# Nonparametric estimation of the division rate of an age dependent branching process 

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Received 17 December 2014; received in revised form 20 November 2015; accepted 23 November 2015
Available online 3 December 2015


#### Abstract

We study the nonparametric estimation of the branching rate $B(x)$ of a supercritical Bellman-Harris population: a particle with age $x$ has a random lifetime governed by $B(x)$; at its death time, it gives rise to $k \geq 2$ children with lifetimes governed by the same division rate and so on. We observe in continuous time the process over $[0, T]$. Asymptotics are taken as $T \rightarrow \infty$; the data are stochastically dependent and one has to face simultaneously censoring, bias selection and non-ancillarity of the number of observations. In this setting, under appropriate ergodicity properties, we construct a kernel-based estimator of $B(x)$ that achieves the rate of convergence $\exp \left(-\lambda_{B} \frac{\beta}{2 \beta+1} T\right)$, where $\lambda_{B}$ is the Malthus parameter and $\beta>0$ is the smoothness of the function $B(x)$ in a vicinity of $x$. We prove that this rate is optimal in a minimax sense and we relate it explicitly to classical nonparametric models such as density estimation observed on an appropriate (parameter dependent) scale. We also shed some light on the fact that estimation with kernel estimators based on data alive at time $T$ only is not sufficient to obtain optimal rates of convergence, a phenomenon which is specific to nonparametric estimation and that has been observed in other related growth-fragmentation models.


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MSC: 35A05; 35B40; 45C05; 45K05; 82D60; 92D25; 62G05; 62G20
Keywords: Growth-fragmentation; Cell division; Nonparametric estimation; Bias selection; Minimax rates of convergence; Bellman-Harris processes

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## 1. Introduction

### 1.1. Motivation

Structured models have been paid particular attention over the last few years, both from a probabilistic and an applied analysis angle, in particular with a view towards a better understanding of population evolution in mathematical biology (see for instance the textbook by Perthame [21] and the references therein). In this context, a more specific focus and need for statistical methods has emerged recently (e.g. Doumic et al. [9,8,7] and the references therein) and this is the topic of the present paper. If $x$ denotes a so-called structuring variable-for instance age, size, any measure of variability or DNA content of a cell or bacteria, and if $n(t, x)$ denotes the number or density of cells at time $t$ of a population starting from a single ancestor at time $t=0$, a sound mathematical model can be obtained by specifying an evolution equation for $n(t, x)$.

Consider for instance the paradigmatic problem of age-dependent cell division, where the evolution of $n(t, x)$ is given by the simplest transport-fragmentation equation

$$
\left\{\begin{array}{l}
\frac{\partial}{\partial t} n(t, x)+\frac{\partial}{\partial x} n(t, x)+B(x) n(t, x)=0  \tag{1}\\
n(t, 0)=m \int_{0}^{\infty} B(y) n(t, y) d y, \quad t>0, n(0, x)=\delta_{0},
\end{array}\right.
$$

where $\delta_{0}$ denotes the Dirac mass at point 0 . In this model, each cell dies according to a division rate $x \leadsto B(x)$ that depends on its age $x$ only (a living cell of age $x$ has probability $B(x) d x$ of dying in the interval $[x, x+d x]$ ) and, at its time of death, it gives rise to $m \geq 2$ children at its time of death. The parameters $(m, B)$ specify the so-called age-dependent model.

In this seemingly simple context, we wish to draw statistical inference on the division rate function $x \leadsto B(x)$ and on $m$ in the most rigorous way, when we observe the evolution of the population through time and when the shape of the function $B$ can be arbitrary, to within a prescribed smoothness class, i.e. in a nonparametric setting. In order to do so, we transfer the deterministic description (1) into a probabilist model that consists of a system of (noninteracting) particles specified by a probability distribution $p$ on the integers (the offspring distribution) and a probability density $f$ on $[0, \infty)$. A particle has a random lifetime drawn according to $f(x) d x$; at the time of its death, it gives rise to $k$ children with probability $p_{k}$ (with $p_{0}=p_{1}=0$ ), each child having independent lifetimes distributed as $f(x) d x$, and so on. The resulting process is a classical supercritical Bellman-Harris, see for instance the textbooks of Harris [12] or Athreya and Ney [2]. It is described by a piecewise deterministic Markov process

$$
\begin{equation*}
X(t)=\left(X_{1}(t), X_{2}(t), \ldots\right), \quad t \geq 0 \tag{2}
\end{equation*}
$$

with values in $\bigcup_{k>1}[0, \infty)^{k}$, where the $X_{i}(t)$ 's denote the (ordered) ages of the living particles at time $t$. The formal link between $X(t)$ and $n(t, \cdot)$ is obtained as follows: define the measure $n(t, d x)$ by $\langle n(t, \cdot), \varphi\rangle=\mathbb{E}\left[\sum_{i=1}^{\infty} \varphi\left(X_{i}(t)\right)\right]$ for smooth test functions with support in $(0, \infty)$. Then $n(t, d x)$ i.e. the empirical measure (in expectation) of the particle system $\left(X_{1}(t), X_{2}(t), \ldots\right)$ solves Eq. (1) in a weak sense, see also [20].

The correspondence between $(m, B)$ and $(f, p)$ is given by

$$
\begin{equation*}
B(x)=\frac{f(x)}{1-\int_{0}^{x} f(s) d s}, \quad x \in[0, \infty), \quad \text { and } \quad m=\sum_{k \geq 2} k p_{k}, \tag{3}
\end{equation*}
$$

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