From biological and clinical experiments to mathematical models

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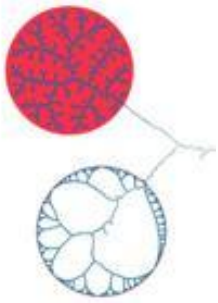

This theme issue discusses the complex cross-disciplinary interactions among the various disciplines involved in the study of a living system (biology, mathematics, and computer sciences). The usual way to formalize, in a rational form, the structure of a biological system is to propose a mathematical formulation of the key processes and of interactions among them which have been identified as fundamental for the studied system. This approach allows one to study, from a mathematical point-of-view, the properties arising from the mathematical model. It is then possible to return to reality with proposals for new experiments in order to validate (or to invalidate) the emergent properties predicted by the mathematical model.

However, the complexity of living systems precludes a complete model of their behaviour, and models of the subsystems of interest are sometimes mathematically intractable. Moreover, compared to a biological system, the simplified hypotheses required to construct a mathematical model may be too unrealistic. In these cases, the model may be too simple to reproduce the interesting behaviour or, at the opposite extreme, too complex to be well understood. In the latter case, the only possible use of such mathematical objects is to mimic the behaviour of the biological system while accepting a limited knowledge of the dynamic behaviour of the mathematical model.

All of these questions raise the need for the development of mathematical methods capable either of reducing the complexity of a mathematical model while keeping the richness of its dynamics or of constructing simple comprehensible models that can generate complex dynamics. The authors in this issue present original approaches in order to answer such questions in many fields of mathematical biology, mainly dynamical systems and evolution PDEs.

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