A θ-SI(R)D MODEL FOR COVID-19

Ettore Rocchi*, Sara Peluso*, Davide Sisti*, Margherita Carletti°

* Urbino University Carlo Bo, Dept. Biomolecular Sciences, Unit of Biostatistics and Biomathematics

° Urbino University Carlo Bo, Dept. Pure and Applied Sciences

Introduction: Many models of the current Covid-19 epidemic have been made in the recent past, mostly SIR and SEIR. We propose a 6-compartment θ-SI(R)D model.

The model: The model, denoted as θ-SI(R)D, is a 6-compartment model, described by as many ordinary differential equations. The six compartments are represented by Susceptible (S), Symptomatic Infected (I_s), Asymptomatic Infected (I_a), Recovered from Asymptomatic fraction (R_a), Recovered from Symptomatic fraction (R_s), Deceased (D).

The biological assumptions are as follows: (i) no entry or exit from the territory (closed territory); (ii) the contagiousness of the infected is immediate (therefore the compartment of the Exposed is not considered); (iii) a loss of immunity is considered (in this version of the model it is considered at a constant rate); (iv) mortality and birth rate affect, as a first approximation, only the Susceptible compartment; (v) the Asymptomatic Infected compartment includes both the fraction identified by laboratory diagnostic evaluation and the unidentified one; (vi) there is no lethality in the Asymptomatic Infected fraction.

The model is the following

$$
\begin{cases}
\dfrac{dS}{dt} = \mu_n S - \mu_m S - \theta \alpha S I_s - (1-\theta)\alpha S I_a + \rho(R_a + R_s) \\[2mm]
\dfrac{dI_a}{dt} = (1-\theta)\alpha S I_a - \beta_a I_a \\[2mm]
\dfrac{dI_s}{dt} = \theta \alpha S I_s - \beta_s I_s \\[2mm]
\dfrac{dR_a}{dt} = \beta_a I_a - \rho R_a \\[2mm]
\dfrac{dR_s}{dt} = (1-\omega_s)\beta_s I_s - \rho R_s \\[2mm]
\dfrac{dD}{dt} = \omega_s \beta_s I_s
\end{cases}
$$

where: α is the disease contact rate; β_a, β_s are the transition rates ($I_a \rightarrow R_a$, $I_s \rightarrow R_s$, respectively); ρ is the rate of loss of immunization, ω_s is the fatality rate in I_s compartment; θ is the proportion of asymptomatic infected; μ_n is the birth rate; μ_m is the mortality rate.

Concerning the parameters, we assumed (taking them from biological literature and pandemic official data) the following values: α = 0.6, β_a = 0.143; β_s = 0.055, ρ = 0.003, μ_n=0.007, μ_m=0.011, θ=0.1, ω_s=0.14.
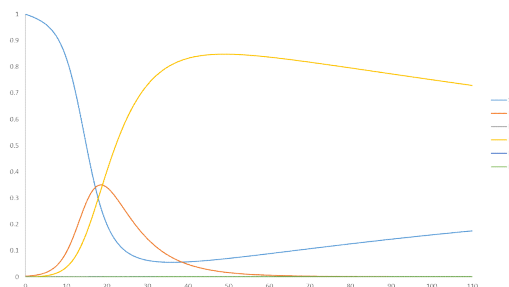
Results: From the above considerations, we have simulated the evolution of pandemic through the model.

Discussions and Conclusions: This model represents a new step towards the complete comprehension of Covid-19 pandemic evolution.