Can the Lotka-Volterra canonical form and mass-action kinetics help for studying epidemiology and virology models?

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June 1, 2022

Abstract

The sister disciplines of (deterministic) mathematical epidemiology and virology, chemical reaction networks (CRN), and biochemical systems started all as collections of examples of non-negative (mostly polynomial) differential dynamical systems, and it is instructive to review their status-quos nowadays.

Deterministic mathematical epidemiology has one celebrated general law, the "R_0 alternative" of Van-den Driessche and Watmough (2002). This states that the local stability condition of a disease free equilibrium assumed to be unique may be expressed under very general conditions as $R_0 < 1$, where R_0, known as "basic reproduction number", is related to the expected number of children in the theory of branching processes. This law seems to be useful in Mathematical Virology as well.

The mathematical epidemiology literature suggests that it may be possible to find other general laws concerning the endemic points, since

1. when $R_0 > 1$, one often encounters a unique fixed endemic point, and

2. the endemic point is typically locally stable when $R_0 > 1$, i.e. when the disease free equilibrium (DFE) isn't.

However, it is difficult to find conditions for the above observations which are both general enough and natural. Let us comment here that most of the mathematical epidemiology literature is, surprisingly, dedicated to conditions which are very rarely met in an epidemic, such as:

1. Conservation of total mass; in lay words, the epidemic causes no deaths.

2. The birth rate is constant; in lay words, there are no births, only immigration, and the immigration precisely balances the natural death rate.

3. Immunity achieved when recovering from sickness is eternal.

Of course, these assumptions may be justified as first caricatures of real epidemics, but the fact that these are gross simplifications seems to be somewhat forgotten, and the study of realistic epidemic models which do not ignore casualties seems somewhat neglected.

We have introduced in [AAK21, AABH22, AAB$^+$21] a "simple", but broad class of "SIR-PH models" with varying population, but only one "susceptible class" (producing new infections), with the express purpose of establishing for these processes the two properties of endemic points above. Since that seemed still hard, we have introduced two further classes "SIR-PH-FA" and "SIR-PH-IA" of approximations for the SIR-PH models, the first of which includes the classic caricatures typically studied in the literature.

It is an interesting question whether general results about this class may be obtained by using Lotka-Volterra canonical forms or CRN representations.

References

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