

This accessible text presents a detailed introduction to the use of a wide range of software tools and modeling environments for use in the biosciences, as well as the fundamental mathematical background. The practical constraints presented by each modeling technique are described in detail, enabling the researcher to determine which software package would be most useful for a particular problem. Features: introduces a basic array of techniques to formulate models of biological systems, and to solve them; discusses agent-based models, stochastic modeling techniques, differential equations, spatial simulations, and Gillespie's stochastic simulation algorithm; provides exercises; describes such useful tools as the Maxima algebra system, the PRISM model checker, and the modeling environments Repast Symphony and Smoldyn; contains appendices on rules of differentiation and integration, Maxima and PRISM notation, and some additional mathematical concepts; offers supplementary material at an associated website.

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