Global sensitivity analysis for models described by continuous time Markov chains with application to epidemic models

Henri Mermoz KOUYE
Paris-Saclay University

Supervisor(s): Gildas Mazo (MaIAGE, INRAE), Elisabeta Vergu (MaIAGE, INRAE) and Clémentine Prieur (LJK, Grenoble-Alpes University)

Address: UR1404 INRAE MaIAGE, 78352 Jouy-en-Josas

Email: henri-mermoz.kouye@inrae.fr

Abstract: Stochastic models are increasingly used in various fields (epidemiology, biology, physics etc) to describe different phenomena. Models can be described by stochastic processes, hence including an intrinsic randomness. Performing global sensitivity analysis (GSA) for such models is challenging, if the intrinsic randomness of the system is considered as a noise on specific quantities of interests (QoIs). The objective of our work is to propose a generic strategy to perform GSA on such stochastic systems.

In order to introduce a more generic framework, our strategy aims firstly at separating the two sources of variability, namely parameters uncertainty and intrinsic randomness and secondly at putting the model functional QoI Y under the form: $Y = f(X, Z)$, where f is a function, X stands for the uncertain parameters and Z represents the intrinsic randomness such as X and Z are independent. For this purpose, two approaches are introduced: Sellke construction [6] and Kurtz representation [1],[3](this later having been recently used for sensitivity analysis of Markov based models in chemical physics [5]). Depending on the class of models, Sellke construction allows to describe Z as a finite-dimensional vector with known distribution while under Kurtz representation, Z is a vector of independent Poisson processes with intensity 1. These two approaches allow not only to estimate the sensitivity indices of the input parameters but also to measure the influence of the intrinsic randomness on the global variability of the QoI under study. Furthermore, Sellke construction can be used to extend to the non-markovian framework.

Then, we put ourselves in various frameworks of sensitivity analysis and implement different methods (global sensitivity indices [4], general metric space sensitivity indices [2], etc) by introducing the indices and their estimators and finally by carrying out the simulations. In order to illustrate the approaches we developed, they will be applied to some SIR-like models which are usually used in stochastic modeling of epidemics.

References

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