

Large population limits in a wide class of individual-based epidemic models

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We present a general and tractable framework for modeling and “nowcasting” the epidemic at a national scale. Our approach is based on a fairly general, individual-based, stochastic model for complex diseases using an arbitrarily large number of types (e.g., infective stage, clinical state, risk factor class). Under the branching assumption, the dynamics of the epidemic is completely determined (in distribution) by a pair (X, \mathcal{P}) , where X is a stochastic process valued in the type space describing the history of an individual infection through time and \mathcal{P} is a point process whose atoms are the times (since infection) at which the individual infects others.

We show how structuring the infected population by its infection age, i.e., time elapsed since infection, allows us to decouple dependencies between types and to time. In the large population limit (obtained either by assumption on the initial condition or as a spontaneous effect of the outbreak), the global scale of the epidemic is well captured by a deterministic McKendrick-Von Foerster 1-d PDE depending only on the expectation of \mathcal{P} and decorated by the one-dimensional marginals of X . We explain how such an approximation allows us to easily obtain parameter estimates and make robust predictions on the fate of the epidemic.

This work is a collective effort of the SMILE group (Stochastic Models for the Inference of Life Evolution) at Sorbonne Université and Collège de France [1].

- [1] F. Foutel-Rodier*, F. Blanquart, P. Courau, P. Czuppon, J.-J. Duchamps, J. Gamblin, É. Kerdoncuff, R. Kulathinal, L. Régnier, L. Vuduc, A. Lambert**, E. Schertzer**. *From individual-based epidemic models to McKendrick-von Foerster PDEs : A guide to modeling and inferring COVID-19 dynamics*. Eprint arXiv :2007.09622, 2020.