematics

Important features of many physical phenomena emerge from the interaction of different physical systems and different temporal or spatial scales. This is particularly true in computational medicine and other biological applications, due to the strong interplay among the systems and components of an organism.

This minisymposium aims at discussing recent coupling strategies both at the modeling level and at the level of numerical discretization. For the former, the interest encompasses multiphysics (over coinciding or neighboring spatial domains) and geometric multiscale modeling (e.g., coupling continuum systems and particle interactions, or 3D and lower dimensional models). At the numerical level, splitting methods such as fractional time-step and staggered schemes may be employed, suitably endowed with interpolation operators and communication algorithms for the exchange of information among spatial domains or time scales. The resulting algebraic systems are typically characterized by a strong imbalance in the number of unknowns or their scaling. Therefore, the design of effective and efficient preconditioners plays a paramount role.

The interest for this minisymposium includes applications in computational biology and medicine such as cardiac and cardiovascular systems, living tissues and their growth, drug delivery, design and implant of biomedical devices, and others.

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