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# COVID-19: $R_0$ is lower where outbreak is larger<sup>☆</sup>

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## ABSTRACT

We use daily data from Lombardy, the Italian region most affected by the COVID-19 outbreak, to calibrate a SIR model on each municipality. Municipalities with a higher initial number of cases feature a lower rate of diffusion, not attributable to herd immunity: there is a robust and strongly significant negative correlation between the estimated basic reproduction number ( $R_0$ ) and the initial outbreak size. This represents novel evidence of the prevalence-response elasticity in a cross-sectional setting, characterized by a same health system and homogeneous social distancing regulations. By ruling out alternative explanations, we conclude that a higher number of cases causes changes of behavior, such as a more strict adoption of social distancing measures among the population, that reduce the spread. This finding calls for the distribution of detailed epidemiological data to populations affected by COVID-19 outbreaks.

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## 1. Introduction

An infectious disease's basic reproduction number, or  $R_0$ , represents the average number of secondary cases produced by a single infected case in an otherwise susceptible population: it is typically used as a reference value to assess the transmissibility of an infectious disease in a given population. Given a number of individuals susceptible to infection, a disease with higher  $R_0$  will infect a larger number of individuals. There is hence an obvious positive relationship between the  $R_0$  and the resulting size of an outbreak [1].

However, the spread of an outbreak does not only depend on ex-ante features of a virus or a population, but potentially also on the response of both population and authorities to the outbreak. A stream of literature has described the possible negative relationship between the prevalence of a disease in a given population and its rate of spread. Indeed, if a population's risk taking behavior is endogenous, then the larger the outbreak size, the more precautions individuals and authorities will take: this is the essence of the prevalence-response elasticity [2–4]. This is particularly important in the context of the COVID-19 pandemic, to which most countries in the world have reacted with some form of social distancing mea-

asures, or lockdown. In absence of a vaccine or effective drugs, these measures are the best weapon to reduce the number of deaths, as well as the number of intensive care unit beds required [5–7] and have been shown to obtain a substantial reduction in the speed of contagion [8–10]. However, their effectiveness crucially relies on the willingness of the population to follow the recommendations.

Several studies have found evidence of the prevalence-response elasticity by employing data from surveys of behavior [11–14], observing for instance an increase in reported condom use in areas with a higher AIDS prevalence. Epidemiological data could allow to overcome the possible problem of response bias, but the task is made non-trivial by the fact that public policies also react to the prevalence of a diseases, and by spillovers across regions due to human mobility. The present study relies on epidemiological panel data on COVID-19 in Lombardy, the region of Italy most heavily affected by the pandemic ([15] provide an accurate description of the early phase of the outbreak in such region). Specifically, we employ daily data on the number of individuals positive to COVID-19 at the municipality level, focusing on a period in which the entire country was subject to a lockdown. All municipalities under analysis share the same public health system and, in the period considered, were subject to the same social distancing regulation. However, at the start of the period, they were characterized by a strong heterogeneity in the number of cases, both in absolute and in per capita terms.

We study a period beginning on March 25, 2020, that is, more than two weeks after the lockdown regulation was put in place, and covering three weeks, during which such regulations still held: this means that movements across municipalities were severely

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restricted, requiring any travelers to present a valid (typically work or health related) justification for their journey. Hence, such municipalities were living in an exceptional state of isolation. At the same time, the period considered is sufficiently longer than the mean serial interval for COVID-19 in Lombardy [15].

We fit a Susceptible-Infected-Recovered (SIR) model [16] on data from each municipality and find that the estimated  $R_0$  is negatively correlated with the prevalence characterizing the municipality at the beginning of our period. This result holds both when considering the absolute and per capita number of cases, and is robust to different specifications and sample disaggregations.

We present and compare different complementary explanations for this finding. Early and widespread testing can increase the reported number of cases and simultaneously allow the authorities to slow the spread of the pandemic by isolating known cases. At the same time, where the number of cases is higher, the population might comply more strictly with the lockdown measures, thus reducing the rate of spread: we show in Section 4 why this latter mechanism is most likely to drive our results.

## 2. Materials and methods

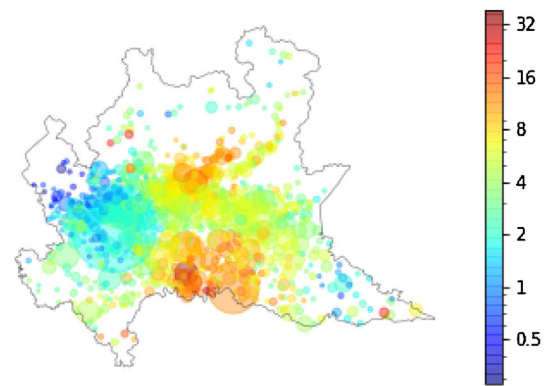
We employ count data of per-municipality (cumulated) recorded cases. These are updated daily and distributed by regional authorities. We do not rely on data on recovered and deceased individuals, as such data are not available with the required geographical disaggregation.

Data are available starting from March 25, 2020. This study focuses on a period of twenty-one days during which lockdown measures were always in place: in Appendix A.1, we perform a sensitivity analysis by employing later data (until April 19). We verify that only minimal deviations appear between regional data and the aggregation of municipal data (with the exception of data from March 24, which is indeed removed from our sample).

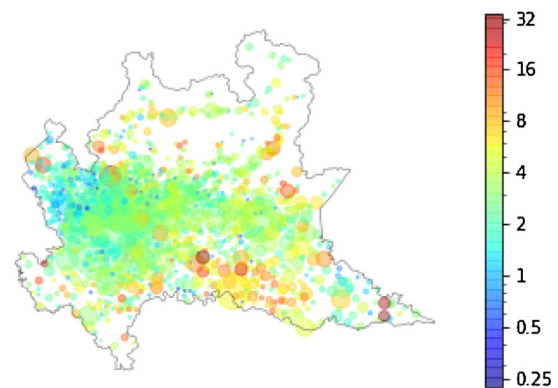
Out of 1507 municipalities in Lombardy, 960 had at least one recorded COVID-19 case as of March 25. Fig. 1a displays the number of cases (size of the dots) and the cases per capita (color of the dots) as of March 25 for each of these 960 municipalities. Similarly, Fig. 1b displays the number of new cases (size of the dots) and the number of new cases per capita (color of the dots) recorded in each municipality during the three weeks under analysis.

It should be noted that official data concerning the COVID-19 outbreak in Italy has been found to be strongly incomplete, both in terms of positive individuals and of casualties: several researchers have estimated an outbreak size much higher than that suggested by official numbers [5] and others have corroborated this with an analysis of anomalies in death rates [17]. Moreover, local testing strategies are known to have deviated from WHO guidelines and to have changed over time, also depending on available resources: towards the end of our period of interest, more subjects with mild symptoms were tested. For this reason, some researchers have put forwards adaptations of the SIR model that account for a threshold in the capacity of the health system [18]. Such problems are not specific to Italy, as official data from a number of countries have been questioned. More in general, the difficulty in obtaining reliable data on the number of infected, deceased and recovered individuals calls for refinements of traditional epidemiological models [19,20].

Given our research question, these caveats are of limited importance. Indeed, the focus of the present work is to document differences in response across municipalities, rather than to precisely estimate the epidemiological parameters of the COVID-19 outbreak in Lombardy. Despite the presence of noise in the data, we show in what follows that the differential patterns identified can be distinguished from such noise.



(a) Cases on March 25



(b) New cases between March 25 and April 14

**Fig. 1.** Distribution of cases and cases increase. *Note:* dot size represent absolute numbers, colors represent cases per one thousand inhabitants. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

Data by municipality on population size, average age, percentage of males (January 1, 2019) and number of foreigners (January 1, 2020) are obtained from the Italian National Institute of Statistics (ISTAT). Data on total taxable income by municipality (year 2018) are retrieved from the Italian Department of Public Finance (MEF). Data on majors' political affiliation are obtained from the Italian Department of Internal and Local Affairs (DAIT): these are used to retrieve information on which municipalities are governed by a civic list, i.e. a list that has no official connection with a national political party and which campaigns on local issues. Out of the 960 municipalities analyzed, 650 are ruled by a civic list. Finally, data on the number of hospital beds per municipality (January 1, 2018) are retrieved from the Department of Public Health. We consider the number of beds in public and private hospitals practicing in agreement with the National Health System. We exclude from the computation beds devoted to rehabilitation and long-stay patients.

### 2.1. Methods

We fit a SIR model on each municipality in the period of three weeks beginning with March 25. Given the short time span considered, we employ a simplified SIR model which does not account for natural rate of mortality. Hence, the model is entirely defined by

setting few parameters:  $\beta$ , which determines the rate at which susceptible ( $S$ ) individuals become infected ( $I$ );  $\gamma$ , which determines the rate at which infected individuals become recovered ( $R$ ); the initial number of infected and recovered individuals, and the population size  $N (= S + I + R)$ .

It is worth mentioning that while  $\beta$  and  $\gamma$  might not be identifiable by analyzing daily *active* cases (for sufficiently low prevalence,  $I$  approximately follows an exponential growth of base  $1 + \beta - \gamma$ ), this concern does not apply to  $I + R$  (see Appendix A.2).

We consider, for each municipality, a discretized version of the continuous SIR model – each period corresponding to a day – and automatically explore the parameter space for  $\beta$ ,  $\gamma$ , and the initial value for  $I$  and  $R$  (we take population size from official statistics), looking for the combination that provides the best fit. Specifically, the goodness of fit is maximized by minimizing the sum of square residuals between the cases count and the sum of the  $I$  and  $R$  pools sizes. The initial values for the free parameters are set to those calibrated on the entire Lombardy region. The optimization algorithm is described in Appendix A.3.

Given that the SIR model assumes a non-null initial population of infected individuals, we only consider the 960 municipalities satisfying this condition. We further drop 48 municipalities which had new cases recorded on only one or two dates, hence reducing to 912 municipalities: the fitting procedure may become unreliable if provided too few updating points. See Fig. 5 in Appendix A.3 for a comparison of fitted SIR models with actual cases count in three representative examples.

Once we find the best SIR parameters for each municipality, we regress the estimated  $R_0$  (the ratio of the estimated  $\beta$  and  $\gamma$ ) on the outbreak size within the municipality as of March 25. We focus on the *per capita* number of cases, as we expect any effect to be related to the *prevalence* of the outbreak – a same number of cases will be perceived in a very different way in Milan or in a small municipality. The choice of relying on the  $R_0$  rather than on the *net* (or *effective*) reproductive number ( $R_t$ ) is far from being an obvious one. Indeed, while the two are closely related ( $R_t = R_0 \cdot \frac{S}{N}$ ) [21], the latter is more often employed to describe later phases of an outbreak, when health policies are in place – as a partial exception, vaccination campaigns, which have a relatively permanent effect on a population's susceptibility, are often described in terms of  $R_0$  [22]. Given our focus on individual behavior (as opposed to, e.g. dynamics affected by herd immunity), we are interested in the *potential* for contagion by infected individuals (in a fully susceptible population), more than in the aggregate evolution of the outbreak (which includes the possible effect of herd immunity). In any case, this choice does not affect our results, as we show by replicating our analysis based on  $R_t$  in Appendix A.4.

We want to emphasize that our estimated  $R_0$  characterizes (apart from statistical fluctuations and possible simplifications related to the estimation approach) contagion dynamics in a context in which several health measures were already in place (first and foremost, the lockdown). Thus, it should not be interpreted as an alternative estimate of the large  $R_0$  measured in the early phases of the outbreak [15], nor as the obvious prosecution of the decreasing trend observed by [15,23].

### 3. Results

Among municipalities with at least one recorded case as of March 25, we find a strong ( $-0.38$ ) and strongly significant ( $p = 0.000$ ) negative correlation between the initial number of cases per one thousand inhabitants and the percentage increase of cases in the period under analysis.

A strong heterogeneity (partly attributed to statistical noise – several municipalities count only a few cases each) can be observed

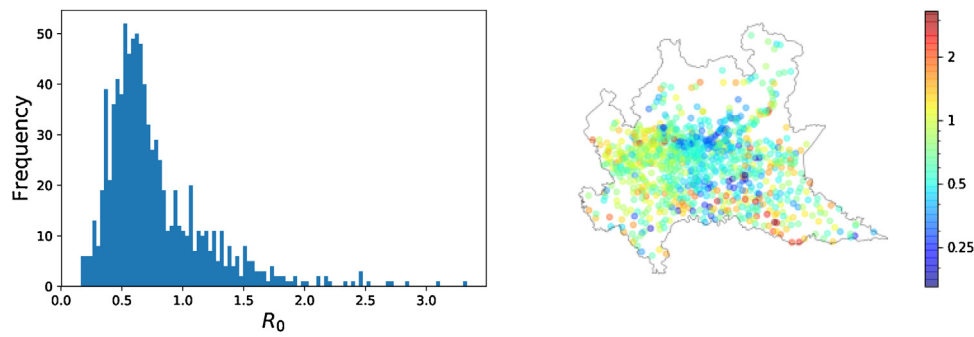
in the distribution of estimated  $R_0$  across municipalities: in what follows, unless differently specified, we trim data by dropping 0.5% of outliers on each side of the distribution of  $R_0$ , hence reducing to 902 municipalities.

Fig. 2 shows the distribution of the estimated values of  $R_0$ : the mean value is 0.77 (0.79 before trimming) and becomes 0.82 when weighted on population; the median is 0.65. In only few municipalities (195) the value of  $R_0$  appears to be larger than the critical threshold of 1: in the remaining 707 municipalities, the outbreak is expected to extinguish without requiring herd immunity.

Table 1 presents the results of the regression analysis. We follow the recommendation of [24] who show that, unless an overwhelming share of the residual in the final model is due to measurement error in the dependent variable (rather than to actual noise in the relation of interest), an OLS with heteroskedastic robust standard errors provides better results than Weighted Least Squares (WLS) – we employ the latter approach as a robustness exercise in Appendix A.1. We see a negative and strongly significant relationship between the initial number of cases per one thousand inhabitants and the estimated  $R_0$  (column (1)); this relationship is robust to controlling for population size (column (2)), and to both the absolute number of cases and the inverse of population size (column (3)), i.e. a full interaction model where the per capita count represents the interaction term [25]. The coefficient for the per capita number of cases can be interpreted as the reduction in  $R_0$  resulting from an increase of one case per one thousand individuals in the prevalence of the outbreak. The value of  $-0.024$  observed in column (2), which we consider as our baseline specification, indicates a sizeable effect: for reference, given that the prevalence in Milan as of March 25 was around 1.7 ‰, the above mentioned result suggests that had it been 2.7 ‰, the average  $R_0$  would have been around 0.860 instead of the observed 0.884. The same negative and strongly significant effect is observed if we consider as explanatory variable the absolute number of cases, controlling for population size (column (4)). This holds also when we consider as explanatory variable the number of *new* cases per capita observed on March 26 as compared to March 25, always controlling for population size (column (5)). While the number of new cases is more noisy than the total number of cases, it might be considered a more up-to-date information on the hazard posed at the local level by the epidemic. Hence, both pieces of information can in principle be relevant for individual behavior: indeed, column (6) shows that they are both strongly significant even when considered simultaneously.

It should be noted that any intrinsic characteristic of municipalities – such as demography, location, structure of the economy – which might explain a larger outbreak size should also favor a larger  $R_0$  [26]. Thus, our minimal model should yield a lower bound for the coefficient of interest in presence of any unobservable variable which influences contagion. Indeed, in column (7) we replicate the analysis presented in column (2) controlling for average age, percentage of males, per capita income, percentage of foreigners, number of hospital beds per capita at the municipality level and a dummy variable indicating whether the municipality is governed by a civic list. As expected, the effect of interest is still significant and even larger in absolute terms (the coefficient for “Cases ‰” changes from  $-0.024$  to  $-0.032$ ). Results also highlight that municipalities characterized by an older population, a lower average income and a stronger presence of foreign residents tend to feature a higher  $R_0$  (the number of hospital beds – which is 0 in most municipalities – becomes statistically significant if considered in absolute terms, with results virtually unchanged).

In principle, an exception to the reasoning above could be represented by systematic differences in the *origin* of local cases. Specifically, if the initial number of cases reflects an inflow of cases from outside the municipality, more than the local outbreak's past expansion, then in theory the effect of interest might be driven



**Fig. 2.** Distribution of  $R_0$ . Note: distribution of estimated per-municipality  $R_0$ , computed as  $\frac{\beta}{\gamma}$ . Not shown: five municipalities with  $R_0 < 0.16$ , five with  $R_0 > 3.33$ .

**Table 1**  
Main results.

	(1)	(2)	(3)	(4)	(5)	(6)	(7)
Intercept	0.888*** (0.021)	0.887*** (0.022)	0.876*** (0.022)	0.786*** (0.015)	0.818*** (0.019)	0.831*** (0.019)	0.282 (1.014)
Cases %	-0.024*** (0.004)	-0.024*** (0.004)	-0.029*** (0.005)				-0.032*** (0.004)
Cases			-0.000 (0.000)	-0.001*** (0.000)		-0.001*** (0.000)	
New cases %					-0.160*** (0.034)	-0.150*** (0.033)	
Population		0.001 (0.001)		0.025*** (0.008)	0.002 (0.001)	0.023*** (0.007)	-0.001 (0.001)
Population <sup>-1</sup>			0.012** (0.006)				
Avg. age							0.046*** (0.007)
Males %							-2.524 (1.627)
Avg. income							-0.157*** (0.059)
Foreigners %							0.868*** (0.332)
Civic list							-0.007 (0.028)
Hospital beds p.c.							-3.018 (1.914)
Observations	902	902	902	902	902	902	902
R <sup>2</sup>	0.047	0.047	0.053	0.019	0.026	0.041	0.121

Note: dependent variable: estimated  $R_0$ . Population and average income are expressed in tens of thousands – of inhabitants and yearly euros, respectively. Hospital beds are expressed in per capita terms. White standard errors reported in parentheses. \* $p < 0.1$ ; \*\* $p < 0.05$ ; \*\*\* $p < 0.01$ .

by the sorting of imported cases in municipalities with lower  $R_0$ . This can be ruled out because, during the lockdown (which started more than two weeks before the period analyzed), opportunities for cross-municipality contagion were minimal compared to before; despite this, our sensitivity analysis shows that the effect is *reinforcing* in the first few days analyzed (Appendix A.1).

We do not include in our main analysis province-level characteristics that may have heterogeneously affected different areas of Lombardy, but we show, via a within-province analysis in Appendix A.1, that results are not driven by specific provinces. This also rules out the possibility of our results being driven by stronger public health interventions (reducing the spread of contagion) being implemented in larger outbreak areas.

#### 4. Discussion

There are a few reasons that might explain why a larger COVID-19 outbreak should result in a *subsequent* lower  $R_0$ .

The first is related to herd immunity, by which areas where the outbreak is initially more present have less scope for further spread because a large share of individuals have already caught, and possibly developed immunity to the virus. This is in principle not a

problem for our approach, as the SIR model accounts for this effect and should estimate an  $R_0$  net of it – in other terms,  $R_0$  describes the evolution of the outbreak in an hypothetical situation in which the pool of susceptible individuals is never reduced. However, the problem might still arise if the count data employed severely underestimate the actual spread of the virus: the number of positive cases could actually be much larger than the detected one, leading to an estimated  $R_0$  lower than the real one because of the undetected effect of herd immunity in reducing the rate of contagion.

The underestimation of infected population might also suggest an alternative explanation of our result, related to *test capacity*: to the extent that a lower detected prevalence reflects a lower ability of health authorities to identify infected individuals, it should then correlate with a lower ability to isolate, hospitalize and cure them, and hence to a faster outbreak growth.

A third, social, explanation is related to the prevalence-response elasticity [14]: if the local population is aware of a larger prevalence of the disease, it reacts by changing its behavior towards a stricter application of social distancing rules, thus leading to a lower  $R_0$ . This might in fact depend from other motives than minimizing the individual risk of infection. Subjects may want to reduce the risk for their fellow citizens, and in particular relatives and family

**Table 2**  
Additional specifications.

	Q 1 (1)	Q 2 (2)	Q 3 (3)	Q 4 (4)	Full (5)
Intercept	1.130*** (0.072)	1.129*** (0.133)	1.027*** (0.211)	0.713*** (0.068)	0.952*** (0.030)
cases%	-0.142*** (0.049)	-0.094** (0.041)	-0.067* (0.041)	-0.004 (0.006)	-0.047*** (0.009)
cases% <sup>2</sup>					0.001*** (0.000)
population	0.000 (0.000)	-0.000** (0.000)	0.000 (0.000)	-0.000** (0.000)	0.000 (0.000)
Observations	226	225	225	226	902
R2	0.036	0.022	0.014	0.008	0.061

Note: Dependent variable: estimated  $R_0$ . White standard errors reported in parentheses. Columns (1) to (4): model restricted to municipalities with a number of cases per thousand inhabitants in the interval (0.278, 2.173], (2.173, 4.11], (4.11, 6.265] and (6.265, 38.743], respectively. Column (5): full sample. \* $p < 0.1$ ; \*\* $p < 0.05$ ; \*\*\* $p < 0.01$ .

members; likewise, they might want to avoid the risk that a larger outbreak results in postponing the end of the lockdown. In what follows, we provide evidence in favor of this social mechanism.

We start by analyzing the first possible explanation, related to herd immunity. Based on ex-post serologic mass tests [27], the share of population attained by the virus as of July 27, 2020 in the two most strongly hit provinces of Bergamo and Cremona was 24% and 19%, respectively. While most municipalities are likely to have reached much lower values (the percentage for the entire Lombardy was found to be 7.5%), to avoid the possibility that an even partial herd immunity effect might be driving the results, we re-estimate our main model on subsamples of municipalities, based on their initial number of cases per capita. Specifically, we split the sample according to quartiles of cases per capita on March 25. The results, presented in columns (1) to (4) of Table 2, show that our findings are not driven by herd immunity, as the coefficient for *cases%* is negative in each quartile. The coefficient is significant, and its absolute value particularly large, for municipalities with a relatively low prevalence (first three quartiles), including municipalities with 2 cases per one thousand inhabitants or less (first quartile).

We then consider the second possible explanation: that a lower detected prevalence signals a lower detection ability, and that this mechanically correlates with a lower ability to track and isolate infected subjects, hence raising the subsequent rate of diffusion. In order to disentangle this *test capacity* explanation from the third, social, one, we sketch two simple models of how these would be expected to affect  $R_0$ .

Let us represent with  $u_t$  the unknown real number of infected subjects per one thousand inhabitants at time  $t$  in a given municipality, and with  $i_t$  the corresponding known number. We are interested in the extent to which unidentified infected subjects (which are  $u_t - i_t$  cases per one thousand inhabitants) will raise the  $R_0$  for the municipality in the subsequent period. More specifically, we can assume that identified and unidentified patients form two different pools of infected subjects and that the latter has a much higher  $\beta$  – probability of infecting susceptible individuals – that leads to a corresponding higher  $R_0$ . Since  $\beta$  enters linearly in  $R_0$  – and assuming for simplicity that  $\gamma$  is constant – the relationship between  $u_t - i_t$  and  $R_0$  would be expected to be *linear*. Moreover, not only identified patients are subject to a stronger form of isolation, but also close contacts of such patient (some of which are not infected) are recommended to self-quarantine: this does not happen in municipalities with a larger number of undetected cases, which implies that the effect of each unidentified patient should be *more* than linear in increasing the  $R_0$ . This would imply a linear or concave relationship between *cases%* and  $R_0$ .

Vice-versa, any social explanation [28,18] is based on the assumption that inhabitants react to the news of the cases in their

municipality. A same increase in per capita cases is likely to be more salient if the initial number of cases is lower. That is, we can expect inhabitants of two towns with respectively 1 and 11 known cases per one thousand inhabitants to differ in their compliance with social distancing prescriptions more than inhabitants of two towns with respectively 20 and 30 known cases per one thousands inhabitants: a same difference of one percentage point in prevalence will have a weaker effect on people behavior where prevalence is higher. This alternative explanation predicts a *convex* relationship (given the negative sign) between *cases %* and  $R_0$ .

To disentangle between the test capacity and the social explanation, we enrich our basic model by introducing a quadratic term in *cases%*. This is done in column (5) of Table 2. We see that the quadratic term has a positive sign and is strongly significant, while the sign of the linear term is still negative and has increased in absolute terms. Hence, while this does not allow us to exclude that the two other explanations might play a role, we can conclude that the *social* explanation is the main driver of the negative relationship between *cases%* and  $R_0$ . Note that the time interval under analysis was sufficient for local populations to react to the perceived threat of contagion, and for such reaction to influence contagion ([15] estimate the mean serial interval – delay between symptoms onset in infector and infectee – in Lombardy at 6.6 days). See Appendix A.1 for additional evidence and sensitivity tests.

[29] describe two possible opposite reactions to the COVID-19 outbreak: a precautionary attitude that leads to a stricter adherence to guidelines, and a “fatalism effect” according to which an individual who is more likely to be infected in the future “*reduces her incentives to be careful today*”. Our results provide strong evidence in favor of the first mechanism.

[10] follow a different approach to model how changes in behavior affect the speed of diffusion in a SIR model. Rather than looking for variations in  $R_0$  as originating from changes in  $\beta$  or  $\gamma$ , they consider such parameters as fixed, and assume instead that in regions with more active cases, more people will isolate (both because of mandatory and voluntary social distancing measures). When this happens, the sample  $S$  of susceptible individuals shrinks: this results in a reduction of the speed of contagion, despite an *increase* in the infection probability for susceptible individuals. Intuitively, the latter effect comes from the assumption that, while a number of sane individuals disconnect from contagion, the remaining ones keep their frequency of contacts unchanged, increasing their chance  $\beta \frac{I}{P_E}$  (with  $P_E$  being the size of the non-isolated population) of contracting the disease. Our model and theirs are complementary, as social distancing can imply a generalized change of habits in the population but also, as a result, the isolation from contagion of a share of the population. In their paradigm, the results we obtain when restricting to quantiles of municipalities (Table 2, columns 1 to 4) and when introducing a quadratic term in the number of

initial cases (Table 2, column 5) can be interpreted as a less-than linear increase in the number of isolated subjects in response to an increase in the number of recorded cases.

The endogeneity of risk taking with respect to outbreak size reveals one of the subtleties in predicting an outbreak's date of extinction [30]. As already observed by [14], a lower prevalence might lead to less precautions been taken and hence to a longer outbreak duration. To the extent that there is habit formation in the population, this might result in a larger outbreak becoming extinct before a smaller one, all else equal, and even in the case  $R_0 < 1$ .

## 5. Conclusions

We show that in the Italian region of Lombardy, during a lockdown, the basic reproduction number for COVID-19 reacts negatively to the initial size of an outbreak at the municipality level, an effect which cannot be explained by the population having reached herd immunity. Limited test capacity – and hence a limited ability by health authorities to isolate and treat affected individuals – appear to have at most a marginal role in explaining our result. Instead, our results provide support for an important role of the prevalence-response elasticity at the local level: population behavior is key to slowing down the contagion and, in particular, information about local outbreaks impacts on diffusion rates. This effect is consistent across all provinces and it is robust to the time period considered.

This is, to the best of our knowledge, the first time that a change of behavior in the population due to the prevalence-response elasticity is observed at a temporal resolution of few weeks. The speed of the contagion and the reduced human mobility across interested municipalities reduce the relevance of geographic spillovers. This allows for a novel identification of the behavioral response directly from local epidemiological data, rather than having to rely on survey-based measures of health behavior. The fact that the behavioral response is particularly strong in municipalities characterized by smaller outbreaks suggests that individuals react more strongly to the first few cases. This aspect is confirmed by the convex relationship we find between the initial size of the outbreak and the  $R_0$ : the marginal effect on behavior of each new case seems to decrease in the number of cases.

Our results provide evidence in favor of a *precautionary* rather than *fatalistic* individual attitude towards the outbreak. Regardless of its motivation (e.g. heuristics or fears versus rationality), it is a socially efficient reaction, as it reduces the likelihood of contagion precisely where it would have the highest potential to spread. Like in many other countries, the Italian response to COVID-19 was characterized on the one hand by a limited access to official, high quality data, which is only in part to be attributed to limits in the detection capability; on the other hand, by a heterogeneous adherence (in particular in later phases of the epidemic) to prescriptions and rules. The evidence provided hence calls for considering populations as an integral part of the decision making process [28]. It suggests that a timely and transparent provision of epidemiological data (possibly mediated by the work of experts and communicators) can affect individual behavior in such a way as to increase the efficacy of a lockdown (as well as social distancing measures in general), hence reducing its negative social and economic impact, and yielding public health benefits at no added cost.

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## Declaration of interest

None declared.

## Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at <https://doi.org/10.1016/j.healthpol.2020.10.017>.

## Declaration of Competing Interest

The authors report no declarations of interest.

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