

A NONLINEAR HEURISTIC MODEL FOR ESTIMATION OF COVID-19 IMPACT TO WORLD POPULATION

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Received April 30, 2020

Abstract. In the current model of first approximation, we suggest a nonlinear heuristic approach by appropriate mathematical modelling, with the main aim – estimate the part of humankind which will survive definitely (in optimistic scenario). As a historical example, let us recall the fate of Inca civilization as pessimistic scenario. It seems to be natural, by the existing traditions in theoretical biology, to use theory of recurrent sets (chains of recurrent sets) for describing how population evolves over time. Such an approach actually determines a non-linear dependence of self-similar rate of evolution process (*or dynamics of infected population*) in regard to the proper residual capacity of non-infected part of all the humankind to overcome the pandemic of K-virus (Covid-19). The last is assumed to be associated with “potential of the niche for absorbing the infection”, defining a catastrophic acceleration (or optimistic deceleration) for the dynamics of the infected part of population.

Key words: Covid-19, self-similar rate of evolution process, recurrent sets, chains of recurrent sets, dynamics of population.

1. INTRODUCTION, MODELLING VIA RECURRENT SETS

The present paper reflects a growing concern on the spreading Covid-19 virus (novel coronavirus nCoV-2019, or K-virus, as noted here and below) over the World to date [1–2]. We consider that a precise mathematical model of the outcome of outbreak remains in need. In the meantime, there are examples of good review articles [3] (which can be applied to the current situation with K-virus or Covid-19), but most of them have been written in a descriptive manner.

In the current model of first approximation, we suggest a heuristic approach by appropriate mathematical modelling, with the main aim – estimate the part of humankind which will survive definitely (in optimistic scenario). As a historical example, let us recall the fate of Inca civilization as pessimistic scenario.

It seems to be natural, by the existing traditions in theoretical biology, to use theory of *recurrent sets* (chains of recurrent sets) for describing how population evolves over time. Such an approach actually determines a nonlinear dependence of self-similar rate of evolution process (*or dynamics of infected population*) in regard to the proper residual capacity of non-infected part of all the humankind to overcome the pandemic. The last is assumed to be associated with “potential of the niche for absorbing the infection”, defining a catastrophic acceleration (or optimistic deceleration) of the dynamics of the infected part of population, as below:

$$x_{n+30} = (1 - \alpha) \cdot x_n + \beta \cdot x_{n+5} + \gamma \cdot x_{n+11}, \quad (1)$$

here $n \in N$, x_n is the number of alive and (presumably) healthy population at the beginning of the current month ($\alpha = \alpha(n)$ is the coefficient of migration to other regions or to the niches inside the population of this region with status of “infected” (5-days period), “being on strong quarantine” (14-days), “mortal case” (~ 22 days), $\alpha \leq 1$ in the most cases in the region with active phase of infection), x_{n+30} is the number of alive population at the end of month (30 days); x_{n+5} is the number of alive population on 5th day ($\beta = \beta(n + 5)$ is the coefficient for those who have been detected as having been infected after passing the 5-days’ period); x_{n+11} is the number of alive population on 11th day ($\gamma = \gamma(n + 11)$ is the coefficient for those who have been detected as not infected after passing the 11-days’ period of quarantine).

We should point out also the reasonable criterion as below *in absence of migration* (besides, we know all the coefficients *retrospectively* only, with respect to the current moment of time):

$$\alpha \cdot x_n = \beta \cdot x_{n+5} + \gamma \cdot x_{n+11} - \chi \cdot x_{n+23}, \quad (2)$$

where $\chi = \chi(n + 23)$ is the coefficient for those who have been detected as died after passing the 23-days’ period (we will suppose here and below $\chi \ll 1$); the term $\beta \cdot x_{n+5}$ in right part of (2) will be then decreased accordingly by those who died, but, nevertheless, α is still constant (for the reason it determines the part of alive population who have been migrated to other regions or to the niches inside the population of this region with status of “infected”, “being on strong quarantine”, “mortal case”). Data with respect to the time-periods of typical evolving of K-virus (Covid-19) is based on research [4].

Applying the ansatz of recurrent sets (chains of recurrent sets, used in the field of researches of theoretical biology), let us assume according to standard methods of solving equations of type (1) [5–6]

$$x_n \sim e^{b \cdot n} \cdot K, \quad (3)$$

here b is the rate of maximum infected population growth ($b < 0$ for healthy part of population, but $b > 0$ if we consider the infected part of population in (3)), K is the size of the maximal niche for absorbing the infection (the maximum of population).

The typical simple asymptotic solutions as (3) above are used to apply for the final prognosis of Human population dynamics; besides, the aforementioned solution of a type (3) can be presented as time-dependent at absorbing the infection inside the maximal niche where amount of healthy people will tend to zero at maximal rate of infected population growth in (3), but at negligible rate of evolving the infection inside the human society the amount of infected population will reach the prescribed level of saturation (Fig. 1):

$$N(t) \sim \left(1 - e^{\int b(t) dt}\right) \cdot K \cong \frac{K}{(1 + e^{\int b(t) dt})} \quad (*)$$

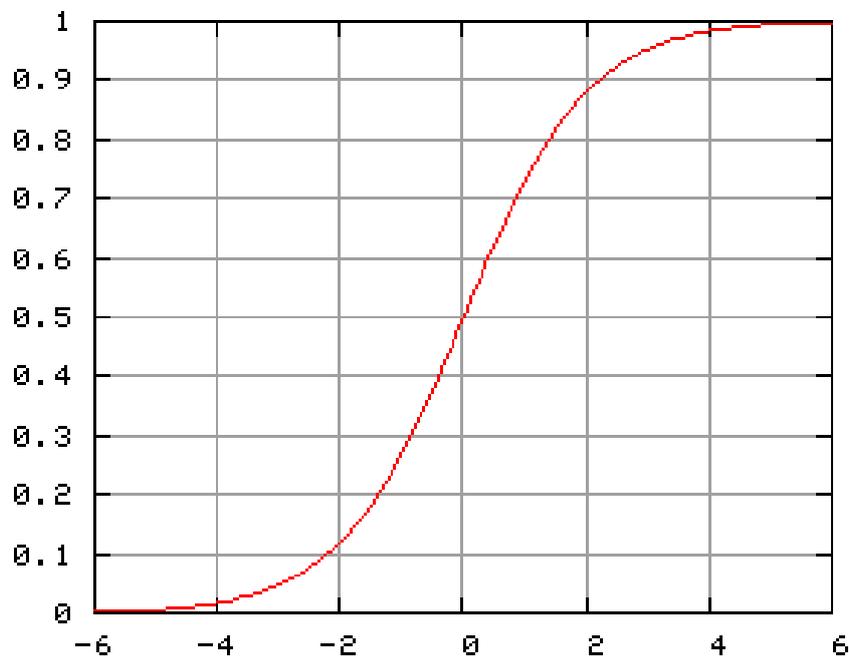


Fig. 1 – Logistic curve for the simple asymptotic solutions of a type (*).

Furthermore, then substituting Eqn. (3) into (1) should yield:

$$\begin{aligned} (1 - \chi) \cdot e^{b(n+30)} &= (1 - \alpha) \cdot e^{bn} + \beta \cdot e^{b(n+5)} + \gamma \cdot e^{b(n+11)}, \\ \Rightarrow e^{b \cdot 30} &\cong (1 - \alpha) + \beta \cdot e^{b \cdot 5} + \gamma \cdot e^{b \cdot 11}, \end{aligned} \quad (4)$$

So, if we denote

$$e^{b \cdot 1} = X, \quad (5)$$

we will obtain from (4)–(5) the algebraic equation of 30th order

$$X^{30} \cong (1 - \alpha) + \beta \cdot X^5 + \gamma \cdot X^{11} \quad (6)$$

which could be solved by numerical methods only. If the real roots exist, we could determine the real self-similar tempo of K-virus (Covid-19) evolving (*or the rate of increasing of the infected population*), depending on coefficients $\{\alpha, \beta, \gamma\}$.

2. DISCUSSION

In principle, it is hard to solve 30-th order algebraic equation (6), that is why we can reduce it to 14-order (not less, because 14 days is the period of strong quarantine):

$$X^{14} \cong (1 - \alpha) + \beta \cdot X^5 + \gamma \cdot X^{11} \quad (7)$$

As for numerical solving, we will need numerical values of “alpha”, “vita”, “gamma” for numerical solving of Eqns. (6) or (7).

Statistical data seems to be verified in various countries, see reference [1]. We can use data for China. Thus, “alpha”, “vita”, “gamma” (at the end of May 2020):

- 1) “alpha” = “vita” + “gamma”;
- 2) “vita” = 82,862/(1,386 billions of people);
- 3) “gamma” = 0.

(Meanwhile, we should especially note that for calculating to be valid, we should use the data of a month ago, to see how many “cases of illness” were registered, how many deaths occurred hereafter in one month period, and to calculate the situation a week forward with respect to the current moment).

We provide the numerical approximated solving the algebraic equations (6)–(7): the dichotomy method has been used for numerical calculating of the solution (with coefficients for the case of China, as calculated from the data above).

The result of numerical calculation is as follows:

1. Solution of equation (6) is $X = 0.9999999999999911$;
2. Solution of equation (7) is $X = 1.0000000000000009$.

So, we obtain from Eqn. (5) the zero actual rate of infection, in case of China (at the end of May 2020): $b \cong 0$ with accuracy of numerical calculation $1e-14$. Besides, we can conclude that equation (7) is more effective for modelling hereafter in case of China.

In general case of local escalating the pandemy, values of "alpha", "vita", "gamma" for numerical solving of Eqns. (6) or (7) should be calculated using the self-scaling condition (2) for them, where the coefficient χ (for those who have been detected as died after passing the 23-days' period) is circa 4.5% of coefficient β (for those who have been detected as having been infected), according to the world-wide statistics [1]. So, in general case we should choose for the aforementioned numerical solving algorithm e.g. as follows: 1) α (or "alpha") $\cong 1$ (during period of a strong quarantine, in absence of migration to the outer regions); 2) β (or "vita", $\beta \ll 1$) should be expressed from (2) in dependence on X , α , γ and χ (or vice versa, γ in dependence on X , α , β , χ , where $\gamma < 1$), taking into account that $\chi \cong 0.045\beta$ (we should note that $\beta \neq 0$ during a real pandemic regime of strong quarantine).

We can assume that X should be slightly more than 1 in this case: $X = 1 + \delta$, where $\delta \ll 1$. Such assumption let transform (2) along with e.g. Eqn. (7) to the system of two simple algebraic equations below (by the series of Taylor expansions):

$$\begin{cases} 1+14\delta \cong (1-\alpha)+\beta\cdot(1+5\delta)+\gamma\cdot(1+11\delta), \\ \alpha = \beta\cdot(1+5\delta)+\gamma\cdot(1+11\delta)-\chi\cdot(1+23\delta), \end{cases} \Rightarrow$$

$$\Rightarrow \quad \{\chi \cong 0.045\beta, \alpha \cong 1\}$$

$$\begin{cases} \alpha + \chi \cong \beta + \gamma \cdot \left(1 + 11 \frac{\chi}{14}\right), \Rightarrow \gamma \cong (\alpha - 0.955\beta) \cdot \left(1 - 11 \cdot \left(\frac{0.045\beta}{14}\right)\right) < 1, \\ \alpha = 1 + 14\delta + \alpha - 1 - \chi \cdot (1 + 23\delta) \Rightarrow \delta = \frac{\chi}{(14 - 23\chi)} \cong \frac{\chi \cdot (1 + (23\chi/14))}{14} \cong \frac{\chi}{14}. \end{cases}$$

Thus, the rate of K-virus (Covid-19) evolving inside the human society (in the absence of migration to the outer regions) is determined from (5) via

expression $X = 1 + \delta$ by the relative amount of “mortal cases” χ at the end of current month.

We can present other, light modification of equation (1) for calculating the number of alive and preferably health part of population (*in the absence of migration to the outer regions*) or for those who known as have absolutely *not been* infected by K-virus (Covid-19):

$$(1 - \chi_{n+29}) \cdot x_{n+30} = (1 - \chi_{n-1}) \cdot x_n - \sum_{m=n}^{n+30} \alpha_m \cdot x_m + \sum_{m=n}^{m=n+16} (\gamma_m \cdot x_m \cdot \theta(m+14)), \quad (8)$$

where $\theta(m+14)$ is the Heaviside step function (which means in (8) the adding at 14th day to society of those who have been on strong quarantine after passing 14 day’s time-period). Such a modification (8) is based on the pessimistic scenario when β in (1) will be zero at all (*i.e.*, zero amount of people with status “infected” will be transferred to society in sufficiently long time-period, but it would not mean the “mortal case” for all of them; $\beta_{(n+5)} = 0$).

Taking into account (8), we obtain

$$(1 - \chi_{n+29}) \cdot e^{b \cdot (n+30)} = (1 - \chi_{n-1}) \cdot e^{b \cdot n} - \sum_{m=n}^{n+30} \alpha_m \cdot e^{b \cdot m} + \sum_{m=n}^{m=n+16} \gamma_m \cdot e^{b \cdot m} \cdot \theta(m+14) \quad (9)$$

Besides, we assume that mandatory condition below should be valid for the discrete self-similar dynamical process, presented by Eqn. (8):

$$-\sum_{m=n}^{n+30} \alpha_m + \sum_{m=n}^{m=n+16} \gamma_m \cdot \theta(m+14) = 0, \quad (10)$$

which means that the total incoming flow of people to the society should be zero during a month (where total balance of incoming flow of healthy (or non-infected) people is combining with the outcoming flow of people who have been placed to the strong quarantine). So, taking into account (10), we obtain from (9)

$$(1 - \chi_{n+29}) \cdot e^{b \cdot (n+30)} = (1 - \chi_{n-1}) \cdot e^{b \cdot n}, \quad (11)$$

$$\Rightarrow e^b = \sqrt[30]{\frac{(1 - \chi_{n-1})}{(1 - \chi_{n+29})}} \cong 1 + \left(\frac{\chi_{n+29} - \chi_{n-1}}{30} \right)$$

Thus, the rate of K-virus (Covid-19) evolving inside the human society (*in the absence of migration to the outer regions*) is determined by relative increasing

of “mortal cases” at the end of current month with respect to the previous month (under mandatory aforementioned condition (10)):

$$(\beta_n + \chi_n) \cdot x_n \cong (\beta_n + \chi_n) \cdot \left(1 + n \left(\frac{\chi_n - \chi_{n-30}}{30} \right) \right) \cdot K, \quad (12)$$

where $(\beta_n + \chi_n) \cdot x_n$ is the part of human society which is corresponding for those who have been infected or died. Taking into account (9)–(12) we have come to conclusion that all population will to be infected, in a sufficiently long time-period (under this pessimistic scenario).

As for why all human population will be infected, it is a reasonable conclusion from (12): K-virus (Covid-19) will be self-enhancing till this death-machine is absorbed by the huge amount of new people. Meanwhile, a lot of the graphical plots from various countries are similar at the beginning of first wave of pandemic to visualization of our formula (*) (see also logistic curve at Fig. 1), let us compare it with *e.g.* the general trend in case of China [1] (with changing scenario in the vicinity of ~ 11–12 of February 2020, see Fig. 2 below):

Total Coronavirus Cases in China

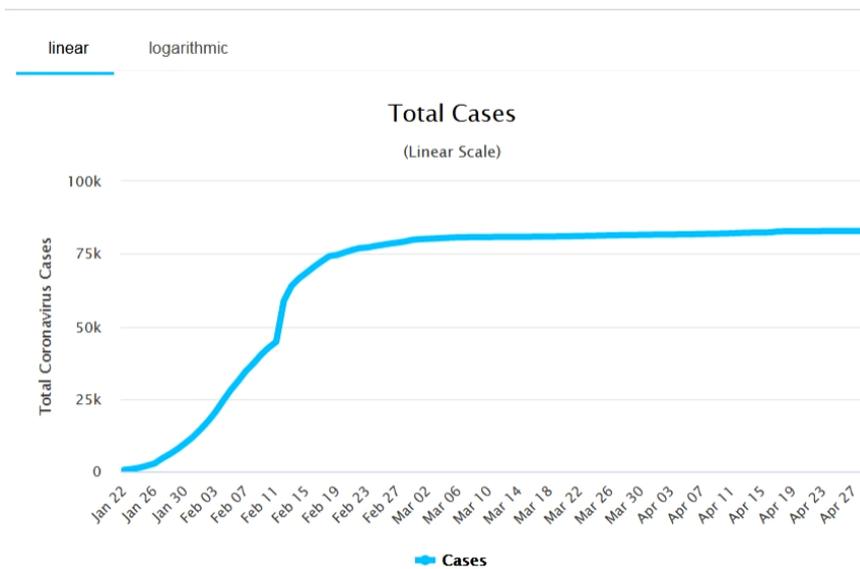


Fig. 2 – Dynamics of total coronavirus cases for China.

– or the classical general trend of a type (*) (Fig. 1) in case of South Korea [1],
Fig. 3:

Total Coronavirus Cases in South Korea

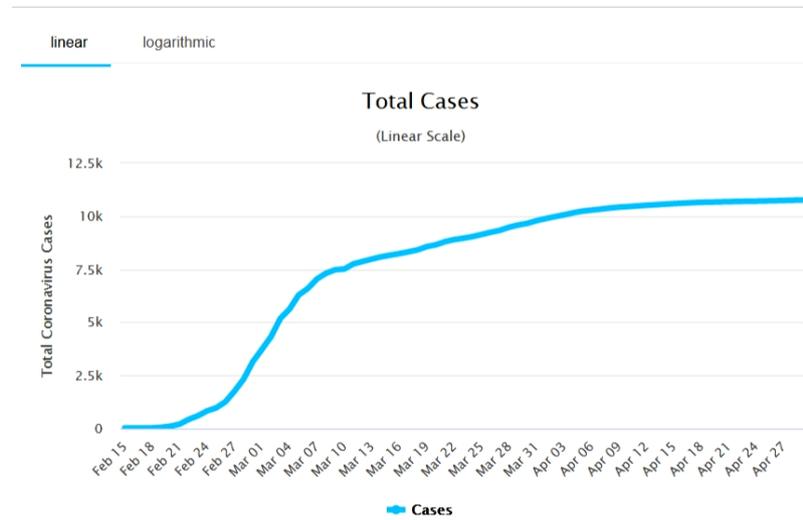


Fig. 3 – Dynamics of total coronavirus cases for South Korea.

– or the exhibiting of classical tendency of a type (*) in case of Austria [1]:

Total Coronavirus Cases in Austria

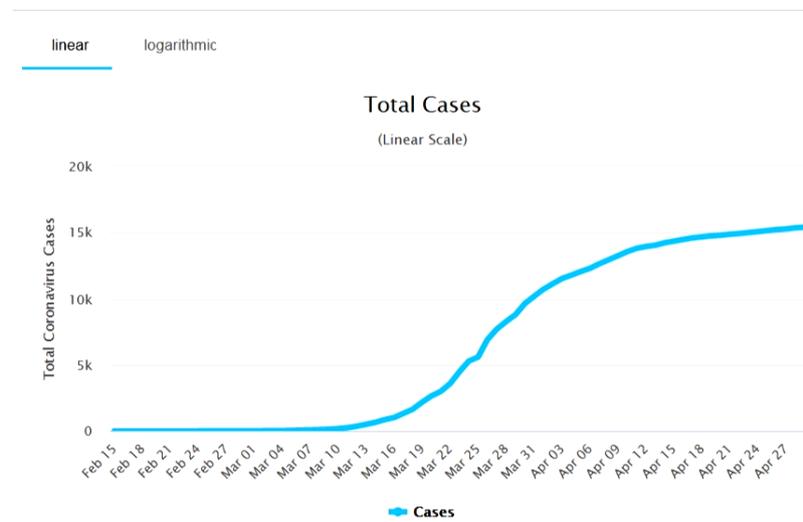


Fig. 4 – Dynamics of total coronavirus cases for Austria.

– Australia [1]:

Total Coronavirus Cases in Australia

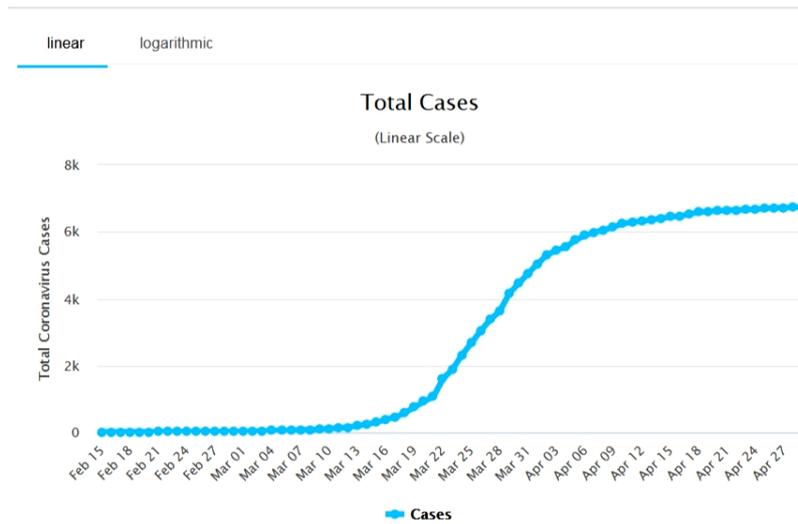


Fig. 5 – Dynamics of total coronavirus cases for Australia.

– Switzerland [1]:

Total Coronavirus Cases in Switzerland

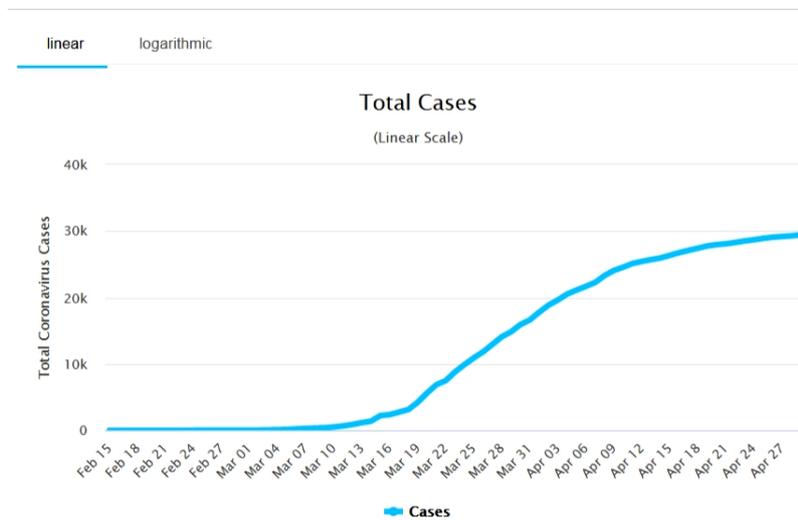


Fig. 6 – Dynamics of total coronavirus cases for Switzerland.

– France [1]:

Total Coronavirus Cases in France

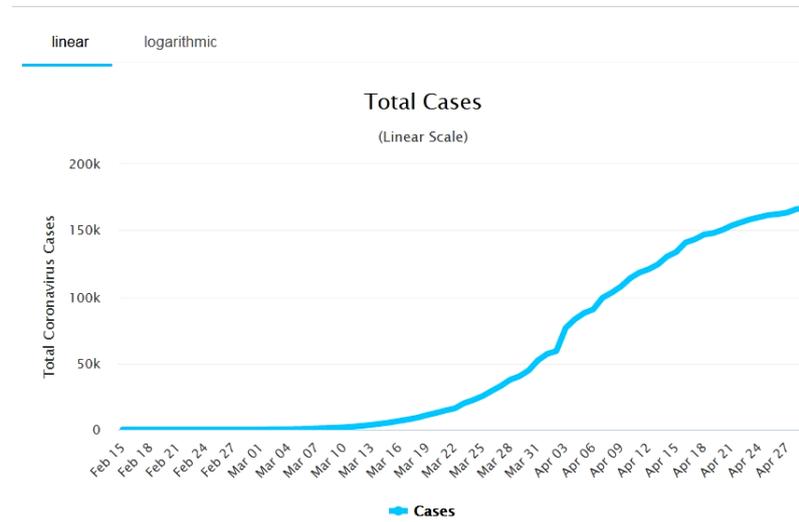


Fig. 7 – Dynamics of total coronavirus cases for France.

– and Germany [1]:

Total Coronavirus Cases in Germany

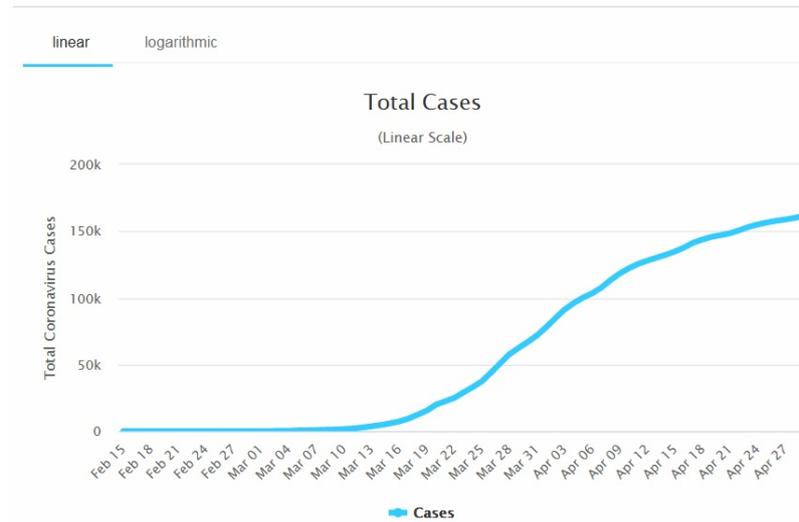


Fig. 8 – Dynamics of total coronavirus cases for Germany.

Also, we should mention the classical general trends of a type (*) in cases of Hong Kong, Taiwan and Vietnam [1] (the statistic data for Vietnam is questionable

due to a negligible amount of officially registered cases of illness of those who have been infected) along with cases of Norway, New Zealand, Luxembourg, Croatia, Israel, Thailand, Channel Islands, Mauritius, Montenegro, Andorra, Japan, Isle of Man, Iceland, Faeroe Islands, Cyprus, Greece, Ireland, Tunisia, Slovenia, Slovakia, Belgium, Italy and Spain at the end of May 2020.

By the way, during its spatial evolving, K-virus (Covid-19) seems to be lost its mortal potential due to mutations. So, we hope its spreading will not be dangerous at the end of 1st year. For this reason, we do not think that eventually more than 35 millions will die from over the World (according to pessimistic estimation in [7], ~1,7 million of people in U.S.). As we hope, it should be less than 5% of the aforesaid overall amount of people.

Nevertheless, we should especially note that, firstly, we have no idea why evolution (in a spatial context) would be related to a loss of infectivity on its own. Secondly, the neutral theory of evolution would suggest that most mutations are neutral, a part of which are deleterious, other part of those are beneficial to the virus. Lastly what does “mortal potential” actually would mean for a virus? Viruses do not have any “potential” on their own, their infectivity and associated mortality are an interplay of virus-host relationship, and may actually have more to do with the host than with virus. In particular the mortality rates for elderly / diabetic / persons with pre-existing unhealthy conditions are $> 10\times$ than for “healthy” younger hosts without those conditions. So it could be said that the “mortal potential” of Covid-19 is in a manner more related to the host than virus.

3. CONCLUSION

In this paper, we present a new approach for modelling the equations of the dynamics of infected population: a new type of the solving procedure is implemented here for the modelling the dynamics of infected part of population (*via* chains of recurrent sets), determined by self-similar rate of evolution process of K-virus (Covid-19) evolving inside the population. Namely, we present a heuristic mathematical model for the outcome of outbreak, which differs from most of the existing theories for describing of the evolution of the viruses in human society (mainly, from those which are based on dynamics by modelling with help of ordinary differential equations or well-known stochastic methods). Meanwhile, the aforementioned mathematical model has been successfully explored with respect to the existence of analytical way for presentation of the solution.

As the main result, the new ansatz is suggested here for such the solving procedure: solving the chains of recurrent sets for modelling the dynamics of infected part of population is reduced to solving algebraic equation of 30th (or, at least, 14th) order, which could be solved by numerical methods only. If the real roots exist, we could determine the real self-similar tempo of K-virus (Covid-19) evolving (*or the rate of increasing of the infected population*), depending on coefficients presenting in the model the healthy part of population, the part of those

who have been infected along with the part of being currently on quarantine, and the part of those who have died (alas!).

All in all, such an approach actually determines a non-linear dependence of self-similar rate of evolution process (*or dynamics of infected population*) in regard to the proper residual capacity of non-infected part of all the humankind. The last is assumed to be associated with “potential of the niche for absorbing the infection”, defining a catastrophic [8] acceleration (or optimistic deceleration) for the dynamics of the infected part of population.

The last but not least, we should especially note that the main aim of applied mathematical (analytical or numerical) approach is, in any case, to obtain the model which should basically realize the fitting or coinciding of real curve of observed dynamics with to theoretical findings. Indeed, only the direct mathematical modelling (based on the data of the real observations for the aforementioned dynamics) should help us to find a key points in decoding of Covid-19 expansion in human society in these extraordinary times.

As the example of applying our ansatz in predicting dynamics of the Covid-19’ evolving in human society, let us consider the case of Russia (the country which seems to be much similar to Germany in culture code in a sense of behaviour of society during pandemic). Total amount of people in Germany is circa 83 millions of people, whereas in Russia 145 millions of people. So, we can interpolate the maximal level of cases of illness in Russia for the current first wave of pandemic as follows (scenario in Russia is worse than in Germany):

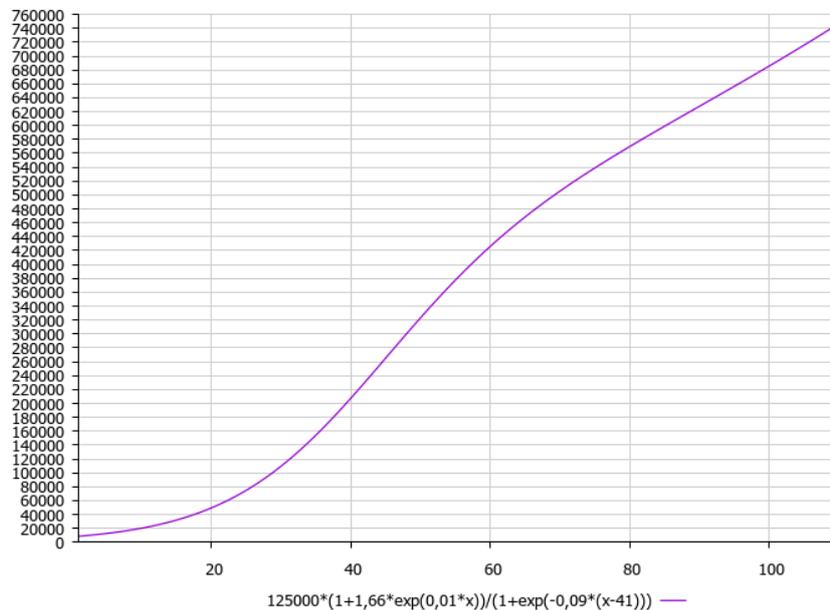


Fig. 9 – A schematic prognosis of the dynamics of total coronavirus cases for Russia. The start is 01 of April 2020 (here we designate $x = t$, in days, just for the aim of presenting the plot of solution).

Let us explain also the non-classical trend of Covid-19 evolving in case of various countries (Fig. 9). We have especially payed attention in (1) to the fact that all the coefficients in (1) might have been dependent on the current step ($n \in N$) of the numerical simulation; namely, $\alpha = \alpha(n)$, $\beta = \beta(n + 5)$, $\gamma = \gamma(n + 11)$. Such dependence could be explained by changing of regime of self-isolation during pandemy (including migration to other regions or to the niches inside the population of this region with status of “infected”, “being on strong quarantine”).

All in all, it means for the cases of non-classical trends of Covid-19 evolving in various countries that we should take into consideration additional correcting coefficients inside formulae of a type (*). For example, it could be presented by the best-fitting formula (13) below for the direct mathematical modelling the Covid-19 dynamics in case of Russia:

$$x_{n(Russia)} = \frac{125000(1 + 1.66\exp(0.01n))}{(1 + \exp(-0.09(n - 41)))}, \quad (13)$$

(where n is the current day from the beginning of April 2020), which yields Fig. 9.

As we can obtain from (13), the deviating of the calculated *vs.* real data of the Covid-19 dynamics in Russia is less than 7% for most of the days, except the first 18 days of April where such difference can be explained by the cumulated delaying in the process of official confirming the non-registered cases of illness (*e.g.*, without symptoms of a disease) which had happened at previous period of pandemy.

The best-fitting formula (14) for the direct mathematical modelling the Covid-19 dynamics in case of Germany should be presented as follows:

$$x_{n(Germany)} = \frac{90000(0.9 + 0.03\exp(0.012n))}{0.47 + \exp(-0.11(n - 28))}, \quad (14)$$

(where n is the current day from 01 of March 2020), which yields Fig. 10.

As we can see from Fig. 10, end of active phase of the current first wave of pandemic will be at the second half of May 2020 in Germany, but there is also no horizontal trend hereafter by the end of active phase of the current first wave of pandemic. Besides, the deviating of the calculated *vs.* real data of the Covid-19 dynamics is less than 7% for most of the days, except the first 26 days of March where such difference less than circa 12750 cases per day (at maximum after first two weeks), in absolute amount of people; such difference can be explained by existing in society the non-registered cases of illness (without symptoms of a disease) which had happened at previous period of pandemy.

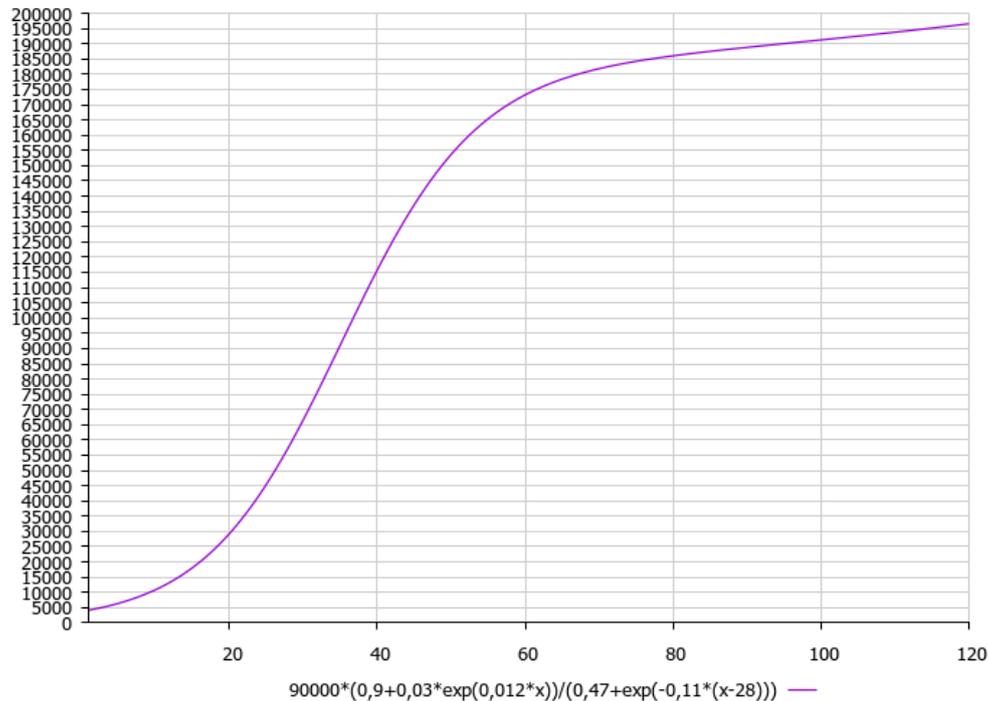


Fig. 10 – A schematic prognosis of the dynamics of total coronavirus cases for Germany.
The start is 01 of March 2020 (here we designate $x = t$, in days).

Also, remarkable articles [9–10] should be cited, which concern the problem under consideration.

CONFLICT OF INTEREST

Authors declare that there is no conflict of interests regarding publication of article.

All data, used in the current research, are available by request addressed for the corresponding author. This research has been made without any funding.

Remark regarding contributions of authors as below:

In this research, Dr. Sergey Ershkov is responsible for the results of the article, the obtaining of exact solutions, simple algebra manipulations, calculations, the representation of a general ansatz and calculations of graphical solutions, approximation and also is responsible for the search of approximate solutions.

Dr. Alla Rachinskaya is responsible for approximated solving of the algebraic equations (6)–(7) by means of advanced numerical methods as well as is responsible for numerical data of calculations.

Dr. Victor Christianto and Dr. Evgenii Prosviryakov are responsible for the deep survey in literature on the problem under consideration.

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