A multi-region variant of the SIR model

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Abstract

In this note, we describe a simple generalization of the basic SIR model for epidemic, in case of a multi-region scenario, to be used for predicting the COVID-19 epidemic spread in Italy.

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MSC: 92C60, 92D30.

1 Introduction

A main concern related to the study of the recent viral pandemic of coronavirus disease (COVID-19) is, of course, to predict its evolution. Concerning its spread in Italy, at the web-page [1] a basic SIR model has been initially used for this purpose. Even though this simple model has displayed interesting potentialities in yielding accurate predictions of the diffusion of the disease for the subsequent few days, it heavily relies on the assumption of *homogeneity* of the spread of epidemic across the country, which is evidently not the case. Furthermore, it cannot capture the possible interactions between the different areas of the country which, as is well known, has played an important role in the diffusion of the epidemic.

We attempt to describe this important aspect by considering a *multi-region* extension of the basic SIR model, to be used for the future forecasts. The basic SIR model is recalled in Section 2, whereas its multi-region extension (mrSIR) is described in Section 3.

2 SIR model

The basic SIR (Susceptible, Infectious, Removed) model for the initial spread of an epidemic disease [2] (see also, e.g., [3, pp. 376–378] or [5]) is

$$\begin{aligned} \dot{x} &= -\beta x y, \\ \dot{y} &= \beta x y - \gamma y, \\ \dot{z} &= \gamma y, \end{aligned} \tag{1}$$

where:

- x is the number of *susceptible*,
- y is the number of *infectictious*,
- z is the number of *removed*,

and

- β is the *coefficient of infection*,
- γ is the *coefficient of removal*.

From (1), one easily realizes that:

$$S(t) = x(t) + y(t) + z(t) \equiv const. \tag{2}$$

We have used this simple model to predict the spread of the COVID-19 disease in Italy [1] but, as is clear from the data available from the Italian Protezione Civile [4], the spread of the disease is not homogeneous in the various regions of Italy. This has caused the predictions to become less accurate, as the spread of the epidemic has going on. For this reason, we here propose a *multi-region* generalization of the basic SIR model, in order to cope with this inhomogeneity.

3 Multi-region SIR (mrSIR) model

In order to generalize the model (1) to a scenario where there are n regions, with a different situation of the epidemic, let us define

$$\boldsymbol{x} = \begin{pmatrix} x_1 \\ \vdots \\ x_n \end{pmatrix}, \qquad \boldsymbol{y} = \begin{pmatrix} y_1 \\ \vdots \\ y_n \end{pmatrix}, \qquad \boldsymbol{z} = \begin{pmatrix} z_1 \\ \vdots \\ z_n \end{pmatrix}, \tag{3}$$

as the vectors of susceptible, infectious, and removed in each region (i.e., x_i, y_i, z_i denote the respective levels in the i-th region). In so doing, the basic model (1) now becomes:

$$\begin{aligned} \dot{\boldsymbol{x}} &= -B\,\boldsymbol{x} \circ \boldsymbol{y} + R\boldsymbol{x}, \\ \dot{\boldsymbol{y}} &= B\,\boldsymbol{x} \circ \boldsymbol{y} - C\boldsymbol{y} + R\boldsymbol{y}, \\ \dot{\boldsymbol{z}} &= C\boldsymbol{y}, \end{aligned} \tag{4}$$

where $\circ$ denotes the Hadamard (i.e., component-wise) product, and

$$B = \begin{pmatrix} \beta_1 & & \\ & \ddots & \\ & & \beta_n \end{pmatrix}, \qquad C = \begin{pmatrix} \gamma_1 & & \\ & \ddots & \\ & & \gamma_n \end{pmatrix}, \qquad R = \begin{pmatrix} \rho_{11} & \dots & \rho_{1n} \\ \vdots & & \vdots \\ \rho_{n1} & \dots & \rho_{nn} \end{pmatrix}, \tag{5}$$

are the matrices with the infection, removal, and *migration* coefficients. In particular, ρ_{ij} is the coefficient of migration from region j to region i. Consequently, in matrix R one assumes:

$$\rho_{jj} \le 0, \qquad \rho_{ij} \ge 0,\ i \ne j, \qquad \sum_{i=1}^{n} \rho_{ij} = 0, \qquad j = 1, \dots, n, \tag{6}$$

with the last condition providing the conservation property

$$S(t) = \sum_{i=1}^{n} [x_i(t) + y_i(t) + z_i(t)] \equiv const, \tag{7}$$

which is the analogous of (2) for the present model. In componetwise form, (4) reads:

$$\begin{aligned} \dot{x}_i &= -\beta_i x_i y_i + \sum_{j=1}^{n} \rho_{ij} x_j, \\ \dot{y}_i &= \beta_i x_i y_i - \gamma_i y_i + \sum_{j=1}^{n} \rho_{ij} y_j, \\ \dot{z}_i &= \gamma_i y_i, \qquad\qquad i = 1, \ldots, n. \end{aligned} \tag{8}$$

In the near future, this model will be used to update the forecasts at the web-site [1].

We conclude this note, by observing that the mrSIR model can be obviously used at different space scales, i.e.: regions within a country; countries within a continent or worldwide; etc.

References

[1] L. Brugnano, F. Iavernaro. `http://web.math.unifi.it/users/brugnano/covid19/`

[2] W.O. Kermack, A.G. Mc Kendrick. A Contribution to the Mathematical Theory of Epidemics. *Proceedings of the Royal Society A* **115**, 772 (1927) 700–721.

[3] D.G. Luenberger. *Introduction to Dynamical Systems, Theory, Models, & Applications.* John Wiley & Sons, New York, 1979.

[4] Dipartimento della Protezione Civile: `http://opendatadpc.maps.arcgis.com/apps/opsdashboard/index.html#/b0c68bce2cce478eaac82fe38d4138b1`

[5] `https://en.wikipedia.org/wiki/Compartmental_models_in_epidemiology` accessed on March 22, 2020.