



Harnessing Biological Complexity: An Introduction to Computational Physiology: 1 (A First Course in "In Silico Medicine")

Taishin Nomura, Yoshiyuki Asai

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The challenge for the biosciences in the twenty-first century is to integrate genome sequencing information into a better understanding of biology, physiology, and human pathology. Such attempts at integration are moving the world toward a new generation of bioscience and bioengineering, where biological, physiological, and pathological information from humans and other living animals can be quantitatively described in silico across multiple scales of time and size and through diverse hierarchies of organization — from molecules to cells and organs, to individuals. To "harness" such complexity, international communities of integrative bioscientists and bioengineers aim to establish frameworks and information infrastructures for describing biological structures and physiological functions on multiple scales of time and space. This textbook includes a public platform to describe physiological functions using mathematical equations and guides the reader to perform mathematical modeling and computer simulations, to combine existing models as well as to create new models. Accessible to biologists, physiologists, and students of the sciences, with illustrative details provided when necessary, this book seeks to achieve a systematic way of harnessing biological complexity. Sharing the databases among communities worldwide will help to find comprehensive answers to all the important questions.



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