

A branching process approach for the propagation of the Bovine Spongiform Encephalopathy in Great-Britain

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Keywords: Branching processes; Extinction; Bayesian estimation; Epidemiology.

AMS: 60J80; 60J85; 92D30

Abstract

The goal of this work is the modelling of the propagation of BSE (Bovine Spongiform Encephalopathy) at the scale of a very large population (Great-Britain) in order to predict its extinction time and to evaluate the efficiency of the main feedback regulation. We first elaborate a multitype branching process in discrete time with age and population dependent individual transitions. The types are the health states at each age. Then, assuming that the disease is rare at the initial time, and assuming a Reed-Frost type assumption for the infection law, we derive from this model a limit process on the incidence of clinical cases, as the initial size of the population increases to ∞ . This limit process may be either considered as a singletype $(a_M - 1)$ -Markovian process with a Poissonian transition distribution, or a multitype Bienaymé-Galton-Watson process having $a_M - 1$ types corresponding to the memory of the process. We derive the bifurcation parameter, the extinction probability and the extinction time distribution from the limit process. Estimations are then done in the Bayesian setting.

Acknowledgements: This work is done in collaboration with L. Maillard, J.-B. Denis, C. Bidot, and was supported by the french government through the project GIS Prions and then by the european ReX Neuroprion

References

- [1] Jacob, C., Maillard, L., Denis, J.-B., Bidot, C. (2008) *Stochastic modelling of the incidence of clinical cases of a rare fatal SEI disease in a large branching population structured in ages. Example of the BSE epidemic in Great-Britain* Technical report, MIA-INRA, Jouy-en-Josas.