Esquível M. L. (New University of Lisbon, Portugal) — **From an Ordinary Differential Equation Model to an Open Population Markov Chain Model, via Stochastic Differential Equations; models for HIV infection in individuals and populations.**

We present an initial exploration of a method for the association of a open population Markov chain model – with a finite number of states – to some phenomena that may be, by force of its intrinsic characteristics, best modeled by ODE, at least in some average sense. The ODE model here presented is formulated as a dynamic change between two regimes; one regime is of mean reverting type and the other is of inverse logistic type. For the general purpose of defining a open Markov chain model for an human population, we associate an Ito process to the OD equations, by means of the addition of Gaussian noise terms which may be thought to model non essential characteristics of the phenomena with small and undifferentiated influences. The next step consists on discretizing the Ito processes and using the sequence of values obtained to define, by simulation, trajectories that, in turn, may define transitions of a finite valued Markov chain, if the state space of the Ito process is partitioned according to some rule. We detail the application of these ideas to the study of the evolution of a Portuguese population of newly diagnosed with HIV. For that purpose the state space of the Ito process referred is partitioned in six infection classes. We detail the evolution of the population in these classes under two different projections for the evolution of the newly diagnosed. The method here presented connects the model for the evolution of the HIV viral load and the CD4 leucocytes count to a Markov chain open model for the Portuguese population of HIV diagnosed.

<div align="center">REFERENCES</div>

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