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Parino, Francesco; Zino, Lorenzo; Rizzo, Alessandro; Porfiri, Maurizio

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A metapopulation activity-driven network model for COVID-19 in Italy

(Special Session: Dynamical Systems to Model and Control Epidemic Spreading: COVID-19 and beyond)

Francesco Parino[1], Lorenzo Zino[2], Maurizio Porfiri[3], and Alessandro Rizzo[1,3]

Context - Several studies suggest that mobility has a key role in shaping the evolution of the COVID-19 outbreak [1, 2]. The proposed mathematical model is designed to capture and reproduce both the spatial spread of the disease and the heterogeneous, time-varying nature of human interactions that supports the pandemic. Our model affords the execution of accurate what/if analyses, which can inform decision-making by policy makers and public health authorities. Specifically, our approach can be used to predict the effect of nontherapeutical interventions (during implementation or gradual re-opening of local borders), of productive activities, and citizen ability to freely move within national borders.

Model - We consider a variant of a metapopulation model [3]. A population of n individuals is partitioned into $H = \{1, \dots, k\}$ geographical areas (or *patches*, which in our case coincide with Italian provinces. Provinces are connected though a weighted graph (H, W), which captures the aggregated inter-provincial commuting patterns; $W \in [0,1]^{k \times k}$ is a row-stochastic matrix such that W_{hk} measures the average fraction of people that live in province h and commute to province k. A schematic of the metapopulation structure is shown in Fig. 1.

Differently from typical metapopulation models that assume homogeneous mixing within patches, our model accounts for the inherent heterogeneous and time-varying nature of human interactions [4]. To this aim, individuals interact on the basis of a mechanism inspired by activity-driven networks [5, 6]. Specifically, individuals are divided into a finite set of activation classes $0 < a_1 < \cdots < a_p \leq 1$, where a_i is probability that an individual in the ith class generates an interaction in a unit time. Different classes are used to capture heterogeneous human behavior, which has been proved to occur in real social systems [4]. At any unit time-step, each individual that belongs to the ith class generates an interaction with probability a_i, independent of the others. Such an individual is called *active.* Interactions are generated according to a probabilistic mechanism, accounting for both individual activity features and mobility patterns. We introduce a parameter $b \in [0,1]$ to measure the propensity of active individuals to commute to other regions. With probability $1-b$, an active individual does not commute and interacts locally with an individual selected uniformly at random within his/her province. With probability b, an active individual commutes to another province, randomly selected according to the routing matrix W, and then generates the interaction therein. At the end of the time-unit, the commuter returns to the province in which he/she lives. The matrix W capture the spatial mobility of these commuters.

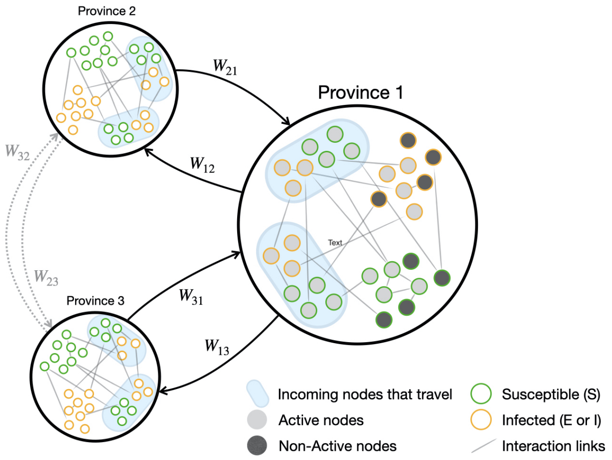

Figure 1: Metapopulation structure.

To model the epidemic progression, we adopt a susceptible–exposed–infected–asymptomatic–removed (SEIAR) model, which allows to capture some key features of COVID-19, including the presence of a phase in which individuals are infected, but asymptomatic, before the possible (but not necessary) emergence of symptoms [7]. Susceptible individuals (S) who contact infectious individuals (either symptomatic or asymptomatic) become exposed (E) with a per-contact probability λ. Then, with probability β, they may become symptomatic (I). Such a transition occurs with probability ν per unit-time. Otherwise, with probability $1-\beta$, they become asymptomatic (A). All infected individuals are eventually removed (that is, they recover or die)[4]. Such a transition occurs with probability γ, if asymptomatic, and with probability μ, if symptomatic. The schematic of all the possible state transitions is represented in Fig. 2.

Let us consider a generic class of activation i and province h, where S_i^h, E_i^h, I_i^h, and A_i^h are the fraction of susceptible, exposed, symptomatic, and asymptomatic individuals belonging to that class and province, respectively. For large-scale systems, we derive an approximate solution of the system of equations, governing the disease spreading

$$\begin{array}{rcl} S_i^h(t+1) & = & (1-\Pi_i^h)S_i^h(t) \\ E_i^h(t+1) & = & \Pi_i^h S_i^h(t) + (1-\nu)E_i^h(t) \\ I_i^h(t+1) & = & \beta\nu E_i^h(t+1) + (1-\nu)I_i^h(t) \\ A_i^h(t+1) & = & (1-\beta)\nu E_i^h(t+1) + (1-\gamma)A_i^h(t). \end{array} \tag{1}$$

where Π_i^h is the probability that an individual with activation class a_i from province h has an interaction with an infected individual. Such an expression has a rather lengthy and convoluted form that depends on the properties of the individual and of the rest of the population, the mobility parameters b and W, and the fraction of exposed and infected individuals for each class and in each province. Here, we omit this expression due to space constraints.

Parametrization - We tailored our model to the 2020 COVID-19 outbreak in Italy. Using census data from ISTAT [8], we partitioned the population into 107 provinces and metropolitan cities,

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[1] Politecnico di Torino [2] University of Groningen [3] New York University

[4] The *removed* state can be further subdivided in the *recovered* and *deceased* classes, including a further parameter. In this preliminary effort, without loss of generality, we adhere to the simpler SEIAR model.

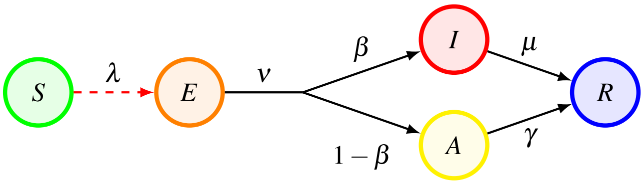

Figure 2: State transitions characterizing the SEIR model.

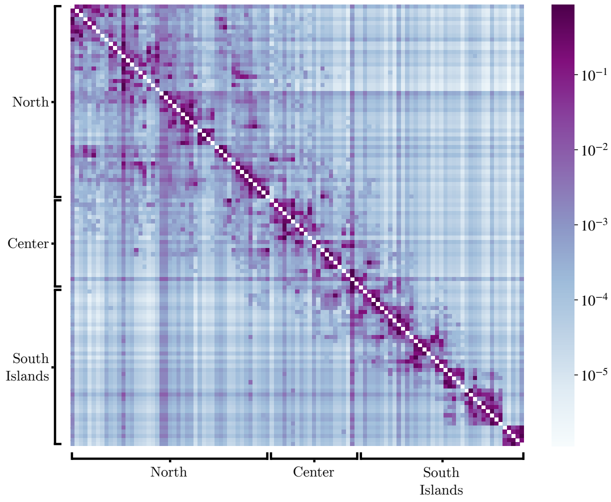

Figure 3: Inter-province mobility matrix W. Darker colors correspond to larger entries.

forming the set H. The weight matrix W was estimated from mobility data from ISTAT [8], as shown in Fig. 3. We set the epidemic progression and diffusion parameters (that is, λ, ν, γ, and μ), utilizing recent and reliable estimates from Prem et al. [9]. Finally, activity classes were identified from official epidemic data from the Dipartimento della Protezione Civile [10]. Specifically, the number and activity values of activity classes were derived from experimental data on social interactions [11], while the distribution of individuals over classes was identified from epidemic data [10]. In such a process, a crucial issue resides in the partial knowledge of the real number of infected individuals. Due to the limited testing capacity, asymptomatic individuals are rarely detected, and there is a high uncertainty on the fraction of asymptomatic individuals [7]. For this reason, the parameter β (which determines the fraction of infected individuals that become symptomatic) was identified together with the remaining parameters, that is, the mobility parameter b and the distribution of the individuals over the activation classes.

Analysis - The main objectives of our study are the investigation of the role of mobility and the effect of past, current, and possible future interventions on the evolution of the epidemic outbreak. We plan to address these issues by means of extensive numerical simulations and rigorous analytical studies.

Through a campaign of numerical simulations, we performed what/if analyses to compare different intervention policies, that is, different strategies to dynamically change the model mobility structure and the individuals' tendency to interact with others to contrast the spread of the disease. Such an analysis allows to assess the effectiveness of different combinations of these two control actions, depending on the time they are implemented (Fig. 4).

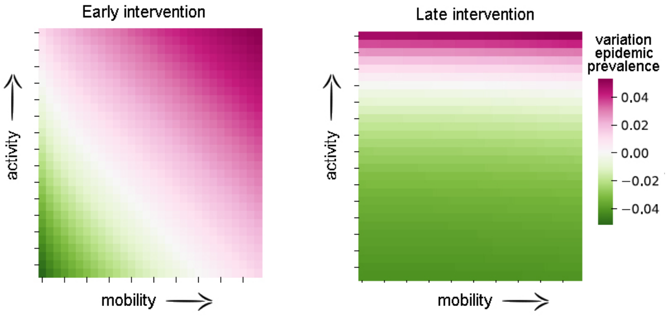

Figure 4: Preliminary simulation results suggest that the epidemic prevalence can be reduced by decreasing the activity or the mobility during the early stages of the epidemics, while for late intervention, reductions on mobility seem to have a minor effect.

From the analytical perspective, we are working to derive the epidemic threshold of the system, through a large-scale approximation of Eq. (1). From the expression of the epidemic threshold, one can understand the role of the model parameters in the early stages of the epidemic outbreaks. We also believe that the effect of re-opening of borders and inter-province mobility can be studied by means of a perturbation technique with respect to the mobility parameters b and W.

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