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Are the Italian government's quarantine measures about the Covid-19 lethality effective? A mathematical statistical analysis

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Abstract

In this paper, the authors present a particular Weighted Least Squares model, the Heteroskedasticity Corrected Linear Model (HCLM), to estimate the impact of the quarantine measures adopted by the Italian government since March 4th 2020 on the lethality rate of the Covid-19 virus. The results obtained suggest that overall these restrictive measures have proven effective, leading to a 3,59% reduction in the lethality rate within 27 days. Furthermore, the authors have decomposed the historical series of the Lethality Rate by identifying, in addition to a first component of easily observable trend, also a second component of noise that is distributed as a white noise. The model shown by the authors, which is absolutely innovative, can also be used to study historical series data relating to any epidemic, be it of bacterial or viral origin.

JEL classification numbers: C01, C02, C13, C22, C60.
Keywords: Covid-19, Lethality rate, Mathematical and statistical models for epidemiology, Time Series Analysis, Health Policy.

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1. Introduction

The initial cases of new acute respiratory disease from SARS-CoV-2 (or more simply from new coronavirus disease 2019, whose acronym is Covid-19) occurred, in December 2019 and January 2020, in Wuhan, in the province of Hubei, in China. Very soon, however, the Covid-19 spread throughout Continental China and in neighboring countries faster than other viruses, such as SARS and MERS, due to the greater globalization and the focus of the epidemic. Wuhan, in fact, is a great junction that connects the north, south, east and west of China through the railways and a large international airport; as a result, the massive rail and air transit, especially during the Chinese New Year, allowed the virus to spread throughout China, raising important global concerns because several cases have also been reported in other countries. In particular, in February 2020 an outbreak of SARS-COV-2 (Covid-19) coronavirus infection was identified in Northern Italy, and since that date an ever-increasing number of cases of infection have been detected.

To emerge of the new coronavirus, SARS-CoV-2, an acute respiratory syndrome that causes severe respiratory tract infections in humans, has thus become a global health emergency. From the same family of the SARS and MERS coronaviruses, the Covid-19 leads to severe cases of pneumonia; the human-to-human transmissions have incubation times between 2 and 10 days and its diffusion is facilitated through droplets, hands or contaminated surfaces.

The health authorities immediately tried to control the disease, isolating people suspected of having the disease, carefully monitoring contacts, collecting epidemiological and clinical data from patients and developing diagnostic and therapeutic procedures. The sampling strategy of the subjects to be tested was, initially, uneven on the national territory but, subsequently, it was transformed and unified and was reduced to a sampling of only symptomatic subjects.

Since it has been observed that the transmission takes place from person to person, drastic measures have been taken to prevent further transmissions in the hope of slowing down the spread of Covid-19, or rather standard containment principles have been adopted, two of which are the isolation of known cases and the quarantine of people deemed to be at high risk of exposure. These measures are necessary to end the transmission of community epidemics and to prevent the importation of new infections and their subsequent transmission chains. To make these outbreaks even more manageable, additional common-sense precautions have been suggested, such as regular hand washing and the use of masks.

In a document, published on the MedrXiv website and elaborated by the group of the Fudan University of Shanghai directed by (Li et al., 2020), was presented a mathematical model to explain that the containment measures are indispensable because "cases tend to multiply by 10 every 19 days". From the same research also reveals another fact: the increase in cases outside of China follows an almost exponential trend overall, with a growth rate of 10 times every 19 days ". According to the model, this is the trend to which the epidemic would tend to grow if containment measures were not adopted. In other words, the model, based on the cases detected from 21 January to 28 February 2020, indicates not only that containment measures are indispensable since the new coronavirus spreads easily, but also that, without the implementation of effective countermeasures, the cases would tend to multiply by 10 every 19 days. For this reason, the authors of the research launch an appeal because are made indispensable containment measures and because "global actions on public health all over the world " are being taken.

The key word to stem the increase in cases, therefore, remains "containment ".

The same concept, namely that measures must be implemented to prevent or reduce transmission in populations at risk, is confirmed in the paper Early Transmission Dynamics in Wuhan, China, of Novel Coronavirus – Infected Pneumonia, published in the New England Journal of Medicine in January 2020 (Qun et al., 2020), in which an analysis of the data on the first 425 cases confirmed in the laboratory in Wuhan was conducted, to describe the epidemiological characteristics and transmission dynamics of Covid-19. Information on demographic characteristics, exposure history and disease times of laboratory-confirmed Covid-19 cases was collected which had been reported by 22 January 2020 and the characteristics of the cases were described and the main epidemiological distributions of delay were assessed. Based on this information, the authors of the paper have shown that there is evidence that human-to-human transmission has occurred between close contacts since mid-December 2019 and that, therefore, considerable efforts are needed to reduce transmission and to control the outbreak.

The results of the study A novel coronavirus outbreak of global health concern (Wang et al., 2020) provide, instead, data on the severity of the emerging infection and on the symptoms deriving from the infection in the prodromal phase, including fever, dry cough and malaises.

In the paper is stressed that the rapid dissemination of information is a top priority for the control and the prevention of diseases; educational campaigns should be launched to promote precautions for the travelers, including frequent hand washing, the label against coughing and the use of personal protective equipment when visiting public places; the public should be motivated to report the fever and other risk factors for coronavirus infection, including close contact with confirmed or suspected cases.

A group of scientists from the University of Maryland, belonging to the Global Virus Network (Sajadi et al., 2020), has established an interesting correlation between the spread and climatic characteristics of the areas in which it occurred and has verified that the outbreak of the epidemic coincides with temperatures relatively stable for more than one month. Another feature of the research is that both the melatonin and the vitamin D, activated by exposure to ultraviolet rays, play a role in the incidence of diseases affecting the respiratory system.

The Maryland study is not, however, the only one that has been done on the subject. In fact, researchers from the University of Guangzhou, China (Guan, 2020), confirmed that the transmission of the virus travels better around 8.7 degrees, while scholars from the University of Tsinghua, in Beijing (Wang et al., 2020), on the base of data from the Chinese Center for the control and the prevention of the disease, showed that there were more cases where temperatures and humidity were lower and not where it was warmer and humidity was higher. So the arrival of summer could significantly reduce the transmission.

A research from the Greifswald Hospital and the Ruhr University in Bochum, Germany, titled Persistence of coronaviruses on inanimate surfaces and their inactivation with biocidal agents, published in the Journal of Hospital Infection (Al-Tawfiq et al., 2019), analyzed the weather of permanence of others human coronavirus on surfaces and has proven that it stays longer in cool and wet situations. On different types of materials (metal, glass, plastic) it can remain contagious from 2 hours to 9 days. At 4 degrees it can remain alive for 28 days. At 30-40 degrees the duration of persistence of highly pathogenic viruses, such as MERS-CoV, TGEV and MHV, disappears in a short time or is reduced.

The results can extend to what has emerged in these days. In fact, a group of American researchers, coordinated by the National Institutes of Health (Nih), with the participation of the University of Princeton and of the University of California, has subjected the new virus to specific laboratory tests to evaluate its resistance over time on different surfaces (something other than transmissibility by contact). The results are published on the MedrXiv website (Van Doremalen et al., 2020). The US researchers have thus discovered that the virus remains active for up to 4 hours on copper and up to 24 hours on cardboard. Its vitality even extends up to 72 hours on plastic (polypropylene) and stainless steel, materials which, fortunately, are easier to clean and disinfect.

After evaluating the resistance of SarsCoV2 on the surfaces, American researchers went even further: they sprayed the virus in the form of aerosols in a closed environment, verifying that it can remain suspended in the air for up to 3 hours. The study was, however, conducted in controlled conditions in laboratory that do not reflect those conditions present in the real world, so the researchers warn that these results do not demonstrate that it is possible to catch the virus simply by breathing in an environment where another infected person was.

Through the models of the Global Virus Network it is now possible to be able to predict the next outbreaks of the virus, which makes it possible to implement precautionary measures to avoid the spread. In this regard, it is foreseeable that the new expansion sites could be located north of the current position. This means, for the United States, that the virus will move to British Columbia, England, Scotland and Ireland (where it could burst between late March and April), and northern China, will be involved, where for now there had been little diffusion.

Some scientists from Beijing University and from Shanghai University have made an important discovery: the virus is not one, but two. In the paper On the origin and continuing evolution of SARS-CoV-2 (Tang, 2020) it is stated that a form, called L-type, is much more aggressive and has already infected 70 percent of people, while the second, S -type, is a lighter form and has affected 30 percent of the population.

These two mutations probably originated from a primitive version, occurred after the human infection and now circulate simultaneously. This implies that other mutations may appear: the virus could mutate again, as it once did. More precisely, genetic population analyzes of 103 SARS-CoV-2 genomes indicated that these viruses evolved into two main types, indicated by L and S. While the first type (L) was more prevalent in the early stages of the epidemic in Wuhan, the frequency of the second type (S) has decreased since the beginning of January 2020.

The analysis of Professor Enrico Bucci, professor of Biology at the Temple University of Philadelphia, carried out with colleagues De Nicolao, Marinari and Parisi, on the regional evolution of the Sars-Cov-2 epidemic (Bucci et al., 2020), claims that from the data can be observed the first results of the social distancing: the doubling time has slowed down, namely the time in which the number of hospitalized and of the dead people doubles, but the conditions of Lombardy region are still critical.

This paper, compared to those previously mentioned, analyzes the historical series of the lethality rate of the virus rather than that of the total number of infected and, using a mathematical statistical approach, highlights that it has an exponential trend too but which it has not a seasonal component, while it has a strong noise component. It also presents an analysis regarding the effectiveness of the restrictive measures imposed by the Italian government to assess their adequacy for policy purposes.

2. Research aims

The main objective of this paper is to estimate the impact, on the lethality rate, of the restrictive measures adopted by the Italian government to contain the infectivity of Covid-19. Since all the variables that determine the lethality of the virus in question currently are not known, it would be inadequate, for the achievement of the objective, a simple linear regression model having as its only explanatory variable a dummy that assumes value 1 in the periods in which the restrictions are operational and 0 in all other periods. Consequently, the authors built a Heteroskedasticity Corrected Linear Model (HCLM), a particular type of Weighted Least Squares (WLS) model, using, as repressors, the Lethality Rate components obtained through an estimate of a Basic Structural Model (BSM). The latter was proposed by Harvey and Peters in 1990 (Harvey and Peters, 1990) and it was improved through subsequent contributions (West and Harrison, 1996) (Kitagawa and Gersch, 1996). However, this method can be freely applied to more general contexts such as epidemiology and has been used in this manuscript also to verify the existence of a seasonal component (i.e. linked to factors such as environmental temperature) of the Lethality Rate. In other words, using a mathematical statistical approach, this paper analyses the historical series of the lethality rate of the virus, rather than that of the total number of infected, and highlights that it also has no seasonal component.

The authors also demonstrated that, under appropriate assumptions not particularly restrictive, it is possible to demonstrate that the HCLM is an undistorted and consistent estimator, subjected to a validation analysis which confirms that it is also suitable for forecasting purposes. In other words, this study allows to evaluate the effectiveness of the restrictive measures imposed by the Italian government, namely the adequacy of the model of mobility limitation chosen by the Italian government to stem the contagion and offers ideas regarding the debate on the opportunity to continue with this model or to adopt an alternative one similar to that of South Korea, based instead on the traceability of people's movements.

The model exposed by the authors has an absolutely innovative character and can also be used to study data in historical series relating to any epidemic, both of bacterial origin both of viral origin.

The paper is organized as follows. In the section 2, after the introduction, the authors present the research aims of the paper, while in the section 3 they formally introduces the problem and search to define and to describe briefly the method by which the mathematical statistical analysis was performed.

In section 4 the results of the estimates are presented. The section 5, finally, provides the conclusions drawn by the authors and contains a general discussion on directions for future research.

3. The model and the estimation procedure

Consider the Basic Structural Model (BSM) proposed by Harvey and Peters, frequently used in the economics for the decomposition of data into historical series but also applied to more general contexts, including the medical one.

The model BSM decomposes a time series into three independent components, namely a trend (μ_t), seasonal (γ_t) and irregular (ε_t) component:

$$y_t = \mu_t + \gamma_t + \varepsilon_t \tag{1}$$

where y_t is a common a random variable, μ_t is a trend, γ_t is a seasonal component, is ε_t a white noise and $T = 1, \dots, T$.

The three terms appearing at the second member of the (1) can be stochastic or deterministic.

For the trend and the seasonal components be valid:

$$\nabla\mu_t = \beta_{t-1} + \eta_t \tag{2}$$

$$\nabla\beta_t = \zeta_t \tag{3}$$

$$\Delta\gamma_t = \Delta\omega_t \tag{4}$$

where the operators ∇ and Δ present in the (2) and in the (4), indicate, respectively, the first difference and the seasonal difference, β_t is named *slope*, and $\eta_t \sim WN(0,\ \sigma_\eta^2)$, $\zeta_t \sim WN(0, \sigma_\zeta^2)$, $\omega_t \sim WN(0, \sigma_\omega^2)$ are mutually uncorrelated white noise processess.

Choosing as dependent variable the lethality rate at time the (1) becomes:

$$L.R._t = \mu_t + \gamma_t + \varepsilon_t \tag{5}$$

where $L.R._t$ is the ratio of the number, D_t, of infected people dead between the time 0 and the time t, and of the number, I_t, of the infected people and it is computed as follows:

$$L.R._t = \frac{D_t}{I_t} \tag{6}$$

The two variables D_t and I_t depend, within the others, also by some seasonal factors (more in particular by weather conditions) that in the (5) are represented by the term γ_t.

Since the (5) is a linear function it is possible to consider the following linear regression model for $L.R._t$:

$$L.R._t = \alpha_0 + \alpha_1\mu_t + \alpha_2\gamma_t + \alpha_3 R_t + z_t \tag{7}$$

where R_t is a dummy variable that take value 1 in that periods in which the restrictions on individual mobility are effective and take value 0 in all other periods, while z_t is an error term that enclose ε_t.

The random component ε_t, in fact, cannot be comprised among the regressors of the (7), because, otherwise, as can be seen by (1), there would be exact collinearity. On the other hand the ε_t is a purely random component of $L.R._t$, and its insertion into the error term z_t does not imply omitted variable bias, because it is not correlated neither with the random variable, nor with the other regressors of the (7). Instead the term ε_t can be enclosed into the (7) if one of the two components of the (1) results not statistically significant on the basis of the BSM. For example, assuming that the not significantly different from zero component is γ_t, (7) becomes:

$$L.R._t = \alpha_0 + \alpha_1\mu_t + \alpha_2\varepsilon_{t_t} + \alpha_3 R_t + z_t \tag{8}$$

Under the following two restrictive hypotheses:

a) The variables μ_t and γ_t are integrated of order 1;

b) The variables μ_t, γ_t and ε_t are estimated correctly through the BSM, namely $\hat{\mu}_t = \mu_t$, $\hat{\varepsilon}_t = \varepsilon_t$ and $\hat{\gamma}_t = \gamma_t$

The (7) can be estimated through a linear regression model such a

$$\nabla L.R._t = \hat{\alpha}_0 + \hat{\alpha}_1 \nabla\mu_t + \hat{\alpha}_2 \nabla\gamma_t + \hat{\alpha}_3 R_t + \hat{z}_t \tag{9}$$

and similarly the (8) can be estimated as:

$$\nabla L.R._t = \hat{\alpha}_0 + \hat{\alpha}_1 \nabla\mu_t + \hat{\alpha}_2 \nabla\varepsilon_t + \hat{\alpha}_3 R_t + \hat{z}_t \tag{10}$$

The compliance with the hypotheses listed above is a necessary and sufficient condition to obtain a consistent and undistorted estimator for the variable $\nabla L.R._t$. The validity of the hypothesis a) can be easily tested by performing a unit root test on the variables $\nabla L.R._t$, $\nabla \mu_t$, and, $\nabla \varepsilon_t$ although it is not necessary to perform a similar test on the latter as it is a white noise.

The size of the coefficient $\hat{\alpha}_1$ in the (9) and in the (10) indicates whether the variation the lethality rate between time t and time $t-1$ depends more on the variation in the lethality or on the variation in the infectivity between the same two periods. In fact $\hat{\alpha}_1 > 1$ implies, according to the (6), that between t and $t-1$ the variation of the lethality trend is greater than the variation of the infectivity trend, while $\hat{\alpha}_1 < 1$ implies, again for the (6), that between t and $t-1$ the variation in the infectivity trend is greater than the change in the lethality trend.

The size of the coefficient $\hat{\alpha}_2$ in the (9) and in the (10) indicate, respectively, the impact on the variation of the lethality rate between the time t and time $t-1$ of the variation of the seasonal factors (for example of the variation of the temperature) and of the variation of the random factors between the same two periods.

The coefficient $\hat{\alpha}_3$ in the (9) and in the (10) quantifies the reduction in the lethality rate between the time t and the time $t-1$ that occurs if at the time t quarantine measures are operative to contain the contagion. In other words, $\hat{\alpha}_3$ quantifies the increase in lethality that would occur between time t and time $t-1$ if the individual mobility restriction measures would not be active.

4. Estimated model

The data considered for the estimations made are historical series, on a daily basis, relating to the total number of individuals positive to the Covid-19 virus in Italy and the historical series, on a daily basis, relating to the total number of individuals who died for Covid-19 in Italy. Both series are defined in the sample period January 31th – March 20th 2020 and have been taken from the database of the European Center for Disease Prevention and Control.

The daily series of the lethality rate for Italy was obtained from the ratio between the total number of individuals died on each day and the total number of infected on each day.

The dummy variable R_t takes on value 1 starting from March 5th. The authors chose this date because the decree introducing limitations on individual movements was approved only on the evening of the day before. However, it should be noted that the country's total lockdown was imposed only starting from March 10th 2020, although the Italians had started to reduce their movements since March 5th.

The Table 1 shows the BSM estimate made by the authors: in it all the components are set as stochastic:

Table 1: Basic Structural Model. Dependent Variable: Lethality Rate
Sample period: 2020-12-31:2020-03-20 (T = 50)
Average log-likelihood = -1.71117
Specification: Stochastic trend, stochastic slope, dummy seasonals (stoch.), irregular component

Coefficient	Estimated value	std. error	z.	p-value
$\widehat{\varepsilon_t}$	0. 243485	0.0702728	3.465	0.0005 ***
$\widehat{\mu_t}$	0.374102	0.0844336	4.431	9.39e-06 ***
$\widehat{\beta_t}$	0.0388520	0.0289602	1.342	0.1797
$\widehat{\gamma_t}$	7.26396e-06	0.0304142	0.0002388	0.9998

As it can be easily seen, the estimated seasonal component $\hat{\gamma}_t$is statistically not significant, while the estimated error component $\hat{\varepsilon}_t$ and the estimated trend component $\hat{\mu}_t$ are statistically very significant. For this reason, the linear regression model to be estimated in the present case is that expressed by (8).

The Figure 1 below shows the time plot of the lethality rate, of $\hat{\mu}_t$ and of $\hat{\varepsilon}_t$. The graph shows that the noise component has quite large oscillations around its average and that, as was easily to suppose, the trend component is strongly increasing. This implies that the data are characterized by a strong heteroskedasticity and that therefore it is necessary to estimate the (8) using a linear regression model whose standard errors are suitably robust both to heteroskedasticity and to autocorrelation.

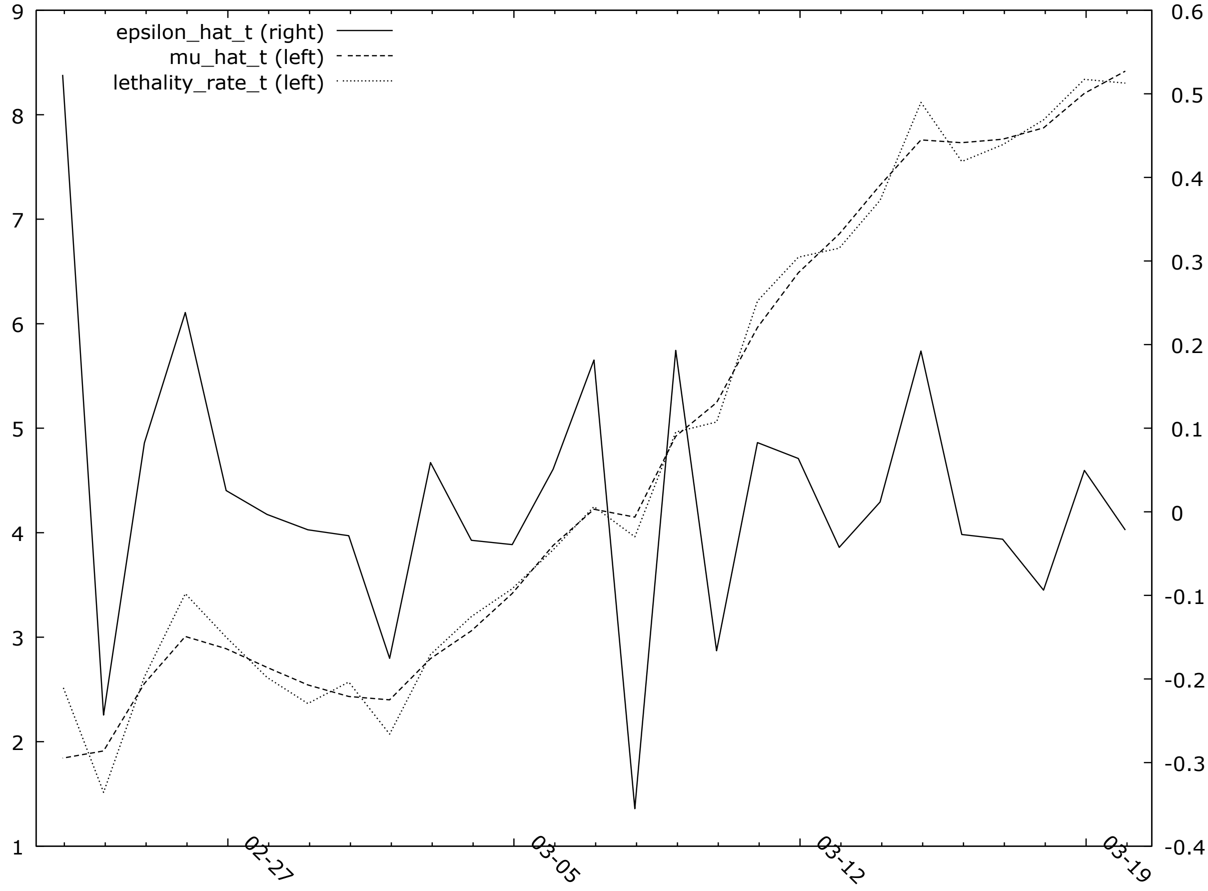


Figure 1: Time plot of the total infected and of the total death, 2020-01-31:2020-03-20 (T = 50)

The authors estimated (8) through a Heteroskedasticity Corrected Linear Model (HCLM) in the sample February 23th (the day the first death for Covid-19 was recorded in Italy) – March 20th 2020.

This model is a particular type of Weighted Least Squares (WLS) and is estimated in three steps:

a) a OLS for the model of interest is estimated;
b) an auxiliary regression is estimated for the variance of the error term;
c) a WLS is estimated using as weight the reciprocal of the error term variance.

The hypothesis a) of the previous paragraph, on which the theoretical model is built, was verified by performing an Augmented Dickey-Fuller test, with constant and trend, with BIC criterion and testing down from order 5 on the variables $L.R._t$, $\hat{\mu}_t$ and $\hat{\varepsilon}_t$, (although, for the reasons explained above, in the case of the last variable it is not necessary to carry out a similar test).

The results are shown in Table 2 below and confirm hypothesis a) of the absence of a unit root for all the variables tested.

Table 2: Augmented Dickey Fuller test. Augmented Dickey Fuller test for $\nabla L.R_t$, $\nabla\mu_t$ and $\nabla\varepsilon_t$ with constant, trend testing down from lag 5 and BIC criterion Null hypothesis: $\alpha = 1$

Variable	Test statistic	p-value
$\nabla L.R_t$	-7.51549	4.194e-006
$\nabla\mu_t$	-4.08891	0.01742
$\nabla\varepsilon_t$	-6.67796	2.018e-008

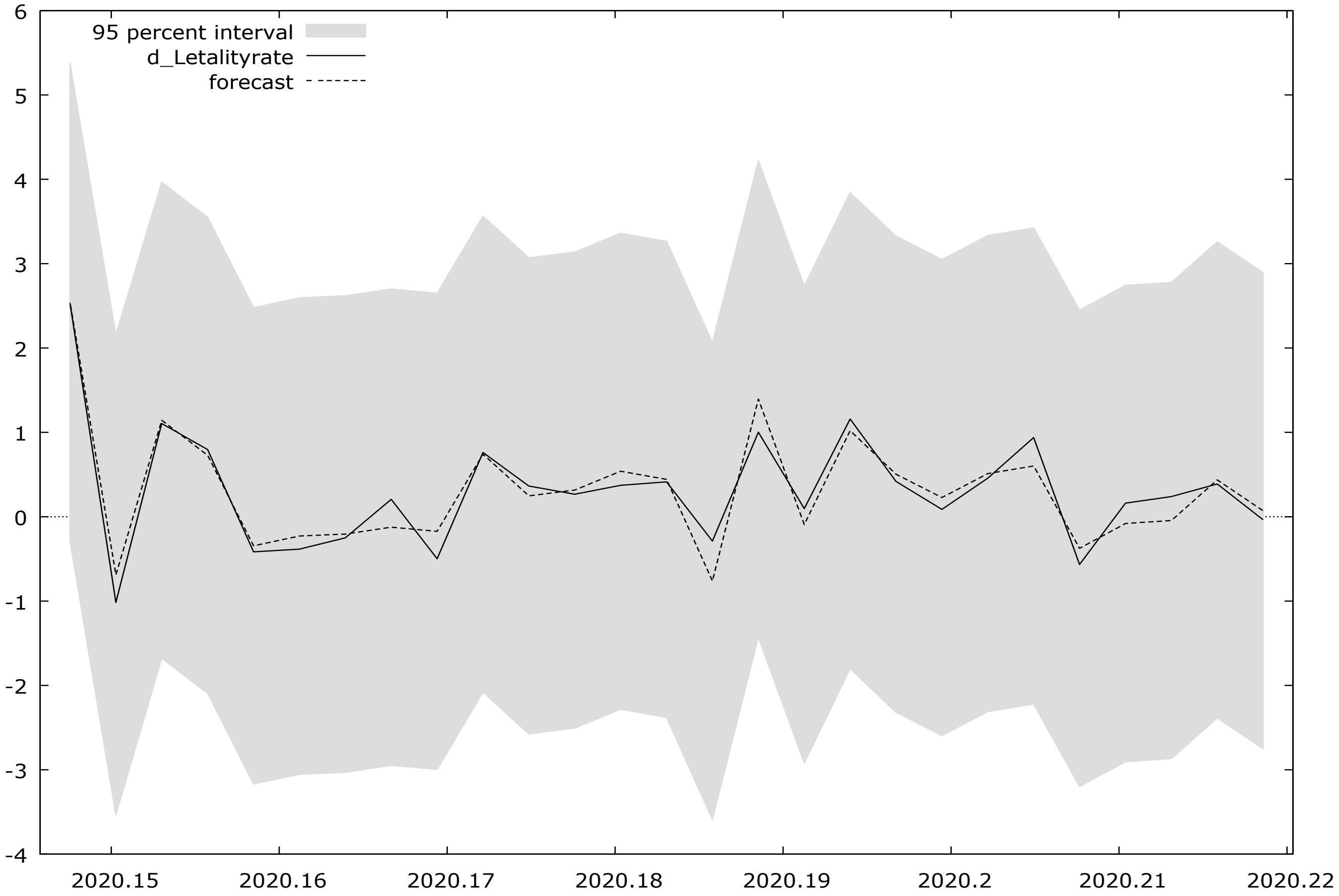
The result of the estimation of the (8) is shown in Table 3:

Table 3: Heteroskedasticity Corrected Linear Model. Dependent variable: Lethality Rate. Sample period 2020-02-23:2020-03-20 (T=27)

Coefficient	Estimated value	std.error	t-ratio	p-value
$\hat{\alpha}_0$	0.0181182	0.0624746	0.2900	0.7744
$\hat{\alpha}_1$	1.22051	0.196844	6.200	2.52e-06 ***
$\hat{\alpha}_2$	1.03347	0.251132	4.115	0.0004 ***
$\hat{\alpha}_3$	−0.133235	0.0761112	−1.751	0.0934 *
Statistics based on the weighted data				
Sum squared resid	42.72256			
R-squared	0.933300			
Adj. R-squared	0.924600			
F(3, 18)	107.2756			
Log-likelihood	−44.50636			
Akaike criterion	97.01272			
Schwarz criterion	102.1961			
Hannan-Quinn	98.55400			
Rho	−0.346238			
S.E. of regression	1.362902			
P-value(F)	1.15e-13			
Durbin-Watson	2.675786			
Statistics based on the original data				
Mean dependent var	0.307506			
S.D. dependent var	0.701035			
S.E. of regression	0.225531			
Sum squared resid	1.169876			
Doornik-Hansen test on the residuals				
Test statistic: Chi-square(2) = 0.725926				
p-value = 0.695612				
ARCH test of order 7 on the residuals				
Test statistic: LM = 10.1858				
p-value = P(Chi-square(7) >10.1858) = 0.178284				

The Doornik-Hansen test and the ARCH test for the residuals indicate that the innovations follow a normal distribution and that they are serially uncorrelated. Since the adjusted R^2 is close to 1, the estimator can also be used to make predictions. The authors validated the model through a static in-sample prediction with confidence interval $\alpha = 0{,}95$. The result is shown in Figure 2 below.

Figure 2: Static prediction for the first difference of the lethality rate, 2020-02-23:2020-03-20 (T = 50)



The relative forecast goodness statistics are shown in Table 4 below.

Table 4: Goodness statistics for the lethality rate statistic and in sample prediction.
Goodness statistics for the lethality rate static and in-sample prediction
Confidence interval $\alpha = 0.95$ Sample period 2020-02-23:2020-03-20 (T=27)

Statistic	**Value**
Mean Error	-0.0015621
Root Mean Squared Error	0.20816
Mean Absolute Error	0.1643
Mean Percentage Error	27.263
Mean Absolute Percentage Error	63.16
Theil's U	0.26848
Bias proportion, UM	5.6318e-005
Regression proportion, UR	0.013904
Disturbance proportion, UD	0.98604

It can be noted that the average forecast error and the Root Mean Squared Error are very low and that the Bias Proportion (UM), the Disturbance Proportion (UD), the Regression Proportion, and Theil Coefficient are close to their respective optimal values.

The coefficient $\hat{\alpha}_1$ is significantly different from zero and has a value greater than 1. This implies, as underlined in the previous paragraph, that the variation in the lethality rate between two consecutive days is mainly explained by the variation in the trend of the lethality between the same two days.

Also the coefficient $\hat{\alpha}_2$ is particularly significant. This means that a variation between two consecutive days of the purely random component of the lethality rate has a very marked effect on the variation of the latter between the same two days.

It is important to observe that the coefficient $\hat{\alpha}_3$ is significant at 10% and that its value is negative and equal to - 0.133235. This indicates that for each day on which the population mobility restrictive measures have been operational, the lethality rate has decreased approximately about 0.13 percentage points.

5. Conclusions

The authors estimated the impact of the quarantine measures adopted by the Italian government on the lethality rate of the Covid-19 virus, using a Heteroskedasticity Corrected Linear Model (HCLM), appropriately obtained with the modalities described in paragraph 3. The HCLM estimator appears internally valid. Moreover, according to the diagnostic tests performed and to the evaluation statistics, it can be used for predictive purposes.

In reality, the authors have decomposed the lethality rate through the Basic Structural Model (BSM) revealing that, in addition to a trend component that is easily ascertainable by observing the data, there is also a noise component that has large oscillations around its average. The absence of a seasonal component is probably explained by the fact that the sample period is too small to include seasonal factors such as temperature.

The estimated values of $\hat{\gamma}_t$ and $\hat{\alpha}_1$ suggest that the turnaround of the lethality rate, which has been registered since March 19th, is not due to a change in the temperature factor, but to the reduction in infectivity which occurred thanks to the quarantine measures adopted by the national government starting from March 4th.

This interpretation is consistent with what can be deduced from the estimated coefficient $\hat{\alpha}_3$ that is, for each day in which the individual mobility restriction measures were operational, lethality decreased by approximately 0.13 percentage points compared to the previous day. In other words, in the absence of such containment measures, the lethality rate between two consecutive days would have increased by approximately 0.13 percentage points more.

It is however important to emphasize that the absence of a seasonal component of the lethality rate is due to the fact that the sample period on which the (1) was estimated reaches up to the month of March. By including the spring and summer months in the sample and repeating the estimate, the result may be different. Therefore the authors' conclusions are valid only for the period considered and are not necessarily in contrast with those of the scholars mentioned in the first paragraph who instead observed a significant effect of environmental conditions on the infectivity of Covid-19**.**

The results derived from the authors' analysis lead to believe that the model adopted by the Italian government to deal with the pandemic has given good results in terms of reducing the lethality rate.

The authors hope that their model, although in its simplicity, can be interesting for the scientific community and for the policy makers and can find wide application both in judging the effectiveness of containment policies of the contagion and both in predicting future trends of lethality. In other words, the authors hope that the results obtained can help to improve future analyses of emerging outbreaks and can represent a guide for health authorities in forecasting and identifying possible preventive measures.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

Ethical Approval

This article does not contain any studies with human participants by any of the authors.

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