Epidemic Modeling and Control: An ARX Approach for Measles Containment

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Abstract: Measles is one of the most dangerous epidemic disease for its high reproduction number and the possible complications on already weakened patients. Effective vaccination is available since the early 60*s* and a suitable vaccination campaign could interrupt this epidemic disease. The most common approach for the disease description considers compartmental models, effective but requiring the identification of model parameters, generally data consuming. A different approach is data driven, that is it consideres autoregressive modeling with exogenous input. The autoregressive modeling is here considered describing measles evolution by using measurable available information, like the number of infected patients and the percentage of vaccinated individuals. A penalized control is herein determined, thus taking into account also limitation in control actions. Numerical results, based on available real data, show the effectivenes of the approach.

1 INTRODUCTION

Despite the existence of a safe and cost-effective vaccination since the early 60*s*, measles is still one of the most dangerous epidemic disease, for the possible complications on already weakened patients and for its high reproduction number, estimated equal to 14. According to the World Health Organization, it is estimated that in 2022 there were 136000 measles death globally, mostly among children under 5 years old, unvaccinated or under-vaccinated. Immunization activities prevented about 57 million deaths between 2000 and 2022 all over the world, (World Health Organization, 2024). Measles is caused by a virus that infects, initially, the respiratory tract; early symptoms (that last up to 7 days) include small white spots inside the cheeks, cough with runny nose and red eyes. A prominent rash begins about 10 days after exposure and it usually lasts less than a week. Most deaths are from complications, like encephalitis, severe diarrhoea, ear infections and severe breathing problems.

The importance of facing measles and its complications is the motivation of many research papers focusing on modeling the evolution of the disease and proposing possible control strategies. Generally, the compartmental modeling results the most effective description, partitioning the population depending on the specific condition with respect to the disease; with the SEIR model, in particular, the population is split into 4 compartments, including susceptible S, exposed E, infected I and removed R individuals. When considering also control actions, the classical SEIR model is further enriched by new elements, like vaccination, as in (A. Kuddus, M. Mohiuddin and A. Rahman, 2021), or by the class of pathogen population, the host of measles virus, as in (H. Alemneh, 2023). More complex models consider also susceptible subjects that cannot be vaccinated and patients that, along with measles, have also complications, (P. Di Giamberardino and D. Iacoviello, 2019a), (P. Di Giamberardino and D. Iacoviello, 2019b), (P. Di Giamberardino and D. Iacoviello, 2020). In this case, the goals are both to provide heard immunity to help subjects that cannot be vaccinated, and to help patients: control actions include prevention, like informative campaign and vaccination, and medication referring both to patients with measles and patients with measles and complications. Optimal control is applied in (H. W. Berhe and O. D. Makinde, 2020), where actions by vaccination, treatment, and prevention by an education campaign are implemented.

The impact of preventive actions is discussed in (O.J. Peter, H.S.Panigoro, M.A. Ibrahim, O.M.Otunuga, T.A.Ayoola and A.O. Oladapo, 2023), where the role of the reproduction number is

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faced. The numerical analysis supports and quantifies the theoretical results, thus suggesting lowering the effective contact with an infected person and increasing the rate of vaccinating susceptible people.

In (Y. Xue, X. Ruan and Y. Xiao, 2021), it is investigated the influences of heterogeneity and immunity on measles transmission, proposing a network model with periodic transmission rate and examining the threshold dynamics.

These compartmental models, while being effective, require the identification of parameters describing the transition from one condition to the others.

A possible different approach is data driven; in this way the analysis and the control strategies are determined just using the measured available data, as, in this case, the number of infected patients and the percentage of vaccinated individuals. In this framework, a useful representation is given by the autoregressive model with exogenous input, namely the ARX and the ARMAX models, (F. Piltan, S. Haghighi and N. Sulaiman, 2017); starting from historical series and by using identification methods, it is possible to describe complex phenomena. The number of infected patients at the current time is expressed as a linear combination of the number of patients in previous years and of the control actions (the vaccinations) previously applied. In the ARX model the number of infected patients is function of the current measure noise, whereas in the ARMAX model also past errors are considered.

In recent studies, (Y. Pei, Q.Pei, H. Lee, M. Qiu and Y. Yang, 2022), historical epidemics data, along with climate and economy ones, have been investigated by means of autoregressive exogenous analysis in the framework of human ecology; in particular, ARX modeling has been used to simulate long-term effects of climate change, economy and epidemics. This approach is particularly useful in presence of missing data, as in (M. Horner, S. Pakzad and N. Gulcec, 2019), where structural health monitoring is faced using also Kalman filtering.

The paper is organized as follows: in Section 2, after a brief recall of the ARX model with the penalized optimal control and the identification of the model parameters, the specific ARX model for epidemic diseases is developed. Numerical results, reported in Section 3, are based on real data, implementing the described procedures, from the data processing, to the ARX model identification, to the penalized optimal control definition and state prediction. In the conclusions the obtained results are summarized, proposing also future developments.

2 MATERIALS AND METHODS

The measles epidemic disease is usually described by means of a compartmental model in which the population is partitioned into groups homogeneous with respect to the disease conditions. For example, often the SEIR model is efficiently used, thus assuming that an healthy subject in the susceptible class S can be infected by an infected patient belonging to the I class. He becomes infected but not infectious yet, thus belonging to the E class of exposed, before the transit to the I class. Successively, he can recover, thus leaving the I class and going to the R one. This description, while being realistic, is not easy to be implemented since it requires the knowledge of the transit parameters from one class to the other. These parameters are strongly connected to the general healthy conditions of the population under study and must be identified considering real data, sometimes not available and consistent. Another approach is data driven, meaning that the description of the measles diffusion is obtained by means of the unique available information, the number of infected patients and of administrated vaccines. The proposed approach falls within this area, considering in particular the autoregressive models with exogenous input, the ARX models. In the next Subsections, this class of models is briefly recalled and adapted to the specificity of the measles disease.

2.1 Brief Recall of the ARX Model

The ARX is an autoregressive model with exogenous input. It is useful the notation of the backward shift operator z^{-1}: for a given scalar process $x(t)$, one has $z^{-1}x(t) = x(t-1)$. The classical ARX model can be represented as follows:

$$A(z^{-1})y(t) = z^{-d}B(z^{-1})u(t) + C(z^{-1})e(t) \quad (1)$$

where:

$$A(z^{-1}) = 1 + a_1 z^{-1} + ... + a_n z^{-n} \quad (2)$$

$$B(z^{-1}) = b_0 + b_1 z^{-1} + ... + b_m z^{-m} \quad (3)$$

$$C(z^{-1}) = 1 \quad (4)$$

with $d > 0$ denoting the delay of the system, $b_0 \neq 0$ and $e(t)$ representing a white noise process, with zero mean value and variance σ^2; $y(t)$ and $u(t)$ are jointly stationary processes representing, in the proposed framework, the number of infected patients and the applied control at time t, respectively. The control

process u up to $t-1$ is realistically assumed independent on the noise process e.

The system (1) represents the situation in which the number of infected patients at time t is function of the sequence of the number of infected patients in the past, up to a chosen time $t-n$, of the applied control actions u, from $t-1$ up to the instant $(t-m-1)$ and of the noise $e(t)$.

For $d=1$, it is useful to represent the current measure $y(t)$ as:

$$y(t) = \phi^T(t)\theta + e(t) \tag{5}$$

where

$$\phi(t) = \begin{bmatrix} -y(t-1) \\ \dots \\ -y(t-n) \\ u(t-1) \\ \dots \\ u(t-m) \end{bmatrix} \tag{6}$$

and

$$\theta = \begin{bmatrix} a_1 \\ \dots \\ a_n \\ b_1 \\ \dots \\ b_m \end{bmatrix} \tag{7}$$

Equation (5) is already in prediction form; therefore, the 1–step predictor can be written as follows:

$$\hat{y}(t|t-1) = \phi^T(t)\theta \tag{8}$$

with the prediction error ε, function of the current instant t and of the set of coefficients θ, given by:

$$\varepsilon(t,\theta) = y(t) - \hat{y}(t|t-1) = \; y(t) - \phi^T(t)\theta \tag{9}$$

With a delay $d>1$, this procedure is no longer useful; it is necessary to solve the Diofantine equation:

$$C(z^{-1}) = A(z^{-1})Q(z^{-1}) + z^{-d}\bar{R}(z^{-1}) \tag{10}$$

that is, it is necessary to solve the long division between $C(z^{-1})$ and $A(z^{-1})$ up to the point in which in the remainder $R(z^{-1})$ it appears the term z^{-d} and therefore it is possible to write $R(z^{-1}) = z^{-d}\bar{R}(z^{-1})$.

The polynomials $Q(z^{-1})$ and $\bar{R}(z^{-1})$ are given by:

$$Q(z^{-1}) = q_0 + q_1 z^{-1} + ... + q_{d-1} z^{-(d-1)} \tag{11}$$

$$\bar{R}(z^{-1}) = r_0 + r_1 z^{-1} + ... + r_{n-1} z^{-(n-1)} \tag{12}$$

The optimal predictor in the general case of $d \geq 1$ is given by:

$$\begin{aligned} C(z^{-1})\hat{y}(t|t-d) &= \bar{R}(z^{-1})y(t-d) \\ &+ B(z^{-1})Q(z^{-1})u(t-d) \end{aligned} \tag{13}$$

that is, with $C(z^{-1}) = 1$ in the ARX case:

$$\hat{y}(t|t-d) = \bar{R}(z^{-1})y(t-d) + B(z^{-1})Q(z^{-1})u(t-d) \tag{14}$$

By using (11), (3), (12), the latter expression can be explicitly written as follows:

$$\begin{aligned} \hat{y}(t|t-d) &= \sum_{i=0}^{n-1}(r_i y(t-d-i)) \\ &+ \sum_{j=0}^{m+(d-1)} \sum_{k=0}^{j} b_k q_{j-k} u(t-d-j) \end{aligned} \tag{15}$$

2.2 Penalised Optimal Control of the ARX Model

The choice of the control action can be done following the goal of an optimal tracking of the variable $y(t)$ to a given reference $y^r(t)$. This can be obtained minimizing the cost index:

$$J = E[(y(t) + \beta u(t-d) - y^r(t-d))^2] \tag{16}$$

with $\beta \geq 0$ the coefficient of a penalty control. This implies that the optimal choice of the control is obtained weighting also its cost, thus aiming at the optimal tracking, penalizing possible too strong control actions. As β increases, generally the behaviour of the control variable becomes more regular.

Let us assume that the autoregressive AR part of the model (1) is asymptotically stable, that is the polynomial $A(z^{-1})$ has poles strictly inside the unit circle. In this case, the minimization of the cost index (16) is obtained once

$$\hat{y}(t|t-d) = -\beta u(t-d) + y^r(t-d) \tag{17}$$

The optimal predictor $\hat{y}(t|t-d)$ with $\beta = 0$ is given by (15); by substituting this expression into (17), the expression

$$\begin{aligned} u^o(t-d) = &\frac{1}{\beta + b_0 q_0}(y^r(t-d) - \sum_{i=0}^{n-1}(r_i y(t-d-i)) \\ &- \sum_{j=1}^{m+(d-1)} \sum_{k=0}^{j} b_k q_{j-k} u(t-d-j)) \end{aligned} \tag{18}$$

is obtained or, equivalently:

$$\begin{aligned} u(t) \quad = \quad &\frac{1}{\beta + b_0 q_0}(y^r(t) - \sum_{i=0}^{n-1}(r_i y(t-i)) \\ &- \sum_{j=1}^{m+(d-1)} \sum_{k=0}^{j} b_k q_{j-k} u(t-j)) \end{aligned} \tag{19}$$

This is the penalized optimal control to be applied at time t to reduce the distance to the reference $y^r(t)$ at time $t+d$.

By using the delay operator, equation (19) can be written as:

$$(\beta + b_0 q_0 + \sum_{j=1}^{m+(d-1)} \sum_{k=0}^{j} b_k q_{j-k} z^{-j}) u(t) = y^r(t) - \sum_{i=0}^{n-1} (r_i y(t) z^{-i}) \quad (20)$$

A block diagram of the ARX model is given in Fig. 1, where the notation

$$M(z^{-1}) = (\beta + b_0 q_0 + \sum_{j=1}^{m+(d-1)} \sum_{k=0}^{j} b_k q_{j-k} z^{-j})$$

is adopted.

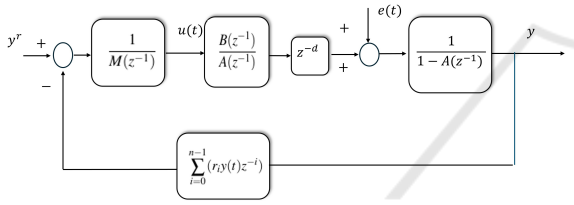

Figure 1: Block diagram of the ARX model.

The transfer function of the loop is given by:

$$L(z^{-1}) = \frac{B(z^{-1}) z^{-d} A(z^{-1}) \sum_{i=0}^{n-1} (r_i z^{-i})}{(\beta + b_0 q_0 + \sum_{j=1}^{m+(d-1)} \sum_{k=0}^{j} b_k q_{j-k} z^{-j})} \quad (21)$$

with the poles of the closed loop obtained from:

$$\Delta = 1 + L(z^{-1}) \quad (22)$$

that is:

$$B(z^{-1}) z^{-d} A(z^{-1}) \sum_{i=0}^{n-1} r_i z^{-i} + \beta + b_0 q_0 + \sum_{j=1}^{m+(d-1)} \sum_{k=0}^{j} b_k q_{j-k} z^{-j} = 0 \quad (23)$$

Note the role of the penalty term β, able to modify the poles of the transfer function of the loop and therefore the system behaviour. The analysis of the poles and of their variation as β goes to infinite will be studied in the numerical section for the specific problem at hand.

2.3 Identification of the ARX Model Parameters

What has been discussed up to now assumes that an identified model ARX is available. It means that the phenomenon under investigation (in the proposed study, the measles evolution when vaccination strategy is applied) has been described by an ARX model with chosen order (n,m) and identified coefficients a_i, $i = 1,...,n$ and b_j, $j = 0,...,m$. Moreover, also the delay with which one wants to determine the optimal control to track a given reference must be established; anyway, this latter can be left as a parameter to be discussed in the numerical section. The identification of the model parameters is obtained by using the least square estimation, minimizing the square of the difference between the model (1) and the available real data. The order of the model is related to the amount of available data, thus resulting from a compromise between the requirement of a model with high order (equivalent to long memory) and the usually limited number N of couples of real inputs $u(t)$ (the administered vaccination) and of real outputs $y(t)$ (the number of positive patients).

Without loosing generality, assume the delay $d = 1$ and consider the prediction in the form (8): it is linear in the parameter vector (7). To estimate θ, by using the prediction error method it is minimized the cost function:

$$J_N(\theta) = \sum_{t=1}^{N} (y(t) - \phi(t)^T \theta)^2 \quad (24)$$

The solution is analogous to the least square estimation:

$$\hat{\theta}_N = (\sum_{t=1}^{N} \phi(t) \phi^{-1}(t))^{-1} (\sum_{t=1}^{N} \phi(t) y(t)) \quad (25)$$

It is possible to find the solution of this identification problem once $N \geq (n+m)$.

2.4 The ARX Model for Epidemiological Environment

The availability of historical data allows the identification of the ARX model, where the measure $y(t)$ is the number of infected patients $I(t)$ per million of people at time t, and the control $u(t)$ is the percentage of vaccinated individual in the population. In the data driven approach used in this paper, the historical series of data are split into two sets; the first one is used for the identification of the ARX, whose order depends on the amount N of data that can be used for the identification, as described previously. The second set is used to validate the identified model, thus checking how much it adequately describes the data not used for the identification.

Note that for the specific application in epidemiology, a reasonable choice for the model's order should

take into account the reproduction number R_0, representing the average number of subjects that can be infected by a unique individual in the period in which he is infectious. This information is important since a low number would slow the epidemic, whereas a high one speeds up the spread by increasing the influence of the number of infected subjects in recent period; in particular, the estimated reproduction number for the measles is 14. Another important aspect is the immunization effects of the vaccine which, for measles, occur almost immediately. The incubation time of the disease, which is about 10 days, while being a fundamental information in a compartmental model, in this case seems less important to be considered for the identification purposes.

If the identification step provides acceptable fitting between real data and the model outputs, a reliable model for the dynamics of the number of infected subjects, connected with the vaccination campaign, becomes available.

This allows, following the procedure of Subsection 2.2, to determine the control action $u(t)$, possibly penalized (by the coefficient β), to minimize the expected value given in (16), that is to make the number of infected patients, $I(t)$, as close as possible to a desired reference, say $I^r(t)$, more manageable by the national health service.

In Subsection (2.2), it is considered also the possibility of yielding the best control at time t to reduce the distance between the predicted number of infected patients $\hat{I}(t+d|t)$, once given the information available at time t, and the desired trend I^r.

In the next Section, the discussed ARX model is identified on real data, showing its effectiveness and limits.

3 NUMERICAL RESULTS

The data considered in this section are taken from (Surveillance atlas of infectious diseases, 2024); they are the sequence of the numbers of infected individuals, per million, in Europe (without considering United Kingdom) between 1999 and 2024, taken monthly, see Fig.2. Moreover, with the same time unit, it is available the percentage of vaccinated individuals, see Fig.3. Since in the ARX model the number of infected patients and the number of vaccinated people are connected by the equation (1), it is necessary to normalize the data.

To filter the real data, without loosing relevant information, a moving average of a windows of 5 samples is assumed; as seen in the cited figures, this allows to cut and smooth some peaks in real data.

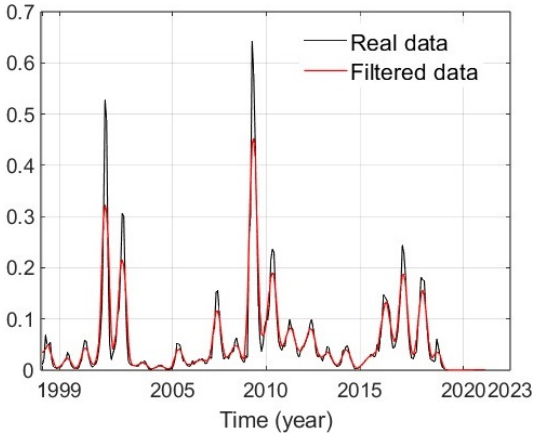

Figure 2: Evolution of the number of infected subjects per million; in black, real data; in red, filtered real data.

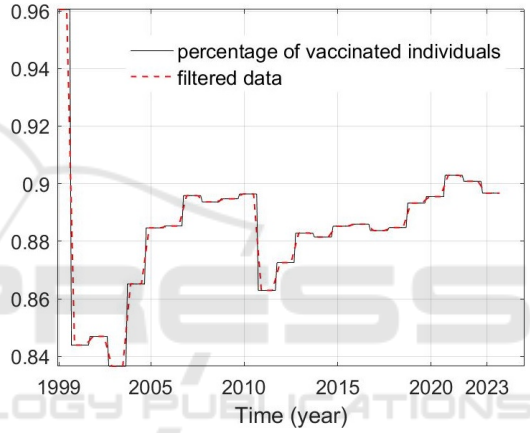

Figure 3: Evolution of the percentage of vaccinated individuals; in black, real data; in red, filtered real data.

The available data cover the period of less than 25 years; for the ARX model identification, it is chosen a period of two years that contains the general periodical trend, thus corresponding to 24 samples. As a first attempt it is chosen an ARX model with $n = m = 3$ and delay $d = 1$. By using the least square estimation method, the identified model is

$$\begin{aligned}&(1+a_1z^{-1}+a_2z^{-2}+a_3z^{-3})y(t)\\&\quad=(b_1z^{-1}+b_2z^{-2}b_3z^{-3})u(t)\end{aligned}\tag{26}$$

that is:

$$\begin{aligned}&(1-1.898z^{-1}+1.274z^{-2}-0.1479z^{-3})y(t)\\&=(-1.533z^{-1}+1.606z^{-2}-0.06802z^{-3})u(t)\end{aligned}\tag{27}$$

In Fig.4 it is shown the comparison between the real data used for the identification and the output of the ARX model. An higher number of data used for the identification yields a low quality; it is possible to obtain higher fitting by reducing the period over

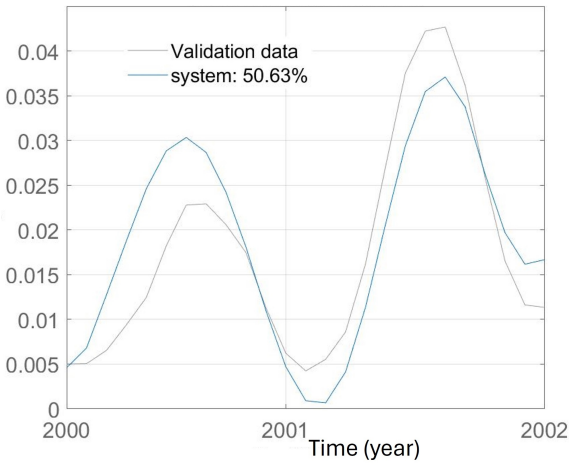

Figure 4: Comparison between real data and the ones reconstructed by the ARX model.

which the model is identified, but the risk is to obtain an overfitting, unable to generalize the model.

By using the model (27) it is possible to determine the characteristics of the noise present in the data regarding two years, assuming, reasonably, that the statistics of the noise remain almost the same in all the control period; the mean value is estimated in $3.16 \cdot 10^{-5}$ with a standard deviation of 0.0015.

The availability of an ARX model allows to predict the possible behaviour of the number of infected patients, once the penalized control (19) is adopted; the windows on which this prediction is determined, along with the penalized control, is chosen corresponding to a period of 18 months. A longer period could yield an unreliable prediction, being based on a model identified on data of a window starting $24+18$ months before, thus referring to a too long period. As a first choice, it is simulated the identified model (27), with no penalization (that is $\beta = 0$), and a realization of noise with the estimated mean value and standard deviation.

In Fig.5 it is shown the simulated behaviour of the number of infected patients once the control (19) is implemented, versus the real trend of infected individuals; in Fig. 6 it is shown the simulated control versus the really applied vaccination strategy. Considering the two Figures 5 and 6, it can be noted that without any penalization, the control can assume high values reaching rapidly about 90% of vaccination coverage and, consequently, the number of infected patients decreases almost immediately.

These results are promising, but it must be considered that no limitations in control actions are introduced; moreover, it is assumed, implicitly, as reference $y^r(t) = 0$, thus requiring a strong effort for a fast reduction of the number of infected patients.

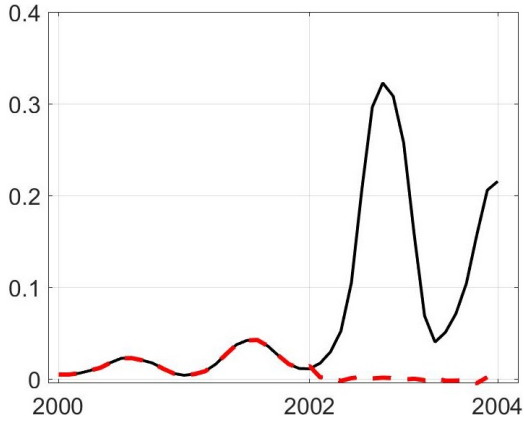

Figure 5: Comparison between real data of infected patients (in black) and the ones reconstructed by the ARX model under the optimal control (19), in red.

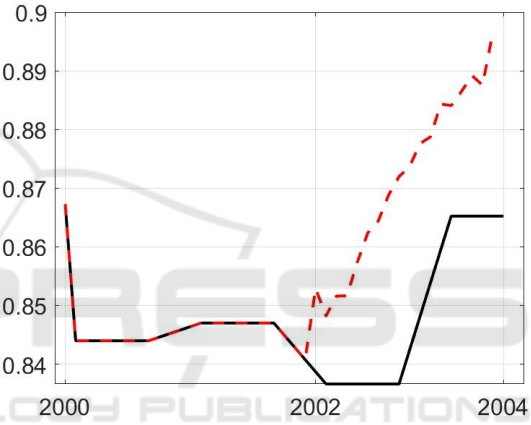

Figure 6: Comparison between real data of vaccination and the the optimal control (19).

If these conditions are not applicable, the proposed approach allows to include a penalization for the strong control actions and, at the same time, accept a less restrictive reference y^r. To stress the influence of β and y^r, behind the basic situation considered, indicated for simplicity as *case 1*, three new cases are analysed:

2. $\beta = 0$ with $y^r = 0.01$
3. $\beta = 0.001$ with $y^r = 0.01$
4. $\beta = 0.005$ with $y^r = 0.01$

The situation 2 is still with a non penalized control with the goal of tracking a low non null number of infected patients; in *case* 3 it is considered also a penalization, as well as in the forth case, with a higher weight for β.

In the non penalized case, the obtained control is able to make the state fluctuate around the reference, Fig. 7, with a low mean value for the tracking error, respectively equal to 0.0065 (*case 1*) and 0.0077 (*case 2*). In the penalized control of *case 4* the tracking

error is of one order higher, equal to 0.0119; this is reasonable, being the control not as efficient as in the first two cases.

Comparing the behaviours of the controls, Fig. 8, besides the higher values obtained in *case 1*, it can be noted that, for *cases 2* and *4*, for the first 8 months the values of $u(t)$ are generally higher in the non penalized case, as obvious; on the other hand, from month 9 on, when the predictive control is less reliable, the trend of the two controls are reverted. Nevertheless, the tracking appears still acceptable. An interesting case is the third, with an intermediate behaviour; the tracking error is the same as in the non penalized control of *case 1*: this can be justified noting that for the system it is easier the tracking to the value 0.01 of (*case 3*) rather than to the value 0 of (*case 1*), requiring, in this latter situation, a stronger action. As far as the control, $u(t)$, its behaviour is between the ones of *case 2* and *4*.

As discussed in Subsection 2.2, it is interesting to study the poles of the closed loop transfer function obtained from (22); for the chosen model identified in (27), the roots to be determined comes from the polynomial (23), that is:

$$\begin{aligned}\Delta = &(1+a_1(\beta-b_1))z^4-(a_1b_2-a_2(\beta-b_1))z^3- \\ &(a_2b_2+a_1b_2-(\beta-b_1)a_3)z^2- \\ &(b_2a_3+b_2a_2)z-b_2a_3 \end{aligned} \quad (28)$$

The stability is reached if all the roots have modulus inside the circle of unit radius.

It is interesting to note the dependency of the roots on the values of β. In absence of penalization, that is assuming $\beta = 0$, there are three roots with modulus less than 1 and one root with modulus equal to 1.6056, thus the system is unstable. As β increases all the roots move away from the zone of instability, as can be noted in Fig. 9; it is shown the evolution of the fours roots as β increases. All the roots have modulus less than 1 for $\beta \geq 3.5$. With a strongly penalized control the system becomes stable, with a more regular action.

4 CONCLUSIONS

In this paper a data driven approach to face the measles epidemic spread control is addressed. The unique available and measurable information are the number of infected patients and the vaccination coverage; the autoregressive model ARX allows to represent the current measurable number of infected patients as function of the characteristics of the pandemics, i.e. the weighted sum of the past numbers

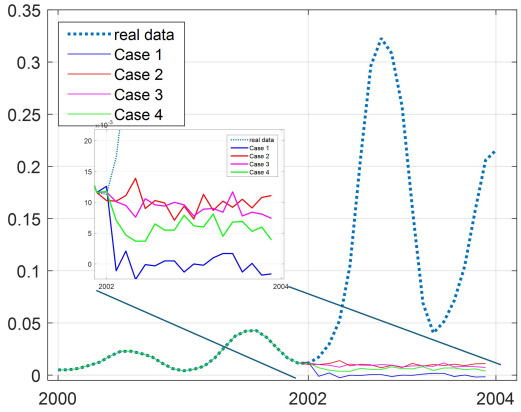

Figure 7: Comparison between real data of Infected patients per million and the corresponding values obtained in Case 1, 2, 3, 4 described in the text.

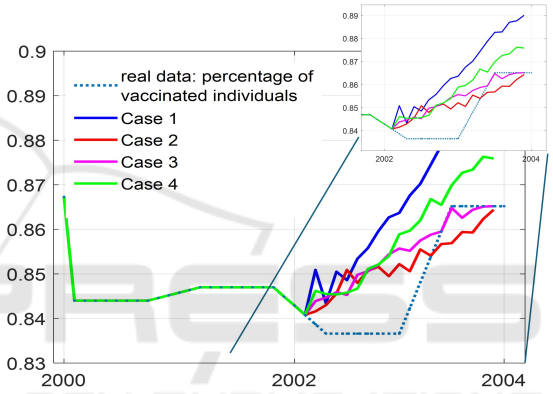

Figure 8: Comparison between real data of percentage of vaccinated patients and the corresponding values obtained in Case 1, 2, 3, 4 described in the text.

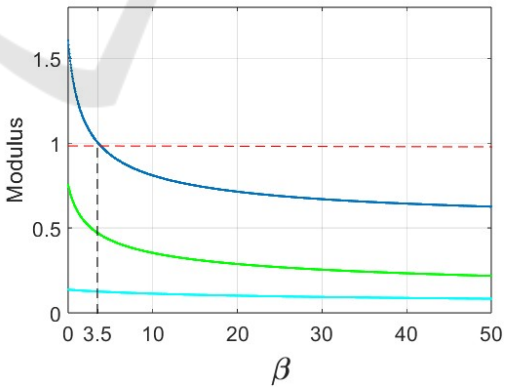

Figure 9: Evolution of the modulus of each root of Δ as penalty parameter β increases. Note that two roots have almost the same modulus and this is the reason for which only three evolutions are evident in the figure.

of infected individuals and of the percentage of vaccinated subjects. It is possible to determine the penalized optimal control (i.e. the vaccination) that reduces the difference between the number of infected

patients and an acceptable threshold, penalising too high values of control actions.

Some general remarks can be summarized:

- the data driven approach considered describes the epidemic spread without using population modeling by means of compartmental description; this allows to avoid identification of parameters, like contact rate, strongly dependent on the specific population;
- the proposed autoregressive approach with exogenous input describes the data by a linear system; this implies that the predictive approach could be limited to few months;
- the ARX model must be identified using historical data; depending on the consistency of the collected data, the identification is more or less reliable;
- in absence of penalization, with the proposed model it is possible to track y^r, with higher control values when the goal to be pursued for infected patients, the reference, is equal to 0;
- with a penalization term by means of the coefficient β, the tracking is in general less efficient, as expected, being the control lower;
- with a strong penalization term the system becomes stable and the control should be lower and more regular. In the proposed analysis, in the predicted evolution this occurs for about one year, as far as the prediction becomes less reliable.

The results, determined on real data, appears promising, showing the effectiveness of the data driven approach, despite some possible criticisms with respect to the ARX model identification.

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REFERENCES

A. Kuddus, M. Mohiuddin and A. Rahman (2021). Mathematical analysis of a measles transmission dynamics model in bangladesh with double dose vaccination. In *Scientific Reports*.

F. Piltan, S. Haghighi and N. Sulaiman (2017). Comparative study between arx and armax system identification. In *I.J. Intelligent Systems and Applications*.

H. Alemneh (2023). Modelling, analysis, and simulation of measles disease transmission dynamics. In *Discrete dynamics in Nature and Society*.

H. W. Berhe and O. D. Makinde (2020). Computational modelling and optimal control of measles epidemic in human population. In *Biosystems*.

M. Horner, S. Pakzad and N. Gulcec (2019). Parameter estimation of autoregressive-exogenous and autoregressive models subject to missing data using expectation maximization. In *Frontiers in Built Environment*. 7.

O.J. Peter, H.S.Panigoro, M.A. Ibrahim, O.M.Otunuga, T.A.Ayoola and A.O. Oladapo (2023). Analysis and dynamics of measles with control strategies: a mathematical modeling approach. In *International Journal of dynamicsa and control*. 7.

P. Di Giamberardino and D. Iacoviello (2019a). Analysis, simulation and control of a new measles epidemic model. In *Proceedings of the 16th International Conference on Informatics in Control, Automation and Robotics*.

P. Di Giamberardino and D. Iacoviello (2019b). Modeling and control of measles epidemic spread with immunodepressed individuals and possible complications. In *Proceedings of the IEEE Conference on Decision and Control*.

P. Di Giamberardino and D. Iacoviello (2020). A new measles epidemic model: analysis, identification and prediction. In *28th Mediterranean Conference on Control and Automation*.

Surveillance atlas of infectious diseases (2024). In *https://atlas.ecdc.europa.eu/public/index.aspx*.

World Health Organization (2024). In *https://www.who.int/*.

Y. Pei, Q.Pei, H. Lee, M. Qiu and Y. Yang (2022). Epidemics in pre-industrial europe: Impacts of climate change, economic well-being, and population. In *Anthropocene*.

Y. Xue, X. Ruan and Y. Xiao (2021). Measles dynamics on network models with optimal control strategies. In *Advances in Continuous and Discrete Models*.