Estimation of the offspring mean in a supercritical or near-critical size-dependent branching process. Application to quantitative PCR.

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We consider a single-type supercritical or near-critical size-dependent branching process $\{N_n\}_n$ such that the offspring mean converges to a limit $m \geq 1$ with a rate of convergence of order N_n^{α}, as the population size N_n grows to ∞, and the variance may increase at the rate N_n^{β}, where $-1 \leq \beta < 1$. We assume that the offspring mean depends on an unknown asymptotically identifiable parameter θ_0 that belongs either to the limit model or to the transient model.
We estimate θ_0 on the non-extinction set of the process from the observations $\{N_h, \ldots, N_n\}$, by using the conditional least squares method weighted by $\{N_{n-1}^{-\gamma}\}_n$. We study the strong consistency of the estimator according to γ, with either h or $n-h$ remaining constant as $n \to \infty$, by using the minimum contrast method [4]. The main sufficient and probably also necessary condition for the consistency of the transient parameter is $\beta + 2\alpha \leq 1$. We also give the asymptotic distribution of the estimator by using Rahimov's central limit theorem for random sums [3] and we show that the best rate of convergence is reached for $\gamma = 1 + \beta$.
We apply our results to the particular setting of the quantitative PCR consisting in the amplification of a DNA molecules population and which aims at quantifying the initial amount N_0 of the population [1]. In the PCR setting, the current quantification method needs many amplification trajectories to estimate the efficiency in order to quantify N_0, where the efficiency is the probability that a molecule will be duplicated. The current quantification uses only one observation per amplification trajectory and is based on inadequate mathematical models. The branching process theory is naturally used to model the PCR amplification process and recently a size-dependent branching process has been developed by Jagers and Klebaner [2]. We propose a new modelling of a PCR amplification trajectory relying on size-dependent branching processes and estimate the reaction efficiency of a single trajectory. We study the properties of the estimators of the efficiency at finite distances using simulations and real-time PCR data.

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