

Time, Space and Social Interactions: Exit Mechanisms for the Covid-19 Epidemics

Antonio Scala^{1,2}, Andrea Flori³, Alessandro Spelta^{4,5}, Emanuele Brugnoli¹, Matteo Cinelli¹, Walter Quattrociocchi^{6,1}, and Fabio Pammolli^{3,5}

¹Applico Lab, CNR-ISC

²Big Data in Health Society

³Impact, Department of Management, Economics and Industrial Engineering, Politecnico di Milano

⁴Univ. di Pavia

⁵Center for Analysis Decisions and Society, Human Technopole and Politecnico di Milano

⁶Univ. di Venezia 'Ca Foscari

April 28, 2020

Abstract

We develop a minimalist compartmental model to study the impact of mobility restrictions in Italy during the Covid-19 outbreak. We show that an early lockdown shifts the epidemic in time and that beyond a critical value of the lockdown strength, the epidemics tend to restart after lifting the restrictions. As a consequence, specific mitigation strategies must be introduced. We then characterize the relative importance of different broad strategies by accounting for two fundamental sources of heterogeneity, i.e. geography and demography. First, we consider Italian regions as separate administrative entities, in which social interactions between age classes occur. Due to the sparsity of the inter-regional mobility matrix, once started the epidemics tend to develop independently across areas, justifying the adoption of solutions specific to individual regions or to clusters of regions. Second, we show that social contacts between age classes play a fundamental role and that measures which take into account the age structure of the population can provide a significant contribution to mitigate the rebound effects. Our approach is general and highlights

the relevance of some key parameters on non-pharmaceutical mitigation mechanisms for the epidemics.

1 Introduction

Different epidemic models and approaches contribute to identify specific mechanisms relevant for policy design [1]. At present, although the World Health Organization (WHO) organizes regular calls for Covid-19 modelers to compare strategies and outcomes, policymakers barely handle the discrepancies between the proposed models (see, e.g.: <https://www.sciencemag.org/news/2020/03/mathematics-life-and-death-how-disease-models-shape-national-shutdowns-and-other>).

To contain the Covid-19 epidemic, governments worldwide have adopted severe social distancing policies, ranging from partial to total population lockdown [2]. Restrictions have led to a sudden stop of economic activities in many sectors, while the majority of Covid-19 infections affect active population (i.e. the age class between 15–64 years) [3]. Overall, the impact of contagion and lockdown measures on health and on economic activities is substantial and pervasive.

Against this background, we introduce a model-based scenario analysis for Covid-19, and we highlight how geographical and demographic variables influence the epidemic spreading and the effects of lockdown solutions, while providing some general indications on relevant exit mechanisms [4].

The general behavior of our framework holds for the vast class of epidemic models where transmission rate is proportional to the number of susceptible people times the density of infected; it is relevant both for deterministic models and for stochastic models as soon as the initial fluctuation regime is overcome [5]. We focus on the determinants of short-term interventions in response to an emerging epidemic when geographic and demographic compartments are included in the model. Our goal is general in nature, since we focus on two relevant decomposability conditions, under which partial dynamics influence the overall configuration of the system (see, e.g., [6, 7, 8, 9]). We study how a) the mobility restriction measures and b) the timing of the lockdown lift affect the total fraction of infected, the peak prevalence, and the delay of the epidemics. Our analysis identifies two fundamental sources of heterogeneity in the diffusion process: regional boundaries and age classes [4]. We show how such dimensions can shape policy interventions aiming at containing the epidemic, irrespective of any detailed quantitative predictions on specific micro level measures.

This paper aims to contribute to the extant literature on trade-offs between mitigation, i.e. slowing down the epidemic contagion, and suppression, i.e. temporarily compressing the risk of contagion [4, 10, 11]. Notwithstanding micro data on individual profiles are not taken into account, our simple compartmental model based on geographical and age classes uncovers relevant aspects, which provide some guidance to policy makers. First, we show that an early lockdown shifts the epidemic in time and that the delay is proportional to the anticipation time, with an intensity which grows with the strength of the lockdown. Beyond a critical threshold, the epidemic would tend to fully recover its strength as soon

as the lockdown is lifted. As a consequence, specific mitigation strategies must be prepared during the lockdown.

To provide some guidance on the relative importance of different general strategies, we first study how the sparsity of the matrix representing mobility flows across administrative regions influences the observed delays of the contagion. The relative strength of intra-regional mobility with respect to inter-regional mobility flows implies that, once the epidemic has started, it then tends to develop independently within each region, as empirically observed in simulations of Covid-19 spread in China [12]. Second, we study the impact of patterns of interaction within and between age classes, finding that the structure of the interactions is of primary importance in estimating post-lockdown effects. According to our results, age-based mitigation strategies can be a key ingredient to contain rebound effects and to protect age-classes with higher incidence of severe cases.

2 Model

To analyze mobility-restriction policies, we introduce a minimalist compartmental model [11, 13]. Although many models, both mechanistic, statistic and stochastic [14], have been proposed for the Covid-19 infection, data collected from national healthcare systems suffer from the lack of homogeneous procedures in medical testing, sampling and data collection [15]. Not to mention the difficulties in assessing the impact of variability in social habits during the epidemics [11, 16]. Moreover, especially in the early phases of the epidemic – i.e. the ones characterised by an exponential growth – different models sharing a given reproduction number R_0 can fit the data with equivalent accuracy (see SI discussion about fitting initial parameters). For these reasons, our aim is to focus on some fundamental qualitative scenarios and not on detailed predictions. We adapt the *SIR* model, the most basic epidemic model for flu-like epidemics, to the observed data available in the Italian case.

The model relies on four compartments, namely: S , I , O , R . Hence, S (usceptible) individuals can become I (nfective) when meeting another infective individual, I (nfectives) either become O (bserved) – i.e. present symptoms acute enough to be detected from the national health-care system – or are R (emoved) from the infection cycle by having recovered; also O (bserved) individuals are eventually R (emoved) from the infection cycle. Notice that we are implicitly absorbing the number of deaths in the R (emoved) compartment of the model; thus R comprises both the *Recovered* people (who hopefully have developed antibodies and are not anymore susceptible) and the small fraction of those who did not overcome the epidemics. In the case of Covid-19, it is not clear yet if there is an asymptomatic phase [17, 18]; in the model, we implicitly assume that asymptomatics are infective and their removal time is the same of the I class. The

model is described by the following differential equations:

$$\begin{aligned}
\partial_t S &= -\beta S \frac{I}{N} \\
\partial_t I &= \beta S \frac{I}{N} - \gamma I \\
\partial_t O &= \rho \gamma I - hO \\
\partial_t R &= (1 - \rho) \gamma I + hO
\end{aligned} \tag{1}$$

$N = S + I + O + R$ is the total number of individuals in a population, the transmission coefficient β is the rate at which a susceptible becomes infected upon meeting an infected individual, γ is the rate at which an infected either becomes observable or is removed from the infection cycle. Like the *SIR* model, the basic reproduction number is $R_0 = \beta/\gamma$; the extra parameters of the *SIOR* model are ρ , the fraction of infected that become observed from the national health-care system, and h , the rate at which observed individuals are removed from the infection cycle. Notice that we consider that O (bserved) individuals not infecting others, being in a strict quarantine.

3 The Italian Lockdown

The Italian lockdown measures of the 8th and 9th of March [19, 20] aimed to change mobility patterns and to reduce the intensity of social contacts, both through quarantine measures and through an increased awareness of the importance of social distancing. We analyze an extensive data set on Facebook (FB) mobility data; those data are part of the Facebook project “Data for Good”, and illustrate mobility patterns of FB users, who allowed the social network to track their location (see <https://dataforgood.fb.com/docs/Covid-19/>) [21]. Our analysis confirms that the lockdown has reduced both the travelled distance and the flow of travelling people.

We consider the effects of lockdown measures on the parameters of our model. Lockdown is a non-pharmaceutical measure; hence the rate γ is the most unaffected parameter, since it is related to the “medical” evolution of the disease. Analogous arguments apply to the rate h of exiting a condition serious enough to be observed and to the probability ρ of being observed by the national healthcare system (although ρ could be influenced variations in testing schemes and alert thresholds). On the other hand, the transmission coefficient β can be thought as the product $C\lambda$ of a contact rate C times a disease-dependent transmission probability λ . Hence, if we assume that the speed of Covid-19 mutation is irrelevant on our timescales, lockdown strategies mostly influence β by reducing the contact rate C between individuals.

To adapt the *SIOR*’s parameters to the Italian data [22], we compare the reported cumulative number of Covid-19 cases Y^{Obs} with the analogous quantity $Y^{\text{model}} = \int \rho \gamma I dt$ in our model. We want to stress that our model fitting is not aimed to produce an accurate model for detailed predictions, but to work in a realistic region of the parameter space.

We first estimate model's parameters by least square fitting on the pre-lockdown period. Since in such range the data Y^{Obs} show an exponential growth trend, it indicates that the pre-lockdown period is an early phase of the epidemic where $\beta - \gamma$ equals the growth rate of Y^{Obs} (see SI for observations on the choices of initial parameters). For fixed $\beta - \gamma$, the time of the epidemic start (that we conventionally assume as the time t_0 where the number of infected is 1) and the fraction ρ of serious cases observed by the national healthcare service, allows some flexibility in estimating the values of β and γ as long as their difference is fixed. Hence, estimating *medical* parameters as the rate γ of escaping the infected state is paramount for calibrating mathematical models.

In response to the outbreak of Covid-19, several estimates of model parameters have been proposed in the literature, revealing a certain amount of uncertainty about some fundamental variables of the epidemic contagion. The European Centre for Disease controls reports an infection time duration τ_I between 5 and 14 days [23]; in our model, we will use $\tau_I = 10$ (i.e. $\gamma = \tau_I^{-1} = 1/10 \text{ days}^{-1}$). According to a report of ISS, the Italian National Health Institute, the time from the start of serious symptoms (i.e. when one gets “observed” from ISS) to the resolution of the symptoms can be estimated as $\tau_H \sim 9 \text{ days}$ [24], corresponding in our model to a value $h = 1/9 \text{ days}^{-1}$. Notice the analysis of 12 different models [14] reports varying estimates for the basic reproduction number R_0 , ranging from 1.5 to 6.47, with mean 3.28 and a median of 2.79.

From fitting the 15 days of Y^{obs} (pre-lockdown phase) and by performing a bootstrap sensitivity analysis of the parameters, we obtain $\beta - \gamma \sim 0.25 \pm 0.01$ and $t_0 = -30 \pm 5 \text{ days}$ by assuming that $\rho = 40\%$. Varying ρ in $[10\%, 100\%]$ varies $\beta - \gamma$ in $[0.22, 0.27]$. On the other hand, for fixed $\beta - \gamma$, R_0 would vary linearly with τ_I ; as an example, R_0 varies in $[2.5, 4.5]$ for the literature parameters $\tau_I \in [5, 14]$; accordingly, to adjust the difference in growth rate, t_0 varies in $[26, 32]$. However, despite the variability of the parameter range, the qualitative behavior of the model – and hence our analysis of the key factors of the epidemic evolution – is unchanged.

We then assume that, after the lockdown day $t_{\text{Lock}} = 15$ (corresponding to the 9th of March), contact rate drops down by a factor α and hence $\beta \rightarrow \alpha\beta$. By fitting the observed data Y^{obs} for a symmetric period of 15 days after t_{Lock} , and by performing a bootstrap sensitivity analysis, we find $\alpha = 0.49 \pm 0.01$, i.e. a $\sim 50\%$ reduction in infectivity and hence in R_0 . Our figure is in line with the observed reduction in R_0 in response to the combined non-pharmaceutical interventions, that across several countries has an average reduction of 64% compared to the pre-intervention values [25]. Notice that Facebook mobility data show a post-lockdown reduction in mobility of 15% at regional level and of 73% at inter-regional level; however, as we will point out later, mobility has a strong impact at the beginning of the epidemics in new regions/countries, while it has much lower effects on the evolution of the epidemics in a region/country.

In the following, we will use the parameters of Tab. 1, corresponding to a basic reproduction number $R_0 = 3.5$. Moreover, since patients in intensive care represent the highest burden for health facilities, in the graphs of the paper we will indicate the number of patients in intensive care, estimated as 3.5% of the

$\beta = 0.35 \text{ day}^{-1}$	$\gamma = 10^{-1} \text{ day}^{-1}$	$h = 1/9 \text{ day}^{-1}$
$t_0 = -30 \text{ days}$	$\rho = 40\%$	$\alpha = 0.49$

Tab. 1. Standard parameters used for the *SIOR* model in the paper.

total patients by using the figures reported by ISS [22].

4 National scenarios and exit mechanisms

Since we are interested on the factors driving the exit dynamics from lockdown, and not on the accurate quantitative predictions of real strategies, we consider several lockdown scenarios, where the lockdown is abruptly lifted and the system let return to the pre-lockdown parameters. Such an approach clearly describes a worst-case estimate of the intensity of the second wave of the contagion after the conclusion of the lockdown. Hence, we consider several simplified scenarios, where we use the *SIOR* model described by System (1) with the parameters of Tab. 1. First, in the simple case of a *SIOR* model fitted on Italian data, we analyze how the post-lockdown dynamics changes according to different starting dates of the epidemics and to different levels of the restrictions implemented by the national authorities. Then, we study the effect of explicitly considering Italy as a collection of separate administrative entities (Regions); finally, we consider the effects of social interactions across age classes.

Interestingly, mobility flows [21] and inter-age social mixing [26] lie at the two opposite range of modelling. In fact, the regional social contact matrix is dense (Fig. 1, left panel), indicating that age classes dynamics are strongly coupled. On the other hand, the inter-regional mobility matrix is very sparse (Fig. 1, right panel), indicating that regions have their own independent dynamics.

We first consider a simple exit strategy consisting in lifting the lockdown at a time t_{Unlock} after the peak of O has occurred. For instance, we hypothesize that infection proceeds uncontrolled up to time t_{Lock} ; in the following lockdown period $[t_{\text{Lock}}, t_{\text{Unlock}}]$, the transmission coefficient β is reduced by a factor α ; finally, β returns to its initial value and only herd immunity is responsible for the dampening of the epidemics. Again, this is a worst case scenarios since it does not considers cautions like keeping social distances and wearing protection devices like masks.

Our results show that the lockdown lowers the peak of O - i.e. the individuals with noticeable symptoms - to $\sim 70\%$ of the free epidemic one, but it also doubles the time of its occurrence from ~ 1.9 months to ~ 3.8 months: an extremely obnoxious effect for the sustainability conditions of the economy of a country. However, since the number of hospitalized patients and - most importantly - the number of patients in intensive care is only a fraction of O , lowering the peak puts less stress on the healthcare system. The ideal situation would be to have accurate data, an accurate model and accurate estimates of the parameters; as an example, in our model lifting the lockdown when the

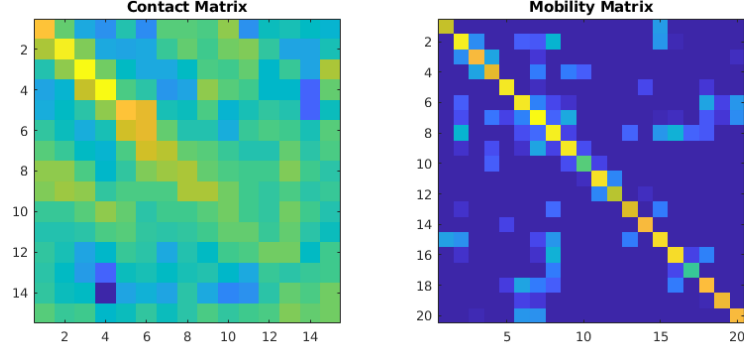


Fig. 1. Left Panel: social contact matrix, from [26]. Right panel: inter-regional mobility matrix, from the Facebook project “Data for Good”. The intensity of a color maps the strength of a matrix element (light colors: high values; dark colors: low values). The inter-age social mixing matrix is dense; hence age classes dynamics are strongly coupled. The inter-regional mobility flows is very sparse (i.e. off diagonal elements are order of magnitudes lower than diagonal elements): this mean that most of the people travel within the same region of origin; hence, the regional dynamics can be considered “almost” decoupled.

number of infected people per unit time $\beta S(t)I(t)/N$ is lower than the average number of recovering people $\gamma I(t)$ would ensure that the number of infections would continue to decrease. In real life, situations are more fuzzy: having not enough information, we could decide to resort on some heuristics, like lifting the lockdown after the observed people O have dropped to a suitable percentage of the maximum peak. As an example, after ~ 4.7 months the peak has reduced to 70% of its initial value, while after ~ 5.2 months to 50%, i.e. ~ 0.5 months later. Notice that, the earlier the lockdown is lifted, the faster O decays to zero even if it starts from higher figures and could even experience a rebound. All such effects are shown in Fig. 2.

Our framework sustains the identification of several mechanisms. The first is related to the timeliness of the lockdown, i.e. to the choice of anticipating t_{Lock} . As expected, early lockdown (i.e. well before the infection peak of the uncontrolled epidemics has developed) reduces the height of the peak at the cost of delaying its appearance and widening the duration of the epidemics. Conversely, lifting the lockdown too soon can make epidemic start again and reach values higher than the ones before the release. A peculiar and counter-intuitive effect can be generated if the lockdown is anticipated too much: in fact, a too early lockdown risks to delay the start of the epidemic without attenuating its severity (see SI for the description of the effects of varying lockdown time). In other words, an early lockdown “buys” time, but only postpones the problem without mitigating its severity.

Another effect is the impact of extreme social and physical distancing mea-

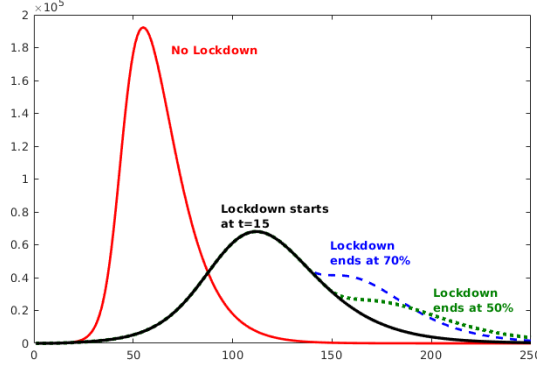


Fig. 2. Comparison of the scenarios where the lockdown is relaxed after the percentage of people with visible symptoms (O) is reached the 70% and the 50% of the reported cases peak. Lifting the lockdown earlier makes the epidemics disappear faster, but has higher impact on the number of hospitalized and intensive care patients; moreover, lifting the lockdown too early can result in a rebound of the number of cases.

asures on the post-lockdown dynamics. Increasing the strength α of the lockdown not only delays the time at which it is lifted, but also induces a stronger re-start of the epidemic in the post-lockdown (see SI for the description of the effects of varying lockdown strength), triggering the need for a new lockdown. Such scenario of repeated lockdowns would obviously be unsustainable, in terms of social and economic costs.

An additional counter-intuitive mechanism must be considered. Since an attenuation of α corresponds to an effective reproduction number $R_0^{\text{eff}} = \alpha R_0$, at the critical value $\alpha_{\text{crit}} = 1/R_0$ the epidemic neither grows nor decreases; to be precise, the decrease becomes sub-exponential, thus taking a practically infinite time when the size of the population is large. Thus, after t_{Lock} the system stays stationary until the lockdown is lifted at t_{Unlock} ; at this point, the epidemic starts growing again as it was before the lockdown. In general, if $\alpha < \alpha_{\text{crit}}$, the system looks to ameliorate (infected, hospitalized, all the infective compartments go down) but as soon as the lockdown is lifted, the epidemic starts again to reach its full strength (see SI). Nevertheless, our estimate $\alpha \sim 0.5 > \alpha_{\text{crit}} \sim 0.3$ for the Italian lockdown gives us hope that, at least in regions where epidemics had an early start, it will not be necessary to follow a repeated seek-and-release strategy in the post-lockdown phase. On the other hand, if it can be attained a lockdown strength $\alpha \sim \alpha_{\text{crit}}$ without disrupting the economy, the epidemic could be contained until the creation, production and distribution of a vaccine.

Tab. 2. Regional delays (in days)

Lombardia	0.0	Molise	10.6
Emilia Romagna	3.1	Umbria	11.8
Marche	4.3	Abruzzo	13.1
Veneto	5.7	Lazio	14.5
Valle d’Aosta	6.4	Campania	15.0
P.A. Trento	6.6	Puglia	15.7
P.A. Bolzano	8.0	Sardegna	16.2
Liguria	8.1	Sicilia	16.6
Friuli Venezia Giulia	8.9	Calabria	17.2
Piemonte	9.0	Basilicata	19.2
Toscana	10.4		

5 Regional Scenarios

Starting with the first confirmed cases in Lombardy on 21 February, by the beginning of March the Covid-19 outbreak had already spread to all Italian regions. While the delay in the beginning of the infection is accounted for by the different mobility interaction between regions, once the epidemic has started in a given area, the intake of external infected people becomes quickly irrelevant (see SI for the description of a metaregional model and its behavior). As a consequence, the normalised growth curves of the epidemic variables tend to converge to a similar shape if epidemiological parameters are uniform across the regions (or the countries; see SI about using normalised data). In fact, regional info graphics released by the Italian National Healthcare Institute (ISS) [22] show that regional diffusion curves have a similar shape and different starting dates (see Fig. 3). This observation can be justified as follows: Italian regions are independent administrative entities, and most of the population tend to work inside the resident region [27]. Hence, epidemics propagate from region to region via the fewer inter-regional exchanges (Incidentally, Lombardy is the Italian region which is most involved in international trade connections [28], being the natural candidate for the initial outbreak of the epidemic). More practically, we estimate the delays by minimizing the distance among the observed curves (see SI for the details of the algorithm); results are reported in Tab. 2. Notice that, assuming Lombardy has been the first region (i.e. delay=0), the resulting regional delays are mostly correlated to geographical distances.

To test the effects of delayed epidemics starts, we build up a synthetic scenario where the Covid-19 outbreak spreads independently in each region; as argued before, given the mobility pattern such an approximation is reasonable after the epidemic has started and is even more accurate under lockdown conditions. Hence, we apply the parameters of table 1 to regional cases, applying eq.1 separately to each region; the maximum number of individuals N_i is the population of the i^{th} (<https://www.istat.it/it/popolazione-e-famiglie?dati>) while the initial time of the infection is taken from table 2. By summing up all the

S_i, \dots, R_i , respectively, we obtain a synthetic model for the global evolution of Covid-19 epidemic throughout Italy. To evaluate the effect of heterogeneity in time delays, we compare the number of daily cases $O^{\text{Delay}} = \sum O_i^{\text{Delay}}$ in our scenario (obtained by taking into account the regional delays t_i as reported in Tab. 2) with the number of daily cases $O^0 = \sum O_i^0$ we would observe by considering the epidemics starts at the same time t_0 in all regions. As expected, heterogeneity flattens the curve and shifts its maximum later in time. This is a first source of errors when fitting an heterogeneous dynamics with a global model. Again, we want to remark that we are exploring realistic qualitative scenarios and we do not aim to predict the real evolution of the epidemics: in fact, Italian regions are different for social contact habits, mobility, organization and capacity of health care provision, as well for factors that affect the medical parameters, like comorbidities, social conditions or pollution levels.

We consider two possible exit strategies: in the first, that we call the *Asynchronous* scenario, each region i lifts the lockdown at the time t_i^{Unlock} when the peak of O_i^{Delay} decreases by 30%; in the second, that we call the *Synchronous* scenario, each region i lifts the lockdown at the same time t^{Unlock} , i.e., when the global peak of O^{Delay} decreases by 30%. The choice of 30% is arbitrary and similar results would hold for choices of values near the peak; it tries to be a sketch of a situation where, due to economic pressure, lockdown is lifted as soon as possible.

Since once an outbreak has started, the epidemic dynamics in a given region i is essentially uncorrelated with the epidemic spreading of any other region $j \neq i$, it could be safe and appropriate to decide the lockdown lifting time on a regional basis, instead of lifting restrictions at the same time. Indeed, it could be unreasonable to keep locked the regions where the epidemic started earlier; on the contrary, regions where the epidemic began with some delay could experience a strong rebound when subjected to a premature lockdown lifting. In Fig. 3 we show the effects of lifting the lockdown at both regional (*Async*) and national (*Sync*) level in Lazio and Lombardy. Since not only epidemics, but also the ruin of an economy is a non-linear process, the *Sync* scenario can turn out to be even more disruptive than the epidemic itself (see also Fig. 2). Notice that analogous arguments hold - mutatis mutandis - also for the world/countries scenario.

6 The role of Age

As we have already observed in the previous Section, heterogeneity strongly impacts on the results within the model [29]. Since the transmission coefficient is proportional to the contact rate between individuals, the rates of social mixing between different age classes represent a well known important source of heterogeneity. This information can be estimated either through large-scales surveys [26] or through virtual populations modeling [30]. While the POLYMOD [26] matrices have been extensively used to estimate the cost-effectiveness of vaccination for different age-classes during the 2009 H1N1 pandemic [31, 32], here

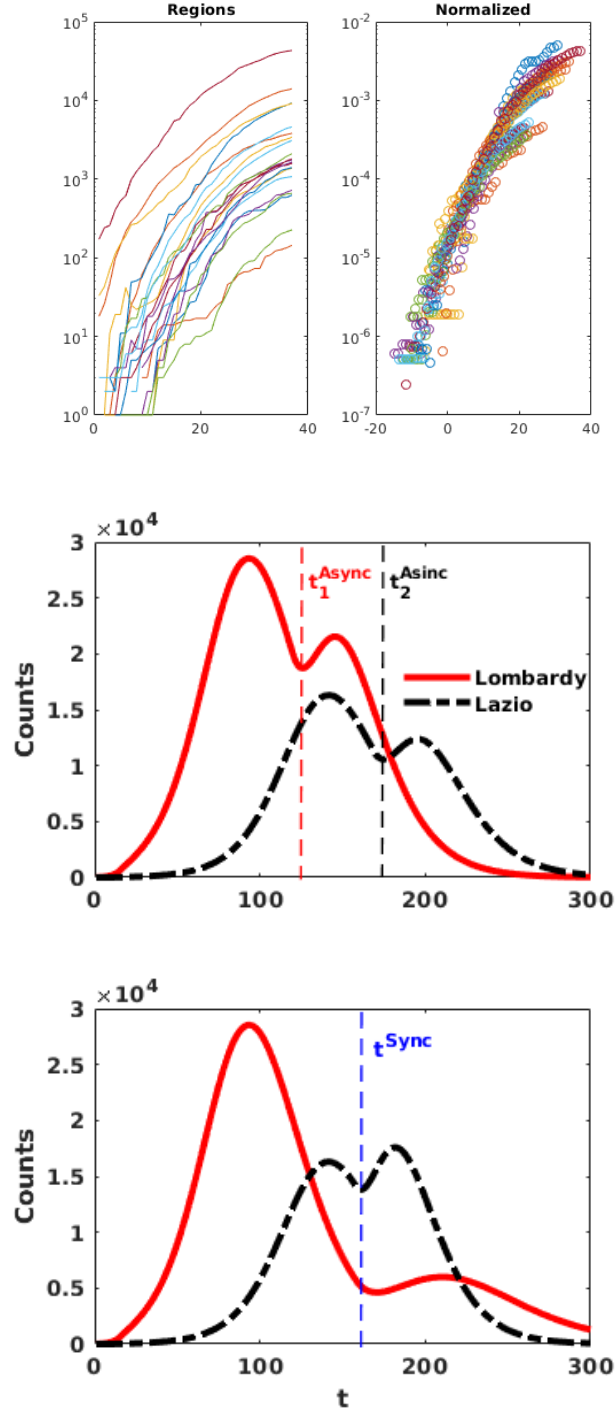


Fig. 3. Upper panels: analysis of time delays among the start of epidemics in different regions (see Tab. 2). Lower panels: sketch of an *Async*(hronous) exit strategy (i.e. each region lifts the lockdown following its own policy) respect to a *Sync*(hronous) exit strategy (i.e. the lockdown lift follows the same policy, but applied to a nation wide scale). In particular, t^{Sync} corresponds to lifting the lockdown in all the region after the peak has fallen by 30% , while t_i^{Async} corresponds to lifting the lockdown in the i^{th} region after the peak of such region has fallen by 30%.

	Y	M	E
Y	2.35	0.44	0.67
M	0.47	0.59	0.50
E	0.50	0.55	0.80

Tab. 3. POLYMOD matrix aggregated for three age classes: Young (00 – 19), Middle (20 – 69) and Elderly (70+).

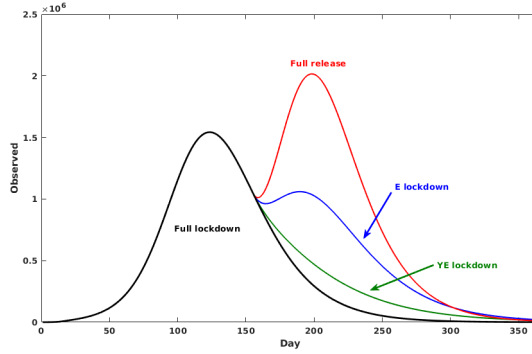


Fig. 4. Comparison of the scenarios where the lockdown is relaxed only for a particular age class with respect to a full release policy. Strategies: YE = quarantine young and elderly, E = quarantine elderly. Notice that we have purposefully left the M class fully unrestrained, in order to show how maintaining a partial, age-based lockdown could deeply change the effectiveness of the exit strategy while maintaining active working force active.

we use them to support the design of a broad class of exit strategies. Hence, to account for age classes, we extend our model by rewriting the transmission coefficient as βC (see SI for a full description of the extended model), where β is the transmission probability of the infection, and C is the sociological matrix describing the contact patterns typical of a given country. For lack of further information, we assume β constant among age classes and C as in [26]. To simplify the analysis, we gather POLYMOD age groups into three classes: Young (00 – 19), Middle (20 – 69) and Elderly (70+) (see Tab 3). Such an aggregation puts together the most “contactful” classes (00 – 19), the classes with the highest mortality risk (70+) [22], and - with a good approximation - the classes corresponding to the active working population (20 – 69).

Fig. 4 shows how the percentage of people with visible symptoms (O) varies once the age class heterogeneity is considered in the model. Differently from fig. 2, fully lifting the lockdown results in a conspicuous rebound of the epidemics, that reaches values even more severe than the pre-exit peak. Thus, models, which do not explicitly consider this source of heterogeneity could severely misforecast the post-exit dynamics. On the other hand, the introduction of the

age structure in the model allows to orient the design of exit strategies based on age-targeted policies, as a way to dampen a possible upturn of contagion. Specifically, social/physical distance measures applied to the elderly may contribute to contain the impact of a renewed upward phase, while relaxing restrictions to the working age class (20-69) would not impair the smoothing of contagion propagation in the post-lockdown phase. Moreover, different strategies would change the relative percentage for age class of people who have undergone the infection; since the incidence of severe cases is strongly age related, this is a crucial issue. Again, it is important to emphasize that we are referring to simple mock-up strategies, which correspond to worst-case scenarios: in real life, community measures and physical distancing, infection prevention and control, personal hygiene habits, face mask usage, etc. will be decisive in contributing to the dampening of the epidemics [23].

7 Conclusions

In this paper we propose and test a general framework to study the Covid-19 contagion through a compartmental model, with a focus on geographical groups and age classes. Our framework shows that the promptness of lockdown measures has a main effect on the timing of the contagion. Strict social distancing policies reduce the severity of the epidemics during the lockdown period, but full recover of the contagion can occur once such measures are relaxed. As a consequence, a mix of specific mitigation strategies must be prepared during the lockdown and implemented thereafter. In order to understand the relative potential impact of different broad strategies, we focus on two broad decomposition criteria within the model, i.e. on geographical mobility and on social interactions between age classes. Our results are driven by the sparsity of the underlying contact matrices, which we measure. First, we show how local dynamics at regional level can be erroneously masked when observing the aggregate national system. Regional heterogeneity tends to lower and widen the curve of the contagion, contributing to a shift forward in time for the peak at the aggregate level. Second, our analysis of mobility data shows that, due to the sparsity of interconnections across regions, contagion develops independently within each region once the epidemic has started. This, in turn, contributes to account for the delays observed in the alignment of the contagion curves across different geographical areas. The independence of regional dynamics is important, since it can justify the adoption of a mix between general mitigation strategies and solutions which are specific to individual regions (or countries) or to clusters of regions. Finally, we investigate the structure of social contacts across different settings and we quantify the relative importance of interactions between age classes in the spreading of contagion. We show that the younger (0-19) and the elder (70+) are the most intensively interacting classes. As a consequence, mitigation strategies specific to these two classes can produce a significant impact on diffusion rates in the post-lockdown phase. In fact, our results show the importance of designing physical distancing measures specific to the elderly

and, in addition, they can orient decisions on the limitation of social contacts for the young. Overall, our results provide guidance on how to relax some of the restrictions to mobility for the active population (20-69), while smoothing and lessening the propagation of contagion in the post-lockdown phase.

Although our study is tuned on the Italian Covid-19 contagion, our modeling approach is general enough to help us understand the role of relevant dimensions, beside the medical and pharmaceutical ones, in identifying the relative importance of different strategies introduced to contain the epidemics and to mitigate its effects. Our framework can contribute to mitigate the stringency of the trade-off between health and economic outcomes. In particular, we show how the timeline of post-lockdown measures should take into account some fundamental compartmental aspects, such as geographical factors and interactions between different age classes. This feature is general, and it can orient the analysis towards fine grained simulations on the impact of specific precautionary interventions, which enforce social distancing while containing the overall burden on the economy and on society.

Additional Information

Competing interests

The author(s) declare no competing interests.

Acknowledgements

A.S., E.B., M.C. and W.Q. acknowledge the support from CNR P0000326 project AMOFI (Analysis and Models OF social medIa) and CNR-PNR National Project DFM.AD004.027 “Crisis-Lab”.

References

- [1] Matt J Keeling. Models of foot-and-mouth disease. *Proceedings of the Royal Society B: Biological Sciences*, 272(1569):1195–1202, 2005.
- [2] Francesco Di Lauro, István Z Kiss, and Joel Miller. The timing of one-shot interventions for epidemic control. *medRxiv*, 2020.
- [3] Vital Surveillances. The epidemiological characteristics of an outbreak of 2019 novel coronavirus diseases (covid-19)—china, 2020. *China CDC Weekly*, 2(8):113–122, 2020.
- [4] Roy M Anderson, Hans Heesterbeek, Don Klinkenberg, and T Déirdre Hollingsworth. How will country-based mitigation measures influence the course of the covid-19 epidemic? *The Lancet*, 395(10228):931–934, 2020.
- [5] Odo Diekmann, Hans Heesterbeek, and Tom Britton. *Mathematical tools for understanding infectious disease dynamics*, volume 7. Princeton University Press, 2012.
- [6] Herbert A Simon and Albert Ando. Aggregation of variables in dynamic systems. *Econometrica: journal of the Econometric Society*, pages 111–138, 1961.
- [7] Albert Ando and Franklin M Fisher. Near-decomposability, partition and aggregation, and the relevance of stability discussions. *International Economic Review*, 4(1):53–67, 1963.
- [8] Herbert A Simon. *The architecture of complexity*. Cambridge, MA: MIT Press, 1996.
- [9] Pierre Jacques Courtois. *Decomposability: queueing and computer system applications*. Academic Press, 2014.
- [10] Neil Ferguson, Daniel Laydon, Gemma Nedjati Gilani, Natsuko Imai, Kylie Ainslie, Marc Baguelin, Sangeeta Bhatia, Adhiratha Boonyasiri, ZULMA Cucunuba Perez, Gina Cuomo-Dannenburg, et al. Report 9: Impact of non-pharmaceutical interventions (npis) to reduce covid19 mortality and healthcare demand. *MRC Centre for Global Infectious Disease Analysis*, 2020.
- [11] Kiesha Prem, Yang Liu, Timothy W Russell, Adam J Kucharski, Rosalind M Eggo, Nicholas Davies, Stefan Flasche, Samuel Clifford, Carl AB Pearson, James D Munday, et al. The effect of control strategies to reduce social mixing on outcomes of the covid-19 epidemic in wuhan, china: a modelling study. *The Lancet Public Health*, 2020.
- [12] Matteo Chinazzi, Jessica T Davis, Marco Ajelli, Corrado Gioannini, Maria Litvinova, Stefano Merler, Ana Pastore y Piontti, Kunpeng Mu, Luca Rossi, Kaiyuan Sun, et al. The effect of travel restrictions on the spread of the 2019 novel coronavirus (covid-19) outbreak. *Science*, 2020.

- [13] Norman TJ Bailey et al. *The mathematical theory of infectious diseases and its applications*. Charles Griffin & Company Ltd, 5a Crendon Street, High Wycombe, Bucks HP13 6LE., 1975.
- [14] Ying Liu, Albert A Gayle, Annelies Wilder-Smith, and Joacim Rocklöv. The reproductive number of covid-19 is higher compared to sars coronavirus. *Journal of travel medicine*, 2020.
- [15] Francesco Casella. Can the covid-19 epidemic be managed on the basis of daily data? *arXiv preprint arXiv:2003.06967*, 2020.
- [16] Sebastian Funk, Marcel Salathé, and Vincent AA Jansen. Modelling the influence of human behaviour on the spread of infectious diseases: a review. *Journal of the Royal Society Interface*, 7(50):1247–1256, 2010.
- [17] Yan Bai, Lingsheng Yao, Tao Wei, Fei Tian, Dong-Yan Jin, Lijuan Chen, and Meiyun Wang. Presumed asymptomatic carrier transmission of covid-19. *Jama*, 2020.
- [18] Hiroshi Nishiura, Tetsuro Kobayashi, Takeshi Miyama, Ayako Suzuki, Sungmok Jung, Katsuma Hayashi, Ryo Kinoshita, Yichi Yang, Baoyin Yuan, Andrei R Akhmetzhanov, et al. Estimation of the asymptomatic ratio of novel coronavirus infections (covid-19). *medRxiv*, 2020.
- [19] Decreto del Presidente del Consiglio dei Ministri. Ulteriori disposizioni attuative del decreto-legge 23 febbraio 2020, n. 6, recante misure urgenti in materia di contenimento e gestione dell'emergenza epidemiologica da covid-19. *Gazzetta Ufficiale*, 59(08-03-2020), 2020.
- [20] Decreto del Presidente del Consiglio dei Ministri. Ulteriori disposizioni attuative del decreto-legge 23 febbraio 2020, n. 6, recante misure urgenti in materia di contenimento e gestione dell'emergenza epidemiologica da covid-19. *Gazzetta Ufficiale*, 62(09-03-2020), 2020.
- [21] Caroline O Buckee, Satchit Balsari, Jennifer Chan, Mercè Crosas, Francesca Dominici, Urs Gasser, Yonatan H Grad, Bryan Grenfell, M Elizabeth Halloran, Moritz UG Kraemer, et al. Aggregated mobility data could help fight covid-19. *Science (New York, NY)*, 2020.
- [22] Istituto Superiore di Sanità. Iss: Sars-cov-2 dati epidemiologici (<https://www.epicentro.iss.it/>). Technical report, ISS, 2020.
- [23] European Centre for Disease Prevention and Control (ECDC). Coronavirus disease 2019 (covid-19) pandemic: increased transmission in the eu/eea and the uk – eighth update, 8 april 2020. 2020.
- [24] Istituto Superiore di Sanità (ISS) COVID-19 Surveillance Group. Characteristics of covid-19 patients dying in italy report based on available data on march 30th, 2020. 2020.

- [25] Seth Flaxman, Swapnil Mishra, Axel Gandy, H Unwin, H Coupland, T Mellan, H Zhu, T Berah, J Eaton, P Perez Guzman, et al. Report 13: Estimating the number of infections and the impact of non-pharmaceutical interventions on covid-19 in 11 european countries. 2020.
- [26] Joël Mossong, Niel Hens, Mark Jit, Philippe Beutels, Kari Auranen, Rafael Mikolajczyk, Marco Massari, Stefania Salmaso, Gianpaolo Scalia Tomba, Jacco Wallinga, et al. Social contacts and mixing patterns relevant to the spread of infectious diseases. *PLoS medicine*, 5(3), 2008.
- [27] Istituto Nazionale di Statistica. Popolazione insistente per studio e lavoro (<https://www.istat.it/it/files//2020/03/Popolazione-insistente.pdf>). Technical report, ISTAT, 2020.
- [28] Istituto Nazionale di Statistica. Commercio estero (<https://www.istat.it/it/commercio-estero>). Technical report, ISTAT, 2020.
- [29] Odo Diekmann, Johan Andre Peter Heesterbeek, and Johan AJ Metz. On the definition and the computation of the basic reproduction ratio r_0 in models for infectious diseases in heterogeneous populations. *Journal of mathematical biology*, 28(4):365–382, 1990.
- [30] Laura Fumanelli, Marco Ajelli, Piero Manfredi, Alessandro Vespignani, and Stefano Merler. Inferring the structure of social contacts from demographic data in the analysis of infectious diseases spread. *PLoS computational biology*, 8(9), 2012.
- [31] Jan Medlock and Alison P Galvani. Optimizing influenza vaccine distribution. *Science*, 325(5948):1705–1708, 2009.
- [32] Marc Baguelin, Albert Jan Van Hoek, Mark Jit, Stefan Flasche, Peter J White, and W John Edmunds. Vaccination against pandemic influenza a/h1n1v in england: a real-time economic evaluation. *Vaccine*, 28(12):2370–2384, 2010.

8 Author Contribution

All authors contributed to the writing and the discussion of the paper. A.Sc. contributed to the modelling and the simulations. M.C., E.B., A.F. and A.Sp. contributed to the data retrieval and analysis. A.Sc. and E.B. contributed to the mathematical analysis of the models. A.Sc., F.P. and W.Q. contributed to the design of the paper and of the strategies to be analysed. F.P., A.F. and A.Sp. contributed to the discussion of the economic impacts of the analysis. W.Q. and M.C. contributed to the mobility analysis.