Data collapse, scaling functions, and analytical solutions of generalized growth models

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(Received 11 October 2010; revised manuscript received 14 April 2011; published 2 June 2011)

We consider a nontrivial one-species population dynamics model with finite and infinite carrying capacities. Time-dependent intrinsic and extrinsic growth rates are considered in these models. Through the model *per capita* growth rate we obtain a heuristic general procedure to generate scaling functions to collapse data into a simple linear behavior even if an extrinsic growth rate is included. With this data collapse, all the models studied become independent from the parameters and initial condition. Analytical solutions are found when time-dependent coefficients are considered. These solutions allow us to perceive nontrivial transitions between species extinction and survival and to calculate the transition's critical exponents. Considering an extrinsic growth rate as a cancer treatment, we show that the relevant quantity depends not only on the intensity of the treatment, but also on when the cancerous cell growth is maximum.

DOI: 10.1103/PhysRevE.83.061902 PACS number(s): 87.23.Cc, 89.75.−k, 05.45.−a

I. INTRODUCTION

Growth models are useful when one tries to understand, describe, or predict the behavior of a wide range of time-dependent processes in physics, chemistry, demography, economics, ecology, epidemiology, just to cite a few disciplines. The simplest way to deal with population growth is to consider that individuals within the population do not interact explicitly with external ones. This is represented by the so-called one-species population dynamics models. These models quantify the population size (number of individuals) $N(t) \geqslant 0$ at a certain time t, given its initial size $N_0 \equiv N(0) > 0$, intrinsic growth rate $\kappa > 0$, and the environment's carrying capacity $K = N(\infty) > 0$. The environment's carrying capacity takes into account all possible interactions among external individuals, species, and resources in a single parameter [1]. If one assumes an environment with unlimited resources (an infinite carrying capacity) and that the *per capita* growth rate $(dN/dt)/N = d\ln N/dt = \kappa$ is constant, then the population grows exponentially (the Malthus model), producing a divergence at an infinite time. However, this divergence can be dismantled considering a finite carrying capacity. The growth of individual organisms [2], tumors [3], and other biological systems [4] are well described by sigmoid curves [5–7] that can be obtained through the Gompertz $[d\ln(N/K)/dt = -\kappa \ln(N/K)]$ or Verhulst model $[d\ln(N/K)/dt = -\kappa(N/K - 1)]$ for instance.

The von Foerster *et al.* [8] model considers the *per capita* growth rate as a power law $d\ln N/dt = \kappa N^{\alpha}$, where the exponent α produces a divergence at a finite time, in constrast to the Malthus model ($\alpha \to 0$). This has been observed for human population growth [8]. The Richards model [9] $\{d\ln(N/K)/dt = -\kappa[(N/K)^{\tilde{q}} - 1]/\tilde{q}\}$ binds the Gompertz ($\tilde{q} \to 0$) and Verhulst ($\tilde{q} = 1$) models through the constant $\tilde{q}$, whose microscopic interpretation is the growth of interacting cells in a fractal medium [10–12]. A power-law growth, similar to the von Foerster *et al.* model, in the Gompertz model $\{d\ln(N/K)/dt = \kappa[\ln(N/K)]^{\gamma}\}$ is known as the hyper-Gompertz model [13,14]. The parameter γ regulates the population size inflection point $p_{\text{inf}} = e^{-\gamma}$, where the growth rate is maximum.

Generalized forms of the classical logistic growth equation are more suitable as predictive models. From the work of Tsoularis [14] we know that ". . .additional growth characteristics are accommodated by this new model, enabling previously unsupported, untypical population dynamics to be modelled by judicious choice of model parameter values alone." As an example, the Tsoularis-Wallace model $\{d\ln(N/K)/dt = \kappa N^{\alpha}\{[(N/K)^{\tilde{q}} - 1]/\tilde{q}\}^{\gamma}\}$ unifies all the cited models and presents an analytical (nonexplicit) solution [15].

Permit us a digression to introduce the concepts of scaling and data collapse. The research of van der Waals was able to rescale data and collapse them into a nontrivial common curve. For a given volume, different real gases liquefy at different temperature and pressure, leading to a first-order transition. Nevertheless, for the critical values of volume, temperature, and pressure, the transition becomes of second order (no latent heat). For each real gas, dividing the temperature, pressure, and volume by their respective critical values, one obtains a collapsed (common) curve. This common curve reveals common aspects of all real gases (a finite particle volume and short-range interaction among them). This data collapse had important consequences as the estimation of the temperature for helium liquefaction, which itself lead to relevant discoveries such as superconductivity and superfluidity [16]. Nowadays, the idea of data collapse is extended to scaling functions [17], which is one particular aspect of the scaling hypothesis [18]. The scaling hypothesis also deals with the scaling laws at critical transition values (such as in the van der Waals mean-field theory) and renormalization-group theory, but this latter aspect is beyond the scope of the present

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work. We attain only the power of the scaling function to connect apparently independent quantities to simple relevant quantities [19] in population dynamics models and to critical transition exponents.

Returning to the analytical solutions obtained from the one-species growth models, we call attention to the following items. For each model, the time t of the population evolution is proportional to the inverse of the intrinsic growth rate κ. This gives rise to a dimensionless characteristic time and can be defined as the system-independent variable $\tau = \kappa t$. Furthermore, we demonstrate how to obtain the scaling function that depends on the combination of quantities such that the models become independent from the initial condition and parameters. A data collapse from the scaling function occurs even in the Tsoularis-Wallace model, where no explicit analytical solution is known.

We also deal with models that consider an extrinsic growth rate, defined as an addition or removal of individuals proportionally to the population size. It can also be seen as the interaction factor when considering multispecies models. Furthermore, in theoretical models of cancer growth, the extrinsic growth rate can be associated with treatment and the knowledge of how the transition between survival and extinction occurs is of utmost importance [20–23]. The concepts of physics in theoretical models of cancer growth were already proposed in Ref. [24] in which the authors obtain a phase transition between tumor growth and latency. A phase transition is also associated with successful cancer treatment in Ref. [25].

Here we obtain analytical solutions for time-dependent intrinsic and extrinsic growth rates and show their data collapse. The steady-state (asymptotic) solution is interpreted as the order parameter. Nontrivial transitions between extinction and survival phases are found and depend on the extrinsic growth rate with well-defined critical exponents. In cancer treatment modeling, we have shown that the relevant quantity in a phase transition depends not only on the intensity of the treatment but also on when the cancerous cell growth is maximum.

This paper is structured as follows. In Sec. II we show the general procedure to obtain the scaling functions and we calculate these functions for the main one-species population dynamics (growth) models. In Sec. III we consider the insertion or removal of individuals through a constant extrinsic growth rate. We show that this quantity does not affect data collapse. Moreover, it induces an extinction-survival transition at well-determined values. We then calculate the transition's critical exponents for the simpler models. We show that both time-dependent intrinsic and extrinsic growth rates do not destroy data collapse. In Sec. IV we present our final remarks. In the Appendix we briefly review the one-parameter generalization of the logarithm and exponential functions and present several of its properties we used herein.

II. GROWTH MODELS AND SCALING FUNCTIONS

One-species growth models are usually represented by

$$\frac{d\ln[p(\tau)]}{d\tau} = G(p), \tag{1}$$

where $\tau = \kappa t$ is the time measurement in terms of the intrinsic growth rate κ and $G(p)$ is the *per capita* growth rate. One-species population dynamics (growth) models fall into two categories: one with infinite and the other with finite carrying capacity. To deal with these two kinds of models, we introduce the variable p. On the one hand, when the resources are unlimited ($K \to \infty$), as is the case of the Malthus model, it is convenient to use $p = N$, where N is the number of individuals. On the other hand, when there are limited resources, as is the case of Verhulst model, it is convenient to express the population size with respect to its equilibrium value, i.e., $p = N/K$. In an environment with limited resources, the steady-state solutions are either species extinction $p^* = 0$ or survival $0 < p^* \leqslant 1$ given by the roots of $G(p^*) = 0$. Optimum environment exploration is achieved when $p(\tau) = 1$.

We have heuristically found that the integral

$$s(\tau) = \int_{p_0}^{p(\tau)} \frac{dp}{pG(p)} = \tau - \tau_0 \tag{2}$$

is a general procedure to obtain the scaling function of the growth models. Here $p_0 = p(\tau_0)$ is the initial condition. This scaling function is linear on τ (see Fig. 1) and data collapses independently of the model parameters and initial condition.

In the infinite carrying capacity case $p(\tau) = N(\tau)$, we write variables with tildes; for instance, the scaling function of Eq. (2) is $\tilde{s}(\tau)$. For $\tilde{G}_\alpha(N) = N^\alpha$ (the von Foerster *et al.* model) [8], where α is a generalization parameter that produces a divergence in a finite (dimensionless) time T, one has the

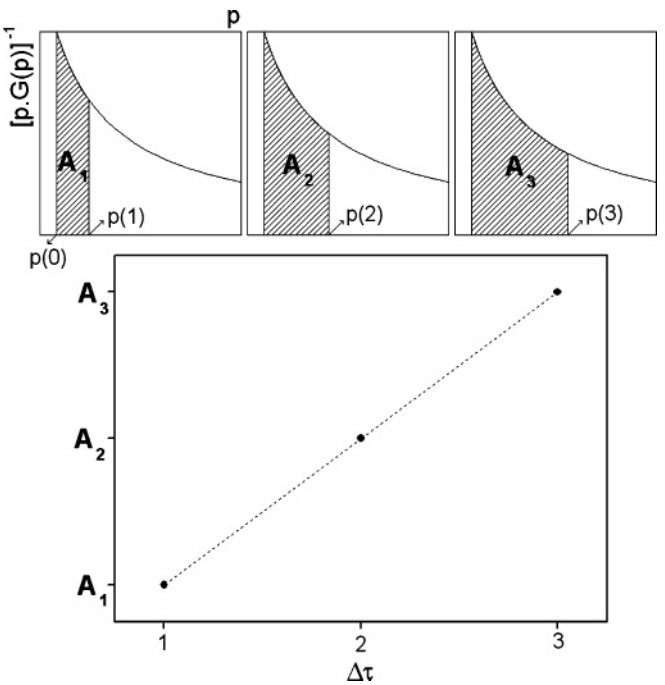

FIG. 1. The area below the curve $1/pG(p)$ grows linearly as a function of $\Delta = \tau - \tau_0$. This behavior does not depend on the model considered.

solution $N(\tau) = 1/[\alpha(T-\tau)]^{1/\alpha}$. The von Foerster *et al.* model scaling function is

$$\tilde{s}_\alpha(\tau) = \frac{N_0^{-\alpha} - N^{-\alpha}(\tau)}{\alpha} = N_0^{-\alpha}\ \ln_{-\alpha}\left(\frac{N(\tau)}{N_0}\right), \qquad (3)$$

where we have used the generalized $\tilde{q}$-logarithmic function (see the Appendix). As $\alpha \to 0$, one retrieves, for the Malthus model $\tilde{G}(N) = 1$, $dN(\tau)/d\tau = N(\tau)$, resulting in the exponential growth $N(\tau)/N_0 = e^\tau$ ($N_0 = e^T$), so that Eq. (3) becomes

$$\tilde{s}_0(\tau) = \ln\left(\frac{N(\tau)}{N_0}\right) \qquad (4)$$

and one obtains a straight line in a plot $\tilde{s}_0\tau$, which is independent from the parameters of the model (intrinsic growth rate κ) and initial condition N_0.

The Richards model [9,12,26,27] can be conveniently written in terms of the $\tilde{q}$-logarithmic function [see Eq. (A1) in the Appendix], $d\ln p(\tau)/d\tau = -\ln_{\tilde{q}}[p(\tau)]$. Based on Refs. [10,11], a microscopic interpretation can be given to $\tilde{q}$ relating it to the range of interaction between cells and the fractal dimension where these cells grow [12]. When discretized, this equation leads to the generalized logistic map [28]. The solution of the model can be written in terms of the generalized exponential and logarithm functions [see Eqs. (A1) and (A2) in the Appendix] as $p(\tau) = 1/e_{\tilde{q}}[\ln_{\tilde{q}}(p_0^{-1})e^{-\tau}]$. The asymptotic limit ($\tau \to \infty$) is $p^* = p(\infty) = 1$, regardless of the choice of $\tilde{q}$. The Gompertz model is retrieved with $\tilde{q} = 0$, so that $d\ln p/d\tau = -\ln p$ and one has the solution $p(\tau) = e^{(\ln p_0)e^{-\tau}}$. The Verhulst model is retrieved with $\tilde{q} = 1$, so that $d\ln p/d\tau = 1 - p$ and $p(\tau) = 1/[1-(1-p_0^{-1})e^{-\tau}]$ is the solution. The scaling function for the Richards model is

$$s_{\tilde{q}}(\tau) = \ln\left(\frac{\ln_{-\tilde{q}}(p_0)}{\ln_{-\tilde{q}}[p(\tau)]}\right), \qquad (5)$$

with the following limiting cases:

$$s_0(\tau) = -\ln\{\ln[p(\tau) - p_0]\}, \qquad (6)$$

$$s_1(\tau) = \ln\left(\frac{p_0^{-1} - 1}{p^{-1}(\tau) - 1}\right). \qquad (7)$$

With this procedure, one gets rid of the dependence on the initial condition and parameters retrieving data collapse. Although Montroll used this transformation for the Verhulst model in Ref. [26], he did not discuss the data collapse.

One way to include the finite carrying capacity K in the von Foerster *et al.* model is to replace N by $p = N/K$, rescale the constants, and replace N^α by $[-\ln(N/K)]^\gamma$ in the saturation function. The von Foerster *et al.* model in the $\ln p$ variable is known as the hyper-Gompertz model [13,14] $d\ln p(\tau)/d\tau = \{-\ln[p(\tau)]\}^\gamma$, whose solution is $p(\tau) = e^{[(\gamma-1)\tau + (\ln p_0)^{1-\gamma}]^{1/(1-\gamma)}}$. The parameter γ regulates the population size inflection point $p_{\rm inf} = e^{-\gamma}$, where the growth rate is maximum. For $\gamma \gg 1$, the inflection point tends to 0; for $\gamma \ll 1$, it tends to the carrying capacity K. The hyper-Gompertz model scaling function is given by

$$s_\gamma(\tau) = -(-\ln p_0)^{1-\gamma}\ \ln_{1-\gamma}\{\ln[p(\tau) - p_0]\}, \qquad (8)$$

so that one retrieves Eq. (6) for $\gamma = 1$.

So far, all the models presented have explicit analytical solutions. However, the Tsoularis-Wallace model does not; nevertheless, its scaling function can still be obtained. In terms of the $\tilde{q}$-logarithm function, the Tsoularis-Wallace model is

$$\frac{d\ln p}{d\tau} = p^\alpha(\tau)\{-\ln_{\tilde{q}}[p(\tau)]\}^\gamma. \qquad (9)$$

The solution $p(\tau)$ of Eq. (9) is the root of $B_{p^{\tilde{q}}(\tau)}(-\alpha/\tilde{q}, 1-\gamma) - B_{p_0^{\tilde{q}}}(-\alpha/\tilde{q}, 1-\gamma) = \tilde{q}^{1-\gamma}\tau$, where $B_x(a,b) = \int_0^x t^{a-1}(1-t)^{b-1}dt$ is the incomplete β function and the scaling function of Eq. (2) is

$$s_{\alpha,\tilde{q},\gamma}(\tau) = \frac{B_{p^{\tilde{q}}(\tau)}\left(-\frac{\alpha}{\tilde{q}}, 1-\gamma\right) - B_{p_0^{\tilde{q}}}\left(-\frac{\alpha}{\tilde{q}}, 1-\gamma\right)}{\tilde{q}^{1-\gamma}}$$

$$= \frac{1}{\tilde{q}^{1-\gamma}} \int_{p_0^{\tilde{q}}}^{p^{\tilde{q}}(\tau)} \frac{dp'}{p'^{1+\alpha/\tilde{q}}(1-p')^\gamma}. \qquad (10)$$

All the models studied can be retrieved by a convenient choice of α, γ, and $\tilde{q}$. For instance, the Richards model is retrieved for $\alpha = 0$ and $\gamma = 1$. By setting $p = N$ and $\gamma = 0$ and rescaling the growth rate, one retrieves the von Foerster *et al.* model.

III. EXTINCTION AND SURVIVAL PHASES: EXTRINSIC GROWTH RATE

The extrinsic growth rate is defined as the addition or removal of individuals proportionally to the population size. It can be seen as the interaction factor when considering multispecies models [29]. In theoretical models of cancer growth, the extrinsic growth rate can be associated with treatment and the knowledge of how the transition between survival and extinction occurs is of the utmost importance [20–23]. The concepts of physics in theoretical models of cancer growth was already proposed in Ref. [24], in which the authors obtained a phase transition between tumor growth and latency. The latency phase is aroused by therapeutic strategies aimed at reducing a growing tumor to dormancy. In addition, cancer treatment consisting in inhibiting angiogenesis has been found to be an interesting therapeutic strategy. A phase transition to a region in the parameter space in which angiogenesis is not successful was proposed in Ref. [25].

Here we obtain the analytical asymptotic solutions for the Tsoularis-Wallace model and investigate the effect of the extrinsic growth rate $\tilde{\epsilon}$ on the data collapse. Further, we show nontrivial transitions between extinction and survival phases. The transition's critical exponents are obtained for the special case $\alpha = 0$, so we exclude models with infinite carrying capacity.

A. Constant extrinsic growth rate

With constant extrinsic growth rates, one can deal with the transitions between the extinction and survival phases. The steady-state solution p^* represents the order parameter since it vanishes in the extinction phase and, at critical points, becomes nonzero, representing survival phases. Let us first consider an

extrinsic growth rate in the Tsoularis-Wallace model [Eq. (9)] and call it the Tsoularis-Wallace-Schaefer model:

$$\frac{d\ln p(\tau)}{d\tau} = p^{\alpha}(\tau)\{-\ln_{\tilde{q}}[p(\tau)]\}^{\gamma} + \epsilon, \tag{11}$$

where $\epsilon = \tilde{\epsilon}/\kappa$.

1. Steady-state solutions, critical value, and exponents

The steady-state solutions are obtained by considering $dp/d\tau = 0$ in Eq. (11), so that $p^*\{p^{*\alpha}[-\ln_{\tilde{q}}(p^*)]^{\gamma} + \epsilon\} = 0$. The solution $p^* = 0$ represents the extinction phase and $p^{*\alpha}[-\ln_{\tilde{q}}(p^*)]^{\gamma} = -\epsilon$ represents the survival phase. The values separating the extinction and survival phases are the roots of

$$(p^*)^{\alpha/\gamma} - (p^*)^{\alpha/\gamma+\tilde{q}} = \tilde{q}(-\epsilon)^{1/\gamma}. \tag{12}$$

For $\alpha = 0$, the solution is

$$p^* = p(\infty) = e_{\tilde{q}}[-(-\epsilon)^{1/\gamma}]. \tag{13}$$

For $\epsilon = 0$, one has $p^* = 1$, as expected. From the definition of the generalized exponential function [Eq. (A2), the survival phase is stable for $\tilde{q}(-\epsilon)^{1/\gamma} < 1$, so that extinction occurs at a critical value

$$\epsilon_c = -\frac{1}{\tilde{q}^{\gamma}}. \tag{14}$$

It is also possible to calculate the transition's critical exponents. For $\epsilon \gtrsim \epsilon_c$, Eq. (13) leads to

$$p^* = (-1)^{1/(\gamma\tilde{q})}(-\tilde{q})^{1/\tilde{q}}(\epsilon^{1/\gamma} - \epsilon_c^{1/\gamma})^{1/\tilde{q}} \sim (\xi - \xi_c)^{\nu_1}. \tag{15}$$

Otherwise, for $\epsilon < \epsilon_c$, according to Eq. (13), one has $p^* = 0$. The relevant quantity is the control parameter $\xi = \epsilon^{1/\gamma}$ and the critical exponent is $\nu_1 = 1/\tilde{q}$. For $\nu_1 = 1/\tilde{q} \leqslant 1$, as the control parameter decreases, the transition from the survival phase to the extinction phase is abrupt: a second-order phase transition. For $\nu_1 = 1/\tilde{q} > 1$, the system presents a continuous transition. When $\tilde{q} = 0$ (the Gompertz model) there is no transition between phases because $\epsilon \to -\infty$, according to Eq. (14). Figure 2 illustrates these transitions. Examples of these behaviors near $(\xi - \xi_c) = 0$ with their corresponding critical exponents are presented in Ref. [30].

One can also introduce the susceptibility of the system $\chi = \partial p^*/\partial\xi$, so that from Eq. (15) we get $\chi \sim (\xi - \xi_c)^{\nu_2}$, with critical exponent $\nu_2 = \nu_1 - 1$. For $\tilde{q} > 1$ (which implies $\nu_1 < 1$), the susceptibility diverges at the critical points. We note the dependence of the critical exponents only on $\tilde{q}$. The exponent γ affects the control parameter, i.e., only where the transition occurs, but it does not affect its form.

Keeping $\alpha = 0$ and taking $\gamma = 1$, one obtains from Eq. (11) the Richards model with constant extrinsic growth rate, which we call the Richards-Schaefer model: $d\ln p(\tau)/d\tau = -\ln_{\tilde{q}}[p(\tau)] + \epsilon$, whose complete solution is $p(\tau) = e_{\tilde{q}}(\epsilon)/e_{\tilde{q}}\{\ln_{\tilde{q}}[e_{\tilde{q}}(\epsilon)/p_0]e^{-(1+\tilde{q}\epsilon)\tau}\}$, where $p_0 = p(0)$ is the initial condition. Its asymptotic behavior is $p^* = p(\infty) = e_{\tilde{q}}(\epsilon)$, which is a particular case of Eq. (13). As in Eq. (13), p^* vanishes for $\tilde{q}\epsilon \leqslant -1$, representing species extinction. Species survival occurs for $\epsilon > \epsilon_c$, where the critical value is $\epsilon_c = -1/\tilde{q}$ and the critical exponents are $\nu_1 = 1/\tilde{q}$ and $\nu_2 = \nu_1 - 1$. For $\alpha \neq 0$, Eq. (12) can be solved for particular cases, which are beyond the scope of this study.

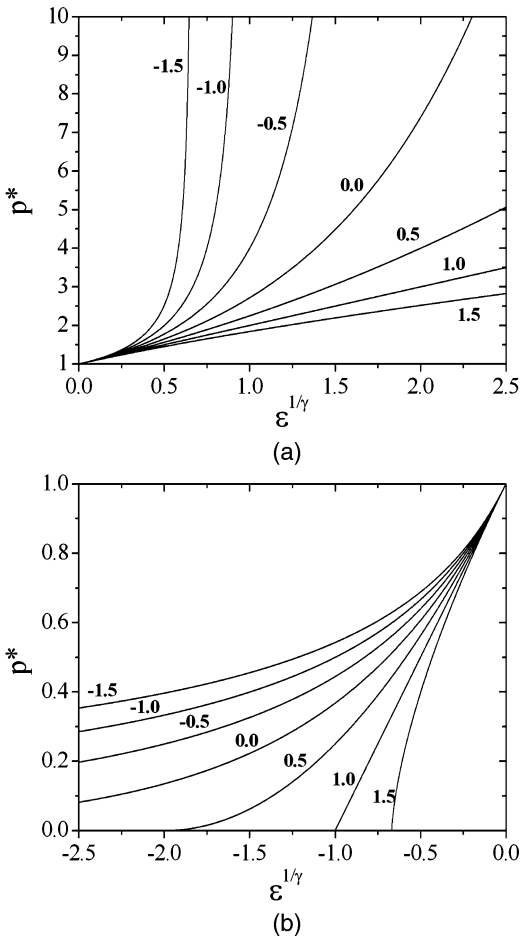

FIG. 2. Plot of the steady-state solution p^* as a function of $\xi = \epsilon^{1/\gamma}$ for different values of $\tilde{q}$. At the critical value the population (a) diverges for $\tilde{q} < 0$ and (b) extinguishes for $\tilde{q} > 0$. There is no transition between phases when $\tilde{q} = 0$ (Gompertz model), there is a continuous transition when $0 < \tilde{q} < 1$, and there is an abrupt (second-order phase) transition when $\tilde{q} > 1$. The parameters used are $\gamma = 1$ and $\tilde{q}$ values are indicated above the curves.

2. Scaling functions

Even in a very general model with an additive term as in the Tsoularis-Wallace-Schaefer model [Eq. (11)], it is possible to obtain the scaling function from Eq. (2):

$$s_{\alpha,\tilde{q},\gamma,\epsilon}(\tau) = \int_{p_0}^{p(\tau)} \frac{dp'}{p'\{p'^{\alpha}[-\ln_{\tilde{q}}(p')]^{\gamma} + \epsilon\}}. \tag{16}$$

Although this is not a general explicit solution, taking $\gamma = 1$ and $\alpha = 0$, we are able to solve the integral and obtain an explicit analytical form for the Richards-Schaefer model:

$$s_{\tilde{q},\epsilon}(\tau) = -[e_{\tilde{q}}(\epsilon)]^{-\tilde{q}} \ln\left(\frac{\ln_{-\tilde{q}}[p(\tau)/e_{\tilde{q}}(\epsilon)]}{\ln_{-\tilde{q}}[p_0/e_{\tilde{q}}(\epsilon)]}\right). \tag{17}$$

For $\epsilon = 0$, $e_{\tilde{q}}(0) = 1$ and one retrieves Eq. (5). Figure 3 depicts data collapse in this very general case. Using three

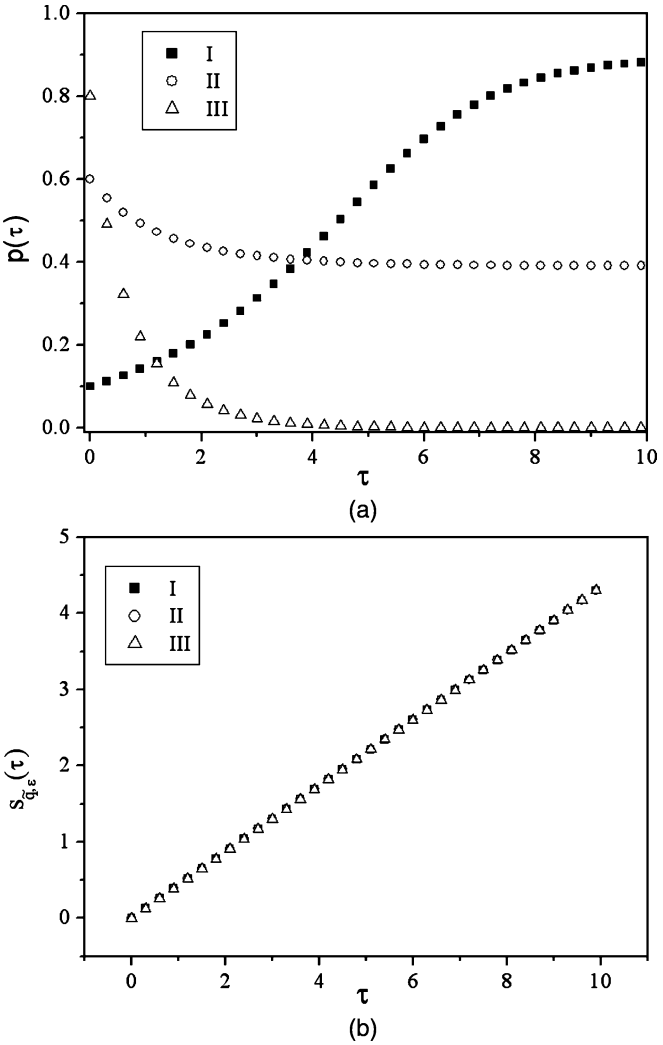

FIG. 3. (a) Plot of the population $p(\tau)$ using the Richards-Schaefer model for three different sets of parameters and initial conditions: (I) $p_0 = 0.1$, $\tilde{q} = 2.0$, and $\epsilon = -0.1$; (II) $p_0 = 0.6$, $\tilde{q} = 0.5$, and $\epsilon = -0.75$; and (III) $p_0 = 0.8$, $\tilde{q} = 1.0$, and $\epsilon = -2.0$. (b) Same set of parameters using the scaled form of the Richards-Schaefer solution $S_{\tilde{q},\epsilon}$. With the appropriate scaling function, all the different behaviors in (a) collapse into a single curve (b).

different sets of parameters, a unique curve is obtained when the appropriate scaling function is used.

B. Time-dependent extrinsic growth rate

Next we consider a very general solution for the Richards model with a time-dependent extrinsic growth rate. We show that data collapse can be done even for the time-dependent intrinsic growth rate. Analytically closed solutions are found for the constant intrinsic growth rate.

1. *Time-dependent intrinsic growth rate*

Consider time dependence in both the intrinsic and extrinsic growth rates:

$$\frac{d\ln[p(t)]}{dt} = -\kappa(t)\ln_{\tilde{q}}[p(t)] + \tilde{\epsilon}(t). \tag{18}$$

Notice that here we use t, instead of τ, as the independent variable and its solution is

$$p(t) = \left[\frac{1}{\tilde{I}(t)}\left(1 + \int_0^t dt'\tilde{I}(t')\kappa(t')\right)\right]^{-1/\tilde{q}}, \tag{19}$$

where

$$\tilde{I}(t) = p_0^{\tilde{q}}\exp\left(\int_0^t dt'\kappa(t') + \tilde{q}\int_0^t dt'\tilde{\epsilon}(t')\right), \tag{20}$$

so that $I(0) = p_0^{\tilde{q}}$.

It is also possible to compute the scaling function, which is

$$s_{\kappa(t),\tilde{q},\tilde{\epsilon}(t)}(t) = \tilde{I}(t)p^{-\tilde{q}}(t) - 1 = \int_0^t dt'\tilde{I}(t')\kappa(t'). \tag{21}$$

For the time-dependent extrinsic growth rate, the insertion or removal of individuals is a function of time. Note that in Eq. (18), one may consider a nontrivial model with multiplicative $\kappa(t)$ and additive $\epsilon(t)$ stochastic noise and the data collapse remains attainable. If $\tilde{\epsilon}(t) = 0$, one can consider the time-dependent growth rate as $\kappa(t) = a_0(t) + a_1\gamma_1(t)$, where $a_0(t)$ is a deterministic growth and $\gamma_1(t)$ may be considered as a multiplicative stochastic noise [31,32].

2. *Constant intrinsic growth rate*

Now consider a constant intrinsic growth rate $\kappa(t) = \kappa$, which we call the Richards-Schaefer model [Eq. (22)] with time-dependent extrinsic growth rate:

$$\frac{d\ln p(\tau)}{d\tau} = -\ln_{\tilde{q}} p(\tau) + \epsilon(\tau). \tag{22}$$

This equation can be explicitly solved and the solution is conveniently written in terms of the generalized logarithm and exponential functions:

$$p(\tau) = \frac{e_{\tilde{q}}[\epsilon(\tau)]}{e_{\tilde{q}}\left[\ln_{\tilde{q}}\left(\frac{e_{\tilde{q}}[\epsilon(0)]}{p_0}\right)\frac{e_{\tilde{q}}[\epsilon(\tau)]}{e_{\tilde{q}}[\epsilon(0)]}e^{-[1+\tilde{q}\overline{\epsilon}(\tau)]\tau}\right]}, \tag{23}$$

where

$$\overline{\epsilon}(\tau) = \frac{1}{\tau}\int_0^\tau d\tau'\epsilon(\tau') \tag{24}$$

is the mean value of $\epsilon(\tau)$ up to time τ. As a particular case, a constant extrinsic growth rate $\epsilon(\tau) = \epsilon$ in Eq. (23) leads to the Richards-Schaefer solution. This very general growth function (Richards) with a time-dependent extrinsic growth rate solution allows us to obtain the stability of the two-species population dynamics model with a time-dependent extrinsic growth rate [29].

The steady-state solution ($\tau \to \infty$) of Eq. (23) is $p^* = p(\infty) = e_{\tilde{q}}(\overline{\epsilon})$, where $\overline{\epsilon} = \overline{\epsilon(\infty)}$ is the true mean value of $\overline{\epsilon(\tau)}$. Species extinction occurs for $\tilde{q}\overline{\epsilon} < -1$. The steady state of the population is $p^* \sim (\overline{\epsilon} - \overline{\epsilon}_c)^{1/\tilde{q}}$, where $\overline{\epsilon}_c = -1/\tilde{q}$ and the susceptibility $\chi = \partial p^*/\partial\overline{\epsilon} \sim (\overline{\epsilon} - \overline{\epsilon}_c)^{1/\tilde{q}-1}$. In this way, regardless of the increasing complexity, the time-dependent extrinsic growth rate, or the constant extrinsic growth rate, the system presents the same critical behavior. The scaling function of the Richards-Schaefer model with a time-dependent

extrinsic growth rate is given by

$$s_{\tilde{q},\epsilon(\tau)}(\tau) = -\{e_{\tilde{q}}[\epsilon(\tau)]\}^{-\tilde{q}} \ln\left(\frac{\ln_{-\tilde{q}}\{p(\tau)/e_{\tilde{q}}[\epsilon(\tau)]\}}{\ln_{-\tilde{q}}\{p_0/e_{\tilde{q}}[\epsilon(0)]\}}\right). \tag{25}$$

If $\epsilon(t)$ is a random variable, then one has the additive stochastic growth equation. In this case, if its mean value vanishes $\overline{\epsilon(\tau)} = 0$ and $\overline{\epsilon(\tau_1)\epsilon(\tau_2)} = \sigma^2\delta(\tau_2 - \tau_1)$ (the Gaussian process), then the probability density function of $v = \ln p$ satisfies the Fokker-Planck equation $\partial_\tau P(v) = \partial_v[P(v)\ln_{\tilde{q}}(v)] + (\sigma^2/2)\partial_v^2[P(v)]$ [26,33,34]. Correlated and Lévy-like noise have also been addressed [23,35,36].

IV. CONCLUSION

Here the concepts of data collapse, scaling functions, phase transitions, and critical exponents are used in population growth models. These statistical physics concepts are widely used in many other research areas [37–40]. Through data collapse, we explicitly show a common characteristic of a wide range of one-species growth models. By including the extrinsic growth rate in the models, we are able to establish scaling and extract associated exponents in equilibrium or nonequilibrium phase transitions. In modeling of cancer treatment, the extrinsic growth rate can be associated with radiotherapy or chemotherapy. The phase transition gives us insight into how cancerous cell extinction occurs. We have shown that the relevant quantity for treatment is $\epsilon^{1/\gamma}$, which depends not only on the intensity of the treatment ϵ, but also on γ, which regulates the time when the growth is maximum. This extrinsic growth rate may also represent the mean-field approximation of the interaction of other species. For this reason, we believe in the data collapse of multispecies models. For time-dependent coefficients, the most general model we have addressed and solved is the Richards-Schaeffer model, whose solutions also present data collapse. Since one can consider stochasticity in the time-dependent coefficient models, with either additive or multiplicative noise, we conjecture that the stochastic models also present data collapse.

ACKNOWLEDGMENTS

A.S.M. acknowledges support from CNPq (Grants No. 303990/2007-4 and No. 476722/2010-1). B.C.T.C. acknowledges support from CAPES. F.R. acknowledges support from CNPq.

APPENDIX: GENERALIZED LOGARITHMIC AND EXPONENTIAL FUNCTIONS

In the following we introduce a one-parameter generalization of the logarithmic and exponential functions and present some of their frequently used properties. These generalizations play a central role [12,28,41,42], as they allow us to easily retrieve particular cases and permit convenient algebraic tricks to handle the expressions.

The $\tilde{q}$-logarithm function is defined as

$$\ln_{\tilde{q}}(x) = \lim_{\tilde{q}'\to\tilde{q}} \frac{x^{\tilde{q}'} - 1}{\tilde{q}'} = \int_1^x \frac{dt}{t^{1-\tilde{q}}}. \tag{A1}$$

This one-parameter generalization of the natural logarithm function, which is retrieved for $\tilde{q} \to 0$, has been introduced in the context of nonextensive statistical mechanics [41,43,44] and is defined as the value of the area underneath the nonsymmetric hyperbole, $f_{\tilde{q}}(t) = 1/t^{1-\tilde{q}}$, in the interval $t \in [1,x]$ [42]. Note that in Eq. (A1), $\ln_{\tilde{q}}(x)$ is not a logarithm x in the base $\tilde{q}$. For $\tilde{q} < 0$, $\ln_{\tilde{q}}(\infty) = -1/\tilde{q}$; for $\tilde{q} > 0$, $\ln_{\tilde{q}}(0) = -1/\tilde{q}$; for all $\tilde{q}$, $\ln_{\tilde{q}}(1) = 0$, $\ln_{\tilde{q}}(x^{-1}) = -\ln_{-\tilde{q}}(x)$, and $d\ln_{\tilde{q}}(x)/dx = x^{\tilde{q}-1}$.

The inverse of the $\tilde{q}$-logarithm function is the $\tilde{q}$-exponential function

$$e_{\tilde{q}}(x) = \begin{cases} \lim_{\tilde{q}'\to\tilde{q}}(1+\tilde{q}'x)^{\frac{1}{\tilde{q}'}} & \text{if} \quad \tilde{q}x > -1 \\ 0 & \text{otherwise,} \end{cases} \tag{A2}$$

so that $e_{\tilde{q}}(0) = 1$ for all $\tilde{q}$ and $[e_{\tilde{q}}(x)]^a = e_{\tilde{q}/a}(ax)$, where a is a constant. For $a = -1$, one has

$$\frac{1}{e_{\tilde{q}}(x)} = e_{-\tilde{q}}(-x). \tag{A3}$$

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