Summary : "Conditional limit theorems for multitype branching processes and illustration in epidemiological risk analysis."

This thesis is concerned with the issue of extinction of populations composed of different types of individuals, and their behavior before extinction and in case of a very late extinction. We approach this question firstly from a strictly probabilistic viewpoint, and secondly from the standpoint of risk analysis related to the extinction of a particular model of population dynamics. In this context we propose several statistical tools.

The population size is modeled by a branching process, which is either a continuous-time multitype Bienaymé-Galton-Watson process (BGWc), or its continuous-state counterpart, the multitype Feller diffusion process. We are interested in different kinds of conditioning on non-extinction, and in the associated equilibrium states. These ways of conditioning have been widely studied in the monotype case. However the literature on multitype processes is much less extensive, and there is no systematic work establishing connections between the results for BGWc processes and those for Feller diffusion processes.

In the first part of this thesis, we investigate the behavior of the population before its extinction by conditioning the associated branching process X_t on non-extinction ($X_t \neq 0$), or more generally on non-extinction in a near future $0 \leq \theta < \infty$ ($X_{t+\theta} \neq 0$), and by letting t tend to infinity. We prove the result, new in the multitype framework and for $\theta > 0$, that this limit exists and is non-degenerate. This reflects a stationary behavior for the dynamics of the population conditioned on non-extinction, and provides a generalization of the so-called Yaglom limit, corresponding to the case $\theta = 0$. In a second step we study the behavior of the population in case of a very late extinction, obtained as the limit when θ tends to infinity of the process conditioned by $X_{t+\theta} \neq 0$. The resulting conditioned process is a known object in the monotype case (sometimes referred to as Q-process), and has also been studied when X_t is a multitype Feller diffusion process. We investigate the not yet considered case where X_t is a multitype BGWc process and prove the existence of the associated Q-process. In addition, we examine its properties, including the asymptotic ones, and propose several interpretations of the process. Finally, we are interested in interchanging the limits in t and θ, as well as in the not yet studied commutativity of these limits with respect to the high-density-type relationship between BGWc processes and Feller processes. We prove an original and exhaustive list of all possible exchanges of limit (long-time limit in t, increasing delay of extinction θ, diffusion limit).

The second part of this work is devoted to the risk analysis related both to the extinction of a population and to its very late extinction. We consider a branching population model (arising notably in the epidemiological context) for which a parameter related to the first moments of the offspring distribution is unknown. We build several estimators adapted to different stages of evolution of the population (phase growth, decay phase, and decay phase when extinction is expected very late), and prove moreover their asymptotic properties (consistency, normality). In particular, we build a least squares estimator adapted to the Q-process, allowing a prediction of the population development in the case of a very late extinction. This would correspond to the best or to the worst-case scenario, depending on whether the population is threatened or invasive. These tools enable us to study the extinction phase of the Bovine Spongiform Encephalopathy epidemic in Great Britain, for which we estimate the infection parameter corresponding to a possible source of horizontal infection persisting after the removal in 1988 of the major route of infection (meat and bone meal). This allows us to predict the evolution of the spread of the disease, including the year of extinction, the number of future cases and the number of infected animals. In particular, we produce a very fine analysis of the evolution of the epidemic in the unlikely event of a very late extinction.