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RESEARCH ARTICLE

Researches on the COVID-19 epidemic in the world within a nonextensive SIR model

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Abstract

The coronavirus disease 2019 (COVID-19) epidemic was investigated within a general Susceptible-Infectious-Removed (SIR) model, especially the distributions of its dead cases and infectious ones. This paper applied its nonextensive modification with respect to more realistic situations. A time-dependent SIR model was modified when particularly regarding control and mitigation measures in response to the societal impacts of epidemics and pandemics. We validated all the theoretical results by fitting the derived q -distributions with data from the COVID-19 pandemic in the world. It was found that not all the changeable fit parameters are independent, some of which shared common properties, a result corroborated by our model prediction. Our modified SIR model was proved to be effective in fitting the COVID-19 epidemic distributions. The relative non-extensive parameter was strongly connected with the freedom of systems, which thus threw a light upon the prevention and treatment of disease next in the world.

Introduction

It has been a kind of global public health emergency[1] since the coronavirus disease 2019 (COVID-19) occurred in December 2019 in Wuhan, China. Coincided with *chunyun*, the period of mass migration for the annual Spring Festival, one outbreak subsequently spread rapidly throughout China and elsewhere in the world. Significant disruption has been caused to the social and economic structure. Actually it has required different methods adding current situations and uncommon medical clinics and travel limitations to relieve its infection. For example, the government of China made lots of important strides like occasion augmentation, hospitalization and isolation and so on. It has been proved to be useful to diminish the infection transmission among the populace.[2,3] However, it is still unknown whether these polisices have a permanent impact and how long they were able to remain there. On the other hand, this epidemic has been a global issue which needs more considerations to assess the effects of these control measures on the development of COVID-19, especially the connections among them.

Nowadays in the market there have already existed plenty of models, for example, susceptible-infected-removed (SIR), susceptible-infected-susceptible (SIS), and susceptible-exposed-infected-removed (SEIR) models, which have been proposed to predict the epidemic progression. A time-dependent dynamic SIR model inspired in a model previously used during the MERS outbreak in South Korea was used to analyse the time trajectories of active and hospitalized cases in Portugal.[4] People also integrated population migration data of COVID-19 into the SEIR model to derive the epidemic curve.[5] All of them were shown to be effective in fitting the epidemic sizes and peaks. Nevertheless, all of these models of infectious disease shared some of ideal hypotheses: a) the reproduction number *R* is often proposed to be exponential which is coming from the classical Boltzmann-Gibbs (BG) statistics; b) the internal interactions are always neglected when considering the propagation of disease, such as the normal human contacts in daily life; c) the total number is recognized as a constant, namely the system is a closed one; d) *etc*..

On the other hand, more and more statistical approaches [6,7] provided powerful tools for medical and epidemiological applications due to predicting the behaviour of certain diseases. In order to take it into consideration that the high inter-connectedness helps increase the probability of occurrence of pandemics, a $\boldsymbol{\kappa}-$ statistical thermodynamic approach [8] to epidemiology was formulated and investigate both the 2003 SARS (Severe Acute Respiratory Syndrome), the 2014 West Africa Ebola epidemic and the present COVID-19 pandemic.

In order to better predict and mitigate the epidemic impact, the ability to parameterize a model for analysing and predicting the behaviour of pandemics is very important. Consequently, we have modified the simple SIR model in order to study the COVID-19 epidemic in China [9] within the framework of non-extensive statistics. The non-extensive statistics, firstly proposed in [10] has attracted various attentions and discussions [11]. Typically, Tsallis introduced a so-called *q*-exponential function to generalize the normal exponential function,

$$\exp_q(x) := [1 + (1-q)x]^{\frac{1}{1-q}} \qquad (1)$$

It returns to the usual exponential function with $\boldsymbol{q} \rightarrow \mathbf{1}$. This function was better to deal with the problems for the appearance of critical fluctuations due to interactions or non-ideal cases. It helps solve such situations where the classical statistics becomes no longer appropriate. Hereby people are approved to re-use this statistical approach but only adding one non-extensive parameter *q* to account for all possible factors violating assumptions of the usual BG cases.

The purpose of this paper is to further clarify the non-extensive effects on the fitting parameters of the modified SIR model for the COVID-19 epidemic. We focus on the situations in the world, where both similarities and differences appear when comparing with the ones in China. In this work we introduce this *q*-statistics as a useful quantitative tool for analysing epidemiological data and providing deeper discussions on these fit parameters. We validate the proposed approach by means of COVID-19 infectious data from various countries available until July of 2021. The physical basis of this statistics will be briefly demonstrated as well as the derivations of relevant equations. Study on the fitting data allows us to test the ability of the derived *q*-functions to describe and forecast infectious outbreaks. The comparisons of the epidemic data between countries are of particular interest when all the fitting parameters, especially our non-extensive parameter *q*, will be deeply investigated.

This paper is organized as follows. In **Methods** we introduce the theoretical framework, where the non-extensive *q*-SIR model is stated as well as the normal SIR one. Their comparisons are shortly explored afterwards. We apply this modified SIR model to analyse the number of infectious cases caused by COVID-19 in different countries until last July next. Section of **Discussions** presents our brief summary and outlook as well as more detailed discussions on the results listed above and shown in figures.

Methods

As we all know, an epidemic is defined as "the occurrence in a community or region of cases of an illness clearly in excess of normal expectancy"[12] , a pandemic is defined as "an epidemic occurring over a very wide area, crossing international boundaries, and usually affecting a large number of people" [13] . Pandemics bring out large-scale outbreaks of infectious diseases and it causes a growth in mortality over a wide geographic area. All of these serious situations lead to the fact that [8] it is suitable to apply statistical approaches to study such medical and epidemiological applications.

In addition to the obvious health consequences, COVID-19 has also affected economic stress and social hardship. Due to its high inter-connectedness of the world nowadays, the classical statistical methods seem not to be correct when analysing it. Different researchers used different fractional operators to fractionalize their models.[3] In the present mathematical model, we go on considering the SIR model but take the non-extensive statistical effects into account. Moreover, we hereby confirm that all methods were carried out in accordance with relevant guidelines and regulations.

As a classical compartmental model in epidemiology, the SIR model was created in 1927 [14] in which a fixed population was considered with only three compartments:

- *S*(*t*), *susceptible*, is used to represent the individuals not yet infected with the disease at time *t*, or those susceptible to the disease of the population.
- *I*(*t*), *infected*, denotes the individuals of the population who have been infected with the disease and are capable of spreading the disease to those in the susceptible category.
- *R*(*t*), *recovered*, is the compartment used for the individuals of the population who have been infected and then removed from the disease, either due to immunization or due to death. Those in this category are not able to be infected again or to transmit the infection to others.

Without so-called vital dynamics (birth and death, sometimes called demography) described above, we can give out the normal SIR model as follows [15-18]:

$$\frac{dS(t)}{dt} = -\beta\, I(t)S(t) \tag{2}$$

$$\frac{dI(t)}{dt} = \beta\, I(t)S(t) - \gamma\, I(t) \tag{3}$$

$$\frac{dR(t)}{dt} = \gamma\, I(t) \tag{4}$$

where β is the average number of contacts per person per time, multiplied by the probability of disease transmission in a contact between a susceptible and an infectious subject, and $\gamma\, I(t)$ is assumed to describe the transition rate between *I*(*t*) and *R*(*t*). The first differential equation is the fraction of those contacts between an infectious and susceptible individual which result in the susceptible person becoming infected. Worth to mention that in which there is no removal from the infectious compartment ($\gamma = 0$), the SIR model reduces to a very simple SI model, which has a logistic solution, in which every individual eventually becomes infected.

In this model, $F = \beta I$, is recognized as the force of infection, modelling the transition rate from the compartment of susceptible individuals to the compartment of infectious individuals. However, for large classes of communicable diseases it is more realistic to consider a force of infection that does not linearly depend on the absolute number of infectious subjects. As for the stock of susceptible population, it has shown us that $S \approx N$ for most of cases due to the large population in SIR system. Consequently, we need to reconsider it with respect to the non-extensive statistical effects. Namely, a non-extensive parameter *q* should be introduced then.

Similar to the non-extensive statistics, the evolution equations above of COVID-19 are modified as follows:

$$\begin{cases} \dfrac{dS(t)}{dt} = 0 & (5) \\ \dfrac{dI(t)}{dt} = b\, I^q(t) - \gamma\, I(t) & (6) \\ \dfrac{dR(t)}{dt} = \gamma\, I(t) & (7) \end{cases}$$

whose solutions are listed as:

$$S(t) = N \qquad (8)$$

$$I(t) = A \cdot \{1 - B \exp\left[-\gamma(1-q)t\right]\}^{\frac{1}{1-q}} \qquad (9)$$

$$R(t) = \frac{A}{\gamma(2-q)} \{1 - B \exp[-\gamma(1-q)t]\}^{1+\frac{1}{1-q}} \qquad (10)$$

With such a q-power modified term of infectious individuals in Eq.(10), we then explore the growth law of confirmed cases over time in Australia, Canada, England, France, Germany, Japan, South Korea and the United States during the first half of 2021. Phenomenological analysis on this non-extensive statistical approach is also performed by combining the specific fitting results. Worthy to mention that for such a q-distribution, some other people appeared to describe satisfactorily the available data for COVID-19 using different non-extensive epidemiological models. For instance, C. Tsallis and U. Tirnakli [19] applied one $q-$statistical functional form in order to predict the peaks around the world. Our numerical results, along with the corresponding discussions, will be shown in the next section.

Data fitting and numerical results

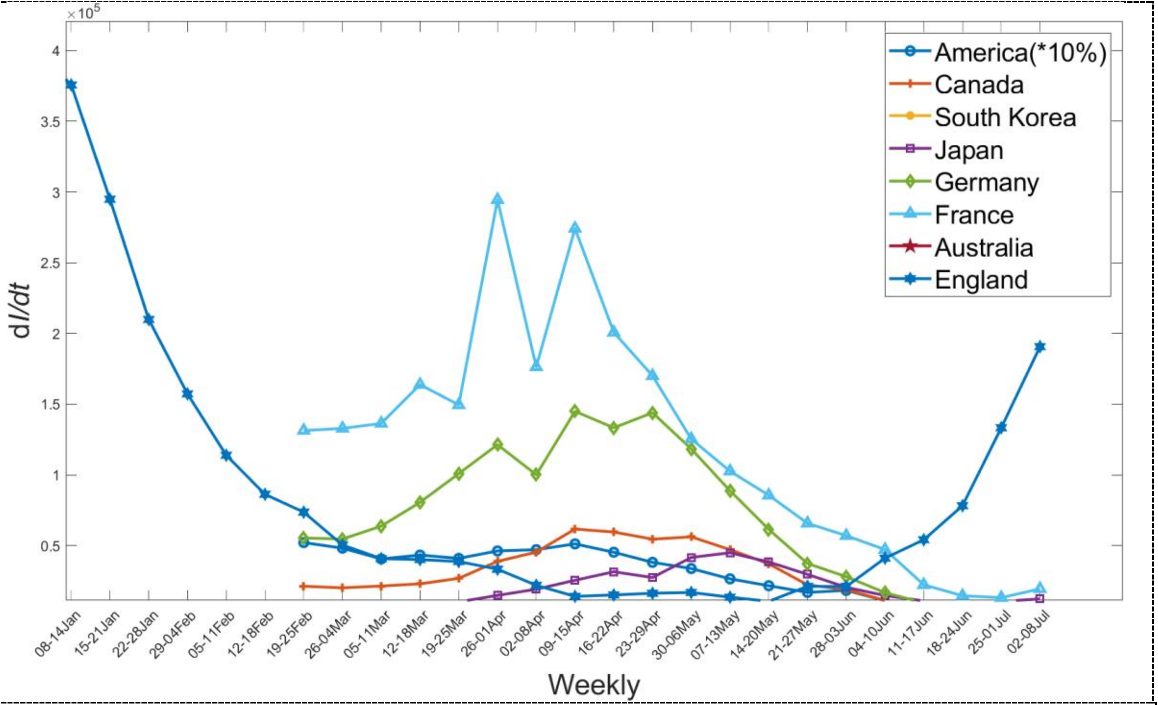

Figure 1. Distributions of the reported data of infected individuals for COVID-19 in various countries in the first half of 2021.

Relevant results are graphically shown. Figure 1 describes the reported cases of infected individuals for COVID-19. For data fitting of model above we have collected the infectious cases of COVID-19 in different countries. Our model solutions were well fitted with the real data in the first half of the year of 2021. All the corresponding fitting parameters are listed in Table 1. Figures 2-5 depict the comparisons between real data in different countries (listed in Table 1) verses present considered model. From the figures it can be noticed that our model shows a strong agreement with collected data available.

Table I. The values of fitting parameters in Eq.(10) in the modified SIR model for different countries:

Countries	A	B	γ	q
England	2.0×10^6	0.89	37.03	0.254
America	6.7×10^6	0.91	29.90	0.476
South Korea	1.0×10^5	-5.98	-25.58	1.671
Germany	1.4×10^6	-10.31	-55.84	1.671
Australia	2.7×10^3	-8.73	-20.76	1.775
Canada	5.9×10^5	-18.13	-49.02	1.775
France	2.2×10^6	-21.50	-53.51	1.980
Japan	4.0×10^5	-61.32	-38.44	1.990

Discussions

First of all, this section provides graphical results of the epidemic progression in these countries in the first half of 2021. According to the report, there exists a secondary outbreak in April, which could be well found in Figure 1. It is very interesting that data shows a big increase at the beginning of the year, which agrees with the fact that the virus for COVID-19 is also active in spring. The number of all the infections is decreasing except for the case in England, which still suffers a heavy situation of COVID-19. This nicely shows the effects caused by control strategies by the government. Moreover, because of the limitation of data source, we only obtained the infectious numbers of COVID-19 in England from January to July of 2021 but others from February to July, which is obviously listed in this figure as well.

In virtue of it the validity of approximation, $S_0 \approx N$, is nicely supported by real data in the world, and the development of recovered individuals in SIR model strongly relies on the case of infectious ones, next we shall focus on the possible interpretations of spread of infections within the non-extensive effect. Worthy to note that small values of time t could recover an exponential function whereas it leads to a Tsallis $q-$exponential distribution, cf. Eq.(1) when $t\to\infty$. γ exhibits the information on the average time for which an individual is infectious. The non-extensive parameter q tells us the departure from the ideal situation, in which the distribution behaves as an exponential function. More specifically, more interactions inside, like mitigation and self-protective measures implemented by the government and the population, lead to larger values of this q parameter. Last but not least, Eq.(9) tells us the mathematical fact that $I(t) \approx A$ when the term of $\gamma(1-q)t$ is large enough.

For data fitting of this modified model, especially Eq.(9), we have analysed the weekly spread of infections from February to July of 2021. In order to better understand the mechanism of the infectious numbers, the cumulative data were fitted by the modified q-distribution, c.f. Eq.(9). Without loss of generality, a mean infectious period of one week was used, and taken to be the same in all cases except for England, where all the infectious number before August of 2021 is available. Therefore, we pick up the data for England from January to July of 2021 as comparisons.

It is obvious to see that the non-extensive parameter q increases among these countries. As discussed above, less intervention strategies were implemented in America and England last year even though it has been over one year since the first case of COVID-19 in human was reported in Wuhan China on December 31st 2019. As for others, this parameter does not display a big discrepancy. Note that the 32th Olympic Games was held in Tokyo last year, which pushed the Japanese government to take lots of important strides like occasion augmentation, hospitalization and isolation and so on. This results in our largest value of q-parameter of all.

Next we go on looking into the simulation results by analyzing the evolution of the cumulative number of active infectious individuals as a function of time.

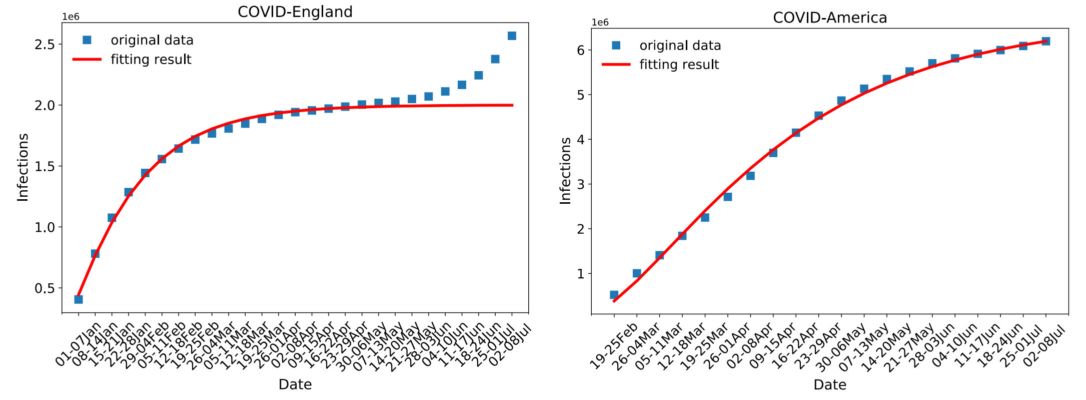

Figure 2. Graphical representation of the modified SIR model to the cumulative data of infectious individuals collected in England and America.

Specifically, Figure 2 reports the fitting results on the weekly evolution of infectious individuals for COVID-19 in England and America. Note that in the case of England we chose the time period from January to July of the year 2021. It is easy to observe that our *q*-function, c.f. Eq.(9), well describes the spread of cumulative data of infections for COVID-19. From the figure we could find that the trend of data in these two countries is kept growing up in the future. This is because of the fact that fewer controlling measures are taken in these two countries, especially in the United Kingdom. The relevant value of non-extensive parameter $q = 0.254$ also supports this point.

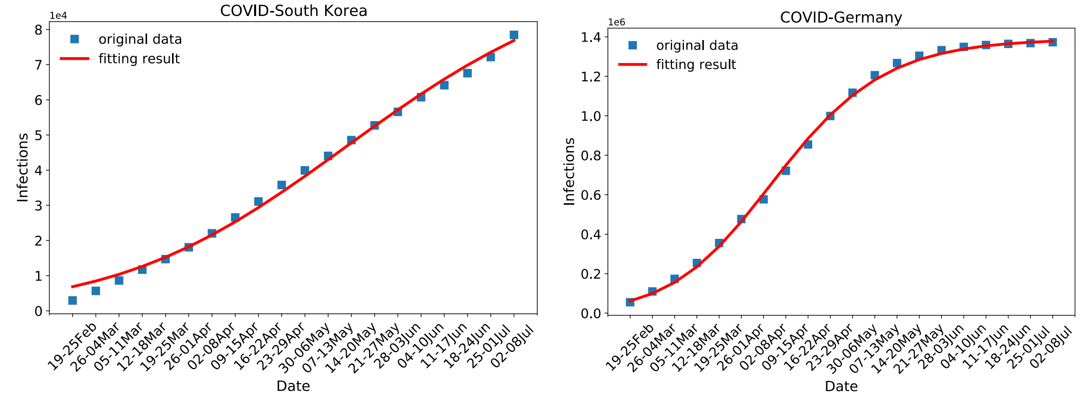

Figure 3. Graphical representation of the modified SIR model to the cumulative data of infectious individuals collected in South Korea and Germany.

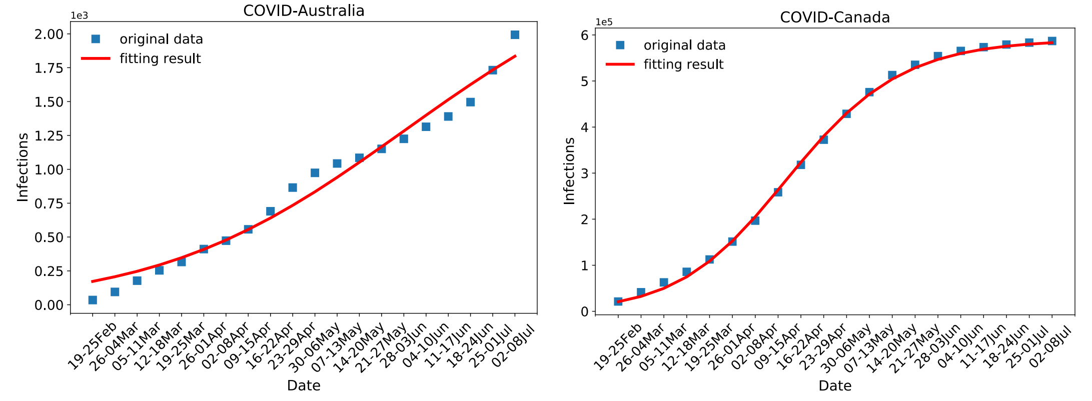

Figure 4. Graphical representation of the modified SIR model to the cumulative data of infectious individuals collected in Australia and Canada.

There are no big differences among the data analysis in South Korea, Germany, Australia and Canada, which are plotted in Figures 3 and 4. The continuous sigmoid curves represent the theoretical prediction of our model as given by Eq.(9), while the dots stand for the cumulative number of infections correspondingly. Similar numbers of parameter q indeed tell us that there is no big difference among these countries, which share almost the same disease containment efforts. Furthermore, with respect to the geographical and demographic factors, there are some similarities of epidemic development between the countries of South Korea and Australia (or Germany and Canada). This is well shown in the graphical representations, especially the shapes of fitting curves, which nicely agrees with the numerical results of parameters B and γ listed in Table 1. The weak fluctuation appeared in the fittings for Australia's infectious distributions. This could be somehow explained by its speciality of geographical location and the second outbreak in April of 2021.

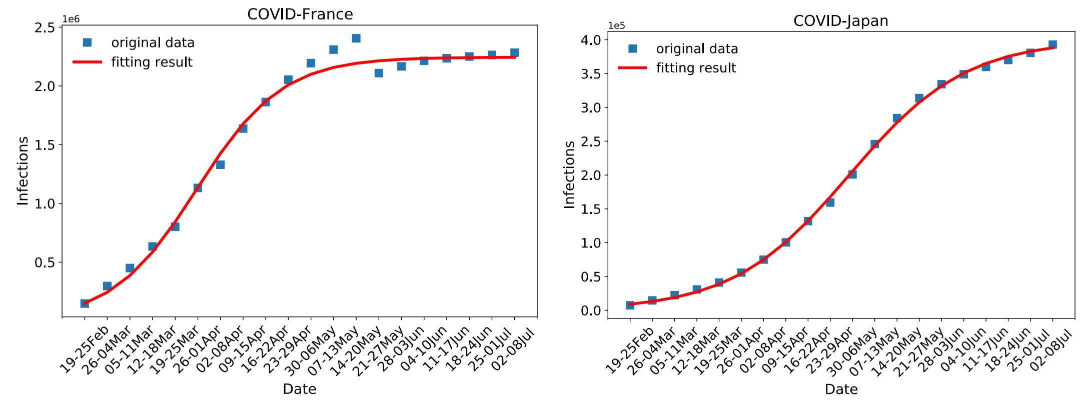

Figure 5. Graphical representation of the modified SIR model to the cumulative data of infectious individuals collected in France and Japan.

On the other hand, the pandemic in France and Japan is well controlled due to the ambitious, agile and aggressive policies by governments. As shown in Figure 5, the trend of cumulative data of infectious number tends towards stability. This leads to the largest values of parameter $q = 1.980$, 1.990, as well as the extreme numbers of both B and γ. Worthy to mention that the government of France did not notice the importance of prevention of COVID-19 initially but soon changed its policies and strategies after the second transmission. It is obviously recalled in the upper panel of Figure 5.

At the same time, one can easily observe an obvious connection between the values of fitting parameter A and the infectious peaks in all countries. For example, the cumulative data of infectious cases for COVID-19 in Japan is getting to a maximum value of 4.0×10^5 by the end of our time period reported. This perfectly satisfies the fitting result of parameter $A = 4.0 \times 10^5$ in Table 1.

In summary, we have developed a non-extensive SIR model to account for the complexity of the epidemic spreads of the COVID-19 in the world. The model focuses on the interplay behind the epidemic distributions based on the analysis of evolution of the COVID-19 disease outbreak in Australia, Canada, England, France, Germany, Japan, South Korea and the United States under different quarantine scenarios. Especially the rapid growth of the number of active cases presenting severe symptoms has saturated the health services in most countries in the continent, which lead to the fact that COVID-19 has been a kind of pandemic. Meanwhile, the impacts of its prevention and isolation measurements become more and more vital when people study epidemic models to explore its outbreaks. On the other hand, the idea of *Global Village* unavoidably affects the exploration of COVID-19 in the world. All lead to it that the system for this epidemic transmission should be considered within the non-extensive application rather than the classical ideal one.

It is of importance to research on the fittings within our modified SIR model, typically Eq.(9), for the various data sets worldwide. In the present article, we have concluded that our model is indeed an alternative tool to investigate the spread of COVID-19 in the world. Through data fitting analysis, the introduced non-extensive parameter q faithfully indicates both the external interference by society, the state or others and the internal interactions inside the system of epidemic transmission. More departure from the classical statistical approach will bring about larger values of q, which means that more effective measurements were taken in the country. Additionally, it is worthy to note that during our comparisons among various fitting parameters, we further illuminate that A approximately stands for the peak value of collected data sets while B and γ better describe the shape of epidemic data development.

All in all, a complete understanding of the physics of these parameters in the study of COVID-19 should be solved in general context. Thus, could we apply it into further and better investigations on both the description of present epidemic distribution and the prediction of future epidemic transmission. In this work we have tried to highlight it from the comparisons among various fittings of provincial data sets in the world. Our model, on the other hand, successfully provides another method to investigate on problems in the scientific researches on the epidemic disease such as COVID-19. Besides, our researches could deeply help understand the physical explanation of the Tsallis non-extensive parameter q, which is also what we will pay attention to in the future.

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Data availability

The datasets generated and/or analysed during the current study are available in the Vision Epidemic Data repository[20]. More details could be seen in the supplementary file as well.

References

[1] WHO: Coronavirus disease 2019 (COVID-19): situation report, 51 (2020).

[2] M. Radha and S. Balamuralitharan, Adv. in Diff. Equa. (2020) 2020:523.

[3] Z. Ahmad, et. al., Scientific. Reports (2020) 10:22268.

[4] Teles P. *Bull World Health Organ*. E-pub: 7 April 2020.

[5] Z. Yang, et. al., J. Thorac. Dis 2020; 12(3): 165-174.

[6] G. Christakos and D. Hristopulos, *Spatiotemporal Environmental Health Modelling*, Springer Science and Business Media, New York, NY 1998.

[7] D. J. Daley and J. Gani, *Epidemic Modelling: An Introduction, vol.15 of Cambridge Studies in Mathematical Biology*, Cambridge University Press, New York, NY 1999.

[8] G. Kaniadakis, M. M. Baldi and T. S. Deisboeck, Sci. Rep. 10, 19949 (2020).

[9] Jiale Wang, Yang Liu, Xusheng Liu and Keming Shen, J. Phys.: Conf. Ser. 2148 012002 (2022).

[10] C. Tsallis, J. Stat. Phys. 52, 479 (1988).

[11] Lists of many applications of non-extensive statistics are available at http://tsallis.cat.cbpf.br/biblio.htm.

[12] N. Madhav, *et al.*, Chapter 17: Pandemics: Risks, impacts and mitigation. In Jamison, D. T. *et. al.* (eds.) *Disease Control Priorities: Improving Health and Reducing Poverty. 3rd edition* (The World Bank, Washington, 2017).

[13] M. Porta, *A Dictionary of Epidemiology. 6th Ed.* (Oxford University Press, Oxford, 2014).

[14] W. O. Kermack and A. G. McKendrick, Bulletin of Mathematical Biology. 53 (1991) 33–55.

[15] E. Kenah and J. M. Robins, J. Theor. Biol. 249, 706 (2007).

[16] E. Kenah and J. M. Robins, Phys. Rev. E 76, 036113 (2007).

[17] S. Cauchemez and N. M. Ferguson, J. R. Soc., Interface 5, 885 (2008).

[18] Yong Tao, Phys. Rev. E 102, 032136 (2020).

[19] C. Tsallis and U. Tirnakli, Fron. Phys. 8: (2020) 217.

[20] Vision epidemic data-the world's most complete epidemic data download station, http://www.sy72.com/world/. All the corresponding data are collected from various official websites.