

# A Lie system approach to resolve compartmental epidemic systems

Epidemic models try to predict the spread of an infectious disease afflicting a specific population. These models are rooted in the works of Bernoulli in the XVIII century, when he proposed a mathematical model to defend the practice of inoculating against smallpox. At the beginning of the XX century, the emergence of compartmental models was starting to develop. Compartmental models are deterministic models in which the population is divided into compartments, each representing a specific stage of the epidemic. For example,  $S$  represents the susceptible individuals to the disease,  $I$  designates the infected individuals, whilst  $R$  stands for the recuperated ones. There are several types of compartmental models, as it can be the SIS model, in which after the infection the individuals do not acquire immunity, a SIRS model, for which immunity only lasts for a short period of time, the MSIR model in which infants are born with immunity, etc. The evolution of these variables in time is represented by a system of ordinary differential equations whose independent variable, the time, is denoted by  $t$ .

A Lie system is a system of ordinary differential equations admitting a superposition principle, that is, a map expressing the general solution of the system of ODEs in terms of a family of particular solutions and a set of constants related to initial conditions. Very surprisingly, it was proven that some new Lie systems admitted Vessiot–Guldberg algebras of Hamiltonian vector fields with respect to some symplectic or Poisson structure. This led to the study of an important particular case of Lie systems, the so called Lie–Hamilton systems.

The goal of our project is to formulate compartmental epidemic models admitting a Hamiltonian formulation in terms of Lie and Lie–Hamilton systems. The important advantage of such a formulation is the possibility to deal with models with time-dependent coefficients in particular recovery and transmission rates. In the next step we want to introduce stochastic variables to the model for the discussion of fluctuations. Stochastic models have a random variable and they estimate probability distributions of potential outcomes by allowing for random variation in one or more inputs over time. Statistics show that the introduction of fluctuations is essential to understand the contagion stages in epidemics. The third goal is to find both analytical and approximated solutions of our system and by a proper choice of initial conditions compare them with the available data.