The SIRn model: coupling seasonality and immunity in the modeling of flu transmission dynamics

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1 Introduction

Influenza or flu disease, caused by the influenza virus, affects about one billion people annually, with the number of severe cases ranging from 3 to 5 million and the number of deaths ranging from 290,000 to 650,000 [1]. The high mutation rate of the multiple flu strains help them to evade adquired immunity and maintain its presence, especially in winter when cold and wet conditions favour transmission [2, 3]. Regarding acquired immunity, whether naturally acquired through infection or through vaccination, it is known that natural infection offers more durable and broader immunity than vaccines, which provide only partial protection influenced by various factors such as cost and public acceptance. Classical flu mathematical models, such as the SIR and SEIR compartmental models, often incorporate seasonal factors, but rarely take into account the gradual loss of immunity over time, and have not separated the seasonal factor from population immunity. In this work, a more advanced model, the seasonal SIRn model [4], is proposed to address this issue by dividing the recovered population into n stages with different levels of immunity and including the classical seasonal transmission rate. To prove its applicability, a case study is presented in which we fit the model to seasonal flu data from Castellón de la Plana, Spain in the 2010-2020 period. Our results show how the SIRn model allows seasonality and immunity terms to be combined in the same model, providing richer and more realistic dynamics of flu transmission.

2 Methods

2.1 Model description

The seasonal SIRn model, which divides the population $N(t)$ into susceptibles $S(t)$, infectious $I(t)$ and n consecutive recovered with different immunity level $R_1(t), \ldots, R_n(t),\ n \geq 2$, is governed by the following first-order differential equations system:

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$$\begin{cases} \dot{S}(t) & = \lambda N(t) - \mu S(t) - \beta(t)\frac{S(t)I(t)}{N(t)}, \\ \dot{I}(t) & = \beta(t)\frac{S(t)I(t)}{N(t)} + \sum_{k=1}^{n}\beta_k(t)\frac{R_k(t)I(t)}{N(t)} - \gamma I(t) - \mu I(t), \\ \dot{R}_1(t) & = \gamma I(t) - \beta_1(t)\frac{R_1(t)I(t)}{N(t)} - r_1 R_1(t) - \mu R_1(t), \\ \vdots & \\ \dot{R}_k(t) & = r_{k-1}R_{k-1}(t) - \beta_k(t)\frac{R_k(t)I(t)}{N(t)} - r_k R_k(t) - \mu R_k(t), \ \forall k = 2, \ldots, n-1 \\ \vdots & \\ \dot{R}_n(t) & = r_{n-1}R_{n-1}(t) - \beta_n(t)\frac{R_n(t)I(t)}{N(t)} - \mu R_n(t), \\ \dot{N(t)} & = S(t) + I(t) + \sum_{k=1}^{n} R_k(t), \end{cases} \tag{1}$$

with $S(0), I(0), R_k(0) \geq 0, \ \forall k = 1, \ldots, n$, as initial conditions, and where $\lambda, \mu \geq 0$ are the birth and death rates, respectively, $\gamma > 0$ is the recovery rate, $\beta(t), \ \beta_k(t) > 0$ are the susceptible and R_k transmission rates, and $r_k > 0$ is the transition rate between R_k and R_{k+1} recovered subpopulations.

For this problem, a constant population size N was considered over time, so that $\lambda = \mu$, and $\beta_k(t) = s(\tau_k)\beta(t)$, where

$$\beta(t) = \frac{\beta_0}{2}\left[1 + \cos\left(\frac{2\pi}{T}t - \phi_0\right)\right]$$

is the classical seasonal transmission rate at time t and $s(\tau_k) \in [0, 1]$ is the susceptibility degree at time after infection τ_k, which is a monotonically increasing function with τ. A recovered individual progressively increases its transmission rate as its degree of susceptibility increases (i.e. its immunity declines) due to its transition through the different recovered stages. As $R_1, \ldots, R_n$ are characterised by a time after infection $\tau_1, \ldots, \tau_n$, and since the choice of the n recovery states can be arbitrary, we have taken it equidistributed such that the transmission rates are equal: $r_k = r = 1/(\tau_{k+1} - \tau_k), \ \forall k = 1, \ldots, n-1$.

2.2 Calibration

The calibration problem consisted of finding a set of model parameters that best fit a real scenario: seasonal flu in Castellón de la Plana in the period 2010-2020. As reference data, the series of weekly urgent cases of flu that visited the General Hospital of Castellón in all the seasons of the chosen period is available. From demographic information, it was known that $N = 282\ 967$ y $\lambda = \mu = 1.622 \cdot 10^{-4}$ weeks^{-1}.

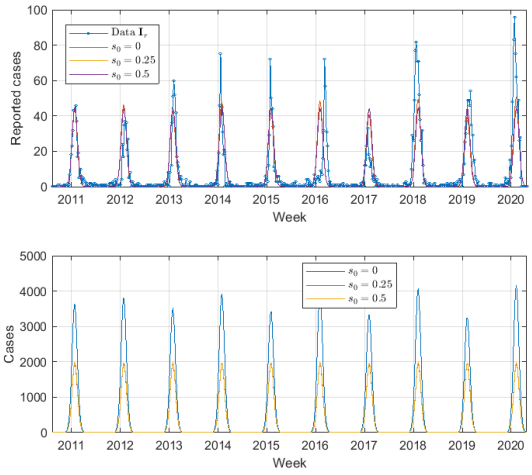
Regarding the SIRn model structure, $n = 520$ weekly recovery states were taken (~ 10 years), with times $\{\tau_1, \tau_2, \ldots, \tau_n\} = \{0, 1, \ldots, 519\}$, so that $r = 1$ weeks^{-1}. For the susceptibility degree, an exponential function of the type $s(\tau) = 1 - (1 - s_0)e^{-at}$ was chosen, and three initial susceptibility degrees $s_0 = 1, \ 0.75, \ 0.5$ were simulated (< 1 are considering cross-immunity). The increasing rate a was derived considering that at 6 years – 312 weeks – susceptibility had recovered to 0.95. The recovery rate for flu was set at $\gamma = 1$ weeks^{-1}. The vector of initial conditions was set to $(S(0), I(0), R_1(0), \ldots, R_n(0)) = (N - 1, 1, 0, \ldots, 0)$, and the simulations were given a warmup time of about 20 years to reach stability before calibration.

As the urgent data series had to be compared with a fraction of the total cases $pI(t)$, the parameters to be calibrated were three: the basal transmission rate β_0, the initial phase ϕ_0 and the reporting fraction p. The deterministic calibration was performed by fixing $\phi_0 = \pi$ (as observed in the data series), simulating the model, calculating an analytical expression of p deduced from the least squares minimisation problem, and finally correcting the initial phase ϕ_0 with a small lag that maximizes the cross-correlation function between the model and data series. In addition,

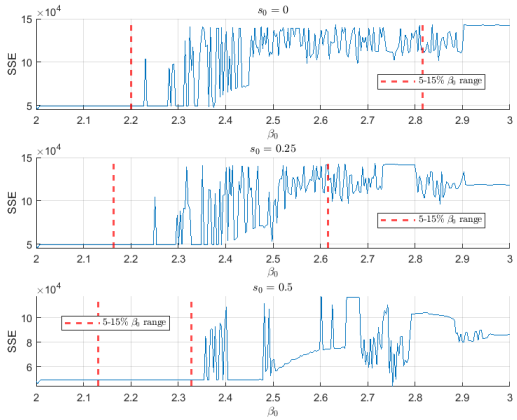
an important constraint was incorporated into the calibration: the infected population after each season is between 5 and 15% of the total population [5]. The calibration was complemented by an identifiability analysis on the β_0 parameter.

3 Results

The results of the fit between the model simulations and the data in Figure 1a shows how the model is able to describe seasonal dynamics under different immunity scenarios. However, Figure 1b, which reflects the evolution of the error by varying the parameter β_0, shows that the error function is ill-conditioned in different regions of space, and that in the range of the 5-15% seasonal infected restriction the solution seems unidentifiable. This is because, given freedom in the ϕ_0 phase, there are multiple pairs of parameters (β_0, p) that generate almost identical simulations.



(a) Best SIRn model fitting.



(b) Error function for different β_0 parameter values and different susceptibility scenarios

The numerical results place the β_0 parameter in the range between 2 and 3 in all scenarios. These values are consistent with those of the basic reproduction number $\mathcal{R}_0$ for flu in the literature. Additionally, the fraction of urgent reporters would be between 1 and 2%.

4 Conclusions

In this paper we have proposed an epidemiological model of flu, the SIRn model, which allows seasonality and immunity to be combined in its design, and which is able to successfully replicate real-world scenarios, such as the case study we have developed. The calibration results show that there are parameters consistent with previous studies, although problems of parameter identifiability may occur. To solve them, additional information would need to be incorporated into the model. All in all, we believe that the SIRn model approaches more realistic dynamics in modelling flu transmission dynamics, and allows us to better analyse and understand complex phenomena such as immunity.

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