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Title: Does lockdown work? A spatial analysis of the spread and concentration of Covid-19 in Italy.

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Summary:

The spread of Covid-19 is a worldwide concern, including and especially in the most developed countries where the rapid spread of the virus has taken governments by surprise. Adopting a spatial approach to the issue allows us, we identify the spatial factors that help to explain why some areas are hit harder than others, based on the Italian example (with the Lombardy region as the epicentre in Europe). Our analysis combines an autoregressive spatial model and a bivariate spatial autocorrelation from a pool of data collected from the Italian provinces. We propose a real-time analysis of the spread and concentration of the virus, as well as the related proximity effects. Our paper suggests that the most globally connected areas are also the worst hit areas. Our findings also indicate that the implementation of a lockdown at the beginning of March was a crucial and effective approach to slowing the spread of the virus further.

Keywords: COVID-19, spatial analysis, geography, lockdown, proximities

1. Introduction

In December 2019, a new virus from the SARS (Severe Acute Respiratory Syndrome) family called COVID-19 (WHO, 2020) began to spread across China and has now reached almost every other country in the world. The coronavirus 2019-nCoV (also known as "Wuhan virus", named after the city of 11 million people where it first broke out) can lead to pneumonia (Wang et al., 2020), and its mortality rate is currently estimated at a maximum of 3% (WHO, 2020). As with the transmission of SARS-CoV, there is evidence that transmission of COVID-19 is person-to-person via airborne respiratory droplets, direct contact with body fluids or secretions, or through contaminated objects (Xu et al., 2020). Initial findings from an epidemiological study (Chen et al., 2020) suggest that the 2019-nCoV virus is 80%

identical to SARS, with 20% of unknown origin, and that it may be less pathogenic than MERS-CoV and SARS-CoV. On the other hand, while the virus strain appears to be less deadly than SARS-CoV, it is more contagious. Consequently, governments are on global alert due to the rapid spread of the epidemic.

As Munster et al (2020) explained, the absence of severe outbreaks of the disease affect our ability to contain the spread of the virus as people do not necessarily know if they are infected or not, and can pass it on unwittingly. In addition, the potentially long incubation period - up to 14 days for Wuhan coronavirus versus about two days for influenza - means that people can become ill and transmit the disease before any symptoms appear (Ren et al., 2020; Wang et al., 2020, Read et al., 2020). As a result, infected people are not immediately aware of how quickly the virus spreads and continue to work and travel, increasing the risk of spreading the virus to their contacts, both at home and abroad.

Given the "alarming levels of spread and inaction" that have been reached, the WHO decided to officially declare a pandemic on 11 March 2020. As of 13 March 2020, Europe in turn became the "epicentre" of the epidemic. In Italy, the population went into full quarantine on 9 March 2020. Spain and France are also heavily affected and have also adopted lockdown measures. The concern is all the more acute as the demographic structure of the European population is relatively old and is thus more vulnerable on average compared to other regions of the world.

In this context, it is important to understand how it spreads in order to better contain it, as there is no epidemic without transmission. The mapping of globalized epidemics, with interpretive maps to show the transmission factors that may have been in play, is an increasingly widespread scientific approach. As Koch and Koch (2005) explain, GIS mapping tools have greatly improved our capacity to study and predict epidemics around the world. They even explain that the mapping studies produced during the Ebola outbreak not only showed the impact of the disease, but also influenced the way the epidemic itself was perceived. Having a geographical reading of epidemics provides a better understanding of how they spread spatially, which can help us to understand the underlying social processes of diffusion. Whether talking about the plague or other diseases, epidemics have often followed major military and trade routes (Lai et al., 2008). Several studies have highlighted the important explanatory role of geographical factors such as air flows during the SARS epidemic in 2003 (Bowen and Laroe, 2006), the porosity of regional borders during the Ebola epidemic of 2014 (Cenciarelli et al., 2015; Kramer et al., 2016) and the impact of urbanisation in the case of Zika in 2015 (Lourenco, 2017).

Traditionally, epidemics spread according to topographical and isotropic factors. This means that they are transmitted from one place to another over large areas – the notion of proximity being defined in kilometres – and this occurs gradually and comprehensively. Two factors should be kept in mind here: a place close to the starting point of the epidemic is almost always affected before a location that is far away from it; and all locations equidistant from the start of the epidemic are expected to be affected at

the same time. Of course, the spread of an outbreak can sometimes experience a "tunnel effect" when the pathogen is transported over long distances by a long-range transport network. In this way, the pathogen skips an entire area and can continue to spread on a much wider scale.

What is important here, however, is topographical diffusion, with the networks ultimately playing only a triggering role allowing the pathogen to spread over a much larger area. According to Cliff et al (2004), authors of the *World Atlas of Epidemic Diseases*, a reference work published in 2004, the spread of epidemic diseases is based on three main modes of diffusion: hierarchical mode (between large cities), local mode (through neighbourhoods) and "jump" mode (along transport routes). This was especially true with HIV/AIDS and SARS, whose spread was largely topological, and where the notion of proximity is defined in terms of connectivity between different points in a network. The rules of diffusion then change completely: a place that is strongly connected to the starting point of the epidemic will generally be affected before a place that is poorly connected, regardless of the distance in kilometres. Places affected at the same time from the same starting point of the epidemic have a similar degree of connection (they can thus be located thousands of kilometres apart). The topographical logic still plays a role, but in parallel with the topological logic, i.e. the network logic. It is thus sometimes possible to distinguish two scales of diffusion for the same epidemic: one local and territorial; the other global and reticular. For example, the 1889-90 influenza in Switzerland spread first from the municipalities served by the railway (Hogbin, 1985) and then via neighbourhoods to surrounding municipalities (Le Goff, 2011). With the increase in mobility and the general development of transport, the flows involved in the rapid spread of pathogens must now be taken into account. The explosion of air flows tends to foster a jumping mode of diffusion. For this reason, airports have become strategic surveillance and control points to try to contain the spread of epidemics. In a recent metapopulation study, Chinazzi et al (2020) model the transmission of COVID-19 to project the impact of travel restrictions on the national and international spread of the epidemic. They show only a modest effect of global travel restrictions unless these measures are combined with behavioural changes advocated by health services. Adiga et al (2020) quantify the risk of population exposure based on decisions to suspend flights, proposing a measurement system to classify vulnerable countries at immediate risk of case emergence.

Hence, one of the key lessons to be learned from the geographical study of epidemics is that we need an effective global health network to deal with such sudden epidemics. This depends in part on our ability to identify potential global health threats and to respond to them at local level. This in turn involves understanding the mechanisms of how disease is spread at global and regional levels. The development of mapping methods has allowed us to make the representation of the epidemic spread of COVID-19 more dynamic and accurate. Consequently, new questions can now be raised: which areas are most affected by the virus? How can these regional variations be explained? And last but not least, has lockdown had the desired effect? Many studies have been conducted on this subject with regard to other

epidemics. Several researchers have thus applied mapping and geostatistical methods to analyse disease spread patterns during epidemics such as tuberculosis (Roth et al., 2016), cholera (Adesina, 1984 ; Ali et al., 2002), SARS-CoV (Lai et al., 2004; Shannon and Willoughby, 2004; Wang et al., 2008; Meade, 2014), MERS-CoV (Cotten et al., 2014), H1N1 influenza (Smallman-Raynor and Cliff, 2008; Souris et al., 2010), HIV (Wallace and Wallace, 1995; Wood et al., 2000) and dengue (Charette et al., 2017; Acharya et al., 2018; Atique et al., 2018; Zhu et al., 2019). Conducted on different scales and for different diseases, these studies highlight the effects of spatial dependence between regions which partly explain the spatial heterogeneity of the spread of epidemics. The spatial dependence effects refer directly to the issue of spatial autocorrelation (Le Gallo, 2014), i.e. the coincidence of similarity of values with similarity of location (Anselin, 1995; Anselin, 1999).

While in medicine, the most common hypothesis involves a process of diffusion across an area by way of gradual transmission, we put forward the hypothesis that the spread of the virus and its spatial concentration is conditioned by the pre-existing spatial organisation (in socio-economic and regional terms). It is within this framework that we attempt to analyse the dynamics of virus spread by (i) highlighting the spatial concentration of COVID-19 cases and (ii) examining the links between the spread of the disease and variables likely to influence it, at the same time taking into account the effects of spatial dependence (neighbourhood effects and spatial autocorrelation). To this end, we adopted an exploratory method in spatial statistics which has not been used to examine such issues to date. Spatial relationships between geographical entities has been a study focus of great interest for geographers for several decades, including in medical geography (Dobis, 2020). One research avenue in this area is the analysis of spatial autocorrelation, which measures the association between objects of the same type (Cliff and Ord, 1972). Existing measures include global (Moran, 1950; Geary, 1954) and local (Anselin, 1995) statistics. Another line of research focuses on spatial correlation or co-location, which measures the spatial relationship between objects of different types (Leslie and Kronenfeld, 2011). We use the method of local indicators of bivariate spatial association (Anselin et al., 2000; Anselin, 2010) to parametrically identify the spatial concentrations of covariations between recorded cases of COVID-19 and various explanatory variables (population density, level of economic development, air traffic, health services). Moreover, in addition to a spatial exploratory approach, we develop a model to explain cases of COVID-19. In this respect, OLS estimators are often biased and inefficient when considering the existence of a spatial autocorrelation event, which calls into question the statistical inference approach. In order to correct this bias, the spatial autoregressive model (SAR) takes into account the spatial dependence of the explanatory variable and, in our case, the impact of the number of infected individuals spreading the virus between neighbouring regions. This model allows us to obtain estimators of the parameter ρ , a parameter that characterizes transmission effects. This is an important factor and several researchers (Spielman and Yoo, 2008; Chen and Wen, 2010; Cromley et al., 2012) have now called for the spatial dimension of neighbourhood effects to be taken into account.

Our study attempts to analyse the mechanisms of the spread of the virus in the national context of Italy that became the European epicentre of the outbreak. We first address the issue of the virus transmission model, examining in particular the spatial autocorrelation of the transmission rates. We then analyse the links between regional factors and the cases identified of infected persons. Finally, the study reflects on the strategies required to contain the epidemic outbreak by highlighting the central role of geography.

2. Materials and method

2.1. Data

Our study focuses on the data presented below. Lee and Wong (2010) show that surveillance data collected on a day-to-day basis can be effectively used to describe an epidemic and its geography, supporting the development of more effective interventions at local level to contain the spread. In 2016, WHO published a study that identified all reported epidemics in Africa from 1970 to 2016. The report showed the difficulty of collecting homogeneous fine scale data and of making temporal comparisons between the data at national level. For our example of the Italy, we collected data from the Ministry of Health in Italy at the level of provinces.

Table 1: The data gathered

Variable	Date	Geographic level	Source
GDP	2018	Provinces (Italy)	Eurostat
NbPassAero	2019	Provinces (Italy)	Eurostat
Density	2018	Provinces (Italy)	Eurostat
Share65+	2018	Provinces (Italy)	Eurostat
PopTot	2018	Provinces (Italy)	Eurostat
NbCases	March, 08, 18 & 28	Provinces (Italy)	Ministry of Health, Italy

Source: authors.

WHO demonstrated (2004) that severe acute respiratory syndrome (SARS) spread rapidly along international air transport routes (the largest outbreaks were observed in air transport hubs or in densely populated areas). This confirms other studies on the virus that underscored these factors (Shannon and Willoughby, 2004; Wang et al., 2008; Meade, 2014). In his article tracing the major factors in the emergence of epidemics and their spread, Mayer (2000) identified migration and mobility as a determining variable. We therefore included a variable in our study to measure this factor (*NbPassAero*).

Several studies have shown the link between the dissemination of epidemics and the socio-economic vulnerability of populations (Barnes, 2014; Stanturf et al., 2015; Bonifay et al., 2018). However, these studies do not focus on the spatial dimensions of the epidemic's transmission, nor do they account for what is at stake in relation to the scale of the analysis. Our hypothesis aims to address these limitations by assuming that the most economically developed areas are the most likely to concentrate the highest

number of cases since they are more closely connected to the rest of the world, especially the other most highly developed regions of the globe. This can in turn lead to heightened exposure of the most vulnerable socio-economic groups at local level. However, it can also keep areas with populations that are highly socio-economically vulnerable more distant from the process of the virus's transmission, or at the very least, reduce their exposure and postpone the moment they might be affected. We therefore added the variable *GDP* which represents GDP/capita in PPP.

Incorporating various examples, Reyes et al (2013) show how the urban environment can be an aggravating factor in the fight against infectious diseases. In their study on swine flu (H1N1) in Hong Kong, Lee and Wong (2010) show that densely populated areas were more affected overall. Given the effects of densely built-up areas, we argue that because the spatial proximity of individuals is more important in dense areas, this then exacerbates more rapid circulation of the virus. We therefore added a variable relative to the population's density (*Density*) as well as one regarding the total population size in the province (*PopTot*). This should allow us to identify the potential effects of thresholds, with the relation between the speed of the virus transmission on the one hand and population density on the other, which is not necessarily in direct proportion. It is possible that there are threshold effects resulting from significant variations between specific areas and societies with regard to the characteristics of housing, the composition of family groups living under the same roof, private and public sociability norms, hygiene practices and proxemic structures (Hall, 1966 & 1968). However, it is not easy to identify such threshold effects within one country as behavioural norms are not sufficiently marked.

Finally, several recent studies have shown that older people have a higher probability of being affected by the virus (Xu et al., 2020 ; Chen et al., 2020). Our model includes the percentage of the population aged over 65 (*Share65+*).

2.2 Methodology

2.2.1. Principles of spatial analysis of COVID-19

Analysis of COVID-19 and its spatialization clearly squares with research undertaken by geographers as well as their methodology. The geographical approach is based on the paradigm that an event's location is not the result of chance. In other words, there are always place effects with respect to the way events spread or are located. This led us to develop a modelling approach to geographical space, highlighting all recurrent forms of organization in an epidemic. Several researchers (Vaneckova et al., 2010; Robertson and Nelson, 2014; Weimann et al., 2016) have highlighted the importance of spatial analysis in understanding how viruses spread. This approach seeks to pin down the exact location of the places where a disease emerges and develops, cross-referencing it with other factors such as population characteristics, infrastructures, etc. Socio-spatial analysis thus allows us to define more or less resilient types of organisation in the face of an external hazard (Sridharan et al., 2007).

The methodology adopted is designed to define a geography of the spatial spread and concentration of the virus, based on the hypothesis from the literature that there are spatial effects (spatial dependence and spatial autocorrelation) in the linkages between the spread of COVID-19 and its explanatory factors. We propose a geography of the outbreak by highlighting the spatial concentration and transmission effects (spatial autocorrelation and co-location effects) associated with a spatial autoregressive model to identify the factors that play a role in explaining the observed event.

2.2.2. Spatial autocorrelation and co-location effects

A co-location analysis technique was first developed by Anselin *et al* (2002) who designed a bivariate local spatial association indicator (BiLISA) to study the spatial correlation pattern between two georeferenced variables (i.e., number of alcohol outlets relative to the number of criminal incidents in the areas in question). BiLISA is used to assess the correlation between one variable in one area and a second variable in neighbouring areas. Bivariate analysis allows the relationship between the dependent variable and the explanatory variables to be isolated one at a time. It is also possible to study spatio-temporal autocorrelation, in other words, the correlation of a variable with reference to the spatial location of a single variable within a given time interval. The correlation of a variable with itself in space and time is then analysed (Anselin *et al.*, 2002). The idea here is to conduct a parametric examination (beyond visual inspection) of the way spatial patterns are correlated between several variables in order to draw conclusions about the spatial dynamics that link a set of localized data. In more technical terms, examining the similarity of spatial processes between variables can be seen as a way to test the robustness or persistence of a given spatial pattern/scheme over time, such as by comparing patterns of local spatial association between COVID-19 and population density (robustness) or between cases of COVID-19 at two reasonably spaced periods in time (persistence) for example. Thus, the method applied allows the spatial covariations of the explanatory factors behind the spatial concentration phenomena of the virus to be captured. We can then identify whether, for each spatial area, the virus is significantly spatially correlated with another variable.

In order to identify and assess the magnitude of spatial relationships, we used Moran's I to measure spatial autocorrelation and identify spatial clusters in the data. Four types of spatial associations can be derived from this statistic for our study: i.e., high-high (HH - spatial concentration of high values of cases and high values of the independent variable from neighbouring regions) and low-low (LL - spatial concentration of low values of cases and low values of the independent variable from neighbouring regions) types for spatial clustering of similar values, and high-low (HL - spatial concentration of high values of cases and low values of the independent variable from neighbouring regions) and low-high (LH - spatial concentration of low values of cases and high values of the independent variable from neighbouring regions) types for spatial clustering of dissimilar values.

The measure of local bivariate spatial autocorrelation using Moran's I statistic, derived from Anselin's (1995) formula, is:

$$I = z_{xi} \sum_{j=1, j \neq i}^N w_{ij} z_{yj}$$

where x_i represents the regional growth and y_j the independent variable for the region i and the neighbouring region j , while z_x z_y are the standardized z-scores of both the variables and x_i y_j . The choice to model spatial proximity and interdependence between territorial units using the spatial weight matrix w_{ij} is a complex and controversial one in spatial analyses. There are a wide range of applications to determine W, depending on the purpose of the study (Anselin et al., 2000, Shi *et al.*, 2006). GeoDa now provides the threshold beyond which spatial correlation ends. For the purpose of our analysis, we tested several weighting matrixes and then selected one from the ten closest neighbours (allowing us to maximise Moran's I).

A permutation approach (here 999) was used to assess the statistical significance of Moran's I and BiLISA results. Randomization assumes that the location of the values and their spatial arrangement are unimportant. Based on randomization, various theoretical standard deviations for Moran's I were obtained, each giving a different p-value as a pseudo-significance. The threshold value of $p = 0.05$ defined its significance. The p-values follow an asymptotically standard-normal distribution, allowing us to evaluate their level of significance by comparing them to a reference distribution (Anselin 1995), and thus defining the thresholds beyond which the HH, LL, LH, HL relationships were no longer significant. The BiLISAs were calculated using GeoDa version 1.12 software (Anselin *et al.*, 2010).

2.2.3. The spatial autoregressive model (SAR)

When dealing with the spatial autocorrelation of data, use of an appropriate econometric model is recommended to avoid any bias in the estimates. To this end, following Anselin and Florax (2012), the *Lagrange multiplier* test allows us to choose between two spatial econometric models (SEM model (spatial autocorrelation of errors) versus a SAR model (spatial autoregressive)). The decision-making rule suggested by the same authors is used to determine the most appropriate specification. If LMLAG is more significant than LMERR, and RLMLAG is significant while RLMERR is not, then the appropriate model is the auto-regressive spatial model. Conversely, if LMERR is more significant than LMLAG, and RLMERR is significant while RLMLAG is not, then the appropriate model is the spatially self-correcting error model. The test results are presented in Table 2. The previous test strategy led to the selection of a model with spatially self-corrected errors. The spatial autoregressive model makes it possible to take the effects of neighbourhood externalities into account. In our case, the number of cases of COVID-19 in an area i is explained by the exogenous variables specific to i , but is also explained by the exogenous variables of its neighbours. The model is also characterized by the presence of a spatial

diffusion effect based on the error process, where a random shock in area i perturbs the number of cases in area I , but also the number of cases in neighbouring areas.

The model is written as follows:

$$Y_{it} = \rho \sum_{j=1}^n w_{ij} y_{jt} + x_{ij} \beta + \theta_{it}$$

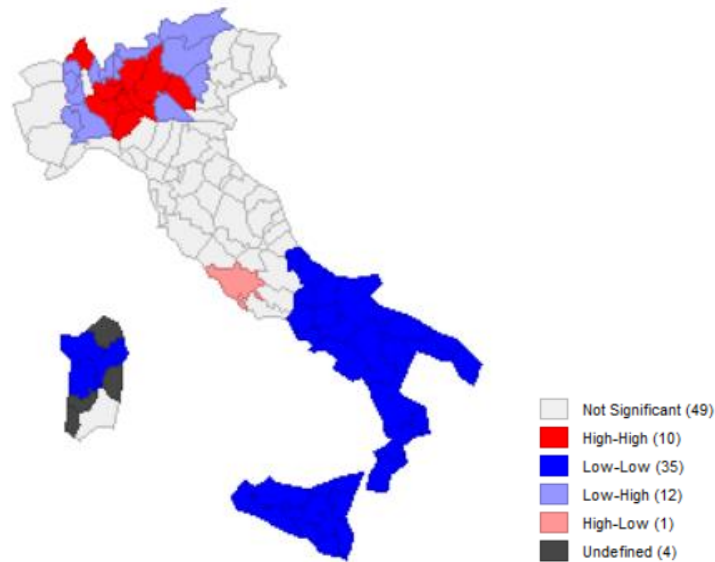
With Y_{it} is the number of cases in territory i at date t , x_{ij} represents the matrix of exogenous variables, the weighting matrix is noted W_{ij} , where ρ is the parameter of the spatially lagged dependent variable that captures the spatial interaction effect indicating the degree to which the number of cases in one province is determined by the number of cases of its neighboring provinces.

3. Results

Analysis of the Italian case is crucial since it was the first country to be confronted with out-of-control transmission of the CoViD-19 epidemic and therefore provides a good basis to assess lockdown strategies. In the case of China, suspicion surrounding the accuracy of the public data released prevents us from fully understanding the kinetics of the epidemic contained through a lockdown strategy. On the other hand, the numerous social, political, economic and institutional similarities between European countries compared to the rest of the world mean that it is possible to draw useful and relevant lessons for other European countries, in particular Spain and France which have also been strongly affected.

Our first goal was therefore to assess the geography of the effects of the spatial concentration of cases of CoViD-19 in Italy. Calculations of Moran's Index on 8 March (first day of the application of the general lockdown decision made by the Italian government), 18 March and 28 March revealed a strong and significant global spatial autocorrelation (Table 2). In order to assess the effects of the spatial dependency of cases, we applied the spatial statistics of the Moran Index at local level. We first looked to test the persistency of the spatial concentration of the number of observed cases over time. To this end, we calculated the BiLISA of the number of cases identified between 8 March and 28 March (Moran's $I = 0,378$) and then mapped them (Figure 1). (i) The provinces where we can observe a spatial concentration of a small number of cases between the two dates in the Mezzogiorno region are in dark blue, (ii) the spatial concentration of a high number of cases between the two dates is in red, (iii) the spatial concentration of a high number of cases by 8 March, in the province of Rome, surrounded by areas with a low number of cases by 28 March is in pink, (iv) the spatial concentration of provinces with a low number of cases surrounded by areas with a high number of cases by 28 March is in light blue. We can thus see a persistency in the spatial concentration of cases in Lombardy (high – areas in red) and in the Italian South (low – areas in dark blue).

Figure 1. Co-localisation of spatial concentration between 8 March and 28 March



Source: Authors.

We can observe a strong concentration of the epidemic in Northern Italy, especially in the central provinces of Lombardy, with a contained spread in the adjacent regions and provinces. On the other hand, the situation in the South of Italy presents a much weaker spatial concentration of the virus and number of cases. Only the capital, in other words, the Rome region, which has strong international connections, experienced an intermediary situation with a relatively high concentration of cases and a moderate spread through the provinces in the vicinity of Lazio.

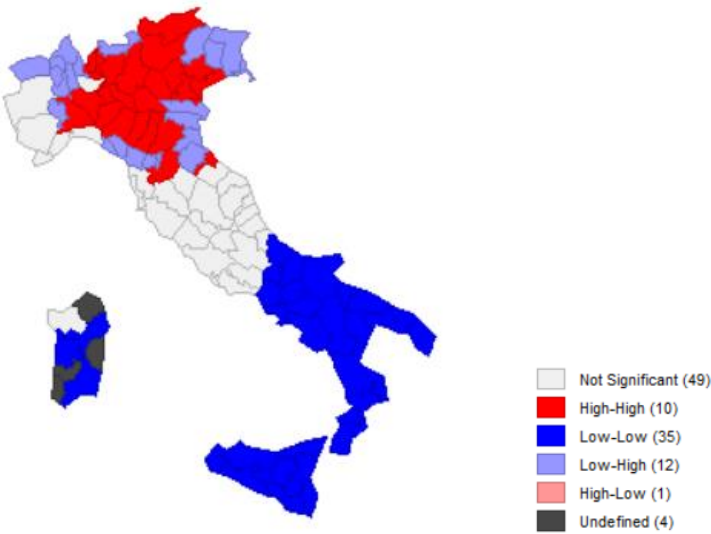
Given the current evidence, it is generally understood that the virus entered Italy through Lombardy and more specifically, the Milan region, notably Codogno in the South East of the city. Its acceleration occurred in Bergamo during a European football match with the Valencia (Spain) football team. A traditional approach would consist of speculating its gradual spread to all areas of the country from the place where this highly contagious agent was introduced, with gradual spatial homogenisation in case density. However, this did not occur. Further analysis of the data shows that between 8 March and 28 March, there was very clear persistence in the relative density of cases (Figure 1). Since the lockdown in Italy began on 8 March, the co-localisation map of the spatial concentration of CoViD-19 cases appears to confirm the anticipated effects of quarantine, especially since eleven towns were locked down from 22 February 2020, six of them in Lombardy.

Whether at country level or at the level of adjacent regions, it appears that when a lockdown is put in place early enough, it does seem to contain the situation, in other words it contains the localisation of areas with a very high density of cases. This result is all the more remarkable since SARS-CoV-2 is both highly contagious and has a large number of asymptomatic cases. The combination of these two factors inevitably hampers detection of the virus’s circulation and reduces the chances of identifying the best moment for a lockdown. In the absence of other means (systematic and reliable testing, targeted quarantine) to introduce other strategies, lockdown appears to be an effective solution in the face of an infectious agent for which we have neither a vaccine nor efficient treatment to treat acute cases that carry a strong risk of death.

Moreover, in addition to examining the efficiency of lockdown, we also calculated the BiLISA of the reported number of cases by 28 March (Moran’s $I= 0,304$) with the GDP/cap, and then mapped them (Figure X). We identified a (i) a spatial concentration of high values of cases and high values of GDP from neighbouring regions and (ii) a spatial concentration of low values of cases and low values of the GDP from neighbouring regions. In light blue, there is also a spatial concentration of low values of cases and high values of GDP from neighbouring regions.

The explanatory economic factors for such discrepancies appear to match the reality. Italy’s North/South economic divide seems to be accentuated by the geography of the epidemic. The highest number of cases is in the most economically globalized areas, which explains the localisation of the place where SARS-CoV-2 first broke out in Italy and the localisation of the first infection cluster. Map 2 is particularly enlightening as it not only shows the localisation of the place where the virus emerged, but also an area of propagation in the country’s most economically developed region and a few adjacent provinces.

Figure 2. Co-localisation of the spatial concentration between the number of cases on 8 March (start date of lockdown) and GDP/cap.



Source: Authors.

Table 2: SAR model of the number of cases in Italy

	OLS	SAR (1)	SAR (2)	SAR (3)
GDP	0,301***	0,359***	0,428***	0,493***
NbPassAero	0,001*	0,002*	0,011*	0,013*
Density	0,016**	0,052**	0,046**	0,002**
Share65+	-0,138	-0,195	-0,151	-0,131
PopTot	-0,005**	-0,006**	0,241**	0,408**
ρ		0,596***	0,514***	0,296***
Observations				
LIK	3384,601	3465,725	3510,882	3591,731
I Moran		0,404***	0,357***	0,341***
Lmerr	17,182**			
LMRerr	5,856			
Lmlag	29,179**			
LMRlag	1,634**			

Source: Auteurs.

NB: * represents the levels of significance. The LM tests compare traditional OLS regression against the alternative SAR and SEM specifications under the null of no spatial dependence. SAR (1) March 8; SAR (2) March 18; SAR (3) March 28

After identifying these spatial concentrations, we drew up a spatial model that allowed us to test the influence of different variables on the number of cases observed (Table 2). We found that ρ is positive and significant, confirming the spatial dependency effect. Digging further, its minimal value declines between 8 March and 28 March, indicating a transmission effect, but one that is very low. We can thus assume that the lockdown implemented on 8 March did indeed help to slow the epidemic.

The findings show that level of wealth informs the number of people infected (strong and highly significant coefficient). We can also note that number of passengers is positive but not particularly significant. For Italy, we can therefore say that the higher the number of visitors at an airport in a province, the higher the number of cases detected. From this perspective, Lombardy is an interesting case as, encompassing the city of Milan and its international airport, it concentrates significant international connections and flows of people in Europe and internationally. Given the intense economic and commercial exchanges between Italy and China, Lombardy is an area that is highly propitious to the emergence of the virus in Italy, especially via Milan, as are the adjacent regions and around the Emilia-Romagna and Veneto regions whose economic activities (industrial districts, tourism) are closely tied to Lombardy and its economic centre. In 2015, for instance, the company ChemChina, the

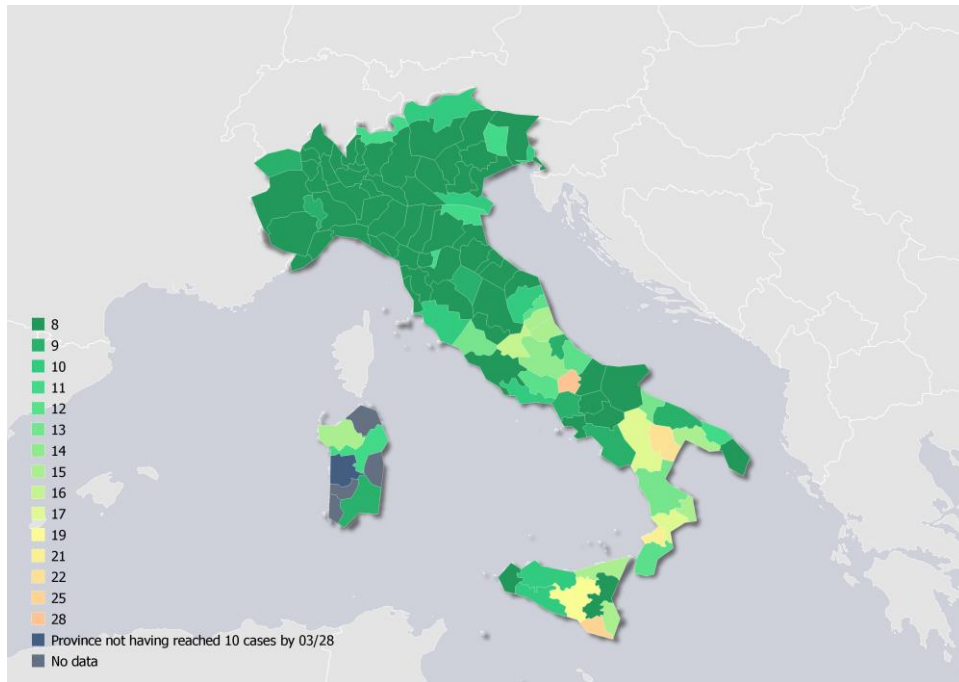
emblematic constructor of Italian tyres whose head office is in Milan, became Pirelli's largest shareholder. High connectivity with the rest of the world is a great asset for regions in terms of economic attractiveness, but our findings show that it rapidly becomes a threat during a health pandemic since these are the areas that are most affected.

Population size and density also seem to play a part in explaining the number of cases observed. With regard to density, the role of spatial proximity in everyday situations is confirmed as a key factor in the spread of viruses such as SARS-CoV-2. Known as the effect of size, it confirms what has already been observed on a global scale where a higher number of cases in big cities has been highlighted.

On the other hand, the percentage of people over 65 in the overall population does not explain the number of cases observed (not significant). It therefore appears that the spatial conditions of social life are more likely to explain the spread of an epidemic than the presence of at-risk populations. This can be explained by the fact that age and personal social attributes have little or no impact on a person's contagiousness, and that they only have an incidence (notably age) on determining populations liable to suffer from acute cases and death. The kinetics of spatial dissemination of SARS-CoV-2 is therefore highly dependent on the spatial organisation of societies from the moment one or several cases is introduced without being immediately detected. This dependency is interesting as, to a certain extent, it can guide the construction of alternative scenarios of spatial dissemination of SARS-CoV-2 in a given area, keeping in mind the scientific knowledge available in terms of its social and economic geography, spatial practices and population(s) (including its mobility habits) and housing characteristics in relation to the composition of households.

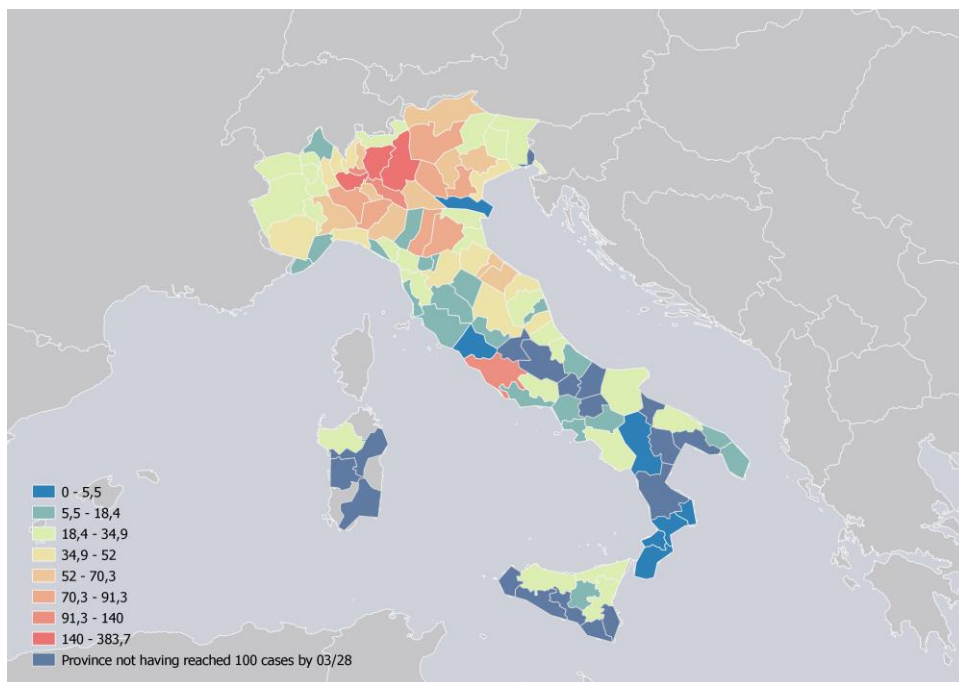
Finally, we observed and measured the kinetics of the epidemic in Italy from two elements on the map: the date on which the threshold of 10 cases was passed in one province (Figure 3) and the speed at which the number of detected cases evolved in each province up to 28 March 2020 (Figure 4).

Figure 3. Process of spatial transmission of the virus between 8 March and 28 March 2020



Source: Authors.

Figure 4. Intra-provincial epidemic kinetics between 8 March and 28 March 2020



Source: Authors.

It appears from Figure 3 that the spread of SARS-CoV-2 was effectively advancing across the whole of Italy by the beginning of March 2020, except in the province of Sardinia which still had not reached the 10 cases threshold by 28 March 2020. The spread towards the South was therefore underway, with a notable ‘delay’ in many of the Mezzogiorno provinces. This delay could range from a few days up to 20 days, especially in Basilicata, Calabria, Sicily and Sardinia, but also in the Abruzzo region. Without any

government intervention, we can therefore calculate that the whole of Italy would have gradually been affected by an upward trend in the circulation of the virus in each region.

The decision to order a lockdown on 8 March 2020 seems not only to have ‘halted’ the epidemic’s intensity in terms of the number of cases and its spatial concentration (Figure 1), but also to have halted and even disassociated the internal kinetics of each area (Figure 4). Indeed, in the period under study, we can see that in the Northern provinces, the spread of the epidemic was extremely rapid, whereas in the Mezzogiorno region (even Naples), the provinces’ internal kinetics were at least 10 times lower than those in the hardest hit Northern provinces. There were still 18 provinces that, by 28 March, had not gone beyond the 100 detected cases threshold. It therefore appears that the lockdown slowed the spread at a very early stage in places where it was implemented in comparison with the intensity of the diffusion of SARS-CoV-2. It also suggests that the lockdown was wholeheartedly respected across the whole of Mezzogiorno. The exception of Naples confirms the importance of the variables regarding density and the impact of demographics in the propagation kinetics of SARS-CoV-2.

Given these very stark contrasts between the north and the south of Italy, it also appears that the earlier a lockdown is put in place, the more effective the preventive containment of the spatial diffusion of highly contagious infectious agents such as SARS-CoV-2 will be. It also suggests that a lockdown that partitions off areas, in this case provinces, is a useful strategy.

4. Conclusion and discussion regarding lockdown strategies against the spread of Covid-19

The COVID-19 outbreak is unprecedented in recent human history. The reasons for its singularity are geographic and spatial (epidemic outbreaks concomitant with areas of high population density and economic development).

Hellewell et al (2020) demonstrated the role of lockdown measures in controlling the spread of COVID-19. The model in our analysis shows a decline in spatial dependency of the variable studied, which could indicate a form of deceleration in its diffusion linked to the effects of the lockdown. On the other hand, our study highlights a geography of areas that are less affected than others. In the case of Italy, the Mezzogiorno region clearly reported a far lower number of cases than the rest of the country. Thus, areas that are generally associated with socio-economic difficulties end up being protected. In addition, the rapid lockdown strategy introduced by the Italian government on 8 March 2020 was almost certainly a key factor in slowing the spread of the virus to the south of the country.

While globalisation can be an accelerator of epidemics or pandemics, it also accounts for the fact that we are now seeing the expansion of ways to prevent and cure it. The largest research centres have undertaken to publish all their work on the virus in open access as soon as possible. At the same time, we could ask whether the globalisation of information is partially responsible

for fuelling panic and fear in the past, since viruses have always been vectors of fear (Smith, 2006; Kott and Limaye, 2016).

The resilience of the COVID-19 epidemic and the exponential growth in its casualties raises numerous questions about the strategies put in place to control it.

The international community refers here to all nation states (or groups of nations, such as the European Union) and their respective public opinions, multilateral organisations and NGOs for health protection and monitoring, and world-renowned health research institutes mobilised to combat the virus and its spread. At the start of the epidemic, however, its international diffusion was not so obvious, so much so that more than a month after its appearance, this new viral outbreak met with almost general polite indifference. The epidemic's spread was indirectly favoured by, on the one hand, underestimation by the major powers, convinced that they were safe from contamination, and on the other hand, procrastination by a large part of the population who did not take the virus and its contagiousness seriously. In addition, we should not forget the widespread suspicion regarding the official data shared by the Chinese authorities concerning the reality of the epidemic in China, especially in Wuhan, the city at the centre of the outbreak.

The analysis presented above based on the Italian case offers some strategic guidelines in the case of a CoViD-19-type epidemic breaking out in one of the major centres of economic globalisation. It certainly appears effective to introduce a general and complete lockdown as early as possible since this would spatially contain the virus and reduce the internal diffusion kinetics within each area. The results are interesting and encouraging for countries such as France and Spain which opted for this strategy due to a lack of resources that could possibly have offered a different approach (mass testing, mass mask wearing, etc.). It is especially useful when compared with pandemic situations that can evolve in countries where the government has introduced neither a targeted strategy nor a lockdown (US, Brazil).

During the first 'preventive' lockdown, the authorities can prepare for a partitioned and targeted lifting of the lockdown, identifying the areas where cases of CoViD-19 are the most concentrated and where epidemic kinetics are highest, and then pursue systematic testing and a targeted rather than generalised lockdown of clusters of infected areas and people. The first areas where the lockdown is lifted, in accordance with the average incubation period, should be those furthest from the initial epidemic centre or from areas that have the most cases and the highest kinetics. The areas "kept distant from the epidemic" should be those that require the lowest amount of testing. In the meantime, the government can concentrate resources on the most infected areas where the most acute cases will be concentrated. However, given the apparent benefits of the initial lockdown suggested by the Italian case, in the course of partitioned and targeted lifting of the lockdown, all inter-territorial mobility will need to be banned or reduced to a minimum. Incidentally, this should also be a fundamental principle from the very outset of the initial lockdown (which was not the case in France that saw numerous movements from Paris to

the French coastal areas between 14 and 17 March). This absence of inter-territorial travel should help to preserve the disassociation observed in the epidemic kinetics between areas thanks to the lockdown.

With regard to the limitations of our study, we do not as yet have the micro-data to map human mobility. Indeed, as Sorichetta et al (2016) argued in the case of malaria, very fine scale data on migration makes it possible to trace the connectivity between regions and population movements, and thus to better identify local and national strategies for eradicating epidemics. Therefore, in future studies, it would be interesting to analyse such intra-territorial mobility. In the case of Northern Italy and in relation to the density of the fabric of economic activity (notably with the presence of industrial districts comprising thousands of SMEs), we can assume that inter and intra-regional migrations of people (between Lombardy, the Veneto region, Emilia Romagna and Piedmont) are relatively high. It would therefore be interesting to take this study further by exploring relational and proximity effects using indicators of people's mobility such as commuting between home and work, for instance.

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