

A Convergent Numerical Algorithm for the Stochastic Growth-Fragmentation Problem

Dawei Wu¹ and Zhennan Zhou^{2,*}

¹ *School of Mathematical Sciences, Peking University, Beijing 100871, China*

² *Beijing International Center for Mathematical Research, Peking University, Beijing 100871, China*

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Abstract. The stochastic growth-fragmentation model describes the temporal evolution of a structured cell population through a discrete-time and continuous-state Markov chain. The simulations of this stochastic process and its invariant measure are of interest. In this paper, we propose a numerical scheme for both the simulation of the process and the computation of the invariant measure, and show that under appropriate assumptions, the numerical chain converges to the continuous growth-fragmentation chain with an explicit error bound. With a triangle inequality argument, we are also able to quantitatively estimate the distance between the invariant measures of these two Markov chains.

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1 Introduction

1.1 Overview of the growth-fragmentation model

Growth-fragmentation models (abbreviated as “GF” henceforth) describe the temporal evolution of a structured population characterized by state variables such

*Corresponding author.

Emails: 2201110052@pku.edu.cn (D. Wu), zhennan@bicmr.pku.edu.cn (Z. Zhou)

as age, size, etc.. As its name suggests, it integrates a “growth process” and a “fragmentation process”. The state variables evolve according to some deterministic equation, but are subject to sudden changes (usually into parts) occurring at stochastic moments. The GF model appears in physics to describe the degradation phenomenon in polymers, droplets and in telecommunications systems to describe some internet protocols [17].

We will focus the GF model on cell division. As is supported by experimental evidence in [19], cells in a culture medium increase in size deterministically and split into two offsprings randomly. The rates at which they grow or break are both determined by their current sizes (state variable). A video from the supplementary material of [23] illustrates this process. A common assumption is that at each fragmentation, the cell splits into two offsprings with equal sizes [6]. Scientists have also analyzed the case where the sizes of the offsprings are random and determined by a kernel [7].

1.2 Stochastic growth-fragmentation model

There are two main approaches to modelling the GF process. One is through an evolutionary partial differential equation regarding the size distribution of the population [7, 17, 18]; the other is through the genealogical tree which is Markovian [2, 3, 5, 10]. We will use the Markovian model proposed in [5] in this paper. Their motivation was the availability of observation schemes at the level of cell individuals, for example, the experiments in [23] where scientists prepared a thin vertical tube with the top open and the bottom sealed, fixed an E.coli cell at the sealed end and watched it grow. When the cell split, exactly one of its descendants was kept at the bottom of the tube, and thus we were able to track a single lineage of cells through time by recording a video of the whole process and identifying those bottom cells. In fact, the new observation scheme did improve on previous rates of convergence obtained by indirect measurements, as in [4]. We will use a slightly different version of their model in this subsection.

Use an infinite binary tree $\mathbb{T} = \bigcup_{n=0}^{\infty} \{0, 1\}^n$ to represent the family of cells. Each node in \mathbb{T} is a finite array of 0's and 1's, and its two children append a 0 and 1 to this array respectively. For example, the node 01 has two child nodes, 010 and 011.

Assign a set of variables (ξ_u, ζ_u, b_u) to each cell $u \in \mathbb{T}$. ξ_u stands for its size at birth, ζ_u stands for its total life span until the fragmentation, and b_u is the moment when it's born. Its size as a function of time is denoted by $x_u(t)$, $t \geq b_u$. A cell grows according to a deterministic rate $g(x)$, and at a certain time it breaks into two equal-sized offsprings. Therefore, if u^+ is either of the daughter cells of u , we have the basic relation

$$2\xi_{u^+} = x_u(b_u + \zeta_u). \quad (1.1)$$