

1 SIOR Model

To model the dynamics, we consider a four compartment epidemic model[1]. In our model, the population is divide in four classes: S =susceptible, I =infected, O =Observed, R =recovered. We consider a dynamics at fixed number N of individuals, i.e. $S + I + O + R = N$. Susceptible individuals can become infected at a rate proportional to an infectivity parameter β times the probability I/N of meeting an infected individual. Notice that β incorporates both the “biological” characteristics of the epidemic (i.e. the probability that the infectious agent surmounts our immunitary defenses) and the “social” characteristics of the epidemic (i.e. the probability that two individuals come at contact). In a SIR model, the recovery parameter γ measures the rate at which and infectious individual recovers; such rate is normally expressed as the inverse of the recovery time τ , a parameter easy to measure from medical surveys. In our case, inspired by the Covid19 dynamics where most of the infected people seem to be asymptomatic, we assume that, after a time $\tau = \gamma^{-1}$, the individual has a probability ϵ of getting so worse that it is observed and a probability $1 - \epsilon$ of full recovery. We assume that the observed individuals cease to spread the infection, either because they are hospitalized or because they undergo to a strict quarantine. Finally, people under observation will also recover with rate h after a time $\tau_h = h^{-1}$. Hence, our $SIOR$ model reads

$$\partial_t \begin{pmatrix} S \\ I \\ O \\ R \end{pmatrix} = \begin{pmatrix} 0 \\ \beta \frac{IS}{N} \\ \epsilon \gamma I \\ (1 - \epsilon) \gamma I + hO \end{pmatrix} - \begin{pmatrix} \beta \frac{IS}{N} \\ \gamma I \\ hO \\ 0 \end{pmatrix}$$

As in the SIR model, the basic reproduction number is $R_0 = \beta/\gamma$ [2]. As noted before, since β contains also social interactions, while γ is disease specific, we expect that at least in the initial stages of the epidemic (i.e. before any policy is actuated or any awareness of the problem is reached) R_0 is a good proxy of the amount of social interactions in a country.

2 Contact Matrix

The outcome of epidemic model critically depend on the contact rates between individuals [4]. Large scale contact surveys are thus a very useful tool for understanding the diffusion of an epidemic before it gets detected or contrasting policies are issued. As shown in [3], mixing patterns and contact characteristics are remarkably similar across different European countries; in particular, contacts are assortatives; notably, schoolchildren and young adults have a much higher contact rate with people of the same age, indicating that 5- to 19-year-olds are expected to take the highest toll from the initial phase of an epidemic.

To consider the mixing patterns of a population, we divide each compartment into n_A age classes and rewrite the infectivity parameter β as βC , where C is the $n_A \times n_A$ contact matrix and C_{ij} measures the average number of contacts

per day between individuals of class i and j . Thus, the *SIOR* model for age classes can be rewritten as

$$\partial_t \begin{pmatrix} \vec{S} \\ \vec{I} \\ \vec{O} \\ \vec{R} \end{pmatrix} = \begin{pmatrix} 0 \\ \frac{\beta}{N} \text{diag}(\vec{S}) C \vec{I} \\ \epsilon \gamma \vec{I} \\ (1 - \epsilon) \gamma \vec{I} + h \vec{O} \end{pmatrix} - \begin{pmatrix} \frac{\beta}{N} \text{diag}(\vec{S}) : C \vec{I} \\ \gamma \vec{I} \\ h \vec{O} \\ 0 \end{pmatrix}$$

where \vec{V} is a vector with $n_{\mathcal{A}}$ components and $\text{diag}(\vec{V})$ is a matrix whose diagonal is \vec{V} . Since there is a sensible change in mortality for ages less and more than 70 years, we renormalize the contact matrix of [3] for Italy to the two age cohorts 0 – 69 and 70+.

3 Incidence

The mortality m_a for age classes $a = 1..n_{\mathcal{A}}$ is derived by dividing the number of deaths d_a by the number of assessed cases c_a . We use the number of cases assessed per age to estimate the incidence Inc_a of serious cases by age as $Inc_a = c_a / \sum c_a$. Hence, we rescale the rates ϵ and $1 - \epsilon$ of getting observed or getting recovered when infected by the diagonal matrix Ξ where $\Xi_{aa} = Inc_a$. Thus, the complete version of the *SIOR* model taking account for contact patterns and disease incidence for age classes can be rewritten as

$$\partial_t \begin{pmatrix} \vec{S} \\ \vec{I} \\ \vec{O} \\ \vec{R} \end{pmatrix} = \begin{pmatrix} 0 \\ \frac{\beta}{N} \text{diag}(\vec{S}) C \vec{I} \\ \gamma \epsilon \Xi \vec{I} \\ \gamma (1 - \epsilon \Xi) \vec{I} + h \vec{O} \end{pmatrix} - \begin{pmatrix} \frac{\beta}{N} \text{diag}(\vec{S}) : C \vec{I} \\ \gamma \vec{I} \\ h \vec{O} \\ 0 \end{pmatrix}$$

Using the approach of [2], we calculate the basic reproduction number as $R_0 = \beta \|C\| / \gamma$, where $\|C\|$ is the spectral radius of the matrix. Notice that the parameter β_{eff} measured using a model with no age classes corresponds to $\beta_{eff} = \beta \|C\|$.

References

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