A Comparative Study of SIRD Model Variations: Assessing the Impact of Different Model Structures on Infectious Disease Outcomes and the Proposal of a New Summary Model

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***Abstract*—The purpose of this paper is twofold: first, to compare different variations of the Susceptible-Infected-Recovered-Deaths (SIRD) models, assessing the differences between them and evaluating its comparative performance; second, to present an aggregated new model that integrates the most significant features of the studied models, aiming to be a more efficient model. The selected models were deliberately chosen to exhibit a spectrum of evolutionary complexity, thereby enabling an in-depth exploration of the nuances associated with the transmission dynamics of infectious diseases. The implementation of all models was executed within the *MATLAB* computational environment, ensuring accurate and efficient analysis. The source code is made available in a public repository.**

I. Introduction

In light of the ease of both intracontinental and intercontinental travel and the increasing interconnectedness of countries, the challenge of containing person-to-person pandemic potential diseases has become more complex [1]. The COVID-19 pandemic has emphasized the importance of mathematical modeling for infectious diseases as a means of guiding the development of strategies and policies to contain the spread of these diseases [2]. Thus, the objective of this paper is to compare various mathematical models that attempt to describe the spread of infectious diseases, assess its comparative differences and provide insight to the design of more efficient models in the future.

All of the models described in this paper are variations on the SIR (Susceptible, Infected, Removed) model, which was developed in the early 1900s by Sir Ronald Ross and Sir William Hamer, among others. This model, which is made up of three ordinary differential equations, contributed to the theoretical foundation for public health interventions. However, this simple model is based on several strong assumptions, and it is clear that this model does not account for several disease transitions and states. The model has three states: Susceptible (individuals who can possibly contract the disease), Infected (individuals who have contracted the disease), and Removed (individuals who have died or recovered from the disease)[3].

The five models studied in this paper are adaptations of models presented by [2] and [4], and a sixth model is proposed, integrating the most significant features of the previously studied models. The results are simulated in Matlab, the results are discussed in this paper and the source code is made available in a public repository. The remainder of this paper is organized as follows: section II provides an introduction to the studied models, starting with the simplest model going up to the most complex one; section III described the methodology to implement these models in Matlab, with a strong emphasis on allowing replicability of these procedure from other interested researchers; section IV presents the results and its discussion; section V concludes this paper proposing steps to be taken when designing the next generation of SIR models.

II. Introducing the models

The nomenclature for the variables used in this study can be found in Table I, which is located in Appendix A of this paper. The models and their respective variables are as follows:

1) **SIRD** - The implemented first model was the SIRD model, which takes into account four states: Susceptible (S), Infected (I), Recovered (R), and Deaths (D). Proposed by [4], this is the most basic model and it considers stages where individuals who can get the disease, those who have contracted it, those who have recovered from it, and those who have died due to the disease.
   Figure 1 depicts a schematic of this model, whereas equations 1 - 4 describe the relevant differential equations. Equation 1 defines the variation of the number of susceptible individuals over time. This is calculated by multiplying the number of susceptible individuals by the number of infected individuals and by a factor -α, to be adjusted in view of different disease scenarios. Equation 2 defines the variation of the number of infected individuals over time. Similarly to equation

1, this is achieved applying specific factors to parcels representing the number of individuals that contribute to this particular stage in the model depicted in figure 1. Equations 3 and 4 are quite simple and self explanatory.

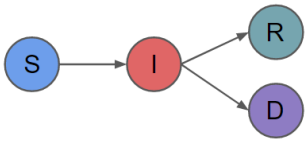

Fig. 1. SIRD model schematic

$$\frac{dS}{dt} = -\alpha SI \tag{1}$$

$$\frac{dI}{dt} = \alpha SI - \delta I - \gamma I \tag{2}$$

$$\frac{dR}{dt} = \delta I \tag{3}$$

$$\frac{dD}{dt} = \gamma I \tag{4}$$

Is it interesting to see that

$$\frac{dI}{dt} = -\frac{dS}{dt} - \frac{dR}{dt} - \frac{dD}{dt} \tag{5}$$

and although this may seem to partially contradict what can be observed in figure 1, because of the negative sign in first parcel, we must note that in this model, the variation on the number of Susceptible individuals is always negative or zero, this is to say, that if the population remains constant (a common assumption for all models), the number of Susceptible individuals yesterday is always bigger (or equal) than the number of Susceptible individuals today, as they keep getting infected at a rate α, and the recovered population is expected to become immune to this disease.

2) **SIRDS** - The next model presented is an adaptation of the SIRD model, also presented in [4]. This model introduces the possibility of individuals who have recovered from the disease to become susceptible to it again, *i.e.* contracting the disease does not guarantee immunity to it. Like the previous model, this model consists of four states: Susceptible (S), Infected (I), Recovered (R), and Deaths (D). The four states can be understood as follows: Susceptible individuals who can contract the disease, Infected individuals who have contracted the disease, Recovered individuals, who have recovered from the disease but can potentially contract it again and thus return to the Susceptible state, and Deaths, which represent individuals who have died due to the disease.
Figure 2 presents a diagram representing this model, and the corresponding differential equations are represented by equations 6 - 9.

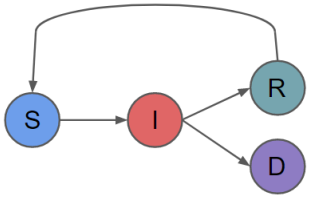

Fig. 2. SIRDS model schematic

$$\frac{dS}{dt} = -\alpha SI + \omega R \tag{6}$$

$$\frac{dI}{dt} = \alpha SI - \delta I - \gamma I \tag{7}$$

$$\frac{dR}{dt} = \delta I - \omega R \tag{8}$$

$$\frac{dD}{dt} = \gamma I \tag{9}$$

Although equation 7 is exactly the same as equation 2, and equation 9 is also equal to equation 4, we chose to replicate these as to allow a better reading and understanding of the models. We note that when compared to the SIRD model, only equations 6 and 8 change, as these consider the flow of individuals from the Recovered to the Susceptible stages. Similar rationale is applicable to the following models, which build on these and consequently, are supported by a set of equations that results from the modified equations of this model.

3) **SEIRDS** - This model, proposed by [2], takes into consideration the fact that an individual must first be exposed to the disease before being considered infected. The model considers five states: Susceptible (S), Exposed (E), Infected (I), Recovered (R), and Deaths (D). The five states can be explained as follows: Susceptible individuals who can contract the disease, individuals who have been exposed to the disease but have not yet contracted it, Infected individuals who have contracted the disease, Recovered individuals who have recovered from the disease, and individuals who have died due to the disease.
Figure 3 presents a diagram representing this model, and the corresponding differential equations are represented by equations 10 – 14.

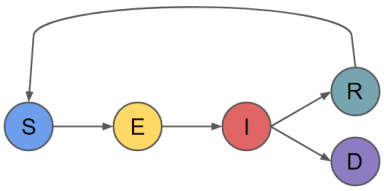

Fig. 3. SEIRDS model schematic.

$$\frac{dS}{dt} = -\alpha SI - \phi SE + \omega R \tag{10}$$

$$\frac{dE}{dt} = \alpha SI + \phi SE - \nu E \tag{11}$$

$$\frac{dI}{dt} = \nu E - \delta I - \gamma I \tag{12}$$

$$\frac{dR}{dt} = \delta I - \omega R \tag{13}$$

$$\frac{dD}{dt} = \gamma I \tag{14}$$

Again, comparing the SEIRDS model with the SIRDS model, we have a new equation representing the number of individuals in the Exposed state, and the equations representing the Susceptible and Infected states were adapted accordingly by the addition of the adequate terms. The new state of Exposed is calculated by adding the number of individuals that transition from the Susceptible state at a rate α, and the number of individuals who become infected at a rate ν. Yet, this state also considers that an individual can remain in the Exposed state for an indefinite amount of time, being this number defined as the product of the number of Exposed individuals by the number of Susceptible individuals by the factor ϕ.

4) **SIIIRRRDS** - This model [4] incorporates multiple severity levels of symptoms experienced by infected individuals. This implies that there will be three levels of infection and three levels of recovery. This is an arbitrary number of levels, and of course, this model should be adapted to the particular disease it aims to model. In this discussion, the authors categorized these three levels as Infected Asymptomatic, Infected with mild symptoms and Infected with severe symptoms. The need to detail different levels of infection is related to the need to account for different rates of disease evolution, as this level of detail allows for a better definition of the ratios that contribute to the next state in the model, thus rendering it more realistic.
Unlike the previous model, this model does not account for the Exposed state, which will be reintroduced in the sixth and final model. The current model comprises eight states: Susceptible (S), Infected Asymptomatic (I_A), Infected with Mild symptoms (I_M), Infected with Severe symptoms (I_S), Recovered from Asymptomatic disease (R_A), Recovered from Mild symptoms (R_M), Recovered from Severe symptoms (R_S), and Deaths (D). These eight states can be explained by individuals who are susceptible to contracting the disease, those who have contracted the disease being asymptomatic or having mild or severe symptoms, those who have recovered from the disease in the same three possible ways, and those who have died. Only individuals who contracted the disease and suffered from severe symptoms were considered eligible to move to Deaths state. The individuals in all three states of Recovered can become Susceptible.
Figure 4 presents a schematic of this model, and the differential equations representing this model are expressed in equations 15 – 22.

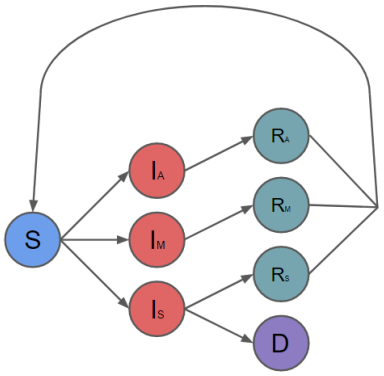

Fig. 4. SIIIRRRDS model schematic

$$\frac{dS}{dt} = -(\alpha_A + \alpha_M + \alpha_S)SI + \omega_A R_A + \omega_M R_M + \omega_S R_S \tag{15}$$

$$\frac{dI_A}{dt} = \alpha_A SI - \delta_A I_A \tag{16}$$

$$\frac{dI_M}{dt} = \alpha_M SI - \delta_M I_M \tag{17}$$

$$\frac{dI_S}{dt} = \alpha_S SI - \delta_S I_S - \gamma I_S \tag{18}$$

$$\frac{dR_A}{dt} = \delta_A I_A - \omega_A R_A \tag{19}$$

$$\frac{dR_M}{dt} = \delta_M I_M - \omega_M R_M \tag{20}$$

$$\frac{dR_S}{dt} = \delta_S I_S - \omega_S R_S \tag{21}$$

$$\frac{dD}{dt} = \gamma I_S \tag{22}$$

where $I = I_A + I_M + I_S$.

5) **SPIIIRRRDS** - In this model [4], a new state is added: the Protected state. As a result, there are now nine possible states: Susceptible (S), Protected (P), Infected Asymptomatic (I_A), Infected with Mild symptoms (I_M), Infected with Severe symptoms (I_S), Recovered from Asymptomatic disease (R_A), Recovered from Mild symptoms (R_M), Recovered from Severe symptoms (R_S), and Deaths (D). These nine states can be explained by individuals who are susceptible to contracting the disease, individuals who have been vaccinated and are therefore protected, those who have contracted the

disease being asymptomatic or having mild or severe symptoms, those who have recovered from the disease in the same three possible ways, and those who have died. Only individuals who contracted the disease and suffered from severe symptoms were considered eligible to move to the Deaths state. Individuals in all three states of Recovered can become Susceptible again, and even those in the Protected state can be considered Susceptible or fall into any of the three states of Infected. Figure 5 presents a schematic of this model, and the differential equations representing this model are expressed in equations 23 - 31.

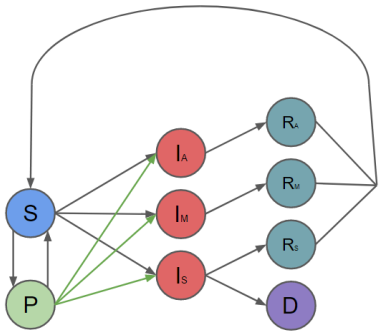

Fig. 5. SPIIIRRRDS model schematic

$$\frac{dS}{dt} = -(\alpha_A + \alpha_M + \alpha_S)SI + \omega_A R_A + \omega_M R_M + \omega_S R_S + \omega_P P - \tau S \quad (23)$$

$$\frac{dI_A}{dt} = \alpha_A SI + \lambda_A PI - \delta_A I_A \quad (24)$$

$$\frac{dI_M}{dt} = \alpha_M SI + \lambda_M PI - \delta_M I_M \quad (25)$$

$$\frac{dI_S}{dt} = \alpha_S SI + \lambda_S PI - \delta_S I_S - \gamma I_S \quad (26)$$

$$\frac{dR_A}{dt} = \delta_A I_A - \omega_A R_A \quad (27)$$

$$\frac{dR_M}{dt} = \delta_M I_M - \omega_M R_M \quad (28)$$

$$\frac{dR_S}{dt} = \delta_S I_S - \omega_S R_S \quad (29)$$

$$\frac{dD}{dt} = \gamma I_S \quad (30)$$

$$\frac{dP}{dt} = \tau S - \omega_P P - (\lambda_A + \lambda_M + \lambda_S)PI \quad (31)$$

where $I = I_A + I_M + I_S$.

6) **SPEEIIIRRRDS** - In this final model, a joint consideration of the previous is now proposed, and two more possible states have been added: non vaccinated Exposed and vaccinated Exposed, resulting in a total of eleven possible states: Susceptible (S), Protected (P), not vaccinated Exposed (E_S), vaccinated Exposed (E_P), Infected Asymptomatic (I_A), Infected with Mild symptoms (I_M), Infected with Severe symptoms (I_S), Recovered from Asymptomatic disease (R_A), Recovered from Mild symptoms (R_M), Recovered from Severe symptoms (R_S), and Deaths (D). These states can be explained by individuals who can contract the disease, those who have been vaccinated and are therefore protected, those who were exposed to the disease from the Susceptible group, those who were exposed to the disease from the Protected group, those who have contracted the disease being asymptomatic or having mild or severe symptoms, those who have recovered from the disease in the same three possible ways, and those who have died. Only individuals who contracted the disease and suffered from severe symptoms were considered eligible to move to the Deaths state. Individuals in all three states of Recovered can become Susceptible again, and even someone exposed from the Protected state can contract the disease. The individuals from the Protected state are eligible to move to the Susceptible state again.
Figure 6 presents a schematic of this model, and the differential equations representing this model are expressed in equations 32 - 42.

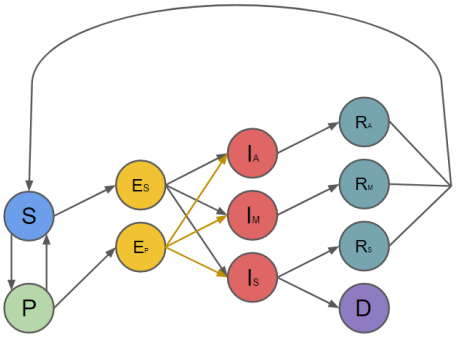

Fig. 6. SPEEIIIRRRDS model schematic

$$\frac{dS}{dt} = -(\alpha_A + \alpha_M + \alpha_S)SI + \omega_A R_A + \omega_M R_M + \omega_S R_S + \omega_P P - \tau S - \phi E_S S \quad (32)$$

$$\frac{dE_S}{dt} = (\alpha_A + \alpha_M + \alpha_S)SI + \phi E_S S - \nu_S E_S \quad (33)$$

$$\frac{dE_P}{dt} = (\lambda_A + \lambda_M + \lambda_S)IP + \phi E_P P - \nu_P E_P \quad (34)$$

$$\frac{dI_A}{dt} = \nu_S \sigma_A E_S + \nu_P \sigma_A E_P - \delta_A I_A \quad (35)$$

$$\frac{dI_M}{dt} = \nu_S \sigma_M E_S + \nu_P \sigma_{M[P]} E_P - \delta_M I_M \quad (36)$$

$$\frac{dI_S}{dt} = \nu_S \sigma_S E_S + \nu_P \sigma_{S[P]} E_P - \delta_S I_S - \gamma I_S \quad (37)$$

$$\frac{dR_A}{dt} = \delta_A I_A - \omega_A R_A \quad (38)$$

$$\frac{dR_M}{dt} = \delta_M I_M - \omega_M R_M \quad (39)$$

$$\frac{dR_S}{dt} = \delta_S I_S - \omega_S R_S \quad (40)$$

$$\frac{dD}{dt} = \gamma I_S \quad (41)$$

$$\frac{dP}{dt} = \tau S - \omega_P P - (\lambda_A + \lambda_M + \lambda_S) PI - \phi E_P P \quad (42)$$

where $I = I_A + I_M + I_S$.

The definition of states as Vaccinated does not imply that a process of vaccination took place, but rather aims at defining a state where immunity has been achieved in a preventive manner, rather than in a infectious manner.

The equations in these models should now have become self-explantory, and in general they account for all the different contributions made to and from preceding and succeding states in the respective model. Each of these contributions is weighted by a specific factor, described in Table I.

III. Methodology

To implement the models described in the previous section, the ***MATLAB*** software was employed. Six functions were developed, each corresponding to a distinct model, where each one receive the adequate variables to the model and returned the time vector and a matrix, where each line corresponds to one compartment of the model and the columns represent the time. The functions were named following the convention `MSM_` plus the model's name. Within each function, it was defined an anonymous function, *i.e.*, a function that is associated with a variable of data type `function_handle`, following which, the `ode45` function was utilized. This function requires three input arguments: `tspan`, `odefun`, and `x0`. The `tspan` argument is a vector with two elements that represent the lower and upper bounds of the integration interval. The `odefun` argument is the `function_handle` for the differential equations system to be solved, while "x0" is the initial condition vector of the same length as "odefun".

To facilitate the usage of the functions described above, a script named `MSM_Main` was developed. Firstly, in this script, all the variables used were initialized as shown in Table II, which is located in Appendix B of this paper. Afterwards, the models were simulated using their corresponding function. The output of each model was then represented in a graphic using the `plot` function in ***MATLAB***. The graphical representations can be found in Figures 7 – 12, which are presented in the next section.

All the files mentioned in this section, and used in this paper can be found in this repository, https://github.com/TiagoAMMSilva/SIRDModel.

IV. Results and Discussion

The obtained graphics with the implemented models are listed below (Figures 7 - 12). The graphics show the percentage of population in each compartment at a given time.

As expected, when adding new compartments, the behavior of the already present states changes. For example, introducing the possibility of a recovered individual becoming susceptible again adds a new dynamic over time. While the first model (SIRD, Fig. 7) eventually remained constant after an initial period of variation, the second model (SIRDS, Fig. 8) continues to change constantly, which can be considered a better approximation to reality, especially for diseases like COVID-19 that have a considerable recurrence rate of around 15% [5].

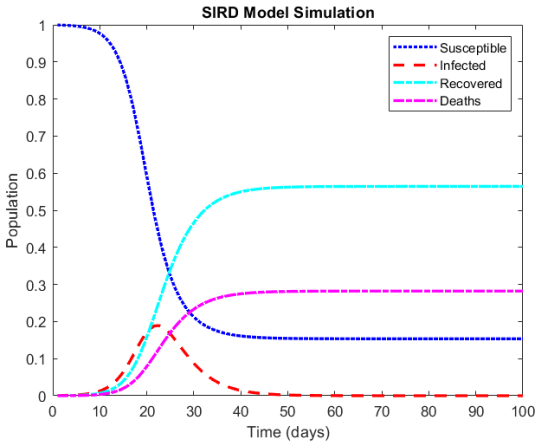

Fig. 7. Graphical representation of the SIRD model

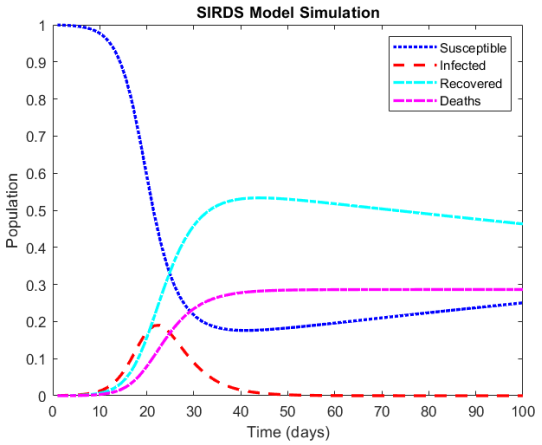

Fig. 8. Graphical representation of the SIRDS model

The addition of the Exposed state (SEIRDS, Fig. 9) resulted in an earlier and more abrupt peak of infection, since the interactions between people are more realistic, accelerating the infection process. It was thought to be more realistic when considering the Exposed state, since not everyone who comes into contact with the disease ends up contracting it.

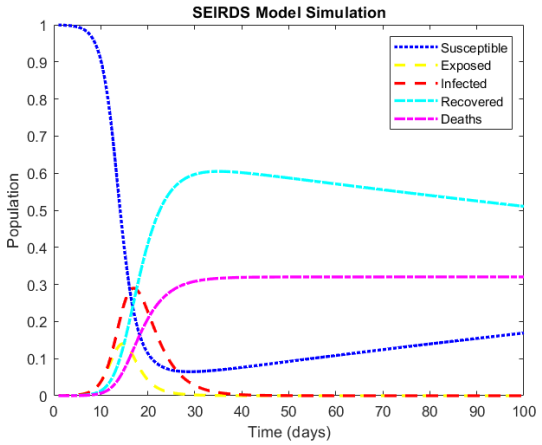

Fig. 9. Graphical representation of the SEIRDS model

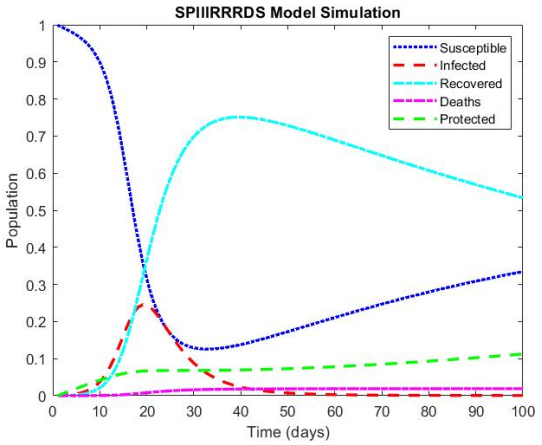

Fig. 11. Graphical representation of the SPIIIRRRDS model

Up until now, the models have considered an excessively large percentage of the population in the Death state. This is because it assumes that anyone infected may die. However, this does not accurately represent reality. Considering various levels of disease severity helps to overcome this assumption, as seen in the change in deaths from the initial graphs to Figures 10 - 12. Nevertheless, assuming that only people with severe symptoms may die could be an exaggeration, but overcoming this would lead the model to even more complicated levels not explored within the scope of this article. One possible solution would be to consider the transition between severity states of the disease.

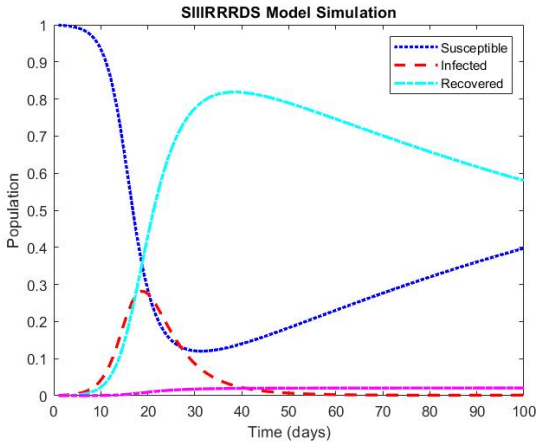

Fig. 10. Graphical representation of the SIIIRRRDS model

The number of infected people decreased as a result of the Protected state being added to the SPIIIRRRDS model (Fig. 11), both in terms of the peak's size and its temporal delay.

All interactions between the variables are examined in the final model (SPEEIIIRRRDS, Fig. 12), since all of the considered variables are present. One of the most notable interactions, in addition to those already mentioned, is the one between exposed and protected individuals. A person may eventually be unable to receive the vaccine after being exposed to the disease, lowering the population's overall vaccination rate and, thus, the efficiency of the protection. It would be important to take into account real-world data and directly compare the produced models in order to determine whether this alteration is more realistic or not.

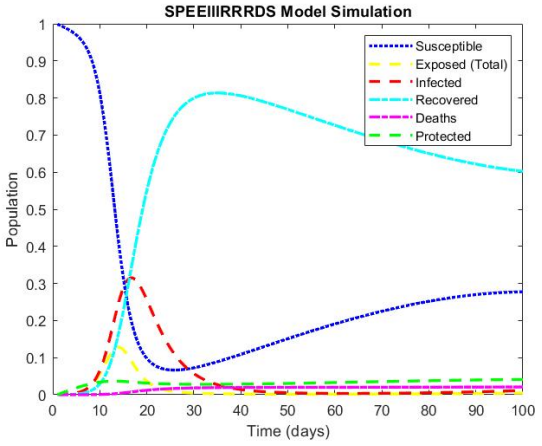

Fig. 12. Graphical representation of the SPEEIIIRRRDS model

The complexity of the models brings greater specificity for a particular target disease, which can be seen as a great advantage for better understanding its behavior and tracking its progression. However, this specificity makes the model less useful for other diseases, as several assumptions are made throughout its development that may not be compatible with the behavior of other diseases. In the transition from the first to the second model, it was considered that the disease can reoccur, and thus it would be unthinkable to use the following models for a disease that can only infect each individual once. Additionally, it is assumed that the rates remain constant, when in reality variations over time have been observed, frequently as a result of changes in social habits, weather

effects, social events, and so on. Also, but not completely different, something very common during the recent COVID-19 pandemic was the emergence of new variants with very different rates of mortality, infection, among others. It is probable that the emergence of new disease variants occurs in other types of diseases, but also possibly, not as well researched as the recent COVID-19 pandemic.

Despite this study considering several combinations of models with a logical stratification of complexity, there are several untested combinations, such as the effect of multiple vaccines or vaccines with multiple doses, which could arguably have some impact on the final results. By definition, modeling all possibilities is unrealistic, as it would not be imaginable or computable with current knowledge and equipment. On the contrary, and because of this, it is necessary to create a consensus on modeling each type of disease in order to accelerate the response to alerts caused by pandemics such as COVID-19.

V. Conclusion

In hindsight, it is evident that utilizing models such as those used in this paper is an extremely useful method to track the progression of infectious diseases in society and predict various outcomes. The role of prediction is extremely important because it allows authorities to assess the benefit (or not) of a given health policy, enabling measures to be taken to prevent both pandemic and endemic emergencies. Furthermore, it can be concluded that even more comprehensive models that closely resemble reality may be beneficial. Hence, testing models with different numbers of states and transitions between them is imperative. The utilization of *MATLAB* as the implementation platform ensures the accuracy and efficiency of the analysis, paving the way for further advancements in disease modeling and control strategies.

Declarations

The authors wish to declare that the numerical values utilized for the variables under investigation were partially sourced from the scholarly article referenced as [4], while the remaining values were estimated by the authors themselves. These values are described in the Matlab source code, available at https://github.com/TiagoAMMSilva/SIRDModel.

Furthermore, the authors would like to state that both Tiago A. M. M. da Silva and Gonçalo M. Rodrigues have contributed equally to this paper.

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APPENDIX A

TABLE I
DESCRIPTION OF THE VARIABLES FROM EQUATIONS 1-42

Notation	Description
$\alpha \rightarrow$	Infection Rate
$\delta \rightarrow$	Recovery Rate
$\gamma \rightarrow$	Mortality Rate
$\omega \rightarrow$	Immunity loss Rate
$\phi \rightarrow$	Rate of Exposition to the disease
$\nu \rightarrow$	Rate of infection after being exposed
$\alpha_A \rightarrow$	Asymptomatic Infection Rate
$\alpha_M \rightarrow$	Mild symptoms Infection Rate
$\alpha_S \rightarrow$	Severe symptoms Infection Rate
$\alpha_P \rightarrow$	Protected population Infection Rate
$\delta_A \rightarrow$	Asymptomatic Recovery Rate
$\delta_M \rightarrow$	Mild symptoms Recovery Rate
$\delta_S \rightarrow$	Severe symptoms Recovery Rate
$\omega_A \rightarrow$	Immunity loss Rate (Asymptomatic
$\omega_M \rightarrow$	Immunity loss Rate (Mild symptoms)
$\omega_S \rightarrow$	Immunity loss Rate (Severe symptoms)
$\omega_P \rightarrow$	Protection loss Rate
$\nu_S \rightarrow$	Rate of infection after being exposed (Susceptible)
$\nu_P \rightarrow$	Rate of infection after being exposed (Protected)
$\sigma_A \rightarrow$	Portion of Infected that are Asymptomatic (From both vaccinated and not vaccinated Exposed)
$\sigma_M \rightarrow$	Portion of Infected that have Mild symptoms (From non vaccinated Exposed)
$\sigma_S \rightarrow$	Portion of Infected that have Severe symptoms (From non vaccinated Exposed)
$\sigma_{M[P]} \rightarrow$	Portion of Infected that have Mild symptoms (From vaccinated Exposed)
$\sigma_{S[P]} \rightarrow$	Portion of Infected that have Severe symptoms (From vaccinated Exposed)
$\tau \rightarrow$	Vaccination Rate
$\lambda_A \rightarrow$	Infection Rate from Protected population (Asymptomatic)
$\lambda_M \rightarrow$	Infection Rate from Protected population (Mild)
$\lambda_S \rightarrow$	Infection Rate from Protected population (Severe)

APPENDIX B

TABLE II
THE VALUE OF THE VARIABLES FROM EQUATIONS 1 - 42. FOR THE MODELS THAT CONSIDER MORE THAN ONE STATE OF INFECTED THE INITIAL VALUE FOR INDIVIDUAL WITH MILD OR SEVERE SYMPTOMS WERE 1 FOR EACH.

Notation	Description
$\alpha \rightarrow$	0.664
$\delta \rightarrow$	0.2
$\gamma \rightarrow$	0.1
$\omega \rightarrow$	0.0028
$\phi \rightarrow$	0.7
$\nu \rightarrow$	0.83
$\alpha_A \rightarrow$	0.1992
$\alpha_M \rightarrow$	0.4316
$\alpha_S \rightarrow$	0.0332
$\alpha_P \rightarrow$	0.0373
$\delta_A \rightarrow$	0.333
$\delta_M \rightarrow$	0.2
$\delta_S \rightarrow$	0.1429
$\omega_A \rightarrow$	0.0111
$\omega_M \rightarrow$	0.0056
$\omega_S \rightarrow$	0.0028
$\omega_P \rightarrow$	0.0056
$\nu_S \rightarrow$	0.83
$\nu_P \rightarrow$	0.031
$\sigma_A \rightarrow$	0.3
$\sigma_M \rightarrow$	0.65
$\sigma_S \rightarrow$	0.05
$\sigma_{M[P]} \rightarrow$	0.69
$\sigma_{S[P]} \rightarrow$	0.01
$\tau \rightarrow$	0.005
$\lambda_A \rightarrow$	0.0112
$\lambda_M \rightarrow$	0.0257
$\lambda_S \rightarrow$	0.0004
Total Population (N)$\rightarrow$	4000
Initial Number of Infected People (a)$\rightarrow$	2
Time Interval $\rightarrow$	[0; 100]