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Abstract: This is a review article to show that delay differential models have a richer mathematical framework (compared with models without memory or after-effects) and a better consistency with biological phenomena such dynamical diseases and cell growth dynamics. The article provides a general computational technique to treat numerically the emerging delay differential models. It introduces the numerical algorithms for parameter estimations, using least squares approach. The article introduces a variational method to evaluate sensitivity of the state variables to small perturbations in the initial conditions and parameters appear in the model. An application to show the consistency of DDE models with cell growth dynamics is also considered.

Keywords: delay differential equations, epidemiology - SIR, immunology, physiology, RK-methods, time-lags, delay, parameter estimation, sensitivity