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The SEI epidemiological model generates natural classes of biological functions: analysis using reaction netwok theory

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The idea of the present research is to find analogies between classical epidemiological models and reaction networks used in chemical reactions in Biology. The Susceptible-Exposed-Infectious (SEI) epidemiological model (see [1], [2]) is considered in the context of the Chemical Reaction Network Theory as a two-step exponential (radioactive) decay reaction chain (Bateman chain): species S is transformed into species E, E is transformed into I, such that the first reaction step (S is transformed into E) is catalyzed by species I.

We study the temporal evolution of the masses/concentrations of the species involved assuming mass action kinetics, focusing mainly on the growth function describing the mass of species I as part of the SEI model. We are especially interested in the situation when one of the chain-links of the SEI model is much faster relative to the other one. We demonstrate that under certain conditions a SEI reaction network can be "approximated" by a single-step reaction, which is either of logistic auto-catalytic type, or, of a first-order exponential non-catalytic type. We thus show that the time evolution graph of the growing species changes its shape between a sigmoidal logistic-type and a concave first-order exponential-type, depending on the ratio of the two rate parameters involved.

This fact motivates us to propose some hints that may be useful for deciding on the choice of an appropriate class of growth functions when numerically simulating a given measurement data set resulting from biological (experimental) processes. More specifically, the modeller should first examine empirically the shape of the specific measurement data set (concavity, sigmoidality, location of the inflection point, lag time, etc.) and then decide what reaction network would better fit the given measurement set [1]–[5].

Keywords: SIR-SEIR models in epidemiology, dynamical systems, (bio-)chemical reaction networks, mass action kinetics, exponential decay chain, Bateman equations, logistic functions, sigmoidal growth functions, population dynamics, parameter identification

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