Gompertzian population growth under some deterministic and stochastic jump schedules

Henry C. Tuckwell¹, ², †,

¹ School of Electrical and Electronic Engineering, University of Adelaide, Adelaide, South Australia 5005, Australia
² School of Mathematical Sciences, Monash University, Clayton, Victoria 3800, Australia
† Email: henry.tuckwell@adelaide.edu.au

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Abstract

Many cell populations, exemplified by certain tumors, grow approximately according to a Gompertzian growth model which has a slower approach to an upper limit than that of logistic growth. Certain populations of animals and other organisms have also recently been analyzed with the Gompertz model. This article addresses the question of how long it takes to reduce the population from one level to a lower one under a schedule of sudden decrements, each of which removes a given fraction of the cell mass or population. A deterministic periodic schedule is first examined and yields exact results for the eradication or extinction time which is defined as that required to reduce the number of cells to less than unity. The decrements in cell mass at each hit could correspond to an approximation to reduction of a tumor by external beam radiation therapy. The effects of variations in magnitude of successive decrements, the time interval between them, the initial population size and the intrinsic growth rate are calculated and results presented graphically.

With a schedule governed by a Poisson process, the number of organisms or cells satisfies a stochastic differential equation whose solution sample paths have downward jumps as random times. The moments of the exit time then satisfy a system of recurrent differential-difference equations. A simple transformation results in a simpler system which has been studied both analytically and numerically in the context of interspike intervals of a model neuron. Results are presented for the mean eradication time for various frequencies and magnitudes of hits and for various eventual and initial population sizes. The standard deviation of the eradication time is also investigated.

Keywords: Gompertz model; tumor; eradication time; jump process; external beam radiation therapy
1 Introduction

An approximate empirically based model for the growth of some biological populations is provided by the Gompertzian function first introduced as a model for human mortality (Gompertz, 1825). An early review of its application to growth curves using differential equations was that of Winsor (1932).

Starting in the 1960s and 1970s, the Gompertz model became popular for its ability to describe the growth of certain tumor cell populations (Laird, 1964; Simpson-Herren and Lloyd, 1970; Smith and Tuckwell, 1974; Norton et al., 1976). This application has continued to the present day. Norton (1988), for example, applied the model to breast cancer. Although the Gompertzian description of tumor growth is purely phenomenological, it can provide a useful simplification which avoids taking into account geometric factors, vascularization, cell types and details of the cell cycles, which require a large number of parameters (Burton, 1966; Jansson and Revesz, 1974; Dibrov et al., 1985; Bajzer et al., 1997). Recently there has appeared an interesting comparison of the predictions of seven ordinary differential equation models, including the Gompertzian, for the growth of tumors (Murphy et al., 2016). It was found that wide discrepancies arise in the application of these models which has implications for the choice of suitable doses of chemotherapeutical agents. Behera and O’Rourke (2008) analyzed the Gompertzian model for tumor growth with additive and multiplicative noise. The familiar logistic model, included in the seven models, sometimes outperforms other models (Vaidya et al., 1982) and has also been analyzed with additive and multiplicative white noises (Ai et al., 2003).

The important issue of modeling the responses of tumors to radiation therapy and chemotherapy has been addressed by several authors. The targets of both forms of treatment is the destruction of the DNA of tumor cells, rendering them incapable of mitosis. Depending on the nature of the treatment a different mathematical formulation is employed. Chemotherapy, applied systemically, usually involves a continuous negative effect on growth (Sachs et al., 2001). The most common form of radiation therapy with an external beam is performed at regular time intervals, often daily for 5 days per week, hence resulting in
discrete and sudden declines in tumor size (Rockne et al., 2009). However tumor size is not a very useful variable for many tumors because dead cells tend to remain in place, at least in the short term. For small tumors in their initial stages, exponential models may be employed (Badri et al., 2016) rather than Gompertzian or other saturating processes. Rockne et al. (2009) explored a spatio-temporal model of tumor growth in the form of a reaction-diffusion system.

The Gompertz model has also often been employed for populations of diverse organisms, one of the first applications being to the human population of the United States (Davies, 1927). Other examples include plant disease (Berger, 1981), several mammalian populations (Zullinger et al., 1984), sage-grouse in North America (Beever and Aldridge, 2011), fish and insects (Eberhardt and Breiwick, 2012) and ungulates (Ferguson and Ponciano, 2015).

2 Description of model

In this article we only study the effects of density independent “disasters” on Gompertzian growth. The deterministic differential equation describing such growth in the unimpeded case for a population of size $N(t)$ at time $t$ contains only two parameters:

$$\frac{dN}{dt} = rN(\ln K - \ln N), \quad N(0) = N_0 \in (0, K), \quad (1)$$

where $r$ is the intrinsic growth rate and $K$ is the asymptotic maximum population size (carrying capacity) when $r$ is positive. Equation (1) can also be written as a system of two differential equations (Simpson-Herren and Lloyd, 1970). The solution of (1) is

$$N(t) = K \exp \left\{ \ln \left[ \frac{N_0}{K} \exp(-rt) \right] \right\}, \quad (2)$$

which shows the slow approach to $K$ as $t \to \infty$.

In the context of populations of organisms, it may be assumed that sudden decrements can occur due to accidents, external attack by hostile species, disease outbreaks, floods or fires etc. Such decrements are usually unpredictable. When tumors are subjected to certain clinical treatments, such as regimes of external radiation therapy, then each successful treatment will result in a decline in the number of viable tumor cells.

In what follows we assume that decrements are proportional to the number of organisms or cells present and that they are rather sudden so that they may be described as downward jumps or discontinuities. Such a dynamic has been depicted in certain chemotherapeutic regimes for tumors by Arroesty et al. (1973) (c.f. Sachs et al., 2001). In such cases a treatment at time $t$ gives, in the manner of a disaster in a population of organisms,

$$N(t^+) = N(t^-) - \epsilon N(t^-), \quad (3)$$

where $\epsilon$ is a positive constant. A more realistic representation would have $\epsilon$ as a random variable but this complication is ignored here. Another possibility, more appropriate for a widely dispersed population, is that the decline is not proportional to the number of cells present but rather is a random number of cells also described by a (constant) random variable,

$$N(t^+) = N(t^-) - \epsilon. \quad (4)$$
However, analysis is able to be performed more readily if the assumption of (3) is made and this case seems to be of practical interest.

3 Deterministic regime

If one assumes that sudden decrements proportional to existing population size occur periodically then the time course of the population can be found analytically, as was observed by Aroesty et al. (1973) in connection with chemotherapy for tumors. Let the population evolve according to

\[ \frac{dN}{dt} = rN(\ln K - \ln N) - N \sum_{i=1}^{\infty} \epsilon \delta(t - iT), \quad N(0) = N_0 \in (0, K), \]

so that the population jumps downward by a fraction \( \epsilon \) of its current size at intervals of \( T \). Putting

\[ k = \ln K, \quad Y = k - \ln N, \quad \alpha = \ln \frac{1}{1 - \epsilon} \]

yields the linear differential equation

\[ \frac{dY}{dt} = -rY + \alpha \sum_{i=1}^{\infty} \delta(t - iT). \]

If the initial value of \( Y \) is \( Y_0 \), then after \( m \) downward jumps in \( N \) have occurred,

\[ Y(mT+) = Y_0 e^{-mrT} + \alpha S_m, \]

where \( S_m \) is a geometric series

\[ S_m = 1 + e^{-rT} + \cdots + e^{-(m-2)rT} + e^{-(m-1)rT} \]

which sums to give

\[ Y(mT+) = Y_0 e^{-mrT} + \alpha e^{-mrT} - 1 \]

The pre-jump value is

\[ Y(mT^-) = Y(mT^+) - \alpha. \]

The asymptotic large time value post jump value is

\[ Y^+(\infty) = \frac{\alpha}{1 - e^{-rT}} \]

with corresponding value for \( N \) of

\[ N^+(\infty) = \exp \left( k - \frac{\alpha}{1 - e^{-rT}} \right). \]

If extinction is defined as achieving a level less than 1, then in terms of the original parameters the condition for extinction is

\[ \ln \left(1 - \epsilon\right) e^{-rT} - 1 > \ln K. \]

If this condition is met, the actual time to extinction \( T_{ext} \) is more easily expressed in terms of \( Y \). The time taken for \( N \) to first become less than 1 is the same as that for \( Y \) to exceed \( k \) so

\[ T_{ext} = T \inf \{ m | Y_0 e^{-mrT} + \alpha e^{-mrT} - 1 > k \}. \]

However when exploring extinction it is more simply done numerically.
3.1 Numerical results

A few examples of trajectory values pre- and post-jump were calculated for $Y$ using the above formulas and converted to values for $N$ using

$$N(t) = e^{k-y}.$$  \hspace{1cm} (14)

The results are displayed in Figures 1 to 4, where only values of $N$ at the pre and post jump values are shown, not the trajectories between jumps. The following set of parameter values was taken as a standard set $K = e^{20} = 4.8517 \times 10^8$, $T = 2$, $\alpha = 0.5$, $N_0 = 0.9K$, $r = 0.02$, together with 15 jumps so that the number of points is 31. The value $\alpha = 0.5$ is equivalent to $\epsilon = 1 - \exp(-\alpha) = 0.3935$ in terms of jumps in $N$.

Results for the standard set are included as blue curves in all of the Figures 1 to 4. In each of the 4 Figures one parameter is varied, being $\alpha$, $T$, $N_0$ and $r$ respectively. In Figure 1, the decline in $N$ is sharp, being roughly exponential, for the standard set, but when $\alpha$ is reduced the decline is much slower and to a larger value as predicted by Equ. (13).

Figure 2 shows very little difference when $T$ is doubled from 2 to 4 but a substantial difference in both the rate of decline and the asymptotic value when $T = 10$. Figure 3 displays results for various $N_0$, but truncated to emphasize the large-time declines. The latter reveal little dependence on $N_0$ as would be expected from Equ. (13). Changes in $r$ from the standard value give results as expected with a much higher asymptotic value attained much sooner for the largest value $r = 0.2$. Results such as these may be of some indicative utility in predicting the effects of various regimes of radio or chemotherapy on tumor reduction.

![Figure 1: Time course of Gompertzian growth with periodic decrements and various $\alpha$ as indicated. Values of $N$ are shown just prior to (e.g., $T^-$) and just after (e.g., $T^+$) each decrement.](image_url)
Figure 2: Time course of Gompertzian growth with periodic decrements and various $T$ as indicated. Values of $N$ are shown just prior to and just after each decrement.

Figure 3: Time course of Gompertzian growth with periodic decrements and various initial sizes $N_0$ as indicated. Values of $N$ are shown just prior to and just after each decrement.

4 Stochastic regime

There are many possible ways to incorporate randomness into models of population growth. One useful and popular method is through stochastic differential equations (SDEs) for Markov processes. Often such processes are continuous and represented by diffusion processes (Tuckwell, 1974, Tuckwell and Le Corfec, 1998, for examples), for which a paradigm in the temporarily homogeneous case is

$$dN = f(N)dt + g(N)dW$$

(15)

where $f$ and $g$ are suitable functions (see for example Gihman and Skorohod, 1972; Oksendal, 2000) and $W$ is a 1-parameter standard Wiener process or Brownian motion with mean zero and $Var(W(t)) = t$. 

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Figure 4: Time course of Gompertzian growth with periodic decrements and various growth rates \( r \) as indicated. Values of \( N \) are shown just prior to and just after each decrement.

4.1 Theory

Solutions of equations like (15) do not contain the possibility of sudden large (discontinuous) changes in \( N \) which may occur in real populations. However, such large random fluctuations can be incorporated by considering more general stochastic differential equations of the form

\[
dN = f(N)dt + g(N)dW + \int_R h(N, u)n(dt, du),
\]

where \( n(t, A) \) for \( A \in B(R) \) is a Poisson process (the number of jumps with magnitudes in the Borel set \( A \) up to time \( t \)) such that if \( E[n(t, A)] = tM(A) \) then

\[
Pr[n(t, A) = k] = \frac{(M(A)t)^k \exp(-M(A)t)}{k!},
\]

for \( k = 0, 1, 2, \ldots \). The theory of such processes was developed by Feller (1940) for a process without a diffusion component and in the more general case by Ito (1951), Skorohod (1965) and Gihman and Skorohod (1972). In the last of these references it is shown how the forward and backward Kolmogorov equations for the transition probability density function can be written down for a process satisfying an SDE of the form of (16). In general such equations are functional partial differential equations and are more difficult to solve than the corresponding equations for the simpler case in which a diffusion process is unaccompanied by a superimposed jumps.

The population size \( N(t) \) is assumed to evolve according to the Gompertzian growth equation (1) between sudden decrements of magnitude \( \epsilon N(t) \) with \( \epsilon > 0 \), which occur at the event times of a Poisson process \( N^*(\lambda; t) \) which has a constant rate parameter \( \lambda \). The stochastic equation for \( N(t) \) is thus

\[
dN(t) = rN(t)(\ln K - \ln N(t))dt - \epsilon N(t)dN^*(\lambda; t),
\]

where \( r, \epsilon \) and \( K \) are all positive. The initial population size is \( N_0 \in (0, K] \). Note that if \( \epsilon = 1 \) then the first event in the Poisson process will annihilate the population so that it will be assumed that \( 0 < \epsilon < 1 \). This means that
the population can never attain the value zero, but it may become arbitrarily close to zero.

Let \( p(N, t|N_0) \) be the transition probability density function of \( N \). From Gihman and Skorohod (1972) we find that \( p \) satisfies the forward Kolmogorov equation

\[
\frac{\partial p}{\partial t} = \frac{\partial}{\partial N} \left[ r N (\ln N - \ln K) p \right] + \lambda [p(N(1 + \epsilon), t) - p(N, t)].
\] (19)
The moments of \( N(t) \) can be found from this equation but closed form expressions do not seem to be available.

The principal objective is to determine how long it will take for the population to attain a certain small value, such as unity, for a given initial size \( N_0 \) and given remaining parameters \( r, \lambda \) and \( K \)? In the case of a tumor or other aggregation of cells, we are asking for the time to eradicate the mass of cells or to greatly reduce its number.

Put \( x = N_0 \); now regarded as a variable. Then define the random variable \( T(x) \) as the time to reduce the population to a level less than unity, for example.

\[
T(x) = \inf \{ t|N(t)|\neq (1, K)|N_0 = x \in (1, K) \},
\] (20)

which is the time that the number of cells first escapes from the interval \((0, K)\) which must occur at \( N < 1 \) because \( N \) cannot exceed \( K \). If the number of cells is \( N(t) \) then \( T(x) \) is the actual time of complete eradication because having less than 1 cell is equivalent to having no cells at all. Letting the \( n \)th moment of \( T(x) \) be \( M_n(x), n = 0, 1, 2, ... \) so that

\[
M_n(x) = E[T^n(x)],
\] (21)

we find, from Tuckwell (1976), that these quantities satisfy the recurrence system of differential-difference equations,

\[
rx(\ln K - \ln x) \frac{dM_n(x)}{dx} + \lambda [M_n(x(1 - \epsilon)) - M_n(x)] = -nM_{n-1}(x),
\] (22)

for \( n = 1, 2, ... \) with \( M_0(x) = 1 \), which is the probability that \( N \) ever escapes from \((1, K)\). For \( n \geq 1 \) the boundary conditions are that \( M_n(x) = 0 \) for \( x \notin (1, K) \) and we also have the requirement that \( M_n(x) \) is bounded and continuous on \((1, K)\). Note, however that this system of differential-difference equations is singular at \( x = K \).

Rather than solving Eqn. (22) directly, it is convenient to note that the simple transformations of Eqn. (6) for the deterministic problem will reduce the stochastic problem to a simpler one for which the author and coworkers have obtained solutions, both analytical and numerical, in the context of the problem of determining the time interval between impulses of a model neuron. The transformations result in the simple SDE

\[
dY(t) = -rY(t)dt + \alpha dN^*(\lambda; t),
\] (23)

which describes a process which decays exponentially towards zero between upward jumps of magnitude \( \alpha \). The time at which the original process \( N^* \) declines below unity for the first time is the same as the time at which \( Y \) first exceeds the value \( k \). This exit time is precisely the same as the time between impulses in a Stein (1965) model neuron with a time constant \( 1/r \) and threshold \( k \) which receives Poisson excitatory postsynaptic potentials with rate \( \lambda \) and amplitude \( \alpha \). This threshold crossing problem for a discontinuous Markov process has been much studied (see Tuckwell 1975 and 1988, and references therein).
4.2 Results

Further simplifications are made by putting $Z = Y/\alpha$, so that $Z$ has jumps of unit magnitude, and scaling time by $\tau = \lambda t$ so the Poisson process has a rate parameter of unity. Thus

$$dZ(\tau) = -\gamma Z(\tau) d\tau + d\hat{N}(\tau)$$

(24)

where $\hat{N}$ has unit rate and $\gamma = r/\lambda$. Defining $\kappa = k/\alpha$ we find that the exit time of interest in (20) is now

$$\Theta(z) = \inf \{ \tau | Z(\tau) > \kappa | Z(0) = z \},$$

(25)

whose moments $\mu_n(z) = E[\Theta^n(z)]$ satisfy the relatively simple system of equations

$$-\gamma z \frac{d\mu_n(z)}{dz} + \mu_n(z + 1) - \mu_n(z) = -n\mu_{n-1}(z),$$

(26)

for $n = 1, 2, \ldots$. Here $z \in (0, \kappa)$ and for $n \geq 1$, $\mu_n(z) = 0$ for $z$ outside this interval.

Explicit expressions for the solutions of Equ. (26) with $n = 1$ can be obtained for values of $\kappa$ between 0 and 3 when $\gamma$ takes on integer or fractional values (see for example Tuckwell and Richter, 1978). These results give the expectation of the time at which $Z$ first reaches or exceeds $\kappa$ for an initial value $z$. For larger values of $\kappa$ numerical methods have been devised to solve the differential-difference equation. In one such approach the differential-difference equation was converted to a system of ordinary differential equations on the unit interval (Tuckwell and Richter, 1978). A different approach was employed in Cope and Tuckwell (1979) whereby an asymptotic expansion at large negative $z$ was matched to the continued solution obtained with boundary conditions at $z = \kappa$ by means of a set of recursion relations. Results for the process $Z$ can be readily converted to corresponding results for the original Gompertzian growth process $N$ because the transformations from $Z$ to $N$ are monotonic.

There are two principal questions we will address.

- How does the extinction time depend on the size of the population whose eventual size would be $K$ in the absence of decrements, for fixed values of the parameters $r$, $\lambda$ and $\epsilon$?

- How does the extinction time depend on the various parameters for different $K$ when the population is initially fully grown or almost fully grown?

Since there are so many combinations of parameters to explore, which makes it difficult to display results for them all, only a few representative cases will be reported here. In the future, tables will be published for the moments of the first exit time of $Z$ from various intervals. From these results for the extinction times of Gompertzian populations can be readily obtained.

- The first set of results, given in Figure 5, is designed to see how the extinction time changes as a function of mean frequency and magnitude of the random decrements. The logarithm of the expectation of the extinction time $T$ for a population at saturation level is plotted against the mean frequency of decrements (in units of $r$) for two values of the decrement $\epsilon = 0.6321$ and $\epsilon = 0.3935$ for $Z$, which two numbers correspond to
jump fractions of $\alpha = 1$ and $\alpha = 0.5$ in the original population $N$. The unit of the extinction time $T$ (corresponding to $T(K)$ in Equ. (20)) is $1/\lambda$.

In the numerical example given here, $K$ is chosen to be $e^8 \approx 2981$ individuals or cells and $T$ is the time taken for the population to become less than 1 individual or cell. From Figure 1 it can be seen that the waiting time for extinction ($< 1$) is extremely large for small and moderate frequencies of decrements and that the logarithm of $E[T]$ goes about like $\exp(-\lambda/r)$ so that $E[T]$ goes about like $\exp(e^{-\lambda/r})$. Note that the values of $\epsilon$ here correspond to relatively large decrements as of order half the population is removed at one hit.

At a given $\lambda/r$ the effect of changing $\epsilon$ is exceedingly pronounced. For example, with $\lambda = 8r$, when $\epsilon$ goes from 0.63 to 0.39, $E[T]$ increases from $2.2/\lambda$ to $337.9/\lambda$! Note that by scaling, the extinction time for $K = e^8$ and $\epsilon = 0.3935$ are the same as for $K = e^{16} \approx 8.9 \times 10^{16}$ and $\epsilon = 0.6321$.

Figure 5: The dependence of the logarithm of the expected time to extinction of a population of size $K = e^8$ with Poisson decrements as a function of their mean rate. Results are shown for cases where each hit removes fractions of $\epsilon = 0.63$ and $\epsilon = 0.39$ of the total population. The unit for the extinction time is $1/\lambda$ where $\lambda$ is the mean rate.

- Next we address the question of how much longer a larger population of individuals or cells will take to eradicate than a smaller one. To this end we plot in Figure 6, for fixed size of decrements $\epsilon = 0.63$, and for various mean rates of their arrival $\lambda = r, 2r, 3r, 4r$ and $5r$, the logarithm of the expectation of the extinction time, in units of $1/\lambda$ against the logarithm of the total population size $K$. For each value of $\lambda$ the dependence of $\ln E[T]$ is approximately linear for small to moderate $K$, but for larger $K$ the growth is more of an exponential character. In one set of results, for $\lambda = 3r$, when $K$ increases from 1000 to 2000 the expected extinction time increases from 49.4/\lambda to 109.9/\lambda which entails an approximate doubling in the extinction time for a doubling of the total population size.

- Another question to address is how the extinction time varies if the destructive decrements of the population commence at the early or late stages of growth. Hence we examine the variation in the mean extinction time as the initial population size changes. An illustrative example is
Figure 6: The logarithm of the expectation of the extinction time is plotted against maximum population size $K$ for various mean frequencies of downward jumps. Each jump removes a fraction 0.63 of the existing population. Units for $T$ as in Figure 1.

depicted in Figure 7. A population of organisms or cells whose eventual size would be $K = e^6$ is subjected to random hits which remove a fraction 0.63 of the population. The mean time to extinction is plotted as a function of the logarithm of the initial population size $N_0$ for two mean rates of hits of $\lambda = 5r$ and $\lambda = 10r$. The curves are drawn through points at which the logarithm of $N_0$ is an integer.

The dependence of $E[T]$ on $\ln N_0$ is quite gentle for the higher frequency of decrements but when the frequency is $\lambda = 5r$ we see that the extinction time increases rather sharply for small $\ln N_0$. This indicates that if the removals of masses of the population starts to occur when the population is quite small, then long extinction times will be avoided and the population will quickly vanish.

- Finally, the variability of the extinction time can be found by calculating the second moment of $T$ from Equ. (22) or equivalently Equ. (26), provided the first moment has already been calculated. In Figure 8 is shown a plot of the logarithm of the standard deviation of the time to extinction of a population at saturation level $K = e^8 \approx 2981$ individuals or cells as a function of the mean arrival rate of decrements for two values of the fraction $\epsilon$ removed by each hit. These curves give the standard deviations for the mean extinction times plotted in Figure 5. The dependences of the mean and standard deviation on mean arrival of hits are very similar. For $\epsilon = 0.63$ the coefficient of variation (CV, standard deviation/mean) is in fact very close to unity, indicative of a wide spread in the distribution, until $\lambda/r \approx 3$ and decreases steadily to about 0.49 by $\lambda/r \approx 10$. For $\epsilon = 0.39$ the CV is near unity until $\lambda/r \approx 8$ whereupon it decreases to attain the value 0.42 by $\lambda/r \approx 18$. 


Summary and conclusions

Gompertz models have been found to fit well the growth of many tumors and have also been considered for certain animal and other populations of organisms. Many articles have addressed the responses of tumors to radiation therapy and chemotherapy, each kind of therapy requiring a different mathematical treatment. In this article the results of removing a fraction of the population at periodic intervals is explored by means of exact results obtained by solving the assumed underlying differential equation. Having defined a standard parameter set, the effect of varying, one at a time, the 4 key parameters of fraction removed ($\epsilon$ or $\alpha$), period ($T$), initial population size ($N_0$) and intrinsic growth rate ($r$) were examined by examples presented in Figures 1 to 4. Surprisingly, as seen in Figure 3, after about 15 decrements (over 15 periods) the resulting population size was practically the same for a wide range of initial values.
the second part of this article the periodic occurrence of decrements was replaced by their occurring at event times in a Poisson process. The resulting discontinuous stochastic process was easily transformed to a simpler one which had been used as a model for nerve firings. Hence results from the interspike interval calculations could be applied to the case of Gompertzian growth with Poissonian downward jumps. The transition density of the process was not found but first and second order moments could be obtained from previous studies. The coefficient of variation of the extinction time was near unity for large ranges of smaller values of mean input frequency.

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