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Modelling the dynamics of exchanged novel coronavirus (2019-nCov) between regions in terms of time and space

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ABSTRACT

To date, many models have been proposed which estimate the transmission risk of COVID-19 in terms of time; however, its dependency on space dimensions has been ignored. In this research, by multiplying risk parameters in certain regions and bridging, we obtain a stable action, which means that the transmission risk worldwide could shrink to a constant. Thus, by increasing the risk parameters in one region, the risk parameters in other regions decrease. Then, by adding space dimensions to the parameters in transmission risk models, and using the wave equations of manifolds for the regions, we obtain the dynamics of the exchanged novel coronavirus (2019-nCov) between countries. We calculate the risk factors of COVID19 for different regions in this model, and observe that they are in good agreement with experimental data.

I. Introduction

The coronavirus epidemic (COVID-19) is the main problem this year that affects all people in the world (Baud et al., 2020). This is an infectious disease caused by a newly discovered coronavirus. This virus is a member of related viruses that cause diseases in mammals and birds. In humans, coronaviruses cause respiratory tract infections that can be mild, such as some cases of the common cold (among other possible causes, predominantly rhinoviruses), and others that can be lethal, such as SARS, MERS, and COVID-19. Among them, COVID-19 is an enveloped viruse with a positive-sense single-stranded RNA genome and a nucleocapsid of helical symmetry. The genome size of coronaviruses ranges from approximately 27 to 34 kilobases, the largest among known RNA viruses (Fehr et al., 2015; Sexton et al., 2016). Until now, many scientists have tried to find methods to cure this disease (Hui David et al., 2019; Wang et al., 2020). Also, many models have been proposed to consider the growth rate of the transmission risk factor for COVID19 (Anzai et al., 2020; Cojocaru et al., 2020; Kaplan, 2019; Khan & Atangana, 2020; Nishiura et al., 2020; Tang et al., 2020a, 2020b). For example, in (Khan & Atangana, 2020), the authors have considered the mathematical modelling and dynamics of the novel corona virus (2019-nCoV). They have described the brief details of interaction among bats and unknown hosts, and then among people and the infection reservoir (seafood market) (Khan & Atangana, 2020). In parallel, another group has estimated the risk of transmission of the novel coronavirus

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(2019-nCov). They have estimated when the effective daily reproduction ratio will fall below 1, and when the epidemic will peak (Tang et al., 2020a). In (Tang et al., 2020b), the authors have adopted a deterministic model to shed light on the transmission dynamics of the novel coronavirus, and assess the impact of public health interventions on infection (Tang et al., 2020b).

In another work, the impact of reduced travel on the exportation dynamics of the novel coronavirus infection (COVID-19) has been considered. It has been shown that the decision to control travel volume through restrictions on freedom of movement should be balanced between the resulting estimated epidemiological impact and predicted economic fallout (Anzai et al., 2020). In another paper, the authors have estimated the rate of under-ascertainment of the novel coronavirus (2019-nCoV) infection. They have done this estimation by using Japanese passenger data on evacuation flights. Assuming that the mean detection window of the virus can be informed by the mean serial interval (estimated at 7.5 days), the ascertainment rate of infection was estimated at 9/100 (Nishiura et al., 2020). In another research, it has been argued that given that a vaccine cannot be developed and deployed for at least a year, preventing further transmission relies upon standard principles of containment, two of which are the isolation of known cases and the quarantine of persons believed at high risk of exposure. That article has presented probability models for assessing the effectiveness of case isolation and quarantine within a community during the initial phase of an outbreak with illustrations based on early observations from Wuhan (Kaplan, 2019). In other investigation, the authors have discussed controlling infection in predator-prey systems with transmission dynamics. They have illustrated if and when applying such preventive treatments leads to a disease prevalence drop in both populations. They have conducted their study using an optimal control model seeking to minimize the treatment cost(s), subject to the transmission dynamics and predator-prey dynamics (Cojocaru et al., 2020).

Motivated by these works, we propose a theory which lives on an (n + m)-dimensional manifold with two regional manifolds and one bridge manifold. We will show that our region is a part of bigger manifold which is connected with other regional manifold by an extra bridge manifold. Two regional manifolds interact with each other via exchanging fields which move along the bridge manifold. These fields are the main cause for the appearance of transmission risk factors in the model.

This paper consists of two main parts. In section II, we show that by adding a bridge manifold to regional one, transmission risk theory is applicable. In section III, we obtain the risk parameters and compare with experimental data.

II. Total action for exchanging COVID19 between countries

Until now, the dependency of transmission risk factors on time has been considered extensively. However, their dependencies on the location have been ignored. In this research, we suggest a model which lets us consider the process of viral transmission between different regions at the same time. In this model, we will make use of some concepts in string theory, and show that all equations in transmission risk theory could be obtained from the string action. In fact, populations seems to be similar to some strings which move between different regions. The behaviour of the infectious, non-infectious and exposed components are similar to gauge, infectious and scalar fields in string theory. This consideration helps us to predict a new pandemic for COVID19.

In Fig. 1, we present the basis of our theory. In this theory, there are two manifolds, each of which includes 8 regions or countries. Also, there is a bridge manifold which includes three regions or countries. The first manifold presents countries which are the origin of COVID19. The bridge manifold depicts countries through which humans travel to a second manifold. The second manifold comprises countries which are targeted by COVID19. Travelling between countries are represented by strings (X). We could formulate this model by using concepts from string theory, and compare with previous results that have been obtained.

Firstly, let us introduce the action of the regional manifold which could be written similar to the acton of strings and is given by (Grignani et al., 2017):

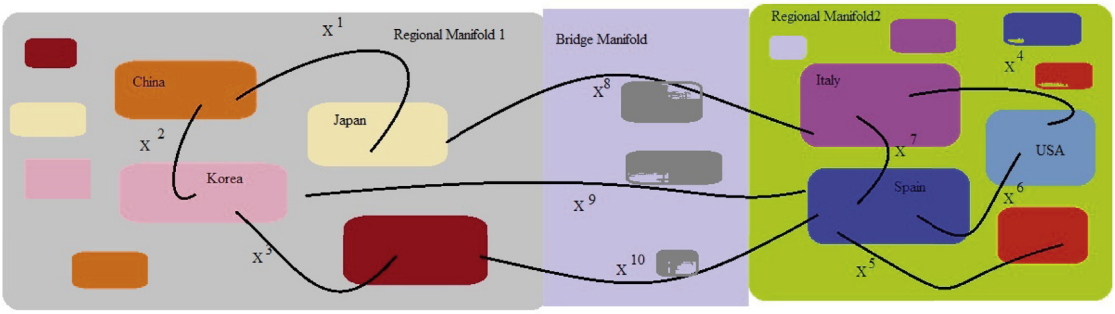

Fig. 1. Two manifolds, each of which includes 8 regions that are connected by a bridge manifold. Exchanged humans are represented by strings.

$$\begin{aligned} &S_{Pendamic-COVID19} = -\int d^n y \sqrt{-\det\left(\overline{\gamma}_{ab} + \left[2\pi l_P^2\right] COV_{ab}\right)}, \\ &\overline{\gamma}_{ab} = g_{\mu\nu}\partial_a P^\mu \partial_b P^\nu, \\ &COV_{ab} = \partial_a C_b - \partial_b C_a \end{aligned} \tag{1}$$

where y is the space-time coordinate for each country or region, C_b is the COVID19 field, COV_{ab} is the field strength related to it, P^μ is the pandemic function for this disease, $g_{\mu\nu}$ is the metric and l_s is the pandemic length. Also, indices (a,b $\mu\nu$) correspond to the countries. For example, for a country like China, we can put $(\mu,\nu = 1,1)$, while for Italy $((\mu,\nu = 3,2))$. By using these indices, we can associate a number to each country, and consider the regional dependency of transmission risk factors. Substituting $P^0 = t$ and doing some mathematical calculations, the action of the regional manifold in equation (1) is given by:

$$S_{Pendamic-COVID19} = -\int d^n y \sqrt{1 + g_{ij}\partial_a P^i \partial^a P^j - 4\pi^2 l_P^4 CO_{ab} CO^{ab}}, \tag{2}$$

This action is not anomaly free. Thus, a bridge action is necessary for anomaly cancellation. Our goal now is to find a good rationale for its inclusion. To this end, we choose a unified form for all transmission risks by using Nambu-Poisson brackets and properties of pandemic fields (P). We write: (Grignani et al., 2017):

$$\begin{aligned} &P^I \approx y^I + y_J COV^{IJ} + y_J \partial^I D \partial^J D \\ &\Rightarrow \left\{P^I, P^J\right\} = \Sigma_{IJ}\varepsilon^{I'J'}\frac{\partial P^I}{\partial y^{I'}}\frac{\partial P^J}{\partial y^{J'}} = COV^{IJ} + \partial^I D \partial^J D + \ldots. \end{aligned} \tag{3}$$

where D is the death parameter. Using N-dimensional instead of 2-dimensional brackets, we may derive the total pandemic term $TOTP_{I_1\ldots I_N} TOTP^{I_1\ldots I_N}$ in the world (Grignani et al., 2017):

$$\begin{aligned} &TOTP^{I_1\ldots I_N} = \left\{P^{I_1}, \ldots., P^{I_N}\right\} = \varepsilon^{I_1\ldots I_N}\frac{\partial P^{I_1}}{\partial y^{I_1}}\ldots..\frac{\partial P^{I_N}}{\partial y^{I_N}} \\ &\Downarrow \\ &S_{\text{cov1}}^{N=n} = \int d^n x\sqrt{g}\left(TOTP_{I_1\ldots I_N} TOTP^{I_1\ldots I_N}\right) = \\ &\int d^n x\sqrt{g}\left(\varepsilon^{I_1\ldots I_N}\frac{\partial P^{I_1}}{\partial y^{I_1}}\ldots..\frac{\partial P^{I_N}}{\partial y^{I_N}}\varepsilon_{I_1\ldots I_N}\frac{\partial P_{I_1}}{\partial y_{I_1}}\ldots..\frac{\partial P_{I_N}}{\partial y_{I_N}}\right). \end{aligned} \tag{4}$$

where N is the number of countries. Equation (4) helps us to extract the bridge terms from the total pandemic terms. To this aim, we will add a bridge manifold to the regional manifold, which connects it to the other regional manifold by applying the properties of (P) in Nambu-Poisson brackets (Grignani et al., 2017):

$$\begin{aligned} &P^I \approx y^I + y_J COV^{IJ} + y_J \partial^I D \partial^J D - + \ldots \\ &\Downarrow \\ &\frac{\partial P^{I_m}}{\partial y^{I_m}} \approx \delta\left(y^{I_5}\right) + \ldots, \\ &\int\limits_{M^{N=m}} \rightarrow \int\limits_{y^{I_1}+\ldots+y^{I_m}} \varepsilon^{I_1\ldots I_m}\frac{\partial P^{I_1}}{\partial y^{I_1}}\ldots\frac{\partial P^{I_m}}{\partial y^{I_m}} = 1 + \ldots, \end{aligned} \tag{5}$$

where ellipses (…) were used to represent higher-order derivatives. Extending the manifold over the additional dimensions extends the integration volume element. By extending the regional manifold in Eq. (4) with the bridge manifold of Eq. (5), we get (Grignani et al., 2017):

$$S_{bridge}^{N=n+m} = \int d^{n+m} x\sqrt{g}\left(Bridge_{I_1\ldots I_m} TOTP_{I_1\ldots I_N} TOTP^{I_1\ldots I_N}\right) \tag{6}$$

where we make the identification (Grignani et al., 2017):

$$Bridge_{I_1\ldots I_m} = \varepsilon^{I_1\ldots I_m}\frac{\partial P^{I_1}}{\partial y^{I_1}}\ldots\frac{\partial P^{I_m}}{\partial y^{I_m}}, \tag{7}$$

Thus, the total action can be written as:

$$S^{N=n+m}_{tot-Pendamic-COVID19} = S^{N=m}_{cov1} + S^{N=n}_{cov1} + S^{N=n+m}_{bridge} \tag{8}$$

The above action is anomaly free because, pandemic fields in two different regions act opposite each other. By increasing the parameters in one action, the parameters in another action decrease. This means that by the growth of covid19 in one region, covid19 in the other region reduces.

III. Testing the model with data

Previously, a method for calculating the Hamiltonian of the action in equation (8) has been proposed. Following (Grignani et al., 2017), we obtain:

$$H^{N=n+m}_{tot-Pendamic-COVID19} = -\int d^{n+m}y\sqrt{1+\left[g_{ij}\partial_a P^i \partial^a P^j\right]^{2n+2m}}F_{n+m} \tag{9}$$

$$F_{n+m} = -\sqrt{1+\frac{k^{2n+2m}_{n+m}}{(t-t_{0-n+m})^{2n+2m}\left[1+\frac{k^{2n+2m-1}_{n+m-1}}{(t-t_{0-n+m})^{2n+2m-1}}\left[1+\ldots\frac{1}{1+\frac{k^2_1}{(t-t_{0-1})^2}}\right]\right]}} \tag{10}$$

Substituting the definition of P in equation (3) into equation (10) and using equations (1)–(8), we can obtain the approximate solutions for the death parameter as:

$$D^i \sim e^{-\int dtG[t,t_{0-1},t_{0-2},\ldots t_{0-n+m-i}]}R[t,t_{0-1},t_{0-2},\ldots t_{0-n+m-i}] \tag{11}$$

where

$$G[t,t_{0-1},t_{0-2},\ldots t_{0-n+m-i}] \sim \Pi^{2n+2m}_{j=1}\frac{F_{n+m}(t_i)}{F_{n+m}(t)-F_{n+m}(t_i)}$$

$$R[t,t_{0-1},t_{0-2},\ldots t_{0-n+m-i}] \sim \left[1+\Sigma^i_{j=1}G^j\right]^{-1} \tag{12}$$

Now, we could obtain the probability of death in terms of time for COVID9 in two different countries (See Figs. 2–4). It is clear that with time, the pandemic rate grows, turns over some peaks, and then decreases. However, decreasing the pandemic

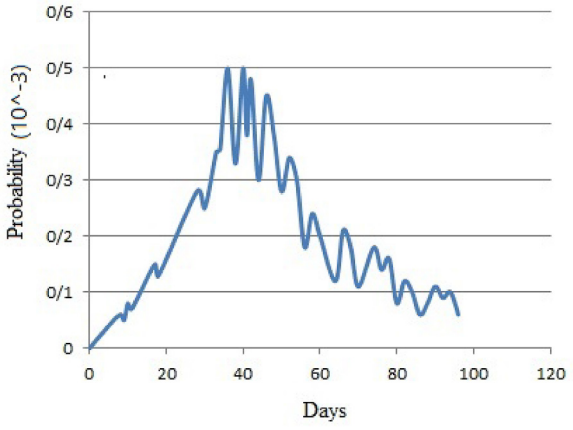

Fig. 2. The probability of death in terms of time for COVID9 ($t_{0-i} = 31i, n = 200, m = 51$). Probabilities could have a coefficient of order 10^{-3}, less or more. This is very the same the pandemic in Europe (Lescureet al, 2020).

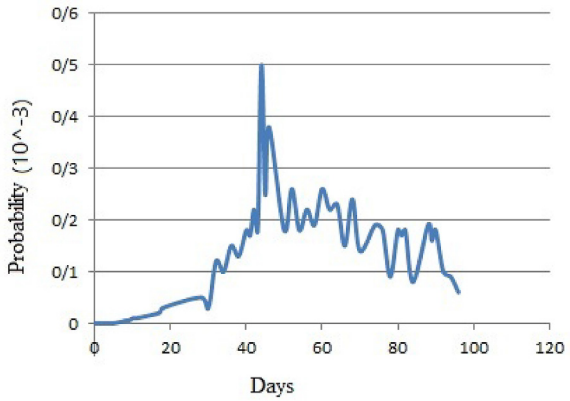

Fig. 3. The probability of death in terms of time for COVID9 ($t_{0-i} = 45i, n = 200, m = 23$). Probabilities could have a coefficient of order 10^{-3}, less or more. This is very similar to the pandemic in North-America (Lescureet al, 2020).

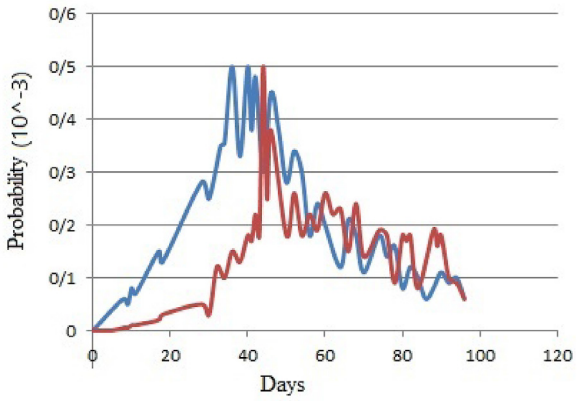

Fig. 4. Comparing the probability of death in terms of time for COVID9 in two different regions. (Probabilities could have a coefficient of order 10^{-3}, less or more.)

rate in one country or region, the virus will be injected into other country, and a new growth in the pandemic rate in other part of the world could be observed. The maximum growth rate in the world seems to be a constant; however, this maximum is exchanged between different countries.

IV. Summary and conclusion

In this research, we have considered the dynamics of exchanged novel coronaviruses (2019-nCov) between countries. We have shown that this action is produced due to the interaction between regional manifolds in (n + m)-dimensional space-time. We have calculated the risk factors of COVID19 and examined our model against experiments. We have shown that multiplying the risk transmission parameters gives a stable action. This means that by increasing these factors in one region, the ones in another region decrease.

Declaration of competing interest

There is no conflict of interest for this paper.

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