MANAGEMENT EPIDEMICS USING HIGH COMPLEXITY MATHEMATICAL MODELING

PART II: SEIMR/R-S GENERAL EPIDEMIC MODEL. THEORY, VALIDATION AND APPLICATIONS

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ABSTRACT

SEIMR/R-S corresponds to a generalized mathematical model of pandemics that enhances traditional, aggregated simulation models when considering inter-regional impacts in a macro region (conurbed); **SEIMR/R-S** also considers the impact of modeling the population divided into socio-demographic segments based on age and economic stratum (it is possible to include other dimensions, for example: ethnics, sex, …).

SEIMR/R-S is the core of the **SEIMR/R-S/OPT** epidemic management optimization model that determines optimal policies (mitigation and confinement) considering the spatial distribution of the population, segmented socio-demographically. The formulation of **SEIMR/R-S/OPT** is presented in another "paper" describing its implementation in GAMS and AMPL, and the implementation for the case of Bogota.

SEIMR/R-S can be understood and used by any epidemiologist, and/or physician, working with SIR, SEIR or similar simulation models, and by professionals working on the issue of public policies for epidemic control.

SEIMR/R-S epidemic model was carried out in a JAVA program. This program may be used by the organizations that considers the **SEIMR/R-S** will be useful for management the COVID-19 pandemic.

1. EPIDEMIC & CONTROL POLICIES MODEL

The **SEIMR/R-S** is a detailed epidemic model that is the result of integrating the **SIR**, **SEIR** and **SEI3RD** model; in these standard models the population is grouped in only one homogenous group. **SEIMR/R-S** extends the modeling to a multi-segment-sociodemographic multi-region system.

SEIMR/R-S model describes the epidemic with following states:

S **Susceptible:** initially covers all population that potentially can be infected (SU)

E **Exposed:** Population that has been infected and are in an incubation (latency) period (EX). The model SIR does not include this state.

IM **Multi-Infected:** Population that has been infected and has active the pathogen in different states of development (I0, I1,I2, … , IN). The active infected states are ordered according to the severity of the infection. The modeled SIR and SEIR consider only one infected state. For convenience, the last state is called "IN"

R **Recovered:** Recovering population (RE)

R-S is related with the Region-Segment model that considers multiples regions where live people classified in multiples socio-demographics segments.

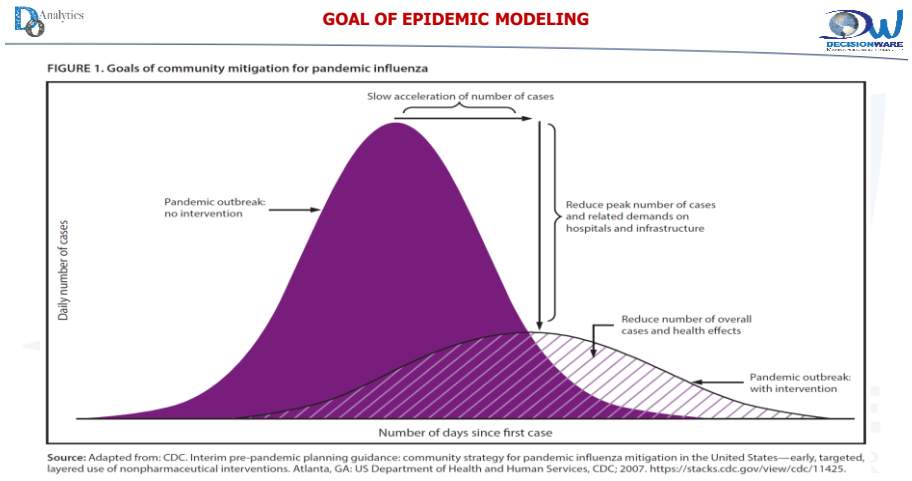
1.1. CONCEPTUAL FRAMEWORK

The following documents have been referenced and used for writing the following numerals:

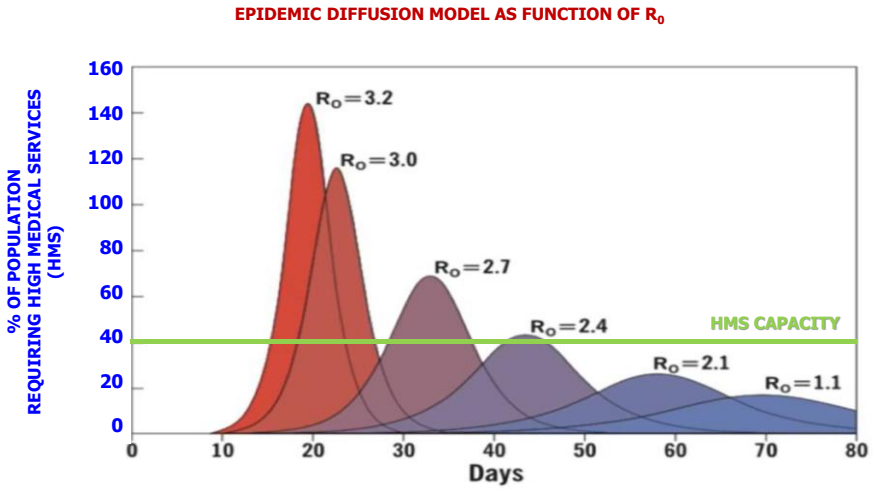
- Brauer, F. and Castillo-Chavez, C. (2000). Mathematical Models in Population Biology and Epidemiology. Springer, New York, 2000.
- Cai, Y., Kang, Y., Banerjee, M., & Wang, W. (2015). A stochastic SIRS epidemic model with infectious force under intervention strategies. Journal of Differential Equations, 259(12), 7463-7502.
- Carcione, J., Santos J. E., Bagaini, C. and Jing, Ba. (2020) A Simulation of a COVID-19 Epidemic Based on a Deterministic SEIR Model.
- Erdem, M., Safan, M., & Castillo-Chavez, C. (2017). Mathematical analysis of an SIQR influenza model with imperfect quarantine. Bulletin of mathematical biology, 79(7), 1612-1636.
- Eubank, S., Eckstrand, I., Lewis, B., Venkatramanan, S., Marathe, M., & Barrett, C. L. (2020). Commentary on Ferguson, et al.,"Impact of Non-pharmaceutical Interventions (NPIs) to Reduce COVID-19 Mortality and Healthcare Demand". Bulletin of Mathematical Biology, 82, 1-7.

- Ferguson, N., Laydon, D., Nedjati Gilani, G., Imai, N., Ainslie, K., Baguelin, M., ... & Dighe, A. (2020). Report 9: Impact of non-pharmaceutical interventions (NPIs) to reduce COVID19 mortality and healthcare demand.
- Hethcote, H. W. (2000). "The Mathematics of Infectious Diseases." SIAM Review 42.4 (2000), pp. 599–653.
- Huang G. (2016). Artificial infectious disease optimization: A SEIQR epidemic dynamic model-based function optimization algorithm. Swarm and evolutionary computation, 27, 31–67. https://doi.org/10.1016/j.swevo.2015.09.007
- Jing, W., Jin, Z., & Zhang, J. (2018). An SIR pairwise epidemic model with infection age and demography. Journal of biological dynamics, 12(1), 486-508.
- Kermack, W.O. and Mc Kendrick, A. G.,(1927) "Contributions to the Mathematical Theory of Epidemics, Part I". Proc. R. Soc. London, Ser. A, 115, 1927, 700-721.
- Liu M. and Liang, J. (2013). Dynamic optimization model for allocating medical resources in epidemic controlling. Journal of Industrial Engineering and Management JIEM, 2013 – 6(1):73-88 – Online ISSN: 2013-0953
- Massad, E., Bruattini, N.M., Coutinho, B. A. F. and Lopez, F. L., (2007). "The 1918 Influenza An Epidemic in the City" of Sao Paulo", Brazil, Medical Hypotheses, 68, 2007, 442-445
- Mejía Becerra, J. D. et. al. (2020). "Modelación Matemática de la Propagación del SARS-CoV-2 en la Ciudad de Bogotá. Documento de Circulación Informal
- Pang, W. (2020). Public Health Policy: COVID-19 Epidemic and SEIR Model with Asymptomatic Viral Carriers. Department of Mathematics and Statistics, McMaster University arXiv:2004.06311v1 [q-bio.PE] 14 Apr 2020.
- Radulescu, A., & Cavanagh, K. (2020). Management strategies in a SEIR model of COVID 19 community spread. arXiv preprint arXiv:2003.11150.
- Samsuzzoha, Md. (2012) . "A Study on Numerical Solutions of Epidemic Models". Doctoral Thesis, Swinburne University of Technology, Australia, 2012.

The goal of epidemic control strategies is to reduce R_0. This can be achieved by reducing susceptibility or contact rates in the population or the infectiousness of infected populations. The potential effectiveness of medical intervention by varying the infectiousness of infected populations and nonmedical interventions by reducing the contact rates in the population have been examined. In medical intervention, use of vaccines and/or antiviral agents for case of treatment can increase the recovery rate and reduce the death rate. On the other hand, in nonmedical interventions, reducing population contact rates through social distancing and travel restrictions can reduce the impact on the transmission process.



Control of an outbreak relies partly on identification of the disease parameters that lead to a significant reduction of the basic reproduction number $\mathbf{R_0}$ that may be function of several parameters of which γ, the recovery rate for clinically ill and β, the transmission coefficient, are the most sensitive parameters. These two parameters can be controlled by medical intervention and nonmedical interventions.



The modeling of epidemics in a solidly developed area of scientific knowledge, widely studied based on simulation models. The master table of epidemic models shows some of the best-known models

TABLE: MAE_EMO			
STATE (COD_EMO)	**DESCRIPTION (DIN_EMO)**	**Reference (COM_EMO)**	**Imple mented**
SIR	Susceptibility (S), Infection (I) and Recovery (R)	Kermack & Mc Kendrick (1927) Jing (2018)	YES
SEIR	Susceptibility (S), Exposure (E), Infection (I) and Recovery (R)	Hethcote (2000)	YES
SEIRA	Susceptibility (S), Exposure (E), Infection (I) and Recovery (R)		NOT
SEI3RD	Susceptibility (S), Exposure (E), 3+1 Infection States (I3), Recovery (R) and Death (D)	Mejía Becerra et. al. (2020)	YES
SEIQR	Susceptibility (S), Exposure (E), Infection (I), Quarantine (Q) and Recovery (R)	Huang (2016)	NOT
SIRS	Susceptibility (S), Infection (I), Recovery (R) and Susceptibility (S)	Cai (2015)	NOT

Then, an epidemiological model is defined based on differential equations that explain the evolution of the process without human intervention. These differential equations can be established based on the population (number of people) who are in a certain "epidemic" state or based on the fraction of the population that is in that state. The epidemic models are nonlinear systems of ordinary differential equations, traditionally this equations system is solved using simulation models based in a discrete approximation for continuous derivatives, be it over time or space. There are many possible schemes. These models are used to analyze several widely discussed (predefined) scenarios and provide evidence on their effectiveness and are not oriented to get the optimal solution of a mix of control policies.

The added value by mathematical programming approach is to convert simulation models into optimization models to be able to combine them with other mathematical programming models, following the principles of structured mathematical modeling that allows join multiple problems of mathematical programming in a single model. Based on the above, the formulation of the models is done by means of algebraic equations that represent how the epidemiological process evolves during the planning horizon.

For the optimization epidemic modeling, the approach is based on multiple state chains that can be associated with semi-Markov chains; initially, it was proposed to model based on the approach of semi-Markovian processes (changing transition matrices over time) but such an approach brings multiple complications in the math formulation of probabilities.

After analyzing the implementation of main (most known) epidemiological models (SIR, SEIR), it was decided to directly model discrete versions of differential equations as they maintain direct connection with biological parameters, which facilitates the connection of these parameters with socio-demographic segments.

Therefore, all epidemiological models considered should be formulated in one of the following terms.

- The time unit of the differential equations is one day.
- The states contain the fraction of the population in each state.
- The time of the optimization model may be divided in periods of multiple days (one week, seven days). In this case, the integration of the differential equations must be made using calculated parameters.

The epidemic states are showed in the master table **MAE_STA**. The models will be implemented using this nomenclature. The table includes the symbol used in the original models and the code used in the information system to reference the state.

EPIDEMIC STATES - TABLE: MAE_STA			
MODEL SYMBOL	**EPIDEMIC STATE (COD_STA)**	**DESCRIPTION (DIN_STA)**	**COMMENTS (DLIN_STA)**
S	SU	Susceptible Population	Those individuals who have not been exposed to the pathogen and are susceptible to being infected by it.
E	EX	Exposed Population	Those individuals who are in the latency state; that is, they have been inoculated by the pathogen but are not yet infectious
I	IN	Infected Population	In SIR and SEIR models is infected population. It must be the most critical state for infected people; this is important for models that have more than one epidemic states to describe the infection process.
I_0	I0	Asymptomatic Infectious	Those individuals in the population who have been inoculated by the virus are infectious but have not developed symptoms. Those infected in this state rarely learn that they have been infected.
I_1	I1	Moderate Symptoms Infectious	Those individuals in the population who are infectious and have mild or moderate symptoms. They are those who can be given management of the disease at home.
I_2	I2	Severe Symptoms Infectious	Those individuals in the population who are infectious and have severe but not critical symptoms. Individuals present in this state require hospitalization.
I_3	IN	Critical Symptoms Infectious	It must be the most critical state for infected people; this is important for models that have more than one epidemic states to describe the infection process. In SIR and SEIR models is infected population
R	RE	Recovered Population	Those individuals recover from infection, having developed antibodies. In most of the models they cannot be re-infected.
	ED	Epidemic Dead	Individuals who fail the infection and die.
	ND	Natural Dead	Individuals who die by other reason different to the epidemic
	NP	New Population	Individuals coming from an exogenous macro-region.

The indexes used in the modeling are presented in the next table.

INDEXES		
Index HEA	**Short Description (Entities)**	**Long Description**
ag	Age	Age
mr	Macro-region	Macro-Region
rg, ro, rd	Region	Region (Basic Territory Unit)
ss	Social Segment	Socio-Demographic Segment
st, s1	Epidemic State	Epidemic State
t, q	Period	

The measurements used must be equal for all models

Measurement Unit Master Table: MAE_UND	
Measurement Unit COD_UND	**Description DES_UND**
1/peo-day	1/ persons-day
fpo/day	Fraction of population per day
peo-day	Persons-day

One of the main limitations of the traditional approach is to assume that the entire population is homogeneous with respect to its epidemiological behavior. It is well known that the epidemic manifests

differently in each socio-demographic stratum and that the composition of socio-demographic segments depends on each region.

In order to enhance the model to be useful in real cases, it is assumed that there is a different pandemic (because it has different parameters) for each pair <region, demographic-segment. These hypotheses may vary according to each case study. In this case, reference has been made to the data used to control the epidemic in a macro-region. It should be noted that the parameters of each epidemiological model vary in quantity but do not vary in the form of calculation, since they are parameters as the same case, which is studied with different mathematical models.

The models are studied under the hypothesis of a homogeneous population in a region, then the epidemic is assumed to be particular to each duple <rg,ss> and the equations are formulated depending on <rg,ss>. The advantage of this approach will be visualized when the epidemic model is coupled with the management of health resources and control policies, which can be individualized for each duple <rg,ss>.

The model parameters can be grouped by the original source of variation, these sources are:
- Pathogen: characteristics of the epidemic due to the pathogen
- Age: It is typical for recovery/worsening times (rates) and probability of recovery to be a function of age.
- Economic stratum: influences the epidemic by means of the intensity of contact, product of the number of contacts, the duration of contacts and the closeness, these variables may also be a combined function of age and economic.

Additionally, may be considered people coming for the exogenous systems (out of the microregion) to the region.

In this case, the socio-demographic segments are a combination of age with an economic stratum. The biological parameters depend on age.

2. GENERAL SIMULATION EPIDEMIC MODEL

Below is presented an aggregate model of epidemic that is the result of integrating the **SIR** model, **SEIR** and **SEI3RD**; in these standard models the population is grouped in only one homogenous group. **SEIMR/R-S** extends the modeling to a multi-segment-sociodemographic multi-region system.

The general assumptions for standard epidemic models are:
- No vaccine exists
- The susceptible population is reduced through infection (moving to infective state).
- People who recovered after catch the virus will be insusceptible of it
- The population of infective class is increased by a fraction of susceptible individuals becoming infective.
- All other people are susceptible
- The population is homogenous
- The population of "critical" infective individuals is reduced by recovery from the disease.

SEIMR/R-S model describes the epidemic with following states:

S **Susceptible:** initially covers all population that potentially can be infected (SU)

E **Exposed:** Population that has been infected and are in an incubation (latency) period (EX). The model SIR does not include this state.

IM **Multi-Infected:** Population that has been infected and has active the pathogen in different states of development (I0, I1,I2, … , IN). The active infected states are ordered according to the severity of the infection. The modeled SIR and SEIR consider only one infected state. For convenience, the last state is called "IN"

R **Recovered:** Recovering population (RE)

R-S is related with the Region-Segment model that considers multiples regions where live people classified in multiples socio-demographics segments.

The next table shows the relation between models and epidemic states.

Model	SEIMR/R-S Model Epidemic States												
	Standard								Extended			Capacity	
	SU	EX	I_0	I_1	I_2	...	I_N	RE	NP	ED	ND	IU	CD
SIR	x						x	x					
SEIR	x	x					x	x					
SEI3RD	x	x	x	x	x	x	x	x		x			
SEIMR/R-S	x	x	x	x	x	x	x	x	x	x	x	x	x

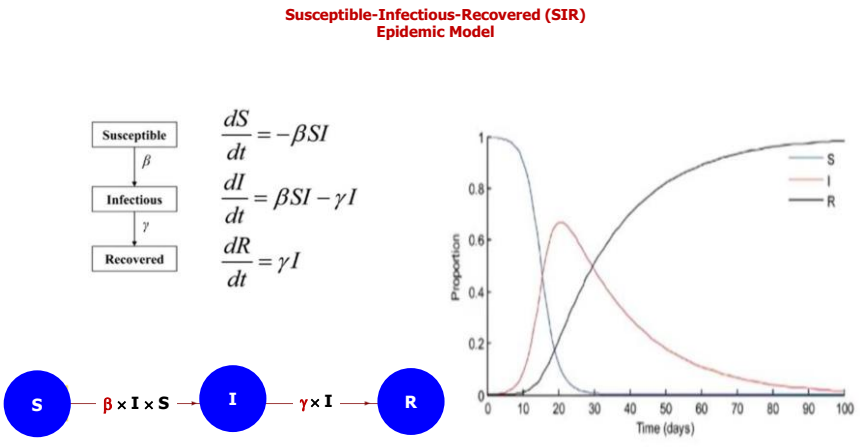
2.1. SIR: EPIDEMIC MODEL

The **SIR** model is a basic model in epidemic modeling (Kermack and Mc Kendrick, 1927). **SIR** process, starting with a susceptible host who becomes infected, the class of infection grow for the infected individuals to be able to transmit the infection to susceptible. When the infected individual is no longer able to transmit infection to susceptible individual, the infected individual is removed from the cycle of diseases transmission in the population. This model is based on the following assumption:

Then, the basic **SIR** model describes the epidemic with three states:
S Susceptible: initially covers all population that potentially can be infected **(SU)**
I Infected: Population that has been infected (IN)
R Recovered: Recovering population (RE)
The diagram shows the behavior of **S(t)**, **I(t)**, and **R(t)** when they are normalized to total of population (**TPOB**) equal to 1. The biological parameters used in SIR and SEIR model are described below.

SIR MODEL - BIOLOGICAL PARAMETERS			
Parameter	**Description**	**Equation**	**Measure Unit**
δ	Contact Intensity – Exogenous Parameter		peo-day
ω	Probability of transmission per contact intensity (infectivity)		
γ	Recovery rate for clinically ill		fpo/day
μ	Epidemic death (mortality) rate		fpo/day
μ^N	Natural mortality rate		fpo/day
κ	The latency period of the virus before developing		day
ψ	Inverse virus latency period	$1/\kappa$	$1/\kappa$
β	Inverse contact intensity × infectivity	$\delta\delta \times \omega$	$\delta\delta \times \omega$
ρ	Relative removal rate	γ/β	
R_0	Basic reproduction ratio/number		

The diagram resumes the standard SIR epidemic model.



SIR model is represented based on three differential equations based on proportions of people in each state (the ratio between the people in a state with the initial population **TPOB**). The measurements between parenthesis.

$$\partial \mathbf{S(t)}/\partial \mathbf{t}\ (\text{fpo/day}) = -\ \beta\ (1/\text{fpo-day}) \times \mathbf{I(t)}\ (\text{fpo}) \times \mathbf{S(t)}\ (\text{fpo})$$

$$\partial \mathbf{I(t)}/\partial \mathbf{t}\ (\text{fpo/day}) = \beta\ (1/\text{fpo-day}) \times \mathbf{I(t)}\ (\text{fpo}) \times \mathbf{S(t)}\ (\text{fpo}) - \gamma\ (\text{fpo/day}) \times \mathbf{I(t)}\ (\text{fpo})$$

$$\partial \mathbf{R(t)}/\partial \mathbf{t}\ (\text{fpo/day}) = \gamma\ (\text{fpo/day}) \times \mathbf{I(t)}\ (\text{fpo})$$

where **S(t)**, **I(t)**, **R(t)** represent the population of susceptible, infected, and recovered individuals, respectively. Adding these equations, the following condition must be hold

$$\partial \mathbf{S(t)}/\partial \mathbf{t} + \partial \mathbf{I(t)}/\partial \mathbf{t} + \partial \mathbf{R(t)}/\partial \mathbf{t} = \mathbf{0}$$

Additionally, **SIR** can be extended with other epidemic states for a more complete description of the system/epidemic:

NP New population entering the system, as people from abroad who in many cases are the ones who cause the epidemic (NP).

ED People who die due to the epidemic (these people die regardless of the management of the epidemic (D).

ND People who die from natural death (N)

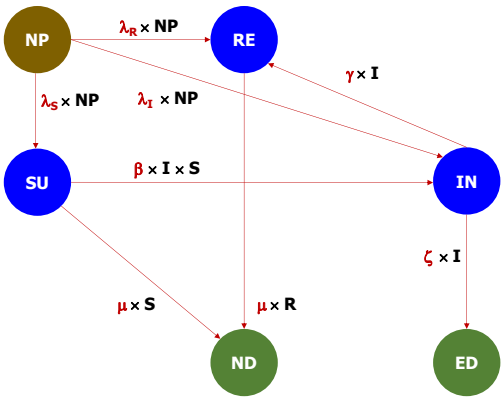
ND and **ED** states should be included if it wants to account for the resources consumed by people who die, who are killed due the epidemic and due by causes other than the epidemic.

For a more general formulation it is included the exogenous variable **NPX(t)** tha represents the proportion of people arriving from an exogenous system, may be births or people arriving from a foreign country/region. The value of **NPX(t)** is a border condition with the foreign system over any value of **t** it is calculated taking as reference the initial population **TPOB**. This adjustment may be important in regions high people exchange rates islands dedicated to tourism. Next table shows the parameters used to this modeling.

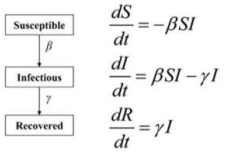
EXOGENOUS SYSTEM PARAMETERS		
Parameter	**Description**	**Measure Unit**
λ^E	Exposed rate coming from the exogenous system	fpo/day
λ^S	Susceptible rate coming from the exogenous system	fpo/day
λ^I	Infectious rate coming from the exogenous system	fpo/day
λ^R	Recovered rate coming from the exogenous system	fpo/day

Next diagram shows the epidemic system modeled.

STATE TRANSITION DIAGRAM - SIR MODEL



STATE	DESCRIPTION
NP	New Population
SU	Susceptive Population
IN	Infective Population
RE	Recovered Population
ND	Natural Dead
ED	Epidemic Dead



Then, the differential SIR equations must be adjusted:

$$\partial S(t)/\partial t = -\ \beta \times I(t)\ \times S(t)\ + \lambda^S \times NPX(t) - \mu^N \times S(t)$$

$$\partial I(t)/\partial t = \beta\ (I(t)\ \times S(t) - (\gamma + \zeta) \times I(t) + \lambda^{I} \times NPX(t)$$

$$\partial R(t)/\partial t = \gamma\ \times I(t)\ - \mu^{N} \times R(t) + \lambda^{R} \times NPX(t)$$

$$\partial D(t)/\partial t = \mu \times I(t)$$

$$\partial N(t)/\partial t = \mu^{N} \times S(t) + \mu^{N} \times R(t)$$

where μ^{N} represents the natural mortality rate and λ^{st} the rates coming from the exogenous system to the state st.

If **TPOB** is the initial total population, and it is constant over time, **NPX(t)=0**, the model meets the hypothesis that at all times

$$\mathbf{S(t) + I(t) + R(t) + D(t) + N(t) = 1}$$

If **NPX(t)** is different from zero the previous equation must be adjusted as

$$\mathbf{S(t) + I(t) + R(t) + D(t) + N(t) = 1 + \int_{q\in[0,t]} \partial NPX(q)\ \partial q}$$

To simulate the process the border conditions at the beginning of the simulation horizon are: **S(0), I(0), R(0), D(0)** and **NPX(t),** for all **t.**

Assuming **NPX(t)** equal to zero, the ratio $\rho = \gamma/\beta$ is called the relative removal rate. Thus, dynamics of infectious depends on the following ratio:

$$\mathbf{R_0 = S(0) \times \gamma/\beta}$$

where $\mathbf{R_0}$, called the basic reproduction ratio/number, is defined as the number of secondary infections produced by a single infectious individual during his/her entire infectious period. The role of the basic reproduction number is especially important. However, the following mathematical analysis describes how the basic reproduction number depends on the host population and the infected host.

At time **t = 0**, $\partial \mathbf{I}/\partial \mathbf{t}$ can be written as

$$\mathbf{\partial I/\partial t = (R_0 - 1) \times \gamma \times I(0)}$$

if $\mathbf{R_0} > 1$ then $\partial \mathbf{I}/\partial \mathbf{t} > 0$ and therefore the disease can spread; but if $\mathbf{R_0} < 1$ then the disease dies out. Making mathematical manipulation it is possible to prove that the maximum number of infective at any time is

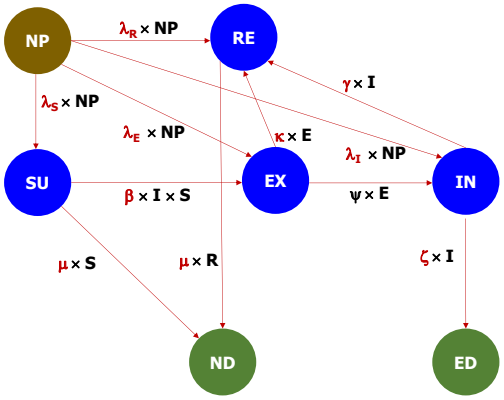
$$\mathbf{TPOB\ (1 - \rho + \rho\ ln\ [\ \rho\ /\ S(0)\ ]\ )}$$

It should be noted that the probability of transition becomes a dynamic variable that must be calculated by the mathematical model, for that reason the **t** index must be included.

2.2. SEIR EPIDEMIC MODEL

The classic SEIR model describes the epidemic dynamics based on the transitions between four different compartments (epidemic states): susceptible (S), exposed (E), infectious (I), and recovered (R) individuals. The SEIR symbols are the same SIR symbols plus the parameter ψ that represents the inverse of the virus latency/incubation period (κ). There are multiple versions of the SEIR model, below are some images summarizing some of the literature consulted: Radulescu & Cavanagh (2020), Hethcote, H. W. (2000), Carcione et a. (2020), Pang, W. (2020), Liu and Liang (2013), Grimm et al. (2020).

STATE TRANSITION DIAGRAM - SEIR MODEL



STATE	DESCRIPTION
NP	New Population
SU	Susceptive Population
EX	Exposed Population
IN	Infective Population
RE	Recovered Population
ND	Natural Dead
ED	Epidemic Dead

$$\frac{dS}{dt} = -\beta I S,$$
$$\frac{dE}{dt} = \beta I S - \varepsilon E,$$
$$\frac{dI}{dt} = \varepsilon E - \gamma I,$$
$$\frac{dR}{dt} = \gamma I,$$

The equations of **SEIR** model are the same as those of **SIR** model considering the following changes:

$$\partial E(t)/\partial t = \beta \times I(t) \times S(t) - \psi \times E(t) + \lambda^E \times NPX(t)$$

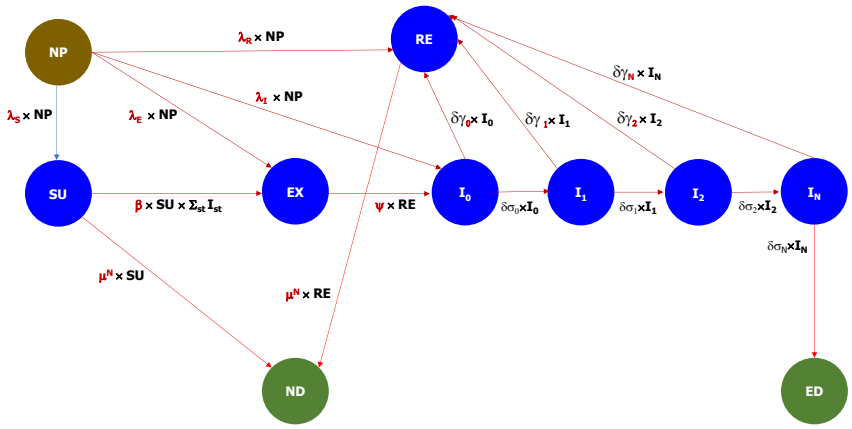
$$\partial I(t)/\partial t = \psi \times E(t) - (\gamma + \zeta) \times I(t) + \lambda^I \times NPX(t)$$

2.3. SEIMR EPIDEMIC MODEL

SEIMR is a generalization of the **SEI3RD** epidemic model that was developed with the aim of simulating the transmission and evolution of acute infections. This simulation assumes that the pathogen causes an infection followed by lifelong immunity or death. Two versions of **SEI3RD** was revised: Grimm et al. (2020) and Mejía Becerra et al. (2020), this version is used in this document.

In **SEI3RD** models the classic **SEIR** model is extended to distinguish between:
i) Several categories of infectiousness; for example: asymptomatic, symptomatic, moderate, and severe cases
ii) Recovered and dead people.
Being able to explicitly distinguish these different groups is important as they can greatly differ in terms of their underlying parameters as well as in terms of their behavioral response to public health interventions compared with the **SEIR** Model.

STATE TRANSITION DIAGRAM – SEI3RD / SEIMRD EPIDEMIC MODELS



The transition between infected states follows this assumptions:
- A person can only be infected by one of the individuals belonging to one of the infected states (I_0, I_1, I_2, I_3, … , I_N). In advance, it will be used the index **st** that is equivalent to index **i**.
- Being inoculated by the pathogen, the individual passes to the group of exposed E.

- After the latency period, the person in the exposed state becomes asymptomatic infectious (I_0 state).
- Once the person is in I_{st} state, there are two possible outcomes: worsening clinical status (moving to mild/moderate/critical infected I_{st+1}) or recovery (R).
- If the person recovers, in any of the states of infection, they enter the absorbent recover state (R).
- Similar logic applies for a larger number of states of infection. It is understood that if an individual of the last state of infection (I3) worsens its clinical condition if it die (E).

Next table shows the biological parameters of **SEI3RD** epidemic model.

BIOLOGICAL PARAMETERS – SEI3RD MODEL			
Parameter	**Description**	**Equation**	**Measure Unit**
μ^N	Natural mortality rate		fpo/day
κ	The latency period of the virus before developing		day
μ	Epidemic mortality rate		fpo/day
ω	Probability of that a person may be contagion		prob
δ_{st}	Probability of I_0, I_1, I_2, I_3, … of recovering		prob
π_{st}	Time a patient in I_0, I_1, I_2, I_3, … recovers		day
η_{st}	Time a patient in I_0, I_1, I_2, I_3, … to next infected state		day
ζ_{st}	Total contact free rate in I_1, I_2, I_3, …		1/day
c_{st}	Free probability of contagion in state I_1, I_2, I_3, …		Prob
γ_{st}	Fraction of people who recover in one day	$1/\pi_{st}$	fpo/day
σ_{st}	Fraction of people who develops symptoms	$1/\eta_{st}$	fpo/day
β_{st}	I_0, I_1, I_2, I_3, … state transmissibility free rate	$-\zeta_{st}\, log(1 - c_{st})$	fpo/day
ψ	Inverse virus latency period	$1/\kappa$	1/day

It should be noted that there are differences in the equations related to transmissibility rate between the formulation presented by Mejía Becerra et al. (2020) and the standard formulations for SIR and SEIR models. This aspect will be analyzed a later numeral.

It is important to understand the relationship between the probability of recovery, the recovery/worsening time, and the rate of departure of people from a state. The output rate from one state to another state may be based on the following expression:

$$\text{Output Rate to State (st)} = \text{Output Probability to State (st)} / \text{Departure Time to State (st)}$$

The total exit rate to any state implies the sum of exit rates to all states.

$$\text{Output Rate} = \Sigma_{st}\ \text{Output Rate to State (st)}$$

The **SEI3RD** equations (Mejía Becerra et al., 2020) of the dynamic model described previously symbolize the proportion of individuals in the population in each of the states (S, E, I_i, R and D), they are:

$$\partial S(t)/\partial t = -\, S(t)\, (\, \beta_0(t) \times\ I_0(t) + \beta_1(t) \times\ I_1(t) + \beta_2 \times\ I_2(t) + \beta_3 \times I_3(t)\,)$$

$$\partial E(t)/\partial t = S(t)\, (\, \beta_0(t) \times\ I_0(t) + \beta_1(t) \times I_1(t) + \beta_2 \times I_2(t) + \beta_3 \times\ I_3(t)\,) - \psi \times\ E(t)$$

$$\partial I_0(t)/\partial t = \psi \times E(t) - \delta_0 \times \gamma_0 \times I_0(t) - (1 - \delta_0) \times \sigma_0 \times I_0(t)$$

$$\partial I_1(t)/\partial t = (1 - \delta_0) \times \sigma_0 \times I_0(t) - \delta_1 \times \gamma_1 \times I_1(t) - (1 - \delta_1) \times \sigma_1 \times I_1(t)$$

$$\partial I_2(t)/\partial t = (1 - \delta_1) \times \sigma_1 \times I_1(t) - \delta_2 \times \gamma_2 \times I_2(t) - (1 - \delta_2) \times \sigma_2 \times I_2(t)$$

$$\partial I_3(t)/\partial t = (1 - \delta_2) \times \sigma_2 \times I_2(t) - \delta_3 \times \gamma_3 \times I_3(t) - (1 - \delta_3) \times \sigma_3 \times I_3(t)$$

$$\partial R(t)/\partial t = \delta_0 \times \gamma_0 \times I_0(t) + \delta_1 \times \gamma_1 \times I_1(t) + \delta_2 \times \gamma_2 \times I_2(t) + \delta_3 \times \gamma_3 \times I_3(t)$$

$$\partial D(t)/\partial t = (1 - \delta_3) \times \sigma_3 \times I_3(t)$$

The following specification must be considered:

1. ψ is the reciprocal of the average latency period.

2. δ_{st} is the likelihood (probability) that an individual in group I_{st} will recover without worsening their clinical condition. This version of SERI3D considers that the people only death, for epidemic reasons, in the last infected state. This limitation may be relaxed but it implies the estimation of more parameters. Then, μ the mortality rate is equal to $\delta_{st,}$ for st equal to the last infected state.

3. γ_{st} is the reciprocal of the average recovery time, without worsening its clinical state, of an individual of class I_{st}.

4. σ_{st} is the reciprocal of the average complication time of a patient in the I_{st} state.

5. β_{st} is the transmissibility rate of an individual in state I_{st}. Mejía Becerra et al. (2020) includes transmissibility rates related with the epidemic control policies, this is ignored in **SEIMR/R-S** general formulation, but it will be presented later in the MBC case.

Then, the equations of **SEI3RD** model are the same as those of the previous **SEIR** model considering the following changes:

$$\partial S(t)/\partial t = -\left[\Sigma_{st\in INF}\,\beta_{st}\times I_{st}(t)\right]\times S(t) + \lambda^{S}\times NPX(t) - \mu^{N}\times S(t)$$

$$\partial E(t)/\partial t = \left[\Sigma_{st\in INF}\,\beta_{st}\times I_{st}(t)\right]\times S(t) - \psi\times E(t) + \lambda^{E}\times NPX(t)$$

$$\partial I_0(t)/\partial t = \psi\times E(t) - \delta\delta_0\times I_0(t) + \lambda^{I}\times NPX(t)$$

$$\partial I_{st}(t)/\partial t = \delta\sigma_{st-1}\times I_{st-1}(t) - \delta\delta_{st}\times I_{st}(t)$$

$$\partial R(t)/\partial t = \Sigma_{st\in INF}\,\delta\gamma_{st}\times I_{st}(t) - \mu^{N}\times R(t) + \lambda^{R}\times NPX(t)$$

$$\partial D(t)/\partial t = \Sigma_{st\in IF}\,\delta\sigma_{st}\times I_{st}(t)$$

The following relations should be considered:

- Equation $\partial \mathbf{I_{st}(t)/\partial t}$ valid for st∈I1F (the set of infected states excluding the first infected state, I_0)
- st∈INF is the set of all infected states
- st∈IF is the set associated to the last infected state.

The following definitions (auxiliary parameters) was included

$$\sigma\delta_{st} = \delta_{st}\times\sigma_{st}$$
$$\delta\sigma_{st} = (1-\delta_{st})\times\sigma_{st} = \sigma_{st} - \sigma\delta_{st}$$
$$\delta\gamma_{st} = \delta_{st}\times\gamma_{st}$$
$$\delta\delta_{st} = (\delta_{st}\times\gamma_{st} + (1-\delta_{st})\times\sigma_{st}) = \delta\gamma_{st} + \delta\sigma_{st}$$
$$\mu = \Sigma_{st\in IF}\,\delta\sigma_{st}$$

The following table resumes the equation included in SEIMR model. The equation has been divided n positive (increment) and negative (decrement) impacts on the state st.

	SEIMR - Differential Equations				
State	st∈SET	State Increment	State Decrement	Natural Dead	Exogenous Increment
$\partial S(t)/\partial t$	SU	$\lambda^{S}\times NPX(t)$	$\beta_{st}\times IS(t)\times S(t)$	$\mu^{N}\times S(t)$	$\lambda^{S}\times NPX(t)$
$\partial E(t)/\partial t$	EX	$\beta_{st}\times IS(t)\times S(t)$	$\psi\times E(t)$		$\lambda^{E}\times NPX(t)$
$\partial I(t)/\partial t$	IN	$\beta_{st}\times IS(t)\times S(t)$	$\delta\delta_{st}\times I_{st}(t)$		$\lambda^{I}\times NPX(t)$
$\partial I_0(t)/\partial t$	I0	$\psi\times E(t)$			$\lambda^{I}\times NPX(t)$
$\partial I_{st}(t)/\partial t$	I1F	$\delta\sigma_{st-1}\times I_{st-1}(t)$			

	SEIMR - Differential Equations				
State	st∈SET	State Increment	State Decrement	Natural Dead	Exogenous Increment
∂R(t)/∂t	RE	$\Sigma_{st\in I1F}\ \delta\gamma_{st} \times I_{st}(t)$		$\mu^N \times R(t)$	$\lambda^R \times NPX(t)$
∂D(t)/∂t	ED	$\Sigma_{st\in IF}\ \mu \times I_{st}(t)$			
		AUXILIARY EQUATION			
		$IS(t) = [\ \Sigma_{st\in INF}\ I_{st}(t)\ ]$			

These equations serve to represent any of the three models studied. The conditions are as follows:

1. SIR Model:
   - Only consider one infected state IN the definitions of the infected state sets are: st∈IF={IN}, st∈I1F={}, st∈I0={}, st∈INF={IN} and st∈IN={IN}
   - Do not include the exposed state (E), that means that st∈EX={}

2. SEIR Model
   - Only consider one infected state IN the definitions of the infected state sets are equal to SIR model.

3. SEIMR Model
   - Considered multiples infected stats {I0, I1, I2,… , IN} IN associate to I_N, do not include the state I_0 that means: st∈IF={I_N}, st∈I1F={I_1, I_2, … , I_N}, st∈I0={I_0}, st∈INF={I_0, I_1, I_2, … , I_N} and st∈IN={I}

The next table presents the SETs of epidemic states needed to model the three epidemics models. The infected sets permit to model any of the three models with the same equations; they are used to define the existence conditions of the equations and in summation limits into the equations.

Epidemic States SETs											
Model	Epidemic States	Non Infected States					Infected States				
	STA	SU	EX	RE	ED	ND	INF	IN	I0	I1F	IF
SIR	S, I, R, D, N	S		R	D	N	I	I			
SEIR	S, E, I, R, D, N	S	E	R	D	N	I	I			
SEIMR	S, E, I_0, I_1, I_2, … , I_N, D, N	S	E	R	D	N	I_0, I_1, I_2, … , I_N		I_0	I_1, I_2, … I_{N-1}	I_N

3. SEIMR/R-S GENERAL EPIDEMIC MODEL

The **SEIMR/R-S** model is built on the basic equations of the **SEIMR** model including the effects of considering the development of the epidemic in a territory (macro-region) that includes multiple regions in which the population socio-demographic segments are distributed in a non-homogeneous manner.

3.1. COMMON ALGEBRAIC NOTATION

Including regional and socio-demographic segment modeling (in this case age and economic stratum) involves associating the biological parameters with these aspects. Therefore, biological parameters may be related to indices: rg (region), ss (socio-demographic segment), ag (age) and/or se (economic stratum).

The next table shows the basic parameters of the **SEIMR** and **SEIMR/R-S** and their relationships.

BIOLOGICAL PARAMETERS – SEI3RD & SEIMR/R-S Models				
SEIMR	**SEIMR/R-S**		**Description**	**Measure Unit**
Parameter	**Parameter**	**Source**		
μ^N	μ^N	Read	Natural mortality rate	fpo/day
κ	κ	Read	The latency period of the virus before developing	day
μ	μ_{ag}	Model	Epidemic mortality rate	fpo/day
ω	$\omega_{rg,ss}$	Model	Probability of that a person may be contagion	prob
δ_{st}	$\delta_{ag,st}$	Model	Probability of I_0, I_1, I_2, I_3, … of recovering	prob
π_{st}	$\pi_{ag,st}$	Model	Time a patient in I_0, I_1, I_2, I_3, … recovers	day

BIOLOGICAL PARAMETERS – SEI3RD & SEIMR/R-S Models				
SEIMR	SEIMR/R-S		Description	Measure Unit
Parameter	Parameter	Source		
η_{st}	$\eta_{ag,st}$	Model	Time a patient in I_0, I_1, I_2, I_3, … to next infected state	day
β_{st}	β	Model	Transmissibility rate of an individual in state st	
ζ_{st}	ζ	Model	Total contact free rate in I_1, I_2, I_3, …	1/day
c_{st}	$c_{ag,st}$	Model	Free probability of contagion in state I_1, I_2, I_3, …	prob

The source **Model** indicates that parameters should be the result of the mathematical model of parameters to be constructed from the regional distribution of socio-demographic segments and their characterization from specific studies developed for the macro-region. This topic will be discussed in detail in the implementation of the City of Bogotá (Velásquez, 2020).

Because the variability of the **SEI3RD** parameters is simpler than that of the **SEIMR/R-S** parameters it is possible to replace the **SEIMR/R-S** parameters with the **SEIMR** to have an equivalent model, but less explanatory of the details that differentiate the epidemic process in the regions.

The calculated biological parameters used in **SEIMR/R-S** model are presented below; they are divided in basic and auxiliary parameters that are included to make easier the implementation process.

BIOLOGICAL PARAMETERS (CALCULATED) - SEIMR/R-S MODEL					
SEIMR		SEIMR/R-S		Description	Measure Unit
Parameter	Equation	Parameter	Equation		
γ_{st}	$1/\pi_{st}$	$\gamma_{ag,st}$	$1/\pi_{ag,st}$	Fraction of people who recover in one day	fpo/day
σ_{st}	$1/\eta_{st}$	$\sigma_{ag,st}$	$1/\eta_{ag,st}$	Fraction of people who develops symptoms	fpo/day
β_{st}	$-\xi_{st}\log(1-c_{st})$	β_{st}	$-\xi_{st}\log(1-c_{ag,st})$	I_0, I_1, I_2, I_3, … state transmissibility rate	fpo/day
ψ	$1/\kappa$	ψ	$1/\kappa$	Inverse virus latency period	1/day
$\sigma\delta_{st}$	$\delta_{st}\,\sigma_{st}$	$\sigma\delta_{ag,st}$	$\delta_{ag,st}\,\sigma_{ag,st}$	$\delta_{ag,st}\,\sigma_{ag,st}$	
$\delta\sigma_{st}$	$(1-\delta_{st})\,\sigma_{st}$	$\delta\sigma_{ag,st}$	$(1-\delta_{ag,st})\,\sigma_{ag,st}$	$(1-\delta_{ag,st})\,\sigma_{ag,st}$	
$\delta\gamma_{st}$	$\delta_{st}\,\gamma_{st}$	$\delta\gamma_{ag,st}$	$\delta_{ag,st}\,\gamma_{ag,st}$	$\delta_{ag,st}\,\gamma_{ag,st}$	
$\delta\delta_{st}$	$\delta\gamma_{st}+\delta\sigma_{st}$	$\delta\delta_{ag,st}$	$\delta\gamma_{ag,st}+\delta\sigma_{ag,st}$	$\delta\gamma_{ag,st}+\delta\sigma_{ag,st}$	
μ	$\Sigma_{st\in IF}\,\delta\sigma_{st}$	μ_{ag}	$\Sigma_{st\in IF}\,\delta\sigma_{ag,st}$	$\Sigma_{st\in IF}\,\delta\sigma_{ag,st}$	
		$\beta\rho_{rg,ss}$	Model	Contagion probability function of regional and socio-demographics characteristics	prob
		$\beta\beta_{rg,ss}$	$\Sigma_{ag\in AGS(ss)}\,\delta\delta_{ag,st}\times\beta\rho_{rg,ss}$	Inverse contact intensity × infectivity	1/fpo-day

3.2. REGIONAL-SEGMENT MODELING

3.2.1. REGIONAL MODELING

To formulate the regional model segmented socio-demographically the following hypotheses are assumed:

- There is no contagion between people living in different regions. This can be true for large regions such as states or departments. But it is questionable for metropolitan areas (cities and conurbed regions) where there is intense traffic between regions.

- The inter-region interrelationship is modeled on the following assumptions:
  - There is traffic of people between regions, which sets for each pair of regions the fraction of each segment, $\varphi_{ro,rg,ss}$, moving from the source region (ro) to the destination region (rg).
  - In addition, the fraction of the time, $\phi_{ro,rg,ss}$, is known to people from the region origin in the destination region during the period (one day).

The calculation process involves determining the impact on the spread of the virus that the population movement has for this purpose it is calculated using the number of infected people who can move between two regions multiplied by the fraction of the time spent in the destination locality. This implies the following effects on the diffusion rate:

1. Infected Movements

   - Increasing the rate of diffusion in the destination locality due to those infected by coming from other regions, it is calculated as:

$$\mathbf{II_{rg}(t)} = \Sigma_{ss \in SSR(rg)} \Sigma_{ro \in ROR(rg)} \varphi_{ro,rg,ss} \times \phi_{ro,rg,ss} \times \mathbf{IS_{ro,ss}(t)}$$

   - Decreased diffusion rate in the source region due to the infected by moving to other regions, it is calculated as:

$$\mathbf{IE_{rg}(t)} = \Sigma_{ss \in SSR(rg)} \Sigma_{rd \in RDE(rg)} \varphi_{rg,rd,ss} \times \phi_{rg,rd,ss} \times \mathbf{IS_{rg,ss}(t)}$$

   The net effect on the rg-region will be:

$$\mathbf{IS_{rg,ss}(t)} = \Sigma_{st \in INF} \mathbf{I_{st,rg,ss}(t)}$$

$$\mathbf{IX_{rg}(t)} = \Sigma_{ss \in SSR(rg)} \mathbf{IS_{rg,ss}(t)}$$

$$\mathbf{IR_{rg}(t)} = \mathbf{IX_{rg}(t)} + \mathbf{II_{rg}(t)} - \mathbf{IE_{rg}(t)}$$

   where

$\mathbf{I_{st,rg,ss}(t)}$	fraction of the population infected in st-epidemic-state living in rg-region and ss-segment.
$\mathbf{IS_{rg,ss}(t)}$	fraction of the population infected living in rg-region and ss-segment.
$\mathbf{IX_{rg}(t)}$	fraction of the population infected living in rg-region
$\mathbf{II_{rg}(t)}$	weighted fraction of the population infected traveling to rg-region
$\mathbf{IE_{rg}(t)}$	weighted fraction of the population infected traveling from rg-region

2. Susceptible Movements

   - Increasing the rate of diffusion in the destination locality (rg-region) due to those susceptible people by coming from other regions that may be infected in rg-region, it is calculated as:

$$\mathbf{SI_{ro,rg,ss}(t)} = \varphi_{ro,rg,ss} \times \phi_{ro,rg,ss} \times \mathbf{S_{ro,ss}(t)}$$

   The following replace of parameter will be included

$$\varphi\phi_{ro,rg,ss} = \varphi_{ro,rg,ss} \times \phi_{ro,rg,ss}$$

   - Decreased diffusion rate in the source region (rg-region) due to the susceptible people by moving to other regions that cannot be infected in rg-region, it is calculated as:

$$\mathbf{SE_{rg,rd,ss}(t)} = \varphi\phi_{rg,rd,ss} \times \mathbf{S_{rd,ss}(t)}$$

   The susceptible population living in the rg-region ss-segment must be decremented by the susceptible people belonging to other regions:

$$\mathbf{SN_{rg,ss}(t)} = \mathbf{S_{rg,ss}(t)} - \Sigma_{rd \in RDE(rg)} \mathbf{SE_{rg,rd,ss}(t)}$$

   where

$\mathbf{S_{rg,ss}(t)}$	fraction of the susceptible population living in rg-region and ss-segment.
$\mathbf{SI_{ro,rg,ss}(t)}$	fraction of the ss-segment susceptible population traveling from ro-region to rg-region
$\mathbf{SE_{rg,rd,ss}(t)}$	fraction of the ss-segment susceptible population traveling from rg-region to rd-region

Next table resume the parameters associated with regional modeling

REGIONAL MODELING PARAMETERS – SEIMR/R-S MODEL			
Parameter	**Source / Equation**	**Description**	**Measure Unit**
$\varphi_{ro,rg,ss}$	Model	Fraction of ss-segment population moving from the source region (ro) to the destination region (rg)	fpo/day
$\phi_{rg,rd,ss}$	Model	Fraction time that spend the ss-segment population of the source region (ro) into the destination region (rg)	hour/day
$\varphi\phi_{rg,rd,ss}$	$\varphi_{rg,rd,ss} \times \phi_{rg,rd,ss}$	$\varphi_{rg,rd,ss} \times \phi_{rg,rd,ss}$	hour/day

3.2.2. SOCIO DEMOGRAPHIC SEGMENT MODELING

An infected person in any segment can infect anyone susceptible in any socio-demographic segment.

The calculation process implies that at the level of one region the population of any segment can infect the population of any other segment. To do this, diffusion (infection of susceptible from infected) is managed at a detailed level in the differential equations for all infected states, but in the differential equation the infected transmission is calculated based on the summation of all infected states in all ss-segments.

In traditional aggregated models, this the transfer rate β (the inverse of contact intensity multiplied by the transmission probability) is assumed fixed for all region and all socio demographics segments. In **SEIMR/R-S** the transfer rate depends on the socio-demographic segment in a region and it is called $\beta\beta_{rg,ss}$, this parameter must be calculated by the parameters model.

Then, the contagion of the susceptible population living in the rg-region and belonging to the ss-segment will be the sum of the contagions that occur in the rg-region (people that do not travel out of the rg-region) plus the contagions that occur in the rd destination regions this is

$$\mathbf{S2I_{rg,ss}(t) = \beta\beta_{rg,ss} \times IR_{rg}(t) \times SN_{rg,ss}(t) + \Sigma_{rd \in RDE(rg)}\, \beta\beta_{rd,ss} \times IR_{rd}(t) \times SE_{rg,rd,ss}(t)}$$

3.3. GENERAL FRAMEWORK

The differential equations of the regional-segmented model are:

$$\partial S_{rg,ss}(t)/\partial t = - S2I_{rg,ss}(t) - \mu^N \times S_{rg,ss}(t) + \lambda^S{}_{rg,ss} \times NPX(t)$$

$$\partial E_{rg,ss}(t)/\partial t = S2I_{rg,ss}(t) - \psi \times E_{rg,ss}(t) + \lambda^E{}_{rg,ss} \times NPX(t)$$

st=I0

$$\partial I_{st,rg,ss}(t)/\partial t = \psi \times E_{rg,ss}(t) - \delta\alpha_{st,ss} \times I_{st-1,rg,ss}(t) + \lambda^I{}_{rg,ss} \times NPX(t)$$

st∈I1F

$$\partial I_{st,rg,ss}(t)/\partial t = \delta\zeta_{st-1,ss} \times I_{st-1,rg,ss}(t) - \delta\alpha_{st,ss} \times I_{st,rg,ss}(t)$$

$$\partial R_{rg,ss}(t)/\partial t = \Sigma_{st \in I1F}\, \delta\beta_{st-1,ss} \times I_{st,rg,ss}(t) - \mu^N \times R_{rg,ss}(t) + \Sigma_{ss \in SSR(rg)}\, \lambda^R{}_{rg,ss} \times NPX(t)$$

$$\partial D_{rg,ss}(t)/\partial t = \Sigma_{st \in I1F}\, \mu\sigma_{ss} \times I_{st,rg,ss}(t)$$

$$\partial NR_{rg}(t)/\partial t = \mu^N \times SR_{rg,ss}(t) + \mu^N \times RR_{rg}(t)$$

where the following rates are defined for the socio-demographic segments

SOCIO-DEMOGRAPHIC BIOLOGICAL PARAMETERS		
Parameter	Equation	Description
$\delta\alpha_{st,ss}$	$\Sigma_{ag \in AGS(ss)}\, \delta\delta_{ag,st}$	Total exit rate
$\delta\zeta_{st,ss}$	$\Sigma_{ag \in AGS(ss)}\, \delta\sigma_{ag,st}$	Worsening exit rate
$\delta\beta_{st,ss}$	$\Sigma_{ag \in AGS(ss)}\, \delta\gamma_{st,ag}$	Recovering exit rate
$\mu\sigma_{ss}$	$\Sigma_{ag \in AGS(ss)}\, \mu_{ag}$	Mortality rate depending on segment
μ_{ag}	$\Sigma_{st \in I1F}\, \delta\sigma_{ag,st}$	Mortality rate depending on age

The definition equations of the regional-segmented model are:

$$IS_{rg,ss}(t) = \Sigma_{st \in INF}\ I_{st,rg,ss}(t)$$
$$IX_{rg}(t) = \Sigma_{ss \in SSR(rg)}\ IS_{rg,ss}(t)$$
$$II_{rg}(t) = \Sigma_{ss \in SSR(rg)}\ \Sigma_{ro \in ROR(rg)}\ \varphi\phi_{ro,rg,ss} \times IS_{ro,ss}(t)$$
$$IE_{rg}(t) = \Sigma_{ss \in SSR(rg)}\ \Sigma_{rd \in RDE(rg)}\ \varphi\phi_{rg,rd,ss} \times IS_{rg,ss}(t)$$
$$IR_{rg}(t) = IX_{rg}(t) + II_{rg}(t) - IE_{rg}(t)$$

$$SR_{rg}(t) = \Sigma_{ss \in SSR(rg)}\ S_{rg,ss}(t)$$
$$SI_{ro,rg,ss}(t) = \varphi\phi_{ro,rg,ss} \times S_{ro,ss}(t)$$
$$SE_{rg,rd,ss}(t) = \varphi\phi_{rg,rd,ss} \times S_{rd,ss}(t)$$
$$SN_{rg,ss}(t) = S_{rg,ss}(t) - \Sigma_{rd \in RDE(rg)}\ SE_{rg,rd,ss}(t)$$
$$SIN_{rg}(t) = \beta\beta_{rg,ss} \times IR_{rg}(t) \times SN_{rg,ss}(t)$$
$$SIE_{rg,ss}(t) = \Sigma_{rd \in RDE(rg)}\ \beta\beta_{rd,ss}\ IR_{rd}(t) \times SE_{rg,rd,ss}(t)$$
$$S2I_{rg,ss}(t) = SIN_{rg}(t) + SIE_{rg}(t)$$

$$RR_{rg}(t) = \Sigma_{ss \in SSR(rg)}\ R_{rg,ss}(t)$$

$$DR_{rg}(t) = \Sigma_{ss \in SSR(rg)}\ D_{rg,ss}(t)$$

From now on, the above mathematical definitions will be summarized as

$$\mathbf{\{\ S,\ E,\ I_{st}\ ,\ D,\ N\ \}} \in \Theta$$

The next table shows the equations dividing the increment and the decrement on each state, it must be considered in the implementation of the mathematical models. The table includes the sets that defined the existence of the equations manly for the infected states.

	SIR Regional – Segmented Model - Differential Equations				
Set	State	State Increment	State Decrement	Natural Dead	Exogenous Increment
	REGIONAL - SEGMENT EQUATIONS				
SU	$\partial S_{rg,ss}(t)/\partial t$		$S2I_{rg,ss}(t)$	$\mu^N \times S_{rg,ss}(t)$	$\lambda^S_{rg,ss} \times NPX(t)$
EX	$\partial E_{rg,ss}(t)/\partial t$	$S2I_{rg,ss}(t)$	$\psi \times E_{rg,ss}(t)$		$\lambda^E_{rg,ss} \times NPX(t)$
I0	$\partial I_{st,rg,ss}(t)/\partial t$	$\psi \times E_{rg,ss}(t)$	$\delta\alpha_{st,ss} \times I_{st,rg,ss}(t)$		$\lambda^I_{rg,ss} \times NPX(t)$
I1F	$\partial I_{st,rg,ss}(t)/\partial t$	$\delta\zeta_{st-1,ss} \times I_{st-1,rg,ss}(t)$			
RE	$\partial R_{rg,ss}(t)/\partial t$	$\Sigma_{st \in I1F}\ \delta\beta_{st,ss} \times I_{st,rg,ss}(t)$		$\mu^N \times R_{rg,ss}(t)$	$\lambda^R_{rg,ss} \times NPX(t)$
ED	$\partial D_{rg,ss}(t)/\partial t$	$\Sigma_{st \in I1F}\ \mu\sigma_{ss} \times I_{st,rg,ss}(t)$			
ND	$\partial NR_{rg}(t)/\partial t$	$\mu^N \times (\ SR_{rg}(t) + RR_{rg}(t)\ )$			

SUSCEPTIBLE STATE EQUATIONS
$SR_{rg}(t) = \Sigma_{ss \in SSR(rg)}\ S_{rg,ss}(t)$
$SI_{ro,rg,ss}(t) = \varphi\phi_{ro,rg,ss} \times S_{ro,ss}(t)$
$SE_{rg,rd,ss}(t) = \varphi\phi_{rg,rd,ss} \times S_{rd,ss}(t)$
$SN_{rg,ss}(t) = S_{rg,ss}(t) - \Sigma_{rd \in RDE(rg)}\ SE_{rg,rd,ss}(t)$
$SIN_{rg,ss}(t) = \beta\beta_{rg,ss} \times IR_{rg}(t) \times SN_{rg,ss}(t)$
$SIE_{rg,ss}(t) = \Sigma_{rd \in RDE(rg)}\ \beta\beta_{rd,ss}\ IR_{rd}(t) \times SE_{rg,rd,ss}(t)$
$S2I_{rg,ss}(t) = SIN_{rg}(t) + SIE_{rg}(t)$
INFECTED STATE EQUATIONS
$IS_{rg,ss}(t) = \Sigma_{st \in INF}\ I_{st,rg,ss}(t)$
$IX_{rg}(t) = \Sigma_{ss \in SSR(rg)}\ IS_{rg,ss}(t)$
$II_{rg}(t) = \Sigma_{ss \in SSR(rg)}\ \Sigma_{ro \in ROR(rg)}\ \varphi\phi_{ro,rg,ss} \times IS_{ro,ss}(t)$
$IE_{rg}(t) = \Sigma_{ss \in SSR(rg)}\ \Sigma_{rd \in RDE(rg)}\ \varphi\phi_{rg,rd,ss} \times IS_{rg,ss}(t)$
OTHER EQUATIONS
$RR_{rg}(t) = \Sigma_{ss \in SSR(rg)}\ R_{rg,ss}(t)$
$DR_{rg}(t) = \Sigma_{ss \in SSR(rg)}\ D_{rg,ss}(t)$

4. CASE: SEI3RD BOGOTA EPIDEMIC MODEL

To validate the **SEIMR/R-S** was selected the **SEI3RD** model used by the Mayor of Bogotá City (**MBC** Colombia). The version used is reported in Mejía Becerra (2020).

4.1. BIOLOGICAL PARAMETERS

The **SEI3RD** (used by MBC) is a particular case of **SEIMR/R-S**, so we should analyze how to enhance equivalent runs in such a way that you can compare the results.

Considering that the parameters used **SEI3RD** do not depend on the age and that they do not are the result of an explicit calculus process it is included an equivalent read parameters process to simulate the case of Bogotá with the **SEIMR/R-S** model. Next table shows the relationship between the two set of parameters. It includes parameters to management simple quarantine control policies (ξ^{Q}_{st} and c^{Q}_{st}).

BIOLOGICAL PARAMETERS – SEI3RD & SEIMR/R-S MODELS			
SEI3RD Parameter	**SEIMR/R-S Parameter**	**Description**	**Measure Unit**
μ^{N}	μ^{N}	Natural mortality rate	fpo/day
κ	κ	The latency period of the virus before developing	day
μ	μ_{ag}	Epidemic mortality rate	fpo/day
ω	$\omega_{rg,ss}$	Probability of that a person may be contagion	prob
δ_{st}	$\delta_{ag,st}$	Probability of I_0, I_1, I_2, I_3, … recovering without worsening the clinical condition.	prob
π_{st}	$\pi_{ag,st}$	Time a patient in I_0, I_1, I_2, I_3, … recovers	day
η_{st}	$\eta_{ag,st}$	Time a patient in I_0, I_1, I_2, I_3, … to next infected state	day
ζ_{st}	ζ	Total contact free rate in I_1, I_2, I_3, …	1/day
ζ^{Q}_{st}	ζ^{Q}	Total contact confined rate in I_1, I_2, I_3, …	1/day
c_{st}	$c_{ag,st}$	Probability of contagion in free state I_1, I_2, I_3, …	prob
c^{Q}_{st}	$c^{Q}_{ag,st}$	Probability of contagion in confined state I_1, I_2, I_3, …	Prob
β_{st}	β	Transmissibility rate of an individual in state st	
β^{Q}_{st}		Transmissibility rate of an individual in state st on quarantine	
$\beta\delta_{t,st}$		Dynamic rate of transmissibility calculated as $\beta\delta_{t,st} = (1 - \theta_{t,st}) \times \beta^{Q}_{st} + \theta_{t,st} \times \beta_{st}$	
$\theta_{t,st}$		Epidemic control parameter (proportion of the st-state that circulates freely)	

Because the variability of the **SEI3RD** parameters is simpler than that of the **SEIMR/R-S** parameters it is possible to replace the **SEIMR/R-S** parameters with the **SEI3RD** and have an equivalent model, but less explanatory of the details that differentiate sociodemographic segments and regions.

4.2. EPIDEMIC CONTROL POLICIES

In the analysis presented by the MBC, two scenarios are established:
i) The population has no restrictions (the individual can move freely), and
ii) The quarantined population (individuals stay in their homes), to achieve this is modeled the dynamic changes in the rate of transmissibility $\beta\delta_{t,st}$.

The MBC calculates $\beta\delta_{st,t}$ as

$$\beta\delta_{st,t} = (1 - \theta_{t,st}) \times \beta^{Q}_{st} + \theta_{t,st} \times \beta_{st}\ ,\ \ \forall st = I0, I1$$

$\beta\delta_{st,t}$ is calculated for moderate asymptomatic and symptomatic individuals. β_{st} and β^{Q}_{st} are transmissibility rates for an asymptomatic or moderate individual who circulates freely within the population and an individual who stays in their home, respectively.

$\Phi_{t,st}$ is the epidemic control variable that represents the population fraction of the st-state that circulates freely in the population ($0 \le \theta_{t,st} \le 1$). β_{st} and β^{Q}_{st} are the transmissibility rates for an individual who circulates freely within the population and an individual who stays in their home, respectively. Q superscript indicates the rate associated to a confined state. $\Phi_{t,st}$ is pre-defined by the user.

β_{st} and β^{Q}_{st} can be expressed as the total contact rate (the total number of contacts susceptible by an effective or non-effective infective individual, per unit of time), multiplied by the probability of infection, given the contact between an infectious and susceptible individual. The formulas for the transmissibility rates are

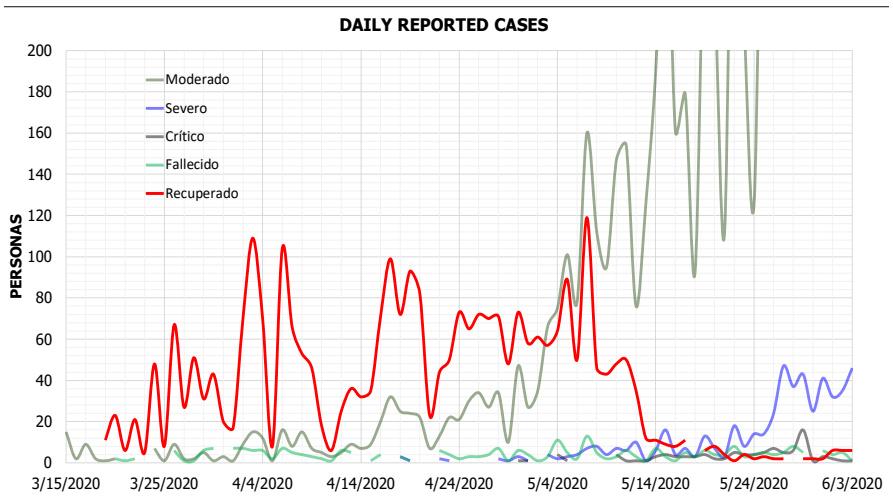
$$\beta_{st} = -\zeta_{st} \log(1 - c_{st}) \approx \zeta_{st} \times c_{st}$$

$$\beta^{Q}_{st} = -\zeta^{Q}_{st} \log(1 - c^{Q}_{st}) \approx \zeta^{Q}_{st} \times c^{Q}_{st}$$

where ζ_{st} and ζ^{Q}_{st} are the average daily effective contact rate for an individual in state I_{st} (i.e. how many contacts a state person has in one day) and c_{st} and c^{Q}_{st} is the contagion probability given effective contact with an individual in the susceptible group.

4.3. HISTORICAL BEHAVIOR OF COVID 19 IN BOGOTA

The first COVID-19 case reported by the Ministry of Health in Colombia was filed on 6 March 2020 and corresponded to a 19-year-old woman in Bogota arriving from Milan, Italy. In Colombia, it has decreed total quarantine in Colombia from 25 March 2020. By the same day, 470 cases had been reported, of which four patients had died (lethality 0.8%) and eight patients had recovered (recovery rate 1.7%). Regarding the source of contagion, a total of 266 (56.6%) cases were imported, 163 (34.7%) related cases and 41 (8.7%) cases were under study. Bogota was 36% of the cases. As of 31 May 2020, 34.1% of the reported cases in Colombia of COVID-19 were in Bogota, with a total of 9,989 confirmed cases of which, 48.2% are women, and the highest concentration of cases according to age, is between 20 and 39 years with a percentage weight of 42.7%. The following figure presents the historical series of the cases reported in the city of Bogotá until May 31, 2020.



Source:

- Instituto Nacional de Salud de Colombia [Internet] Coronavirus (CO-VID-19) en Colombia. 2020. Citado 1 de junio de 2020. Disponible en: Disponible en: https://bit.ly/2UNnOtl
- Observatorio de Salud de Bogotá. [Internet]. Subsecretaría de Salud Pública. Secretaría Distrital de Salud. 2020. Citado 1 de junio de 2020. Disponible en: http://saludata.saludcapital.gov.co/osb/index.php/datos-de-salud/enfermedades-trasmisibles/covid19/

4.4. DATA USED BY MAYOR OF BOGOTA CITY

The experiments taken as a reference was made by the Mayor of City of Bogotá (**MBC**) correspond to those reported on April 4, 2020 and have as a start date of March 15, 2020, to consider that there is a period between the start date of symptomatic and the date of diagnosis, on this date it was recorded: an individual hospitalized and 115 more symptomatic moderate moderates, in addition, R_0=2.6 was taken, and the MBC assumed, by expert discretion, the average latency time of one day (κ=1). The population of Bogota used was 7'413,000 inhabitants (corresponds to the estimated population for Bogota for 2018, according to Population Projections 2018-2023, DANE). MBC modeling assumes that the entire population

is homogeneous, i.e. no differentiation of the location, age, economic stratum, and activity of individuals is made.

However, following the document "Análisis Demográfico y Proyecciones Poblacionales de Bogotá" (published by MBC in March 2018), the population of Bogotá amounts to the sum 8'380,801 inhabitants. On the other hand, according to MBC's SALUD DATA (HEALTH DATA), the population of Bogotá projected for 2020 was 8,273,319 inhabitants (regardless of the rural town of Sumapaz), which corresponds to an understatement of the population of the order of 11.61%; referring (divisor) the population estimated by the MBC to plan the COVID-19 epidemic. This implies that the amounts estimated by MBC models, to be compared with the reality reported in SALUD DATA, must be multiplied by a factor of 1.1161. This difference in population should not make a difference in the information established in the modelling of fractions of the population, but if it is of fundamental importance when the use of hospital resources is involved in modeling.

Parameter	ASSUMPTIONS AND CONSIDERATIONS MADE BY THE MAYOR OF BOGOTÁ
δ_{st}	Likelihood (probability) of an individual in the st state recovering without worsening their clinical condition. The basic theory of probability to calculate δ_{st} may be used. ▪ Asymptomatic $\delta_{st=I0}$, by expert medical criterion and in accordance with [3, 5] MBC established that 30% of cases are asymptomatic and rarely reported by the authorities. As a result, 70% of the remaining cases are symptomatic. ▪ Symptomatic moderated $\delta_{st=I1}$, according to the report of the world health organization, 80% of the reported cases (which are assumed almost all symptomatic) are mild and moderate. This assumption implies that 80% of symptomatic cases (assumed very similar in magnitude to the reported cases) recover without worsening their condition. ▪ Symptomatic severe $\delta_{st=I2}$, it is assumed that 5 out of 7 cases with severe symptoms recover. This means that, of symptomatic cases, approximately 14.3% (similar to 13.8% reported by [6]) have severe symptoms and recover. ▪ Symptomatic critic $\delta_{st=I3}$, it is assumed that an individual entering the critical state has a 50% chance of recovering. That is, 2% of all cases die. This assumption is the same as that made by Imperial College (IC) [2].
π_{st}	Average recovery time, without worsening their st status: ▪ $\pi_{st=I0}$, according to medical criteria, an infected individual who never develops symptoms is infectious for 10 days. ▪ $\pi_{st=I1}$, a person with moderate symptoms recovers on average on the eighth day of the onset of symptoms. Assumption established from the criterion of the expert physician. ▪ $\pi_{st=I2}$, a person occupies a general hospitalization bed 8 days before recovering. (assumed by (IC)). ▪ $\pi_{st=I3}$, it is estimated that a person lasts ten days in intensive care before recovering. This assumption is the same as that made by (IC).
η_{st}	The average complication time of a patient in the state st ▪ $\eta_{st=I0}$, after the latency period, an individual takes 4.1 days to develop symptoms (taking into account the latency period, this means that the incubation period is 5.1 days, in accordance with [4]) ▪ $\eta_{st=I1}$, from the moment an individual develops moderate symptoms, it takes 5 days to require hospitalization care (assumed by (IC)). ▪ $\eta_{st=I2}$, before moving to ICU a severe symptomatic spends on average six days in a general hospitalization bed (assumed by (IC)). ▪ $\eta_{st=I3}$, it is estimated that a person lasts ten days in intensive care before death (assumed by (IC)).
ε_{st}	Contacts of infected people if there is no quarantine ▪ $\varepsilon_{st=I0}$, is estimated with the basic reproduction number R_0 equivalent to 2.6, the number of people with which an asymptomatic individual has effective contact is 7.16. ▪ $\varepsilon_{st=I1}$, i.e., it is assumed that people with moderate symptoms circulating freely in the population have effective contact with 10 people a day (assumed by (IC)). ▪ $\varepsilon_{st=I2}$, it is assumed that a hospitalized (severe symptomatic) has on average two effective daily contacts ▪ $\varepsilon_{st=I3}$, it is assumed that a person in intensive care has on average two effective contacts (medical expert criterion).
ε^{Q}_{st}	Contacts of infected people if there is no quarantine ▪ $\varepsilon^{Q}_{st=I0}$, it is assumed that asymptomatic people who stay at home have effective contact on average with 2.98 people per day (average number of people per household according to the 2017 multipurpose survey of the district planning secretariat) ▪ $\varepsilon^{Q}_{st=I1}$, it is estimated that a symptomatic individual who stays at home only has contact with the people in the household , which on average is 2.98. ▪ $\varepsilon^{Q}_{st=I2}$, it is assumed that a hospitalized (severe symptomatic) has on average two effective daily contacts. ▪ $\varepsilon^{Q}_{st=I3}$, it is assumed that a person in intensive care also has on average two effective contacts (medical expert criterion).
c_{st}	Probability of contagion if there is no quarantine ▪ $c_{st=I0}$, is estimated with the basic number of reproduction R_0 equivalent to 2.6, the chance of contagion is 10%. ▪ $c_{st=I1}$, it is assumed that for each effective contact you have a possibility of contagion of 1.5%. That is, for every 200 effective contacts between a symptomatic and a moderate symptomatic individual, 3 new cases are generated on average (medical expert criterion).

	▪ $c_{st=I2,I3}$ assumed a 1% chance of contagion for each effective contact (medical expert criterion).
c^{Q}_{st}	Probability of contagion if there is quarantine ▪ $c^{Q}_{st=I0}$, possibility of contagion of 1% for each effective contact. That is, for every 100 effective contacts of a susceptible with an infectious asymptomatic in the population, a new case is generated on average. ▪ $c^{Q}_{st=I1}$, it is assumed that for each effective contact you have a possibility of contagion of 1.5% (medical expert criterion). ▪ $c^{Q}_{st=I2,I3}$, a 1% chance of contagion is assumed for each effective contact (medical expert criterion).

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[3] Mizumoto, K., Kagaya, K., Zarebski, A., &Chowell, G. (2020). Estimating the Asymptomatic Proportion of Coronavirus Disease 2019 (COVID-19) Cases on Board the Diamond Princess Cruise Ship, Yokohama, Japan, 2020. Eurosurveillance, 25(10), 2000180.

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[5] Nishiura, Kobayashi, Miyama, Suzuki, Jung, Hayas- hi, Kinoshita, Yang, Yuan, Akhmetzhanov, and Lin- ton. Estimating the Asymptomatic Proportion of Coronavirus Disease 2019 (COVID-19) cases on Board the Diamond Princess Cruise Ship, Yokoha- ma, Japan, 2020. Osaka Institute of Public Health, 2020.

[6] World Health Organization. Report of the WHO-China Joint Mission on Coronavirus Disease 2019 (COVID-19). 2020.

To use the MBC model, the following assumptions were made with respect to transmissibility rates:

- β_0 = 0.3271875,
  Transmissibility rate of an asymptomatic individual circulating freely in the region. It was estimated in such a way that in the absence of intervention, the basic number of reproduction is equivalent to 2.6 (R_0 is also known as secondary infection rate or contagion rate). Value assumed by b_0, free movement policy.

- β^{Q}_{0} = 0.02995 = 2.98 log(1 – 0.01) ≈ 0.0298. Difference 0.5008%
  It assumes that asymptomatic people who stay at home have effective contact on average with 2.98 people (average people per household in Bogotá, according to the DANE survey) and are assumed, a contagion probability of 0.01 for each effective contact. Value assumed for quarantine policy.

- β_1 = 0.15114 = 10 log(1 – 0.015) ≈ 0.015. Difference 0.7519%
  People with moderate symptoms circulating freely in the population are supposed to have effective contact with 10 people a day and assume that for each effective contact there is a 1.5% chance of contagion. (That is, for every 200 effective contacts between a symptomatic and a moderate symptomatic individual are generated on average 3 new cases).

- β^{Q}_{1} = 0.04504 = 2.98 log(1 – 0.015) ≈ 0.0298. Difference 0.5008%.
  It is estimated that a symptomatic individual who stays at home only has contact with the people in the household. Value assumed for quarantine policy.

- β_2 = 0.0201 = - 2.00 log(1 – 0.015) ≈ 0.02. Difference 0.5008%.
  It is assumed that a hospitalized (severe infected) has on average two effective daily contacts, with a chance of contagion of 1% for each effective contact (medical expert criterion). This probability is lower than that assumed for a moderate infected as biosecurity measures are assumed.

- β_3 = 0.0201 = - 2.00 log(1 – 0.015) ≈ 0.02. Difference 0.5008%.
  It is assumed that a person in intensive care also has on average two effective contacts (medical expert criterion).

According to Mejia Becerra et al. (2020), the assumptions raised by MBC represent the most pessimistic estimates of academic literature. In short, the parameters used are:

1. General Parameters:
   The following table presents general biological parameters:

GENERAL BIOLOGICAL PARAMETER – MBC SEIR3D MODEL				
Parameter	**OPTEX Parameter**	**Description**	**Value**	**Measurement Unit**
μ^N	MIUN	Natural mortality rate	0.00005	fpo/day
κ	KAPP	The latency period of the virus before developing	1	day
μ	MIUUB	Epidemic mortality rate	?	fpo/day
ω	PCONB	Probability of that a person may be contagion	?	prob

2. Epidemic State Dependent Parameters:
   The following table presents epidemic state dependent parameters:

STATE DEPENDENT BIOLOGICAL PARAMETER – MBC SEIR3D MODEL									
State	β_{st}	β^Q_{st}	δ_{st}	π_{st}	η_{st}	ε_{st}	ε^Q_{st}	c_{st}	c^Q_{st}
			(Probability)		**(day)**	**(contacts/day)**		**(Probability)**	
I0	0.3271875	0.02995	0.3000	10.0	4.1	7.16	2.980	0.10	0.010
I1	0.15114	0.04504	0.8000	8.0	5.0	10.00	2.980	0.015	0.015
I2	0.0201	0.0201	0.7143	8.0	6.0	2.00	2.000	0.01	0.01
I3	0.0201	0.0201	0.5000	10.0	10.0	2.00	2.000	0.01	0.01

3. Initial Conditions:
   The following table presents the initial conditions (fraction of the population in each epidemic state)

State	Population Fraction	Population
I0	0.000030352100000000000	225000
I1	0.000015513287467961700	115000
I2	0.000001348980000000000	1
I3	0.000001348980000000000	1
RE	0	0
ND	0	0
ED	0.000026979600000000000	200000
EX	0.000026979630379063800	200000
SU	0.999899905586153000000	7'412258
TOTAL	1	7'413000

MBC calibrated the model in such a way that as of March 31, there are about 6 deaths.

4.5. SCENARIOS ANALYZED BY MAYOR OF BOGOTA CITY

MBC study considered , three scenarios of decisions:

1. No action is taken.

2. There is 30% isolation from 15 March to 20 March, from this date it is assumed that there is an isolation of 60% until 27 April, from where isolation of 30% for the susceptible and 50% for moderate symptomatic is maintained. There is 30% isolation from 15 March to 20 March, then it is assumed.

3. There is 30% isolation from 15 March to 20 March, then 70% isolation is assumed for three months: from 20 March to 20 June and 30% isolation for asymptomatic and 50% for symptomatic from this date.

The simulated period was one year. The values assumed for $\theta_{t,st}$ in the scenarios are presented in the following table (t in days):

State st	**Scenario 1**		**Scenario 2**		**Scenario 3**	
	Period	$\theta_{t,st}$	Period	$\theta_{t,st}$	Period	$\theta_{t,st}$
I0	$\forall t$	0	$0 \le t < 5$	0.3	$0 \le t < 5$	0.3
			$5 \le t < 43$	0.6	$5 \le t < 97$	0.7
			$43 \le t$	0.3	$97 \le t$	0.3
I1		0	$0 \le t < 5$	0.3	$0 \le t < 5$	0.3

State st	Scenario 1		Scenario 2		Scenario 3	
	Period	$\theta_{t,st}$	Period	$\theta_{t,st}$	Period	$\theta_{t,st}$
	$\forall t$		$5 \leq t < 43$	0.6	$5 \leq t < 97$	0.7
			$43 \leq t$	0.5	$97 \leq t$	0.5

4.6. RESULTS

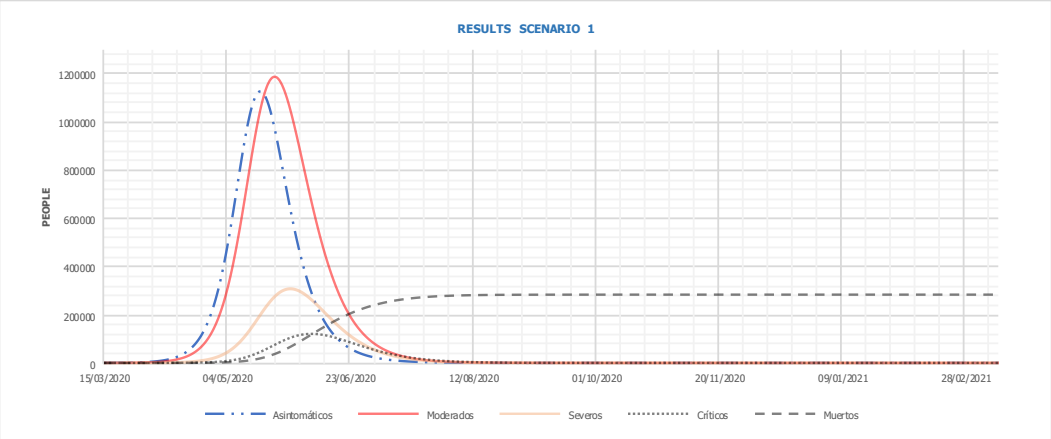
The model used by MBC serves to understand the dynamics of the transmission of a disease such as COVID-19 in the city of Bogota and the effects of isolation policies. While this aggregate model is conceptually appropriate to explain the dynamics of the transmission, the uncertainty of various sensitive parameters and the lack of: i) regionalization and ii) an age group structure, make this model a tool for qualitative evaluation of intervention actions in hypothetical decision-making scenarios, rather than as a model to support decision-making with high precision and optimization criteria.

4.6.1. SCENARIO 1. NO QUARANTINE

This scenario shows a high number of deaths, severe cases, and critical patients who according to the MBC would surely have saturated the health system as of April 14. Results of projection on the stage without quarantine. R_t symbolizes the effective number of transmission calculated by MBC with the next generation matrix method (). The results presented by the MBC are presented below

Día	Susceptibles	Expuestos	Asintomáticos	Moderados	Severos	Críticos	Recuperados	Muertos	R_t
7/04/2020	7390210	3126	8729	5006	678	124	5092	35	2.59
14/04/2020	7344217	9338	26172	15057	2047	377	15678	114	2.58
21/04/2020	7209022	27198	77112	44767	6124	1136	47285	356	2.53
28/04/2020	6832922	73685	215996	128741	17921	3369	139289	1076	2.40
05/05/2020	5929707	165011	528704	338317	49377	9606	389106	3170	2.00

According to MBC, this scenario has a maximum overall hospitalization demand of 306,370 on May 30, 2020 and a peak of critical cases on June 7 (124,346 critical cases). In addition, the disease would reach 90.5% of the population, leaving 283,532 deaths during the testing period (one year).

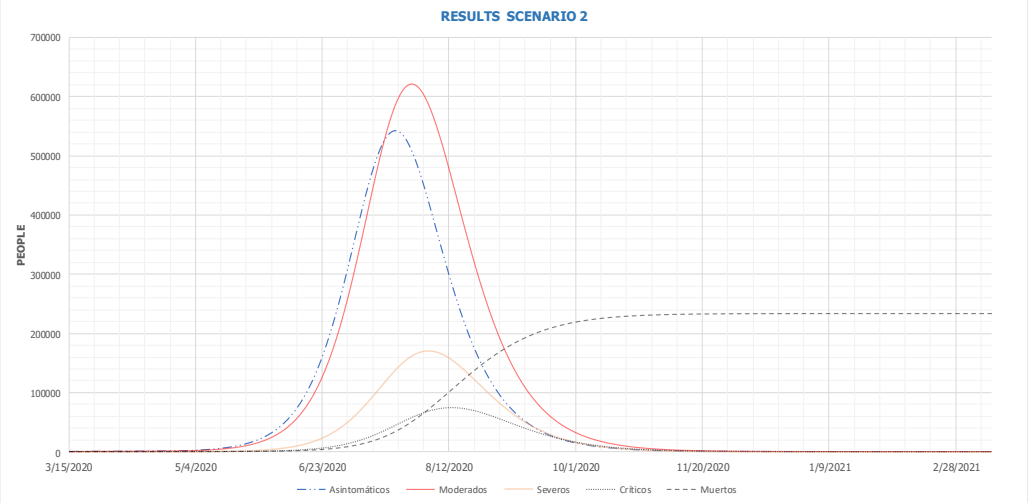


4.6.2. SCENARIO 2. QUARANTINE UNTIL APRIL 27

In this hypothetical scenario there is a substantial decrease in demands for health resources at the peak of the epidemic and a postponement of this compared to the previous scenario. It is estimated that 300 critical cases are exceeded on 19 May; the number of individuals who have severe symptWHO in this scenario amounts to 170. 913 cases on 4 August and 74520 critical cases on 13 August. It is appreciated that the decrease in cases is given to a greater magnitude by measures that persist over time; deferral of demand for health resources takes place to a greater extent through mandatory preventive isolation. In this scenario, the virus affects approximately 75.5% of the population leaving 233,352 dead during the testing period.

The results presented by MBC are presented below

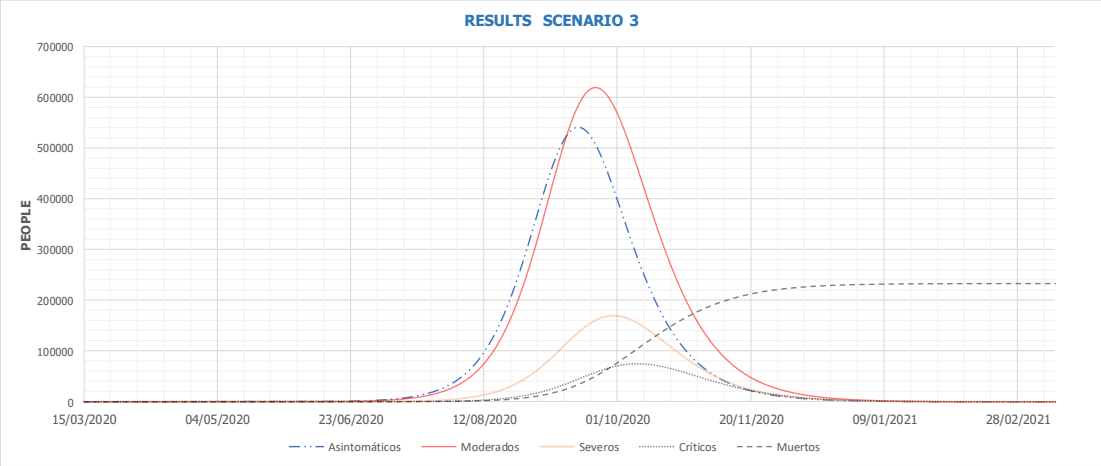
Día	Susceptibles	Expuestos	Asintomáticos	Moderados	Severos	Críticos	Recuperados	Muertos	R_t
7/04/2020	7410025.31	147.32	631.98	623.35	140.10	40.93	1373.05	17.96	1.33
14/04/2020	7408827.28	185.52	794.32	784.74	182.28	59.46	2130.90	35.50	1.32
21/04/2020	7407318.53	233.59	999.89	987.56	231.70	79.65	3089.30	59.78	1.32
28/04/2020	7405292.29	375.18	1301.63	1245.66	292.52	102.96	4298.14	91.62	1.83
05/05/2020	7401082.00	740.00	2536.00	1969.00	399.00	134.00	6017.00	134.00	1.00



4.6.3. SCENARIO 3. QUARANTINE UNTIL JUNE 20

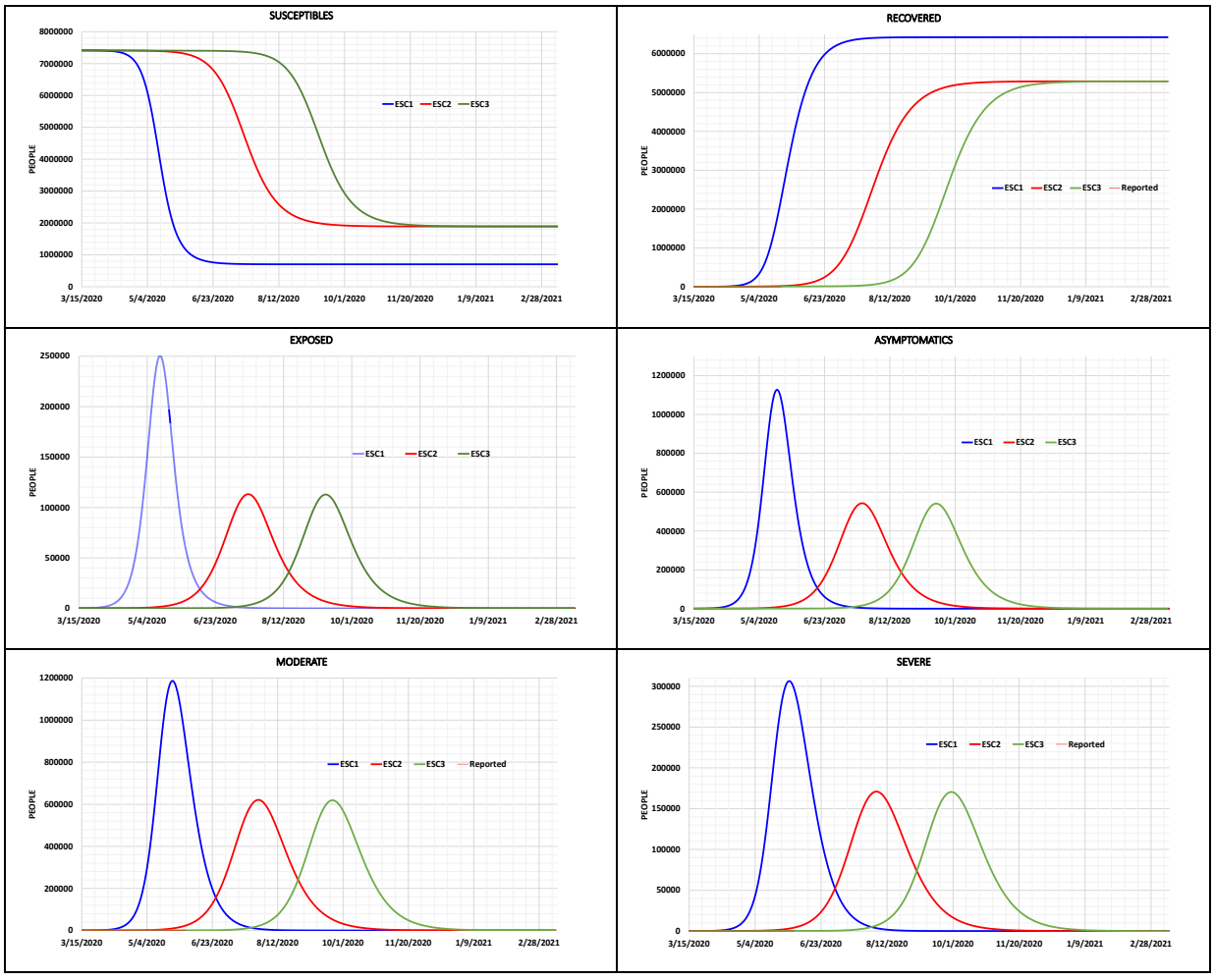
This scenario follows a logic analogous to that of the previous scenario; only the length of mandatory preventive insulation is increased until 20 June and the effectiveness of the mandatory preventive insulation is increased (to 70%). Figure shows the results through April 28 of this scenario. The difference between this scenario and 2 lies in the postponement of the highest demand for health resources. Maintaining maximum demands at similar levels: 170416 severe cases on September 30. 74318 critical cases on October 9. 300 critical cases are exceeded on 14 July and the epidemic affects approximately 75.5% of the population, leaving 233270 dead during the testing period.

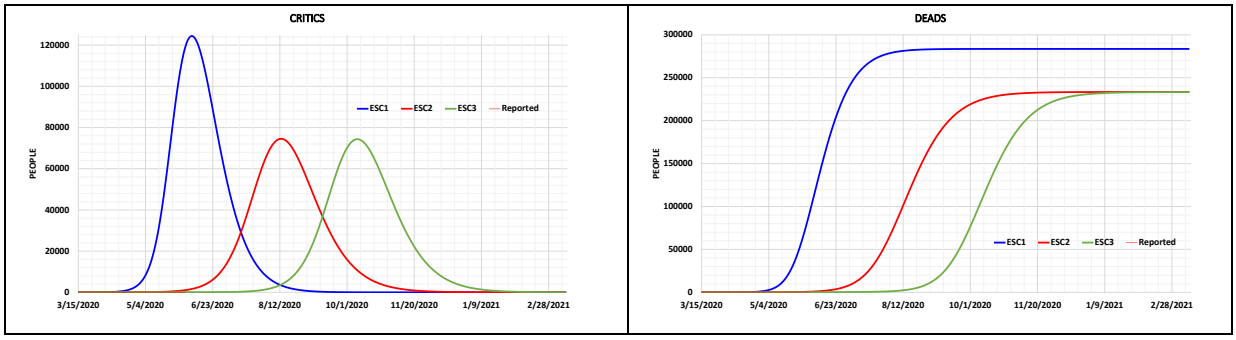
Día	Susceptibles	Expuestos	Asintomáticos	Moderados	Severos	Críticos	Recuperados	Muertos	R_t
7/04/2020	7410673.79	86.21	408.82	461.26	115.53	36.62	1200.71	17.05	1.11
14/04/2020	7410038.72	93.30	440.60	498.31	131.24	48.07	1717.82	31.95	1.11
21/04/2020	7409351.41	100.98	476.38	538.28	144.20	57.09	2281.24	50.41	1.11
28/04/2020	7408607.49	109.30	515.48	582.02	156.76	64.60	2892.61	71.74	1.11
05/05/20	7407802.00	118.0	558.00	630.00	170.00	71.00	3556.00	96.00	1.00



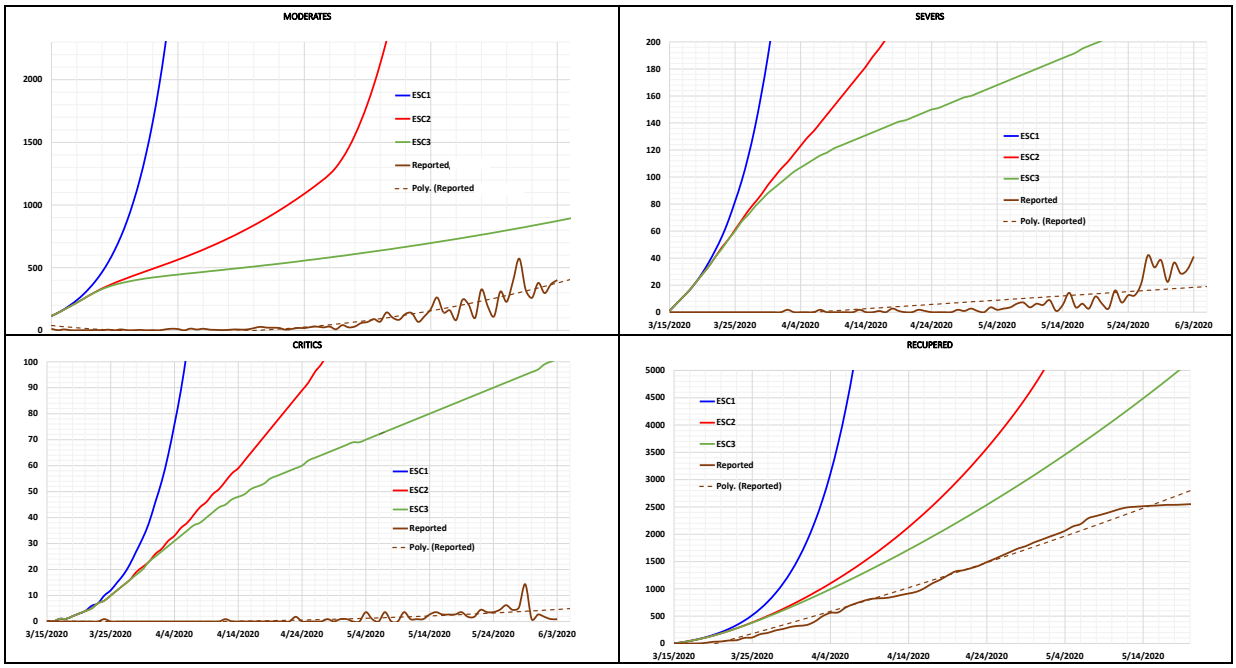
4.6.4. AGGREGATE ANALYSIS

To develop comparative curves with reality, historical data were divided by 1,1161, this due to the difference between the population data of the MBC which according to SALUD DATA is outdated. Below is the system behavior for each of the epidemiological states of the SEI3RD model.





The following graphs present the comparison of the results of the scenarios analyzed by MBC and the reality reported by the same MBC.



The significant difference between the states "predicted" by the MBC and reality, reported by the MBC, reaffirms that "the most pessimistic estimates of academic literature" (Mejía Becerra et al., 2020) have been used, which may force governments to take very drastic (draconian) actions with high economic impact.

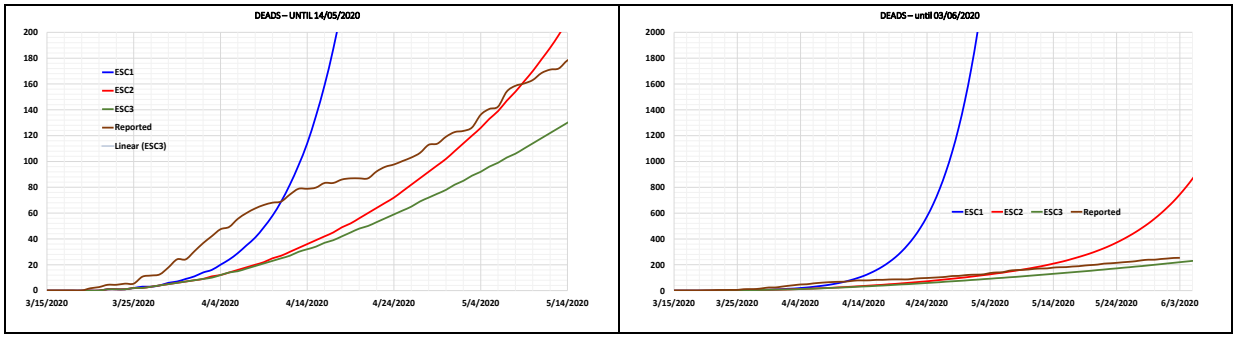
These models are based on exponential growth that, with a constant R_0 number above 1, may predict that the majority of the population would become critically infected, which would then quickly result in a large number of deaths. Historic data seems to indicate that the behavior of "curves" is not exponential, rather sub-exponential; this, which seems to be a simple technical characterization; but, it has very important, in this case transcendental, implications.

When using simulation models, in most cases, scenario analysis is used by to test the impact of decisions and not so much to analyze uncertainty. In this case, it seems that, the reality is totally out of the way for the MBC, this entails serious implications, since this situation implies that it faces at least one of the following situations:

- The mathematical model describing the epidemic used is not the appropriate
- Computational implementation of the mathematical model may have errors
- The biological and socio-demographic parameters used for simulation are not appropriate
- Measurements representing the historical sample do not correspond to reality.

If all is correct, the representativeness of the mathematical model would be appropriate and its support for decisions will be effective.

The following graphs present the results for the dead.



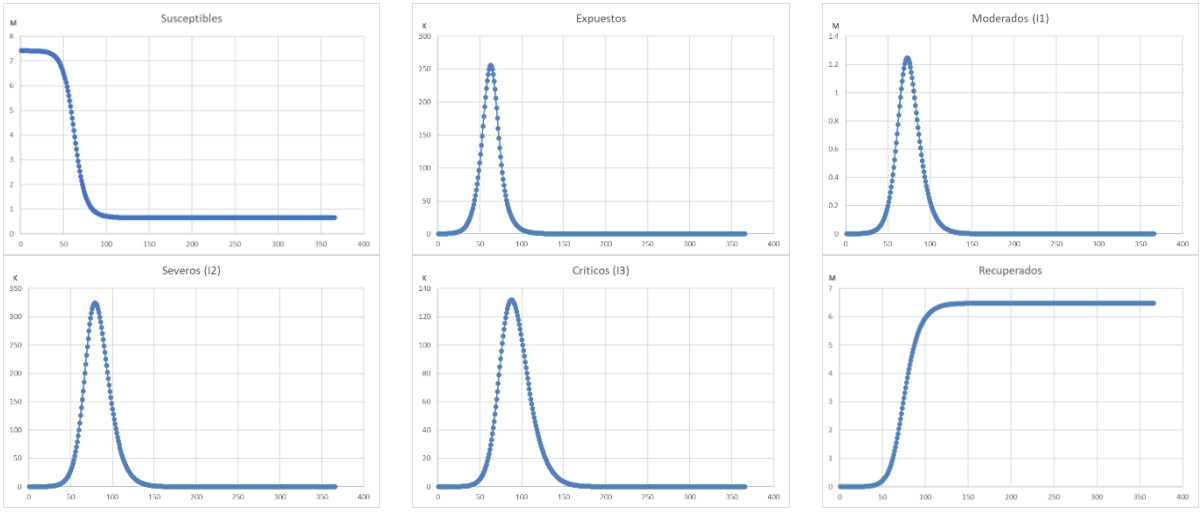
In the case of deaths, reality outperforms the most drastic scenario, this happens from the beginning of the simulation. There can be many reasons, it should be borne in mind that it appears that the initial conditions of the model influence the death toll, it should be remembered that the MBC calibrated the model in such a way that as of March 31 there are about 6 deaths.

The graphs presented were constructed with information taken from:

- Mejía Becerra. J. D. Modelación Matemática de la Propagación del SARS-CoV-2 en la Ciudad de Bogotá Segunda Versión. https://observatoriocovid19.sv/doc/biblioteca/internac/Ficha_Metodologica.pdf y
- Base de datos de casos confirmados COVID-19. Subsecretaría de Salud Pública. Secretaría Distrital de Salud. 2020. Corte: 10 de junio 2020.

4.7. COMPARISON WITH BOGOTÁ OFICIAL MODEL

This experiment is based on reproducing the results published by the Mayor of the city of Bogotá (MCB) for the SEI3RD model, as the official model used to manage the COVID-19 pandemic. Scenario 1 reported by MCB was reproduced, which does not consider confinement or mitigation policies. The reference population is 7'413,000. The results are presented below and are the same as those reported by MCB.



$I_{st\text{-}1,rg,ss}(t)$

5. CASE: $I_{st\text{-}1,rg,ss}(t)$ MADERO - TAMPICO - ALTAMIRA CASE

6. FUNDING

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