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Newsletter of the International Society of Difference Equations



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Newsletter Editor: Małgorzata Guzowska



A LETTER FROM THE PRESIDENT



Dear ISDE members

This year's annual ISDE meeting (ICDEA 2020) in Sarajevo had to be postponed until next summer due to the ongoing Coronavirus pandemic. ICDEA 2021 will be held on 26th-30th July, 2021, Sarajevo (icdea2020.pmf.unsa.ba). Hopefully by that time, a vaccine would be available worldwide. Consequently, next ICDEA meetings will be delayed one year. Next ICDEAs are planned to be held in Paris (2022), Thailand (2023), Paris (2023). Tentatively, there are plans to hold ICDEAs in Guangzhou (2025), Pisa (2026), and Okayama (2027).

Our society's second meeting is the 23rd European Conference on Iteration Theory (ECIT 2020) which has to be postponed until next summer. ECIT 2021 will be held on 27th June- 1st July 2021 at Reichenau (Austria). Next Progress on Difference Equations (PODE) will be held in Szczecin, Poland, in 2022.

I know some societies decided to have their conferences virtual. Most of these conferences, however, are local. When we discussed this issue in the last meeting of the Board of Directors, the decision to postpone ICDEA 2020 was unanimous. The fact that our membership is from all five continents made it impossible to have a virtual conference.

It is quite remarkable that the mathematical community all over the world has made significant contributions to our understanding of the coronavirus dynamics. Discrete and continuous mathematical models have been used to make prediction of the spread of Covid-19 and to identify its controlling mechanisms. Who would have predicted that the net

reproduction rate of the infection R_0 would become a household word? I am proud to inform you that we have received 7 publications on Covid-19 written by ISDE members. These papers or their abstracts may be found in ISDE website.

Since 2013, the society has established the annual best JDEA paper award, which is sponsored by Taylor & Francis. The winners of the 2019 best paper award are Anna Cima and Sundus Zafar for their paper “Invariant fibrations for some birational maps of \mathbb{C}^2 , JDEA 25(8), 2019, 1107-1133”. In memory of the first president and Co-Founder of ISDE, Bernd Aulbach, the society has established the prestigious life-time Achievement Award “Aulbach Award” which is awarded biannually in odd years. The winner will be announced at the next meeting of the society during ICDEA 2021 in Sarajevo.

I wish you all a safe and productive fall semester.

Saber Elaydi, President

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P.S. For access to ISDE membership, please use (user id: isded, password: isded).

INTRODUCTION FROM THE NEWSLETTER EDITOR

Dear Colleagues:

It is, with great pleasure, I present to you the new issue of ISDE Newsletter. I hope that you will enjoy reading this new issue.

I would like to thank all ISDE members who have sent news and information for this newsletter.

I would also like to ask the members of the Society to contribute information and articles about their faculty, new books, new conferences, new grants and job opportunities to the newsletter and webpage, as well as any relevant information about mathematics or about our members.

All information may be emailed (for now) to:

malgosiaguzowska@gmail.com

Hope see You all soon
Małgorzata (Malgosia)Guzowska

M. Guzowska



BEST JDEA PAPER 2020 AWARD

The winners of the 2019 best paper award are **Anna Cima** and **Sundus Zafar** for their paper
“Invariant fibrations for some birational maps of \mathbb{C}^2 ”

Published in the Journal of Difference Equations and Applications 25(8), 2019, 1107-1133.

This has a monetary award in the amount of £ 500

Congratulations!

JOURNAL OF DIFFERENCE EQUATIONS AND APPLICATIONS
 2019, VOL. 25, NO. 8, 1107–1133
<https://doi.org/10.1080/10236198.2019.1654464>



Invariant fibrations for some birational maps of \mathbb{C}^2

Anna Cima and Sundus Zafar

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ABSTRACT

In this article, we extract and study the zero entropy subfamilies of a certain family of birational maps of the plane. We find these zero entropy mappings and give the invariant fibrations associated to them.

ARTICLE HISTORY

Received 3 July 2018
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KEYWORDS

Birational maps; algebraic entropy; first integrals; fibrations; blowing-up; integrability; periodicity

MATHEMATICS SUBJECT CLASSIFICATION 2010

14E05; 26C15; 28D20; 34K19; 37C15; 39A23

1. Introduction

A mapping $f = (f_1, f_2) : \mathbb{C}^2 \rightarrow \mathbb{C}^2$ is said to be rational if each coordinate function is rational, that is, f_i is a quotient of polynomials for $i = 1, 2$. These maps can be naturally extended to the projective plane $P\mathbb{C}^2$ by considering the embedding $(x_1, x_2) \in \mathbb{C}^2 \rightarrow [1 : x_1 : x_2] \in P\mathbb{C}^2$. The induced mapping $F : P\mathbb{C}^2 \rightarrow P\mathbb{C}^2$ has three components $F_i[x_0 : x_1 : x_2]$ which are homogeneous polynomials of the same degree. If F_1, F_2, F_3 have no common factors and have degree d , we say that f or F has degree d . Similarly we can define the degree of $F^n = F \circ \dots \circ F$ for each $n \in \mathbb{N}$.

We are interested in birational maps. It is said that a rational mapping $f : \mathbb{C}^2 \rightarrow \mathbb{C}^2$ is birational if there exists an algebraic curve C and another rational map g such that $f \circ g = g \circ f = id$ in $\mathbb{C}^2 \setminus C$.

The study of the dynamics generated by birational mappings in the plane has been growing in recent years, see for instance [2,3,6,8,11,15–20,23].

UPCOMING CONFERENCES



ICDEA
2020/2021

**26th INTERNATIONAL CONFERENCE
ON DIFFERENCE EQUATIONS
AND APPLICATIONS**

26-30 July 2021, Sarajevo, Bosnia and Herzegovina

The **26th International Conference on Difference Equations and Applications (ICDEA 2020)** will be held at the **University of Sarajevo, School of Economics and Business** on **26-30 of July 2021**. ICDEA is the official conference of the International Society of Difference Equations (ISDE) and hosts its General Meeting.

The purpose of ICDEA 2020 is to bring together Researchers, PhD students and Postdocs to present and discuss research results in Difference Equations, Discrete Dynamical Systems and related topics.

There will be invited plenary talks (50 min+10 min), contributed talks (25 min+ 5 min), plus facilities for posters.

Previous ICDEA conferences were held in London (UK) in 2019, Dresden (Germany) in 2018, Timisoara (Romania) in 2017, Osaka (Japan) in 2016, Bialystok (Poland) in 2015, Wuhan (Hubei, China) in 2014, Muscat (Oman) in 2013, Barcelona (Spain) in 2012, Trois-Rivières (Quebec, Canada) in 2011, Riga (Latvia) in 2010, Estoril (Portugal) in 2009, Istanbul (Turkey) in 2008, Lisbon (Portugal) in 2007, Kyoto (Japan) in 2006, Munich (Germany) in 2005, Los Angeles (California, USA) in 2004, Brno (Czech Republic) in 2003, Changsha (China) in 2002, Augsburg (Germany) in 2001, Temuco (Chile) in 2000, Poznan (Poland) in 1998, Taipei (Taiwan) in 1997, Veszprém (Hungary) in 1995 and San Antonio (Texas, USA) in 1994.

Plenary speakers are experts chosen from the many areas of difference equations, discrete dynamical systems and their interplay with nonlinear science. Contributed talks in any area of difference equations and discrete dynamical systems are welcome.

<http://www.pmf.unsa.ba/icdea2020/>

PLENARY SPEAKERS

John Appleby, Dublin City University, Ireland

Saber Elaydi, Trinity University, USA

Lubomir Snoha, Matej Bel University, Banska Bistrica, Slovakia

Walter Van Assche, Department of Mathematics, KU Leuven, Belgium

Gail S.K. Wolkowicz, Department of Mathematics and Statistics, McMaster University, Canada

Jianshe Yu, Center for Applied Mathematics, Guangzhou University, China

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Nedim Bušatlija (University of Sarajevo , BIH)



ECIT 2020

23rd European Conference on Iteration Theory

Reichenau an der Rax

15th June 2020 – 19th June 2020



The conference is postponed to the period between Sunday, **27th June 2021** and Thursday, **1st July 2021**.

TOPICS

As its name states the main topic of this conference is iteration theory. In particular among the main topics are discrete dynamical systems and functional equations. Questions of this type arise for example in biology, physics, economics and engineering.

HISTORY OF ECIT

The first European Conference on Iteration Theory took place 1973 in Toulouse (France). It was continued 1977 in Graz (Austria), 1980 in Marburg (Germany), 1982 in Toulouse (France), 1984 in Lochau (Austria), 1987 in Caldes de Malavella (Spain), 1989 in Batschuns (Austria), 1991 in Lisboa (Portugal), 1992 in Batschuns (Austria), 1994 in Opava (Czechia), 1996 in Urbino (Italy), 1998 in Muszyna (Poland), 2000 in La Manga del Mar Menor (Spain), 2002 in Évora (Portugal), 2004 in Batschuns (Austria), 2006 in Gargnano (Italy), 2008 in Yalta (Ukraine), 2010 in Nant (France), 2012 in Ponta Delgada (Portugal), 2014 in Łagów (Poland), 2016 in Innsbruck (Austria) and 2018 in Murcia (Spain).

TALKS

According to the tradition of the European Conferences on Iteration Theory there are 20 minutes talks with 5 minutes for discussion. There will be no parallel sessions. Moreover, there will be no special plenary speakers. Official language of this conference is English.

More information: <https://www.univie.ac.at/projektservice-mathematik/e/?event=ecit2020>

SCIENTIFIC COMMITTEE

- Laura Gardini, Urbino (Italy)
- Witold Jarczyk, Zielona Góra (Poland)
- Wolfgang Förg-Rob, Innsbruck (Austria)
- Francisco Balibrea, Murcia (Spain)
- Jaroslav Smítal, Opava (Czechia)
- Henrique Oliveira, Lisboa (Portugal)
- Daniele Fournier-Prunaret, Toulouse (France)
- Marta Štefánková, Opava (Czechia)
- Alexander Sharkovsky, Kyiv (Ukraine)
- Armengol Gasull, Barcelona (Catalonia)
- Stefan Siegmund, Dresden (Germany)

HONORARY MEMBERS OF THE SCIENTIFIC COMMITTEE

- Christian Mira, Toulouse (France)
- Ludwig Reich, Graz (Austria)
- Marek Cezary Zdun, Kraków (Poland)

ORGANIZING COMMITTEE

- Peter Raith, Vienna (Austria)



Reichenau an der Rax, source: Wikipedia

PUBLICATIONS ON COVID-19 WRITTEN BY ISDE MEMBERS

- Gowrisankar, A., Rondoni, L., & Banerjee, S. (2020). **Can India develop herd immunity against COVID-19?** *The European Physical Journal Plus*, 135(6), 1-9.
- Bozkurt, F., Yousef, A., Baleanu, D., & Alzabut, J. (2020). **A Mathematical Model of the Evolution and Spread of Pathogenic Coronaviruses from Natural Host to Human Host.** *Chaos, Solitons & Fractals*, 109931.
- Moussaoui, A., & Auger, P. (2020). **PREDICTION OF CONFINEMENT EFFECTS ON THE NUMBER OF COVID-19 OUTBREAK IN ALGERIA.** *Math. Model. Nat. Phenom* 15.
DOI: <https://doi.org/10.1051/mmnp/2020028>
- Upadhyay, R. K., Chatterjee, S., Saha, S., & Azad, R. K. (2020). **Age-group targeted testing for COVID-19 as new prevention strategy.** DOI: 10.21203/rs.3.rs-31786/v1
- Livadiotis, G. (2020). **Statistical analysis of the impact of environmental temperature on the exponential growth rate of cases infected by COVID-19.** *Plos one*, 15(5), e0233875.
- Ndairou, F., Area, I., Nieto, J. J., & Torres, D. F. (2020). **Mathematical modeling of COVID-19 transmission dynamics with a case study of Wuhan.** *Chaos, Solitons & Fractals*, 109846.
- Silva, C. J., Cruz, C., Torres, D. F., Munuzuri, A. P., Carballosa, A., Area, I., ... & Abreu, W. (2020). **Optimal control of the COVID-19 pandemic: controlled sanitary deconfinement in Portugal.** *arXiv preprint arXiv:2009.00660*.



Can India develop herd immunity against COVID-19?

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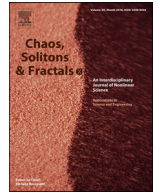
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Abstract World Health Organization declared the novel coronavirus disease 2019 (COVID-19) outbreak to be a public health crisis of international concern. Further, it provided advice to the global community that countries should place strong measures to detect disease early, isolate and treat cases, trace contacts and promote “social distancing” measures commensurate with the risk. This study analyses the COVID-19 infection data from the top 15 affected countries in which we observed heterogeneous growth patterns of the virus. Hence, this paper applies multifractal formalism on COVID-19 data with the notion that country-specific infection rates follow a power law growth behaviour. According to the estimated generalized fractal dimension curves, the effects of drastic containment measures on the pandemic in India indicate that a significant reduction of the infection rate as its population is concern. Also, comparison results with other countries demonstrate that India has less death rate or more immunity against COVID-19.

1 Introduction

The novel coronavirus disease 2019 (COVID-19) is an emerging epidemic responsible for infecting lots of people and killing lakhs globally since the first report till today, according to the World Health Organization (WHO). The WHO China Country Office has informed of cases of pneumonia unknown aetiology detected in Wuhan, Hubei Province of China, on 31 December 2019. A total of 44 case patients with pneumonia of unknown aetiology have reported to WHO by the national authorities in China since 31 December 2019 through 3 January 2020. Further, WHO received the information from the National Health Commission China that the outbreak is associated with exposures in one seafood market in Wuhan on 11 and 12 January 2020. The Chinese authorities identified a new type of coronavirus, which has been isolated on 7 January 2020. China shared the genetic sequence of the novel coronavirus for countries to use in developing specific diagnostic kits. During the period 13–20 January 2020, the Ministry of Public Health, Thailand, reported the first imported case of laboratory-confirmed novel COVID-19 from Wuhan, China, and the Ministry of Health, Labour and Welfare, Japan (MHLW), reported an imported case of laboratory-confirmed COVID-19 from

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A mathematical model of the evolution and spread of pathogenic coronaviruses from natural host to human host

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Allee effect

Neimark-Sacker Bifurcation

ABSTRACT

Coronaviruses are highly transmissible and are pathogenic viruses of the 21st century worldwide. In general, these viruses are originated in bats or rodents. At the same time, the transmission of the infection to the human host is caused by domestic animals that represent in the habitat the intermediate host. In this study, we review the currently collected information about coronaviruses and establish a model of differential equations with piecewise constant arguments to discuss the spread of the infection from the natural host to the intermediate, and from them to the human host, while we focus on the potential spillover of bat-borne coronaviruses. The local stability of the positive equilibrium point of the model is considered via the Linearized Stability Theorem. Besides, we discuss global stability by employing an appropriate Lyapunov function. To analyze the outbreak in early detection, we incorporate the Allee effect at time t and obtain stability conditions for the dynamical behavior. Furthermore, it is shown that the model demonstrates the Neimark-Sacker Bifurcation. Finally, we conduct numerical simulations to support the theoretical findings.

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1. Introduction

According to the International Committee on Taxonomy of Viruses (ICTV), coronaviruses are members of the sub-family *Coronavirinae* in the family *Coronaviridae* and the order *Nidovirales*. *Coronavirinae* consists of four genera groups; α -coronavirus, β -coronavirus, γ -coronavirus, and δ -coronavirus [1,2]. Recently, these groups are divided in terms of phylogenetic clustering while before they were sorted based on serology. All viruses of *Nidovirales* order are enveloped, non-segmented positive-sense RNA viruses, where within this, the *coronaviridae* has the most significant identified RNA genomes, containing approximately 30 kgbases (kb) genomes. On the other hand, all coronaviruses have animal origin [2,3]. Table 1 below shows that the four genera of coronaviruses originated from animals.

The HCoV-NL63 and HCoV-229E are α -coronaviruses that cause mild infections in humans. On the other hand, SARS-CoV, which has swine as an intermediate host role, does not show any

evidence of infections in humans. HCoV-OC43 and HCoV-HKU1 are both β -coronaviruses and are also mostly harmless to the human body that has a rodent-borne origin. HCoV-229E and HCoV-OC43 were isolated nearly 50 years ago, while HCoV-NL63 and HCoV-HKU1 were identified in 2003. Coronaviruses have not considered as highly pathogenic until the outbreak of SARS-CoV in 2003 and MERS-CoV in 2012. The spread of SARS-CoV in China (Guangdong) indicated that a coronavirus was transmitted from bats to an intermediate host like market civets, and from there to the human host, while the outbreak of MERS-CoV in the middle east countries also came from bats to dromedary camels as an intermediate host, and then, it was transmitted to human [4–8]. These viruses cause respiratory and intestinal infections, including fever, dizziness, and cough.

On the 12th of December 2019, a new virus form of *Coronaviridae* was reported in China (Wuhan). The outbreak was associated again with intermediate hosts like reptilians, while the natural host was assumed as bats. This novel virus was designated at first as WH-Human 1 and was referred after that as COVID-19 by the WHO. COVID-19 was characterized by two members of β -coronavirus; human-origin coronavirus (SARS-CoV Tor2) and bat-

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PREDICTION OF CONFINEMENT EFFECTS ON THE NUMBER OF COVID-19 OUTBREAK IN ALGERIA

ALI MOUSSAOUI^{1,*} AND PIERRE AUGER^{2,3}

Abstract. The first case of coronavirus disease 2019 (COVID-19) in Algeria was reported on 25 February 2020. Since then, it has progressed rapidly and the number of cases grow exponentially each day. In this article, we utilize *SEIR* modelling to forecast COVID-19 outbreak in Algeria under two scenarios by using the real-time data from March 01 to April 10, 2020. In the first scenario: no control measures are put into place, we estimate that the basic reproduction number for the epidemic in Algeria is 2.1, the number of new cases in Algeria will peak from around late May to early June and up to 82% of the Algerian population will likely contract the coronavirus. In the second scenario, at a certain date T , drastic control measures are taken, people are being advised to self-isolate or to quarantine and will be able to leave their homes only if necessary. We use *SEIR* model with fast change between fully protected and risky states. We prove that the final size of the epidemic depends strongly on the cumulative number of cases at the date when we implement intervention and on the fraction of the population in confinement. Our analysis shows that the longer we wait, the worse the situation will be and this very quickly produces.

Mathematics Subject Classification. 92B05, 92C60.

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1. INTRODUCTION

The cumulative number since 25 February, when the first case was diagnosed, to present day, is 1761 cases, including 529 from the city of Blida and 310 from Algiers. Since then, the infection has become more virulent, and the number of cases has been increasing. It should be noted that screening remains very low in relation to the means available. Figure 1 shows the cumulative number of detected cases of coronavirus in Algeria between March 01 and April 10, 2020. Between these two dates, the cumulative number of cases increased from 03 to 1761. The spread of the epidemic adjusts very well (which is well known in epidemiology) with an exponential growth for the number of contaminated cases I over time:

$$I(t) = I_0 e^{\lambda t} \quad (1.1)$$

Keywords and phrases: COVID-19, *SEIR* compartmental model, basic reproduction number, time scales, aggregation of variables.

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Age-group-targeted testing for COVID-19 as a new prevention strategy

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Abstract Robust testing and tracing are key to fighting the menace of coronavirus disease 2019 (COVID-19). This outbreak has progressed with tremendous impact on human life, society and economy. In this paper, we propose an age-structured SIQR model to track the progression of the pandemic in India, Italy and USA, taking into account the different age structures of these countries. We have made predictions about the disease dynamics, identified the most infected age groups and analysed the effectiveness of social distancing measures taken in the early stages of infection. The basic reproductive ratio \mathfrak{R}_0 has been numerically calculated for each country. We propose a strategy of age-targeted testing, with increased testing in the most proportionally infected age groups. We observe a marked flattening of the infection curve upon simulating increased testing in the 15–40 year age groups in India. Thus, we conclude that social distancing and

widespread testing are effective methods of control, with emphasis on testing and identifying the hot spots of highly infected populations. It has also been suggested that a complete lockdown, followed by lockdowns in selected regions, is more effective than the reverse.

Keywords Epidemic model · COVID-19 · Age-structured SIQR model · Basic reproductive ratio · Age-targeted testing

1 Introduction

COVID-19, a respiratory disease caused by a new strain of coronavirus (SARS-CoV-2), has spread to almost every part of the world, since first reported in 31 December 2019 [1]. WHO declared this outbreak a ‘Public Health Emergency of International Concern’ on 30 January 2020. As of 30 April 2020, it has caused 2,33,824 deaths with 33,03,544 confirmed cases of infection. Till date, USA has the largest number of fatalities, followed by Italy. USA reports 1,095,023 cases, with 3226 cases per million people, though the statistics have still been evolving due to the large variability in testing performed by different countries as of now [2].

In the absence of any vaccine to prevent and contain the spread of novel coronavirus disease, COVID-19, as well as the lack of an established treatment regimen to cure this disease (beyond mitigation of symptoms),

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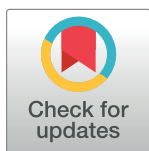
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RESEARCH ARTICLE

Statistical analysis of the impact of environmental temperature on the exponential growth rate of cases infected by COVID-19

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Southwest Research Institute, San Antonio, TX, United States of America

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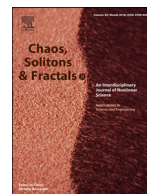
Abstract

We perform a statistical analysis for understanding the effect of the environmental temperature on the exponential growth rate of the cases infected by COVID-19 for US and Italian regions. In particular, we analyze the datasets of regional infected cases, derive the growth rates for regions characterized by a readable exponential growth phase in their evolution spread curve and plot them against the environmental temperatures averaged within the same regions, derive the relationship between temperature and growth rate, and evaluate its statistical confidence. The results clearly support the first reported statistically significant relationship of negative correlation between the average environmental temperature and exponential growth rates of the infected cases. The critical temperature, which eliminates the exponential growth, and thus the COVID-19 spread in US regions, is estimated to be $T_C = 86.1 \pm 4.3 \text{ F}^\circ$.

1. Introduction

The daily number of new cases infected by COVID-19 is currently exponentially growing for most countries affected by the virus. However, this exponential growth rate varies significantly for different regions over the globe. It is urgent and timely to understand the reasons behind this regional variation of the exponential growth rates. Little information is known about this matter, while there are indications that the environmental temperature may be a factor; for instance, northern and colder US and Italian regions experienced much more incidents than others.

Typically, the evolution curve of the spread of the coronavirus initiates with a pre-exponential phase, which is characterized by a mild logarithmic growth, followed by the outbreak, that is, the phase of the exponential growth. Social-distancing measures against the spread may affect the evolution curve in a way that the exponential growth slows down (decelerated phase) and starts to decline (decline or decay phase [1]), depending though on the effectiveness and applicability of these measures. However, after the decline of the spread at some place, new infected cases may outbreak in other places, marked with insignificant number of cases until



Mathematical modeling of COVID-19 transmission dynamics with a case study of Wuhan

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Numerical simulations

ABSTRACT

We propose a compartmental mathematical model for the spread of the COVID-19 disease with special focus on the transmissibility of super-spreaders individuals. We compute the basic reproduction number threshold, we study the local stability of the disease free equilibrium in terms of the basic reproduction number, and we investigate the sensitivity of the model with respect to the variation of each one of its parameters. Numerical simulations show the suitability of the proposed COVID-19 model for the outbreak that occurred in Wuhan, China.

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1. Introduction

Mathematical models of infectious disease transmission dynamics are now ubiquitous. Such models play an important role in helping to quantify possible infectious disease control and mitigation strategies [1–3]. There exist a number of models for infectious diseases; as for compartmental models, starting from the very classical SIR model to more complex proposals [4].

Coronavirus disease 2019 (COVID-19) is an infectious disease caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). The disease was first identified December 2019 in Wuhan, the capital of Hubei, China, and has since spread globally, resulting in the ongoing 2020 pandemic outbreak [5]. The COVID-19 pandemic is considered as the biggest global threat worldwide because of thousands of confirmed infections, accompanied by thousands deaths over the world. Notice, by March 26, 2020, report 503,274 confirmed cumulative cases with 22,342 deaths. At the time of this revision, the numbers have increased to

1,353,361 confirmed cumulative cases with 79,235 deaths, according to the report dated by April 8, 2020, by the World Health Organization.

The global problem of the outbreak has attracted the interest of researchers of different areas, giving rise to a number of proposals to analyze and predict the evolution of the pandemic [6,7]. Our main contribution is related with considering the class of super-spreaders, which is now appearing in medical journals (see, e.g., [8,9]). This new class, as added to any compartmental model, implies a number of analysis about disease free equilibrium points, which is also considered in this work.

The manuscript is organized as follows. In Section 2, we propose a new model for COVID-19. A qualitative analysis of the model is investigated in Section 3: in Section 3.1, we compute the basic reproduction number R_0 of the COVID-19 system model; in Section 3.2, we study the local stability of the disease free equilibrium in terms of R_0 . The sensitivity of the basic reproduction number R_0 with respect to the parameters of the system model is given in Section 4. The usefulness of our model is then illustrated in Section 5 of numerical simulations, where we use real data from Wuhan. We end with Section 6 of conclusions, discussion, and future research.

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Optimal control of the COVID-19 pandemic: controlled sanitary deconfinement in Portugal

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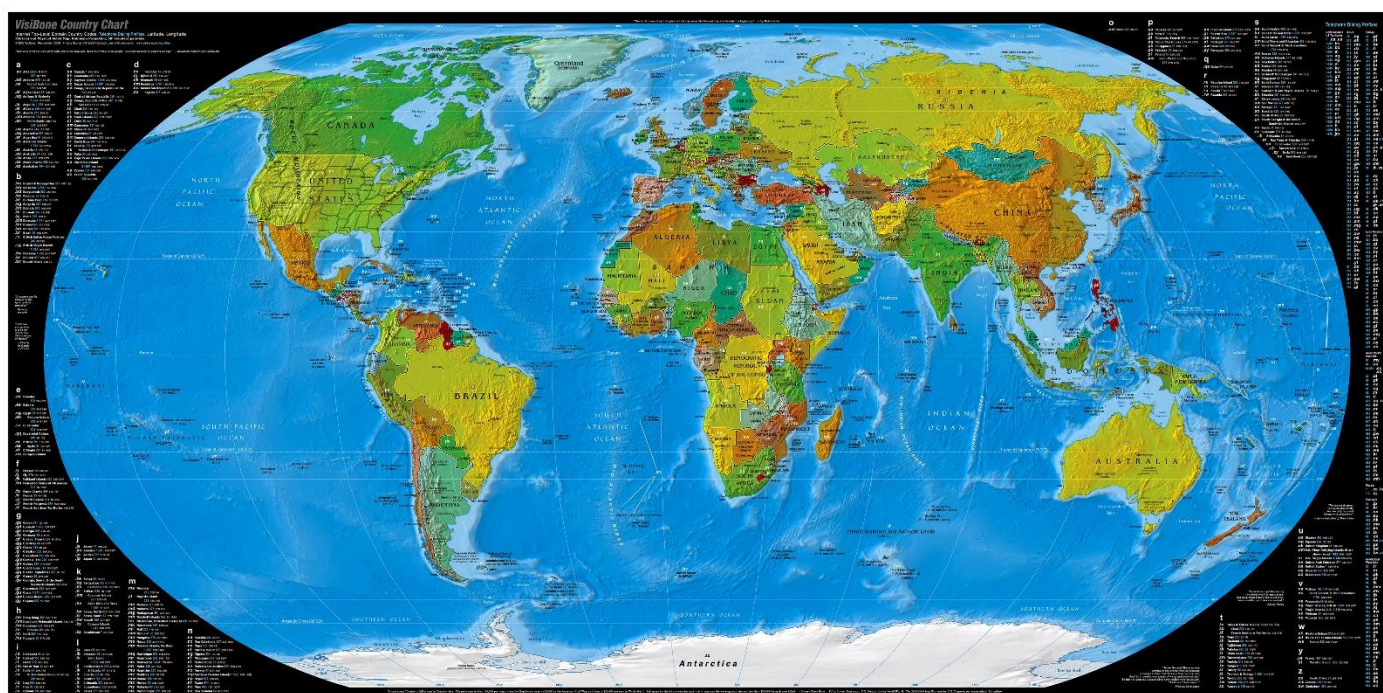
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Abstract

The COVID-19 pandemic has forced policy makers to decree urgent confinements to stop a rapid and massive contagion. However, after that stage, societies are being forced to find an equilibrium between the need to reduce contagion rates and the need to reopen their economies. The experience hitherto lived has provided data on the evolution of the pandemic, in particular the population dynamics as a result of the public health measures enacted. This allows the formulation of forecasting mathematical models to anticipate the consequences of political decisions. Here we propose a model to do so and apply it to the case of Portugal. With a mathematical deterministic model, described by a system of ordinary differential equations, we fit the real evolution of COVID-19 in this country. It is complemented with an analysis of the Portuguese social network, which allows detecting changes in public opinion and provides a feedback to update the model parameters. With this, we apply control theory to maximize the number of people returning to “normal life” and minimizing the number of active infected individuals with minimal economical costs while warranting a low level of hospitalizations. This work allows testing various scenarios of pandemic management (closure of sectors of the economy, partial/total compliance with protection measures by citizens, number of beds in intensive care units, etc.), ensuring the responsiveness of the health system, thus being a public health decision support tool.

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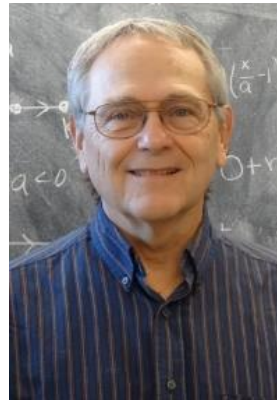
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