Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.
Non-extensive thermodynamic entropy to predict the dynamics behavior of COVID-19

Ahmad Ghanbari a, Reza Khordad a,*, Mostafa Ghaderi-Zefreh b

a Department of Physics, College of Science, Yasouj University, Yasouj, 75918-74934, Iran
b Department of Animal Genetics, Yasouj University, Yasouj, 75918-74934, Iran

ARTICLE INFO

Keywords:
Covid-19
Entropy
Tsallis

ABSTRACT

The current world observations in COVID-19 are hardly tractable as a whole, making situations of information to be incompleteness. In pandemic era, mathematical modeling helps epidemiological scientists to take informing decisions about pandemic planning and predict the disease behavior in the future. In this work, we proposed a non-extensive entropy-based model on the thermodynamic approach for predicting the dynamics of COVID-19 disease. To do so, the epidemic details were considered into a single and time-dependent coefficients model. Their four constraints, including the existence of a maximum point were determined analytically. The model was worked out to give a log-normal distribution for the spread rate using the Tsallis entropy. The width of the distribution function was characterized by maximizing the rate of entropy production. The model predicted the number of daily cases and daily deaths with a fairly good agreement with the World Health Organization (WHO) reported data for world-wide, Iran and China over 2019-2020-time span. The proposed model in this work can be further calibrated to fit on different complex distribution COVID-19 data over different range of times.

1. Introduction

In medicine, infectious disease is a process caused by various biological agents including bacteria, viruses, fungi, protozoans and worms impairing individual health [1]. In many cases, infectious diseases like HIV [2] and malaria [3-6] can be directly or indirectly spread from person to person yielding a significant burden to international health and global economics [7] leading to current cause of increasing premature rate in humans and other species [8]. Coronaviruses were first described in 1966 [14]. They are enveloped, positive single-stranded large RNA viruses that infect humans, but also a wide range of animals. Severe acute respiratory syndrome (SARS) that began in southern China and resulted in 774 deaths out of 8098 infected patients in 29 countries and the Middle East respiratory syndrome (MERS) originated in Saudi Arabia and responsible for 848 deaths among 2458 patients in 27 countries [11-13]. In the 2019, an outbreak of epidemic was triggered in December 2019 by a novel coronavirus in Wuhan, China [10, 14] and called COVID-19 [9]. This is one kind of seventh known coronavirus that spread quickly between people through unknown mechanisms [10] and it is sought that COVID-19 likely has an animal origin [15-19]. Important achievements have been made for deciphering the COVID-19 transmission dynamic using various mathematical models [20-30]. Amongst them are growth models, DE equations [31-37]. However, statistical mechanics paradigm has scarcely, if any thoroughly, used in this area. Statistical mechanics is a branch of theoretical physics and chemistry that applies thought through tools to study systems containing large number of particles [38]. In the past few years, many works have adopted statistical mechanics in various branches of science like computational neuroscience, biomechanics, engineering and physical and chemical approach [39-44]. Entropy is related to the missing information on the concrete state of a system and it shows a measure of the disorder of a system. Herein, we use an entropic-based statistical mechanics model for predicting COVID-19 daily cases and deaths of people in world-wide, Iran and China. Also we attempt to develop an entropy-based approach to predict dynamic of the COVID-19 epidemic worldwide. The proposed models are based on a modified susceptible-exposed-infectious-recovered (SEIR) computational framework. It is now evident that behavior of COVID-19 epidemic depends on many factors such as medical interventions, public-service announcements, isolation of people, restriction of individual and social activities. Therefore, it would be very difficult to find all those details of the epidemic by a mathematical model. However, in this study we try to lay

* Corresponding author.
E-mail address: rezakh2025@yahoo.com (R. Khordad).

https://doi.org/10.1016/j.physb.2021.413448
Received 7 December 2020; Accepted 28 September 2021
Available online 30 September 2021

out a way to put these factors in mathematical model using non-extensive entropy method. Unlike the most general physical systems in which the non-extensivity entropy is very naive, we believe that COVID-19 epidemic systems have visible and very strong non-extensivity entropy.

2. Entropy based model

In our approach, we first defined density function \( f(t) \) as the number of daily COVID-19 cases. Daily deaths due to COVID-19 and recovery ones were subtracted from this parameter since death and recovery are two active agents in thermodynamic systems. The epidemic is remarkably vague and cannot be expressed by an explicit functional form. Therefore, we supposed the epidemic to be as a thermodynamic system and according to the approach for the rate of vibration excitation and chemical reaction \([1] \), we considered the rate of change of \( f(t) \) as

\[
\frac{df(t)}{dt} = a(t)f(t),
\]

where \( a(t) \) is a time-dependent parameter. The balance between the epidemic spread and the control mechanisms during the public intervention are two important rationale tools that could make up \( a(t) \) parameter. Accordingly, a coupled system of differential equations should be applied to model this scenario. To this end, we use a statistic background by supposing that all the spreading and controlling mechanisms effects could be incorporated into the \( a(t) \) parameter.

To proceeding along, here, we impose four constraints on this \( a(t) \) parameter:

(i) The parameter \( a(t) \) must have the dimension of \( t^{-1} \). We know that Eq. (1) is the Master equation and \( a(t) \) shows the transition probabilities for various pairs of states. The parameter is proportional to inverse time. Therefore, we have selected the simplest choice as \( a(t) \sim t^{-1} \). With this selection, the following constraint is satisfied \((t \rightarrow 0, a \rightarrow \infty)\).

(ii) There is an exponential enhancement of smooth spread at the initial stage, \( a(0) \rightarrow \infty \).

(iii) On a given day, \( t = L \), the rate must decrease. Mathematically, it means that \( \frac{df(t)}{dt} \) vanishes at \( t = L \), this is so called inflexion date. Substituting Eq. (1) into \( \frac{df(t)}{dt} = 0 \) yields

\[
\frac{da}{dt} + a^2 = 0, \quad t = L
\]

(iv) \( f(t) \) has a maximum, this means that for \( t = D, a(D) = 0 \).

As could be seen in the above, it is further assumed that \( a(t) \) has an analytical function. Many functions could be searched for, however, the sufficiently simple function satisfying the four constraints could be as follows

\[
a(t) = -\frac{c \ln(f_D)}{t}
\]

where \( c = \frac{1}{\ln\left(\frac{t_0}{t_D}\right)} \) and \( L \) is cumulated days to reach the inflexion point counting from the initial date. Inserting Eq. (2) into Eq. (1) and by some computation, we could deduce the following relation

\[
f(t) = \frac{k}{\sqrt{2\pi \sigma^2}} \exp\left(-\frac{(\ln(t) - \mu)^2}{2\sigma^2}\right)
\]

Here \( k \) is proportion constant, \( \mu = \ln D + \sigma^2 \) and \( \sigma \) is proportion constant and determined through the use of the principle of the extreme rate of entropy production.

3. Principle of entropy production

The principle of entropy production has attracted the wide attention of many researchers. Paszynski et al. \([46]\) have studied entropy production in open systems. They showed that the entropy production in small-open systems coupled to environments is predominantly caused by the displacement from equilibrium. Santos et al. \([47]\) showed that the entropy production of a quantum system undergoing open-system dynamics can be formally split into a term that only depends on population unbalances, and one that is underpinned by quantum coherences. Shiraiishi et al. \([48]\) investigated the fundamental relation between entropy production and heat current. They establish the fact that quick energy exchange inevitably induces large entropy production in a quantitative form. Tsuruya \([49]\) considering the locality of the second law of thermodynamics, addressed that entropy can be divided into entropy derived from a chemical reaction and entropy produced by the diffusion of signaling molecule. He showed that the conserved production rate can be defined as the channel capacity of the given signal transduction cascade. We used the principle of maximum/minimum entropy production as a useful method to determine model parameters. In this way, the \( \sigma \) characterizes the width of the \( f(t) \) density curve. As the curve gets wider, the entropy became larger and as the maximum dissipation rate is reached, the width would cease to enhance. The dissipation rate is proportional to the rate of entropy production. Maximum dissipation rate corresponds to the extreme rate of the entropy production which again corresponds to

\[
\frac{d^2 S(\sigma)}{d\sigma^2} = 0
\]

where \( S(\sigma) \) is the tsallis entropy and express as

\[
S(\sigma) = \frac{k}{q-1} \left( 1 - \sum_{i=1}^{n} (f_i(t))^q \right)
\]

where \( n \) is the total number of possibilities of the system and \( k \) is a positive constant. Substituting Eq. (4) into Eq. (6), the entropy is obtained by

\[
S(\sigma) = \frac{\sigma^q}{q} \exp\left[ (1-q)\mu - \frac{(q-1)\sigma^2}{2} \right] \exp\left[ q \left( \ln(\mu^2) - \frac{1-q}{q} - \frac{q}{2} \right) \right]
\]

Here, the symbol \( \text{erf} \) denotes the imaginary error function as \( \text{erf}(x) = \frac{2}{\sqrt{\pi}} \int_0^x e^{t^2} dt \). Due to above formula, Eq. (5) is authentic if and only if

\[
\sigma \approx 0.3802
\]

At this value for \( \sigma \), the intrinsic spread mechanism is balanced by the dissipation mechanism (controlling effect). The relationship between date \( D \), maximum number of daily cases and \( L \), inflexion point, could be obtained by inserting Eq. (4) into the inflexion point \( \frac{df(t)}{dt} \bigg|_{t=L} = 0 \). Then, we could deduce the following relation as

\[
D = L \exp\left(\frac{1}{2} \sigma^2 + \frac{1}{5} \sqrt{4\sigma^2 + \sigma^4} \right)
\]

Also, using Eq. (4), \( f(D) \) has related with \( f(L) \) as

\[
f(D) = f(L) \exp\left( -\sigma^2 - \frac{1}{2} \sqrt{4\sigma^2 + \sigma^4} + \frac{3}{5} \left( \frac{3}{2} \sigma + \frac{1}{2} \sqrt{4 + \sigma^2} \right)^2 \right)
\]

According to Eq. (4), two important relations have been obtained
By these two relations, we can predict the maximal number of daily COVID-19 cases and deaths over every time and location point. Also, the inflexion point, $L$, is characterized through the data at the earlier stage of epidemic. To this end, we calculated the rate of enhance $\frac{df}{dt}$ at $t = L$. So using Eq. (4) and by some computation, the following equation yields

$$\frac{df}{dt}\bigg|_{t=L} = -\frac{1}{\sigma^2 L} f(L) \ln \frac{L}{D}$$

Therefore, the solution of above equation is as follow

$$L = \left( \frac{1}{\frac{1}{2} + \frac{1}{2} \sqrt{1 + 4 \frac{3 f(L)}{\frac{df}{dt}\bigg|_{t=L}}} \prime} \right) \frac{f(L)}{\frac{df}{dt}\bigg|_{t=L}}$$

4. Results and discussion

Before using our thermodynamic model, we need to determine the parameters. To do this firstly, we specified the value $F = f(L)$ using the reported data at the inflexion point (the data $\frac{df}{dt}$ reaches to decrease). Also, the proportion constant, $k$, has characterized by inserting $f(L) = F$ in Eq. (3) and we used Eq. (12) to find $L$. Afterward, using Eq. (10) we predicted $D$ and $f(D)$ and plot the curve $f(t)$. To determine the inflexion point, we record the reported number $f(t)$ for each day and plotted the curve $g(t) = f(t) - f(t - 1)$. Finally, the inflexion point, $L$, is the peak point at $g(t)$ (denoted as $G$). However, significant cases must be considered:

(a) It is possible to have report delay of case in the initial stage of the epidemic. So a false peak must be made.

(b) At places with always small reported data, it is difficult to observe a clear peak.

(c) Due to new outbreak, sometimes there are multiple inflexion points.

Also, as mention above, $L$ is calculated numerically as

$$L = \frac{3F}{G}$$
where $\mathcal{F} = \frac{1}{2} (\mathcal{F} - \mathcal{G})$ is the number of $\mathcal{F}$ averaged over two consecutive dates.

After determining the parameters, we use the model for daily COVID-19 cases and deaths of WW, Iran and China reported by the World Health Organization (WHO) from January 23, 2020 to May 6, 2020. In Figs. 1 (a) and 2(b), we have compared our analytical model with daily cases and daily deaths of WW, respectively. As can be seen for an initial period of the epidemic, there is fairly good agreement between our proposed model and the reported data. However, as time passes, WW data became much smoother and flatter, a matter that shows some sort of deviation from our model prediction. We interpret this that people behavior around the world to COVID-19 epidemic has changed over time. Moreover, we can see that the non-extensive parameter tends to $1, q \rightarrow 1$, showing a better treatment for the model. Fig. 2(a) and (b) show a comparison of the model with daily cases and daily deaths for different $q$ for the same period of time for Iran. In this case, there is fairly good agreement between the model and the WHO reported data. As can be seen, as $q \rightarrow 1$, the level of model fitting with data disappears. In Fig. 3(a) and (b), the model has been compared with reported daily cases and daily deaths of China. In this case, as $q \rightarrow 1$, we see a better agreement and generally, there is a good agreement between the model and reported data. Fig. (4) shows entropy versus $q$ for different $q$. As it can be seen, the entropy first level down to a special time then it jumps to the initial time, and then it behaves in a smooth line. According to the general concordance of proposed model with the data of WHO data, we would think that one can use our proposed model in this study to predict the number of daily cases and daily deaths of COVID-19 and its dynamic.

However, the main assumption of this study that there was only one peak available in COVID-19 data and it disappeared as time passed on. For this reason, we tackled with this phenomenon, as discussed in the paper, that $a(t)$ must have the dimension of $t^{-1}$. However, for some data, e.g. Iran COVID-19 data, we could see that as time passes on, the COVID-19 does not have only one peak and several peaks are observed. For this reason, it is suggested that $a(t)$ be defined as $a(t) = \frac{a(t)}{t}$, this makes the $f(t)$ to be periodic function and the next peaks can be predicted. Also, the effect of various factors influencing on COVID-19, such as wearing mask, social distance, staying at home, etc., could be included in the $a(t)$ function. Therefore, having a different density functions of COVID-19 and a suitable functional form for $a(t)$ function, one can come up with a model that would answer a wide range of different questions. This study can provide such a platform to conduct these sorts of studies in the future.

5. Conclusion

In this work, we developed a nonextensive entropic based model to contain and decipher COVID-19 outbreak. To this end, we used the principle of thermodynamic to come up with a mathematical model to explore WHO’s COVID-19 data. We showed that by means our proposed model one can predict the COVID-19’s number of daily cases and deaths and its dynamic. It should note that the simplicity of the model is an advantage point. In this model, the details of epidemic have been ignored. We have used the model for the first peak in the infection. More comparisons need to be done to further assess the validity our model. This can be considered in future studies.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

References

[1] P. Waltevkar, R. Gannamani, T. Govender, Combination drug therapy via nanocarriers against infectious diseases, Eur. J. Pharmaceut. Sci. 127 (2019) 121–141.
[2] D. Pillay, M. Zambon, Antiviral drug resistance, BMJ 317 (1998) 660–662.
[3] N.J. White, Antimalarial drug resistance, J. Clin. Invest. 113 (2004) 1084–1092.
[4] R.S. Kallapur, N. Suleman, C. Mocktar, N. Seedar, T. Govender, Nanoengineered drug delivery systems for enhancing antibiotic therapy, J. Pharmaceut. Sci. 104 (2015) 872–905.
[5] B.J. Ausg, Novel formulation strategies for improving oral bioavailability of drugs with poor membrane permeation or presystemic metabolism, J. Pharmaceut. Sci. 99 (2017) 45–65.
[6] A. Signore, About inflammation and infection, EJNNMI Res. 3 (2013) 8.
[7] L. Lozano, M. Naghavi, K. Foreman, S. Lim, K. Shibuya, V. Aboyans, J. Abraham, T. Adair, R. Aggarwal, S.Y. Ahn, Global and regional mortality from 235 causes of death for 20 age groups in 1990 and 2010: a systematic analysis for the Global Burden of Disease Study 2010, Lancet 380 (2012) 2095-2128.
[8] J.A. Bacher, D. Klinkenberg, J. Wallinga, Incubation period of 2019 novel coronavirus (2019-nCoV) infections among travellers from Wuhan, China, Jan 28-2020, Euro Surveill. 25 (2020), 200062.
[9] N. Zhu, D. Zhang, W. Wang, X. Li, B. Yang, J. Song, X. Zhao, B. Huang, W. Shi, R. Li, et al., A novel coronavirus from patients with pneumonia in China, 2019, N. Engl. J. Med. 382 (2020) 727.
[10] D. Wang, B. Hu, C. Hu, F. Zhu, X. Liu, J. Zhang, B. Wang, H. Xiang, Z. Cheng, Y. Xiong, Clinical characteristics of 138 hospitalized patients with 2019 novel coronavirus-infected pneumonia in Wuhan, China, JAMA 323 (2020) 1061–1069.
[11] C.W. Lam, M.H. Chan, C.K. Wong, Severe acute respiratory syndrome: clinical and laboratory manifestations, Clin. Biochem. Rev. 25 (2004), 2004.
[12] E.I. Azhar, D.S. Hui, Z.A. Memish, C. Drosten, A. Zumla, The Middle East respiratory syndrome (MERS), Infect. Disease Clin. 33 (2019) 891–905.
[13] W. Tan, X. Zhao, X. Ma, W. Wang, P. Niu, W. Xu, G.F. Gao, G. Wu, A novel coronavirus genome identified in a cluster of pneumonia cases—Wuhan, 2019—2020, China CDC Weekly 2 (2020) 61–62.
[14] J.F.W. Chan, S. Yuan, K.-H. Kek, K.K.W. To, H. Chu, J. Yang, F. Xing, J. Liu, C.C.-Y. Yip, R.W.S. Poon, A familial cluster of pneumonia associated with the 2019 novel coronavirus indicating person-to-person transmission: a study of a family cluster, Lancet 395 (2020) S14-S23.
[15] C. Huang, Y. Wang, X. Li, L. Ren, J. Zhao, Y. Hu, L. Zhang, C. Fan, J. Xu, G. Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China, Lancet 395 (2020) 497–506.
[16] L.T. Phan, T.V. Nguy, Q.C. Luong, T.V. Nguyen, H.T. Nguyen, H.Q. Le, T.T. Nguyen, T.M. Cao, Q.D. Pham, Importation and human-to-human transmission of a novel coronavirus in Vietnam, N. Engl. J. Med. 382 (2020) 872–874.
[17] Q. Li, X. Guan, P. Wu, X. Wang, L. Zhou, Y. Tong, R. Ren, K.S. Leung, E.H. Lau, J. Y. Wong, et al., Early transmission dynamics in Wuhan, China, of novel coronavirus-infected pneumonia, N. Engl. J. Med. 382 (2020) 1199.
[18] Z.Y. Zu, M.D. Jiang, P.P. Xu, W. Chen, Q.Q. Ni, G.M. Lu, L.J. Zhang, Coronavirus disease 2019 (COVID-19): a perspective from China, Radiology (2020), 204089.
[19] C.A. Donnelly, A.C. Ghani, M.G. Leung, A.J. Hedley, C. Fraser, S. Riley, L.J. Abu Raddad, L.M. Ho, T.Q. Thach, P. Chau, Epidemiologic determinants of spread of causal agent of severe acute respiratory syndrome in Hong Kong, Lancet 361 (2003) 1761–1766.
[20] S. Riley, C. Fraser, C.A. Donnelly, A.C. Ghani, L.J. Abu Raddad, A.J. Hedley, G.M. Leung, L.M. Ho, T.H. Lam, T.Q. Thach, Transmission dynamics of the etiological agent of SARS in Hong Kong: impact of public health interventions, Science 300 (2003) 1961–1966.
[22] M. Lipsitch, T. Cohen, B. Cooper, J.M. Robbins, S. Ma, L. James, G. Gopalakrishna, S. K. Chew, C.C. Tan, M.H. Samore, Transmission dynamics and control of severe acute respiratory syndrome, Science 300 (2003) 1966–1970.
[23] C. Dye, N. Gay, Modeling the SARS epidemic, Science 300 (2003) 1884–1885.
[24] N. Jia, L. Tsui, Epidemic modelling using SARS as a case study, North Am. Actuar. J. 9 (2005) 28–42.
[25] D.J. Watts, R. Muhammad, D.C. Medina, P.S. Dodds, Multiscale, resurgent epidemics in a hierarchical metapopulation model, Proc. Natl. Acad. Sci. Unit. States Am. 102 (2005) 11157–11162.
[26] E. Kenah, J.M. Robins, Second look at the spread of epidemics on networks, Phys. Rev. 76 (2007), 036113.
[27] L. Bian, D. Liebner, A network model for dispersion of communicable diseases, Trans. GIS 11 (2007) 155–173.
[28] X.-l. Yu, X.-y. Wang, D.-m. Zhang, F. Li, S. Wu, Mathematical expressions for epidemics and immunization in small-world networks, Phys. Stat. Mech. Appl. 387 (2008) 1421–1430.
[29] B. Dybiec, SIR model of epidemic spread with accumulated exposure, Phys. J. B 67 (2009) 377–383.
[30] B. Dybiec, A. Kleczkowski, C.A. Gilligan, Modelling control of epidemics spreading by long-range interactions, J. R. Soc. Interface 6 (2009) 941–950.
[31] T. Ganyani, C. Faes, N. Hens, Inference of the generalized-growth model via maximum likelihood estimation: a reflection on the impact of overdispersion, J. Theor. Biol. 484 (2020), 110029.
[32] E. Akkoyun, S.T. Kwon, A.C. Acar, W. Lee, S. Bark, Predicting abdominal aortic aneurysm growth using patient-oriented growth models with two-step Bayesian inference, Comput. Biol. Med. (2020), 103620.
[33] P. Agarwal, S. Denis, S. Jain, A.A. Alderremy, S. Aly, A new analysis of a partial differential equation arising in biology and population genetics via semi analytical techniques, Phys. Stat. Mech. Appl. 542 (2020), 122769.
[34] I. Balázs, P. Getto, G. Röst, A Continuous Semiflow on a Space of Lipschitz Functions for a Differential Equation with State-dependent Delay from Cell Biology, 2019 arXiv preprint arXiv:1903.01774.
[35] J.D. Anderson Jr., Hypersonic and High-Temperature Gas Dynamics, American Institute of Aeronautics and Astronautics, 2006.
[36] S. Bornholdt, S. Kauffman, Ensembles, dynamics, and cell types revisiting the statistical mechanics perspective on cellular regulation, J. Theor. Biol. 467 (2019) 15–22.
[37] J.A. González, M. Acanda, Z. Akhtar, D. Andrews, J. Azqueta, E. Bass, A. Bellorín, J. Couso, M.A. García-Nustes, Y. Infante, New Combinational Therapies for Cancer Using Modern Statistical Mechanics, 2019 arXiv preprint arXiv:1902.00728.
[38] D. Watts, R. Muhammad, D.C. Medina, P.S. Dodds, Multiscale, resurgent epidemics in a hierarchical metapopulation model, Proc. Natl. Acad. Sci. Unit. States Am. 102 (2005) 11157–11162.
[39] E. Kenah, J.M. Robins, Second look at the spread of epidemics on networks, Phys. Rev. 76 (2007), 036113.