Parameter Identification in a System of Differential Equations Modeling Evolution of Epidemic Diseases

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A mathematical model for the prediction of time evolution of sexually transmitted diseases has been developed. It consists of nine coupled ordinary differential equations and includes 22 user-specified parameters. These parameters have specific physical meanings and a relatively well defined upper and lower bounds, but their exact values are unknown. Therefore, it is of utmost importance to determine values of these 22 parameters so that the results of numerical integration match as closely as possible certain aggregate quantities (such as mortality rates of infants due to an infectious disease such as syphilis that was acquired at birth) for which actual field data exist in medical statistics. This is a practical example of parameter identification problem which was solved by minimizing an L_2 norm of the difference between the predicted mortality of infants and the observed mortality of infants during a period of 70 years (1900-1970). Because of the relatively large number of parameters and the highly coupled system of ordinary differential equations, one could expect that the objective function space has a number of local minima and any standard gradient based minimization algorithm would thus terminate in the nearest feasible minimum. Therefore, we used our robust hybrid optimization algorithm which automatically switches among several gradient based and evolutionary minimization algorithms in order to maximize the convergence rate of the minimization process towards the global minimum. This parameter identification problem was accomplished successfully.