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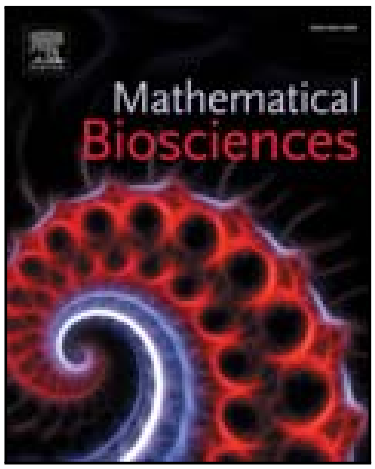

Identification of Parameters in Systems Biology

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Highlights

- Numerical method is developed for solving inverse problem on the identification of the finite dimensional set of parameters in systems biology models described by nonlinear ODEs
- Method combines the ideas of Pontryagin optimization, Bellman quasilinearization and Tikhonov regularization
- Well-posedness and convergence of the method is directly associated with the identifiability of the parameters
- Accompanied with regularization the method presents a robust algorithm to address practical non-identifiabilty cases
- Method is applied to solve inverse problem on the identification of parameters for Lotka Volterra system, bistable switch model in genetic regulatory network, gene regulation and repressilator models in synthetic biology.
- Effects of Tikhonov regularization with optimal choice of regularization parameter for the identification of the large parameter sets, noisy data and quadratic convergence is analyzed.
- The method has an advantage over popular methods such as lsqnonlin, fmincon, nl2sol in terms of computational time, number of iterations and function evaluations.

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