Epidemic Impact of Temporary Large People Mass Fluxes: The COVID-19 and the Jubilee 2025 Reference Case

Paolo Di Giamberardino[a] and Daniela Iacoviello[b]

Department of Computer, Control and Management Engineering Antonio Ruberti, Sapienza University of Rome, Italy
{paolo.digiamberardino, daniela.iacoviello}@uniroma1.it

Keywords: Epidemic Spread, COVID–19, Multigroup Interactions, Population Flows, Jubilee 2025.

Abstract: In the paper, the problem of the interaction between two separated population is considered when an infectious disease is presented. An asymmetric behaviour is studied, with one smaller population receiving a people flow from a second more numerous one. For each of them, the different conditions with respect to the epidemic status are considered as well as different numbers of flowing individuals. The reference case in mind is the possible COVID-19 epidemic during the next Jubilee 2025, where a very large amount of pilgrims are expected to come in Italy and, mainly, in Rome, with numbers comparable with the usual living population. A theorical study about the effects on the equilibria conditions, completed with a numerical analysis of different possible scenarios, is reported in the paper, showing that it must be expected a sensible increment of the number of infected individuals.

1 INTRODUCTION

The analysis of epidemic spread over a population has been widely addressed, (Daley and Gani, 1999; Martcheva, 2015), introducing compartmental models with increasing number of compartments as the complexity of the epidemic dynamics required: SIR (Di Giamberardino and Iacoviello, 2017), SIS, SEIR (Casagrandi et al., 2006) and others, whose names are given by the initials of the compartments names: Susceptible, Infected, Recovered, Exposed, and so on.

Following the particular characteristics of the epidemic modeled, higher dimensional models have been introduced. This has happened in the very recent years for the study of the COVID–19, being important to distinguish level of infections, different contagious ways, response to contagious, illness epilogue, in view of finding effective containment solutions (Iranzo and Pérez–González, 2021).

Advanced modeling of COVID-19 addressed also the dynamics of interactions between homogeneous groups of individuals in the same population (Contreras et al., 2020), clustered by age (Di Giamberardino et al., 2020; Yue et al., 2023), by work, by fragility due to co–morbidities, etc.

A further interactions in the epidemic modeling,

analysis and control is among populations: mobility of infected people contributes to the virus spread. Mobility from and to Wuhan have been addresses since the beginning of the infection (Ng et al., 2020), and then studied for different populations or sub-populations interactions (Di Giamberardino et al., 2021b).

In this paper, a slightly different point of view is assumed in the analysis of multi-group interactions: the unidirectional people motion from one population to another and the analysis of the effect on the receiving population only. The phenomena addressed are all those situations in which the number of individuals in one population in some quite long (months) time periods suddenly increase doubling or more the number of individuals. This is usually the situation of some holiday places that in particular periods of the year host a number of guests much higher than the usual population. However, although the relative increment is quite sensible, the absolute values are quite contained.

A similar effect with much higher numbers is expected for the next Jubilee 2025, during which Italy, but in particular Rome, will be interest by the presence of a very high number of pilgrims/tourists, numbers almost comparable with the population of the city.

This event is then assumed as a case study in the analysis of the effects of large fluxes of individuals

[a] https://orcid.org/0000-0002-9113-8608
[b] https://orcid.org/0000-0003-3506-1455

567

towards a population from outside regions, assumed behaving like a second population.

The paper is organized as follows. Section 2 is devoted to address the SEIR model adopted, recalling dynamic characteristics in terms of equilibria and stability, and according to classical epidemic indicators like the reproduction number. Then, the model under study, which includes the population flux and the source second population dynamics, is introduced and described in section 3. The full dynamics is studied in Section 4 for what concerns new equilibria and their stability, while in Section 5 the transient evolutions in function of characteristic parameters of the infection are presented, described and analyzed. A concluding Section 6 summarizes the main results and introduces the ongoing and the next steps of the present research.

2 THE MATHEMATICAL MODEL

For sake of simplicity, the epidemic modeling is performed referring to the SEIR model, the most generic one able to include also an incubation period which can reduce the effects of possible infected mobility limitations.

2.1 First Population: Recalls on SEIR Model

The situation described takes into consideration one population with an epidemic steady state condition, which can be the epidemic free situation or the endemic one if the infection is already present in the country. These two possibilities are obtained starting from the equations

$$
\begin{align}
\dot{S}_1 &= -\beta_1 S_1 I_1 - \mu_{S_1} S_1 + N_1 \tag{1} \\
\dot{E}_1 &= \beta_1 S_1 I_1 - \delta_1 E_1 - \mu_{E_1} E_1 \tag{2} \\
\dot{I}_1 &= \delta_1 E_1 - \gamma_1 I_1 - \mu_{I_1} I_1 \tag{3} \\
\dot{R}_1 &= \gamma_1 I_1 - \mu_{R_1} R_1 \tag{4}
\end{align}
$$

This is a classical SEIR model, where the dynamics of the Susceptible (S), Exposed (E), Infected (I) and Removed (R) individuals of a population interested by an infection is modeled; they correspond, respectively, to the healthy individuals that can be infected, the infected but not yet infectious persons, the infected individuals and the healed ones respectively. The parameters describe the infection rate β, the death rates μ_*, the incubation time $\frac{1}{\delta}$, the average healing time $\frac{1}{\gamma}$ and the newborn individuals N. The subscript "1" denoted the first system here introduced, in view of the description in next Section 3.

For such a system it is well known that there are two equilibrium points: the epidemic free one

$$
P_{1,e}^1 = \begin{pmatrix} S_{1,e}^1 \\ E_{1,e}^1 \\ I_{1,e}^1 \\ R_{1,e}^1 \end{pmatrix} = \begin{pmatrix} \frac{N_1}{\mu_{S_1}} \\ 0 \\ 0 \\ 0 \end{pmatrix} \tag{5}
$$

and the endemic condition

$$
P_{1,e}^2 = \begin{pmatrix} S_{1,e}^2 \\ E_{1,e}^2 \\ I_{1,e}^2 \\ R_{1,e}^2 \end{pmatrix} = \begin{pmatrix} \frac{(\delta_1+\mu_{E_1})(\gamma_1+\mu_{I_1})}{\beta_1 \delta_1} \\ \frac{N_1}{(\delta_1+\mu_{E_1})} - \frac{\mu_{S_1}(\gamma_1+\mu_{I_1})}{\beta_1 \delta_1} \\ \frac{N_1 \delta_1}{(\delta_1+\mu_{E_1})(\gamma_1+\mu_{I_1})} - \frac{\mu_{S_1}}{\beta_1} \\ \frac{N_1 \delta_1 \gamma_1}{\mu_{R_1}(\delta_1+\mu_{E_1})(\gamma_1+\mu_{I_1})} - \frac{\mu_{S_1}\gamma_1}{\beta_1 \mu_{R_1}} \end{pmatrix} \tag{6}
$$

While the first point always exists, for $P_{1,e}^2$ the condition

$$
\beta_1 \geq \frac{\mu_{S_1}(\delta_1 + \mu_{E_1})(\gamma_1 + \mu_{I_1})}{N_1 \delta_1} \tag{7}
$$

must be satisfied in order to have all the state components non negative.

At steady state, the disease condition clearly depends on the stability of the two equilibrium points. In order to obtain the conditions of the stability, a local study can be performed starting from the computation of the Jacobian for (1)–(4) evaluated in each equilibrium point, corresponding to the dynamic matrix of the linear approximation of the nonlinear dynamics.

For the Jacobian, one has

$$
J = \begin{pmatrix} -\beta_1 I_1 - \mu_{S_1} & 0 & -\beta_1 S_1 & 0 \\ \beta_1 I_1 & -\delta_1 - \mu_{E_1} & \beta_1 S_1 & 0 \\ 0 & \delta_1 & -\gamma_1 - \mu_{I_1} & 0 \\ 0 & 0 & \gamma_1 & -\mu_{R_1} \end{pmatrix} \tag{8}
$$

Setting, for shortening the expressions length,

$$
m_{1,1} = (\delta_1 + \mu_{E_1}); \qquad m_{2,1} = (\gamma_1 + \mu_{I_1}) \tag{9}
$$

and evaluating (8) at $P_{1,e}^1$, matrix

$$
J(P_{1,e}^1) = \begin{pmatrix} -\mu_{S_1} & 0 & -\beta_1 \frac{N_1}{\mu_{S_1}} & 0 \\ 0 & -m_{1,1} & \beta_1 \frac{N_1}{\mu_{S_1}} & 0 \\ 0 & \delta_1 & -m_{2,1} & 0 \\ 0 & 0 & \gamma_1 & -\mu_{R_1} \end{pmatrix} \tag{10}
$$

is obtained. Stability can be deduced looking at its eigenvalues. Two of them are $\lambda_1 = -\mu_{S_1}$ and $\lambda_2 = -\mu_{R_1}$, strictly negative by parameters definition. For the remaining two, the roots of the polynomial

$$
\lambda^2 + (m_{1,1} + m_{2,1})\lambda + m_{1,1}m_{2,1} - \beta_1 \delta_1 \frac{N_1}{\mu_{S_1}} \tag{11}
$$

must be computed. The condition for local asymptotic stability is the negativeness of all the eigenvalues and in this case it holds true once

$$
m_{1,1}m_{2,1} - \beta_1 \delta_1 \frac{N_1}{\mu_{S_1}} > 0 \tag{12}
$$

that can be rewritten putting in evidence the epidemic transmission factor,

$$\beta_1 < \frac{\mu_{S_1} m_{1,1} m_{2,1}}{N\delta} \qquad (13)$$

For the second equilibrium point, the local dynamics is described by the matrix

$$J(P_{1,e}^2) = \begin{pmatrix} -\frac{\beta_1 N_1 \delta_1}{m_{1,1} m_{2,1}} & 0 & -\frac{m_{1,1} m_{2,1}}{\delta_1} & 0 \\ \frac{\beta_1 N_1 \delta_1}{m_{1,1} m_{2,1}} - \mu_{S_1} & -m_{1,1} & \frac{m_{1,1} m_{2,1}}{\delta_1} & 0 \\ 0 & \delta_1 & -m_{2,1} & 0 \\ 0 & 0 & \gamma_1 & -\mu_{R_1} \end{pmatrix}$$

Here the negative eigenvalue $\lambda_1 = -\mu_{R_1}$ is immediately obtained. For the other three ones, the roots of the polynomial

$$\lambda^3 + a_2 \lambda^2 + a_1 \lambda + a_0 \qquad (14)$$

must be studies, with

$$a_2 = \frac{\beta N_1 \delta_1}{m_{1,1} m_{2,1}} + m_{1,1} + m_{2,1}$$

$$a_1 = \beta_1 N_1 \delta_1 \frac{m_{1,1} + m_{2,1}}{m_{1,1} m_{2,1}}$$

$$a_0 = \beta_1 N_1 \delta_1 - \mu_{S_1} m_{1,1} m_{2,1}$$

A necessary condition to have all the roots with negative real part is the positiveness of all the coefficients, in this case

$$1 - \frac{\mu_{S_1} m_{1,1} m_{2,1}}{\beta_1 N_1 \delta_1} > 0 \quad \Leftrightarrow \quad \beta_1 > \frac{\mu_{S_1} m_{1,1} m_{2,1}}{N_1 \delta_1} \quad (15)$$

to be compared with the equilibrium point existence condition (7).

Making use fo the Routh-Hurwitz criterion, necessary and sufficient conditions for negativeness of the roots are

$$a_0 > 0, \qquad a_2 > 0, \qquad a_1 a_2 - a_0 > 0 \qquad (16)$$

The first coincides with the necessary condition (15), the second is always verified. For the third, one has to check if

$$a_1 a_2 - a_0 =$$
$$\beta_1 N_1 \delta_1 \left(\frac{1}{m_{2,1}} + \frac{1}{m_{1,1}} \right) \left(\frac{\beta N_1 \delta_1}{m_{1,1} m_{2,1}} + m_{1,1} + m_{2,1} \right)$$
$$- (\beta_1 N_1 \delta_1 - \mu_{S_1} m_{1,1} m_{2,1}) > 0$$

Easy computations give

$$(\beta_1 N_1 \delta_1)^2 \frac{m_{1,1} + m_{2,1}}{m_{1,1}^2 m_{2,1}^2} + \beta_1 N_1 \delta_1 \frac{(m_{1,1} + m_{2,1})^2}{m_{1,1} m_{2,1}}$$
$$- \beta_1 N_1 \delta_1 + \mu_{S_1} m_{1,1} m_{2,1} > 0$$

showing a second order inequality

$$(\frac{\beta_1 N_1 \delta_1}{m_{1,1} m_{2,1}})^2 (m_{1,1} + m_{2,1})$$
$$+ \frac{\beta_1 N_1 \delta_1}{m_{1,1} m_{2,1}} \left((m_{1,1} + m_{2,1})^2 - m_{1,1} m_{2,1} \right)$$
$$+ \mu_{S_1} m_{1,1} m_{2,1} > 0 \qquad (17)$$

with respect to the term

$$\frac{\beta_1 N_1 \delta_1}{m_{1,1} m_{2,1}}$$

put in evidence. Since

$$(m_{1,1} + m_{2,1})^2 - m_{1,1} m_{2,1} = m_{1,1}^2 + m_{2,1}^2 + m_{1,1} m_{2,1} > 0 \qquad (18)$$

then, with respect to the quantity

$$\frac{\beta_1 N_1 \delta_1}{m_{1,1} m_{2,1}} \qquad (19)$$

it is easy to verify, without any computation, that the inequality (17) is satisfied for all $\frac{\beta_1 N_1 \delta_1}{m_{1,1} m_{2,1}}$ if the roots r_1 and r_2 are complex (with negative real part), or for

$$\frac{\beta_1 N_1 \delta_1}{m_{1,1} m_{2,1}} < -r_1 \quad \cup \quad \frac{\beta_1 N_1 \delta_1}{m_{1,1} m_{2,1}} > -r_2 \qquad (20)$$

with $r_1 > r_2 > 0$, if they are real. Recalling that condition (15) can be rewritten as

$$\frac{\beta_1 N_1 \delta_1}{m_{1,1} m_{2,1}} > \mu_{S_1} \qquad (21)$$

it is possible to conclude that the equilibrium point $P_{1,e}^2$ is stable (locally asymptotically) if (21), coincident with the existence condition (7), holds.

2.1.1 The Reproduction Number

For this population, it is possible to evaluate the basic reproduction number $\mathbf{R}_0$ (van den Driessche, 2017) as well as the reproduction number under endemic conditions, $\mathbf{R}_e$. The approach followed is the classical next generation matrix computation (Ledzewicz and Schattler, 2011), whose spectral radius is the reproduction number estimation. To this aim, the partial dynamics with direct infection and propagation is taken

$$\begin{pmatrix} \dot{E}_1 \\ \dot{I}_1 \end{pmatrix} = \begin{pmatrix} \beta_1 S_1 I_1 \\ 0 \end{pmatrix} - \begin{pmatrix} (\delta_1 + \mu_{E_1}) E_1 \\ -\delta_1 E_1 + (\gamma_1 + \mu_{I_1}) I_1 \end{pmatrix}$$
$$= \mathcal{F} - \mathcal{V} \qquad (22)$$

and the local approximating matrices

$$F = \frac{\partial \mathcal{F}}{\partial (E,I)} = \begin{pmatrix} 0 & \beta_1 S_1 \\ 0 & 0 \end{pmatrix} \qquad (23)$$

$$V = \frac{\partial \mathcal{V}}{\partial (E,I)} = \begin{pmatrix} m_{1,1} & 0 \\ -\delta & m_{2,1} \end{pmatrix} \qquad (24)$$

are computed, making use also of substitutions (9). From these, through their evaluation in the conditions under analysis and computing the spectral radius of FV^{-1}, one has

$$\mathbf{R}_0 = \sigma \left(FV^{-1} \right) \big|_{P_{1,e}^1}$$

$$= \sigma \left(\begin{pmatrix} 0 & \beta_1 S_1 \\ 0 & 0 \end{pmatrix} \begin{pmatrix} \frac{1}{m_{1,1}} & 0 \\ \frac{\delta}{m_{1,1}m_{2,1}} & \frac{1}{m_{2,1}} \end{pmatrix} \right)_{P_{1,e}^1}$$

$$= \sigma \begin{pmatrix} \frac{\delta\beta_1 S_e^1}{m_{1,1}m_{2,1}} & \frac{\beta S_e^1}{m_{2,1}} \\ 0 & 0 \end{pmatrix} = \frac{\delta_1 \beta_1 N_1}{\mu_{S_1} m_{1,1} m_{2,1}} \quad (25)$$

$$\mathbf{R}_e = \sigma \left(FV^{-1} \right) \big|_{P_{1,e}^2} = \frac{\delta_1 \beta_1 S_{1,e}^2}{m_{1,1}m_{2,1}} = 1 \quad (26)$$

In the transient conditions, the *current* reproduction number $\mathbf{R}_t$ can be considered

$$\mathbf{R}_t = \frac{\delta_1 \beta_1 S_1(t)}{m_{1,1}m_{2,1}} \quad (27)$$

The reproduction numbers are indexes usually adopted to characterise the spread of the epidemic: if $\mathbf{R}_0 < 1$, the infections asymptotically vanishes; it corresponds to the stability condition of the epidemic free equilibrium point. If $\mathbf{R}_0 > 1$, the epidemics is spreading, with the number of infected individuals always different from zero. If $\mathbf{R}_e = 1$, the endemic equilibrium is the current situation, with constant non null infected individuals present, with severity of the conditions depending on the infection factor β_1. Clearly, if $\mathbf{R}_e = 1$, $\mathbf{R}_0 > 1$. Both these two parameters refer to steady state conditions. The current reproduction number $\mathbf{R}_t$ follows the same conditions but it is referred to the time varying situation.

3 THE INCOMING POPULATION FLUX

The population referred in the previous Section is assumed subject to a high intense people incoming flux for a time period sufficiently high to participate to the infection process.

In a first approximation, an average epidemic condition for incoming individuals is assumed, so that it is possible to consider one unique source for population transfer without dividing them according to different countries with non homogeneous conditions. The full population source of the incoming flux can be described by a second SEIR model, and the population variation can be modelled as an increment of each class of the population in (1)–(4) given by a fraction of the external people.

In order to introduce the population variation, the external averaged source of incoming people is here represented as a second SEIR model; also the incoming population is subject to the same epidemic spread but with different conditions, being possible to have a better or a worst behaviour of the disease.

The result is the same as (1)–(4), but with different parameters and number of individuals in the classes

$$\dot{S}_2 = -\beta_2 S_2 I_2 - \mu_{S_2} S_2 + N_2 \quad (28)$$

$$\dot{E}_2 = \beta_2 S_2 I_2 - \delta_2 E_2 - \mu_{E_2} E_2 \quad (29)$$

$$\dot{I}_2 = \delta_2 E_2 - \gamma_2 I_2 - \mu_{I_2} I_2 \quad (30)$$

$$\dot{R}_2 = \gamma_2 I_2 - \mu_{R_2} R_2 \quad (31)$$

For such a system, the same computations performed for the dynamics 1 are possible, showing that the two equilibrium points are $P_{2,e}^1$ and $P_{2,e}^2$, whose expressions are the same as (5) and (6) respectively, with subscript 2 instead of 1. Analogously, the stability conditions (13) and (7) holds, with the substitution of the subscript. Finally, also the reproduction numbers, here denoted by adding superscript "2" ($\mathbf{R}_0^2$, $\mathbf{R}_e^2$ and $\mathbf{R}_t^2$), have the same expressions.

Assume a permanent uniform flux of people going from system 2 to system 1 and then coming back, with a time limited permanence but sufficiently long to be fully involved in the epidemic evolution of system 1; this means that after a few days, a steady state condition is reached and a first approximated model can be given, for the population 1 under incoming, assuming that the total number of each class members becomes

$$S = S_1 + \alpha_1 S_2; \quad E = E_1 + \alpha_2 E_2;$$
$$I = I_1 + \alpha_3 I_2; \quad R = R_1 + \alpha_4 R_2$$

so that

$$S_1 = S - \alpha_1 S_2; \quad E_1 = E - \alpha_2 E_2;$$
$$I_1 = I - \alpha_3 I_2; \quad R_1 = R - \alpha_4 R_2$$

Actually, assuming four different fractions α_i characterising each class may be a too generic position. It is assumed here for sake of generalization, but some particular cases will be discussed in the sequel.

The new total population dynamics is then modelled by

$$\dot{S} = -\beta_1 SI - \mu_{S_1} S + N_1 + \alpha_1 N_2$$
$$+ \alpha_3 \beta_1 I_2 S + \alpha_1 \beta_1 S_2 I - \alpha_1 (\alpha_3 \beta_1 + \beta_2) S_2 I_2$$
$$+ \alpha_1 (\mu_{S_1} - \mu_{S_2}) S_2 \quad (32)$$

$$\dot{E} = \beta_1 SI - m_{1,1} E - \alpha_3 \beta_1 I_2 S - \alpha_1 \beta_1 S_2 I$$
$$+ \alpha_1 \alpha_3 \beta_1 S_2 I_2 + \alpha_2 \beta_2 S_2 I_2$$
$$+ \alpha_2 (m_{1,1} - m_{2,1}) E_2 \quad (33)$$

$$\dot{I} = \delta_1 E - m_{1,2} I - \alpha_2 \delta_1 E_2 + \alpha_3 \delta_2 E_2$$
$$+ \alpha_3 (m_{1,2} - m_{2,2}) I_2 \quad (34)$$

$$\dot{R} = \gamma_1 I - \mu_{R_1} R - \alpha_3 \gamma_1 I_2 + \alpha_4 \gamma_2 I_2$$
$$+ \alpha_4 (\mu_{R_1} - \mu_{R_2}) R_2 \tag{35}$$

The full model is then represented by equations (32)–(35) along with (28)–(31).

4 ANALYSIS OF THE DYNAMICS

Formally, using a compact notation

$$x_i = \begin{pmatrix} S_i & E_i & I_i & R_i \end{pmatrix}^T \tag{36}$$

with all the consequent meanings of the use of superscript and subscript, if the dynamics of the first population (1)–(4) is denoted by

$$\dot{x}_1 = f_1(x_1) \tag{37}$$

while the dynamics of the second one (28)–(31) is expressed by

$$\dot{x}_2 = f_2(x_2) \tag{38}$$

a flux from the second population to the first can be modelled introducing $\bar{x}_1 = x_1 + \alpha x_2$ as the new augmented state of the first dynamics; consequently, $\bar{x}_2 = x_2 - \alpha x_2 = (1 - \alpha) x_2$ denotes the decreased population of the second system. Note that $\alpha \in R$ if all $\alpha_i = \alpha$, while $\alpha = diag\{\alpha_i\}$ in case of different values of α_i. Assume, without lost of generality in the results, the case of $\alpha \in R$ to simplify the expressions. Otherwise, $(1 - \alpha)^{-1}$ should replace $\frac{1}{1-\alpha}$. The full dynamics is then

$$\dot{\bar{x}}_1 = \dot{x}_1 + \alpha \dot{x}_2 = f_1(x_1) + \alpha f_2(x_2)$$
$$= f_1(\bar{x}_1 - \alpha x_2) + \alpha f_2(\bar{x}_2 + \alpha x_2)$$
$$= f_1\left(\bar{x}_1 - \frac{\alpha}{(1-\alpha)}\bar{x}_2\right) + \alpha f_2\left(\frac{1}{(1-\alpha)}\bar{x}_2\right)$$
$$= \bar{f}_1(\alpha; \bar{x}_1, \bar{x}_2)$$

$$\dot{\bar{x}}_2 = (1-\alpha)\dot{x}_2 = (1-\alpha)f_2\left(\frac{1}{(1-\alpha)}\bar{x}_2\right)$$
$$= \bar{f}_2(\alpha; \bar{x}_2)$$

The new equilibrium points $\bar{x}_1^e$ and $\bar{x}_2^e$ can be computed from

$$f_1\left(\bar{x}_1^e - \frac{\alpha}{(1-\alpha)}\bar{x}_2^e\right) + \alpha f_2\left(\frac{1}{(1-\alpha)}\bar{x}_2^e\right) = 0 \tag{39}$$

$$(1-\alpha)f_2\left(\frac{1}{(1-\alpha)}\bar{x}_2^e\right) = 0 \tag{40}$$

The second equation gives

$$\frac{1}{(1-\alpha)}\bar{x}_2^e = P_{2,e} \quad \Rightarrow \quad \bar{x}_2^e = (1-\alpha)P_{2,e} \tag{41}$$

where $P_{2,e}$ can be $P_{2,e}^1$ or $P_{2,e}^2$, according to the system conditions; by substitution in the first one,

$$f_1(\bar{x}_1^e - \alpha P_{2,e}) = 0 \tag{42}$$

allowing to find

$$\bar{x}_1^e - \alpha P_{2,e} = P_{1,e} \quad \Rightarrow \quad \bar{x}_1^e = P_{1,e} + \alpha P_{2,e} \tag{43}$$

with $P_{1,e}$ with the same definition as $P_{2,e}$ above.

Stability of the four possible equilibria can be studied making reference to the Jacobian matrix

$$J = \begin{pmatrix} \frac{\partial \bar{f}_1(\alpha; \bar{x}_1, \bar{x}_2)}{\partial \bar{x}_1} & \frac{\partial \bar{f}_1(\alpha; \bar{x}_1, \bar{x}_2)}{\partial \bar{x}_2} \\ 0 & \frac{\partial \bar{f}_2(\alpha; \bar{x}_2)}{\partial \bar{x}_2} \end{pmatrix}$$
$$= \begin{pmatrix} \frac{\partial f_1(\bar{x}_1 - \frac{\alpha}{(1-\alpha)}\bar{x}_2)}{\partial \bar{x}_1} & \frac{\partial f_1(\bar{x}_1 - \frac{\alpha}{(1-\alpha)}\bar{x}_2)}{\partial \bar{x}_2} + \alpha \frac{\partial f_2(\frac{1}{(1-\alpha)}\bar{x}_2)}{\partial \bar{x}_2} \\ 0 & (1-\alpha)\frac{\partial f_2(\frac{1}{(1-\alpha)}\bar{x}_2)}{\partial \bar{x}_2} \end{pmatrix} \tag{44}$$

In detail, component–wise, computations of (44) give

$$J_{11} = \frac{\partial f_1(\bar{x}_1 - \frac{\alpha}{(1-\alpha)}\bar{x}_2)}{\partial \bar{x}_1} = \frac{\partial f_1(x_1)}{\partial x_1}\bigg|_{x_1 = (\bar{x}_1 - \frac{\alpha}{(1-\alpha)}\bar{x}_2)}$$

$$J_{12} = \frac{\partial f_1(\bar{x}_1 - \frac{\alpha}{(1-\alpha)}\bar{x}_2)}{\partial \bar{x}_2} + \alpha \frac{\partial f_2(\frac{1}{(1-\alpha)}\bar{x}_2)}{\partial \bar{x}_2}$$
$$= -\frac{\alpha}{(1-\alpha)} \frac{\partial f_1(x_1)}{\partial x_1}\bigg|_{x_1 = (\bar{x}_1 - \frac{\alpha}{(1-\alpha)}\bar{x}_2)}$$
$$+ \frac{\alpha}{(1-\alpha)} \frac{\partial f_2(x_2)}{\partial x_2}\bigg|_{x_2 = (\frac{1}{(1-\alpha)}\bar{x}_2)}$$

$$J_{22} = (1-\alpha)\frac{\partial f_2(\frac{1}{(1-\alpha)}\bar{x}_2)}{\partial \bar{x}_2} = \frac{\partial f_2(x_2)}{\partial x_2}\bigg|_{x_2 = (\frac{1}{(1-\alpha)}\bar{x}_2)}$$

The evaluations at any equilibrium point give

$$J_{11} = \frac{\partial f_1(x_1)}{\partial x_1}\bigg|_{x_1 = ((P_{1,e} + \alpha P_{2,e}) - \frac{\alpha}{(1-\alpha)}(1-\alpha)P_{2,e})}$$
$$= \frac{\partial f_1(x_1)}{\partial x_1}\bigg|_{x_1 = P_{1,e}} \tag{45}$$

$$J_{12} = -\frac{\alpha}{(1-\alpha)} \frac{\partial f_1(x_1)}{\partial x_1}\bigg|_{x_1 = P_{1,e}}$$
$$+ \frac{\alpha}{(1-\alpha)} \frac{\partial f_2(x_2)}{\partial x_2}\bigg|_{x_2 = P_{2,e}} \tag{46}$$

$$J_{22} = \frac{\partial f_2(x_2)}{\partial x_2}\bigg|_{x_2 = P_{2,e}} \tag{47}$$

Thanks to the block triangular structure, it is possible to verify that after the people flow from the second population to the first, at steady state each population remains in its previous status of epidemic free or endemic conditions.

However, in case of motion of individuals, they sum to the already present ones and, moreover, they act as an initial perturbation producing a transient evolution which depend on the $\mathbf{R}_0$ of the hosting population. The new equilibrium points take into account the flux, decreasing for the second system ($\bar{x}_2^e = (1-\alpha)P_{2,e}$) while increasing for the first one ($\bar{x}_1^e = P_{1,e} + \alpha P_{2,e}$). Since the equilibrium changes, some consequences are expected for the reproduction number too.

4.1 Effects on the Reproduction Number

The computation of the new reproduction number follows the approach already used in Section 2 but making use of the the new dynamics (32)–(35), in particular the (E,I) part of the dynamics (33) and (34)

$$
\begin{aligned}
\dot{E} = {} & \beta_1 SI - m_{1,1}E - \alpha_3\beta_1 I_2 S - \alpha_1\beta_1 S_2 I \\
& + \alpha_1\alpha_3\beta_1 S_2 I_2 + \alpha_2\beta_2 S_2 I_2 \\
& + \alpha_2(m_{1,1} - m_{2,1})E_2 \qquad (48) \\
\dot{I} = {} & \delta_1 E - m_{2,1}I - \alpha_2\delta_1 E_2 + \alpha_3\delta_2 E_2 \\
& + \alpha_3(m_{1,2} - m_{2,2})I_2 \qquad (49)
\end{aligned}
$$

Following the previous computations, the $\mathcal{F}$ and $\mathcal{V}$ are defined as

$$
\mathcal{F} = \begin{pmatrix} \beta_1 SI \\ 0 \end{pmatrix} \qquad (50)
$$

$$
\mathcal{V} = \begin{pmatrix} m_{1,1}E + \alpha_3\beta_1 I_2 S + \alpha_1\beta_1 S_2 I - \alpha_1\alpha_3\beta_1 S_2 I_2 \\ -\delta_1 E + m_{2,1}I + \alpha_2\delta_1 E_2 \end{pmatrix}
$$
$$
+ \begin{pmatrix} -\alpha_2\beta_2 S_2 I_2 - \alpha_2(m_{1,1} - m_{2,1})E_2 \\ -\alpha_3\delta_2 E_2 - \alpha_3(m_{1,2} - m_{2,2})I_2 \end{pmatrix} \qquad (51)
$$

and consequently

$$
F = \begin{pmatrix} 0 & \beta_1 S \\ 0 & 0 \end{pmatrix}_{\bar{x}^e}
$$

$$
V = \begin{pmatrix} m_{1,1} & \alpha_1\beta_1 S_2 \\ -\delta_1 & m_{2,1} \end{pmatrix}_{\bar{x}^e}
$$

$$
V^{-1} = \frac{1}{m_{1,1}m_{2,1} + \delta_1\alpha_1\beta_1 S_2} \begin{pmatrix} m_{2,1} & -\alpha_1\beta_1 S_2 \\ \delta_1 & m_{1,1} \end{pmatrix}_{\bar{x}^e}
$$

$$
FV^{-1} = \frac{1}{m_{1,1}m_{2,1} + \delta_1\alpha_1\beta_1 S_2} \begin{pmatrix} \delta_1\beta_1 S & \beta_1 m_{1,1}S \\ 0 & 0 \end{pmatrix}_{\bar{x}^e}
$$

and its spectral radius, tanks to the matrix structure, is given by

$$
\sigma\left(FV^{-1}\right) = \frac{\delta_1\beta_1 S}{m_{1,1}m_{2,1} + \delta_1\alpha_1\beta_1 S_2}\bigg|_{\bar{x}^e} \qquad (52)
$$

The four cases of equilibrium conditions must be considered. For the first system, the basic reproduction number is obtained evaluating in $\bar{x}^e = \bar{x}_1^e = P_{1,e} + \alpha P_{2,e}$ both the epidemic free (5) and endemic (6) conditions for the second system.

For the first case,

$$
\bar{\mathbf{R}}_0^1 = \frac{\delta_1\beta_1(S_{1,e}^1 + \alpha_1 S_{2,e}^1)}{m_{1,1}m_{2,1} + \delta_1\alpha_1\beta_1 S_{2,e}^1} \qquad (53)
$$

while for the second one

$$
\bar{\mathbf{R}}_0^2 = \frac{\delta_1\beta_1(S_{1,e}^1 + \alpha_1 S_{2,e}^2)}{m_{1,1}m_{2,1} + \delta_1\alpha_1\beta_1 S_{2,e}^2} \qquad (54)
$$

In both cases a consistency condition is verified, since

$$
\bar{\mathbf{R}}_0^1\big|_{\alpha=0} = \bar{\mathbf{R}}_0^2\big|_{\alpha=0} = \bar{\mathbf{R}}_0 \qquad (55)
$$

The effect of the people flux can be observed in the dependency of $\bar{\mathbf{R}}_0^1$ from the $\alpha_1 S_{2,e}^1$ and $\bar{\mathbf{R}}_0^2$ from the $\alpha_1 S_{2,e}^2$; while the pre existing status is unchanged, so that if the system is in epidemic free condition, it will always be in the same condition, the increment of population produces a change in the epidemic spread capabilities changing the reproduction number worsening it. In particular, note that

$$
\lim_{\alpha_1 \to +\infty} \bar{\mathbf{R}}_0^1 = \lim_{\alpha_1 \to +\infty} \bar{\mathbf{R}}_0^2 = 1 \qquad (56)
$$

that is asymptotically the behaviour in any case tends to be equivalent to an endemic condition.

On the other hand, if the first system is in endemic conditions, as previously computed, in absence of flux

$$
\mathbf{R}_e = 1 \qquad (57)
$$

is obtained evaluating the next generation matrix in the endemic equilibrium point.

Under the people motion, two possible cases are addressed: the second system is in epidemic free condition, so that $S_2 = S_{2,e}^1$, or in endemic status, so that $S_2 = S_{2,e}^2$; the new expressions for the reproduction numbers are obtained evaluating the spectral radius of the next generation matrix in such two cases:

$$
\bar{\mathbf{R}}_e^1 = \frac{\delta_1\beta_1(S_{1,e}^2 + \alpha_1 S_{2,e}^1)}{m_{1,1}m_{2,1} + \delta_1\alpha_1\beta_1 S_{2,e}^1} \qquad (58)
$$

and

$$
\bar{\mathbf{R}}_e^2 = \frac{\delta_1\beta_1(S_{1,e}^2 + \alpha_1 S_{2,e}^2)}{m_{1,1}m_{2,1} + \delta_1\alpha_1\beta_1 S_{2,e}^2} \qquad (59)
$$

In order to study the effects of the incoming flux, expression (58) can be rewritten as

$$
\bar{\mathbf{R}}_e^1 = \frac{1 + \frac{\alpha_1 S_{2,e}^1}{S_{1,e}^2}}{1 + \frac{\alpha_1 S_{2,e}^1}{S_{1,e}^2}} = 1 \quad \forall\alpha_1 \geq 0 \qquad (60)
$$

making use of the identity (26); the same holds for expression (59).

This result proves that the modified dynamics remains in endemic conditions, changing the equilibrium point, that is the number of infected individuals at steady state according to the new equilibrium point.

A deeper analytical analysis involves large and meaningless expressions. However, to face the problem, some assumptions can be introduced to simplify the model without lost of generality. A first hypothesis assumed is that the initial conditions for both the original (population 1) and the external (population 2) systems are at one of their steady state conditions. With the addition of the observation that the fractions α_i are very low, when cases as the reference one are addressed, it is possible to assume that the flux is a very small perturbation for system 2 and its steady state condition does not vary. One of the main consequences is that in system (28)–(31), the variables S_2, E_2, I_2 and R_2 can be assumed constant and equal to $P_{2,e}^1$ if the external population is assumed epidemic free, or by $P_{2,e}^2$ if the endemic condition is the case. A last hypothesis is the uniformity of the flux in the sense that no selection is performed on the basis of the epidemic status and then the fractions α_i can be assumed all equal and denoted by α.

In the present analysis, once that the asymptotic behaviour is defined, it is important to evaluate also the transients.

This analysis is performed by means of numerical simulation addressing the different combinations discussed above with different levels of epidemic spread.

5 NUMERICAL ANALYSIS

In this section numerical simulations are carried on in order to put in evidence the transient behaviour for each case of populations conditions. They all are performed starting from the new equilibrium points as computed in previous Section and applying a small perturbation.

The choice of the parameters are performed to respect the reference case, but clearly qualitative results can be applied to any populations combinations.

So, for the first system, the following parameters in Table 1 have been chosen

to best fitting with Italian case (Di Giamberardino et al., 2021a) in a SEIR model. Different values for β_1 are assumed in the four simulation cases to change the possible combination of epidemic conditions.

The second system has been chosen with similar characteristics of system 1 except for the number of individuals, assumed a little more than 10 times the

Table 1: Parameters values for system 1.

Parameter	Value
N_1	$1.69 \cdot 10^3$
δ_1	$1/3$
γ_1	$1/10$
$\mu_{S_1} = \mu_{E_1} = \mu_{R_1}$	$2.81 \cdot 10^{-5}$
μ_{I_1}	$2 * 2.81 \cdot 10^{-5}$

first. The idea is to simulate Europe vs. Italy, but also in this case a simple change of values let the model be adaptable to any conditions. Also for this system, the

Table 2: Parameters values for system 2.

Parameter	Value
N_2	$2 \cdot 10^4$
δ_2	$1/3$
γ_2	$1.2 * (1/10)$
$\mu_{S_2} = \mu_{E_2} = \mu_{R_2}$	$0.8 * 2.81 \cdot 10^{-5}$
μ_{I_2}	$2 * 2.81 \cdot 10^{-5}$

values of β_2 is assumed in next Subsections according to the epidemic characteristics under analysis.

The time scale is one day and the simulations have been performed over two years (730 days) to show the effects over the first year of interest and to stress the transient characteristics of the infection evolution according to the stability conditions verified.

Although the actual case study proposed, people flux in Italy (Rome) during the Jubilee 2025, should consider two populations with endemic characteristics, this case will be addressed after the analysis of the behaviours in the other three possible combinations.

5.1 Both Population in Epidemic Free Equilibrium Conditions

In this case, the two populations are assumed to be both in epidemic free conditions. The first one is characterised by a basic reproduction number $\mathbf{R}_0^1 = 0.85$, with an infection factor $\beta_1 = 1.5 \, 10^{-9}$. The results of a first set of simulations are reported in Figure 1, where a factor $\mathbf{R}_0^2 = 0.81$, with a infection parameter $\beta_2 = 1.1 \, 10^{-10}$, has been assumed for the second systems. Three different flux intensities are tested: $\alpha = 0.01$, a low flux, corresponding, with the present numbers, to an increment of about 10% of living population, $\alpha = 0.1$, a flux corresponding about to double the living population, and $\alpha = 0.99$, for an evaluation of asymptotic behaviours, with a population which increases ten time the usual number.

It is possible to note that the epidemic free asymptotic condition assures that the number of infected
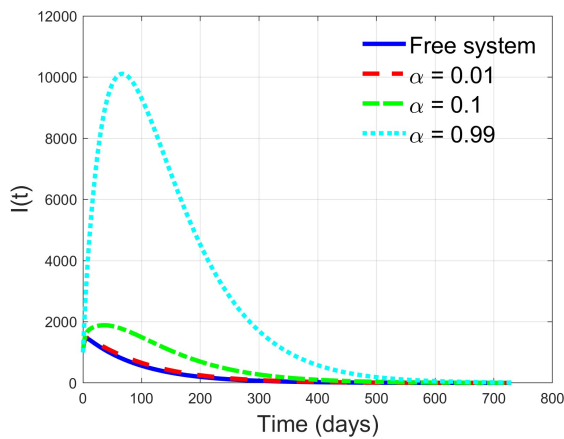
Figure 1: Time history of $I(t)$ in epidemic free cases for different flux intensities.

goes to zero as time passes, but the peak value, as well as the time in which the number is sensibly high, become greater as the flux increments.

A different analysis is reported in Figure 2, where under an average flux ($\alpha = 0.1$), three reproduction number values for the incoming population are taken, still remaining in the epidemic free conditions. So $\beta_2 = 0.9\ 10^{-10}$, $\beta_2 = 1.1\ 10^{-10}$ and $\beta_2 = 1.3\ 10^{-10}$ are assumed, yielding to $\mathbf{R}_0^2 = 0.67$, $\mathbf{R}_0^2 = 0.81$ and $\mathbf{R}_0^2 = 0.97$ respectively.
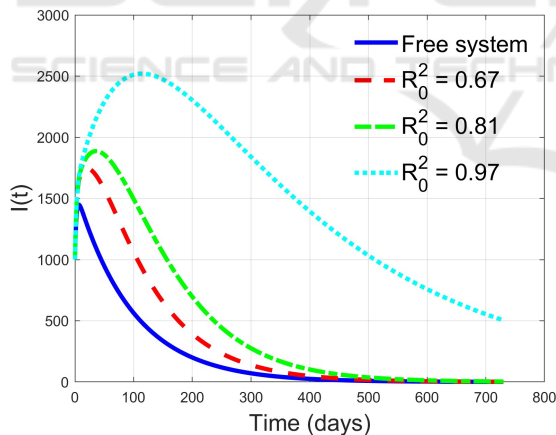
Figure 2: Time history of $I(t)$ for medium income flux $\alpha = 0.1$ from population with different basic reproduction numbers

Also in this case, the lower is the stability condition $\mathbf{R}_0^2$, the higher are the amplitude and the time length of the transient. An interesting observation is that while from a qualitative point of view a small worsening of the medical situation can be expected, the results here presented show that the intensity of such a worsening can be higher than expected.

The extremes of the possible behaviours are sum-

marised in Figure 3 where the best and the worst situations are reported. The first one is referred to the minimum flux ($\alpha = 0.01$) from a population with low reproduction number ($\mathbf{R}_0^2 = 0.67$), while for the second one a very high flux ($\alpha = 0.99$) from population with a high reproduction number ($\mathbf{R}_0^2 = 0.97$) is considered. The peak value and the time length of high value are proportionally very high.
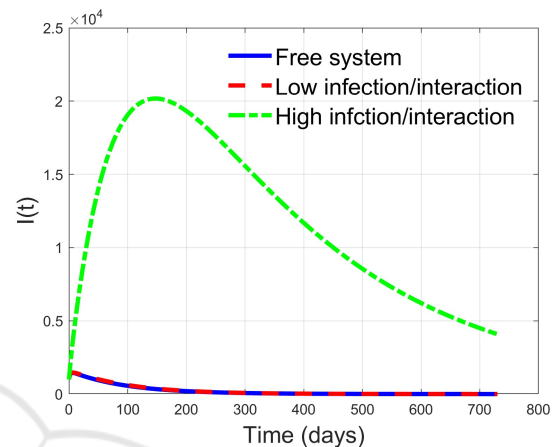

Figure 3: Time history of $I(t)$ for the lowest and the highest dangerous situation according to the choice of epidemic characteristics and population flow.

5.2 Epidemic Free Receiving Population from One in Endemic Condition

This set of simulations has the goal to evaluate if and how an epidemic free population can be affected by a flux from a population where the epidemics is in an endemic condition. In all the simulations, for the first population, a value of $\mathbf{R}_0^1 = 0.85$ has been chosen, corresponding to a $\beta_1 = 1.5\ 10^{-9}$. The first set of simulations, analogously to the previous case, has been performed assuming the same different rates of flux: $\alpha = 0.01$, a low flux, $\alpha = 0.1$, a flux corresponding about to double the living population, and $\alpha = 0.99$, for an evaluation of asymptotic behaviours. The results are reported in Figure 4, showing a sensible contribution to the worsening of the epidemic in terms of number of infected individuals even for medium fluxes.

It is intuitive that different levels of stability, equivalent to different $\mathbf{R}_0^1$ values, for the receiving epidemic free population produce variations in the number of infected individuals I_1. This is a condition that the hosting population can evaluate regardless the infection conditions of the incoming people.

On the other hand, it can be more useful and interesting to evaluate how much the epidemic conditions of the source population, denoted by the values of $\mathbf{R}_0^2$,
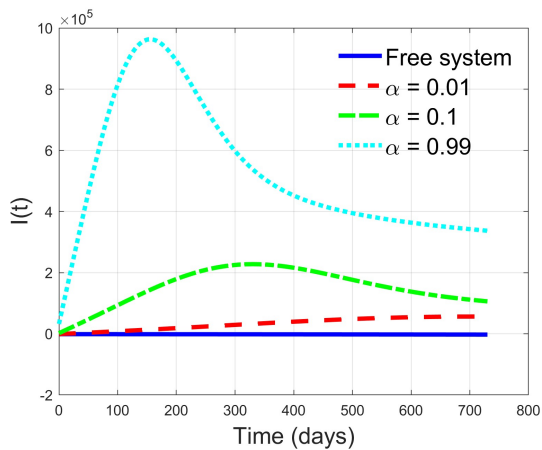
Figure 4: Time history of $I(t)$, in case of epidemic free population with flux from one with endemic conditions, for different incoming intensities.

can affect the dangerousness of the flux with respect to the receiving population for prevention purposes.

In Figure 5, the results of a set of simulations in which the flux rate is kept constant and equal to the median value $\alpha = 0.1$, the reproduction number of the population 1 is fixed to $\mathbf{R}_0^1 = 0.85$ while the $\mathbf{R}_0^2$ has changed, with values $\mathbf{R}_0^1 = 1.11$, $\mathbf{R}_0^1 = 1.4$ and $\mathbf{R}_0^1 = 1.4$.
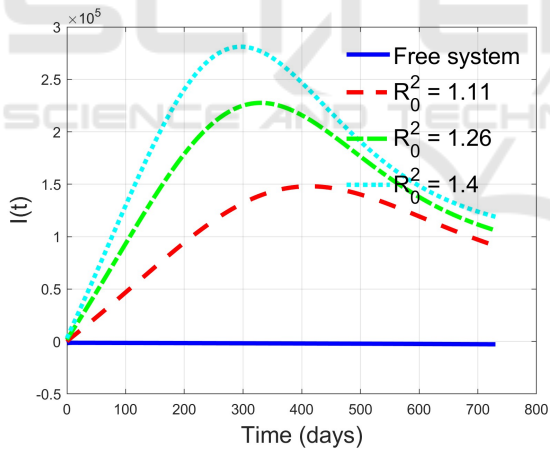
Figure 5: Time history of $I(t)$ for medium income flux $\alpha = 0.1$ from population with different basic reproduction numbers.

In Figure 5 it is evidenced that the contribution of the epidemic condition of the external population 2 is in a worsening of the receiving population, but specifically concentrated in the transient with the behaviour that tends to became equally dangerous at the end of the second year.

An overall evaluation of the effects on the increment of infected individuals in amplitude and in time length is reported in Figure 6, where the lowest effect,

with the minimum flow ($\alpha = 0.01$) and minimum infection rate ($\beta_2 = 1.5\,10^{-10}$, that is $\mathbf{R}_0^2 = 1.11$), and the highest contribution, for high flow ($\alpha = 0.99$) and high $\beta_2 = 1.9\,10^{-10}$ ($\mathbf{R}_0^2 = 1.4$), are reported compared with the absence of flow.
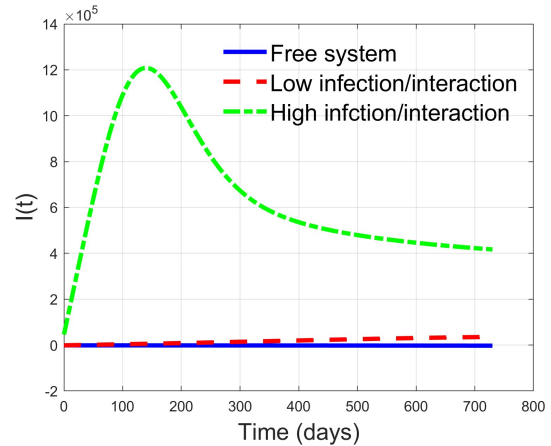

Figure 6: Time history of $I(t)$ for the lowest and the highest dangerous situation according to the choice of epidemic characteristics and population flow.

5.3 Flow from Epidemic Free to Endemic Populations

The case here considered seems the less dangerous among the ones studied, since the incoming population has the best situation with respect to the epidemics, being in epidemic free condition. This status is modelled assuming $\beta_2 = 1.1\,10^{-10}$, corresponding to $\mathbf{R}_0^2 = 0.81$.

The effects of different flows and different contact rates for the first population are analysed. In Figure 7 the reproduction number for the first system is set to $\mathbf{R}_0^1 = 1.42$, corresponding to $\beta_1 = 2.5\,10^{-9}$, for the second one is set to $\mathbf{R}_0^2 = 0.81$, for $\beta_2 = 1.1\,10^{-10}$, while the moving population is quantified by $\alpha = 0.01$, $\alpha = 0.1$ and the asymptotic $\alpha = 0.99$. The result is that also this case presents a sensible level of dangerousness, making worse and worse the infected situation as the flow increases, despite the health situation of the incoming individuals.

The dual situation is reported in Figure 8, where with a fixed medium value for the flow, different reproduction number values for the second system are set, still remaining in the epidemic free condition ($\mathbf{R}_0^2 < 1$): $\mathbf{R}_0^2 = 0.67$, $\mathbf{R}_0^2 = 0.81$ and $\mathbf{R}_0^2 = 0.97$, given by choosing $\beta_2 = 0.9\,10^{-10}$, $\beta_2 = 1.1\,10^{-10}$ and $\beta_2 = 1.3\,10^{-10}$ respectively.

Looking at the plots in Figure 8, even in healthy situation for incoming people, the infected individuals more or less double with a quite long transient.
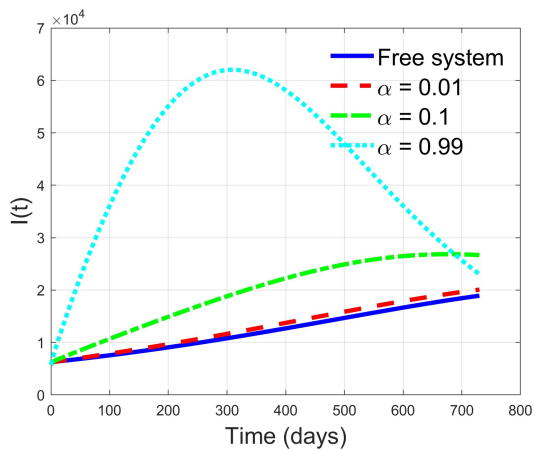
Figure 7: Time history of $I(t)$, in case of population with endemic conditions receiving income people from one in epidemic free status, for different flux intensities.
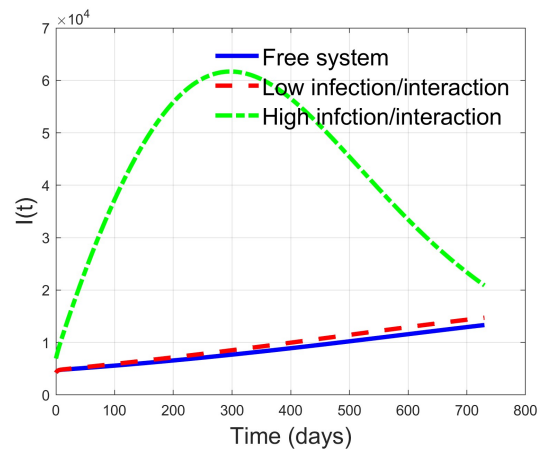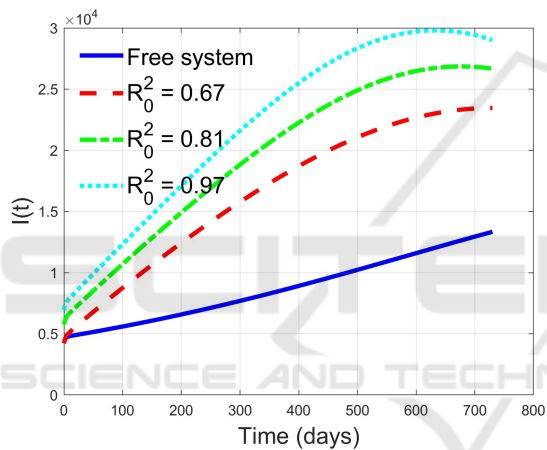

Figure 8: Time history of $I(t)$ for medium income flux $\alpha = 0.1$ from population with different basic reproduction numbers.

Lastly, also in this case an estimation of the bound interval between the best condition (low flux and low infection rate) and the worst one (high flux, high infection rate), is reported in Figure 9, which put in evidence the possibility of a great worsening of the disease situation in terms of number of infected individuals, with a peak about at the end of the first year.

5.4 Flow from Endemic to Endemic Populations

The present situation all over the world with respect to any known infection with large diffusion, including COVID–19, is represented by the presence of the virus with a stable limited number of infected individuals at a physiological level. That is, the endemic condition can be assumed, with different values for

Figure 9: Time history of $I(t)$ for the lowest and the highest dangerous situation according to the choice of epidemic characteristics and population flow.

the equilibrium point according to local characterization of the parameters. So, this is the real situation that will be faced in the reference case studied.

However, since the actual conditions in terms of infection situation at the beginning of the event considered, more or less the end of the present year (2024), following the previous analysis, a (small) range of possible infection rates has to be considered, both for the receiving population 1 and for the incoming population 2.

Then, the effect of the intensity of the people flow α is considered in a first set of simulations in which the reproduction numbers for the two systems are varied: $\mathbf{R}_0^1 = 1.25$ and $\mathbf{R}_0^2 = 1.11$ for Figure 10, $\mathbf{R}_0^1 = 1.25$ and $\mathbf{R}_0^2 = 1.4$ for Figure 11, $\mathbf{R}_0^1 = 1.59$ and $\mathbf{R}_0^2 = 1.11$ for Figure 12 and $\mathbf{R}_0^1 = 1.59$ and $\mathbf{R}_0^2 = 1.4$ for Figure 13. While the qualitative variations seem similar, it is clear comparing Figures 10 and 12 with Figures 11 and 13 that, despite the variation of the $\mathbf{R}_0^i$ is almost the same for both the systems, the effect of variation of the second system produces a doubling in the effect on the infected increment.

The same considerations can be deduced from Figure 14 where, for $\alpha = 0.1$, the two plots associated with the higher value for $\mathbf{R}_0^2$ show a double number of infected individuals with respect to the lower ones, quite independently from the $\mathbf{R}_0^1$.

The comparison between the behaviour with the lowest infection values and flow and the highest ones, corresponding to the best and the worst conditions in the range here studied, is reported in Figure 15, when it is possible to understand that it must be expected a possible sensible increment of individuals that require medical support, with a peak of ten times the usual number of patients and the low decrement towards the new equilibrium condition.
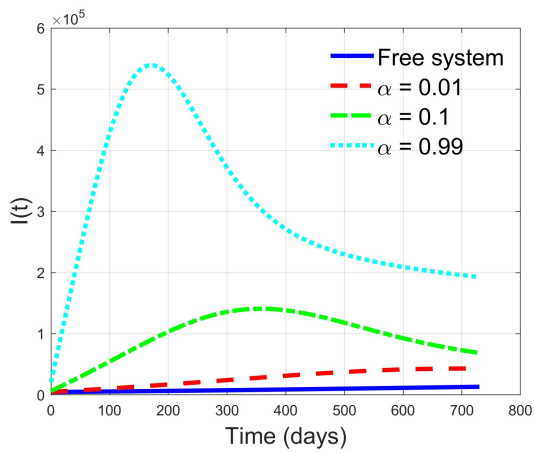
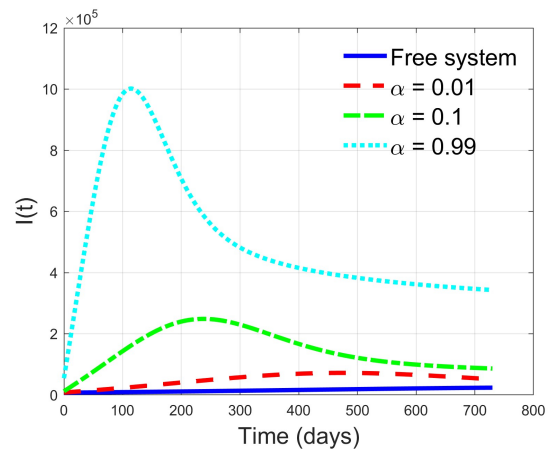Figure 10: Time history of $I(t)$ for $\mathbf{R}_0^1 = 1.25$ and $\mathbf{R}_0^2 = 1.11$, under different flux intensities.
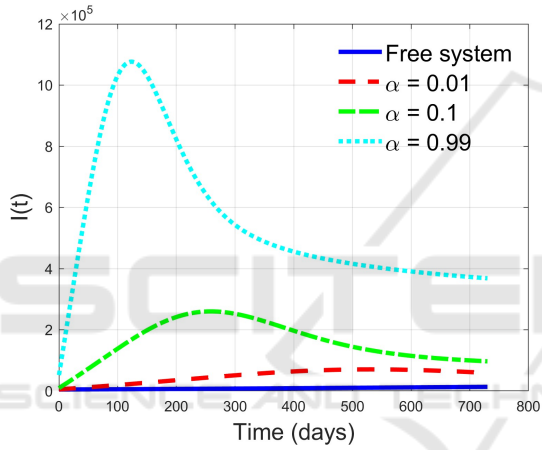

Figure 11: Time history of $I(t)$ for $\mathbf{R}_0^1 = 1.25$ and $\mathbf{R}_0^2 = 1.4$, under different flux intensities.

Figure 12: Time history of $I(t)$ for $\mathbf{R}_0^1 = 1.59$ and $\mathbf{R}_0^2 = 1.11$, under different flux intensities.

Figure 13: Time history of $I(t)$ for $\mathbf{R}_0^1 = 1.59$ and $\mathbf{R}_0^2 = 1.4$, under different flux intensities.
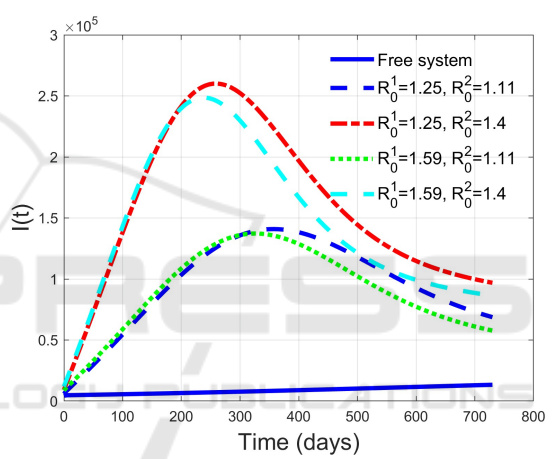

Figure 14: Time history of $I(t)$ for medium income flux $\alpha = 0.1$: effects of different combinations of basic reproduction numbers.
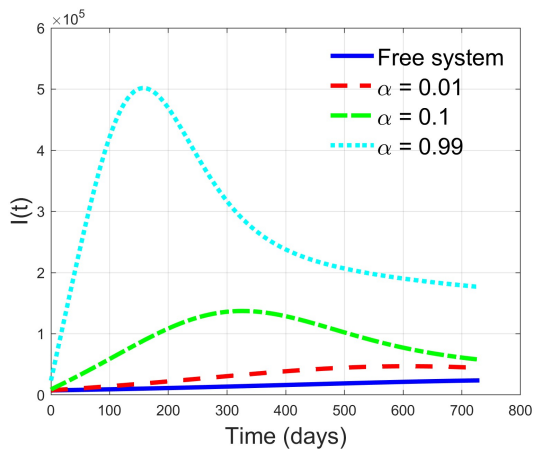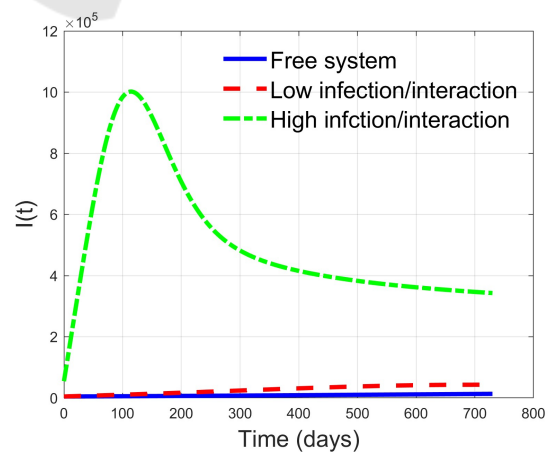

Figure 15: Time history of $I(t)$ for the lowest and the highest dangerous situation according to the choice of epidemic characteristics and population flow.

6 CONCLUSIONS AND FUTURE WORK

In the paper the analysis of the effects of a temporary increment of a population on the epidemic characteristics and on the increment of the number of infected individuals. The flux is assumed coming from a second population with its own infection status. A SEIR model is assumed for describing both the population, being important to put in evidence the effects on the infected individuals only. Steady state conditions are initially considered, with the analysis carried out analytically, giving the conditions for having the classical epidemic free or endemic status, along with their stability conditions. A reference to the reproduction number has been also addressed to evaluate the epidemic spread conditions.

While at steady state it is easy to evaluate the effects of the people flux, being the new equilibria the combinations of the previous ones, a different approach has been used to study the transients, trying to quantify the effects in terms of increment of infected individuals in population 1. This analysis has been performed in a numerical way, studying the effects of the possible different contributions of the people variation and of the epidemic status of the populations to the worsening of the infection conditions. Numerically, the case study in mind has been the analysis of the possible epidemic effects of the Jubilee 2025 on the Italian or, suitably scaled, Roman situation during the year of intense pilgrim/tourists income.

The main result is that it would be necessary to considered a sanitary prevention plan for an effective approach to the effects of the disease containment. Moreover, these considerations can be extended, qualitatively, to any infectious illness: improving the analytical aspects it is possible to address a more general class of infections and different populations, being possible to extend the results, suitably scaled, also to several different case like high density touristic places. Moreover, a more specific analysis of how and how much these fast increments of populations can affect the infection rate β is going to be faced.

REFERENCES

Casagrandi, R., Bolzoni, L., Levin, S., and Andreasen, V. (2006). The SIRC model and influenza. *A. Mathematical Biosciences*, 200:152–169.

Contreras, S., Villavicencio, H., Medina-Ortiz, D., Biron-Lattes, J., and Olivera-Nappa, A. (2020). A multi-group seira model for the spread of covid-19 among heterogeneous populations. *Chaos, Solitons and Fractals*, 136.

Daley, D. J. and Gani, J. (1999). *Epidemic Modelling: An Introduction*. Cambridge Studies in Mathematical Biology. Cambridge University Press.

Di Giamberardino, P., Caldarella, R., and Iacoviello, D. (2021a). A control based mathematical model for the evaluation of intervention lines in COVID-19 epidemic spread: The Italian case study. *Symmetry*, 13(5).

Di Giamberardino, P. and Iacoviello, D. (2017). Optimal control of SIR epidemic model with state dependent switching cost index. *Biomedical Signal Processing and Control*, 31.

Di Giamberardino, P., Iacoviello, D., Albano, F., and Frasca, F. (2020). Age based modelling of sars-cov-2 contagion: The italian case. pages 274–279.

Di Giamberardino, P., Iacoviello, D., Papa, F., and Sinisgalli, C. (2021b). A data-driven model of the covid-19 spread among interconnected populations: epidemiological and mobility aspects following the lockdown in italy. *Nonlinear Dynamics*, 106(2):1239–1266.

Iranzo, V. and Pérez–González, S. (2021). Epidemiological models and covid-19: a comparative view. *Hist Philos Life Sci.*, 43(3).

Ledzewicz, U. and Schattler, E. (2011). On optimal singular controls for a general SIR-model with vaccination and treatment. *Discrete and continuous dynamical systems*, pages 981–990.

Martcheva, M. (2015). An introduction to mathematical epidemiology. *Text in Applied Mathematics 61, Springer*.

Ng, O., Marimuthu, K., Chia, P., Koh, V., Chiew, C., and et al. (2020). SARS-CoV-2 infection among travelers returning from wuhan, china. *N Engl J Med.*, 382(15):1476–1478.

van den Driessche, P. (2017). Reproduction numbers of infectious disease models. *Infectious Disease Modelling*, 2:288–303.

Yue, Y., Tan, Y., and Tang, S. (2023). Stability analysis of the covid-19 model with age structure under media effect. *Computational and Applied Mathematics*, 42(5).