On a Class of Generalized Gompertz-Bateman Growth-decay Models

Svetoslav Markov

Institute of Mathematics and Informatics,
Bulgarian Academy of Sciences
smarkov@bio.bas.bg

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Abstract. A recently proposed reaction network induces the classical Gompertz equations. The network consists of two reactions, one reaction for a decaying species S and another reaction for a sigmoidally growing species X catalyzed by species S. The proposed reaction network provides for a separation of the dynamical evolutions of the two species. More specifically, the reaction equation for the decaying species S is totally independent on the growing species X, while species X uses species S simultaneously both as a catalyst and as a (food) resource. Based on the idea of such a separation, in this work we propose a class of growth-decay models formulated in terms of reaction networks that includes the Bateman exponential decay chain for the evolution of the catalyst/resource species. In this note we show that the Gompertz-type reaction network can be generalized into a class of Gompertzian-type growth-decay models by replacing the first species

from the Bateman exponential decay chain by the second species in the chain, that now can play the role of a catalyst/resource for the growing species. A further generalization would be to use the third species (or the k-th species) in the Bateman decay chain as a catalyst/resource for the growing species. An important advantage of the new class of models is the possibility of obtaining a prolonged lag time of the sigmoidal solutions of the growing species.

Key words: Dynamical growth models; logistic function; Gompertz function; Bateman equations; sigmoidal functions; dynamical systems; reaction networks, first integral; conservation equation.

1   Introduction

A reaction network inducing the classical Gompertz growth model [5] is recently proposed [11]. The proposed reaction network involves two reaction equations over two species: a catalyst/resource species S that declines tending to 0 with $t \longrightarrow \infty$, and a sigmoidally growing species X catalyzed by species S. The reaction network provides for separate dynamics of the two species S and X, due to the independent (uncoupled) behavior of species S from that of X. The idea of such independency is supported by several authors, e.g. [4], [12], [15], [16], [17], [19]. Based on the idea of such a separation, and noticing that the resource species S is the first one in the Bateman exponential decay chain [2], in this work we point attention to a general class of growth-decay models where the resource species is replaced by some consecutive species appearing further in the Bateman chain. An important advantage of the proposed class of models is the prolonged lag phase of the sigmoidally growing species X—a property often needed when fitting biological data of growth-decay processes, studied e.g. in microbiology, marine ecology, tumor research, etc. [4], [13], [14], [19].

In Section 2 we recall the classical Gompertz model from the perspective of reaction networks theory [3], [10], [11]. In Section 3 we introduce an extension of the Gompertz model using the Bateman exponential decay chain and study some simple properties of the induced dynamical system. Section 4 contains the solutions of the proposed

Gompertz-type model system. Section 5 describes a further generalization of the Gompertzian model combining the latter with the Bateman exponential decay chain or considering the Gompertzian model as an operator over an input resource function.

2 The Gompertz reaction network

The classical Gompertz model can be formulated in terms of a reaction network involving species S, X, P as follows [11]:

$$
\begin{aligned}
S &\xrightarrow{k_1} P \\
S + X &\xrightarrow{k} 2X + S.
\end{aligned}
\tag{1}
$$
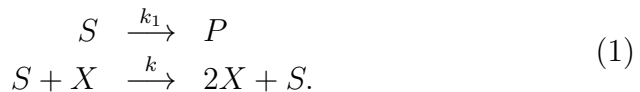
Assume that species S, X, P are homogeneously distributed in a fixed volume and denote their concentrations resp. by s, x, p. Consider the following dynamical system of reaction equations for the rates of concentrations s, x, p of species resp. S, X, P:

$$
\begin{aligned}
s' &= -k_1 s, \\
p' &= k_1 s, \\
x' &= k s x.
\end{aligned}
\tag{2}
$$

Based on the general theory of reaction networks [3], [10], assuming mass action kinetics, one arrives to the following:

Proposition 1 [11]. Reaction network (1) induces via mass action law the system of reaction equations (2).

Assume in system (2) the following initial conditions:

$$
s(0) = s_0 > 0; \ p(0) = p_0 \geq 0; \ x(0) = x_0 > 0.
\tag{3}
$$

Proposition 2 [11]. For the initial value problem (2)–(3) we have the following properties for the variables $s, x \in [0, \infty)$:
i) a conservation relation:

$$
(k/k_1)s = c - \ln x, \ \ c = (k/k_1)s_0 + \ln x_0;
\tag{4}
$$

ii) the variable x satisfies the classical Gompertz equation.

Proof. Ignoring in (2) the uncoupled equation for p', we obtain the dynamical system

$$s' = -k_1 s, \quad x' = ksx, \tag{5}$$

which is an S-system [15], [16]. System (5) generates the relation

$$s'/k_1 + x'/(kx) = 0. \tag{6}$$

Using initial conditions (3), we obtain the first integral (4).

Substituting s from (4) in equation $x' = ksx$, we obtain the familiar Gompertz differential equation

$$x' = k_1 x(c - \ln x), \; x(0) = x_0, \tag{7}$$

for the mass/concentration x of the growth species X. The assumption $x(\infty) = 1$ determines the constant c as $c = 0$. The solution of equation (7) is the familiar Gompertz function

$$x(t) = x_0 e^{-e^{-k_1 t}}. \tag{8}$$

The graph of the solution $x = x(t)$ given by (8) is visualized on Fig. 1 for two different values of the rate parameter k_1.
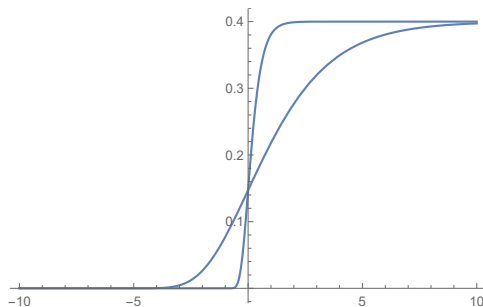

Figure 1: The Gompertz function (8) for $s_0 = 0.4$, $x_0 = 0.14$, $k_1 = 0.5$ and $k_1 = 5$ (the steeper graph)

3 A Gompertz-Bateman growth-decay model

The first reaction of reaction network (1) determines the dynamics of species S showing that the evolution of S does not depend on species X; mathematically, this is seen from the first equation in system (2).

The second reaction shows that species S is a catalyst in the reaction, thus again S is not influenced (consumed) by X. For comparison, in the logistic reaction network $S + X \longrightarrow 2X$ species X uses S as a food resource and the dynamics of both species are interconnected, namely the biomass of X gains as much as the biomass of S loses.

Differently to species S, in network (1) the dynamics of X strongly depends on S, since S acts as catalyst on the reproduction of X. Let us note once more that species X does not influence the (bio)mass of S during the process of reproduction, that is X does not consume S as food but uses S merely as a catalyst.

The idea of building a model of two interacting species S, X, such that the dynamics of the catalyst species S is separately determined independently on that of the growing species X, is inherently incorporated in the classical Gompertz model (1). This idea is further developed in the present work as follows.

Reaction $S \xrightarrow{k_1} P$ says that at time moment t_0 a concentration quantity s_0 instantly appears in the environment of the growing species X and the process immediately starts. Such an instant appearance of S, thereby homogeneously distributed in the volume, seems not very realistic. We shall next modify the reaction $S \longrightarrow P$ so that the catalyst species arrives smoothly in time in the form of a wave, possibly starting from an arbitrary small value greater or equal zero. In order to simulate such a situation, let us look at reaction $S \xrightarrow{k_1} P$ as a first step (chain-link) of an n-step exponential growth-decay Bateman chain [2]:

$$S \xrightarrow{k_1} P \xrightarrow{k_2} Q \xrightarrow{k_3} R \xrightarrow{k_4} ... \qquad (9)$$
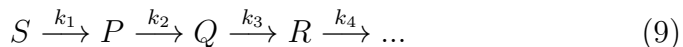
The Bateman chain (9) suggests that, instead of the first species S in the chain, we may use some species next in the chain to play the role

of a catalyst for the growing species X. To be more specific, we shall use for that purpose the second species P in the Bateman chain. In other words, consider the case of a two-step Bateman chain:

$$S \xrightarrow{k_1} P \xrightarrow{k_2} Q \tag{10}$$

and use species P from reaction network (9) to play the role of the catalyst species in the second reaction of Gompertz reaction network (1). Thus, we obtain the following reaction network:

$$\begin{aligned} S &\xrightarrow{k_1} P \xrightarrow{k_2} Q \\ P + X &\xrightarrow{k} 2X + P, \end{aligned} \tag{11}$$
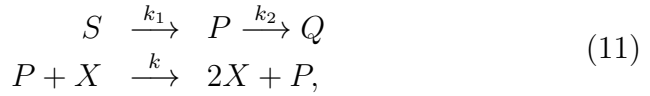
to be further referred as Gompertz-Bateman model of order 1 (the classical Gompertz model being a Gompertz-Bateman model of order 0).

As usually, assume that species S, P, X are homogeneously distributed in a fixed volume and denote their concentrations (masses) resp. by s, p, x. Consider then the following dynamical system of reaction equations for the rates of variables s, x, p:

$$\begin{aligned} s' &= -k_1 s, \\ p' &= k_1 s - k_2 p, \\ x' &= kxp. \end{aligned} \tag{12}$$

On the base of the reaction networks theory [3], [10], assuming mass action kinetics, we arrive at the following:

Proposition 3. Reaction network (11) induces the dynamical system of reaction equations (12).

Let us equip system (12) with the following initial conditions to hold in the interval $[0, \infty)$:

$$s(0) = s_0 > 0; \ p(0) = p_0 \geq 0; \ x(0) = x_0 > 0. \tag{13}$$

Proposition 4. The dynamical system (12) with initial conditions (13) induces the conservation relation

$$(k/k_2)(p + s) = c - \ln x, \quad c = (k/k_2)(p_0 + s_0) + \ln x_0. \tag{14}$$

Proof. To prove (14) note that system (12) implies

$$p' + s' = -k_2 p = -k_2[x'/(kx)],$$

hence

$$(k/k_2)(p' + s') = -[x'/x]. \tag{15}$$

Integrating (15) we obtain (14) as a first integral.

4 Solutions to Gompertz-Bateman growth-decay model of order 1

Let us now concentrate on the solutions for the variables s, p, x of initial value problem (12)–(13). The solutions for functions s and p are well-known as being part of the Bateman equations [2]. More specifically, we recall that in the interval $[0, \infty)$ the following expression holds true for s:

$$s(t) = s_0 e^{-k_1 t}. \tag{16}$$

For the variable p the expression holds true:

$$p = \begin{cases} (k_1/(k_2 - k_1))s_0(e^{-k_1 t} - e^{-k_2 t}) + p_0 e^{-k_2 t}, & k_1 \neq k_2 \\ e^{-k_1 t}(p_0 + k_1 s_0 t), & k_1 = k_2 \end{cases} \tag{17}$$
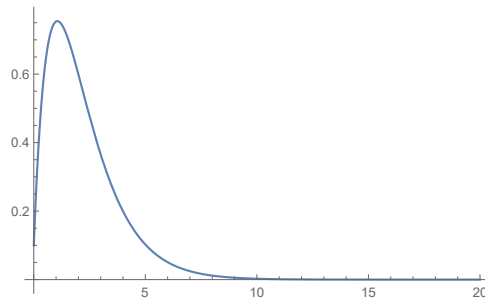

Figure 2: The function p for $k_1 = 1, k_2 = 1.2, p_0 = 0.1, s_0 = 1.74$

The graph of solution p for $k_1 = 1, k_2 = 1.2, p_0 = 0.1, s_0 = 1.74$ is presented on Fig. 2.

For the variable x the following propositions hold true:

Proposition 5. The initial value dynamical problem (12)–(13) possesses an unique solution for the variable x in the interval $[0, \infty)$, which is a solution to the differential equation: $x' = kxp$, wherein p is defined by expression (17). Hence, the Gompertz-Bateman model (11) can be formulated as a differential equation for the growth function x as follows:

$$x' = kxp = \begin{cases} kx[(k_1/(k_2 - k_1))s_0(e^{-k_1 t} - e^{-k_2 t}) + p_0 e^{-k_2 t}], & k_1 \neq k_2 \\ kxe^{-k_1 t}(p_0 + k_1 s_0 t), & k_1 = k_2 \end{cases}$$
(18)

Expression (18) induces the following growth rate per capita (also known as Gompertz "mortality law"):

$$\frac{x'}{x} = kp = \begin{cases} k[(k_1/(k_2 - k_1))s_0(e^{-k_1 t} - e^{-k_2 t}) + p_0 e^{-k_2 t}], & k_1 \neq k_2 \\ ke^{-k_1 t}(p_0 + k_1 s_0 t), & k_1 = k_2 \end{cases}$$
(19)

An explicit expression for the solution x can be obtained from the conservation relation (14), written in the form

$$\ln x = c - (k/k_2)(p + s), \quad c = (k/k_2)(p_0 + s_0) + \ln x_0. \tag{20}$$

Substituting the expressions for s and p, namely (16) and (17), in (20), we obtain the following

Proposition 6. The Gompertz-Bateman growth function x defined as solution of differential equation (18) can be expressed as follows:

$$x(t) = \begin{cases} x_0 e^{\frac{ke^{-(k_1+k_2)t}(-e^{k_2 t}k_2 s_0 + e^{(k_1+k_2)t}(k_2-k_1)(p_0+s_0)+e^{k_1 t}(k_2 p_0 + k_1(-p_0+s_0)))}{k_2(k_2-k_1)}}, & k_1 \neq k_2, \\ x_0 e^{\frac{k(p_0+s_0 - e^{-k_1 t}(p_0+s_0+k_1 s_0 t))}{k_1}}, & k_1 = k_2. \end{cases}$$
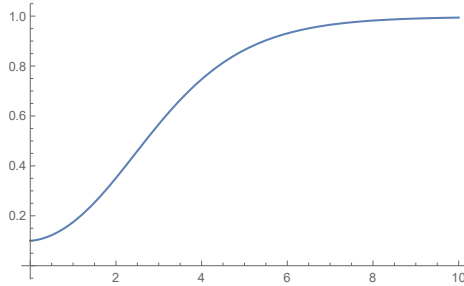(21)

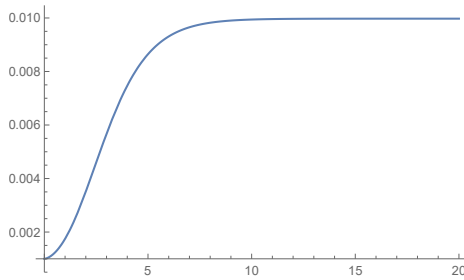Figure 3: The solution x for $k_1 = 1$, $k_2 = 0.8$, $s_0 = 1.74$, $p_0 = 0.1$, $x_0 = 0.1$.

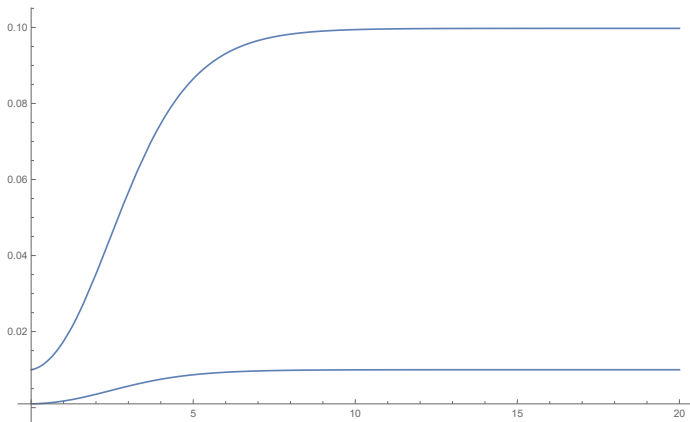Figure 4: The solution x for $k_1 = 1$, $k_2 = 0.8$, $s_0 = 1.74$, $p_0 = 0.1$, $x_0 = 0.001$.

Figure 5: The solutions x for two sets of parameters: i) $k_1 = 1$, $k_2 = 0.8$, $s_0 = 1.74$, $p_0 = 0.1$, $x_0 = 0.1$, and ii) for $k_1 = 1$, $k_2 = 0.8$, $s_0 = 1.74$, $p_0 = 0.01$, $x_0 = 0.01$.
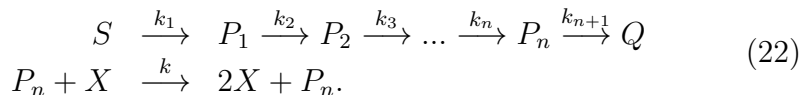
The solutions x for various values of the parameters and the initial conditions are visualized on Figures 3–5. The sigmoidal behavior of function x and its lag phase are clearly expressed.

5   Notes on the Gompertz-Bateman model

We briefly present two ideas for possible generalizations of the Gompertz-Bateman model arising from the perspective of reaction networks theory.

5.1   A note on a generalization of the Gompertz-Bateman model

Based on the idea of a separation of the dynamics of the declining (resource) species from that of the growth species, the Gompertz-Bateman model of order 1 can be naturally generalized by replacing the second species P by the n-th consecutive species in the Bateman chain arriving thus to the following reaction network:

$$
\begin{aligned}
S \quad &\xrightarrow{k_1} \quad P_1 \xrightarrow{k_2} P_2 \xrightarrow{k_3} ... \xrightarrow{k_n} P_n \xrightarrow{k_{n+1}} Q \\
P_n + X \quad &\xrightarrow{k} \quad 2X + P_n.
\end{aligned}
\tag{22}
$$

to be further referred as Gompertz-Bateman model of order n. Under such terminology the classical Gompertz model should be considered as a Gompertz-Bateman mode of order 0.

5.2   The Gompertzian model as an operator

The Gompertz-Bateman model of order n (23) suggests that the last reaction of the model of the form

$$
P_n + X \xrightarrow{k} 2X + P_n
\tag{23}
$$

can be looked as an operator reaction transforming an input species P_n into an output species X. In terms of dynamical reaction equations

the "Gompertzian" differential operator

$$x' = kxp \tag{24}$$

acts on a given input function p, producing an output function x. Such a setting raises the question of admissible input functions p that produce meaningful solutions x with required properties, e.g. bounded, sigmoidal, etc.

6   Concluding remarks

The idea of building a model of two interaction species S and X, where the dynamics of the catalyst species S is separately determined and independent from that of the growing species X, is incorporated in the classical Gompertz model. This idea can be further developed by looking for various possibilities for the dynamics of the catalyst species S. Reaction $S \longrightarrow P$ used in the classical Gompertz model says that in time moment t_0 a quantity s_0 appears in the environment of the growth species and the process immediately starts. Such an instant appearance seems not quite realistic. In this work, we modify the reaction $S \longrightarrow P$ so that the catalyst species penetrates the environment of the growing species smoothly in time in the form of a wave. In order to simulate such a situation, we look at the reaction $S \longrightarrow P$ as at a first chain-link of an n-step exponential growth-decay Bateman chain. We then generalize the classical Gompertz growth-decay model by replacing the first species from the Bateman exponential decay chain by involving the second species in the chain, that now plays the role of a catalyst/resource for the growing species X. A further generalization would be to use the third species (or the k-th species) in the Bateman exponential decay chain as a catalyst/resource for the growing species.

When studying the classical Gompertz growth models from the perspective of the reaction networks theory we are surprised by the interesting reaction mechanism of the model. Based on this mechanism, in the paper we define a new class of Gompertz-like models. We propose an one-dimensional differential equations for the growth

(resp. decay) species, by finding a first integral leading to a conservation relation. Another consequence is the resulting new form of the Gompertzian mortality law. The proposed reaction networks are simple and may seem trivial but are of some importance to those who construct new models to study biological growth processes whose underlying mechanism is unknown. The proposed reaction network realization of the Gompertz growth model can be interpreted from the perspective of demographic and socio-economic sciences. It is remarkable that the Gompertz reaction network comprises a reaction equation describing biological activity that is characteristic for highly organized biological organs, organisms or populations. This explains why using the Gompertz model in areas, such as marine and plant ecology, demographic studies and cancer research, is so successful [4], [12], [13], [14], [19]. The reaction network approach clearly explains the close links between the Gompertz model and the Verhulst logistic model [1], [11]. Let us also mention that sigmoidal Gompertzian type functions find numerous applications in fitting real-life biological, ecological, socio-economic etc. experimental measurement data [6]–[9], [17], [19].

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