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# A one dimensional model of population growth

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## HIGHLIGHTS

- A model based on individual–individual distance-dependent interaction is proposed.
- The model presents full analytic solution.
- A rich phase diagram to which the population has access is observed.
- The phases are: exponential growth, convergence, divergence, and extinction.

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## ABSTRACT

In this work, a one dimensional population growth model is proposed. The model, based on the cooperative and competitive individual–individual distance-dependent interaction, allows us to get a full analytical solution. With this analytical approach, it was possible to investigate the dynamics of the population according to some parameters, as intrinsic growth rate, strength of the interaction between individuals, and the distance-dependent interaction. As a consequence of the individuals' interaction, a rich phase diagram to which the population has access was observed. The phases observed are: convergence to carrying capacity, exponential growth, divergence at finite time, and extinction. Moreover, it was also observed that some phases are strictly dependent on the initial condition. For instance, in the cooperative regime with negative intrinsic growth rate, the population can diverge or become extinct according to the initial population size. The phases accessible to the population can be seen as a macroscopic behavior which emerges from the interaction among the individuals (the microscopic level).



## 1. Introduction

The understanding of the population growth behavior at individual level interaction is a pertinent question which has caught the attention of the scientific community in the last years [1–4]. This approach introduces a more fundamental understanding about the properties of ecosystems and can cast some light about universal laws which govern population dynamics [5–13]. The idea of understanding macroscopic behavior by means of the microscopic properties of a system is common in physics, for instance, understanding macroscopic properties of fluids as a consequence of the interaction of an Avogadro number of atoms or molecules [14,15]. However, only recently, has this idea gained force in context of biological systems.

Mombach et al. proposed in Ref. [16] modeling the competitive interaction between two individuals according to the distance between them. More specifically, they proposed an individual–individual interaction which decreases with the distance. They showed that some well-known phenomenological population growth models – as Verhulst, Gompers, and

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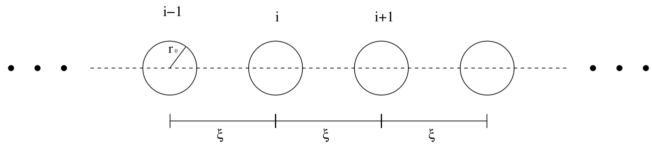


**Fig. 1.** One-dimensional cells arrangement.

Richards (see Refs. [17–21]) – emerge from this kind of interaction. They also showed that the population growth behavior is entirely dependent on the dimension of the media in which the population is embedded and the fractal dimension formed by the own population (see also Ref. [22]). The result of this work allows a better understanding of tumor cells growth, which presents fractal structure [23].

It has been shown recently in Ref. [1] that when cooperation is included in the model of Mombach et al., other phenomenological models, as the Bertalanffy [24] and Von Foerster models [25], emerge from the individual level interaction. One important characteristic of the Bertalanffy and von Foerster models is that they can present population blow-up at finite time. That is, the population growth is faster than the exponential growth. It is interesting that the von Foerster model was used in the sixties to describe human population growth and recently it has been analyzed again in Ref. [26]. In both studies the data-fit of the model was successful. It suggests, as was written by von Foerster, that if the human population continues to grow like it has in the last centuries, the population must diverge at finite time. Another model, proposed in Ref. [27] based on the energy consumption and power law properties of social interaction, also predicts a divergence of human population at finite time. Of course all these models are valid only until a limit of population size. When the population becomes very large, other aspects must dominate, and then these models lose their validity.

In the present work, we continue with the idea of Refs. [16,1] to deal with the context of cooperative and competitive interaction dependent on the distance between individuals. However, we will restrict ourselves to the case of a population which grows in a one-dimensional medium. This restriction, as will be presented in more details as follows, brings some simplification into the previous models. This simplification allows a full analytical solution of the population dynamics, and then allows us to identify other population behaviors which were not identified previously. For instance, in a one-dimensional model we can study the population dynamics according to parameters which were not studied in previous works, just because of the difficulty of the analysis in a more generic situation. In the present work, the analysis of the dynamics, according to the intrinsic growth rate and the strength of interaction among the individuals, is presented. Moreover it is possible to identify some regimes which are entirely dependent on the initial condition.

The paper is organized as follows. In Section 2 we present the one-dimensional population growth model. The model is entirely based on individual–individual interaction which decreases with the distance. In the same section we show that the proposed model has full analytical solution. It is also presented that the model can be solved numerically and then we have two approaches to compare the results. In Section 3 we present the analysis of the model in the context of competition between the individuals and then in Section 4 the analysis is in the case of cooperation between the individuals. In Section 5 we present a complete analysis of the accessible equilibrium phases. We will show that the population described by the model can reach the equilibrium in the following phases: (i) convergence to the carrying capacity; (ii) extinction; (iii) exponential growth; and (iv) divergence at finite time. The phase into which the population goes depends on the choice of the parameters of the model and, in some cases, on the initial population size. The conclusion is presented in Section 6.

## 2. The one-dimensional model

Consider a one-dimensional arrangement of $N$ individuals – or cells – at a given time $t$, according to Fig. 1. This arrangement can be seen as a stylized model which describes population growth in a thin tube, for instance, cells which grow in a blood vessel. Each cell has a radius $r_0$ and each two neighbor cells are at a distance $\xi$ of each other. By convenience $\xi \geq 2r_0$, so that the inner structure of the cells is preserved. We adopt a periodic boundary condition; that is, the $(N+1)$-th and the 1-th cells are the same.

The replication rate $R_i$ of the $i$th cell of the population is given by its self stimulus for replication and the stimulus/inhibition $JI_i$ from the other cells of the population. That is

$$R_i = k + JI_i. \tag{1}$$

The parameter $k$ represents an individual replication property. Then it does not depend on its interaction with other agents, and consequently it does not depend on $N$. Based on these assumptions, we adopt $k$ as a constant and identical, by convenience, for all individuals of the population. This way, $k$ can be interpreted as the *intrinsic growth rate* (more details as follows). The parameter $J$ represents the interaction strength between two cells and the way of interaction, if cooperation ($J > 0$) or competition ($J < 0$). And then, $I_i$ represents the interaction field (always positive) which the $i$th individual feels from all the other individuals of the population. $I_i$ is the result of the interaction of this individual with all the other individuals of the population, that is $I_i = I_i(N) = \sum_{j \neq i} I_{ij}$, where $I_{ij}$ is the interaction field between $i$ and $j$. Following the ideas presented in Ref. [16] and recently analyzed in Refs. [1,22], we will consider that $I_{ij}$ decays with the distance $r_{ij}$ between the