ISSN 2007-9737

A Computational Approach to Finding SEIR Model Parameters that Best Explain Infected and Recovered Time Series for SARS-CoV 2

Jairo Rojas-Delgado[1], Mario Pupo-Meriño[2], Jorge Gulín-González[1]

[1] Universidad de las Ciencias Informáticas,
Centro de Estudios de Matemática Computacional (CEMC),
Cuba

[3] Universidad de las Ciencias Informáticas,
Departamento de Bioinformática,
Cuba

jrojasdelgado@bcamath.org, {mpupom, gulinj}@uci.cu

Abstract. The novel SARS-CoV 2 coronavirus has grown to become a global pandemic. Since then, several approaches have been adopted and developed to provide insights into epidemic origins, worldwide dispersal and epidemiological history. The Susceptible, Exposed, Infected and Recovered (SEIR) models are among the widely used approaches to study the further progression of the pandemic. However, finding such model parameters remains a difficult task, especially in small geographical areas where details of the initial compartments and the model parameters deviates from global distributions. The main result of our paper is a meta-heuristic approach to find SEIR model parameters that best explains the infected time series. Our approach, allows studying different future scenarios considering not only the most likely future, but a set of possible SEIR parameters that explains current epidemic trends. We show that there are several possible parameters sets of such models able to explain current epidemic trends and by studding them is possible to obtain insights into the future possible outcomes.

Keywords. SARS-CoV 2, SEIR, meta-heuristic.

1 Introduction

Since the detection of the novel coronavirus SARS-CoV 2 we have seen it grow to become a pandemic [7]. Studding epidemic origins, worldwide dispersal and epidemiological history is critical for decision making and issuing accurate information to the population.

SEIR models are among the widely used approaches to study infectious diseases [1, 17, 20]. SEIR models and its several variations, have many parameters that usually depends on geographical distributions, initial population and the specific diseases under study.

The combination of dynamical modelling with substantial fluctuations calls for data assimilation methods for parameter inference [4]. Hence, fitting the SEIR model parameters is a difficult task and at the same time of paramount importance.

Several recent studies aim to include restriction policies in the modelling SARS-CoV 2 epidemic. In [4], the authors estimate the per-capita transmission rate of a stochastic SEIR model based on available data. The per-capita transmission rate is considered a function of time that accounts for the application of restriction policies. This work only considers the best fitting parameters and neglects other possible explanations of currently observed data.

Other works have successfully modelled the application of restriction policies in a different way, for example, by including a compartment for patients in quarantine [21].

Other introduced models do not consider the application of restriction policies at all.

doi: 10.13053/CyS-25-2-3462

For example, the authors of [13] use a machine learning approach as an alternative to SEIR models producing accurate results as long as no significant interruption occurs, such as, the application restriction policies. It is worth noticing that the accuracy of such models is evaluated in a time interval of nine days, hence, no empirical results suggest long time accuracy.

From a different perspective, some authors have successfully used meta-heuristic algorithms to fit SEIR model parameters. In a work by Mulder, the Simulated Annealing algorithm is used to fit SEIR model parameters using active infected and recovered time series [12]. It only considers the best fitting parameters and does not consider other possible explanations of currently observed data and does not study the effect of restriction policies in the epidemic development. In [14], the Particle Swarm Optimization algorithm is used to fit SEIR model parameters. This work does not address the possibility of multiple explanations of currently observed data nor study the effect of restriction policies in the epidemic development.

Recently, Rajiv Chowdhury et al. conducted a scenario analysis of SARS-CoV 2 coronavirus in more than 16 countries [2]. They used the most up-to-date SEIR transmission parameters to construct their adaptive models from previous works, hence, analyses were based on several transmission parameter assumptions. In such work, authors assumed a constant transmission rate during each modeled cycle, which is likely to vary by a population's adherence to the restriction policies and a mix of specific measures put in place.

In this paper, we introduce an approach to find SEIR parameters that best explains the observed infected and recovered time series. Here, we refer to observed infected time series to the times series of active infected patients, that is, patients that are infected not yet recovered. In addition, we refer to observed recovered time series to the time series of patients that were infected at some point but are currently recovered.

We define a search space containing SEIR parameters and a fitness function that accounts for the error between the SEIR model forecasting and the observed times series: infected and recovered.

We provide intuition and previous experimental results behind our hypothesis that such fitness function is multi-modal with several local minima that accounts for different outcomes of the epidemic in the future. Here we use the terms SEIR model parameters, local minima and future possible outcomes indistinctly.

Our goal is not to find the global optimum of the fitness function, but to locate the local minima in the search space. In order to do so, we use a meta-heuristic optimization method named Firefly Algorithm (FA) [19]. Inspired in the social behavior of fireflies, FA keeps a set of solutions during the course of optimization. Previous, experimental results suggest that the solutions optimized by FA converges in clusters around local minima [16].

Here we focus on SARS-CoV 2 data from Cuba, Spain and Italy. Results show the formation of clusters of possible SEIR parameters around local minima. We sample the four best possible local minima according to its fitness value (how much each local minima fits current observed data) and its diversity (how much different is each local minima from the others). We ended up with four groups of SEIR model parameter sets that describes possible outcomes in the future and can be used by epidemiological specialists to take decisions and study the statistical distributions of the SEIR parameters.

Different to other works, our approach considers the application of restriction policies to reduce the per-capita transmission rate in different scenarios. The rate at which the restriction policies affect the model parameters are directly learned from the data without relying in parameter distributions from previous works. Secondly, as we use a meta-heuristic approach, the way we fit SEIR model parameters is expected to be robust to noise in the active infected and recovered time series. Finally, we are not considering a single best fitting of the SEIR model parameters, but several of them, which should provide wider insights on the epidemic development.

The organization of this paper is as follow: Section 2 formally introduces our approach for finding SEIR model parameters and describes the SEIR model used to fit current observed data and the FA meta-heuristic algorithm .

Section 3 shows the results of finding local minima in the SEIR parameter's space and the parameter distributions for the possible outcomes of the pandemic in the future. We discuss limitations and advantages of the introduced approach in Section 4.

2 Methods

In this section we introduce our approach for searching SEIR model parameters based on current active infected and recovered time series. In addition, we describe the SEIR model used to study the SARS-CoV 2 epidemic and for completeness we also describe FA optimization algorithm. Throughout this article we use x for scalars, $\boldsymbol{x}$ for vectors and X for sets.

2.1 Searching SEIR Model Parameters

Let $\boldsymbol{\Delta}_I, \boldsymbol{\Delta}_R \in \Delta \subset \mathbb{R}^d$ be the current observed infected and recovered times series for d days and $\boldsymbol{w} = (w_1, w_2, ..., w_n)$ be a vector where w_i are the parameters of a SEIR model such as $\boldsymbol{w} \in \Omega$, usually $\Omega \subset \mathbb{R}^n$. Considering $g_I : \Omega \to \Delta$ a function that maps a given set of SEIR model parameters and its corresponding infected time series and $g_R : \Omega \to \Delta$ a function that maps a given set of SEIR model parameters and its corresponding recovered time series we define $f : \Omega \times \Delta \times \Delta \to \mathbb{R}$ as a function that evaluates the quality of a SEIR model parameter vector defined as:

$$f(\boldsymbol{w}, \boldsymbol{\Delta}_I, \boldsymbol{\Delta}_R) = \frac{||(g_I(\boldsymbol{w}) - \boldsymbol{\Delta}_I||_2^2}{d\sigma_I^2} + \frac{||g_R(\boldsymbol{w}) - \boldsymbol{\Delta}_R||_2^2}{d\sigma_R^2}, \tag{1}$$

where $||.||_2$ is the L^2-norm and σ_I^2 and σ_R^2 are the variance of $\boldsymbol{\Delta}_I$ and $\boldsymbol{\Delta}_R$ respectively. Notice that we use the NMSE between the current active infected time series and SEIR predicted infected times series and also the NMSE between the current recovered time series and SEIR predicted recovered times series. Here we are actually combining two goals: to fit infected time series and to fit recovered time series, hence, we use NMSE to avoid one goal dominate over the other.

A valid option here would be to use multi-objective optimization and should be studied in the future. We are interesting in solving the following optimization problem:

$$\boldsymbol{w} = \operatorname*{argmin}_{\boldsymbol{w} \in \Omega} f(\boldsymbol{w}, \boldsymbol{\Delta}_I, \boldsymbol{\Delta}_R). \tag{2}$$

Here we will only consider the case of $\Omega \in \mathbb{R}^n$, hence, we are dealing with a continuous optimization problem. In addition, we will consider several restrictions that affects the SEIR model parameters w_i that are dependent on the specific model variant and are described in section 2.2. Regarding the fitness function, we can expect that two different vectors of model parameters w_i and w_j are able to simultaneously explain the current observations, that is for $t < d$. However, for $t > d$ the two parameter vectors can indeed produce different future outcomes. The intuition behind this idea suggest that we can expect several SEIR parameters to have the same fitness value, producing a multi-modal landscape with several local minima. Recent experimental results provide evidence of this [6]. However, we did not perform any theoretical level analysis of this fitness function to provide a formal proof.

Finding the local minima in the SEIR parameter space, as defined in equation 2, can be rephrased as finding the most likely outcomes in the future that explain current observations. Algorithm 1 clarifies the steeps proposed in the present work to search and summarize such outcomes.

In step 1, we initialize the set of possible future outcomes T as empty. In step 3, we search for local minima in the SEIR parameter space and after this we create groups of similar local minima obtaining a representative sampling in step 4. We select the b best local minima based on its fitness value and diversity, storing them in the set of possible future outcomes T, steps 5-6. As the search of local minima is a non-deterministic stochastic process, we repeat the previously described steps a number k times. In step 8, we create b groups of local minima from T. In the following subsections we describe Algorithm 1 in detail.

2.1.1 Finding Local Minima of Fitness Function

In step 3, we must find the local minima of the fitness function. Considering the scenario

Algorithm 1 Searching SEIR model parameters that best explain observed data

```
Require: Currently observed times series: $\mathbf{\Delta}_I, \mathbf{\Delta}_R$.
Require: Initial susceptible and infected population.
Ensure: SEIR parameter distributions of future outcomes.
1: Set $T = \{\}$
2: for $i = 1$ to $k$ do
3:     Find local minima of fitness function.
4:     Create groups of similar local minima.
5:     Select $b$ local minima based on its fitness value and diversity.
6:     Store the $b$ best local minima in $T$
7: end for
8: Create $b$ groups of local minima from $T$.
9: Provide SEIR parameter distributions for each of the $b$ groups.
```

of a multi-modal fitness function, gradient based optimization methods are discouraged as those are usually intended for local optimization [3], although, a local search method with restart may be an option here. Therefore, we focus in global optimization methods and specifically in meta-heuristic methods.

Meta-heuristic are approximate, stochastic search algorithms. Most population-based-meta-heuristics[1] have been designed for global optimization. Meta-heuristic algorithms do not provide any warranty of convergence or optimality. However, we must consider that the current observed times series are actually a noisy measure of the real number of infected or recovered cases (for example: there are undetected cases). In such scenario, looking for an exact solution may be misleading.

Currently, there are several global optimization meta-heuristic algorithms based in populations in the literature. The FA algorithm is a nature inspired meta-heuristic that is based in populations and share some features with the more widely known Particle Swarm Optimization (PSO) meta-heuristic. In PSO, each solution explores the search space considering the position of the best solution found so far and the best previous position of each solution. However, in FA each solution explores the search space considering all solutions that have a better fitness value. This particular feature allows FA optimized solutions to converge in clusters near the local minima and not only in a single, possibly global optimum. For completeness, we provide a detailed description of FA algorithm in section 2.3.

2.1.2 Creating Groups of Similar Local Minima

In step 4, we take all the solutions optimized by FA algorithm, and remove redundant and very similar solutions that may have converged nearby. By doing this, we expect to reduce the number of local minima while keeping a representative sampling of the search space. In addition, having repeated or very similar local minima may artificially alter the statistical distributions of the SEIR model parameters. We propose to conduct an unsupervised clustering analysis and to take the final cluster centroids as future outcomes.

Here we face two possible approaches: hierarchical or agglomerative clustering analysis. Hierarchical analysis has the advantage of not requiring an initial pre-defined number of clusters to perform the analysis as opposed to agglomerative clustering. However, at the end in both cases we must manually select the number of clusters that better describe the data based in some inter/intra cluster measure. Here, we propose to consider K-Means algorithm to perform the clustering analysis and the Silhouette Coefficient (SC) to select the final number of clusters [22].

[1] We use population-based-meta-heuristics to refer to meta-heuristic algorithms that keep a set of solutions during the course of optimization. Do not confuse the term population, as in population-based meta-heuristic, with human population.

2.1.3 Selecting the Best Local Minima based on its Fitness Value and Diversity

In step 5, we select future outcomes based on its fitness function and diversity, that is, the cluster centroids provided by the K-Means algorithm. First, the selection is based in how well such centroids, that represent sets of parameters of the SEIR model, explains the current number of infected and recovered cases. The fitness function, as defined in equation 1, models how well a given set of SEIR model parameters fit current observed data.

Secondly, we want to select centroids that are different from each other, for example, two centroids may have a similar fitness value but are distant in the search space. This will allow to examine different future outcomes of the epidemic outbreak that may explain current trends. Given a sequence of centroids provided by the K-Means algorithm $\boldsymbol{w}_1, \boldsymbol{w}_2, ..., \boldsymbol{w}_r$, Algorithm 2 describes how the best local minima are selected based on its fitness value and diversity.

Algorithm 2 Selecting best local minima based on its fitness function and diversity

```
Require: Sequence of centroids: $\boldsymbol{w}_1, \boldsymbol{w}_2, ..., \boldsymbol{w}_r$.
Require: Number of centroids to select: $b < r$.
Ensure: Best centroids.
1: Sort the sequence of centroids in ascending order according to its fitness value
2: Sort the sequence of centroids in ascending order according to the following criterion:
       $o_i = \frac{i \cdot f(\boldsymbol{w}_i, \boldsymbol{\Delta}_I, \boldsymbol{\Delta}_R)}{\sum_{j=1}^{i} d_{i,j}},$   (3)
   where $d_{i,j}$ is the Euclidean distance between $\boldsymbol{w}_i$ and $\boldsymbol{w}_j$.
3: Return the first $b$ centroids of the ordered sequence.
```

The centroids that best fit the infected and recovered time series are located at the beginning of the sequence in step 1. After this, in step 2, the sequence of centroids is re-ordered based not only on the fitness value of the centroids, but also based on how close they are in the search space.

The idea is to push back in the sequence centroids that are similar to the previous ones. This provides a chance to different future outcomes, that still explains current observed data, to be studied and analyzed. The equation 3 models this idea by dividing the centroid fitness value by the average Euclidean distance of each centroid with the previous ones in the sequence.

Here is critical to notice the balance between the fitness value and the diversity. The fitness value is of paramount importance (centroids that do not explain current observed data with accuracy are not useful) but diversity is required to avoid losing possible future outcomes of the epidemic.

2.1.4 Summarizing Future Outcomes

After running several times the FA optimization algorithm and having a set of future outcomes from the FA solutions in steps 3-6, we have a number of $k \cdot b$ local minima that represent future outcomes of the epidemic. The $k \cdot b$ local minima should represent, at least, the top b local minima in the search space that fit current observed data. In step 8, we use K-Means with a number of clusters equals to b to group the local minima stored in T. This should compensate the non-deterministic nature of FA algorithm and K-Means, providing statistical stability and confidence intervals for the SEIR model parameters. Finally, in step 9 we provide SEIR model parameter distribution for each future outcome based on the different centroids.

2.2 SEIR Model and Description of Scenarios

This section describes the SEIR model used in this work to study SARS-CoV 2. This SEIR model have four main compartments:

- Susceptible: population that can be infected.
- Exposed: population that has being exposed to the infection but cannot infect others yet.
- Infected: population that can infect others.
- Recovered: population that had the infection and do not infect others anymore.

The parameters of the model are the per-capita transmission rate, the exposed-to-infectious rate and the infectious-to-recovered rate. Each of these parameters describe how the population migrates from one compartment to another:

— Per-capita transmission rate (β): number of susceptible persons that are exposed per each infected person.

— Exposed-to-infectious rate (γ_0): number of exposed persons that go to transmissible compartment.

— Infectious-to-recovered rate (γ_1): number of infected persons that go to recovered compartment.

Each parameter is usually treated as a constant. However, in order to model restriction policies, we treat the per-capita transmission rate as a function of time $\beta : \mathbb{R} \to \mathbb{R}$. Here, the main challenge is figuring out the value of $\beta(0)$, especially when the situation of COVID-19 is characterized by extreme spatial heterogeneity [4]. At the beginning of the epidemic spread, the number of initial cases is not known, hence, estimating the value of $\beta(0)$ from infected grow is very difficult: either we have a large value of $\beta(0)$ with a small number of initially infected patients or a more discrete value of $\beta(0)$ with a large number of initially infected patients. In addition, the migration rates from other countries, that was an important factor before frontiers closed, makes this even more difficult.

In order to narrow the possible values of $\beta(t)$ to an interval already observed for SARS-CoV 2, we set the maximum value of this parameter to be $\beta_{max} = \bar{R}_0 \cdot \gamma_1$ where $\bar{R}_0$ is the maximum basic reproduction number observed for SARS-CoV 2. Here we use a value of $\bar{R}_0 = 6.49$ reported in [11]. The value of β_{max} should correspond to the per-capita transmission rate for a naive population completely unaware of the epidemic spread.

No-pharmacological preventing solutions are available for the control of COVID-19 pandemic. Thus, at present, the intervention politics are the best way to control the national and international expansion of this disease. Policies are mainly based on isolation and quarantine measures. Isolation separates sick people with a contagious disease from people who are not sick. Quarantine[2] separates and restricts the movement of people who were exposed to a contagious disease to see if they become sick. In most cases a combination of isolation and quarantine measures have been applied by governments.

In our study, we propose several scenarios in order to model real situations. We assume that the disease is present with a relative extension in the entity (country, state, province, city) and that isolation and/or quarantine measures have been taken. To define the scenarios, three states related to the applied politics were considered:

State A: Voluntary home quarantine for the majority of people, closure of schools, universities, majority of services, shopping and social distancing measures. At national level means partial or total closure of national borders (immigration is not an infection factor) and inside the country closure of state borders, province and/or county borders.

State B: It consists in a relaxation of the restriction politics mentioned in state A. For example: opening of public spaces with a limited number of people, opening of schools, universities and factories while keeping social distancing measures.

State C: Stricter polices with respect to state A are considered. For example, mandatory home quarantine for the majority of people, mandatory use of mask.

Considering these states, we are interested in modelling three scenarios: relaxing restriction policies at the current time and hardening such policies after some time, keeping restriction policies as they are currently implemented or with even more strict policies for as long as required and relaxing and hardening restriction policies.

1. **Relaxing restriction policies at the current time and hardening such policies after some time**. For this, we will model the per-capita transmission rate as a wave function of time:

$$\beta_1(t) = \frac{\beta_{max} - \beta_{min}}{2} \cdot \Big(cos(t\beta_{lag}) + 1\Big) + \beta_{min}, \quad (4)$$

[2] See: http://www.cdc.gov/quarantine/index.html

where β_{min} is a parameter that represents the minimum value of the per-capita transmission rate and β_{lag} controls the period of the wave function. Considering such function we can define a search space with four continuous search parameters: $w_1 = \beta_{min} \in [0,1], w_2 = \beta_{lag} \in [0,1], w_3 = \gamma_0 \in [1/14, 1/2], w_4 = \gamma_1 \in [1/42, 1/7]$.

Starting from state A, at $t = 0$ such state is kept until the current day, then, restriction policies are completely lifted. After that, an increase in the number of infected is expected and then a hardening policy will be applied again as in state A.

2. **Keeping restriction policies as they are currently implemented or with even more strict policies for as long as required**. In this scenario, we will model the per-capita transmission rate as an exponentially decreasing function of time similar to [5]:

$$\beta_2(t) = (\beta_{max} - \beta_{min}) \cdot e^{-t\beta_{lag}} + \beta_{min}, \quad (5)$$

where β_{min} is a parameter that represents the minimum value of the per-capita transmission rate and β_{lag} controls how fast the per-capita transmission rate decreases at the beginning of the spread. Considering such function we can define a search space with four continuous search parameters: $w_1 = \beta_{min} \in [0,1], w_2 = \beta_{lag} \in [0,1], w_3 = \gamma_0 \in [1/14, 1/2], w_4 = \gamma_1 \in [1/42, 1/7]$.

This scenario involves in the transition from state A to state C (almost total quarantine for all the people). For this scenario, the per-capita transmission rate abruptly decreases in time. This scenario is very similar to that applied in Wuhan, Hubei, China. Here, is important to consider that the per-capita transmission rate will be adjusted to the specific country infected and recovered time series, hence, if no state C have been implemented during that time, the per-capita transmission rate will not reflect a decrease.

3. **Relaxing and hardening restriction policies**. Here, we will combine the previous two scenarios with a damped cosine wave, modelling restriction policies being relaxed and hardened as required. The per-capita transmission as a function of time can be defined as:

$$\beta_3(t) = \frac{\beta_1(t) \cdot \beta_2(t)}{\beta_{max}}. \quad (6)$$

Considering such function we can define a search space with four continuous search parameters: $w_1 = \beta_{min} \in [0,1], w_2 = \beta_{lag} \in [0,1], w_3 = \gamma_0 \in [1/14, 1/2], w_4 = \gamma_1 \in [1/42, 1/7]$.

In this scenario, starting from state A, we move to state B and then back to state A again. As we move from state A to state B, a few relaxation of policies are applied but not all.

The dynamics of the SEIR model used in the present work can be described by the following equations. Let, $N(t) = S(t) + E(t) + I(t) + J(t) + R(t)$ where $S(t)$ is the number of susceptible patients, $E(t)$ is the number of exposed patients, $I(t)$ is the number of infected patients and $R(t)$ is the number of recovered patients in time t:

1. Susceptible population: susceptible population diminishes in proportion to the per-capita transmission rate. As the susceptible population diminishes, also the rate $S(t)/N(t)$ decreases as well:

$$\frac{d}{dt}S(t) = -\frac{\beta_i(t) \cdot I(t) \cdot S(t)}{N(t)}. \quad (7)$$

2. Exposed population: exposed population increases in the same rate that the susceptible population decreases. When the decrease in susceptible population is significant, the exposed-to-infectious rate begins to dominate, making the exposed population start a decrease dynamic:

$$\frac{d}{dt}E(t) = \frac{\beta_i(t) \cdot I(t) \cdot S(t)}{N(t)} - \gamma_0 \cdot E(t). \quad (8)$$

3. Infectious population: infectious population grows in the same rate that exposed population decreases. When the decrease in exposed population is significant, the infectious-to-recovered rate begins to dominate, making the infectious population start a decrease dynamic:

$$\frac{d}{dt}I(t) = \gamma_0 E(t) - \gamma_1 \cdot I(T). \tag{9}$$

4. Recovered population: the recovered population grows in the same rate that infectious-to-recovered rate and the infectious population:

$$\frac{d}{dt}R(t) = \gamma_1 \cdot I(T). \tag{10}$$

2.3 The Firefly Meta-Heuristic Algorithm

The FA is a meta-heuristic optimization algorithm introduced in 2009 inspired in the flashing behavior of fireflies [19]. When considering this algorithm, each candidate solution is represented by a firefly. The basic idea is that fireflies use their light to attract others of its kind. This way, the fireflies with stronger light, or fitness, will attract more than others. The equation to move a firefly i to a brighter one j is given by equation 11:

$$\boldsymbol{w}_i = \boldsymbol{w}_i + \beta^{\dagger} \exp(-\gamma^{\dagger} d_{i,j}^2)(\boldsymbol{w}_j - \boldsymbol{w}_i) + \eta r, \tag{11}$$

where $d_{i,j}$, as before, is the Euclidean distance between $\boldsymbol{w}_i$ and $\boldsymbol{w}_j$.

In equation 11, $\beta^{\dagger}$ is the bright of a firefly when the distance is zero, $\gamma^{\dagger}$ is the light absorption coefficient, η is a parameter that controls randomness and $r \in [-0.5, 0.5]$ is a random number generated from a uniform distribution. The constants $\beta^{\dagger}$, $\gamma^{\dagger}$ and η are known as hyper-parameters that control the exploration/exploitation capabilities of the algorithm. In addition, the number of solutions is another important hyper-parameter that we denote as p. The pseudo code for FA algorithm is given in Algorithm 3.

In step 1 of Algorithm 3, the SEIR model parameters, represented here by the concept of firefly solution, are initialized randomly using a uniform distribution. At each iteration, each firefly fitness is compared with the rest in step 7. In case that a firefly has more bright than another, the one with less bright is moved to the brighter in step 3. This makes that the solutions of this algorithm, do not move to the same, possibly global best solution, but to all solutions that have a better fitness value. This is essential in order to find several local minima in the search space and not only the global optimum, as optimized solutions usually form clusters around them [16].

Algorithm 3 The Firefly meta-heuristic algorithm (FA)

```
 1: Initialize firefly solutions $\boldsymbol{w}_i$ for $1 \leq i \leq p$.
 2: for i = 1 to Max. Number of Iterations do
 3:     for j = 1 to $p$ do
 4:         for k = 1 to $p$ do
 5:             $f_j = f(\boldsymbol{w}_j, \boldsymbol{\Delta}_I, \boldsymbol{\Delta}_R)$
 6:             $f_k = f(\boldsymbol{w}_k, \boldsymbol{\Delta}_I, \boldsymbol{\Delta}_R)$
 7:             if $f_j > f_k$ then
 8:                 Move firefly $j$ to firefly $k$.
 9:             end if
10:         end for
11:     end for
12: end for
13: Return the best $\boldsymbol{w}$ according to its fitness value.
```

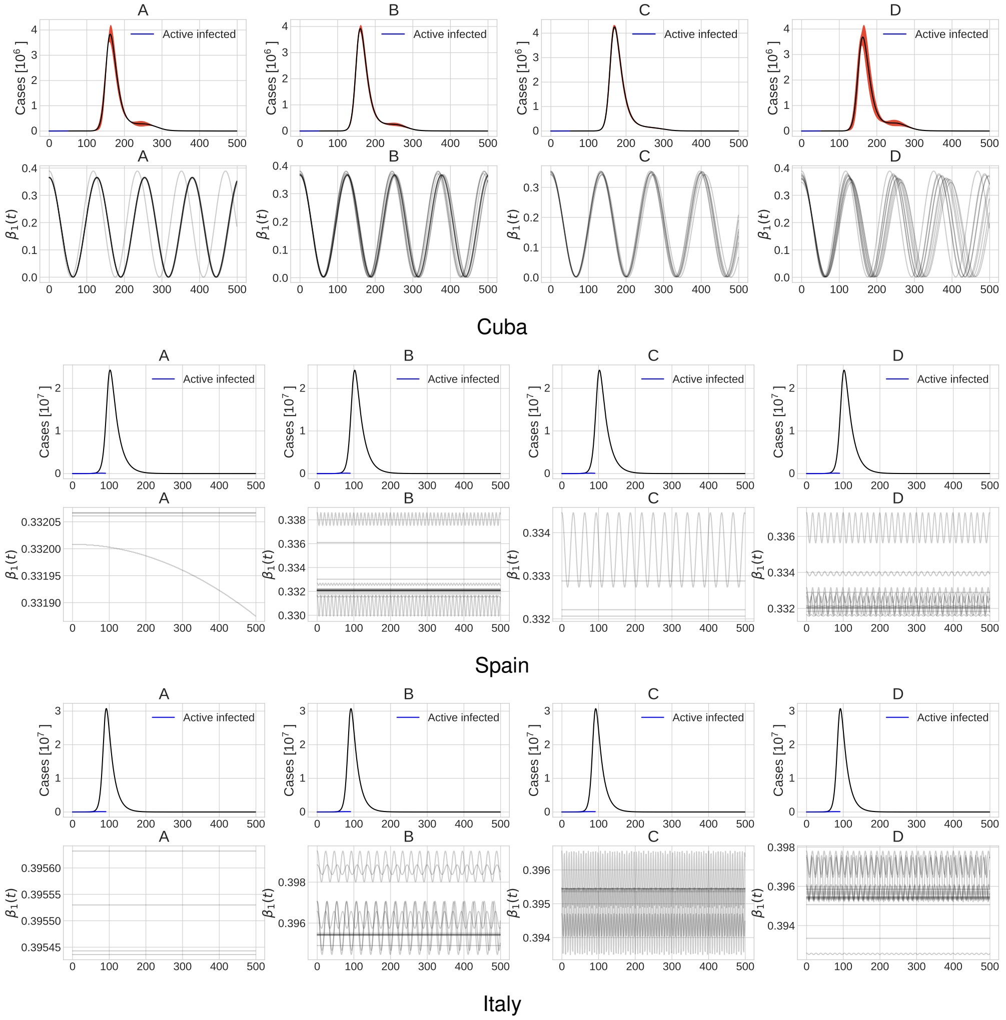
3 Results

In this section we describe the data used in the present paper to analyze SARS-CoV 2 in Cuba, Spain and Italy. In addition, we present the results of finding SEIR model parameter distributions of possible future outcomes using the three scenarios explained in Section 2.2.

3.1 SARS-CoV 2 Data

SARS-CoV2 data was retrieved from the World Health Organization reports[3]. Using this data, we create a daily time series of the number of active infected and recovered patients. The start of the epidemic for each country is selected based in the apparition of the first cases, hence, the time series length is different for each country.

[3] Available at: https://covid19.who.int.



Cuba

Spain

Italy

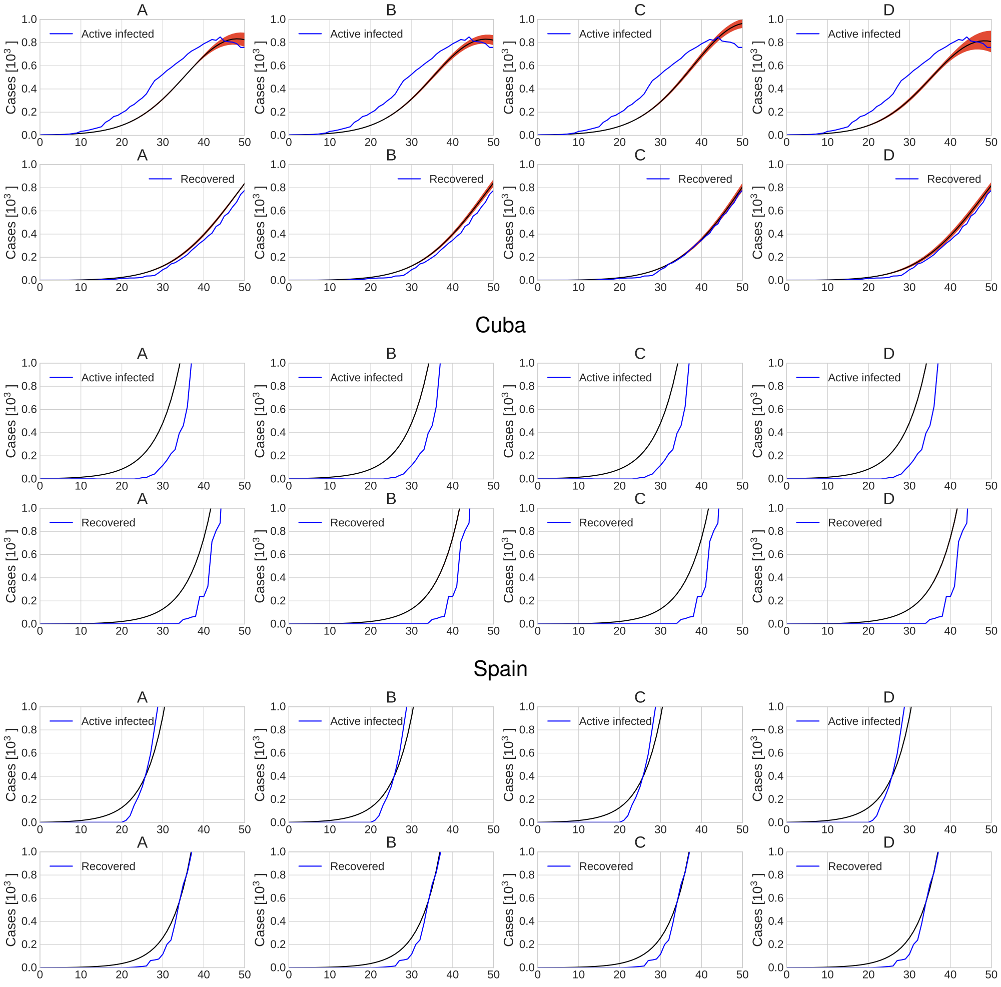
Fig. 1. Number of active infected patients and values of the per-capita transmission rate in the first 500 days corresponding to scenario 1. Plots A, B, C and D show clusters of different possible future outcomes

To optimize our SEIR model parameters we will use information of the first 50 days only. All data and source code for the experiments is provided publicly at Internet: `https://github.com/ml-opt/cys-covid`.

3.2 Searching the Set of Possible Outcomes

We use FA algorithm to find local minima in the SEIR parameter space, which corresponds to step 3 of Algorithm 1. FA algorithm hyper-parameters are selected based in the literature standard recommendations, that is: $\beta^\dagger = 0.8$, $\gamma^\dagger = 0.6$, $\eta = 0.3$ and $p = 400$. We perform a number of 200 iterations of the FA algorithm. The large number of fireflies $p = 400$ comes from the fact that we want to achieve clusters around all local minima without actually knowing how many are there.

Using the optimized FA solutions as points in $\Omega = \mathbb{R}^n$, we perform unsupervised clustering analysis using K-Means algorithm as defined in step 4 of Algorithm 1. K-Means algorithm requires to specify an initial number of clusters that we do not know based on obtained data. We perform



Cuba

Spain

Italy

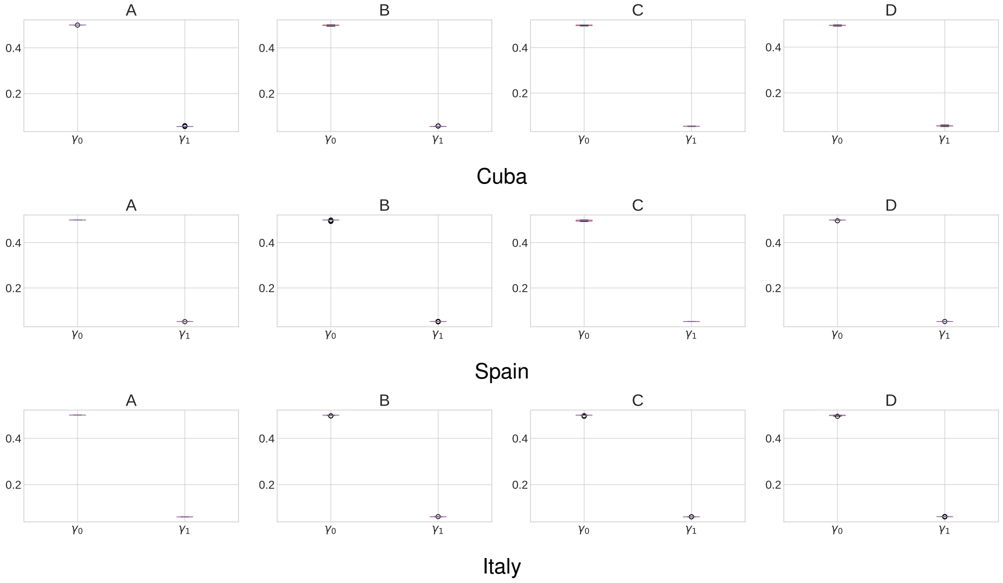
Fig. 2. Active infected and recovered time series forecast and the current observed times series in blue corresponding to scenario 1. Plots A, B, C and D show clusters of different possible future outcomes

a grid search, considering different numbers of clusters from 10 to 100 with a step of 10. For each number of cluster, we calculate the Silhouette Coefficient which is a intra/extra cluster measure of how separated and consistent are the obtained clusters. The Silhouette Coefficient is a number in $[0, 1]$. A lower value of the Silhouette Coefficient stands for poor quality of the cluster analysis and a higher value stands for a better cluster analysis.

After this, we select the top $b = 4$ clusters based on its fitness value and diversity according to step 5 of Algorithm 1. We repeat the previously described steps 3-6 a number of $k = 10$ times. This is done for each of the three scenarios in Section 2.2.

3.3 Summarizing Possible Outcomes

We present the epidemiological development for each of the three scenarios described in section 2.2. We present an epidemic forecast of the number of infected patients for the first 500 days and information on how well such forecast fits observed infected and recovered cases.



Cuba

Spain

Italy

Fig. 3. Box plots presenting the SEIR model parameters distribution for each outcome corresponding to scenario 1. Plots A, B, C and D show SEIR model parameters distributions of different possible future outcomes

In addition, we present the SEIR model parameter distributions for each scenario and how the per-capita transmission rate controls the epidemic outbreak.

3.3.1 Scenario 1: Relaxing Restriction Policies at the Current Time and Hardening such Policies After some Time

In Figure 1, we show the number of active infected cases and the value of the per-capita transmission rate in the first 500 days of SARS-CoV 2 in Cuba, Spain and Italy. In the figure, we show the top $b = 4$ clusters found by Algorithm 1, denoted as A, B, C and D. The red area around the mean represents the standard error.

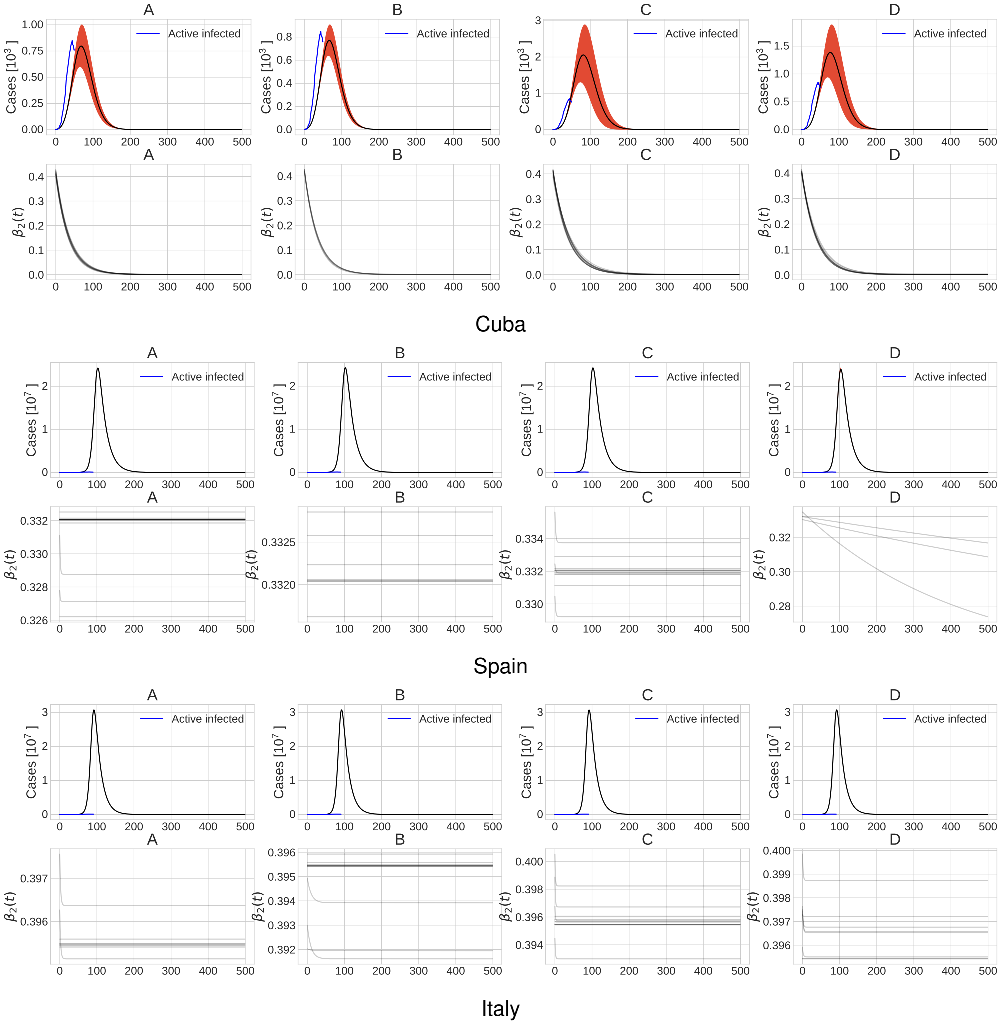
Figure 2 presents a zoom in the first 50 days of the active infected patients and recovered patients adding the current observed times series in blue lines.

As before, the black line represents the mean of the local minima of each of the top $b = 4$ clusters, denoted as A, B, C and D.

In case of Cuba, the four possible outcomes show that the value of the per-capita transmission rate in the 50-th day was between 0.1 and 0.2. Relaxing restriction policies in the 60-th to 80-th days, makes the number of active infected patients to raise to about four million. This even holds if the restriction policies are hardened in approximately the 120-th day. This exemplifies the extremely important fact of not relaxing restriction policies too much or too soon.

These findings are consistent with those in Hubei, China where lifting quarantine would have led to a second epidemic peak in March [20]. Moreover, notice that restriction policies are being lifted since the 60-th to 80-th day, but, we see an exponential increase in the active infected time series nearly in the 120-th day. This give us an important hint in how much caution we must have when relaxing restriction policies.

In case of Spain and Italy the values of the per-capita transmission rate are nearly constant in this period. This shows how the epidemic spread went without control during the first 50 days. Actually, in Spain the quarantine lockdown was applied in about day 45, hence, the per-capita transmission rate do not record any decrease in the first 50 days. This scenario is similar to the findings of [21] where under a regime without restriction



Cuba

Spain

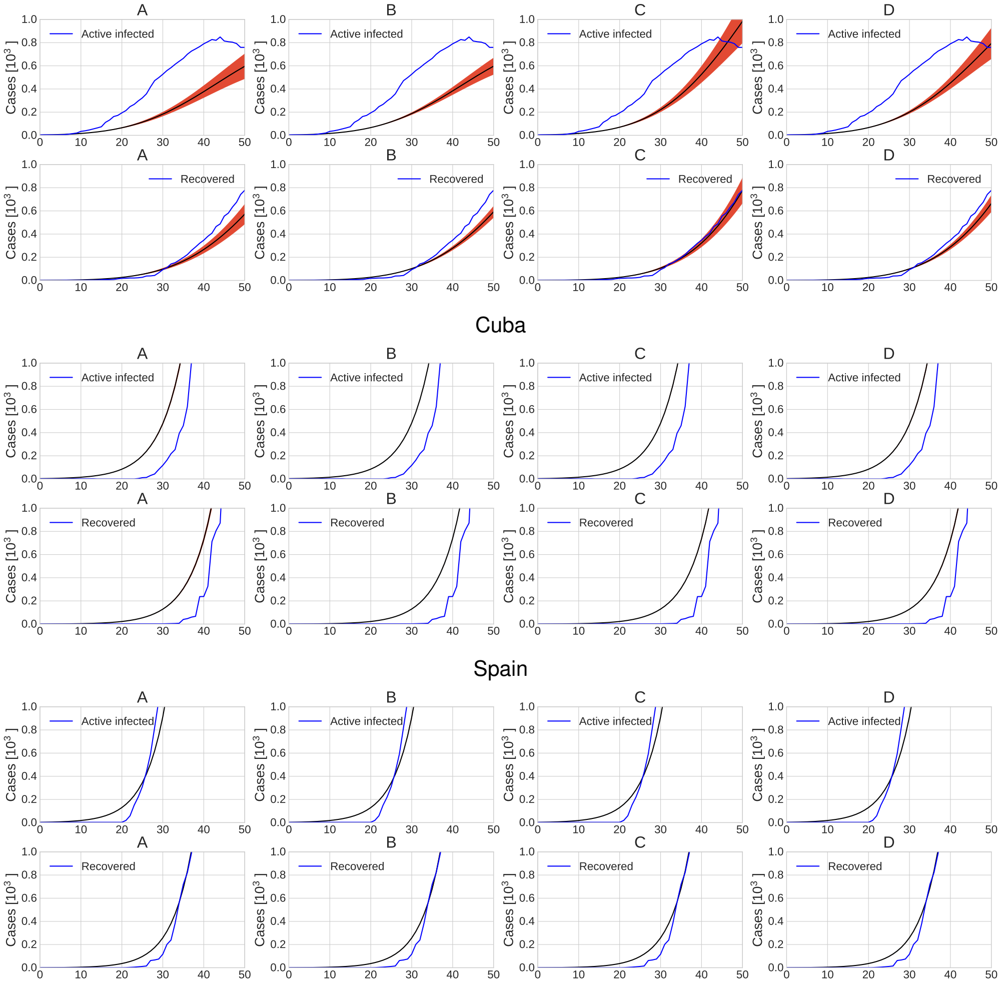
Italy

Fig. 4. Number of active infected patients and values of the per-capita transmission rate in the first 500 days corresponding to scenario 2. Plots A, B, C and D show clusters of different possible future outcomes

policies, the peak of active infected cases is predicted to happen in the first 270-650 days representing about 10-20% of the total population. Figure 3 shows the SEIR model parameters distribution for each of the top $b = 4$ possible outcomes studied in the present work. The bottom and top lines in the box plots represents the first and third quartiles, the line in the middle represents the median of the measurements and the whiskers represents standard deviation. Notice how the values of γ_0 and γ_1 are similar across the different countries.

3.3.2 Scenario 2: Keeping Restriction Policies as they are Currently Implemented

Figure 4 shows the number of active infected cases in the first 500 days of SARS-CoV 2. The figure, as in the previous scenario, shows four possible outcomes of the epidemic. In the figure, we show that the per-capita transmission rate diminishes in the first days of the outbreak to a minimum and then the restriction policies are kept in time. Here is interesting to see how the predicted value of $\beta_2(t)$ keeps diminishing in time after day 50 in the



Cuba

Spain

Italy

Fig. 5. Active infected and recovered time series forecast and the current observed times series in blue corresponding to scenario 2. Plots A, B, C and D show clusters of different possible future outcomes

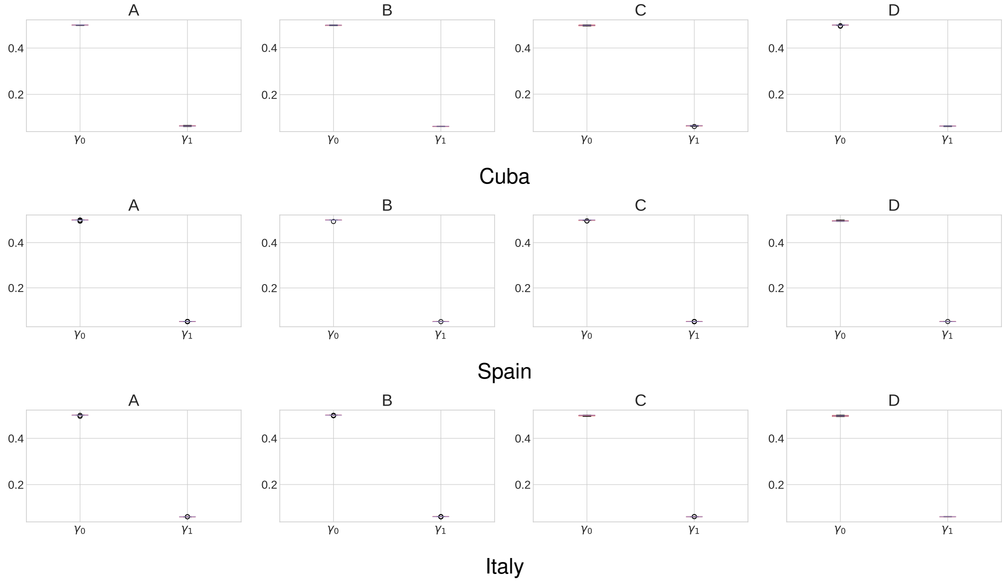
case of Cuba. In the case of Spain and Italy, we again observe a nearly constant value for the per-capita transmission rate, which is consistent with the outcomes of the first scenario. Here is interesting to notice how scenario 1 and scenario 2 mostly agree on the per-capita transmission rate and number of infected cases before day 50 and depicts different outcomes for the future.

Figure 5 presents a zoom in the first 50 days of the active infected patients and recovered patients adding the current observed times series in blue lines. Furthermore, Figure 6 shows the SEIR model parameters distribution for each of the top $b = 4$ possible outcomes under consideration.

3.3.3 Scenario 3: Relaxing and Hardening Restriction Policies as Required

Figure 7 shows the number of active infected cases in the first 500 days of SARS-CoV 2. As before, we present four possible outcomes of the epidemic development.

In the case of Cuba, it can be observed what would happen if the restriction policies are



Cuba

Spain

Italy

Fig. 6. Box plots presenting the SEIR model parameters distribution for each outcome corresponding to scenario 2. Plots A, B, C and D show SEIR model parameters distributions of different possible future outcomes

hardened and relaxed, but only partially. Notice that special care should be taken when relaxing restriction policies: if the restriction policies are relaxed too much, that would create a peak of infected cases, as can be confirmed from the first scenario. What we see now in scenario 3, is that a considerable peak can also happen, tough in a much smaller scale (take into account the error in the plot ranging from less than half million cases to four million cases).

Figure 8 presents a zoom in the first 50 days of the active infected patients and recovered patients adding the current observed times series in blue lines. As before, the black line represents the mean of the local minima of each of the top $b = 4$ clusters, denoted as A, B, C and D. The red area around the mean represents the standard error of the mean.

Notice that this scenario is fundamentally different from scenario 2, where restriction policies are kept for a long time, which is really difficult to achieve from a practical point of view. In the cases of Spain and Italy, the per-capita transmission rate is kept mainly constant as the data do not capture the effect of restriction policies at this point.

Figure 9 shows the SEIR model parameters distribution for each of the top $b = 4$ possible outcomes studied in the present work. As before, the results obtained in this scenario are similar to the already obtained values of γ_0 and γ_1 in the first and second scenario. This somehow highlight how our meta-heuristic approach is able to find such parameters even under different per-capita transmission regimes.

4 Discussion

Our proposal allows a fast analysis of several scenarios with adequate accuracy. This approach has the potential of fitting SEIR models not only for an entire country, but also for provinces, municipalities and small geographical regions based only in the data. Considering the case of Cuba, where social distance measures were applied in the first 50 days, we observe a reduction of about 65-80% of the per-capita transmission rate in that period of time. Interestingly, similar results were obtained by Jarvis et al. who reported a 73% reduction in the average daily number of contacts

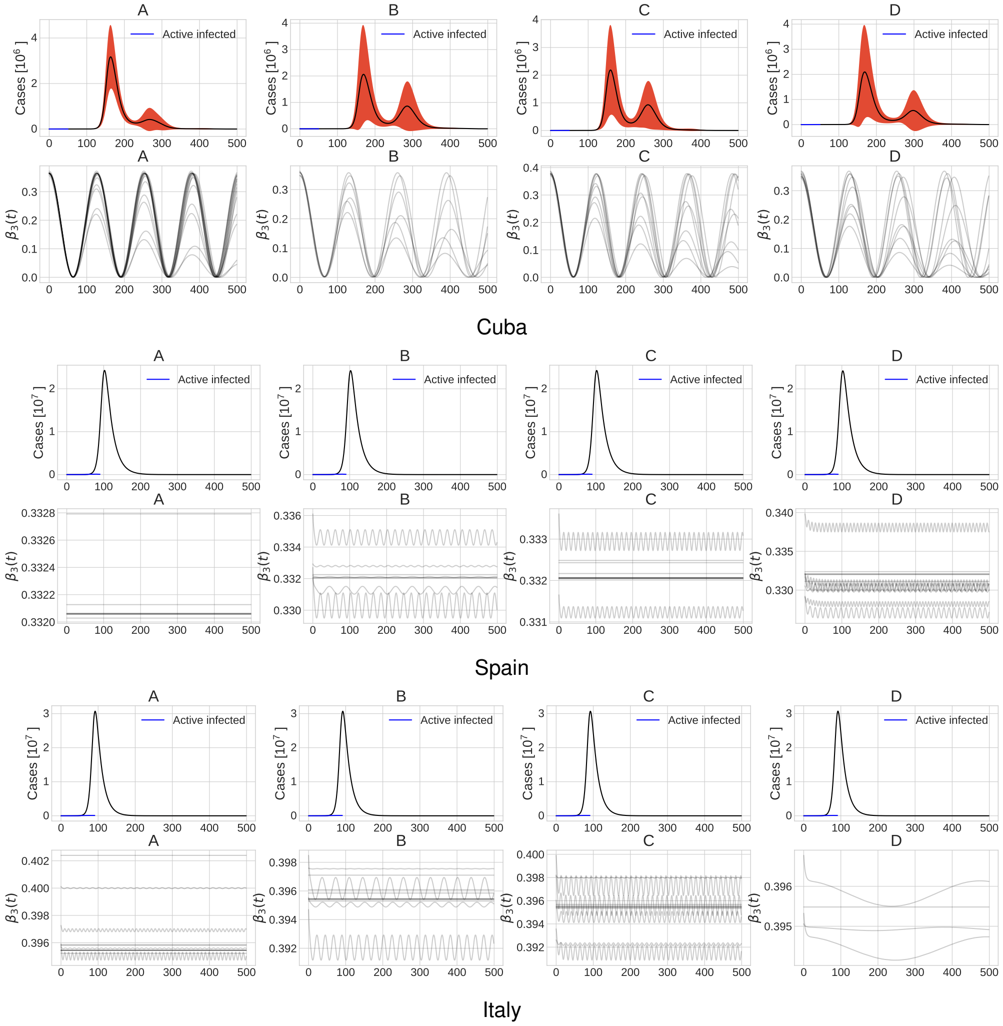
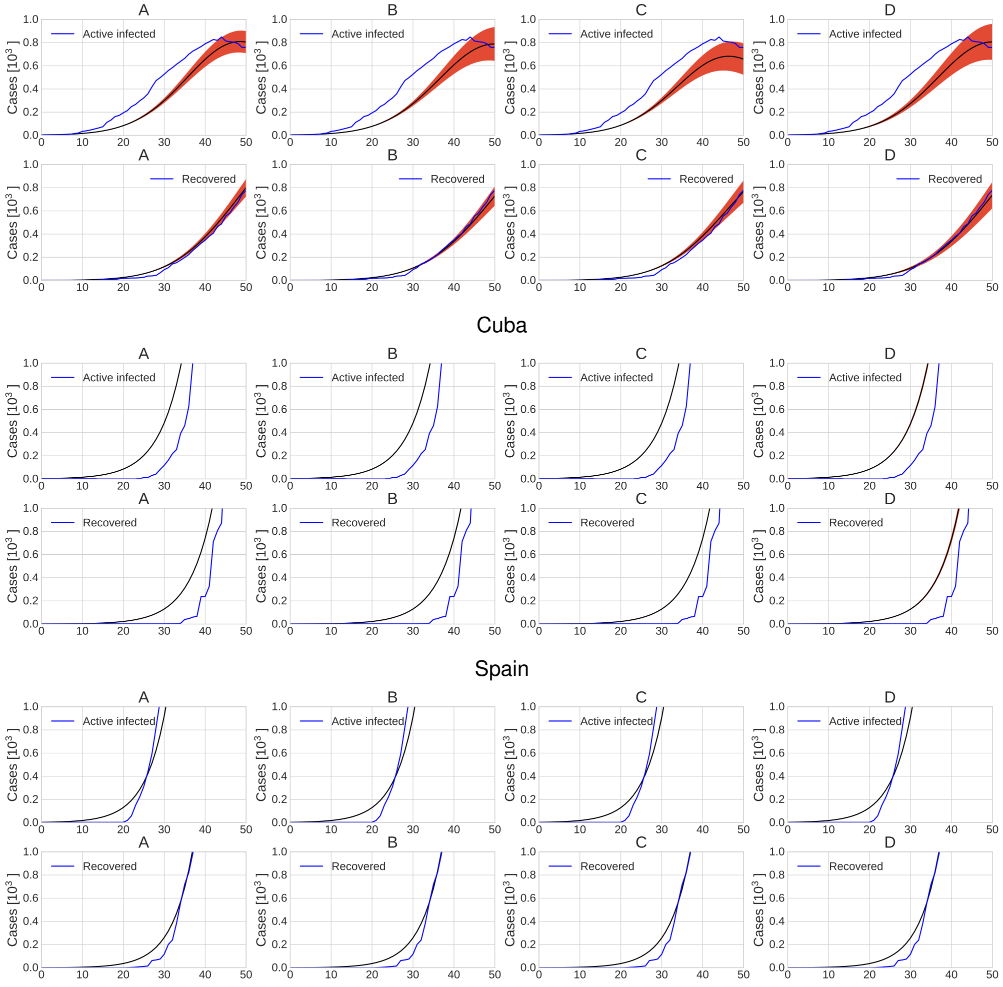


Fig. 7. Number of active infected patients and values of the per-capita transmission rate in the first 500 days corresponding to scenario 3. Plots A, B, C and D show clusters of different possible future outcomes

observed per participant after the implementation of restriction policies [8].

For the case of Spain and Italy, we do not observe any reduction in the per-capita transmission rate during this period of time. This is somehow consistent with the delay in the application of social distance measures (for example, in the case of Spain the lockdown was imposed in approximately day 45 of the epidemic). Moreover, this situation highlights an important limitation of our scenario modelling, as neither the wave function of scenario 1 and 3 nor the exponentially decreasing function of scenario 2 will be able to fit accurately the expected decay in the per-capita transmission rate after day 50 in such countries. Future work should account for a function with more degrees of freedom to model such situation.

Surprisingly, the exposed-to-infectious rate for the three studied countries was similar in approximately $\gamma_0 \approx 0.5$. This even holds when we consider the three scenarios under study. This value of the exposed-to-infectious rate is similar to other results obtained for Spain and Italy [6] but



Cuba

Spain

Italy

Fig. 8. Active infected and recovered time series forecast and the current observed times series in blue corresponding to scenario 3. Plots A, B, C and D show clusters of different possible future outcomes

different to the exposed-to-infectious rate $\gamma_0 \approx 0.2$ observed in China [10].

The analysis of the scenarios highlights the importance of keeping restriction policies during a reasonable time, providing further evidence of its efficacy in preventing future waves of infection [18]. At this point, the main limitation of our approach is the accuracy of the real infected time series that may be biased. Despite this, even when the official infected time series may not be accurate, we may expect it to be correlated with the actual number of infected patients.

In practice, the real number of infected patients is larger than that officially reported by countries and institutions[4]. The informed official number critically depend on the applied tests. For this reason, in our study, we have selected countries with a good system of data retrieval, which allows us to conduct analysis on this data with a reasonable confidence. Moreover, reports show that the real number of infected patients for the three studied countries in the first wave of the disease is very low compared

[4] See: https://coronavirus.jhu.edu/data/mortality

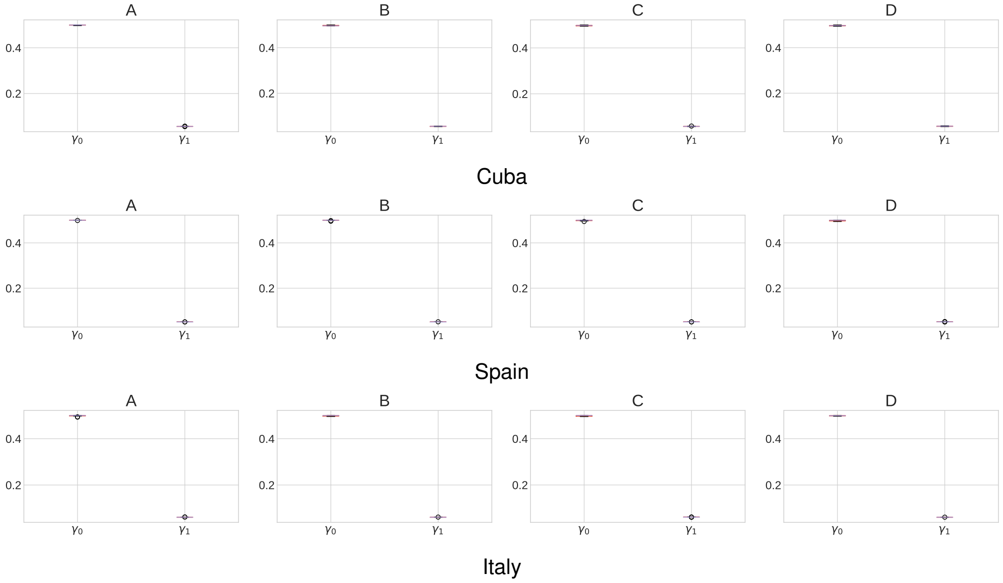


Fig. 9. Box plots presenting the SEIR model parameters distribution for each outcome corresponding to scenario 3. Plots A, B, C and D show SEIR model parameters distributions of different possible future outcomes

to the total population. For example, surveys based on PCR tests have found that around 4-5% of the population in Spain has been infected[5]. This means that, at present, the susceptible population is more than 95% of the total population.

In addition, to reach herd immunity, a significant fraction of the population has to get infected [15]. In that condition we guess that our predictions will be semi-quantitatively correct and useful in order to take decisions about relaxing or restricting policies. Particularly, the modelled results of scenario 2 (keeping restriction policies as they are currently implemented), is compatible with the excellent results obtained by China in the management of the crisis in Wuhan, Hubei.

We need to consider several core limitations of our approach. First, the meta-heuristic FA search algorithm is a stochastic search method, hence, there is not warranties of finding all possible fittings. Moreover, FA hyper-parameter optimization is a difficult task as, in general, this is a class of challenging optimization problems, whose objective functions tend to be non-smooth, discontinuous, unpredictably varying in computational expense and include continuous, nominal and/or discrete variables [9].

Our approach might be used carefully and it is critical to take into account the following elements:

— Care must be taken in selecting the number of iterations of the FA algorithm. A low number of iteration will cause poor fitting around local minima while a large number of iterations will cause a lack of diversity of the firefly solutions.

— Care must be taken in selecting the number of top b clusters. Choosing a small value of b may leave important outcomes out of the analysis, while a large number will render too many future outcomes, increasing the difficulty of studding them.

— Finally, our approach cannot be used before having data, hence, it will be only available after the epidemic have already began. However, as the epidemic advance, the number of possible future outcomes will reduce, increasing the forecasting accuracy.

[5] Available at: https://www.lamoncloa.gob.es/lang/en/gobierno/news/Paginas/2020/20200513enecovid19-study.aspx.

5 Conclusions

We have developed a meta-heuristic approach to find parameters of the SEIR model that best explains the observed infected and recovered time series. Further, we have shown that there are several possible parameter vectors of such models able to explain current epidemic trends and by studding them is possible to obtain insights into the future possible outcomes. Our approach allowed to study several scenarios in different countries at medium and long term. The proposed method could be more exact depending on the time series accuracy. In this sense, as the time passes, the number of possible future outcomes will reduce, increasing the forecasting accuracy.

References

1. **Berger, D. W., Herkenhoff, K. F., Mongey, S. (2020).** An seir infectious disease model with testing and conditional quarantine. Working Paper 26901, National Bureau of Economic Research.
2. Chowdhury, R., Heng, K., Shawon, M. S. R., Goh, G., Okonofua, D., Ochoa-Rosales, C., Gonzalez-Jaramillo, V., Bhuiya, A., Reidpath, D., Prathapan, S., others **(2020).** Dynamic interventions to control covid-19 pandemic: a multivariate prediction modelling study comparing 16 worldwide countries. European journal of epidemiology, Vol. 35, No. 5, pp. 389–399.
3. **Du, K.-L., Swamy, M. (2016).** Search and optimization by metaheuristics. Birkhäuser.
4. **Engbert, R., Rabe, M. M., Kliegl, R., Reich, S. (2021).** Sequential data assimilation of the stochastic seir epidemic model for regional covid-19 dynamics. Bulletin of mathematical biology, Vol. 83, No. 1, pp. 1–16.
5. **Fanelli, D., Piazza, F. (2020).** Analysis and forecast of covid-19 spreading in china, italy and france. Chaos, Solitons & Fractals, Vol. 134, pp. 109761.
6. **Godio, A., Pace, F., Vergnano, A. (2020).** Seir modeling of the italian epidemic of sars-cov-2 using computational swarm intelligence.
7. **Huang, C., Wang, Y., Li, X., Ren, L., Zhao, J., Hu, Y., Zhang, L., Fan, G., Xu, J., Gu, X., Cheng, Z., Yu, T., Xia, J., Wei, Y., Wu, W., Xie, X., Yin, W., Li, H., Liu, M., Xiao, Y., Gao, H., Guo, L., Xie, J., Wang, G., Jiang, R., Gao, Z., Jin, Q., Wang, J., Cao, B. (2020).** Clinical features of patients infected with 2019 novel coronavirus in wuhan, china. The Lancet, Vol. 395, No. 10223, pp. 497 – 506.
8. **Jarvis, C. I., Van Zandvoort, K., Gimma, A., Prem, K., Klepac, P., Rubin, G. J., Edmunds, W. J. (2020).** Quantifying the impact of physical distance measures on the transmission of covid-19 in the uk. BMC medicine, Vol. 18, pp. 1–10.
9. **Koch, P., Golovidov, O., Gardner, S., Wujek, B., Griffin, J., Xu, Y. (2018).** Autotune: A derivative-free optimization framework for hyperparameter tuning. Proceedings of the 24th ACM SIGKDD International Conference on Knowledge Discovery & Data Mining, KDD 18, Association for Computing Machinery, New York, NY, USA, pp. 443 – 452.
10. Li, Q., Guan, X., Wu, P., Wang, X., Zhou, L., Tong, Y., Ren, R., Leung, K. S., Lau, E. H., Wong, J. Y., others **(2020).** Early transmission dynamics in wuhan, china, of novel coronavirus–infected pneumonia. New England Journal of Medicine, Vol. 382, No. 13, pp. 1199–1207. PMID: 31995857.
11. **Liu, Y., Gayle, A. A., Wilder-Smith, A., Rocklöv, J. (2020).** The reproductive number of COVID-19 is higher compared to SARS coronavirus. Journal of Travel Medicine, Vol. 27, No. 2. Taaa021.
12. **Mulder, L. (2020).** Use of simulated annealing to determine the operational parameters of the seir model for the coronavirus for various jurisdictions. Bulletin of the World Health Organization.
13. **Pinter, G., Felde, I., Mosavi, A., Ghamisi, P., Gloaguen, R. (2020).** Covid-19 pandemic prediction for hungary; a hybrid machine learning approach. Mathematics, Vol. 8, No. 6.
14. **Putra, S., Khozin Mu'tamar, Z. (2019).** Estimation of parameters in the sir epidemic model using particle swarm optimization. American Journal of Mathematical and Computer Modelling, Vol. 4, No. 4, pp. 83–93.
15. **Randolph, H. E., Barreiro, L. B. (2020).** Herd immunity: Understanding covid-19. Immunity, Vol. 52, No. 5, pp. 737 – 741.
16. **Senthilnath, J., Omkar, S., Mani, V. (2011).** Clustering using firefly algorithm: Performance study. Swarm and Evolutionary Computation, Vol. 1, No. 3, pp. 164 – 171.
17. **Wang, X., Peng, H., Shi, B., Jiang, D., Zhang, S., Chen, B. (2019).** Optimal vaccination strategy of a constrained time-varying seir epidemic model. Communications in Nonlinear Science and Numerical Simulation, Vol. 67, pp. 37 – 48.

18. **Xu, S., Li, Y. (2020).** Beware of the second wave of covid-19. The Lancet, Vol. 395, No. 10233, pp. 1321–1322.

19. **Yang, X.-S. (2009).** Firefly algorithms for multimodal optimization. **Watanabe, O., Zeugmann, T.**, editors, Stochastic Algorithms: Foundations and Applications, Springer Berlin Heidelberg, Berlin, Heidelberg, pp. 169–178.

20. Yang, Z., Zeng, Z., Wang, K., Wong, S.-S., Liang, W., Zanin, M., Liu, P., Cao, X., Gao, Z., Mai, Z., others **(2020).** Modified seir and ai prediction of the epidemics trend of covid-19 in china under public health interventions. Journal of Thoracic Disease, Vol. 12, No. 3, pp. 165.

21. **Zhou, X., Ma, X., Hong, N., Su, L., Ma, Y., He, J., Jiang, H., Liu, C., Shan, G., Zhu, W., Zhang, S., Long, Y. (2020).** Forecasting the worldwide spread of covid-19 based on logistic model and seir model. medRxiv.

22. **Zhu, L., Ma, B., Zhao, X. (2010).** Clustering validity analysis based on silhouette coefficient. Journal of Computer Applications, Vol. 30, No. 2, pp. 139–141.

Article received on 07/08/2020; accepted on 25/03/2021.
Corresponding author is Jairo Rojas-Delgado.