Report Covid-19 for Spain: April-04

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A dynamical model to predict the Covid-19 in Spain

The model used to predict the Covid-19 evolution in Spain is based on the classical Kermack-Mackendrick models. These models provide a coupled system of three differential equations for the main variables of an epidemic: susceptible, infected and recovered populations.

The model here proposed generalises these models by including continuum delays as integral equations in some model parts, in order to consider the evolution delay of some model variables. Thus, the model becomes a coupled system of integro-diferential equations.

In addition, the Jay W. Forrester methodology, developed in the MIT and generalised in the "Escola d'Investigació Operativa i Sistemes de la ciutat de Valéncia" is used. This methodology uses a universal language, represented by the hydrodynamic diagram (Section 1), to build dynamical models of complex systems.

The model presented has input variables or parameters (whose values must be provided) and output variables (Section 2) computed by the system of integro-diferential equations (Section 3). To get the parameter values for Spain the model is calibrated by using the experimental data provided by the Spanish Health Ministry (Section 4). We also provide a day to day model update, predicting the infected population values: at short time term for the next three days, and at long time term computing the day and the value of the maximum infected population (Section 5). For any other information, please contact the authors through their electronic mails.

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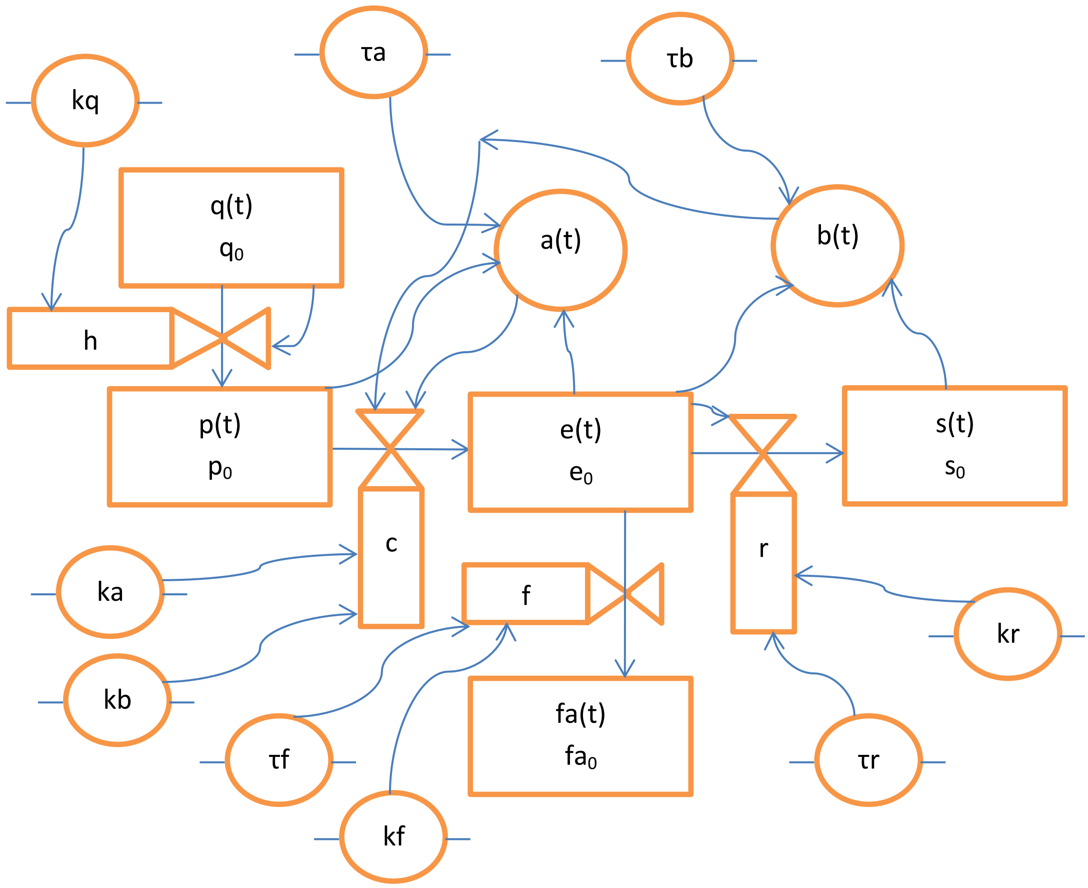
1. Hydrodynamic Diagram



2. Model variables

2.1. Input variables or parameters:

kq: susceptibility rate

τa: continuum susceptible-infected populations interaction delay

τb: continuum susceptible-recovered populations interaction delay

ka: susceptible-infected populations interaction rate

kb: susceptible-recovered populations interaction rate

τf: continuum infected population deaths delay

kf: infected population deaths rate

τr: continuum recovered population delay

kr: recovering population rate

2.2. Output variables (with equation):

q(t): country population (Spain)

h(t): susceptible population flow

p(t): susceptible population

c(t): infection flow
e(t): infected population
f(t): deaths flow
fa(t): cumulated deaths
r(t): recovered population flow
s(t): cumulated recovered population

3. Model equations

$$\frac{dq(t)}{dt} = -h(t)$$

$$h(t) = kq \cdot q(t)$$

$$\frac{dpt)}{dt} = h(t) - c(t)$$

$$c(t) = ka \cdot a(t) + kb \cdot b(t)$$

$$a(t) = \int_{t_0}^{t} \mathrm{e}^{\frac{x-t}{\tau a}} p(x)e(x)dx$$

$$b(t) = \int_{t_0}^{t} \mathrm{e}^{\frac{x-t}{\tau b}} p(x)s(x)dx$$

$$\frac{de(t)}{dt} = c(t) - f(t) - r(t)$$

$$f(t) = kf \int_{t_0}^{t} \mathrm{e}^{\frac{x-t}{\tau f}} e(x)dx$$

$$r(t) = kr \int_{t_0}^{t} \mathrm{e}^{\frac{x-t}{\tau r}} e(x)dx$$

$$\frac{ds(t)}{dt} = r(t)$$

Remark: the equations also consider the computation of infected population by the interaction between this population and the recovered population.

4. Model calibration

The model is calibrated by using the experimental data corresponding to the c(t), e(t), f(t) and r(t) variables. They are provided day to day by the Spanish Health Ministry, which can be found in the link:

"https://www.mscbs.gob.es/profesionales/saludPublica/ccayes/alertasActual/nCov-China/situacionActual.htm"

The model calibration is made by the random number generation method for the parameter values.

First of all, the comparison between the experimental data of the infected population and the theoretical values corresponding to the calibrated model is presented. The comparison for today is presented in Figure 1:

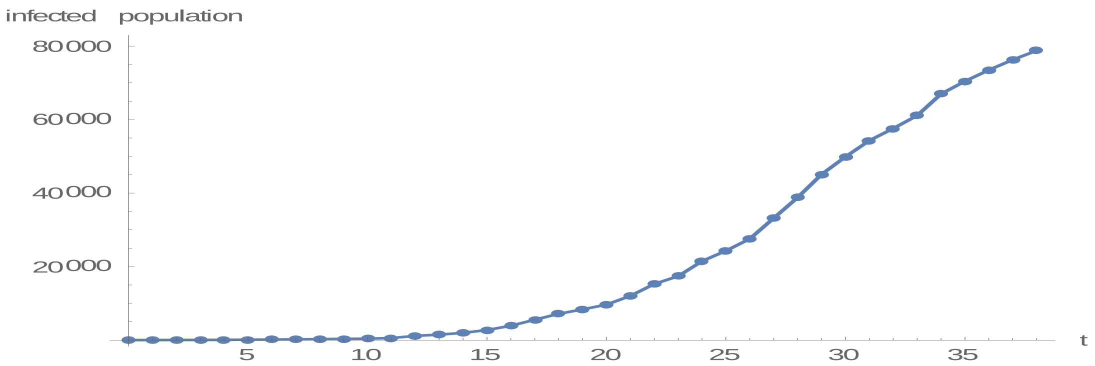


Figure 1: Infected population (dots) and the predicted infected population by the calibrated model (curve) versus time in days (the zero day is 2020 February 31). Determination Coefficient R^2=0.886.

<u>Remark</u>: The determination coefficient varies between 0 and 1. The closer the unit the better the model fits the considered reality.

5. Short and long time term prediction

The prediction objective at short time term is to provide the infected population estimation for the next three days, that is:

Day 05/04/2020: 85769 infected
Day 06/04/2020: 93292 infected
Day 07/04/2020: 101512 infected

The prediction objective at long time term is to find the infected population peak: the day which the infected population starts to decrease from. See Figure 2, which provides a prediction for 60 days, starting from February 26:

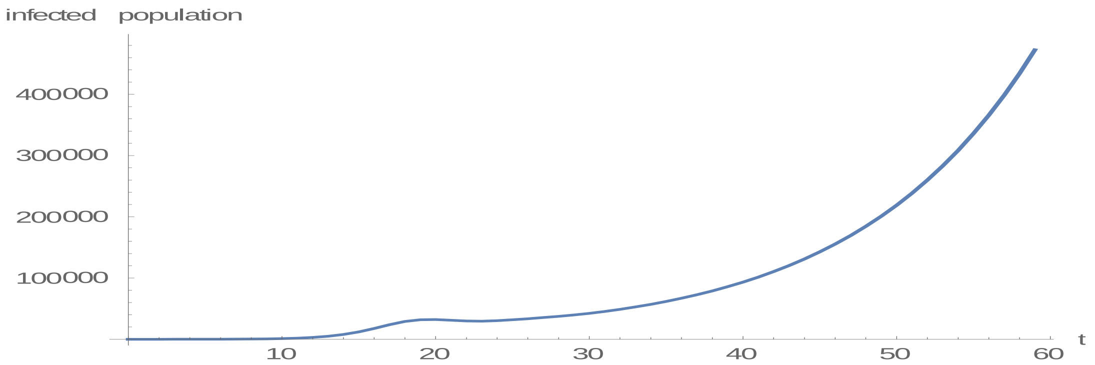


Figure 2: Infected population prediction (curve) versus time in days (the zero day is 2020 February 26).

Figure 2 provides that **the infected population peak will not be reached yet in April 26**.

6. Comments

Take into account that the model just provides estimations but not exact values, for both short and long time term predictions. In addition, these predictions can change by considering the incorporation of new data in the model calibration.

The model can be improved by:
(a) Formulating it as a stochastic model, that is, by providing every day predictions with confidence intervals. This improvement would afford more reliability to the model.
(b) Calibrating the model by using a genetic algorithm instead a simple random number generation. This method would provide a better fitting between the model results and the experimental data and, as a consequence, better predictions.
(c) Introducing the political decisions as influences on the parameters. Thus, the model could be a ruling tool for future similar crises.

These improvements will be tried in the collaboration with more scientists, taking into account the present restrictions due to the crisis. For similar comparable approaches see also the following links:
https://www.systemdynamics.org/covid-19
https://covid19.webs.upv.es
https://biocomsc.upc.edu/en/covid-19