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Coronavirus and Migration: Analysis of Human Mobility and the Spread of COVID-19

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Abstract

Reactions, measures as well as discourses dealing with the current pandemic vary significantly across the world. While some countries were completely locked down, as was the case in Italy, some had claimed to have very few or no cases, as was the case in Turkey and Indonesia by March 10th, 2020. Nevertheless, the spread of COVID-19 from China has been clearly linked to those travelling from Wuhan in Hubei province in Central China. Therefore, it is important to understand the travel density/volume of passengers carried as well as routes from Wuhan through connected main regional air travel hubs across China. In this study, we developed a model on migration and travel intensity that can explain outbreak and spread of COVID-19 since it appeared at the end of 2019. We show that the presence of migrant stock populations of Chinese origin and the immigrant stock in China are useful indicators in the prediction of the spread of the outbreak worldwide in the event of interaction with several other macro factors. We argue that monitoring immigrant stock data and travel volume data based on human mobility corridors (i.e. origins and destinations), countries could have been better prepared and taken early measures to contain the spread of COVID-19.

Keywords: *Coronavirus; COVID-19; epidemic; migration; human mobility; air travel; spatial diffusion; public health; China; Italy; France; Germany; Spain; UK; USA; Turkey.*

Introduction

COVID-19 / 2019-nCoV or Coronavirus as commonly known, has probably been as terrifying as the Spanish Flu and Swine Flu (Jilani *et al.,* 2019). We have written this article at a relatively early stage of the pandemic. Therefore, the number of cases and death toll were rising[3] but not as shocking as these historic pandemics. However, still reactions, measures, as well as accompanying political discourses vary greatly across the world, while some countries are regionally locked down as was the case in Italy by 21st of February 2020[4], some others claim there is none or a few cases only as was the case in Turkey and Indonesia by 10th of March 2020.

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[3] Worldwide number of infected people were 666,211 along with 30,864 deaths by 29 March 2020.

[4] Complete, nationwide, lockdown was announced on 9th March 2020.

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The origin of COVID-19 pandemic, initially, has been linked (i.e. suspected but not yet confirmed) to the cases identified in Wuhan, the capital of Hubei province in Central China.[5] Therefore, it is important to take into account the travel density / volume of passengers carried and routes from Wuhan through connected main regional air travel hubs across China along with the final destinations abroad relating to many of these travellers. The travel volumes are likely to be linked to the Chinese immigrant stock populations in these destination countries following the cultures of migration model, which suggests increasing mobility and traffic between countries of destination and origin over time (Cohen and Sirkeci, 2011).

According to the World Health Organisation (WHO, 2020a), coronaviruses (CoV) are a large family of viruses that cause illness ranging from the common cold to more severe diseases, such as Middle East Respiratory Syndrome (MERS-CoV) (WHO, 2020d) and Severe Acute Respiratory Syndrome (SARS-CoV) (WHO, 2020e). The most recent coronavirus, also known as COVID-19, has not been previously observed in humans, with these types of viruses being known to be transmitted between animals and humans (WHO, 2020f). This was confirmed when the earlier cases were identified in Wuhan, China (Chan *et al.*, 2020). Symptoms of COVID-19 are also known to be similar to common flu, but the spread is much speedier. These symptoms include fever, cough, and breathing difficulties and unfortunately can lead to death (WHO, 2020a). Therefore, the risks to public health are grave and cannot be ignored without serious risk of casualties. In sum, the COVID-19 pandemic is now a major health threat globally (Ferguson *et al.,* 2020: 3). As of 1 April 2020, there have been 905,279 cases and 45,371 deaths confirmed worldwide and the global spread has been extremely rapid (ECDC, 2020).

The purpose of this article is to offer insights using international migration data taking into account a series of basic macro indicators. We argue that monitoring immigrant stock data and travel volume data based on human mobility corridors (i.e. origins and destinations), countries could have been better prepared and taken much earlier measures to contain the spread of COVID-19 or other similar diseases. After introducing the conceptual framework, we explain the data and methods used, following which we discuss our findings, having mapped clusters of countries based on their profiles and numbers of COVID-19 cases. In the subsequent section, we discuss the results of a regression model, which can be used in predicting the potential spread of a pandemic, thereby providing more effective targeted and timely responses to similar outbreaks in the future. Lastly, the limitations of this study and some future avenues for research are presented.

Conceptualising the Spread of Virus and Migration Relationship

We have looked at two sets of literature to gain an understanding the current COVID-19 spread crisis: human mobility/migration literature and studies on the spatial spread of diseases. One of the models in migration literature, namely "cultures of migration", argues that over time, i.e. as migration experiences accumulate in an area and through a route between the origin and destination, mobility continues almost irrespective of changes in the drivers of migration that were in place at the beginning (Cohen and Sirkeci, 2011; Cohen, 2004). Thus, we expect an increasing volume of migration over time through established migration corridors. This can be measured by examining

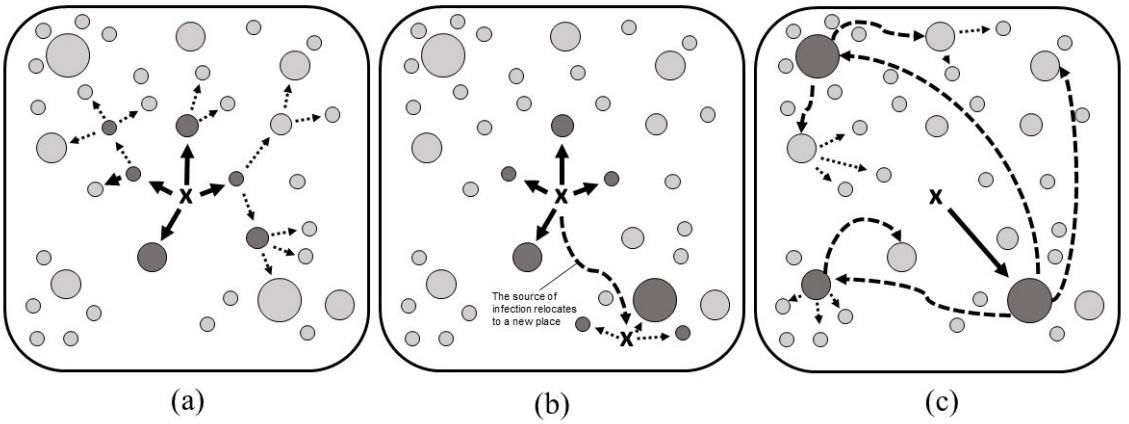
[5] According to a World Health Organisation report the source of the virus has not been confirmed yet (https://www.who.int/docs/default-source/coronaviruse/who-china-joint-mission-on-COVID-19-final-report.pdf), while a recent study has established two different strains of the virus: one prevalent in Wuhan, and the other being found everywhere else (https://www.researchgate.net/publication/339461351_Variant_analysis_of_COVID-19_genomes). It should be noted that, whilst the virus was first diagnosed in Wuhan this does not prove that it originated there.

the volume of travel between destinations and place of origin. Therefore, we are expecting a correlation between the travel volume between a country of origin and a destination country and immigrant stock of a group in the latter. Hence, mapping the volume of migration flows from the origin of a disease can be useful in understanding the spread and thus, being equipped to set up appropriate containment measures. In the current COVID-19 crisis, this potential proxy indicator seems to be underestimated despite the mass flight cancellations declared in February and March 2020.

It is argued that the increase in emerging infectious diseases[6] is related to environmental change and to human encroachment into remote areas, which increases the contact between human and non-human species, thereby allowing for cross-species transfers of pathogens (Mayer, 2000; Anthamatten and Hazen, 2011). For example, the emergence of SARS in China in 2003 was linked to close contact between humans and the Himalayan palm civet, sold as meat in Chinese markets (Klempner and Shapiro, 2004; Anthamatten and Hazen, 2011: 41-42), whilst the most recent case of COVID-19 has been linked to bats (Lai *et al.*, 2020a).

Disease spread patterns are known to be moderated by human activities ranging from agriculture to conflicts, however, further critical insights may be found in spatial approaches to health (Jones *et al.*, 2008: 91; Anthamatten and Hazen, 2011: 42). Spatial approaches help us understand diffusion patterns of emerging infectious diseases. Diffusion refers to the spread of an phenomenon across space. Anthamatten and Hazen (2011) identified three primary types of diffusion (Figure 1).

Figure 1. Three types of spatial-diffusion patterns of viruses and/or contagious diseases



Note: (a) Expansion diffusion; (b) Relocation diffusion; (c) Hierarchical diffusion; The "x" symbolizes the original source of diffusion and the circles symbolize population settlements; larger circles represent larger settlements, and bold circles represent infected settlements.
Source: This figure was prepared based on Anthamatten and Hazen (2011: 44)

Spread of viruses outward from a source is called *expansion diffusion*. Diseases, such as COVID-19, as well as simple head lice, that spread by direct transmission are referred to as

[6] COVID-19 is not unique in one respect in that about 30 deadly diseases have been identified since the 1980s (Walters, 2003). If we also consider the new strains of existing diseases, the figures are even higher, whereby 335 infectious diseases emerged between 1940 and 2004 (Jones et al., 2008). HIV-1 and SARS are considered to be completely new to human populations (Anthamatten and Hazen, 2011: 41).

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contagious diffusion. On the other hand, with *relocation diffusion*, a virus is introduced to a location outside its original range, this often coming with migration, which moves specific cultural practices as well as diseases. A historical example is the introduction of smallpox to the Americas by the conquistadors, whilst a more recent one is the epidemic of cholera that affected Latin America in 1991. This was thought to have been initiated by the release of the cholera pathogen in Peru by a ship arriving from Asia (Mayer, 2000; Anthamatten and Hazen, 2011: 42). It is clear that in the era of super-mobility and ubiquitous connectedness[7], air travel carries pathogens rapidly across the globe (Anthamatten and Hazen, 2011: 42). This was the case in 2003 when SARS quickly spread via air passengers around the world. Pathogens and vectors can be transported rapidly with travel and also by transported goods (Masterton and Green, 1991; Anthamatten and Hazen, 2011: 42). For instance, outbreaks of food poisoning have been traced to shipments of food arriving from abroad. Ho *et al.*, (2002) stated that since 1995, several US outbreaks of cyclosporiasis have been connected to raspberries imported from Guatemala (Anthamatten and Hazen, 2011: 44).

Hierarchical diffusion assumes a spatial hierarchy in the spreading of things. In particular, large metropolitan areas see a much speedier spread of diseases compared to small villages. This is simply due to the sheer number of people and goods travelling in and out of such large settlement areas. Due to population density, among other features, proliferation of diseases in cities is faster as people interact with each other in many public spaces (Anthamatten and Hazen, 2011: 45). The early diffusion of Acquired Immune Deficiency Syndrome (AIDS) in the US is an example of hierarchical diffusion. It had started in a few large cities at first, but over a decade it had spread beyond, first to other cities and then to smaller towns. The spread of HIV in Sub-Saharan Africa saw a very similar pattern[8] (Gould, 1993; Anthamatten and Hazen, 2011: 45).

Data and Method

The chronology of reporting of the COVID-19 cases is important for our analysis. It was first the case that undiagnosed cases marked by pneumonia in people associated with a seafood market appeared in Wuhan, Hubei Province, China, which were reported on 31 December 2019 (e.g. Holshue *et al.*, 2020). Chinese authorities[9] reported this cluster of cases and confirmed the coronavirus for the first time on 11 January 2020 in the Wuhan Municipal Health and Health Commission's Report on Unexplained Viral Pneumonia (NHCPRC, 2020a, 2020b). A local doctor in Wuhan had apparently been alerting others to the potential coronavirus cases as early as mid-December 2019. The development of the symptoms for the COVID-19 seemingly confirms such a start date (Chan *et al.*, 2020). The earliest date for spotting the first COVID-19 case appears as being 17 November 2019, although it was not recognised as such at that time (Ma, 2020) and inadvertently, it was carried to other countries (Lipsitch *et al.*, 2020). This means all countries were exposed to the unchecked spread of the virus between up until mid-January in the case of China, whilst laggard countries failed to take any action until the middle March (e.g. Turkey). Hence, millions of more interactions took place, including trips to and from China and other connected destinations until social distancing and other stricter measures were put in place.

The first case in the USA was diagnosed on 19 January 2020, and the first in Italy was diagnosed on 31 January 2020. For many other countries, reports of the first cases came much later.

[7] For connectedness and connected consumers, see Sirkeci (2013).

[8] HIV/AIDS rates in rural areas of Ghana were higher than those in urban areas throughout the course of its epidemic (Oppong, 1998; Anthamatten and Hazen, 2011: 45).

[9] Information comes from the official website of the National Health and Health Commission in the People's Republic of China.

For example, Turkey announced the first case on 11 March 2020 (McKernan, 2020). In these countries, the number of cases has been rapidly rising since soon after the first one were reported[10], which means the virus has been spreading unchecked for a lengthy period. It has been well documented that, without measures preventing spread, the number of infected people will increase much more rapidly than were this not the case. The United Kingdom has been one of the laggard countries, where practically no measures were in place until early March against the spread of COVID-19 (Hunter, 2020).

In our exploration of the spread of the disease, some assumptions were formulated. First, we assumed a normal distribution of the cases diagnosed in Wuhan, Hubei, China. We have calculated the crude rate for COVID-19 cases in Hubei province by dividing the number of cases recorded by the total population and each resident in the province is assumed to have had an equal chance of being infected by this virus. This leads to the second assumption: the same crude rate of COVID-19 spread (CRS) is true for the people who have travelled from Wuhan. Accordingly, we have estimated the CRS for Hubei province, as abovementioned, the region of the origin, in China. The CRS for the province is estimated to be 1.14 per thousand through the formula (1) [i.e. the number of diagnosed cases (c) divided by the total population (p)]:

$$CRS = c/p \times 1000 \qquad (1)$$

This gives us a probable number of people infected who travelled abroad. These numbers of infected travellers are pro-rata distributed to destination countries, according to the volume of travel to each destination. This is the number of infected people that arrived in each country, which should be treated as the minimum number of cases for each destination at the beginning of the pandemic.

We first established the correlation (see Table 1c, Appendix) between migration data and Wuhan's air travel data, as the latter was not available for all countries, to understand the link between human mobility and the spread of COVID-19. We used the 2017 data on immigrant stock in all countries (WB, 2020) as an indicator of travel intensity between countries. In addition, we included some other contextual indicators that may have been moderating the relationship between these independent variables and the dependant variable (i.e. the number of cases of COVID-19 reported by World Health Organisation - WHO). We tested the Gross National Income (GNI) and Human Development Index (HDI) as potential indicators of the macro environment and decided to use HDI as it reflects a much more holistic picture of individual countries. Population size and population density alongside median age were included in our analyses as moderating demographic variables. We also used the Cato Institute's Human Freedom Score (HFS) (CATO, 2020) to control for the possibility of some countries not accurately reporting the COVID-19 cases and related death statistics. We created cross-tabulations summarising the number of cases, the number of deaths according to the WHO (2020a,b,c), airline travellers volumes from Lai *et al.* (2020b: 15) and Chinese migrant stock from WB (2020) in top 30 destination countries along with the probable number of cases in these destinations using the CRS (Tables 1a and 1b, Appendix).

Methodologically, firstly we used correlation analysis to understand the relationship between the number of COVID-19 cases of infection and death as well as potential moderating factors, where the focus is on human mobility drivers (Table 1c, Appendix). Secondly, we ran multivariate regression models to understand the determinants of the number of COVID-19 cases by country.

[10] For earlier analyses of such a development, see: https://freelonia.org/coronavirus-italian-job/ and https://freelonia.org/gec-kalan-ulkelerde-vaka-sayisi-hizla-artiyor/

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This can also offer a basis for developing a predictive model. Thirdly, we used cluster analysis in order to determine the spatial clustering with the exploratory data from the selected 111 countries[11]. The above described analyses were carried out using the IBM PASW Statistics (Predictive Analytics Software Statistics) program. Cluster analysis was calculated using the k-means algorithm[12]. Cluster analysis is one of the most widely used methods of statistical analysis in social sciences (Rencher, 2002). It considers the similarities of individuals, objects, or spatial units (countries in this study) and groups them into two or more sub-groups (Everitt and Dunn, 1991; Afifi and Clark, 1999; Rencher, 2002; Addio and Ercole, 2005; Yüceşahin and Tulga, 2017). The analysis indicates the spatial units (countries) assigned to the same cluster that are similar in terms of the values of the variables.

Findings and Discussion

We, first, examined the patterns of COVID-19 spread around the world and identified four clusters of countries reflecting their profiles and the volume of cases and deaths along with some key macro indicators as moderating factors. We explored the global data and what has been reported by individual countries and tried to understand the patterns in relation to immigrant stocks from China along with other contextual factors. The following equations were used in the three multivariate regression models run to assess the relative importance of different factors in explaining the total number of COVID-19 cases (TCC), i.e. our dependent variable (Table 1 and 2):

$$\hat{y}= \beta_0 \text{ (constant)}+ \beta_1(\text{TPO})+ \beta_2(\text{POD})+ \beta_3(\text{MEA})+ \beta_4(\text{HDI})+ \beta_5(\text{HFS})+ \beta_6(\text{ISFC})+\text{Ɛ} \quad \text{(Model 1)}$$

$$\hat{y}=2.313+1.678+8.258+0.026+4.951+0.048+6.852+0.523$$

$$\hat{y}= \beta_0 \text{ (constant)}+ \beta_1(\text{TPO})+ \beta_2(\text{POD})+ \beta_3(\text{MEA})+ \beta_4(\text{HDI})+ \beta_5(\text{HFS})+ \beta_6(\text{ISIC})+\text{Ɛ} \quad \text{(Model 2)}$$

$$\hat{y}=2.543+1.637+6.477+0.023+5.094+0.018+6.725+0.499$$

$$\hat{y}= \beta_0 \text{ (constant)}+ \beta_1(\text{TPO})+ \beta_2(\text{POD})+ \beta_3(\text{MEA})+ \beta_4(\text{HDI})+ \beta_5(\text{HFS})+ \beta_6(\text{HMO})+\text{Ɛ} \quad \text{(Model 3)}$$

$$\hat{y}=2.454+1.765+5.827+0.025+5.112+0.035+6.517+0.517$$

Moderating variables in the regression models included total population (TPO), population density (POD), median age (MEA), HDI, HFS, immigrant stock from China (ISFC), immigrant stock in China (ISIC) and human mobility[13] (HMO). The correlation matrix (Table 1) confirms that all the independent variables, except for the TPO and POD, are significantly correlated with the TCC[14]. However, there are some collinearity problems between the MEA and HDI; the GNI and HDI; and the ISFC and HMO. The correlation coefficient (r) between the MEA and HDI is 0.876;

[11] The selection of 111 countries was data driven, whereby we dropped countries where immigrant stock and/or Covid-19 case statistics were not available.

[12] For the details of and justifications for K-means clustering, please see Afifi and Clark (1999: 395); Bacher (2002: 105); and Rencher (2002: 482).

[13] In order to represent the size of international human mobility, this variable is obtained by multiplying ISFC by ISIC.

[14] We transformed and used logarithmic equivalents (i.e. Log_{10}TCC) of the number of cases in the dependent variable, TCC.

between the GNI and HDI is 0.837 and between the ISFC and HMO is 0.838. To explore the differences and delineate the relationship, three different models were run, as shown in Table 2.

Table 1. Correlation matrix for the exploratory multiple regression analyses (n=111)

	TPO	POD	MEA	HDI	GNI	HFS	ISFC	ISIC	HMO
Total COVID-19 cases (TCC)	0.177	0.064	-0.714**	-0.761**	-0.664**	-0.561**	0.375**	0.313**	0.297**
Total Population (TPO)	1	0.018	-0.056	-0.087	-0.081	-0.106	0.192*	0.213*	0.161
Population density (POD)		1	-0.124	-0.126	-0.323**	-0.097	0.160	0.052	0.034
Median age (MEA)			-1	-0.876**	-0.698**	-0.713**	0.227*	0.124	0.170
Human Development Index (HDI)				-1	-0.837**	-0.751**	0.270**	0.116	0.190*
Gross National Income (GNI)					-1	-0.660**	0.352**	0.086	0.226*
Human Freedom Score (HFS)						-1	0.261**	0.069	0.184
Immigrant stock from China (ISFC)							1	0.456**	0.838**
Immigrant stock in China (ISIC)								1	0.708**
Human mobility (HMO)									1

** Correlation is significant at the 0.01 level (2-tailed)

* Correlation is significant at the 0.05 level (2-tailed)

Regression results confirmed that the total number of cases for each country is significantly moderated by the factors included in our model. In Model 1, the TPO, POD, MEA, HDI, HFS, and ISFC explain 65% of the variance in the number of COVID-19 cases in each county. In this model, in which the ISIC and HMO are excluded because of the high-level correlation among them, both the TPO and HDI are the most significant factors affecting the TCCs. Despite the high-level of correlation between MEA and HDI, we included these two variables in the model since they are conceptually quite different indicators. At the same time, the volume of immigrant stock in destination countries (ISFC) is a statistically significant indicator for the volume of COVID-19 cases (TCCs).

Despite there being no collinearity problem between ISFC and ISIC, we used these indicators in the models 1 and 2 in order to present their explanatory power separately. Similar to the first model, the five variables (TPO, POD, MEA, HDI, HFS, and ISIC) were significant in determining the number of COVID-19 cases and the model 2 also explains 66% of the variance, with HDI being the most significant factor. Moreover, TPO and ISIC are the significant factors in Model 2. Confirming the role of ISIC and ISFC in these two models support our argument that human mobility is a significant determinant of the spread and volume of COVID-19 cases (TCCs) across the world. Therefore, in the third model, instead of ISFC and ISIC, we have included an interaction of the two, i.e. Human mobility (HMO) along with other contextual variables, namely TPO, POD, MEA, HDI, and HFS. These included independent variables explain 64% of the variance in TCCs in each country. The TPO and HDI are the most important indicators for the TCCs. Moreover, human mobility is a statistically significant factor for the TCCs in the countries.

Considering the spread of COVID-19 among 110 countries, for the three models we can argue that countries with larger populations, and higher HDI scores have the highest COVID-19-case levels. Some of these factors are probably more or less self-explanatory. For example, population size is directly related to the pool size for potentially infected individuals. HDI is significant and it shows that relatively poor countries will be affected worse from the COVID-19 pandemic. However, we found no significant relationships between the TCC and population density (POD) and HFS. These results tell us that every one unit increase in the HDI score may mean about five more COVID-19 cases being reported according to these models. In all three models, a one person increase in population size indicates over 1.6 more COVID-19 cases. HFI scores were found to be

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insignificant in determining the number of cases reported, thus not supporting the negative relationship that was expected.

Table 2. Results of multiple regressions for the dependent variable TCCs by country (n=110[b])

Variable[s]	Model 1		Model 2		Model 3	
	β coefficient	t-value	β coefficient	t-value	β coefficient	t-value
(Constant)	-2.313	-4.423***	-2.543	-5.094***	-2.454	-4.747***
Total Population (TPO)	1.678E-09	3.529**	1.637E-09	3.492**	1.765E-09	3.720***
Population density (POD)	-8.258E-05	-1.028	-6.477E-05	-0.823	-5.827E-05	-0.726
Median age (MEA)	0.026	1.709	0.023	1.525	0.025	1.588
Human development index (HDI)	4.951	4.652***	5.094	4.876***	5.112	4.791***
Human freedom score (HFS)	-0.048	-0.501	-0.018	-0.196	-0.035	-0.373
Immigrant stock from China (ISFC)	6.852E-07	2.383*	–	–	–	–
Immigrant stock in China (ISIC)	–	–	6.725E-06	2.909**	–	–
Human mobility (HMO)	–	–	–	–	6.517E-12	2.004*
Adjusted R^2	*0.65*		*0.66*		*0.64*	
F	*34.205*		*35.519*		*33.419*	

Source: Data from ECDC (2020); UN (2019, 2020); WB (2020); Vásquez and Porčnik (2019), authors' calculations.
Significance: ***$p < 0.001$; **$p < 0.01$; *$p < 0.05$.
[a] For further information on some of the variables by countries, see Table 2a, b, c, and d in the Appendix.
[b] Although Myanmar is involved in the Covid-19 case and death list, obtained from ECDC (2020), the case and the death cells have zero. Therefore, the regression analyses omitted this country during the analysing processes. In addition, China is excluded from both the data (Table 2a, b, c, and d in the Appendix) and analyses since this country does not have (Chinese) any migrant stock.

We have tested the role of migration in three models. In model 1, we have shown that every additional immigrant from China (ISFC) in a given destination country indicates a 6.9 increase in the number of COVID-19 cases. In model 2, every additional immigrant in China (ISIC) from a destination country means 6.73 more COVID-19 cases being found in that country. In model 3, we have used an interaction variable (product of ISFC and ISIC) to show that every one unit increase in HMO leads to 6.52 more COVID-19 cases. Thus, we argue it is not the number of Chinese immigrants, but rather, the totality of human mobility in both directions, i.e. including immigrants in China, that matters.

The volume of migration in each migration corridor linking the countries of origin and destination appears as a strong indicator for the spread of the pandemic. This can be an important proxy to see how countries can predict the scale of and prepare for a pandemic. The role of migration is also explain why similarly large and developed countries have varying numbers of cases emerging. Using migration data alongside the other indicators we have used in the analyses may be helpful for organising the global response to similar pandemics in terms of where to concentrate the resources at early stages so as to contain the spread. This relates to our next question. We discuss in the following passages which countries are more vulnerable and which are more resistant.

We have determined the spatial clustering (i.e. similarities and disparities) of the selected countries using the total number of COVID-19 cases (WHO, 2020a, b, c and ECDC, 2020)[15] along with other all contextual variables. The data for the chosen 10 variables have different units for the 111 focal countries and thus, all have been analysed after logarithmic transformation[16]. As a result of the cluster analysis, the values in log format averages (final cluster centres) of the variables are presented in Table 3. Accordingly, we have assigned 51 of the 111 countries to cluster 1; 35 countries to cluster 2; 15 countries to cluster 3, and 10 countries to cluster 4. The values in log format in Table 3 have been converted into a plot diagram to illustrate clearly the differences between the clusters and the countries in each (Figure 2).

The cluster analysis has shown certain spatial and perhaps socioeconomic patterns across the world. The first cluster (1) is marked by relatively low numbers of COVID-19 cases (Table 3 and Figure 2). In this cluster, total deaths, total population, population density, median age, human development index, gross national income, human freedom score, immigrant stock from China, and immigrant stock in China are also slightly lower than for the countries in other clusters. Most of these countries, if not all, are also considered to be low-income countries, with few exceptions, such as Malta and Brunei Darussalam.

Table 3. Final cluster centres obtained from the cluster analysis (n=111)

		Variables[a]									
		TCC	TDE	TPO	POD	MEA	HDI	GNI	HFS	ISFC	ISIC
Log_{10}	Cluster 1	1.21	0.02	6.61	1.72	1.44	-0.17	3.92	0.84	2.84	2.48
	Cluster 2	2.60	0.67	7.17	1.88	1.54	-0.09	4.32	0.85	3.72	3.01
	Cluster 3	2.67	0.98	7.86	2.02	1.54	-0.11	4.24	0.85	4.95	4.36
	Cluster 4	4.11	2.49	7.65	2.31	1.63	-0.04	4.64	0.92	5.16	3.98
Anova Test	*F Value*	*78.39*	*63.82*	*22.29*	*2.88*	*12.02*	*15.17*	*14.20*	*4.84*	*77.17*	*60.92*
	P	***	***	***	*	***	***	***	**	***	***

Source: Data from ECDC (2020); UN (2019, 2020); WB (2020); Vásquez and Porčnik (2019), with authors' calculations

[a] TCC: Total COVID-19 cases; TDE: Total COVID-19 related deaths; TPO: Total population; POD: Population density; MEA: Median age; HDI: Human Development Index; GNI: Gross National Income; HFS: Human Freedom Score; ISFC: Immigrant Stock from China; ISIC: Immigrant Stock in China.

Significance: ***$p < 0.001$; **$p < 0.01$; *$p < 0.05$

In cluster 2, all the indicators are higher than with the first cluster, whereas the gross national income is higher than for cluster 3; median age is equal to that of cluster 3; and immigrant stock from China and immigrant stock in China from the origin countries are lower than for cluster 3.

In cluster 3, total COVID-19 cases is higher than for cluster 1 and 2. The countries in cluster 3 have higher deaths, population density, median age, immigrant stock from China and immigrant stock in China compared to the countries in the first two clusters. In cluster 3, the total population and immigrant stock in China are higher than the two other clusters. In addition, median age and HFS are equal to cluster 2. In this cluster, 8 countries are located in South and East Asia along with Australia, Canada, New Zealand and Brazil and Russia, two emerging economies.

[15] The total number of COVID-19 cases by country is presented in Tables 2a, b, c, and d in the Appendix.

[16] Logarithmic transformation is a method of standardising data values in log (log_{10}) format. Cluster analysis is a sensitive analysis for large variables, which can lead to incorrect results because the analysis tries to parse large sets of values. For this reason, the variables to be used in the analysis must either be the same (for example, all percentages) or transformed. Since the units of the variables used in the analysis differ from each other (numbers, years, rates, percentages, scores etc.), they have been standardised and transformed into log (Log_{10}) format. A large log_{10} value shows that the variable is high in terms of the rate, speed, or score, while a small log_{10} value shows that they are low.

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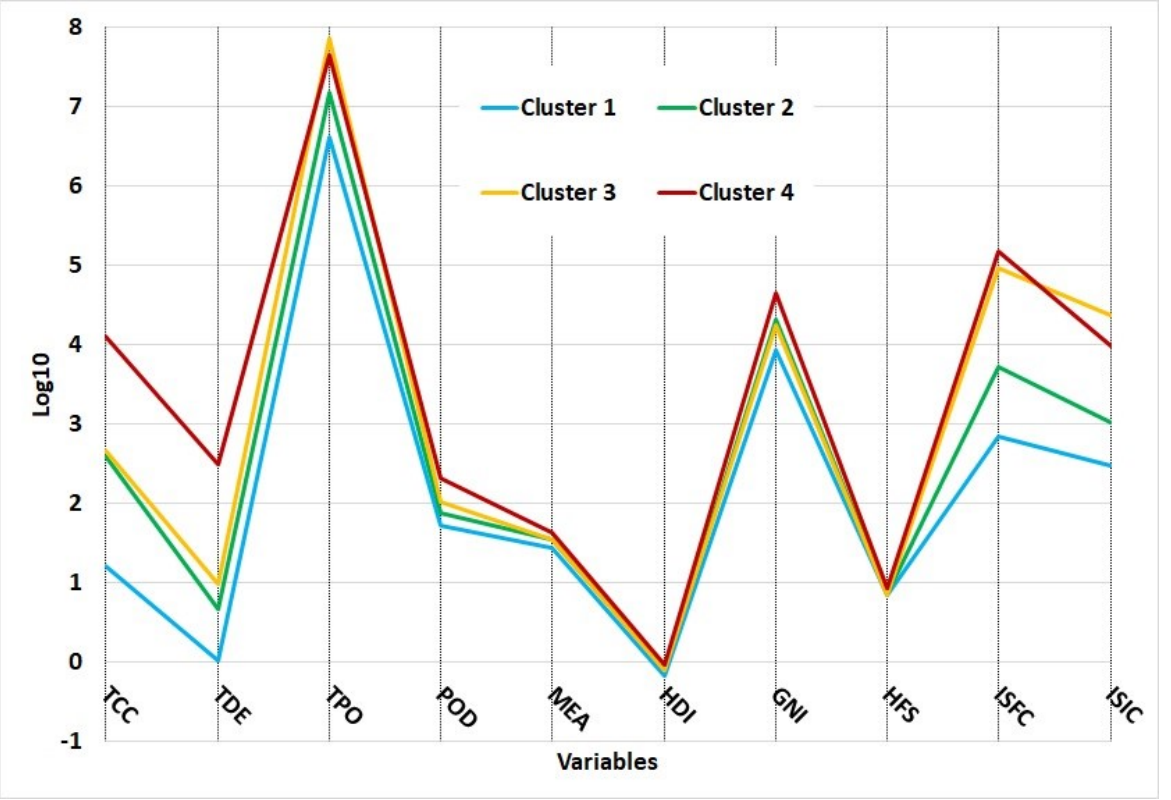
Figure 2. Clustering of countries and the final cluster centres of the variables



Cluster 1	Cluster 2	Cluster 3	Cluster 4
Azerbaijan, Bahamas, Barbados, Bhutan, Bolivia, Bosnia and Herzegovina, Brunei Darussalam, Cambodia, Central African Republic, Congo, Croatia, Cyprus, El Salvador, Estonia, Fiji, Gabon, Georgia, Ghana, Guatemala, Guinea, Guyana, Haiti, Honduras, Iceland, Kenya, Kyrgyzstan, Latvia, Lithuania, Madagascar, Malta, Mauritania, Mauritius, Moldova, Mongolia, Namibia, Nepal, Papua New Guinea, Paraguay, Rwanda, Serbia, Seychelles, Slovakia, Sudan, Suriname, Timor Leste, Togo, Trinidad and Tobago, Uganda, Uruguay, Tanzania, and Zambia	Argentina, Algeria, Austria, Bulgaria, Chile, Costa Rica, Czechia, Denmark, Dominican Republic, Ecuador, Egypt, Finland, Greece, Hungary, Ireland, Israel, Jordan, Kazakhstan, Lebanon, Luxembourg, Mexico, Norway, Pakistan, Panama, Peru, Poland, Portugal, Romania, Slovenia, South Africa, Sri Lanka, Sweden, Turkey, Ukraine, and Venezuela	Australia, Bangladesh, Brazil, Canada, India, Indonesia, Japan, Malaysia, Myanmar, New Zealand, Philippines, Russia, Singapore, Thailand, and Vietnam	Belgium, France, Germany, Italy, the Netherlands, South Korea, Spain, Switzerland, the UK, and the USA

Note: This plot diagram was prepared by the final cluster centres obtained from the cluster analysis (see Table 3).
Explanation: TCC: Total COVID-19 cases; TDE: Total COVID-19 related deaths; TPO: Total population; POD: Population density; MEA: Median age; HDI: Human Development Index; GNI: Gross National Income; HFS: Human Freedom Score; ISFC: Immigrant Stock from China; ISIC: Immigrant Stock in China.

Cluster 4 comprises the USA, Belgium, Germany, Italy, the Netherlands, the UK, Switzerland, Spain, France, and South Korea, all high-income countries with strong health infrastructures. In this cluster total population is as high as in cluster 3. These countries are marked by a remarkably high volume of COVID-19 cases and large diasporas from China as well as higher population density compared to the other clusters. Remarkably, in this cluster, immigrant stock in China from the other countries is lower than for Cluster 3.

The F values in the cluster analysis show that the most important variables contributing to the clustering regarding the countries' convergence or divergence are, respectively, the total COVID-19 cases (78.39), immigrant stock from China (77.17), total deaths (63.82), immigrant stock in China (60.92), total population (22.29), HDI (15.17), GNI (14.20), HFS (4.84), and population density (2.88) (Table 3). The top four most important variables contributing to this clustering are the total COVID-19 cases (TCC) (F=78.39), immigrant stock from China (F=77.17), total deaths (F=63.82), and immigrant stock in China (F=60.92). As can be seen from the red line in Figure 2, ten countries in cluster 4 are in relocation areas of the spatial diffusion pattern of COVID-19. These ten countries are located in three regions: (1) origin-region (China and a neighbouring country, South Korea); (2) first relocation-region (Western Europe); and (3) second relocation-region (USA).

It is important to note that we are examining the predicting power of immigrant populations/diasporas from China and immigrants/diasporas in China for understanding the spread (and volume) of COVID-19 cases, also being in line with the diffusion theories explained at the beginning. However, we are not making a causal relationship, but rather, identifying a proxy to understand the diffusion. Migration relationships or corridors of human mobility established over time as cultures of migration emerge are indicators of developing social and economic relationships between the countries involved. This means more investment and more remittance flows, more holiday trips, and a significant growth regarding other relationships.

Conclusion

The spread of COVID-19 seems to follow a relocation diffusion pattern beyond the neighbouring countries. A hierarchical diffusion pattern was also observed regarding many countries in cluster 4 we have identified. These countries marked by high HDI scores, relatively large populations, high income and sizeable Chinese diasporas have seen the largest volumes of infected populations. However, there was also evidence confirming an expansion to neighbouring countries, as expected, towards Japan and South Korea and other South-East Asian neighbours where initially a significant number of cases were reported.

The statistical models that we have applied clearly show that the COVID-19 spread around the world could have been estimated and mapped out to a substantial degree of accuracy by simply taking into account some macro variables, such as the population size, HDI scores, and immigrant stock from the origin at each destination. We have applied the statistical model at the country level. However, where data are available, this model can be used to identify certain regional or local level concentration of infected individuals. It emerges from the most recent data that large metropolitan areas and global cities, such as London and New York, are taking the lion share of cases in their respective countries. Therefore, further spread from these centres could also be examined using a similar approach. What matters in this model is that viruses relocate to surrounding areas or beyond by transport following the diffusion theory we presented at the beginning of this work.

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Our analyses of the data available show that governments around the world could have been more proactive and prepared in responding to the COVID-19 pandemic, if they had utilised model(s) like the one suggested in this article. So far, late and reactionary responses to the crisis have seemingly led to sharp increases in the number of cases and deaths in many countries. We argue that this could have been avoided, if travel data had been used during the early stages of diffusion. By monitoring immigrant stock data and/or travel volume data based on human mobility corridors (i.e. origins and destinations), countries could have been better prepared to tackle the spread of COVID-19. This is one of the lessons that should be learnt for tackling future pandemics more effectively than the present one.

Another important note is that despite some racist exchanges by politicians in early phases of the COVID-19 crisis, the spread of the virus does not have an ethnic origin. We have shown the role of human mobility patterns irrespective of ethnic or national origins. Many other studies by scientists also point that the origin of the viruses have not been confirmed. Given the fact that human settlements more and more expand into living spaces of animals, there is likely to be more transfer of such viruses from animals to humans. Focusing on this latter challenge may mean better use of our resources and energy for future generations.

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Appendix

Table 1a. Key indicators for top 30 destination countries receiving air travellers from Wuhan, Hubei Province, China (n=30)

Country	Airline travellers' volume (in thousand)	Total Covid-19 cases*	Total Covid-19 deaths*	Total population (in thousand)	Crude rate of spread (CRS) per thousand	Population density (persons per square km)	Median age (years)
Thailand	485.6	721	1	69,626	0,0104	136.3	40.1
Japan	382.8	1,089	41	126,860	0,0086	348.0	48.4
Hong Kong	244.4	274	4	7,436	0,0368	7,082.1	44.8
Taiwan	237.7	165	2	23,774	0,0069	671.4	42.5
South Korea	230.2	8,961	113	51,225	0,1749	526.8	43.7
USA	189.1	35,206	471	329,065	0,1070	36.0	38.3
Malaysia	150.6	1,306	10	31,950	0,0409	97.2	30.3
Singapore	138.6	455	2	5,804	0,0784	8,291.9	42.2
Viet Nam	115.6	118	0	96,462	0,0012	311.1	32.5
Australia	109.8	1,709	7	25,203	0,0678	3.3	37.9
Indonesia	99.6	514	48	270,626	0,0019	149.4	29.7
Cambodia	64.3	86	0	16,487	0,0052	93.4	25.6
Macao, PRC	62.3	19	0	640	0,0297	21,419.6	39.3
Germany	58.0	24,774	94	83,517	0,2966	239.6	45.7
Philippines	61.6	380	25	108,117	0,0035	362.6	25.7
UK	46.7	5,683	281	67,530	0,0842	279.1	40.5
Canada	50.7	1,430	18	37,411	0,0382	4.1	41.1
Italy	36.9	59,138	5,476	60,550	0,9767	205.9	47.3
UAE	38.7	153	2	9,771	0,0157	116.9	32.6
Russian Fed.	36.9	438	0	145,872	0,0030	8.9	39.6
France	32.9	16,018	674	65,130	0,2459	118.9	42.3
India	26.0	439	7	1,366,418	0,0003	459.6	28.4
N. Zealand	29.5	102	0	4,783	0,0213	18.2	38.0
Spain	26.1	28,572	1,720	46,737	0,6113	93.7	44.9
Egypt	14.3	294	10	100,388	0,0029	100.8	24.6
Maldives	12.2	13	0	531	0,0245	1,769.9	29.9
Sri Lanka	13.8	87	0	21,324	0,0041	340.0	34.0
Turkey	16.5	1,236	30	83,430	0,0148	108.4	31.5
Laos	8.6	0	0	7,169	0,0000	31.1	24.4
Myanmar	10.4	0	0	54,045	0,0000	82.7	29.0

Source: CATO (2020); Lai *et al.* (2020b); UN (2019 and 2020); Vásquez and Porčnik (2019); WB (2020); WHO (2020a, b, and c).
* Covid-19 case and death statistics are from 23 March 2020.

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Table 1b. Key indicators for top 30 destination countries receiving air travellers from Wuhan, Hubei Province, China (n=30)

Country	Human development index	Gross national income	Immigrant stock from China (in thousand)	Human freedom index
Thailand	0.765	16,129	149,352	6.55
Japan	0.915	40,799	741,022	8.28
Hong Kong	0.939	60,221	2,343,868	8.81
Taiwan	0.882	28,128	0	8.4
South Korea	0.906	36,757	656,846	8.2
USA	0.920	56,140	2,130,352	8.46
Malaysia	0.804	27,227	54,980	6.52
Singapore	0.935	83,793	462,632	8.11
Viet Nam	0.693	6,220	8,639	6.29
Australia	0.938	44,097	526,040	8.62
Indonesia	0.707	11,256	73,971	6.83
Cambodia	0.581	3,597	1,566	7.13
Macao, PRC	0.907	79,110	290,609	n/a
Germany	0.939	46,946	129,150	8.53
Philippines	0.712	9,540	37,083	6.88
UK	0.920	39,507	226,000	8.47
Canada	0.922	43,602	711,555	8.65
Italy	0.883	36,141	212,173	8.04
UAE	0.866	66,912	0	6.13
Russian Fed.	0.824	25,036	56,210	6.34
France	0.891	40,511	111,717	8.02
India	0.647	6,829	7,035	6.64
N. Zealand	0.921	35,108	98,109	8.88
Spain	0.893	35,041	183,583	8.12
Egypt	0.700	10,744	1,266	4.5
Maldives	0.719	12,549	0	n/a
Sri Lanka	0.780	11,611	2,482	6.41
Turkey	0.806	24,905	2,190	6.21
Laos	0.604	6,317	13,951	6.2
Myanmar	0.584	5,764	47,742	5.44

Source: CATO (2020); Lai *et al.* (2020b); UN (2019 and 2020); Vásquez and Porčnik (2019); WB (2020); WHO (2020a, b, and c).

Table 1c. Correlation matrix for the exploratory variables in top 30 destination countries (n=30)

	Total Covid-19 cases	Total deaths	Total population	Population density	Median age	Human development index	Gross national income	Immigrant stock from China	Crude rate of spread	Human freedom index
Airline travellers' volume	-0.081	-0.139	-0.068	0.035	0.428*	0.258	0.163	0.409*	-0.147	0.263
Total Covid-19 cases	1	0.855**	0.009	-0.142	0.470**	0.337	0.211	0.224	0.904**	0.353
Total deaths		1	-0.043	-,0.90	0.369*	0.182	0.076	-0.002	0.930**	0.194
Total population			1	-0.123	-0.207	-0.269	-0.236	-0.006	-0.088	-0.129
Population density				1	0.177	0.248	0.582**	0.202	-0.083	0.269
Median age					1	0.845**	0.632**	0.413*	0.504**	0.759**
Human development index						1	0.823**	0.467**	0.321	0.776**
Gross national income							1	0.494**	0.182	0.617**
Immigrant stock from China								1	0.015	0.508**
Crude rate of spread									1	0.325
Human freedom index										1

*. Correlation is significant at the 0.05 level (2-tailed).
**. Correlation is significant at the 0.01 level (2-tailed).

Table 2a. Moderating indicators by selected countries: Argentina to Latvia (n=111) [23/03/2020]

Country	Total Covid-19 cases	Total deaths	Total population (in thousand)	Population density (persons per square km)	Median age (years)
Argentina	266	4	44,781	16.4	31.5
Algeria	102	15	43,053	18.1	28.5
Australia	1,709	7	25,203	3.3	37.9
Austria	3,631	16	8,995	108.7	43.5
Azerbaijan	65	1	10,048	121.6	32.3
Bahamas	4	0	389	38.9	32.2
Bangladesh	27	3	163,046	1,252.6	27.6
Barbados	17	0	287	667.5	40.5
Belgium	3,401	75	11,539	381.1	41.9
Bhutan	2	0	763	20.0	28.1
Bolivia	27	0	11,513	10.6	25.6
Bosnia and Herzegovina	125	1	3,301	64.7	43.1
Brazil	1,546	25	211,050	25.3	33.5
Brunei Darussalam	88	0	433	82.2	32.3
Bulgaria	185	3	7,000	64.5	44.6
Cambodia	86	0	16,487	93.4	25.6
Canada	1,430	18	37,411	4.1	41.1
Central African Republic	4	0	4,745	7.6	17.6
Chile	632	1	18,952	25.5	35.3
Congo	4	0	5,381	15.8	19.2
Costa Rica	134	2	5,048	98.9	33.5
Croatia	235	1	4,130	73.8	44.3
Cyprus	95	0	1,199	129.7	37.2
Czechia	1,165	1	10,689	138.4	43.2
Denmark	1,395	13	5,772	136.0	42.3
Dominican Republic	203	3	10,739	222.2	28.0
Ecuador	789	14	17,374	70.0	27.9
Egypt	294	10	100,388	100.8	24.6
El Salvador	3	0	6,454	311.5	27.6
Estonia	326	0	1,326	31.3	42.4
Fiji	3	0	890	48.7	27.9
Finland	626	1	5,532	18.2	43.1
France	16,018	674	65,130	118.9	42.3
Gabon	6	1	2,173	8.4	22.5
Georgia	54	0	3,997	57.5	38.3
Germany	24,774	94	83,517	239.6	45.7
Ghana	24	1	30,418	133.7	21.5
Greece	624	15	10,473	81.3	45.6
Guatemala	19	1	17,581	164.1	22.9
Guinea	2	0	12,771	52.0	18.0
Guyana	5	1	783	4.0	26.7
Haiti	2	0	11,263	408.7	24.0
Honduras	27	0	9,746	87.1	24.3
Hungary	167	7	9,685	107.0	43.3
Iceland	568	1	339	3.4	37.5
India	439	7	1,366,418	459.6	28.4
Indonesia	514	48	270,626	149.4	29.7
Ireland	906	4	4,882	70.9	38.2
Israel	1,071	1	8,519	393.7	30.5
Italy	59,138	5476	60,550	205.9	47.3
Japan	1,089	41	126,860	348.0	48.4
Jordan	114	0	10,102	113.8	23.8
Kazakhstan	60	0	18,551	6.9	30.7
Kenya	15	0	52,574	92.4	20.1
Kyrgyzstan	14	0	6,416	33.5	26.0
Latvia	139	0	1,907	30.7	43.9

Source: CATO (2020); UN (2019 and 2020); Vásquez and Porčnik (2019); WB (2020); WHO (2020a, b, and c).

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Table 2b. Moderating indicators by selected countries: Argentina to Latvia (n=111) [23/03/2020]

Country	Human development index	Gross national income	Human freedom index	Immigrant stock from China (in thousand)	Immigrant stock in China (in thousand)
Argentina	0.830	17,611	6.86	15,924	1,933
Algeria	0.759	13,639	4.99	683	554
Australia	0.938	44,097	8.62	526,040	13,286
Austria	0.914	46,231	8.48	15,986	1,054
Azerbaijan	0.754	15,240	6.22	427	530
Bahamas	0.805	28,395	7.56	179	0
Bangladesh	0.614	4,057	5.77	174,487	6,282
Barbados	0.813	15,912	7.02	43	0
Belgium	0.919	43,821	8.29	19,813	1,578
Bhutan	0.617	8,609	6.53	973	539
Bolivia	0.703	6,849	6.65	1,173	175
Bosnia and Herzegovina	0.769	12,690	7.37	18	0
Brazil	0.761	14,068	6.48	23,769	115,347
Brunei Darussalam	0.845	76,389	5.69	2,172	0
Bulgaria	0.816	19,646	7.79	1,471	246
Cambodia	0.581	3,597	7.13	1,566	464
Canada	0.922	43,602	8.65	711,555	19,990
Central African Rep.	0.381	777	5.41	127	0
Chile	0.847	21,972	8.15	9,823	411
Congo	0.608	5,804	5.36	937	870
Costa Rica	0.794	14,790	7.70	9,422	107
Croatia	0.837	23,061	7.86	434	136
Cyprus	0.873	33,100	7.93	1,884	0
Czechia	0.891	31,597	8.34	5,219	359
Denmark	0.930	48,836	8.56	10,611	1,759
Dominican Republic	0.745	15,074	6.95	4,995	0
Ecuador	0.758	10,141	6.82	4,265	290
Egypt	0.700	10,744	4.50	1,266	1,294
El Salvador	0.667	6,973	6.89	260	0
Estonia	0.882	30,379	8.46	312	0
Fiji	0.724	9,110	7.17	935	136
Finland	0.925	41,779	8.53	9,956	1,349
France	0.891	40,511	8.02	111,717	15,087
Gabon	0.702	15,794	5.99	331	150
Georgia	0.786	9,570	7.74	256	0
Germany	0.939	46,946	8.53	129,150	14,446
Ghana	0.596	4,099	6.94	264	1,165
Greece	0.872	24,909	7.33	4,414	370
Guatemala	0.651	7,378	7.07	683	0
Guinea	0.466	2,211	5.61	164	357
Guyana	0.670	7,615	6.74	1,166	0
Haiti	0.503	1,665	6.71	739	0
Honduras	0.623	4,258	6.81	601	0
Hungary	0.845	27,144	7.65	18,193	380
Iceland	0.938	47,566	8.41	609	112
India	0.647	6,829	6.64	7,035	15,051
Indonesia	0.707	11,256	6.83	73,971	58,639
Ireland	0.942	55,660	8.52	13,640	969
Israel	0.906	33,650	7.61	1,130	757
Italy	0.883	36,141	8.04	212,173	5,958
Japan	0.915	40,799	8.28	741,022	66,159
Jordan	0.723	8,268	6.84	20,936	864
Kazakhstan	0.817	22,168	6.90	5,142	4,680
Kenya	0.579	3,052	6.85	1,487	661
Kyrgyzstan	0.674	3,317	6.98	303	988
Latvia	0.854	26,301	8.29	237	100

Source: CATO (2020); UN (2019 and 2020); Vásquez and Porčnik (2019); WB (2020); WHO (2020a, b, and c).

Table 2c. Moderating indicators by selected countries: Lebanon to Zambia (n=111) [23/03/2020]

Country	Total Covid-19 cases	Total deaths	Total population (in thousand)	Population density (persons per square km)	Median age (years)
Lebanon	248	4	6,856	670.2	29.6
Lithuania	143	1	2,760	44.0	45.1
Luxembourg	798	8	616	237.7	39.7
Madagascar	3	0	26,969	46.4	19.6
Malaysia	1,306	10	31,950	97.2	30.3
Malta	90	0	440	1,376.2	42.6
Mauritania	14	1	4,526	4.4	20.1
Mauritius	28	2	1,270	625.5	37.5
Mexico	316	2	127,576	65.6	29.2
Moldova	94	1	4,043	123.1	37.6
Mongolia	10	0	3,225	2.1	28.2
Myanmar	0	0	54,045	82.7	29.0
Namibia	3	0	2,495	3.0	21.8
Nepal	1	0	28,609	199.6	24.6
Netherlands	4,217	179	17,097	507.0	43.3
New Zealand	102	0	4,783	18.2	38.0
Norway	2,132	7	5,379	14.7	39.8
Pakistan	784	5	216,565	280.9	22.8
Panama	313	3	4,246	57.1	29.7
Papua New Guinea	1	0	8,776	19.4	22.4
Paraguay	22	1	7,045	17.7	26.3
Peru	363	5	32,510	25.4	31.0
Philippines	380	25	108,117	362.6	25.7
Poland	634	7	37,888	123.7	41.7
Portugal	1,600	14	10,226	111.7	46.2
Romania	433	2	19,365	84.1	43.2
Russian Federation	438	0	145,872	8.9	39.6
Rwanda	19	0	12,627	511.8	20.0
Serbia	188	1	8,772	100.3	41.6
Seychelles	7	0	98	212.5	34.2
Singapore	455	2	5,804	8,291.9	42.2
Slovakia	185	0	5,457	113.5	41.2
Slovenia	414	1	2,079	103.2	44.5
South Africa	274	0	58,558	48.3	27.6
South Korea	8,961	113	51,225	526.8	43.7
Spain	28,572	1720	46,737	93.7	44.9
Sri Lanka	87	0	21,324	340.0	34.0
Sudan	2	1	42,813	24.3	19.7
Suriname	5	0	581	3.7	29.0
Sweden	1,906	21	10,036	24.5	41.1
Switzerland	6,971	60	8,591	217.4	43.1
Thailand	721	1	69,626	136.3	40.1
Timor-Leste	1	0	1,293	87.0	20.8
Togo	16	0	8,082	148.6	19.4
Trinidad and Tobago	50	0	1,395	271.9	36.2
Turkey	1,236	30	83,430	108.4	31.5
Uganda	1	0	44,270	221.6	16.7
Ukraine	47	3	43,994	75.9	41.2
United Kingdom	5,683	281	67,530	279.1	40.5
U. Rep. of Tanzania	12	0	58,005	65.5	18.0
United States of America	35,206	471	329,065	36.0	38.3
Uruguay	158	0	3,462	19.8	35.8
Venezuela	36	0	28,516	32.3	29.6
Vietnam	118	0	96,462	311.1	32.5
Zambia	3	0	17,861	24.0	17.6

Source: CATO (2020); UN (2019 and 2020); Vásquez and Porčnik (2019); WB (2020); WHO (2020a, b, and c).

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Table 2d. Moderating indicators by selected countries: Lebanon to Zambia (n=111) [23/03/2020]

Country	Human development index	Gross national income	Human freedom index	Immigrant stock from China (in thousand)	Immigrant stock in China (in thousand)
Lebanon	0.730	11,136	6.74	2,987	399
Lithuania	0.869	29,775	8.32	280	100
Luxembourg	0.909	65,543	8.56	1,117	0
Madagascar	0.521	1,404	6.32	2,813	238
Malaysia	0.804	27,227	6.52	54,980	10,954
Malta	0.885	34,795	8.37	447	0
Mauritania	0.527	3,746	5.47	346	204
Mauritius	0.796	22,724	7.52	23,210	660
Mexico	0.767	17,628	6.65	8,860	1,261
Moldova	0.711	6,833	6.93	361	137
Mongolia	0.735	10,784	7.61	9,683	4,546
Myanmar	0.584	5,764	5.44	47,742	39,776
Namibia	0.645	9,683	6.75	2,881	134
Nepal	0.579	2,748	6.51	24,394	2,401
Netherlands	0.933	50,013	8.50	54,413	3,378
New Zealand	0.921	35,108	8.88	98,109	3,656
Norway	0.954	68,059	8.44	11,520	850
Pakistan	0.560	5,190	5.69	312	7,746
Panama	0.795	20,455	7.69	19,273	905
Papua New Guinea	0.543	3,686	6.60	92	100
Paraguay	0.724	11,720	6.90	800	0
Peru	0.759	12,323	7.55	4,751	21,641
Philippines	0.712	9,540	6.88	37,083	121,320
Poland	0.872	27,626	7.78	1,262	794
Portugal	0.850	27,935	8.27	10,806	375
Romania	0.816	23,906	8.11	4,909	460
Russian Federation	0.824	25,036	6.34	56,210	9,714
Rwanda	0.536	1,959	6.82	105	176
Serbia	0.799	15,218	7.30	1,750	149
Seychelles	0.801	25,077	7.16	515	0
Singapore	0.935	83,793	8.11	462,632	12,191
Slovakia	0.857	30,672	8.02	1,135	203
Slovenia	0.902	32,143	7.97	1,038	0
South Africa	0.705	11,756	7.08	38,684	1,925
South Korea	0.906	36,757	8.20	656,846	222,276
Spain	0.893	35,041	8.12	183,583	3,425
Sri Lanka	0.780	11,611	6.41	2,482	6,361
Sudan	0.507	3,962	4.44	1,310	0
Suriname	0.724	11,933	7.48	5,436	105
Sweden	0.937	47,955	8.50	28,410	2,566
Switzerland	0.946	59,375	8.82	22,286	1,348
Thailand	0.765	16,129	6.55	149,352	23,357
Timor-Leste	0.626	7,527	6.76	1,249	0
Togo	0.513	1,593	6.31	530	191
Trinidad and Tobago	0.799	28,497	6.62	871	0
Turkey	0.806	24,905	6.21	2,190	1,750
Uganda	0.528	1,752	6.61	597	321
Ukraine	0.750	7,994	6.26	6,625	1,437
United Kingdom	0.920	39,507	8.47	226,000	12,623
United Republic of Tanzania	0.528	2,805	6.26	22,542	498
United States of America	0.920	56,140	8.46	2,130,352	71,493
Uruguay	0.808	19,435	7.74	165	0
Venezuela	0.726	9,070	3.80	14,081	2,127
Vietnam	0.693	6,220	6.29	8,639	36,205
Zambia	0.591	3,582	6.49	1,055	310

Source: CATO (2020); UN (2019 and 2020); Vásquez and Porčnik (2019); WB (2020); WHO (2020a, b, and c).