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Identification of Parameters in Mathematical Biology. Preliminary report.

We consider inverse problems for the identification of both constant and functional parameters for systems of nonlinear ODEs arising in mathematical biology. We implement a numerical method suggested in U.G.Abdulla, Journal of Optimization Theory and Applications, 85, 3(1995), 509-526(Part I); 527-543(Part 2). The idea of the method is based on the combination of Bellman's quasilinearization with sensitivity analysis in Banach spaces setting and Tikhonov's regularization. We apply the method to various biological models such as Lotka-Volterra system, bistable switch model in genetic regulatory networks, a three-step pathway modelled by 8 nonlinear ordinary differential equations, etc. Then we test the robustness of the method in the presence of random noise. Numerical results confirm the quadratic convergence. (Received September 19, 2015)