A family of evolution equations with nonlinear diffusion, Verhulst growth, and global regulation: Exact time-dependent solutions

P. Troncoso[a], O. Fierro[a], S. Curilef[a], A.R. Plastino[b,c],*

[a]Departamento de Física,Universidad Católica del Norte, Antofagasta, Chile
[b]Physics Department, University of Pretoria, Pretoria 0002, South Africa
[c]Faculty of Astronomy and Geophysics, National University La Plata and Conicet, Casilla de Correo 727, La Plata 1900, Argentina

Abstract

A family of evolution equations describing a power-law nonlinear diffusion process coupled with a local Verhulst-like growth dynamics, and incorporating a global regulation mechanism, is considered. These equations admit an interpretation in terms of population dynamics, and are related to the so-called conserved Fisher equation. Exact time-dependent solutions exhibiting a maximum nonextensive q-entropy shape are obtained.
© 2006 Elsevier B.V. All rights reserved.

1. Introduction

There has been in recent years an intense research effort in connection with the study of exact solutions of diverse evolution equations involving nonlinear diffusion terms [1–26]. A comprehensive and up to date discussion on many aspects of these lines of enquiry can be found in the monograph [1]. Research on evolution equations endowed with nonlinear power-law diffusion terms has been greatly stimulated by the fact that these equations often admit exact solutions exhibiting a maximum q-entropy (q-maxent) form [27,28]. That is, they admit solutions maximizing a power-law q-entropy [27] under appropriate, simple constraints [1,22]. The q-maxent probability distributions, and the associated thermostatistical formalism, have attracted consider-able interest during the last decade and have been applied to the study of diverse systems and processes in physics, biology, economics, and other fields (see Refs. [27–33] and references therein). The q-maxent solutions of evolution equations involving nonlinear, power-law diffusion have played an important role in some of these developments. To give just a couple of examples, we can mention the successful generalization of the Black–Scholes equation in mathematical finance advanced by Borland [31], and the general framework for

*Corresponding author.

E-mail addresses: arplastino@maple.up.ac.za, vdfsarp9@uib.es (A.R. Plastino).

determining from experimental data the degree of nonextensivity exhibited by a system, proposed by Frank and Friedrich [32].

An interesting new version of the celebrated Fisher equation has been recently advanced by Newman, Kolomeisky and Antonovics (NKA) [34]. The standard Fisher equation [35] constitutes a basic and well-studied model in population biology [36], providing the simplest spatial generalization of the Verhulst logistic equation [37–40] for population dynamics. The Fisher equation describes a biological population whose density $\rho(x, t)$ is locally governed by a Verhulst dynamics and, at the same time, is diffusing in space. Besides its importance in population biology, the Fisher equation also appears naturally in various other fields, such as chemical reaction-fronts dynamics [41] and nonlinear optics [42]. These diverse applications of Fisher equation constitute a strong motivation to study its properties and to explore its possible extensions or generalizations.

Due to the Verhulst component, the Fisher equation is not a continuity equation and, consequently, the total population

$$P_T = \int \rho(x, t)\, \mathrm{d}x \tag{1}$$

is not constant in time. The NKA equation constitutes a conserved version of the Fisher equation. As happens with the standard Fisher equation, the NKA equation also comprises two terms: a diffusion term and a Verhulst term. However, in the NKA equation the parameters characterizing the Verhulst term exhibit a time dependence leading to a constant global population size P_T. The aim of the present contribution is to study a variant of the NKA equation incorporating a nonlinear power-law diffusion term, and exhibiting exact analytical, maximum q-entropy time-dependent solutions. The global regulation mechanism advanced by NKA, or the one explored by us, can be interpreted as a phenomeno-logical description of a population whose growth is controlled, for instance, by an agent (chemical or biological) that diffuses much faster than the population itself [34]. The nonlinearity in the diffusion term considered by us provides a way to include into the model the effects of interactions between the members of the diffusing population. Interactions are already included, in a sense, in the nonlinear component of the Verhulst term. But this nonlinearity affects only the growth process, not the diffusion one. If the population density is high enough for the nonlinearity in the Verhulst term to be important, it is not unreasonable to consider the possibility that nonlinearities in the diffusion process may have some effect as well. The reaction–diffusion-like equations consider here, admitting exact analytical solutions, may be useful as a starting point for the development of more realistic models, or as particular instances to test numerical integration schemes.

The paper is organized as follows. In Section 2 we briefly review the main features of the Fisher and the NKA equations. In Section 3 we introduce our Fisher-like family of evolution equations with nonlinear diffusion and global regulation. A maximum q-entropy ansatz generating exact time-dependent solutions is discussed in Section 4. Particular examples are provided in Section 5. Finally, some conclusions are drawn in Section 6.

2. The Fisher and the NKA equations

The standard Fisher equation in one spatial dimension reads,

$$\frac{\partial \rho(x, t)}{\partial t} = D \frac{\partial^2 \rho(x, t)}{\partial x^2} + r\rho(x, t) - \mu\rho^2(x, t), \tag{2}$$

where D is the diffusion coefficient, and r and μ are two real parameters that characterize the (local) Verhulst dynamics. The parameter r describes the reproduction rate while the (nonnegative) parameter μ regulates the population density through competition. The local equilibrium population density that can be supported at a given location in space is given by

$$\rho_{\text{eq.}} = \frac{r}{\mu}. \tag{3}$$

As already mentioned, it is plain that the Fisher equation (2) is not a continuity equation. The total population is not conserved. Indeed, if we integrate Eq. (2) over the spatial variable x we obtain

$$\frac{dP_T(t)}{dt} = D \int dx \frac{\partial^2 \rho(x,t)}{\partial x^2} + r(t)P_T(t) - \mu(t) \int dx \, \rho^2(x,t). \tag{4}$$

Noticing that the integrand in the first term in the right-hand side of the above equation is a perfect derivative, and assuming that $\rho(x,t)$ (and $\partial\rho(x,t)/\partial x$) go to zero-fast enough when $|x| \to \infty$ one gets

$$\int dx \frac{\partial^2 \rho(x,t)}{\partial x^2} = 0. \tag{5}$$

This means that all the time dependence exhibited by the total population P_T is due to the Verhulst term. This basic fact leads in a natural way to the NKA proposal for a conserved Fisher equation: to assume an appropriate time dependence on the Verhulst parameters r and μ in order to make the total population time independent. In fact, a pair of time-dependent parameters $r(t)$ and $\mu(t)$ verifying the auxiliary equation

$$r(t) = \frac{\mu(t)}{P_T} \int dx \, \rho^2(x,t) \tag{6}$$

yields a constant total population P_T [34]. In other words, within the NKA model, the birth and death rates are continually adjusted to ensure that the population has a fixed size.

3. Fisher-like population dynamics with nonlinear diffusion and global regulation

In the present study we consider a family of nonlinear reaction–diffusion equations, akin to the Fisher and the NKA models, describing a nonlinear diffusion process coupled to a Verhulst growth dynamics with global regulation

$$\frac{\partial\rho(x,t)}{\partial t} = D\frac{\partial^2 \rho^\alpha(x,t)}{\partial x^2} + r\rho(x,t) - \mu^*[1 - p + p\mu(t)]c(x)\rho^q(x,t), \tag{7}$$

where μ^* is a positive constant, the parameter p and the function $c(x)$ satisfy $p \in [0,1]$ and $c(x) = h_1 + h_2 x^2$, with $h_{1,2}$ constants. As we are going to see shortly, the parameter p determines how strong are the global effects within the Verhulst regulation term. The case $p = 0$ corresponds to a situation like the one described by the standard Fisher equation (2) where the regulation mechanism is completely local. On the other hand, $p = 1$ describes a case where the global regulation effects are maximum. Intermediate values of p correspond to a partial global regulation. It is reasonable to expect that in real populations, even in the presence of global regulation, some local contribution to the regulation mechanism may still be important. That is the main motivation for introducing the parameter p.

The x-dependence of the function $c(x)$ introduces a spatial dependence in the Verhulst term which can be associated, for instance, with a nonhomogeneous distribution of the local resources needed by (and limiting) the population growth. As an illustration of this spatial dependence, we have adopted a quadratic form for the function $c(x)$. This form of $c(x)$ can be regarded as describing the Verhulst dynamics in a region around a local maximum or minimum of the function $c(x)$.

Integrating Eq. (8) over the spatial coordinate x we obtain

$$\frac{dP_T(t)}{dt} = r(t)P_T(t) - \mu^*[1 - p + p\mu(t)] \int dx \, c(x)\rho^q(x,t). \tag{8}$$

We are going to consider two different mechanisms of global regulation for the total population: (i) one leading to a Verhulst-like equation of motion for the total population and (ii) one leading to a constant total population.

3.1. Total population with Verhulst-like dynamics

If we set $p = 1$ and consider a global regulation mechanism given by the function

$$\mu(t) = \frac{[\int \mathrm{d}x\, \rho(x,t)]^q}{\int \mathrm{d}x\, c(x)\rho^q(x,t)} \tag{9}$$

we obtain a Verhulst-like equation of motion for the total population

$$\frac{\mathrm{d}P_T}{\mathrm{d}t} = rP_T - \mu^* P_T^q. \tag{10}$$

Eq. (10) describes a law of population growth qualitatively similar to the one given by the celebrated Verhulst population dynamics model [37–40]. In point of fact, the standard Verhulst equation is recovered when $q = 2$. For other values of parameter q (with $q > 1$) the generalized Verhulst equation (10) determines a qualitatively analogous type of self limiting population growth, with an asymptotic equilibrium population given by

$$P_T^{(\mathrm{eq.})} = \left(\frac{r}{\mu^*}\right)^{1/(q-1)}. \tag{11}$$

Other values of the parameter $p \in [0,1]$ in Eq. (7) (always with the same global control determined by the function $\mu(t)$ given by expression (9)) describe a situation where the Verhulst term in Eq. (7) is only partially affected by the global control mechanism. In fact, the value of p measures the weight of the global control upon the local Verhulst dynamics. The value $p = 1$ corresponds to a Verhulst term fully affected by the global mechanism. On the other hand, $p = 0$ corresponds to a local Verhulst dynamics that is unaffected by any global control. If we also have, in this last case $r = \mathrm{const.}$, we recover a model akin to the standard Fisher one, but with nonlinear diffusion.

3.2. Constant total population

If, alternatively, we assume a global regulation mechanism given by time-dependent functions $r(t)$ and $\mu(t)$ related by

$$r(t) = \mu^* \frac{[1 - p + p\mu(t)]}{P_T} \int \mathrm{d}x\, c(x)\rho^q(x,t), \tag{12}$$

a constant total population is obtained (see Eq. (8)).

4. Maximum q-entropy ansatz for the population density

As already mentioned in the Introduction, the maximum entropy formalism based upon the Tsallis q-entropic measures [27,28,33]

$$S_q = \frac{1}{q-1}\left[1 - \int \rho^q\, \mathrm{d}x\right], \tag{13}$$

proved to be a useful tool to find exact time-dependent solutions to evolution equations involving power-law nonlinear diffusion. Following this approach, let us consider a q-maxent ansatz for the time-dependent population density $\rho(x;t)$,

$$\rho(x,t) = \frac{1}{Z(t)}[1 - (1-q)(\lambda_1(t)x + \lambda_2(t)x^2)]^{1/(1-q)}. \tag{14}$$

The above ansatz can be regarded as arising from the optimization of the q-entropy (13) under the constraints imposed by normalization and the mean values of x and x^2. The quantities Z, λ_1, and λ_2 are the corresponding normalization parameter ("partition function") and Lagrange multipliers. Notice that, for the evolving populations that we consider here, the distribution is not normalized to 1, but to a possibly time-dependent total population P_T. The q-distribution (14) depends on time only through Z and the Lagrange multipliers.

Previous experience with q-maxent solutions of nonlinear evolution equations [1,22,23] indicates that it is convenient to recast the q-maxent ansatz as

$$\rho(x,t) = N(t)[1 - (1-q)\beta(t)(x - x_0(t))^2]^{1/(1-q)}. \tag{15}$$

The total population size P_T, as a function of time t is then given by

$$P_T = \int \mathrm{d}x \, \rho(x,t)$$
$$= \sqrt{\frac{\pi}{(q-1)} \frac{\Gamma((3-q)/2(q-1))}{\Gamma(1/(q-1))}} \frac{N(t)}{\sqrt{\beta(t)}}. \tag{16}$$

The explicit form of the integral in the right side of Eq. (8) reads

$$\int \mathrm{d}x \, c(x)\rho^q(x,t) = \int \mathrm{d}x(h_1 + h_2 x^2)\rho^q(x,t)$$
$$= N^q(t)\frac{3-q}{2}\left[\sqrt{\frac{\pi}{(q-1)\beta(t)}}\frac{\Gamma((3-q)/2(q-1))}{\Gamma(1/(q-1))}\right]\left(c(x_0(t)) + \frac{h_2}{(3-q)\beta(t)}\right). \tag{17}$$

For our present purposes we are going to need the following two expressions involving the q-maxent ansatz. On the one hand, we have $\dot{\rho} = (\partial\rho/\partial t)$, given by

$$\dot{\rho}(x,t) = \frac{1}{N(t)}\dot{N}(t)\rho(x,t) + 2[N(t)]^{1-q}(t)\rho^q(x,t)\dot{x}_0(t)\beta(t)(x-x_0(t)) - [N(t)]^{1-q}\rho^q(x,t)\dot{\beta}(t)(x-x_0(t))^2. \tag{18}$$

On the other hand, we have $\partial^2\rho^{2-q}/\partial x^2$, given by

$$\frac{\partial^2[\rho(x,t)]^{2-q}}{\partial x^2} = -2(2-q)[N(t)]^{1-q}\beta(t)\rho + 4(2-q)[N(t)]^{2(1-q)}\rho^q\beta^2(t)(x-x_0(t))^2. \tag{19}$$

It is possible to show after some algebra, from Eqs. (18)–(19), that the ansatz (15) constitutes an exact time-dependent solution of the nonlinear reaction–diffusion equation (8), provided that we set $\alpha = 2 - q$ and the quantities x_0, N, and β comply with the set of coupled, nonlinear, ordinary differential equations given by

$$\dot{x}_0(t) = -\mu^*[1 - p + p\mu(t)]\frac{h_2}{\beta(t)}N(t)^{q-1}x_0(t), \tag{20}$$

$$\dot{N}(t) = r(t)N(t) - \mu^*[1 - p + p\mu(t)](h_1 + h_2 x_0(t)^2)N(t)^q - 2D(2-q)N(t)^{2-q}\beta(t), \tag{21}$$

$$\dot{\beta}(t) = \mu^*[1 - p + p\mu(t)](h_2 + (1-q)\beta(t)(h_1 + h_2 x_0(t)^2))N(t)^{q-1} - 4D(2-q)\beta(t)^2 N(t)^{1-q}. \tag{22}$$

Choosing now appropriate forms for $r(t)$ and $\mu(t)$ we can implement the regulation models leading either to a total population exhibiting a global Verhulst dynamics or, alternatively, to a constant total population.

5. Particular examples

5.1. Partial global regulation and Verhulst-like dynamics of the total population

Replacing the ansatz (15) into expression (9) for $\mu(t)$, we get

$$\mu(t) = \left(\frac{2}{3-q}\right)\left[\frac{\Gamma((3-q)/2(q-1))}{\Gamma(1/(q-1))}\sqrt{\frac{\pi}{(q-1)\beta(t)}}\right]^{q-1}\left(c(x_0) + \frac{h_2}{(3-q)\beta(t)}\right)^{-1}. \tag{23}$$

In Fig. 1, we show the trend of the total population for the parameter values $q = 1.5$, $\mu^* = 1$, $r = 2$, $h_1 = h_2 = 1$, $D = 1$, and initial conditions for the system (20) given by $N(0) = 0.05$, $\beta(0) = 1$, and $x(0) = 0$. Several values of the parameter p were considered: $p = 0, \frac{1}{2}, 1$. In every case the total population approaches an equilibrium value. Notice that only the case $p = 0$ corresponds to a fully global regulation leading to a total population P_T evolving in accordance with the Verhulst-like equation (10).
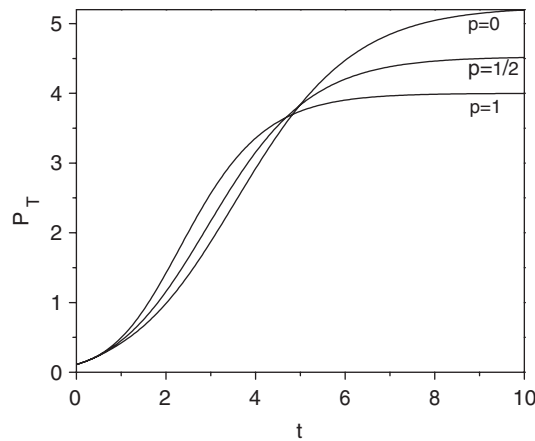
Fig. 1. The total population P_T is depicted as a function of time t. The parameter $q = 1.5$ and the initial conditions $N(0) = 0.05$ and $\beta(0) = 1$ define the total initial population. The initial distribution is also characterized by $x_0(0) = 0$. The rest of the parameters appearing in the reaction–diffusion equation are $\mu^* = 1$, $r = 2$, $h_1 = h_2 = 1$ and $D = 1$ and several values of p are considered; namely, $p = 0, \frac{1}{2}, 1$.
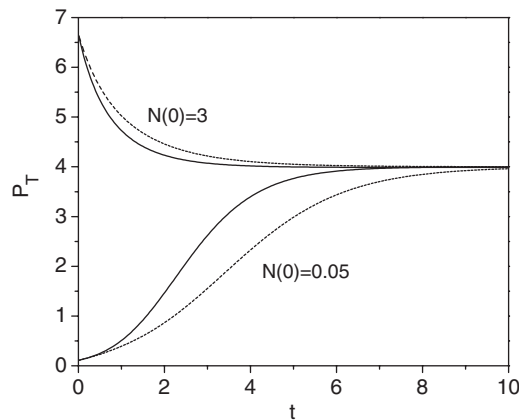

Fig. 2. Two sets of curves are shown corresponding to different initial conditions, which are given by $N(0) = 0.05$ and $N(0) = 3$. The evolution in time of $P_T(t)$ for $p = 1$ is depicted, namely Verhulst solution (solid line) in comparison with the $P_T(t)$ for $p = 0$ and $h_1 = h_2 = 1.127753$ (dashed line).

It is interesting to compare, for the same initial population density (that is, the same initial conditions for the dynamical system (20)) the evolution of the total population corresponding to complete global regulation ($p = 1$) with the evolution given by no global regulation ($p = 0$). A couple of examples of such a comparison are shown in Fig. 2. The two sets of initial conditions for (20) considered in Fig. 2 correspond to $N(0) = 0.05$ and $N(0) = 3$ (the initial values for β and x_0 are the same as in Fig. 1). For the two mentioned initial conditions, the solid lines in Fig. 2 correspond to $p = 1$ and the dashed lines to $p = 0$. In the case of no global regulation ($p = 0$), the values of the parameters h_1 and h_2 were chosen in such a way as to obtain the same equilibrium values for the total population as those obtained with global regulation ($p = 1$). A similar situation is illustrated in Fig. 3. Here, the behavior of the total population P_T with global regulation ($p = 1$ and the same parameters as in Fig. 2) is compared to the solution of the Verhulst-like equation (10) with fitting parameters, namely, $p = 1.4$ and $\mu^* = 0.7$. In Fig. 4, the evolution of the square root of the mean square displacement (which we are going to call from now on the "mean displacement") $\sigma = \sqrt{\langle (x - x_0)^2 \rangle}$ is depicted as a function of time t for $p = 0, \frac{1}{2}, 1$, and the same initial conditions and parameters as in Fig. 1.

In addition, in Fig. 5 the total population P_T as a function of t is depicted for a periodic function $h_2(t) = 1 - \frac{1}{2}\sin(t)$. This periodic dependence of h_2 represents a periodic change in the local properties of the
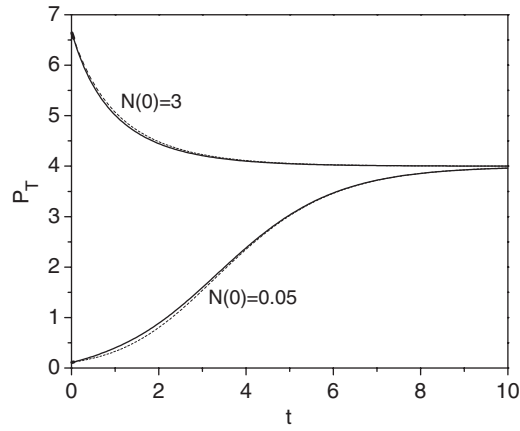
Fig. 3. $P_T(t)$ for $p = 0$ and $h_1 = h_2 = 1.127753$ (solid line) and a Verhulst-like solution (dashed line) are depicted. Verhulst-like equation $dP_T/dt = rP_T(t) - \mu P_T^q$ and fitting parameters $r = 1.4$ and $\mu = 0.7$ are used.
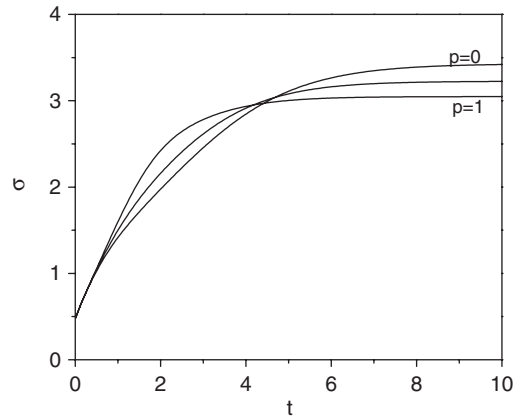

Fig. 4. The quantity $\sigma = \sqrt{\langle (x - x_0)^2 \rangle}$ is plotted as a function of time t for $p = 0, \frac{1}{2}, 1$. Initial conditions are given by $N(0) = 0.05$, $x_0(0) = 0$ and $\beta(0) = 1$.
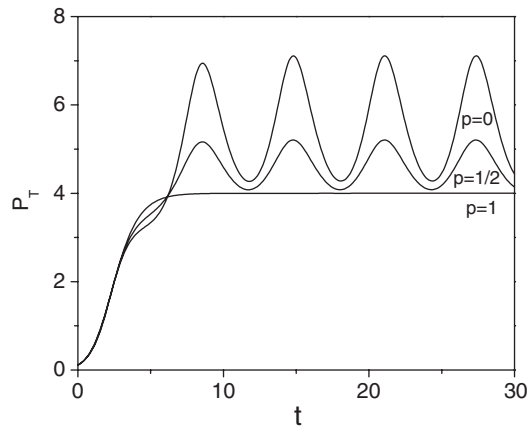

Fig. 5. P_T as a function of t is depicted. A periodic function for $h_2(t)$, given by $h_2 = 1 - \frac{1}{2}\sin(t)$, is considered.
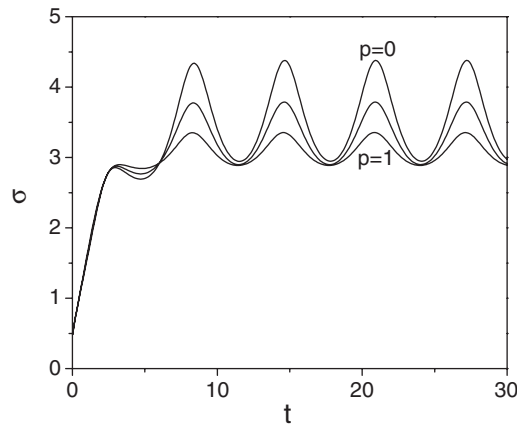
Fig. 6. Evolution of $\sigma = \sqrt{\langle (x - x_0)^2 \rangle}$ as a function of t is depicted. A periodic function for $h_2(t)$, given by $h_2 = 1 - \frac{1}{2} \sin(t)$, is considered.

environment due, for instance, to seasonal effects. In Fig. 6 we show the mean displacement $\sigma = \sqrt{\langle (x - x_0)^2 \rangle}$ as a function of the time t.

5.2. Global regulation determining a constant total population

We are going to consider now a model with a global regulation scheme leading to a constant value of the total population size, $P_T = \int \rho \, dx$. A possible relation between $r(t)$ and $\mu(t)$ yielding a constant population is given by Eq. (12), that is here rewritten for the sake of convenience

$$r(t) = \mu^* \frac{[1 - p + p\mu(t)]}{P_T} \int dx \, c(x) \rho^q(x, t). \tag{24}$$

For a given constant value P_T of the total population, the q-maxent ansatz (15) and the parameter $N(t)$ can be written in terms of the two remaining parameters determining the shape of the population density, $\beta(t)$ and $x_0(t)$,

$$\rho(x, t) = P_T \sqrt{\frac{(q-1)\beta(t)}{\pi}} \frac{\Gamma(1/(q-1))}{\Gamma((3-q)/2(q-1))} [1 - (1-q)\beta(t)(x - x_0(t))^2]^{1/(1-q)}, \tag{25}$$

and

$$N(t) = P_T \sqrt{\frac{(q-1)}{\pi}} \frac{\Gamma(1/(q-1))}{\Gamma((3-q)/2(q-1))} \beta^{1/2}(t). \tag{26}$$

Then, the relation connecting the function $r(t)$ and $\mu(t)$ can be cast, respectively, as

$$\begin{aligned} r(t) &= \mu^* \frac{1 - p + p\mu(t)}{P_T} \int dx \, c(x) \rho^q(x, t) \\ &= \mu^* \frac{3 - q}{2} [1 - p + p\mu(t)] \left(c(x_0(t)) + \frac{h_2}{(3-q)\beta(t)} \right). \end{aligned} \tag{27}$$

Substituting now the ansatz (25) in the evolution equation (7), and taking into account the relation (27) between $r(t)$ and $\mu(t)$, we obtain a set of two coupled differential equations of motion for β and x_0,

$$\dot{x}_0(t) = -\mu^* [1 - p + p\mu(t)] \frac{h_2}{\beta(t)^{(q+1)/2}} N_q^{q-1} x_0(t), \tag{28}$$

$$\dot{\beta}(t) = \mu^* [1 - p + p\mu(t)](h_2 + (1-q)\beta(t)(h_1 + h_2 x_0(t)^2)) N_q^{q-1} \beta(t)^{(q-1)/2} - 4D(2-q)\beta(t)^{(5-q)/2} N_q^{1-q}, \tag{29}$$
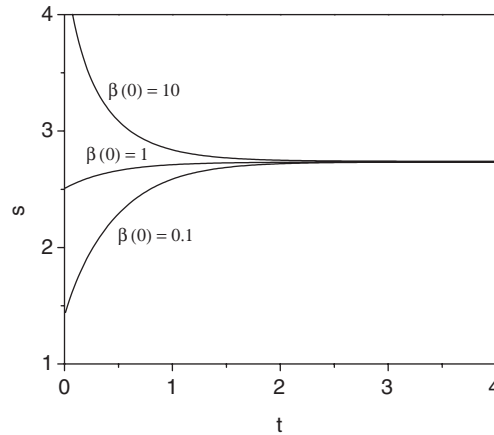
Fig. 7. The evolution of $\sigma = \sqrt{\langle (x - x_0)^2 \rangle}$ as a function of t is plotted. $P_T = 4$ is taken to be constant. The following parameters are considered $q = 1.5$, $D = 1$, $h_1 = h_2 = 1.0$, $p = 0$, and $x_0(0) = 0$, for several values of $\beta(0)$ (these are, 0.1, 1, 10).

where

$$N_q = P_T \sqrt{\frac{(q-1)}{\pi}} \frac{\Gamma(1/(q-1))}{\Gamma((3-q)/2(q-1))}. \tag{30}$$

In Fig. 7, the evolution of the mean displacement $\sigma = \sqrt{\langle (x - x_0)^2 \rangle}$ is depicted as a function of the time t, for the case of global regulation with constant total population. The total population P_T is taken to be constant, namely $P_T = 4$, and the used values of the parameters are $q = 1.5$, $\mu^* = 1$, $D = 1$, $h_1 = h_2 = 1.0$, $p = 0$, and $x_0(0) = 0$. Several values of $\beta(0)$ were considered: 0.1, 1, and 10.

6. Conclusions

In the present contribution we introduced and investigated some of the main properties of a family of reaction–diffusion equations describing a power-law nonlinear diffusion process coupled with a local (but globally regulated) Verhulst-like population dynamics. These equations are related to the conserved Fisher equation recently advanced by Newman, Kolomeisky and Antonovics. The standard Fisher equation does not have the form of a continuity equation. Consequently, the total population size is not conserved. The NKA model incorporates a global regulation mechanism (affecting the coefficients of the Verhulst term) that makes the total population size constant. In the family of models advanced here, a different regulation mechanism was investigated that makes the total population obey a Verhulst-like ordinary differential equation. An alternative globally regulated model, different from the NKA one but also endowed with a conserved total population, was also considered.

Exact time-dependent solutions exhibiting a maximum q-entropy shape were obtained for the models investigated. These solutions maximize the Tsallis q-entropy under the (time-dependent) constraints imposed by normalization and the mean values of x and x^2. The dynamics of these maximum entropy solutions is governed by a set of three coupled, nonlinear ordinary differential equations (reducing to just two equations in the case of the model with constant population). A few particular examples illustrating the behavior of these equations of motion were provided. The numerical integration of the alluded set of ordinary differential equations indicates that the associated q-maxent solutions approach, as $t \to \infty$, stationary distributions. This is consistent with the fact that, for $p = 1$, the total population approaches the asymptotic equilibrium value given by Eq. (11). The stationary values of the parameters entering the q-maxent solutions can be determined by solving the equations obtained when the left-hand sides of equations (20) are set equal to zero. Unfortunately, the resulting equations (with the exception of the one corresponding to x_0, whose equilibrium solution is $x_0 = 0$) do not admit a simple analytical solution. In connection with the problem of the asymptotic

behavior of the solutions to Eq. (7), it must be mentioned that there exist H-theorems for some reaction–diffusion equations similar to this equation (but with constant coefficients) [13]. It would be interesting to explore the possibility of formulating an H-theorem for Eq. (7).

The present effort provides further evidence for the usefulness of Tsallis maximum entropy principle for the construction of time-dependent solutions of evolution equations involving nonlinear, power-law diffusion terms.

Acknowledgment

References

[1] T.D. Frank, Nonlinear Fokker–Planck Equations, Springer, Berlin, 2005.
[2] T.D. Frank, A. Daffertshofer, Physica A 272 (1999) 497.
[3] T.D. Frank, Phys. Lett. A 267 (2000) 298.
[4] T.D. Frank, Physica A 285 (2000) 351.
[5] T.D. Frank, A. Daffertshofer, Physica A 295 (2001) 455.
[6] T.D. Frank, A. Daffertshofer, Physica A 292 (2001) 392.
[7] T.D. Frank, Phys. Lett. A 280 (2001) 91.
[8] T.D. Frank, Physica A 301 (2001) 52.
[9] T.D. Frank, Phys. Lett. A 290 (2001) 93.
[10] T.D. Frank, Physica A 310 (2002) 397.
[11] T.D. Frank, Phys. Lett. A 305 (2002) 150.
[12] T.D. Frank, J. Math. Phys. 43 (2002) 344.
[13] T.D. Frank, Ann. Phys. 13 (2004) 461.
[14] T.D. Frank, Eur. Phys. J. B 37 (2004) 139.
[15] T.D. Frank, Physica A 340 (2004) 251.
[16] E.K. Lenzi, C. Anteneodo, L. Borland, Phys. Rev. E 63 (2001) 1109.
[17] L.C. Malacarne, R.S. Mendes, I.T. Pedron, E.K. Lenzi, Phys. Rev. E 63 (2001) 0101.
[18] L.C. Malacarne, R.S. Mendes, I.T. Pedron, E.K. Lenzi, Phys. Rev. E 65 (2002) 2101.
[19] P.C. da Silva, L.R. da Silva, E.K. Lenzi, R.S. Mendes, L.C. Malacarne, Physica A 342 (2004) 16.
[20] L.R. da Silva, L.S. Lucena, P.C. da Silva, E.K. Lenzi, R.S. Mendes, Physica A 357 (2005) 103.
[21] I.T. Pedron, R.S. Mendes, T.J. Buratta, L.C. Malacarne, E.K. Lenzi, Phys. Rev. E 72 (2005) 1106.
[22] A.R. Plastino, A. Plastino, Physica A 222 (1995) 347.
[23] C. Tsallis, D. Buckman, Phys. Rev. E 54 (1996) 2197.
[24] L. Borland, F. Pennini, A.R. Plastino, A. Plastino, Eur. Phys. J. B 12 (1999) 285.
[25] A.R. Plastino, M. Casas, A. Plastino, Physica A 280 (2000) 289.
[26] A. Rigo, A.R. Plastino, M. Casas, A. Plastino, Physica A 276 (2000) 97.
[27] M. Gell-Mann, C. Tsallis (Eds.), Nonextensive Entropy: Interdisciplinary Applications, Oxford University Press, Oxford, 2004.
[28] J.P. Boon, C. Tsallis (Eds.), Europhysics News (Special Issue), vol. 36, November/December 2005.
[29] B. Boghosian, Phys. Rev. E 53 (1996) 4754.
[30] A. Taruya, M. Sakagami, Mon. Not. R. Astron. Soc. 364 (2005) 990.
[31] L. Borland, Phys. Rev. Lett. 89 (2002) 098701.
[32] T.D. Frank, R. Friedrich, Physica A 347 (2005) 65.
[33] J.A.S. Lima, R. Silva, A.R. Plastino, Phys. Rev. Lett. 86 (2001) 2938.
[34] T.J. Newman, E.B. Kolomeisky, J. Antonovics, Phys. Rev. Lett. 92 (2004) 228103.
[35] R.A. Fisher, Ann. Eugen. 7 (1937) 355.
[36] J. Murray, Mathematical Biology, Springer, Berlin, 1989.
[37] P.F. Verhulst, Mem. Acad. R. Belg. 18 (1845) 1.
[38] J. Mazumdar, An Introduction to Mathematical Physiology and Biology, Cambridge University Press, Cambridge, UK, 1999.
[39] G.E. Hutchinson, An Introduction to Population Ecology, Yale University Press, 1978.
[40] P.G.L. Leach, K. Andriopoulos, Chaos Solitons Fractals 22 (2004) 1183.
[41] J. Riordan, C.R. Doering, D. ben Avraham, Phys. Rev. Lett. 75 (1995) 565.
[42] S. Coen, M. Tlidi, P. Empli, M. Haelterman, Phys. Rev. Lett. 83 (1999) 2328.