A NEW MODIFICATIONS OF THE SIR/SEIR MODELS
WITH "INTERVENTION POLYNOMIAL FACTOR".
METHODOLOGICAL ASPECTS

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ABSTRACT: We develop a novel modification of the classic Kermack–McKendrick SIR (Susceptible–Infectious–Recovered) model. The new SIR model with "intervention polynomial factor" (SIR-IPF) can be used successfully to model and play different scenarios for the infectious disease spread. A generalized "reproduction number" is introduced. A similar modifications are proposed for the classic SEIR and G-SEIR models. The specialists working in the field of "reaction-kinetic mechanisms" have the word.

Numerical examples, illustrating our results are given using *CAS Mathematica*.

1. INTRODUCTION

Dynamical models consisting of a systems of "reaction" differential equations are commonly used in chemistry, there the differential equations are called *reaction equations*. In chemistry reaction differential equations are induced by chemical reactions networks via reaction kinetic principles, such as *mass action kinetics* [1]–[2]. In [3]–[4] the author focuses his attention on growth functions (models) formulated as solutions to differential equations or systems of differential equation. For some modifications and extensions, see [5]–[11]. In the field of epidemiology [12]–[13], several mathematical approaches aiming to describe the infectious disease spread have been employed. The classic Kermack–McKendrick [14]–[16] SIR (Susceptible–Infectious–Recovered) model can be formulated as a chemical reaction network by [17]:

$$
\begin{aligned}
S + I & \xrightarrow{\frac{k_1}{K}} & 2I \\
I & \xrightarrow{k_2} & R.
\end{aligned}
\tag{1}
$$

The reaction network (1) induces the following differential system:

$$
\begin{cases}
\dfrac{ds}{dt} & = & -\dfrac{k_1}{K}s(t)i(t) \\
\dfrac{di}{dt} & = & \dfrac{k_1}{K}s(t)i(t) - k_2 i(t) \\
\dfrac{dr}{dt} & = & k_2 i(t)
\end{cases}
\tag{2}
$$

where $s(t)$ - number of individuals susceptible but not yet to infected with an infectious disease at time t; $i(t)$ - number of infected individuals at time t and can spread the infectious disease to susceptible individuals; $r(t)$ - number of recovered (or deceased) individuals at time t and assumed to be immune for life; k_1 - transmission rate through the exposure of the infectious disease; k_2 - rate of recovering from the infectious disease and $\frac{1}{k_2}$ is the mean period during which an infected individual can pass it on. In the SIR model, the determination of the basic reproduction number

$$
\tilde{R} = \frac{k_1}{k_2}
\tag{3}
$$

is a challenging task for COVID-19 infectious disease. In [18] the authors discussed the following SIR model with "intervention factor":

$$
\begin{cases}
\dfrac{ds}{dt} & = & -\dfrac{(1-\rho)k_1}{K}s(t)i(t) \\
\dfrac{di}{dt} & = & \dfrac{(1-\rho)k_1}{K}s(t)i(t) - k_2 i(t) \\
\dfrac{dr}{dt} & = & k_2 i(t)
\end{cases}
\tag{4}
$$

where $\rho \in [0, 1]$ is "intervention parameter". For some models, see [19]–[23].

In this paper we consider a new modification of the SIR model with "intervention polynomial factor". A new reproduction number is introduced. If desired, this new model can be assigned to the "class of dynamic models" for the analysis of epidemiological diseases. A similar modification is proposed for the classic SEIR and generalized G-SEIR models. Numerical examples, illustrating our results are given using CAS $Mathematica$.

2. MAIN RESULTS

2.1. A NEW MODIFICATION OF THE SIR MODEL WITH "INTERVENTION POLYNOMIAL FACTOR" (SIR-IPF)

We consider the following reaction network:

$$S + I \xrightarrow{\frac{f(t)}{K}} 2I$$
$$I \xrightarrow{g(t)} R. \tag{5}$$

The reaction network (5) induces the following differential system:

$$\begin{cases} \dfrac{ds(t)}{dt} &= -\dfrac{f(t)}{K}s(t)i(t) \\ \dfrac{di(t)}{dt} &= \dfrac{f(t)}{K}s(t)i(t) - g(t)i(t) \\ \dfrac{dr(t)}{dt} &= g(t)i(t) \end{cases} \tag{6}$$

where

$$f(t) = \sum_{i=1}^{m} k_{2i-1} t^{i-1}; \quad g(t) = \sum_{i=1}^{m} k_{2i} t^{i-1}.$$

From the relation

$$\lim_{t \to \infty} \frac{f(t)}{g(t)} = \frac{k_{2m-1}}{k_{2m}} \tag{7}$$

we see, that the new reproduction number has the form:

$$\tilde{R}_{new} = \frac{k_{2m-1}}{k_{2m}}. \tag{8}$$

Evidently, for $m = 1$, we get the classic Kermack–McKendrick SIR model (2).

Our main goal was to offer to the attention of specialists and other tools for possible simulation and playback of scenarios in the analysis of infectious disease spread using
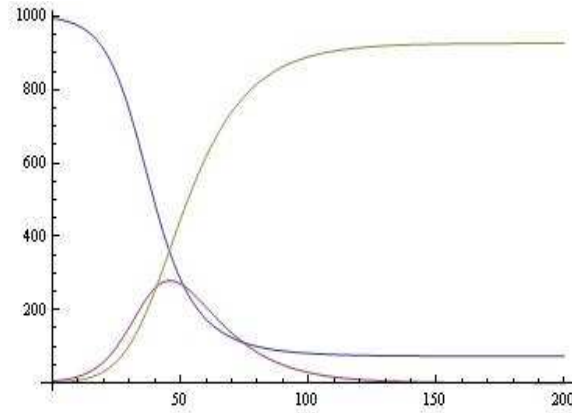
Figure 1: $K = 1000$; $k_1 = 0.2$; $k_2 = 0.071$; $s_0 = s(0) = 995$; $i_0 = i(0) = 5$; $r_0 = r(0) = 0$ [18].

a new technique - "intervention polynomial factor" and the resulting "reproduction numbers".

2.2. SIMULATIONS USING (SIR-IPF) MODEL

The new SIR model with "intervention polynomial factor" (SIR-IPF) can be used successfully to model and play different scenarios for the distribution of COVID-19. For the analysis of COVID-19 cases in India, in [18] the authors solved system of differential equations (2) for $K = 1000$; $k_1 = 0.2$; $k_2 = 0.071$; $s_0 = s(0) = 995$; $i_0 = i(0) = 5$; $r_0 = r(0) = 0$ (see, Fig. 1).

Consider the model (SIR–IFP) for fixed $m = 3$ and $K = 1000$; $k_1 = 0.2$; $k_3 = 0.05$; $k_5 = 0.005$; $k_2 = 0.071$; $k_4 = 0.005$; $k_6 = 0.002$; $s_0 = s(0) = 995$; $i_0 = i(0) = 5$; $r_0 = r(0) = 0$. The solutions are visualized on Fig. 2 in the interval $(0, 200)$. For fixed $m = 2$ and $K = 1000$; $k_1 = 0.2$; $k_3 = 0.01$; $k_2 = 0.071$; $k_4 = 0.01$; $s_0 = s(0) = 995$; $i_0 = i(0) = 5$; $r_0 = r(0) = 0$ see, Fig. 3.

If desired, this new model can be assigned to the "class of dynamic models" for the analysis of epidemiological diseases.
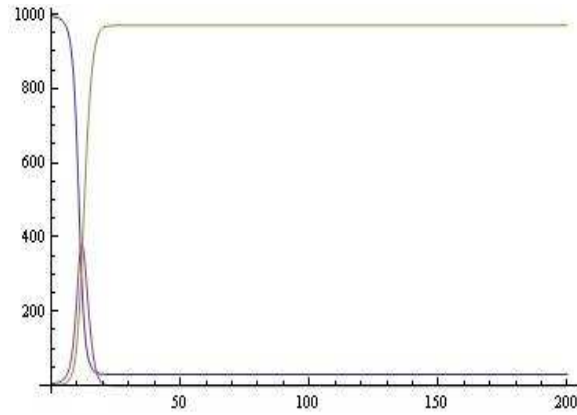
Figure 2: The model (SIR–IFP) for fixed $m = 3$ and $K = 1000$; $k_1 = 0.2$; $k_3 = 0.05$; $k_5 = 0.005$; $k_2 = 0.071$; $k_4 = 0.005$; $k_6 = 0.002$; $s_0 = s(0) = 995$; $i_0 = i(0) = 5$; $r_0 = r(0) = 0$.
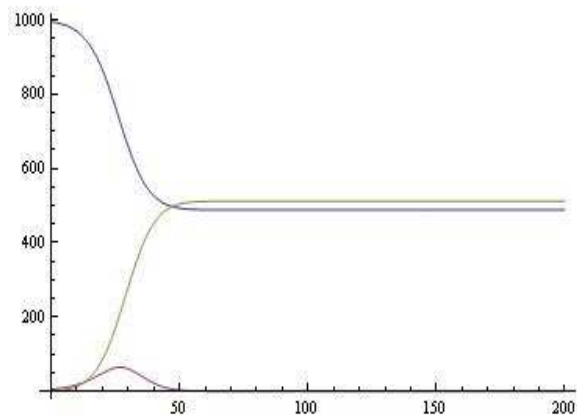

Figure 3: The model (SIR–IFP) for fixed $m = 2$ and $K = 1000$; $k_1 = 0.2$; $k_3 = 0.01$; $k_2 = 0.071$; $k_4 = 0.01$; $s_0 = s(0) = 995$; $i_0 = i(0) = 5$; $r_0 = r(0) = 0$.

2.3. A NEW MODIFICATION OF THE SEIR MODEL WITH "INTERVENTION POLYNOMIAL FACTOR" (SEIR-IPF)

Other mathematical models can be used to investigate the spread of diseases, such as SEIR. MSEIR, SEIRS and MSEIRS [19]–[23]. For the SEIR (Susceptible–Exposed–Infectious–Recovered) model, the corresponding system of differential equations is:

$$
\begin{cases}
\dfrac{ds(t)}{dt} &= -\dfrac{f(t)}{K}s(t)i(t) \\[2mm]
\dfrac{de(t)}{dt} &= \dfrac{f(t)}{K}s(t)i(t) - \sigma e(t) \\[2mm]
\dfrac{di(t)}{dt} &= \sigma e(t) - g(t)i(t) \\[2mm]
\dfrac{dr(t)}{dt} &= g(t)i(t).
\end{cases}
\tag{9}
$$

Here the term $\frac{f(t)}{K}i(t)$ expresses the rate at which new individuals (as a proportion of the total population size) are infected by the already infectious $i(t)$ individuals; $f(t)$ is called transmission rate of the infection; $g(t)$ is the removal rate. For some details, see [20]. In [20] the authors developed a novel SEIR spline model for analysis of coronavirus infection. Here we will consider a modification of the model (9) with a special choice of the functions $f(t)$ and $g(t)$. More precisely, $f(t)$ and $g(t)$ are polynomials of the form:

$$
f(t) = \sum_{i=1}^{m} k_{2i-1}t^{i-1}; \quad g(t) = \sum_{i=1}^{m} k_{2i}t^{i-1}.
$$

We will call the new modification SEIR model with "intervention polynomial factor" – (SEIR-IPF). Different scenarios for parameter variation and fixed degree of polynomials f and $g - (m = 2)$ using the (SEIR-IPF) model are given in Fig. 4.

2.4. A LOOK AT THE GENERALIZED SEIR MODEL PROPOSED BY PENG, YANG ET AL. [?]

A generalized SEIR model is proposed by Peng, Yang et al. in [25] (see, Fig. 5). In the considered system of differential equations, the functions $\lambda(t)$ and $k(t)$ are respectively increasing and decreasing in the fixed time interval. A modification of the SEIR model with a special choice of decreasing function is considered by Anguelov et al. in [24].

Here we will consider a modification of the model with a special choice of the functions $\lambda(t)$ and $k(t)$. More precisely, $\lambda(t)$ and $k(t)$ are polynomials of the form:

$$
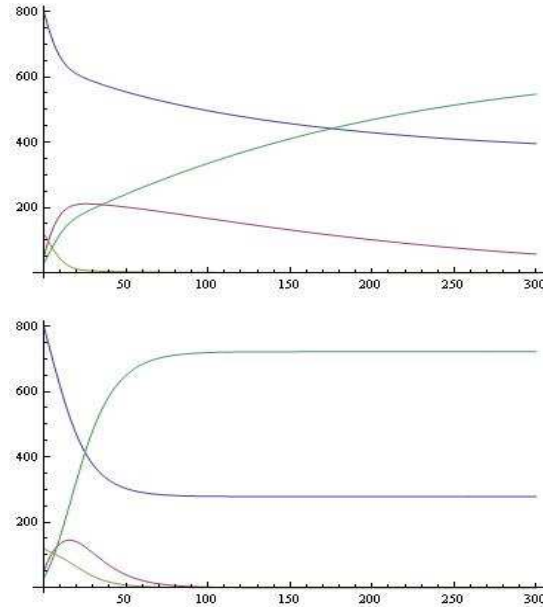\lambda(t) = \sum_{i=1}^{m} k_{2i-1}t^{i-1}; \quad k(t) = \sum_{i=1}^{m} k_{2i}t^{i-1}.
$$

Figure 4: Different scenarios for parameter variation and fixed degree of polynomials f and g - ($m = 2$) using the (SEIR-IPF) model.

We will call the new modification G-SEIR model with "intervention polynomial factor" – (G-SEIR-IPF).

We will explicitly note that in this new formulation the model has many degrees of freedom (the coefficients of the polynomials $\lambda(t)$ and $k(t)$), and this makes it attractive in the study and simulation of such dynamic models.

For fixed $m = 3$ and $K = 1000$; $k_1 = 100$; $k_3 = 1$; $k_5 = 0.1$; $k_2 = 100$; $k_4 = -0.12$; $k_6 = -0.008$; $s_0 = 800$; $e_0 = 40$, $i_0 = 80$; $q_0 = 20$, $r_0 = 20$, $d_0 = 20$, $p_0 = 20$, $\beta = 0.1$, $\alpha = 0.15$, $\gamma = 0.08$, $\delta = 0.1$ the simulation is depicted on Fig. 6.

For fixed $m = 3$ and $K = 800$; $k_1 = 100$; $k_3 = 0.2$; $k_5 = 0.1$; $k_2 = 120$; $k_4 = 0.1$; $k_6 = -0.005$; $s_0 = 500$; $e_0 = 80$; $i_0 = 20$; $q_0 = 30$; $r_0 = 100$; $d_0 = 20$; $p_0 = 50$; $\beta = 0.2$; $\alpha = 0.3$; $\gamma = 0.1$; $\delta = 0.15$ the simulation is depicted on Fig. 7.
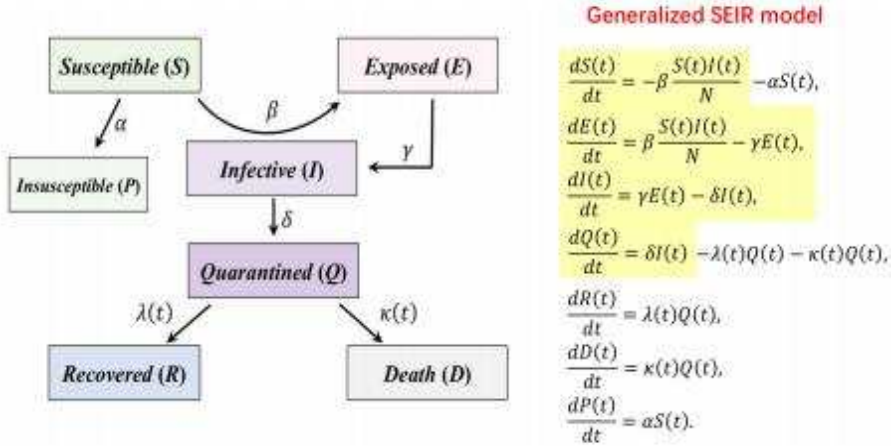
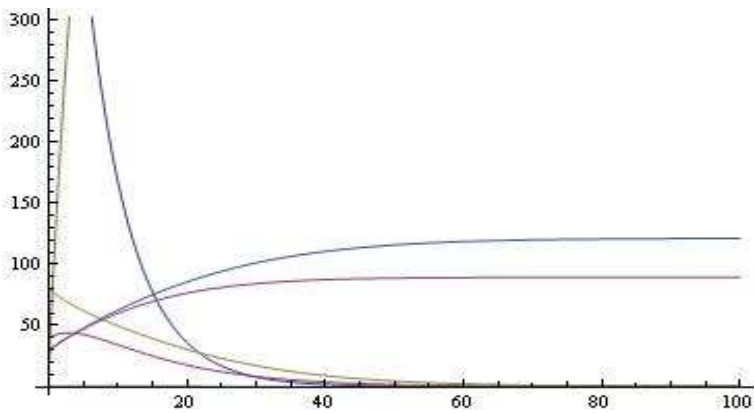Figure 5: The generalized SEIR model by Peng, Yang et al. [25].

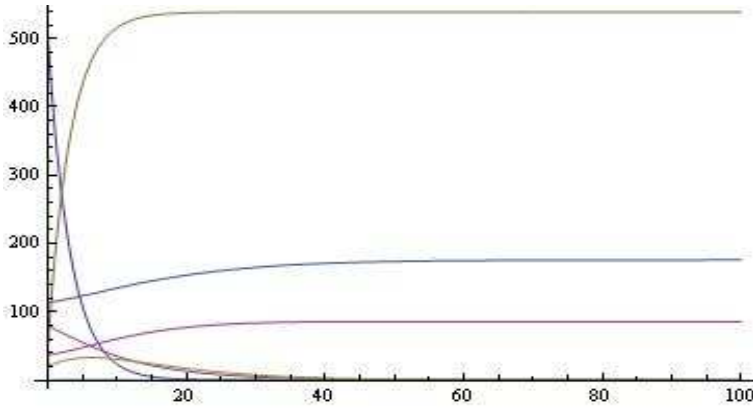Figure 6: The simulation using (G-SEIR-IPF) model.

Figure 7: The simulation using (G-SEIR-IPF) model.

2.5. A LOOK AT THE SEIRDP (SUSCEPTIBLE-EXPOSED-INFECTED-RECOVERED-DEATH-INSUSCEPTIBLE (P)) MODEL [?]

The SEIRDP (Susceptible, Exposed, Infected, Recovered, Death, Insusceptible (P)) model can be described by [26] (see, Fig. 8):

$$\begin{cases} \dfrac{ds(t)}{dt} &= -\dfrac{\beta}{K}s(t)i(t) - \alpha s(t) \\ \dfrac{de(t)}{dt} &= \dfrac{\beta}{K}s(t)i(t) - \gamma e(t) \\ \dfrac{di(t)}{dt} &= \gamma e(t) - \lambda(t)i(t) - k(t)i(t) \\ \dfrac{dr(t)}{dt} &= \lambda(t)i(t) \\ \dfrac{dd(t)}{dt} &= k(t)i(t) \\ \dfrac{dp(t)}{dt} &= \alpha s(t) \end{cases} \qquad (10)$$

where

- $S(t)$: Susceptible population;

- $E(t)$: Population who are exposed to the virus, but not yet infectious in latent period;

- $I(t)$: Population who get laboratory positive confirmation and with infectious capacity;
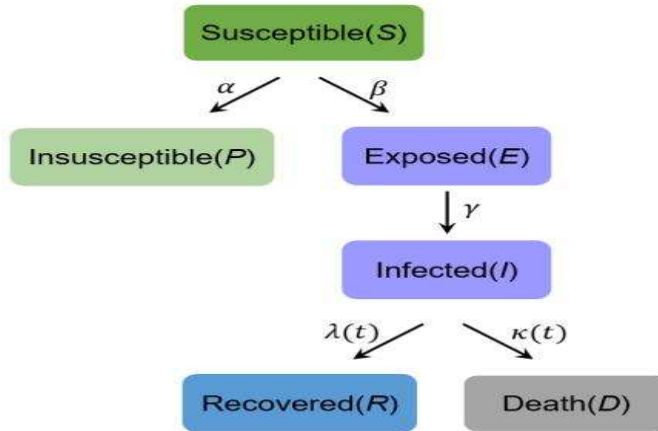
- $R(t)$: Recovery cases;

- $D(t)$: Death number;

Figure 8: The generalized SEIRDP model by Lounis and Azevedo [26].

- $P(t)$: Insusceptible cases;

- α : Protection rate (include people exposed to the infectious patients and people exposed to the asymptomatic patients);

- β : Infection rate;

- γ^{-1} : Average latent time;

- $\lambda(t)$: Coefficient used in the time-dependent cure rate;

- $k(t)$: Coefficient used in the time-dependent mortality rate.

In [26], the authors consider the functions (see, Fig. 9):

$$\lambda(t) = \frac{\lambda_0}{1 + e^{-\lambda_1(t - \lambda_2)}}$$

$$k(t) = k_0 e^{-k_1 t} \tag{11}$$

2.6. A NEW MODIFICATION OF THE SEIRDP MODEL WITH "INTERVENTION POLYNOMIAL FACTOR" (SEIRDP-IPF)

From methodological aspects, here we will consider a modification of the model with a special choice of the functions $\lambda(t)$ and $k(t)$.
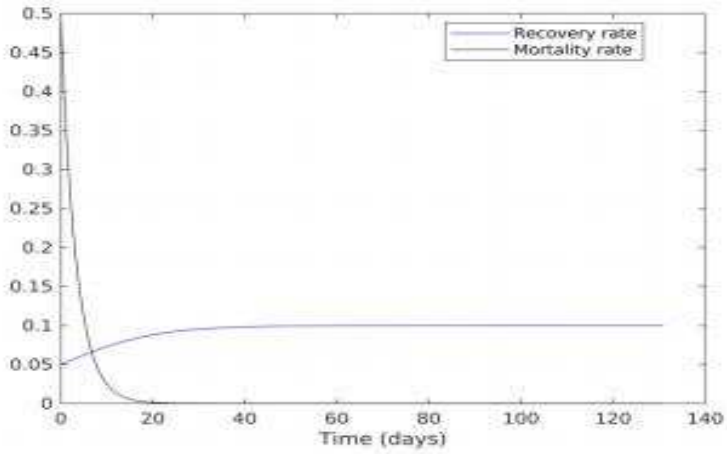
Figure 9: Plot of recovery and mortality rates [26].

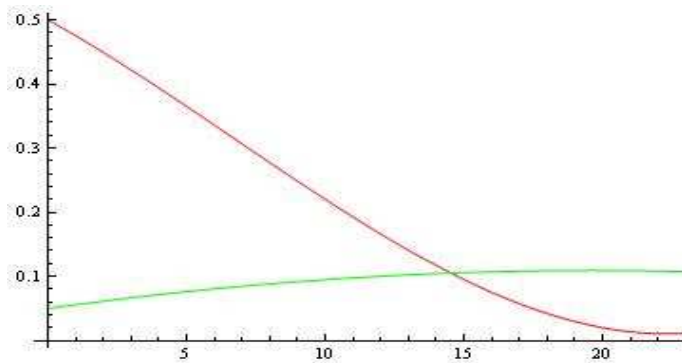Figure 10: Plot of recovery and mortality rates (the new functions $\lambda^*(t)$ and $k^*(t)$) .

More precisely, $\lambda^*(t)$ and $k^*(t)$ are polynomials of the form:

$$\lambda^*(t) = \sum_{i=1}^{m} k_{2i-1} t^{i-1}$$

$$k^*(t) = \sum_{i=1}^{m} k_{2i} t^{i-1}.$$

(12)

We will call the new modification SEIRDP model with "intervention polynomial factor"
– (SEIRDP-IPF).

For example, let

$$\lambda^*(t) = 0.05 + 0.006t - 0.00015t^2 - 0.0000001t^3$$

$$k^*(t) = 0.5 - 0.024t - 0.0008t^2 + 0.00004t^3$$

(see, Fig. 10.).

For fixed $K = 1$, $\lambda^*(t)$ and $k^*(t)$ and

$$\beta = 0.1;\ \alpha = 0.15;\ \gamma = 0.08;\ s_0 = 0.6;\ e_0 = 0.2;\ i_0 = 0.1;$$

$$r_0 = 0.05;\ d_0 = 0.05;\ p_0 = 0$$

the simulation is depicted on Fig. 11.

For fixed $K = 1$, $\lambda^*(t)$ and $k^*(t)$ and

$$\beta = 0.1;\ \alpha = 0.15;\ \gamma = 0.08;\ s_0 = 0.9;\ e_0 = 0.06;\ i_0 = 0.01;$$

$$r_0 = 0.01;\ d_0 = 0.01;\ p_0 = 0.01$$

the simulation is depicted on Fig. 12.

3. CONCLUSION.

In the last 2 years several thousand publications have appeared, incl. and these arti-
cles in arXiv.org on SIR/SEIR/GSEIR models. Of course, the SIR-IPF/SEIR-IPF/G-
SEIR-IPF/SEIRDP-IPF models are very sensitive with respect to the coefficients k_i of
the polynomials. One of the good hits in our development is that in some private cases
we get some classic and newer SIR/SEIR/GSEIR models. For example, we develop
a novel modification of the classic Kermack–McKendrick SIR (Susceptible–Infectious–
Recovered) model with new reproduction numbers $\rho_0, \rho_1, \ldots \rho_l$ in appropriate intervals
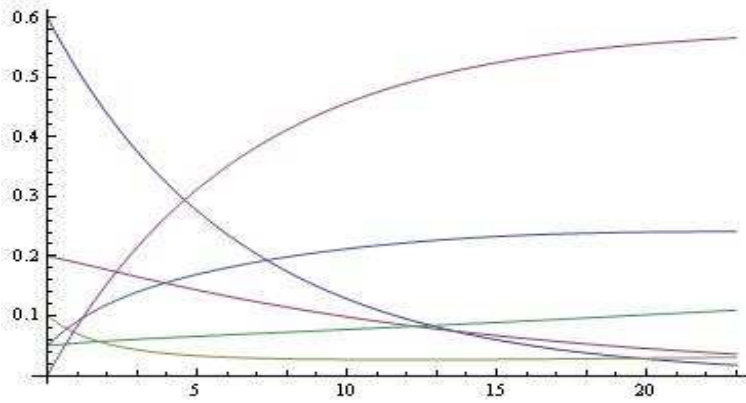
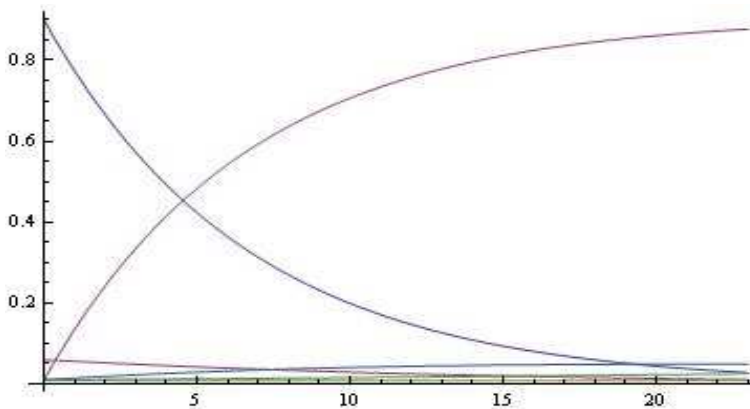Figure 11: The simulation using (GSEIRDP-IPF) model.

Figure 12: The simulation using (GSEIRDP-IPF) model.

$(t_0, t_1), (t_1, t_2), \ldots (t_l, t_{l+1})$. The new (SIR-IPF) can be used successfully to model and play different scenarios for the infectious disease spread. Our research is a natural continuation of previous results in approximating specific data of a strictly exponential nature (e.g., COVID-19 Bulgaria, Cuba, China, South Korea, etc.) using modified logistics and other models in which the typical reaction constants were replaced by "polynomial variable transfer" and showed good results in performing the regression analysis. We note that the choice of "input functions", especially for the GSEIR model, is quite specific and is almost subject to the requirement for these functions to be increasing and decreasing respectively in a fixed time interval. Only in the already cited article [20] the classic technique is used - spline functions! Our article opens up possibilities for generating a number of "reproduction numbers" for characteristic time intervals and simulating and playing different scenarios. We will explicitly note that the article contains the explorations only of a model nature and much more complex issues related to the resistance and stability of the solution of such stratified systems differential equations (especially for the GSEIR model) can be considered as open, until specialists working in the field of "reaction kinetics mechanisms and models" decide that there is reason to use our modest explorations. It is planned to upgrade the Distributed Platform for e-Learning - DisPeL [27]–[28], including a specialized module for simulation of chemical kinetics, module for solving nonlinear differential equations and verifying the mass action balance and module for simulation by the introduced new reproduction number.

ACKNOWLEDGMENTS

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