

On the Numerical Simulation of Exponential Decay and Outbreak Data Sets Involving Uncertainties

Milen Borisov¹[0000–0002–2172–3879] and Svetoslav Markov²[0000–0001–6810–8796]

¹ Institute of Mathematics and Informatics, Bulgarian Academy of Sciences
Acad. Georgi Bonchev Str., Block 8, 1113 Sofia, Bulgaria
`milen_kb@math.bas.bg`

² Institute of Mathematics and Informatics, Bulgarian Academy of Sciences
Acad. Georgi Bonchev Str., Block 8, 1113 Sofia, Bulgaria
`smarkov@bio.bas.bg`

Abstract. Measurement data sets collected when observing epidemiological outbreaks of various diseases often have specific shapes, thereby the data may contain uncertainties. A number of epidemiological mathematical models formulated in terms of ODE's (or reaction networks) offer solutions that have the potential to simulate and fit well the observed measurement data sets. These solutions are usually smooth functions of time depending on one or more rate parameters. In this work we are especially interested in solutions whose graphs are either of "decay" shape or of a specific wave-like shape briefly denoted as "outbreak" shape. Furthermore we are concerned with the numerical simulation of measurement data sets involving uncertainties, possibly coming from one of the simplest epidemiological models, namely the two-step exponential decay process (Bateman chain). To this end we define a basic exponential outbreak function and study its properties as far as they are needed for the numerical simulations. Stepping on the properties of the basic exponential decay-outbreak functions, we propose numerical algorithms for the estimation of the rate parameters whenever the measurement data sets are available in numeric or interval-valued form.

Keywords: Least square approximation · Numerical simulation · Decay and outbreak data.

1 Introduction: the Exponential Decay Chain

Consider briefly the exponential (radioactive) decay chain (Bateman chain) [2] in the special cases of one and two reaction steps. These two reaction networks find numerous applications not only in nuclear physics and nuclear medicine, but in biology, in particular in population dynamics, fishery research, pharmacodynamics and mathematical epidemiology [5, 7, 12, 15, 16].

The exponential decay function. The one-step exponential (radioactive) decay (1SED) model is a first order reaction step transforming a species S into another species P. The model is presented by the reaction network $S \xrightarrow{k_1} P$, where k_1 is a positive rate parameter. Assuming mass action kinetics, this reaction network translates into a system of two ordinary differential equations (ODE's) for the density functions $s = s(t)$ and $p = p(t)$, corresponding to species S and P, resp. in $t \in [0, \infty]$:

$$\begin{aligned} s' &= -k_1 s, \\ p' &= k_1 s. \end{aligned} \tag{1}$$

Under initial values $s(0) = s_0 > 0$; $p(0) = p_0 \geq 0$ the solutions to (1) can be presented in the time interval $T = [0, \infty)$ as [5]:

$$\begin{aligned} s(t) &= s_0 e^{-k_1 t}, \\ p(t) &= c - s_0 e^{-k_1 t}, \quad c = s_0 + p_0. \end{aligned} \tag{2}$$

Let us focus on solution $s = s(t)$. Assume $s_0 = 1$, then solution s from (2) is a function of variables k and t of the form:

$$\eta(k; t) = e^{-kt}. \tag{3}$$

In reality the rate parameter k in (3) takes specific distinct values in each particular biochemical process, however from mathematical perspective we can consider parameter k as a continuous function variable. So, function $\eta(k; t)$ is continuous, differentiable and monotonically decreasing with respect to both variables k and t . Function (3) will be further referred as *basic exponential decay function*, briefly *basic decay function*. For the derivatives of (3) with respect to t we have $(e^{-kt})' = -k e^{-kt}$ and $(e^{-kt})'' = k^2 e^{-kt} > 0$. The latter inequality says that function s , resp. the basic decay function e^{-kt} , is convex in R^+ .

Another characteristics of the basic decay function is:

$$t_h = \ln 2 / k, \tag{4}$$

wherein time instant t_h is known in nuclear physics as “half-life time” or just “half-life”. The half-life (4) satisfies the relation $\eta(t_h) = 1/2$, resp. $s(t_h) = s_0/2$, cf. Fig. 1. From (4) the rate parameter k can be expressed as:

$$k = \ln 2 / t_h \approx 0.693 / t_h. \tag{5}$$

Consider two basic decay functions: $e^{-k_1 t}$, $e^{-k_2 t}$. For a fixed t , the following monotonicity property takes place:

$$k_1 \leq k_2 \implies e^{-k_1 t} \geq e^{-k_2 t}. \tag{6}$$

Assume that the rate parameter k in function (3) is known within an error bound $\Delta \geq 0$. As an illustration, the upper graph on Figures 2 and 3 presents the function: $e^{-(k-\Delta)t}$, whereas the lower graph presents the function: $e^{-(k+\Delta)t}$.

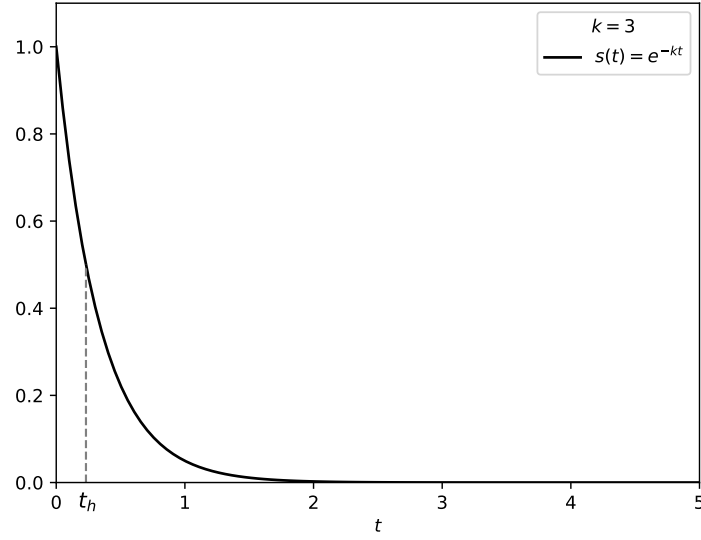


Fig. 1. Graph of function $\eta(t) = e^{-kt}$ for $k = 3$. The half-life $t_h = \ln 2/k$ is visualized.

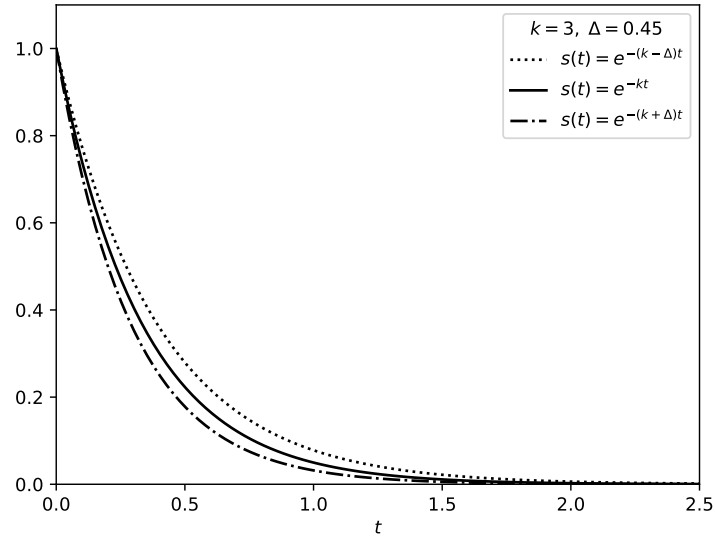


Fig. 2. Upper function $e^{-(k-\Delta)t}$ and lower function $e^{-(k+\Delta)t}$ for $k = 3, \Delta = 0.45$

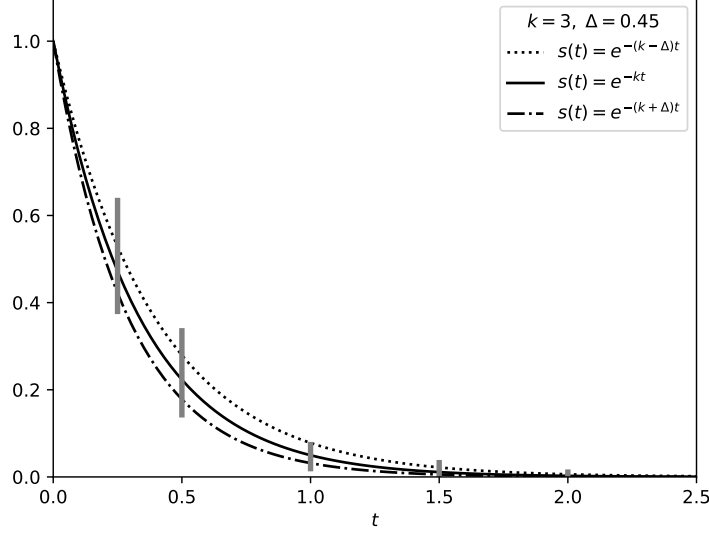


Fig. 3. A provisional interval-valued data set visualized

Denote $K = [k - \Delta, k + \Delta]$. We wish to know how the error in the parameter k influences the error in the value of function η , that is the *interval hull*:

$$\eta(K; t) = \{\eta(k; t) : k \in K\}. \quad (7)$$

Proposition 1. *Using the monotonicity of function (3) with respect to rate parameter k , for the interval hull (7) we have*

$$\eta(K; t) = [e^{-(k+\Delta)t}, e^{-(k-\Delta)t}]. \quad (8)$$

Proposition 1 allows for an easy computation of the interval hull (7). Fig. 2 visualises the upper function $e^{-(k+\Delta)t}$ and lower function $e^{-(k-\Delta)t}$ for $k = 3$, $\Delta = 0.45$.

A parameter identification problem for the exponential decay model.

Assume that at some instances t_i , $i = 1, \dots, n$, experimental data with interval-valued uncertainties $(t_1, X_1), \dots, (t_n, X_n)$, are available, wherein $X_i = [\underline{x}_i, \bar{x}_i]$ are some real intervals. We wish to estimate the value of the rate parameter k so that exponential decay solution η “fits well” the given experimental data. In particular, we shall additionally require that the values of function η are included in all the experimental intervals at the given time instances as shown on Fig. 3. We shall come back to the parameter identification problem for the exponential decay model in Section 4.

2 The Two-step Exponential Decay-outbreak Model: Properties

The two-step exponential (radioactive) decay-outbreak (2SED) model involves two first-order reaction steps in the transition of three species, say S, P, Q, into each other. More specifically, the 2SED model is presented by the reaction network $S \xrightarrow{k_1} P \xrightarrow{k_2} Q$, or, in canonical form [13]:



where k_1, k_2 are positive rate parameters. Assuming mass action kinetics, reaction network (9) translates into a system of ODE's for the density functions $s = s(t), p = p(t), q = q(t)$, corresponding to species S, P, Q, resp. in $t \in [0, \infty]$. Skipping the uncoupled equation ($q' = k_2 p$) for function q , we have:

$$\begin{aligned} s' &= -k_1 s, \\ p' &= k_1 s - k_2 p. \end{aligned} \quad (10)$$

Assume initial value conditions to dynamical system (10) as follows:

$$s(0) = s_0 > 0; \quad p(0) = p_0 = 0. \quad (11)$$

The solutions s, p to initial value problem (10)–(11) can be explicitly presented in the time interval $T = [0, \infty)$ as follows [5]:

$$\begin{aligned} s(k_1; t) &= s_0 e^{-k_1 t}; \\ p(k_1, k_2; t) &= s_0 \begin{cases} \frac{k_1}{k_2 - k_1} (e^{-k_1 t} - e^{-k_2 t}), & k_1 \neq k_2, \\ k t e^{-k t}, & k_1 = k_2 = k. \end{cases} \end{aligned} \quad (12)$$

In order to study analytically solution $p(k_1, k_2; t)$ from (12) we define and study a simplified function called “basic outbreak function”. As seen from (12) the expression for function $p(k_1, k_2; t)$ when $k_1 \neq k_2$ makes an essential use of the difference $(e^{-k_1 t} - e^{-k_2 t})$ of two decay functions as visualized on Fig. 4. The graph of function $p(k_1, k_2; t)$ using rate parameters $k_1 = 3$ and $k_2 = 1$ is presented on Fig. 5.

2.1 A Basic Wave-like Function

Definition 1. Define function

$$\varepsilon(m, n; t) = \begin{cases} \frac{1}{n-m} (e^{-m t} - e^{-n t}), & m \neq n, \\ t e^{-k t}, & m = n = k. \end{cases} \quad (13)$$

for $m > 0, n > 0, t \in [0, \infty)$.

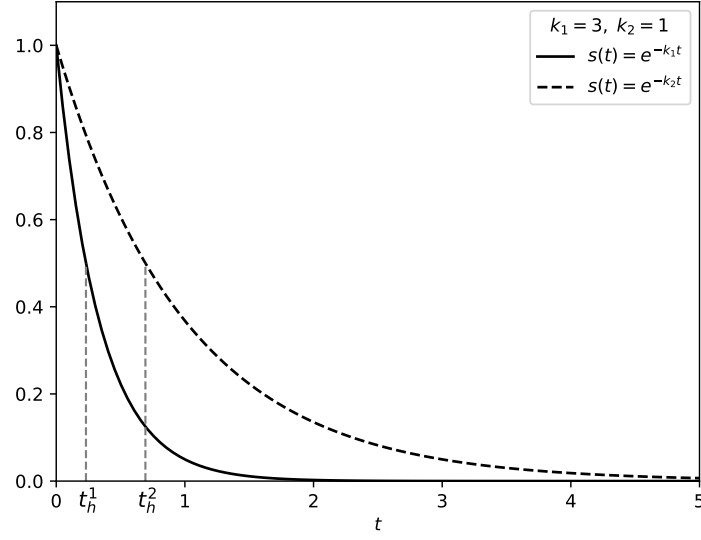


Fig. 4. Two decay functions with rate parameters $k_1 = 3$, resp. $k_2 = 1$; the half-life times are visualized.

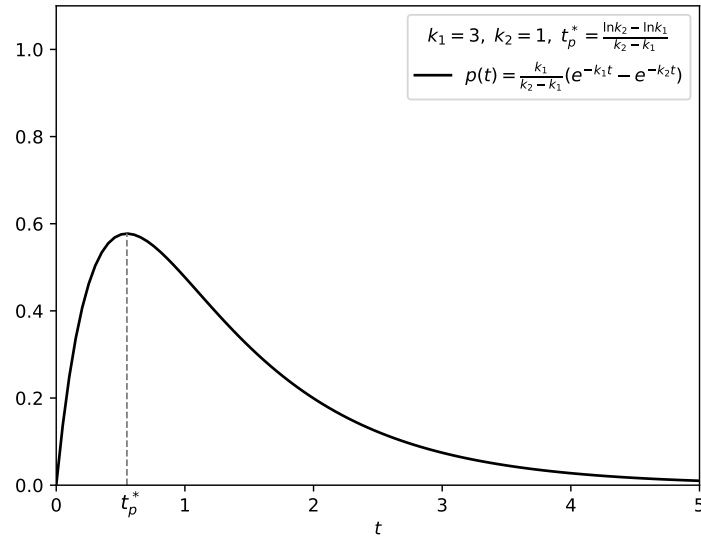


Fig. 5. A basic exponential outbreak function: $k_1 = 3, k_2 = 1, t_p^* = \frac{\ln k_2 - \ln k_1}{k_2 - k_1}$

Consider the special case $m \neq n$, that is function:

$$\varepsilon(m, n; t)|_{m \neq n} = \frac{e^{-m t} - e^{-n t}}{n - m}. \quad (14)$$

Using (14), function $\varepsilon(m, n; t)$ is defined in the case $m = n$ naturally as follows:

$$\begin{aligned} \varepsilon(m, n; t)|_{m=n} &= \lim_{k \rightarrow n, k \neq n} \varepsilon(k, n; t) \\ &= - \lim_{k \rightarrow n, k \neq n} \frac{e^{-k t} - e^{-n t}}{k - n} \\ &= - \frac{\partial e^{-k t}}{\partial k} = t e^{-k t}. \end{aligned} \quad (15)$$

Combining cases (14) and (15) we obtain the general definition (13).

Note that $\varepsilon(m, n; t) > 0$ for $t \in R^+$. Note also that $p(k_1, k_2; t) = s_0 k_1 e(k_1, k_2; t)$.

For the derivative $\varepsilon(m, n; t)'$ of function (13) in the case $m \neq n$ we calculate:

$$\begin{aligned} \varepsilon(m, n; t)' &= (n - m)^{-1} d(e^{-m t} - e^{-n t}) / dt \\ &= (-m e^{-m t} + n e^{-n t}) / (n - m), \\ &= \frac{n e^{-n t} - m e^{-m t}}{n - m}. \end{aligned} \quad (16)$$

In the case $m = n$ we have:

$$\varepsilon(m, n; t)'|_{m=n=k} = (t e^{-k t})' = (1 - k t) e^{-k t}. \quad (17)$$

Combining cases (16), (17), we obtain:

$$\varepsilon(m, n; t)' = \begin{cases} \frac{n e^{-n t} - m e^{-m t}}{n - m} & m \neq n, \\ (1 - k t) e^{-k t}, & m = n = k. \end{cases} \quad (18)$$

Proposition 2. *Function $k_1 \varepsilon(k_1, k_2; t)$ satisfies the ODE initial value problem:*

$$p' = k_1 s - k_2 p, \quad p(0) = 0, \quad (19)$$

wherein $s = s(t) = e^{-k_1 t}$ is the basic decay function (3).

Proof. Using definition (13) and equations (12), (18) the proof follows.

According to Proposition 2 function $k_1 \varepsilon(k_1, k_2)$ satisfies the 2SED reaction network in the case $s_0 = 1, p_0 = 0$. This property allows us to name function $\varepsilon(m, n)$ a basic outbreak function (using "epidemiological" terminology). We next give some more properties of function $\varepsilon(m, n)$.

2.2 The basic outbreak function: maximum value and inflection point

Let us compute the time instant t_ε^* when the outbreak function $\varepsilon(m, n)$ attains its maximum. Using $(e^{-kt})' = -ke^{-kt}$, and (18), we have for case $m \neq n$:

$$\varepsilon(m, n; t)' = \frac{-me^{-mt} + ne^{-nt}}{n - m}. \quad (20)$$

To compute t_ε^* we need to solve equation $\varepsilon(m, n; t)' = 0$ with respect to t . We obtain that $t = t_\varepsilon^*$ satisfies equation $-me^{-mt} + ne^{-nt} = 0$, or

$$\frac{e^{-mt}}{e^{-nt}} = e^{-(m-n)t}. \quad (21)$$

From (21) we obtain:

$$e^{-(m-n)t_\varepsilon^*} = \frac{n}{m},$$

hence (for $n \neq m$):

$$t_\varepsilon^* = \ln\left(\frac{n}{m}\right)/(n - m) = \frac{\ln n - \ln m}{n - m} = \ln\left(\frac{n}{m}\right)^{\frac{1}{n-m}}.$$

To compute inflection point t_ε^* for the case $k_1 = k_2 = k$ we solve equation:

$$\varepsilon(k_1, k_2; t)'|_{k_1=k_2=k} = (te^{-kt})' = (1 - kt)e^{-kt} = 0,$$

for $t = t_\varepsilon^*$ to obtain $t_\varepsilon^* = 1/k$. In the general case $m > 0, n > 0$ we obtain the following

Proposition 3. *The basic outbreak function attains its maximum at time instant*

$$t_\varepsilon^* = \begin{cases} \frac{\ln n - \ln m}{n - m} = \ln\left(\frac{n}{m}\right)^{\frac{1}{n-m}}, & n \neq m, \\ 1/k. & n = m = k. \end{cases} \quad (22)$$

We next compute the (maximum) value of the outbreak function $\varepsilon(k_1, k_2; t)$ at point $t = t_\varepsilon^*$. Using (13) we compute

$$\varepsilon(k_1, k_2; t_\varepsilon^*) = \begin{cases} \frac{e^{-k_1 t_\varepsilon^*} - e^{-k_2 t_\varepsilon^*}}{k_2 - k_1}, & k_1 \neq k_2, \\ t_\varepsilon^* e^{-k t_\varepsilon^*}, & k_1 = k_2 = k. \end{cases} \quad (23)$$

We have for $k_1 \neq k_2$ and $i = 1, 2$:

$$e^{-k_i t_\varepsilon^*} = e^{-k_i \ln\left(\frac{k_2}{k_1}\right)^{\frac{1}{k_2 - k_1}}} = e^{\ln\left(\frac{k_2}{k_1}\right)^{\frac{-k_i}{k_2 - k_1}}} = \left(\frac{k_2}{k_1}\right)^{\frac{-k_i}{k_2 - k_1}}.$$

Thus formula (23) becomes

$$\varepsilon(k_1, k_2; t_\varepsilon^*) = \begin{cases} \left[\left(\frac{k_2}{k_1} \right)^{\frac{-k_1}{k_2-k_1}} - \left(\frac{k_2}{k_1} \right)^{\frac{-k_2}{k_2-k_1}} \right] / (k_2 - k_1), & k_1 \neq k_2, \\ \frac{1}{ke}, & k_1 = k_2 = k. \end{cases} \quad (24)$$

Let us now compute the time instant t_ε^{**} , when the outbreak function $\varepsilon(m, n)$ attains its inflection point. To this end we have to solve equation $\varepsilon(m, n; t)'' = 0$ for $t = t_\varepsilon^{**}$, or

$$(-m\eta(m; t) + n\eta(n; t))' = m^2\eta(m; t) - n^2\eta(n; t) = 0,$$

or

$$\frac{\eta(m; t)}{\eta(n; t)} = \frac{n^2}{m^2} = \left(\frac{n}{m} \right)^2.$$

We obtain

$$\eta(m - n; t_\varepsilon^{**}) = \left(\frac{n}{m} \right)^2,$$

or

$$-(m - n)t_\varepsilon^{**} = 2 \ln \frac{n}{m},$$

hence

Proposition 4. *The outbreak function $\varepsilon(m, n)$ attains its inflection point at*

$$t_\varepsilon^{**} = 2 \frac{\ln n - \ln m}{n - m} = 2 t_\varepsilon^*. \quad (25)$$

The outbreak function plays an important role in a number of epidemiological and pharmacokinetic models.

3 Least-square approximations: fitting the exponential decay function

3.1 Fitting the exponential decay function to a numeric data set

Consider the exponential function

$$x(t) = ae^{bt}, \quad (26)$$

wherein $a > 0$ and $b < 0$ are unknown parameters. Let $(t_i, x_i), i = 1, 2, \dots, n$, be a given (numeric) measurement data set observed from some decay process, to be briefly denoted as a “decay data set”. To determine the optimum parameter

values of function (26), a and b , using least-square approximation, we minimize the functional

$$\Phi(a, b) = \sum_{i=1}^n (x_i - ae^{bt_i})^2, \quad (27)$$

with respect to a and b .

Fitting the one-parameter exponential decay function. Let the parameter a be known as $a = 1$, so that the function to be fitted is of the form

$$x(t) = e^{bt}, \quad (28)$$

then functional (27) obtains the form:

$$\Phi_1(b) = \sum_{i=1}^n (x_i - e^{bt_i})^2. \quad (29)$$

For the derivative of (29) with respect to b we obtain:

$$\frac{d\Phi_1(b)}{db} = -2 \sum_{i=1}^n (x_i - e^{bt_i}) t_i e^{bt_i} = 0. \quad (30)$$

Equation (30) can be written as:

$$\sum_{i=1}^n t_i x_i e^{bt_i} - \sum_{i=1}^n t_i e^{2bt_i} = 0. \quad (31)$$

To solve equation (31) with respect to b we shall need to use a numeric procedure, such as the Newton-Raphson method. An important part of such an iteration procedure is to determine an initial approximation for the parameter b . This can be done by a visual inspection of the shape of the decay data set $(t_i, x_i), i = 1, 2, \dots, n$, in order to establish approximately the half-life time instant t_h . Using expression (4) we can determine an initial approximation for the rate parameter b , namely $b \approx \ln 2/t_h$.

The two-parameter exponential decay function. Consider now the case when both parameters a, b in (27) are unknown. From equation:

$$\frac{\partial \Phi(a, b)}{\partial a} = -2 \sum_{i=1}^n e^{bt_i} (x_i - ae^{bt_i}) = 0, \quad (32)$$

we calculate:

$$a = \frac{\sum_{i=1}^n x_i e^{bt_i}}{\sum_{i=1}^n e^{2bt_i}} = \frac{S_1}{S_2}. \quad (33)$$

The condition for minimization of functional (27) with respect to b obtains the form:

$$\frac{\partial \Phi(a, b)}{\partial b} = -2 \sum_{i=1}^n (x_i - ae^{bt_i}) \left(\frac{da}{db} e^{bt_i} + at_i e^{bt_i} \right) = 0. \quad (34)$$

We now need to solve equation

$$\sum_{i=1}^n (x_i - ae^{bt_i}) \left(\frac{da}{db} e^{bt_i} + at_i e^{bt_i} \right) = 0, \quad (35)$$

wherein

$$\frac{da}{db} = \frac{1}{S_2^2} \left(S_2 \frac{dS_1}{db} - S_1 \frac{dS_2}{db} \right), \quad \frac{dS_1}{db} = \sum_{i=1}^n t_i x_i e^{bt_i}, \quad \frac{dS_2}{db} = 2 \sum_{i=1}^n x_i e^{bt_i}. \quad (36)$$

We can use a numerical iterative procedure for solving problem (35)–(36). In practice, the two-parameter setting can be avoided via a suitable normalization of the decay data set, so that the parameter a can be set to 1 (possibly by visual inspection of the data set).

3.2 Fitting the exponential decay function to an interval-valued data set

In the literature there are a number of research papers dealing with numerical simulation of the exponential decay models. Many authors focus on the case when imprecise/uncertain input data sets are available. Such data sets can be considered under various statistical assumptions, see e.g. [8, 9, 11]. A number of researchers assume that the input data are available in the form of intervals, that is the data are “interval-valued”, see e.g. [1, 3, 4, 6, 10, 14].

For the exponential decay model let us assume that an interval-valued decay data set is available, (t_i, X_i) , $i = 1, 2, \dots, k$, $X_i = [\underline{x}_i, \bar{x}_i]$, as mentioned at the end of Section 1 and depicted in Fig. 3.

A numerical algorithm. For the solution of the interval-valued optimization problems we propose the following algorithm:

Step 1. Find an initial numeric value for the parameter k , such that the solution e^{-kt} is included in all interval-valued data (t_i, X_i) , $i = 1, 2, \dots, k$. To this end a visual inspection of the decay data set can be performed aiming at finding an approximation of the half-life time t_h , resp. the rate parameter $k = \ln 2/t_h$.

Step 2. Choose a sufficiently small value for $\Delta > 0$. Check if the interval enclosure (7): e^{-Kt} for $K = [k - \Delta, k + \Delta]$, $\Delta > 0$, for the chosen Δ is included in the interval-valued decay data set, if so, then increase Δ and repeat the procedure. If the interval enclosure is not included in the interval-valued data set, then STOP. The final result of this procedure is the last Δ , resp. last interval $K = [k - \Delta, k + \Delta]$.

4 Numerical simulations involving the basic exponential decay-outbreak model

Consider next a biological process based on reaction network (9) involving two species S and P, resp. the two rate parameters k_1 and k_2 in the induced dynamical system (10). In reality such a situation appears in a number of areas, e.g. in epidemiology, where researchers collect information simultaneously for the decay of the susceptible and for the outbreak of the infected/infectious individuals. Since the decay part does not depend on the outbreak part of the process, we shall assume that the decay part has been solved using the methods presented in the previous Section 3 and thus the decay rate parameter (k_1) has been computed. Hence we can concentrate on the numerical computation of the outbreak rate parameter (k_2) using an available outbreak data set for the decay-outbreak process.

The numeric problem for the decay-outbreak process . Mathematically, consider the basic outbreak function (13). Assume that the decay rate parameter m is already available, as computed from a given decay data set (t_i, x_i) , $i = 1, 2, \dots, k$, according to instructions given in Section 3. Assume that an “outbreak data set” (t_j, y_j) , $j = 1, 2, \dots, l$, is available from experimental observations on the decay-outbreak process. Then, we have to minimize the functional

$$\Psi(m, n) = \sum_{j=1}^l (y_j - \varepsilon(m, n; t_j))^2, \quad (37)$$

with respect to rate parameter n . Expression (37) leads to the following

Proposition 5. *To minimize functional (37) with respect to rate parameter n we need to solve equation*

$$\frac{\partial \Psi(m, n)}{\partial n} = -2 \sum_{j=1}^l (y_j - \varepsilon(m, n; t_j)) \cdot \frac{\partial \varepsilon(m, n)}{\partial n} \Big|_{t_i} = 0, \quad (38)$$

wherein

$$\frac{\partial \varepsilon(m, n)}{\partial n} \Big|_{t_i} = \frac{m}{n - m} [(n - m)te^{-nt} - (e^{-mt} - e^{-nt})] \Big|_{t=t_i}. \quad (39)$$

Problem (38)-(39) can be solved numerically using appropriate numerical methods.

Initial conditions for the rate parameter n . By visual inspection on the outbreak data set one can find approximately an initial condition for the outbreak maximum time t_ε^* . Using expression (13) we have

$$\ln k_2 - k_2 t_\varepsilon^* = \ln k_1 - k_1 t_\varepsilon^*. \quad (40)$$

Equation (40) can be solved for k_2 using appropriate numerical method. If the available data set does not provide a good (visual) approximation for the value t_ε^* , then one may try to inspect visually the inflection point $2t_\varepsilon^*$, cf. expression (25) for t_ε^{**} .

The interval-valued problem for the decay-outbreak process can be formulated and treated in similar lines as done for the decay function, see previous Section 3. For the relevant numerical procedure the following condition may be applied.

Consistency condition. Using (13) we have for $K_1 = [k_1 - \Delta, k_1 + \Delta]$, $\Delta > 0$, resp. for interval enclosure

$$\varepsilon(K_1, k_2; t) = \{\varepsilon(k_1, k_2; t) : k_1 \in K_1\}, \quad (41)$$

the following expression:

$$\varepsilon(K_1, k_2; t) = \begin{cases} \frac{e^{-K_1 t} - e^{-k_2 t}}{k_2 - K_1}, & k_2 \notin K_1, \\ t e^{-K_1 t}, & k_2 \in K_1. \end{cases} \quad (42)$$

The consistency condition now reads: $\varepsilon(K_1, k_2; t_j) \in (t_j, Y_j)$, $j = 1, 2, \dots, l$.

Two basic decay functions with interval-valued rates $k_1 = 3, \Delta_1 = 0.45, k_2 = 1, \Delta_2 = 0.15$ are visualised on Fig. 6. A basic exponential outbreak function with interval valued rates: $k_1 = 3, \Delta_1 = 0.45, k_2 = 1, \Delta_2 = 0.15$ is presented on Fig. 7. A basic exponential outbreak function fitted to interval-valued data set; $k_1 = 3, \Delta_1 = 0.45, k_2 = 1, \Delta_2 = 0.15$ visualized graphically on Fig. 8.

5 Concluding remarks

In the present work we focus on a nonlinear least-squares approximation problem related to decay-outbreak biological processes. In particular we consider the two-step exponential decay chain (2SED) model, that has numerous applications in epidemiology, pharmacokinetics, nuclear medicine etc. This model is of considerable interest when analysing experimental measurement data sets coming from various decay-outbreak processes. Such data sets may or may not be fitted well by solutions of a 2SED model due to different mechanisms of the decay-outbreak process. For example, the SIR and SEI epidemiological models possess different shapes of the outbreak data, due to the presence of catalytic actions, e.g. an autocatalytic action on the first reaction in the SIR model, and a catalytic action from a third species on the first reaction in the case of the SEI model. Such catalytic actions model specific patterns of the disease transmission. So, discovering the underlying mechanism of the decay-outbreak process is as important as is the establishment of a linear mechanism in the familiar linear case (linear regression).

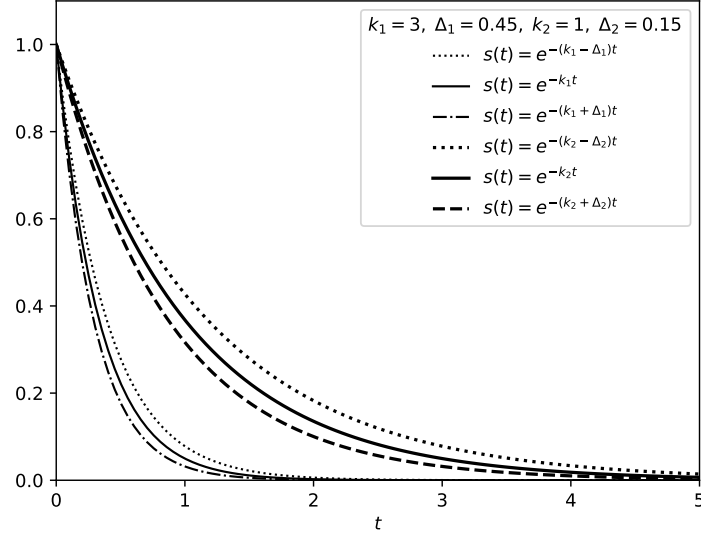


Fig. 6. Two basic decay functions with interval-valued rates: $k_1 = 3, \Delta_1 = 0.45, k_2 = 1, \Delta_2 = 0.15$

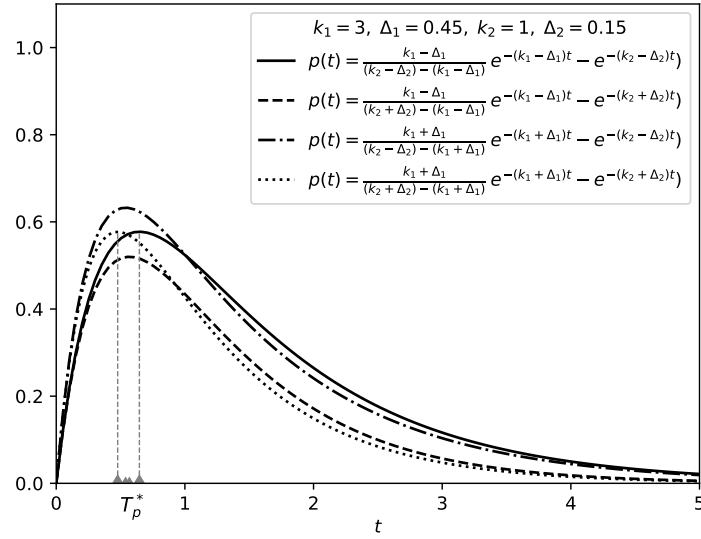


Fig. 7. A basic exponential outbreak function with interval valued rates: $k_1 = 3, \Delta_1 = 0.45, k_2 = 1, \Delta_2 = 0.15$

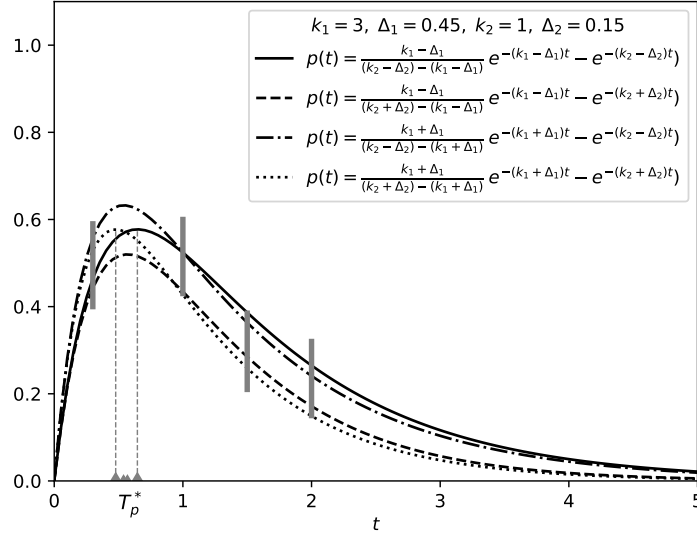


Fig. 8. A basic exponential outbreak function fitted to interval-valued data set; $k_1 = 3, \Delta_1 = 0.45, k_2 = 1, \Delta_2 = 0.15$

In addition, we are concerned with the situation of uncertainties in the data sets, focusing on the so-called interval-valued decay and outbreak data sets. In order to offer a precise definition of the term “numerical simulation” in such a setting, we begin with basic outbreak functions. In the course of the discussion it becomes necessary to provide a mathematical analysis of the decay and outbreak functions. This analysis turns to be useful when the data sets are inspected for specific peculiarities in their shapes, which can produce initial approximations for the induced numerical problems.

Acknowledgements The second author (SM) gratefully acknowledges financial support for project KP-06-N52/1 of 2021 at Bulgarian NSF entitled “New mathematical models for analysis of big data, with applications to medicine and epidemiology”.

References

1. Ahn, M. Peng, C. Park, Y. Jeon, A resampling approach for interval-valued data regression, Stat. Anal. Data Min. 5 (4) (2012) 336–348.
2. Bateman H., The solution of a system of differential equations occurring in the theory of radio-active transformations, Proc. Cambridge Phil. Soc. 15 (1910), 423–427.

3. Blanco-Fernández, Angela et al., Extensions of linear regression models based on set arithmetic for interval data. *arXiv: Statistics Theory* (2012): n. pag.
4. Billard, L., E. Diday, Regression analysis for interval-valued data, in: *Proceedings of the Seventh Conference of the International Federation of Classification Societies on Data Analysis, Classification and Related Methods*, 2000, pp. 369–374.
5. Borisov, M., S. Markov, The two-step exponential decay reaction network: analysis of the solutions and relation to epidemiological SIR models with logistic and Gompertz type infection contact patterns, *Journal of Mathematical Chemistry*, 59(5), 1283–1315, DOI: 10.1007/s10910-021-01240-8
6. Brito, P., A.P.D. Silva, Modeling interval data with normal and skew-normal distributions, *J. Appl. Stat.* 39 (2012) 157–170.
7. Chellaboina V., Bhat S. P., Haddad W. M., D. S. Bernstein, Modeling and Analysis of Mass-Action Kinetics. *IEEE Control Systems Magazine* 2009; 60–78.
8. Dette, H., H.-M. Neugebauer (1996). Bayesian optimal one point designs for one parameter nonlinear models. *Journal of Statistical Planning and Inference*, 52, 1, 17–31.
9. Dette, H., Martinez Lopez, I., Ortiz Rodriguez, I. M., A. Pepelyshev, Efficient design of experiment for exponential regression models, Technical Report, Universität Dortmund, SFB 475, No. 2004,08. <http://hdl.handle.net/10419/49337>
10. Gil, M., Lubiano, M., Montenegro, M., & López, M. (2002). Least squares fitting of an affine function and strength of association for interval-valued data. *Metrika*, 56(2), 97–111.
11. Han, C., K. Chaloner (2003). D- and c-optimal designs for exponential regression models used in pharmacokinetics and viral dynamics. *Journal of Statistical Planning and Inference*. 115, 585–601.
12. Hethcote, H. W., The Mathematics of Infectious Diseases, *SIAM REVIEW*, 42, 4, 599–653 (2000).
13. Lente G., Deterministic Kinetics in Chemistry and Systems Biology. *Briefs in Molecular Science*, Springer 2016.
14. Lima Neto, E., Cordeiro, G., De Carvalho, F. (2011). Bivariate symbolic regression models for interval-valued variables. *Journal of Statistical Computation and Simulation*, 81(11), 1727–1744.
15. Muench, H., Catalytic models in epidemiology, Cambridge (MA), Harvard University Press; 1959.
16. Murray, J D., Mathematical Biology: I. An Introduction, Third Edition. *Springer* 2002.