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SEIMR/R-S. General Epidemic Simulation Model Multi-Infected States - Multi Sociodemographic Segments - Multi-Region Mobility. Theory

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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 sociodemographic segments based on age and economic stratum (it is possible to include other dimensions, for example: ethnics, gender, ...). 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 sociodemographically and multiple type of vaccines. The formulation of SEIMR/R-S/OPT is presented by Velasquez-Bermudez (2021a) that includes the modeling of the vaccination process. 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. Following the theory presented in this document, ITCM (Instituto Tecnológico de Ciudad Madero, México) implemented the SEIMR/R-S epidemic model in a JAVA program (Velasquez-Bermudez et. al, 2021). This program may be

used by the organizations that considers the SEIMR/R-S will be useful for management the COVID-19 pandemic, it is presented by Velasquez-Bermudez et al. (2021).

Keywords: Pandemic Management, Epidemic Mathematics, Optimization, Health Decision Support Systems

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-sociodemographic-segment 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"

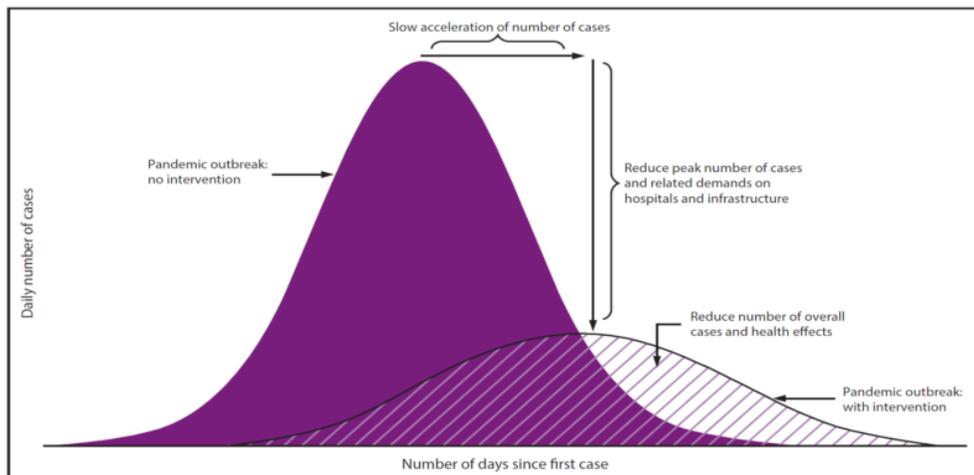
R Recovered: Recovering population (RE)

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

1.1. Conceptual Framewor

The goal of epidemic control strategies is to reduce the basic reproduction number 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

Figure 1. GOAL OF EPIDEMIC MODELING



Source: Adapted from: CDC. Interim pre-pandemic planning guidance: community strategy for pandemic influenza mitigation in the United States—early, targeted, layered use of nonpharmaceutical interventions. Atlanta, GA: US Department of Health and Human Services, CDC; 2007. <https://stacks.cdc.gov/view/cdc/11425>.

Control of an outbreak relies partly on identification of the disease parameters that lead to a significant reduction R_0 that may be function of several parameters of which γ , the recovery rate for clinically ill and b , 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 table of epidemic models shows some of the best-known models

The following documents have been consulted, referenced and/or used for writing the following numerals:

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Table 1. Traditional Epidemic Models		
Model	Description	Reference
SIR	Susceptibility (S), Infection (I) and Recovery (R)	Kermack & Mc Kendrick (1927) Jing (2018)
SEIR	Susceptibility (S), Exposure (E), Infection (I) and Recovery (R)	Hethcote (2000)
SEI3RD	Susceptibility (S), Exposure (E), 3+1 Infection States (I3), Recovery (R) and Death (D)	Mejía Becerra et. al. (2020)
SEIQR	Susceptibility (S), Exposure (E), Infection (I), Quarantine (Q) and Recovery (R)	Huang (2016)
SIRS	Susceptibility (S), Infection (I), Recovery (R) and Susceptibility (S)	Cai (2015)

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 sociodemographic 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 next table. The models will be implemented using this nomenclature. The table includes the symbol used in the original models and the code used in this document.

Table 2. Epidemic States

Model Symbol	Epidemic State	Description	Comments
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 algebraic notation are presented in the next table, each index is associated to an entity of the information system.

Index	Short Description	Long Description
ag	Age	Age
mr	Macro-region	Macro-Region
rg, ro, rd	Region	Region (Basic Territory Unit)
ss	Social Segment	Sociodemographic Segment
st, sl	Epidemic State	Epidemic State
t, q	Period	

The measurement units used are equal for all models

Measurement Unit	Description
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 sociodemographic segment and that the composition of sociodemographic 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, sociodemographic-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.

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, the duration, and the closeness of contact.

These parameters may also be a combined function of age and economic. In this document, the sociodemographic segments are a combination of age with an economic stratum. The biological parameters depend on age.

Additionally, may be considered people coming for the exogenous systems the macroregion, epidemic state NP.

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-sociodemographic-segment 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 sociodemographic segments.

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

Table 5. SEIMR/R-S Model Epidemic States

Model	Model Epidemic States												
	Standard								Extended			Capacity	
	S U	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)

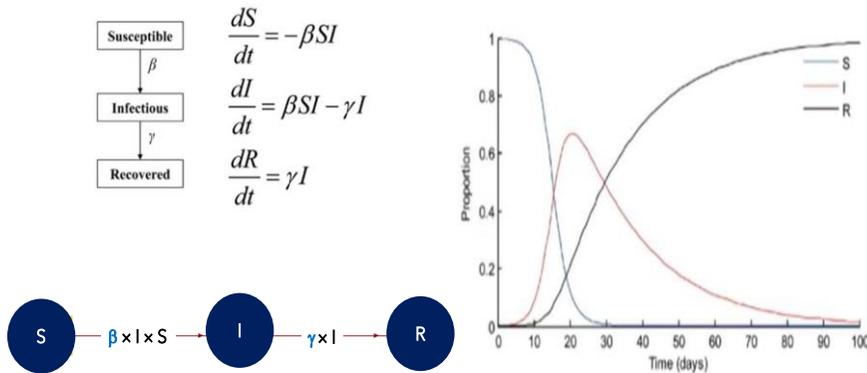
The diagram shows the behavior of S(t), I(t), and R(t) when they are normalized using the initial population equal to 1. The biological parameters used in SIR and SEIR model are described below.

Table 6. SIR Model - Biological Parameters

Parameter	Description	Equation	Measure Unit
d	Contact Intensity – Exogenous Parameter		peo-day
w	Probability of transmission per contact intensity (infectivity)		
γ	Recovery rate for clinically ill		fpo/day
m	Epidemic death (mortality) rate		fpo/day
m ^N	Natural mortality rate		fpo/day
k	The latency period of the virus before developing		day
y	Inverse virus latency period	1/ k	1/ k
b	Inverse contact intensity × infectivity	dd × w	dd × w
r	Relative removal rate	γ/b	
R ₀	Basic reproduction ratio/number		

The diagram resumes the standard SIR epidemic model.

Figure 2. Susceptible-Infectious-Recovered (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 parentheses.

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

$$\frac{\partial I(t)}{\partial t} \text{ (fpo/day)} = \beta \text{ (1/fpo-day)} \times I(t) \text{ (fpo)} \times S(t) \text{ (fpo)} - \gamma \text{ (fpo/day)} \times I(t) \text{ (fpo)} \quad (2)$$

$$\frac{\partial R(t)}{\partial t} \text{ (fpo/day)} = \gamma \text{ (fpo/day)} \times I(t) \text{ (fpo)} \quad (3)$$

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

$$\frac{\partial S(t)}{\partial t} + \frac{\partial I(t)}{\partial t} + \frac{\partial R(t)}{\partial t} = 0 \quad (4)$$

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)

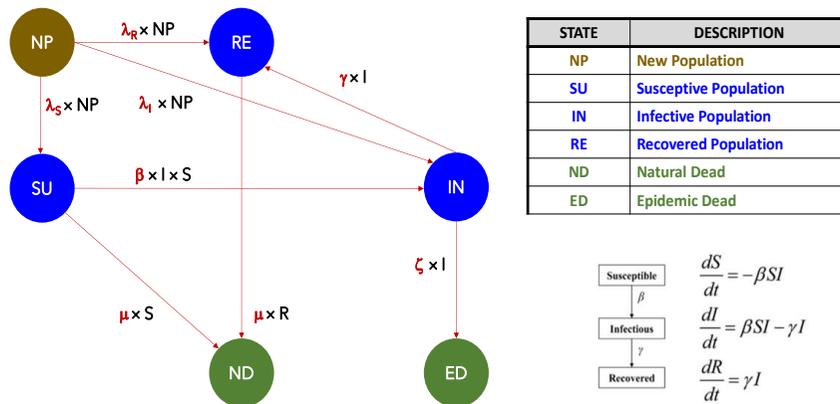
ND and ED states should be included if it wants to account for the resources consumed by people who die, who are killed due the epidemic and due by causes other than the epidemic.

For a more general formulation it is included the exogenous variable $NPX(t)$ that 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 with high people exchange rates, e.g., islands dedicated to tourism. Next table shows the parameters used to this modeling.

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

Next diagram shows the epidemic system modeled.

Figure 3. STATE TRANSITION DIAGRAM - SIR MODEL



Then, the differential SIR equations must be adjusted:

$$\partial S(t)/\partial t = -\beta \times I(t) \times S(t) + \lambda^S \times NPX(t) - \mu^N \times S(t) \tag{5}$$

$$\partial I(t)/\partial t = \beta (I(t) \times S(t) - (\gamma + \zeta) \times I(t) + \lambda^I \times NPX(t) \tag{6}$$

$$\partial R(t)/\partial t = \gamma \times I(t) - \mu^N \times R(t) + \lambda^R \times NPX(t) \tag{7}$$

$$\partial D(t)/\partial t = \mu \times I(t) \tag{8}$$

$$\partial N(t)/\partial t = \mu^N \times S(t) + \mu^N \times R(t) \tag{9}$$

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

$$S(t) + I(t) + R(t) + D(t) + N(t) = 1 \tag{10}$$

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

$$S(t) + I(t) + R(t) + D(t) + N(t) = 1 + \int_{q \in [0,t]} \partial NPX(q) \partial q \tag{11}$$

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:

$$R_0 = S(0) \times \gamma/\beta \tag{12}$$

where 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 $t = 0$, $\partial I/\partial t$ can be written as

$$\partial I/\partial t = (R_0 - 1) \times \gamma \times I(0) \tag{13}$$

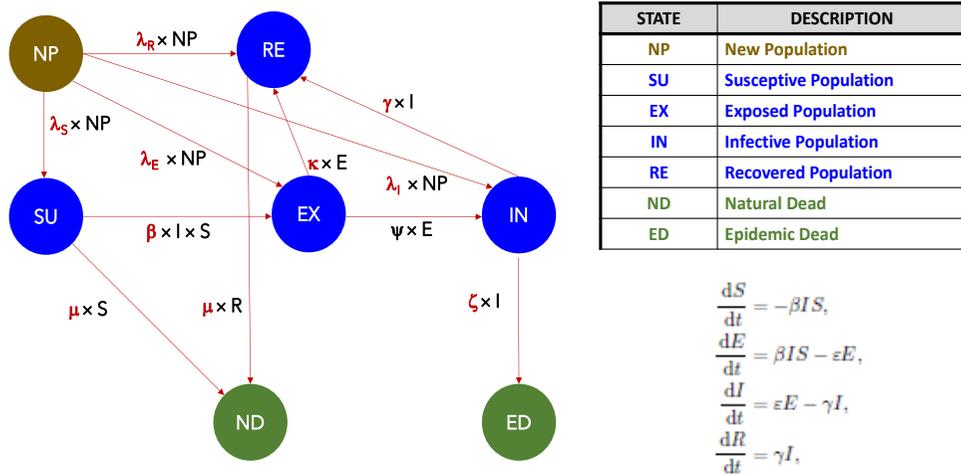
if $R_0 > 1$ then $\partial I/\partial t > 0$ and therefore the disease can spread; but if $R_0 < 1$ then the disease dies out. Making mathematical manipulation it is possible to prove that the maximum number of infective at any time is

$$TPOB \times (1 - \rho + \rho \ln [\rho / S(0)]) \tag{14}$$

2.2. SEIR Epidemic Model

The classic SEIR model describes the epidemic dynamics based on the transitions between four different epidemic states: susceptible (S), exposed (E), infectious (I), and recovered (R) individuals. The SEIR symbols are the same SIR symbols plus the parameter γ that represents the inverse of the virus latency/incubation period (k). There are multiple versions of the SEIR model, 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).

Figure 4. STATE TRANSITION DIAGRAM - SEIR MODEL



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

$$\frac{\partial E(t)}{\partial t} = \beta \times I(t) \times S(t) - \psi \times E(t) + \lambda^E \times NPX(t) \quad (15)$$

$$\frac{\partial I(t)}{\partial t} = \psi \times E(t) - (\gamma + \zeta) \times I(t) + \lambda^I \times NPX(t) \quad (16)$$

2.3. SEIMR Epidemic Model

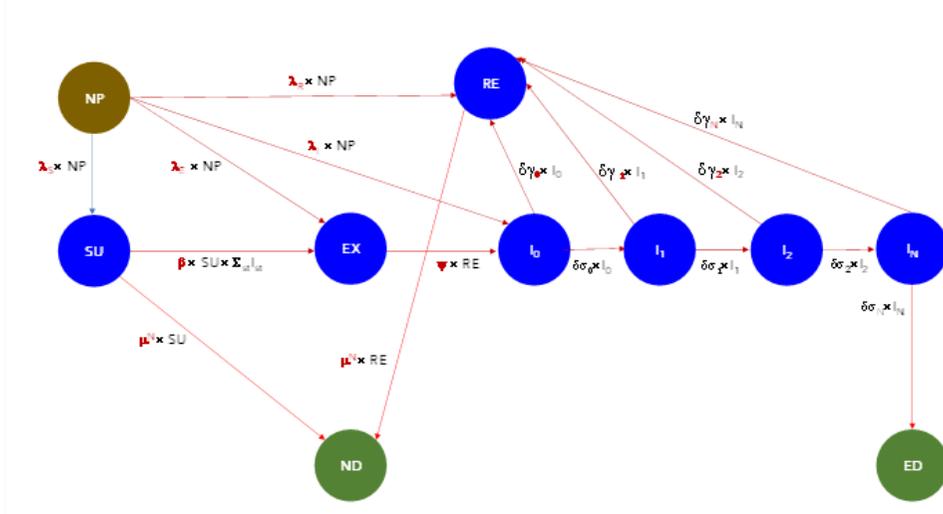
SEIMR is a generalization of the SEI3RD epidemic model that was developed with the aim of simulating the transmission and evolution of acute infections. This simulation assumes that the pathogen causes an infection followed by lifelong immunity or death. Two versions of SEI3RD were revised: Grimm et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

Figure 5. 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 ($I_0, I_1, I_2, I_3, \dots, I_N$). 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 (I_3) worsens its clinical condition if it die (E).

Next table shows the biological parameters of SEI3RD epidemic model.

Table 8. Biological Parameters – SEI3RD Model

Parameter	Description	Equation	Measure Unit
m^N	Natural mortality rate		fpo/day
k	The latency period of the virus before developing		day
m	Epidemic mortality rate		fpo/day
w	Probability of that a person may be contagion		prob
d_{st}	Probability of $I_0, I_1, I_2, I_3, \dots$ of recovering		prob
p_{st}	Time a patient in $I_0, I_1, I_2, I_3, \dots$ recovers		day
h_{st}	Time a patient in $I_0, I_1, I_2, I_3, \dots$ to next infected state		day
z_{st}	Total contact free rate in I_1, I_2, I_3, \dots		1/day
c_{st}	Free probability of contagion in state I_1, I_2, I_3, \dots		Prob
g_{st}	Fraction of people who recover in one day	$1/p_{st}$	fpo/day
s_{st}	Fraction of people who develops symptoms	$1/h_{st}$	fpo/day
b_{st}	$I_0, I_1, I_2, I_3, \dots$ state transmissibility free rate	$- z_{st} \log(1 - c_{st})$	fpo/day
y	Inverse virus latency period	$1/k$	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.

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.
 Output Rate = S_{st} 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:

$$\partial S(t)/\partial t = - S(t) (\beta_0(t) \times I_0(t) + \beta_1(t) \times I_1(t) + \beta_2 \times I_2(t) + \beta_3 \times I_3(t)) \quad (17)$$

$$\partial E(t)/\partial t = S(t) (\beta_0(t) \times I_0(t) + \beta_1(t) \times I_1(t) + \beta_2 \times I_2(t) + \beta_3 \times I_3(t)) - \psi \times E(t) \quad (18)$$

$$\partial I_0(t)/\partial t = \psi \times E(t) - \delta_0 \times \gamma_0 \times I_0(t) - (1 - \delta_0) \times \sigma_0 \times I_0(t) \quad (19)$$

$$\partial I_1(t)/\partial t = (1 - \delta_0) \times \sigma_0 \times I_0(t) - \delta_1 \times \gamma_1 \times I_1(t) - (1 - \delta_1) \times \sigma_1 \times I_1(t) \quad (20)$$

$$\partial I_2(t)/\partial t = (1 - \delta_1) \times \sigma_1 \times I_1(t) - \delta_2 \times \gamma_2 \times I_2(t) - (1 - \delta_2) \times \sigma_2 \times I_2(t) \quad (21)$$

$$\partial I_3(t)/\partial t = (1 - \delta_2) \times \sigma_2 \times I_2(t) - \delta_3 \times \gamma_3 \times I_3(t) - (1 - \delta_3) \times \sigma_3 \times I_3(t) \quad (22)$$

$$\partial R(t)/\partial t = \delta_0 \times \gamma_0 \times I_0(t) + \delta_1 \times \gamma_1 \times I_1(t) + \delta_2 \times \gamma_2 \times I_2(t) + \delta_3 \times \gamma_3 \times I_3(t) \quad (23)$$

$$\partial D(t)/\partial t = (1 - \delta_3) \times \sigma_3 \times I_3(t) \quad (24)$$

The following specification must be considered:

1. y is the reciprocal of the average latency period.
2. d_{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, m the mortality rate is equal to d_{st} , for st equal to the last infected state.
3. g_{st} is the reciprocal of the average recovery time, without worsening its clinical state, of an individual of class I_{st} .
4. s_{st} is the reciprocal of the average complication time of a patient in the I_{st} state.
5. b_{st} is the transmissibility rate of an individual in state I_{st} . must be noted that Mejía Becerra et al. (2020) includes transmissibility rates related with the epidemic control policies, this is ignored in this document

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

$$\partial S(t)/\partial t = - [\sum_{st \in INF} \beta_{st} \times I_{st}(t)] \times S(t) + \lambda^S \times NPX(t) - \mu^N \times S(t) \quad (25)$$

$$\partial E(t)/\partial t = [\sum_{st \in INF} \beta_{st} \times I_{st}(t)] \times S(t) - \psi \times E(t) + \lambda^E \times NPX(t) \quad (26)$$

$$\partial I_0(t)/\partial t = \psi \times E(t) - \delta \delta_0 \times I_0(t) + \lambda^I \times NPX(t) \quad (27)$$

$$\partial I_{st}(t)/\partial t = \delta \sigma_{st-1} \times I_{st-1}(t) - \delta \delta_{st} \times I_{st}(t) \quad (28)$$

$$\partial R(t)/\partial t = \sum_{st \in INF} \delta \gamma_{st} \times I_{st}(t) - \mu^N \times R(t) + \lambda^R \times NPX(t) \quad (29)$$

$$\partial D(t)/\partial t = \sum_{st \in IF} \delta \sigma_{st} \times I_{st}(t) \quad (30)$$

The following relations should be considered:

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

The following definitions (auxiliary parameters) was included

$$\sigma \delta_{st} = \delta_{st} \times \sigma_{st} \quad (31)$$

$$\delta \sigma_{st} = (1 - \delta_{st}) \times \sigma_{st} = \sigma_{st} - \sigma \delta_{st} \quad (32)$$

$$\delta \gamma_{st} = \delta_{st} \times \gamma_{st} \quad (33)$$

$$\delta \delta_{st} = (\delta_{st} \times \gamma_{st} + (1 - \delta_{st}) \times \sigma_{st}) = \delta \gamma_{st} + \delta \sigma_{st} \quad (34)$$

$$\mu = \sum_{st \in IF} \delta \sigma_{st} \quad (35)$$

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

Table 9. SEIMR - Differential Equations

st∈SET	State Increment	State Decrement	Natural Dead	Exogenous Increment
SU	$I^S \times NPX(t)$	$IS(t) \times S(t)$	$m^N \times S(t)$	$I^S \times NPX(t)$
EX	$IS(t) \times S(t)$	$y \times E(t)$		$I^E \times NPX(t)$
IN	$IS(t) \times S(t)$	$dd_{st} \times I_{st}(t)$		$I^I \times NPX(t)$
I0	$y \times E(t)$			$I^I \times NPX(t)$
I1F	$ds_{st-1} \times I_{st-1}(t)$			
RE	$S_{st \in I1F} dg_{st} \times I_{st}(t)$		$m^N \times R(t)$	$I^R \times NPX(t)$
ED	$S_{st \in IF} m \times I_{st}(t)$			
Auxiliary Equation				
$IS(t) = [S_{st \in INF} b_{st}(t) \times I_{st}(t)]$				

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:
 $st \in IF = \{IN\}$, $st \in I1F = \{\}$, $st \in I0 = \{\}$, $st \in INF = \{IN\}$ and $st \in IN = \{IN\}$
- Do not include the exposed state (E), that means that $st \in EX = \{\}$

2. SEIR Model

- Only consider one infected state IN.

3. SEIMR Model

- Considered multiples infected stats $\{I0, I1, I2, \dots, IN\}$ IN associate to I_N , do not include the state I_0 that means:
 $st \in IF = \{I_N\}$, $st \in I1F = \{I_1, I_2, \dots, I_N\}$, $st \in I0 = \{I_0\}$, $st \in INF = \{I_0, I_1, I_2, \dots, I_N\}$ and $st \in IN = \{I\}$

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.

Table 10. Epidemic States SETs

Model	Epidemic States	Non Infected States					Infected States				
	STA	SU	EX	RE	ED	ND	INF	I_N	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, I0, I1, I2, ... IN, D, N	S	E	R	D	N	$I_0, I_1, I_2 \dots I_N$		I0	$I_1, I_2 \dots I_{N-1}$	I_N

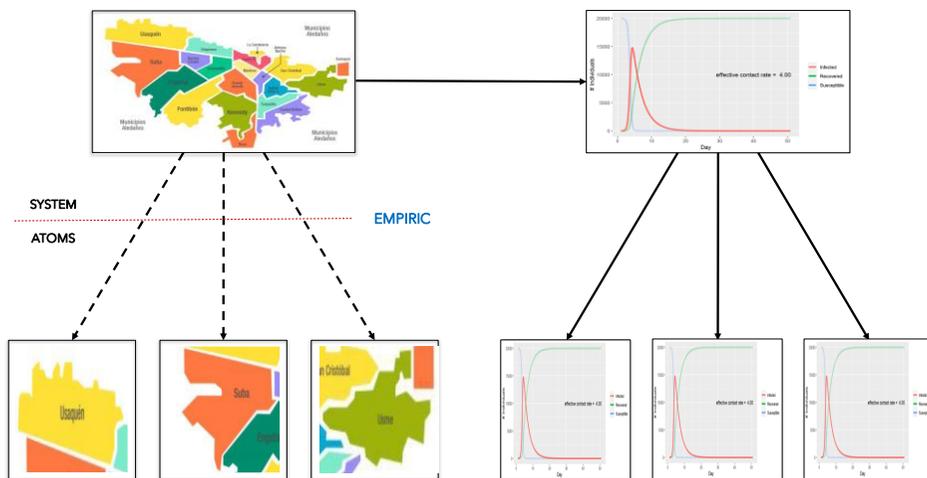
3. SEIMR/R-S General Epidemic Model

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 sociodemographic segments are distributed in a non-homogeneous manner.

3.1. Framework

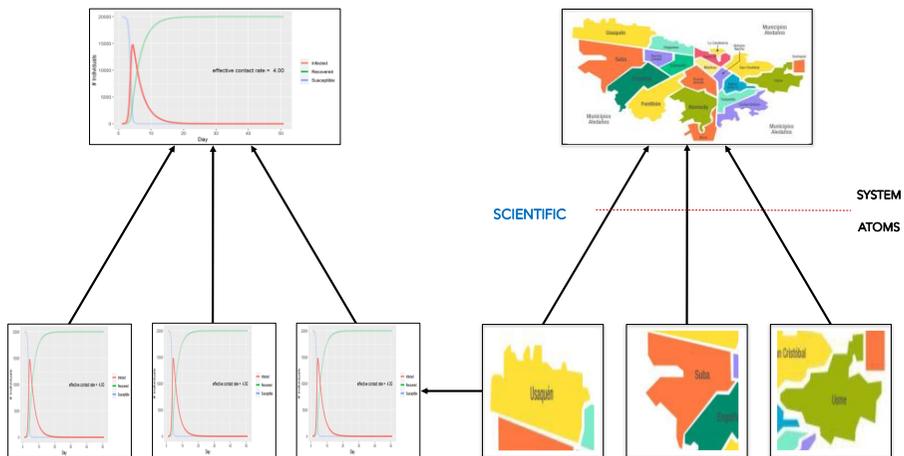
The focus SEIMR/R-S is on building the epidemic modelling with a bottom-up approach, rather than the traditional top-down approach in which multi-region territory (macro-region) is modeled in an aggregated manner and what happens in regions is inferred through disaggregation processes, usually based on empirical rules and mental models.

Figure 6. LOW MATHEMATICAL COMPLEXITY TOP-DOWN MODELING



In the bottom-up approach, SEIMR/R-S models what happens in each atom (region-sociodemographic segment) and the relationships that occur between atoms, that in the case of the pandemic focuses on the mobility of people. Modeling is based on the epidemic process characterized by different behavior in each sociodemographic segment (e.g., age and economic stratum) and the distribution of segments in each of the regions, modeling what happens in each <region-segment>.

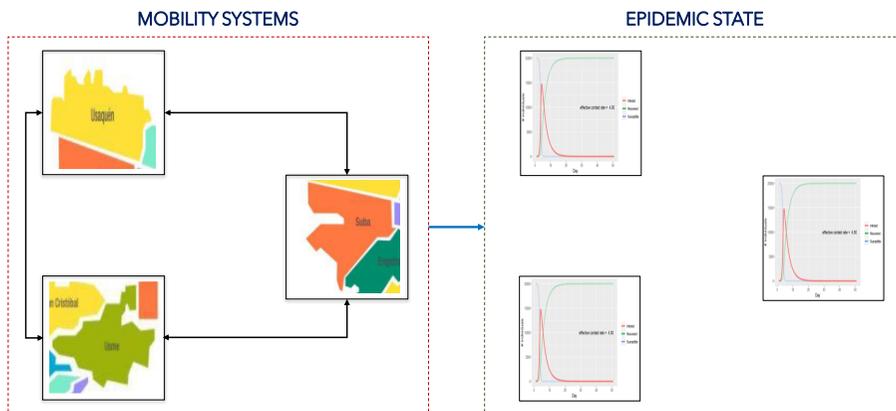
Figure 7. HIGH MATHEMATICAL COMPLEXITY BOTTOM-UP MODELING



On the other hand, the mobility of the population between regions is characterized by the number and the duration of travels, it could also be considered the closeness of people during the trip, which depends on the transport mode. In this way the epidemic spreads between regions. Only one transport mode is considered in the formulation, but it is straight forward the extension to multiple transport modes.

The mobility is the more important part of SEIMR/R-S, because if it is ignored, the differential equation model would be reduced to $NR \times NS$ parallel systems of simultaneous equations without interaction between them, which is not consistent with what happens in reality. NR represents the number of regions and NS represents the number of sociodemographic segments.

Figure 8. MOBILITY BETWEEN REGIONS & EPIDEMIC STATE



The structure of SEIMR/R-S allows the decision maker to simulate, or optimize, epidemic control policies by acting directly on an <region, segment> atom and/or on a connectivity arc (mode of transport) between regions. This cannot be achieved with traditional top-down modeling.

3.2. Common Algebraic Notation

Including regional and sociodemographic 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 (sociodemographic 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.

Table 11. Biological Parameters – SEI3RD & SEIMR/R-S Models

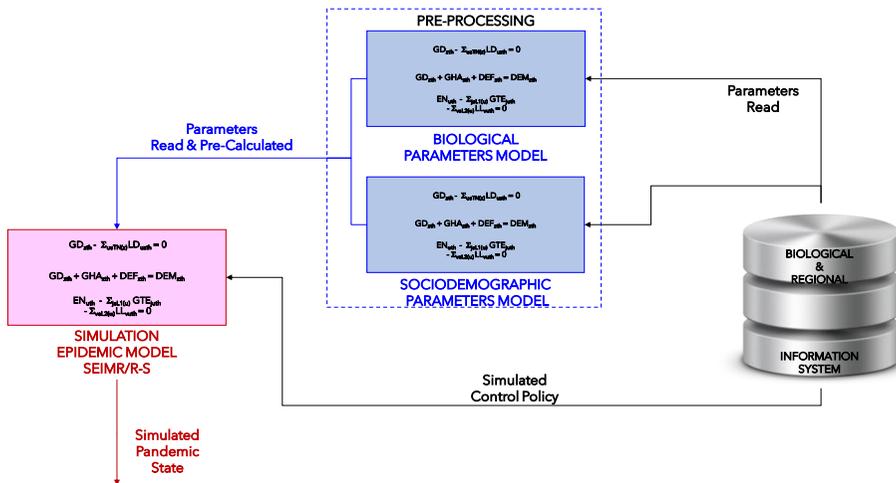
SEIMR	SEIMR/R-S		Description	Measure Unit
Parameter	Parameter	Source		
m^N	m^N	Read	Natural mortality rate	fpo/day
k	k	Read	The latency period of the virus before developing	day
m	m_{ag}	Model	Epidemic mortality rate	fpo/day
w	$w_{rg,ss}$	Model	Probability of that a person may be contagion	prob
δ_{st}	$\delta_{ag,st}$	Model	Probability of $I_0, I_1, I_2, I_3, \dots$ of recovering	prob
p_{st}	$p_{ag,st}$	Model	Time a patient in $I_0, I_1, I_2, I_3, \dots$ recovers	day
h_{st}	$h_{ag,st}$	Model	Time a patient in $I_0, I_1, I_2, I_3, \dots$ to next infected state	day
b_{st}	b	Model	Transmissibility rate of an individual in state st	
z_{st}	z	Model	Total contact free rate in I_1, I_2, I_3, \dots	1/day
c_{st}	$c_{ag,st}$	Model	Free probability of contagion in state I_1, I_2, I_3, \dots	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 sociodemographic segments and their characterization from specific studies developed for the macro-region. In advance this model will be referred as Parameters Model which must be built on the basis of the territory's sociodemographic information system. An example of the database built for the city of Bogota is located at:

<http://www.doanalytics.net/Documents/DW-2A-ITM-SEIMR-R-S-Epidemic-Model-Case-Bogota.pdf>

The following diagram presents the connectivity of the SEIMR/R-S model use process to be used as a pandemic simulation tool under different control policies studied by the decision maker.

Figure 9. CONNECTIVITY OF THE SEIMR/R-S MODELS



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 is presented below; they are divided in basic and auxiliary parameters that are included to make easier the implementation process.

Table 12. Biological Parameters (Calculated) - SEIMR/R-S Model					
SEIMR		SEIMR/R-S		Description	Measure Unit
Parameter	Equation	Parameter	Equation		
g_{st}	$1/p_{st}$	$g_{ag,st}$	$1/p_{ag,st}$	Fraction of people recovered in 1 day	fpo/day
s_{st}	$1/h_{st}$	$s_{ag,st}$	$1/h_{ag,st}$	Fraction of people develops symptoms	fpo/day
b_{st}	$-\xi_{st} \log(1 - c_{st})$	b_{st}	$-\xi_{st} \log(1 - c_{ag,st})$	$I_0, I_1, I_2, I_3, \dots$ state transmissibility rate	fpo/day
y	$1/k$	y	$1/k$	Inverse virus latency period	1/day
sd_{st}	$d_{st} s_{st}$	$sd_{ag,st}$	$d_{ag,st} s_{ag,st}$	$d_{ag,st} s_{ag,st}$	
ds_{st}	$(1 - d_{st}) s_{st}$	$ds_{ag,st}$	$(1 - d_{ag,st}) s_{ag,st}$	$(1 - d_{ag,st}) s_{ag,st}$	
dg_{st}	$d_{st} g_{st}$	$dg_{ag,st}$	$d_{ag,st} g_{ag,st}$	$d_{ag,st} g_{ag,st}$	
dd_{st}	$dg_{st} + ds_{st}$	$dd_{ag,st}$	$dg_{ag,st} + ds_{ag,st}$	$dg_{ag,st} + ds_{ag,st}$	
m	$S_{st \in IF} ds_{st}$	m_{ag}	$S_{st \in IF} ds_{ag,st}$	$S_{st \in IF} ds_{ag,st}$	

		$br_{rg,ss}$	Model	Contagion probability function of regional and sociodemographic	prob
		$bb_{rg,ss}$	$S_{ag \in AGS(ss)}$ $dd_{ag,st} \times$ $br_{rg,ss}$	Inverse contact intensity by infectivity	1/fpo-day

3.3. Regional-Segment Modeling

3.3.1. Regional Modeling

To formulate the regional model segmented sociodemographically the following hypotheses are assumed:

1. There is no direct 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 that must be represented by the mobility system.
2. 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, $j_{ro,rg,ss}$, moving from the source region (ro) to the destination region (rg).
 - In addition, the fraction of the time, $f_{ro,rg,ss}$, is known to people from the region origin in the destination region during the period (one day).
3. Modeling does not include different modes of inter-region transport. One way to include this aspect is to associate the tm-index with the entity transport mode and differentiate the population by means of the transport mode that they use, which involves redefining the parameter $j_{ro,rg,ss}$ as a function of tm, that is $j_{ro,rg,ss,tm}$. In addition, a parameter linking the closeness of people during the trip should be included, which should increase the likelihood of contagion that should be inversely proportional to closeness.

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:

$$II_{rg}(t) = S_{ss \in SSR(rg)} S_{ro \in ROR(rg)} j_{ro,rg,ss} \times f_{ro,rg,ss} \times IS_{ro,ss}(t) \tag{36}$$

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

$$IE_{rg}(t) = S_{ss \in SSR(rg)} S_{rd \in RDE(rg)} j_{rg,rd,ss} \times f_{rg,rd,ss} \times IS_{rg,ss}(t) \tag{37}$$

The net effect on the rg-region will be:

$$IS_{rg,ss}(t) = S_{st \in INF} I_{st,rg,ss}(t) \quad (38)$$

$$IX_{rg}(t) = S_{ss \in SSR(rg)} IS_{rg,ss}(t) \quad (39)$$

$$IR_{rg}(t) = IX_{rg}(t) + II_{rg}(t) - IE_{rg}(t) \quad (40)$$

where

$I_{st,rg,ss}(t)$ fraction of the population infected in st-epidemic-state living in rg-region and ss-segment.

$IS_{rg,ss}(t)$ fraction of the population infected living in rg-region and ss-segment.

$IX_{rg}(t)$ fraction of the population infected living in rg-region

$II_{rg}(t)$ weighted fraction of the population infected traveling to rg-region

$IE_{rg}(t)$ 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:

$$SI_{ro,rg,ss}(t) = j_{ro,rg,ss} \times f_{ro,rg,ss} \times S_{ro,ss}(t) \quad (41)$$

The following replace of parameter will be included

$$jf_{ro,rg,ss} = j_{ro,rg,ss} \times f_{ro,rg,ss} \quad (42)$$

- 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:

$$SE_{rg,rd,ss}(t) = jf_{rg,rd,ss} \times S_{rd,ss}(t) \quad (43)$$

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

$$SN_{rg,ss}(t) = S_{rg,ss}(t) - S_{rd \in RDE(rg)} SE_{rg,rd,ss}(t) \quad (44)$$

where

$S_{rg,ss}(t)$ fraction of the susceptible population living in rg-region and ss-segment.

$SI_{ro,rg,ss}(t)$ fraction of the ss-segment susceptible population traveling from ro-region to rg-region

$SE_{rg,rd,ss}(t)$ fraction of the ss-segment susceptible population traveling from rg-region to rd-region

Next table resume the parameters associated with regional modeling:

Table 13. Regional Modeling Parameters – SEIMR/R-S Model			
Parameter	Source / Equation	Description	Measure Unit
$j_{ro,rg,ss}$	Model	Fraction of ss-segment population moving from the source region (ro) to the destination region (rg)	fpo/day
$f_{rg,rd,ss}$	Model	Fraction time that spends the ss-segment population of the source region (ro) into the destination region (rg)	hour/day
$j_{rg,rd,ss}$	$j_{rg,rd,ss} \wedge f_{rg,rd,ss}$	$j_{rg,rd,ss} \wedge f_{rg,rd,ss}$	hour/day

3.3.2. Socio Demographic Segment Modeling

The basic hypothesis is that an infected person in any segment can infect anyone susceptible in any sociodemographic 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 \square (the inverse of contact intensity multiplied by the transmission probability) is assumed fixed for all region and all sociodemographic segments. In SEIMR/R-S the transfer rate depends on the sociodemographic segment in a region and it is called $bb_{rg,ss}$, 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

$$S2I_{rg,ss}(t) = bb_{rg,ss} \times IR_{rg}(t) \times SN_{rg,ss}(t) + S_{rd \in RDE(rg)} bb_{rd,ss} \times IR_{rd}(t) \times SE_{rg,rd,ss}(t)$$

3.4. General Framework

The differential equations of the regional-segmented model are:

$$\partial S_{rg,ss}(t)/\partial t = - S2I_{rg,ss}(t) - \mu^N \times S_{rg,ss}(t) + \lambda^S_{rg,ss} \times NPX(t) \tag{45}$$

$$\partial E_{rg,ss}(t)/\partial t = S2I_{rg,ss}(t) - \psi \times E_{rg,ss}(t) + \lambda^E_{rg,ss} \times NPX(t) \tag{46}$$

st=I0

$$\partial I_{st,rg,ss}(t)/\partial t = \psi \times E_{rg,ss}(t) - \delta \alpha_{st,ss} \times I_{st-1,rg,ss}(t) + \lambda^I_{rg,ss} \times NPX(t) \tag{47}$$

st ∈ IIF

$$\partial I_{st,rg,ss}(t)/\partial t = \delta \zeta_{st-1,ss} \times I_{st-1,rg,ss}(t) - \delta \alpha_{st,ss} \times I_{st,rg,ss}(t) \tag{48}$$

$$\partial R_{rg,ss}(t)/\partial t = \sum_{st \in IIF} \delta \beta_{st-1,ss} \times I_{st,rg,ss}(t) - \mu^N \times R_{rg,ss}(t) + \sum_{ss \in SSR(rg)} \lambda^R_{rg,ss} \times NPX(t) \tag{49}$$

$$\partial D_{rg,ss}(t)/\partial t = \sum_{st \in IIF} \mu \sigma_{ss} \times I_{st,rg,ss}(t) \tag{50}$$

$$\partial NR_{rg}(t)/\partial t = \mu^N \times SR_{rg,ss}(t) + \mu^N \times RR_{rg}(t) \tag{51}$$

where the following rates are defined for the sociodemographic segments

Table 14. Sociodemographic Biological Parameters		
Parameter	Equation	Description
$da_{st,ss}$	$S_{ag \in AGS(ss)} dd_{ag,st}$	Total exit rate
$dz_{st,ss}$	$S_{ag \in AGS(ss)} ds_{ag,st}$	Worsening exit rate
$db_{st,ss}$	$S_{ag \in AGS(ss)} dg_{st,ag}$	Recovering exit rate
ms_{ss}	$S_{ag \in AGS(ss)} m_{ag}$	Mortality rate depending on segment
m_{ag}	$S_{st \in IIF} ds_{ag,st}$	Mortality rate depending on age

The definition equations of the regional-segmented model are:

$$IS_{rg,ss}(t) = S_{st \in INF} b_{st,rg,ss}(t) I_{st,rg,ss}(t) \tag{52}$$

$$IX_{rg}(t) = S_{ss \in SSR(rg)} IS_{rg,ss}(t) \tag{53}$$

$$II_{rg}(t) = S_{ss \in SSR(rg)} S_{ro \in ROR(rg)} jf_{ro,rg,ss} \times IS_{ro,ss}(t) \tag{54}$$

$$IE_{rg}(t) = S_{ss \in SSR(rg)} S_{rd \in RDE(rg)} jf_{rg,rd,ss} \times IS_{rg,ss}(t) \tag{55}$$

$$IR_{rg}(t) = IX_{rg}(t) + II_{rg}(t) - IE_{rg}(t) \tag{56}$$

$$SR_{rg}(t) = S_{ss \in SSR(rg)} S_{rg,ss}(t) \tag{57}$$

$$SI_{ro,rg,ss}(t) = jf_{ro,rg,ss} \times S_{ro,ss}(t) \tag{58}$$

$$SE_{rg,rd,ss}(t) = jf_{rg,rd,ss} \times S_{rd,ss}(t) \tag{59}$$

$$SN_{rg,ss}(t) = S_{rg,ss}(t) - S_{rd \in RDE(rg)} SE_{rg,rd,ss}(t) \tag{60}$$

$$SIN_{rg}(t) = bb_{rg,ss} \cdot IR_{rg}(t) \times SN_{rg,ss}(t) \tag{61}$$

$$SIE_{rg,ss}(t) = S_{rd \in RDE(rg)} bb_{rd,ss} \cdot IR_{rd}(t) \cdot SE_{rg,rd,ss}(t) \tag{62}$$

$$S2I_{rg,ss}(t) = SIN_{rg}(t) + SIE_{rg}(t) \tag{63}$$

$$RR_{rg}(t) = S_{ss \in SSR(rg)} R_{rg,ss}(t) \tag{64}$$

$$DR_{rg}(t) = S_{ss \in SSR(rg)} D_{rg,ss}(t) \tag{65}$$

From now on, the above mathematical definitions will be summarized as $\{ S, E, I_{st}, D, N \} \in Q$

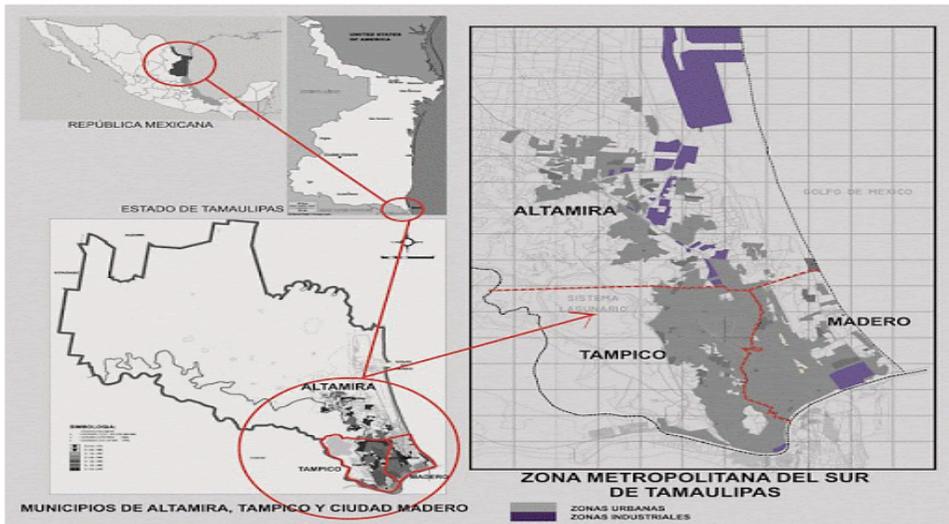
The next table shows the equations dividing the increment and the decrement on each state, it must be considered in the implementation of the mathematical models. The table includes the sets that defined the existence of the equations mainly for the infected states.

Table 15. 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	$\partial I_{st,rg,ss}(t)/\partial t$	$\psi \times E_{rg,ss}(t)$	$\delta\alpha_{st,ss} \times I_{st,rg,ss}(t)$		$\lambda^I_{rg,ss} \times NPX(t)$
IIF	$\partial I_{st,rg,ss}(t)/\partial t$	$\delta\zeta_{st-1,ss} \times I_{st-1,rg,ss}(t)$			
RE	$\partial R_{rg,ss}(t)/\partial t$	$\sum_{st \in IIF} \delta\beta_{st,ss} \times I_{st,rg,ss}(t)$		$\mu^N \times R_{rg,ss}(t)$	$\lambda^R_{rg,ss} \times NPX(t)$
ED	$\partial D_{rg,ss}(t)/\partial t$	$\sum_{st \in IIF} \mu\sigma_{ss} \times I_{st,rg,ss}(t)$			
ND	$\partial NR_{rg}(t)/\partial t$	$\mu^N \times (SR_{rg}(t) + RR_{rg}(t))$			
SUSCEPTIBLE STATE EQUATIONS					
$SR_{rg}(t) = \sum_{ss \in SSR(rg)} S_{rg,ss}(t)$					
$SI_{ro,rg,ss}(t) = \varphi\phi_{ro,rg,ss} \times S_{ro,ss}(t)$					
$SE_{rg,rd,ss}(t) = \varphi\phi_{rg,rd,ss} \times S_{rd,ss}(t)$					
$SN_{rg,ss}(t) = S_{rg,ss}(t) - \sum_{rd \in RDE(rg)} SE_{rg,rd,ss}(t)$					
$SIN_{rg,ss}(t) = \beta\beta_{rg,ss} \times IR_{rg}(t) \times SN_{rg,ss}(t)$					
$SIE_{rg,ss}(t) = \sum_{rd \in RDE(rg)} \beta\beta_{rd,ss} IR_{rd}(t) \times SE_{rg,rd,ss}(t)$					
$S2I_{rg,ss}(t) = SIN_{rg}(t) + SIE_{rg}(t)$					
INFECTED STATE EQUATIONS					
$IS_{rg,ss}(t) = \sum_{st \in INF} \beta_{st,rg,ss}(t) I_{st,rg,ss}(t)$					
$IX_{rg}(t) = \sum_{ss \in SSR(rg)} IS_{rg,ss}(t)$					
$\Pi_{rg}(t) = \sum_{ss \in SSR(rg)} \sum_{ro \in ROR(rg)} \varphi\phi_{ro,rg,ss} \times IS_{ro,ss}(t)$					
$IE_{rg}(t) = \sum_{ss \in SSR(rg)} \sum_{rd \in RDE(rg)} \varphi\phi_{rg,rd,ss} \times IS_{rg,ss}(t)$					
OTHER EQUATIONS					
$RR_{rg}(t) = \sum_{ss \in SSR(rg)} R_{rg,ss}(t)$					

4. Implementation

The model was implemented by the Technological Institute of Mexico, specifically by the ITCM (Instituto Tecnológico de Ciudad Madero) and was applied to three municipalities of the south of the State of Tamaulipas in Mexico which are: Tampico, Ciudad Madero and Altamira, which also make up a conurbated metropolitan area.

Figure 10. Tampico, Ciudad Madero and Altamira Metropolitan Area (TMA)



The population of the TMA metropolitan area is presented in the following table:

Table 16. Metropolitan Area Tampico, Ciudad Madero and Altamira

Region	ID	Population (inhabitants)	Type
Tampico	TAM	327308	Downtown
Madero	MAD	216664	Tourist
Altamira	ALT	246549	Industrial
Metropolitan Area	TMA	790521	

For sociodemographic segments:

- Eighteen age groups were established as shown in next table including the distribution in TMA and the epidemic mortality.

Table 17. Population by Age Group

ID	Group	Region			Epidemic Mortality
		Altamira	Madero	Tampico	
Y00	0 a 4 años	22436	14299	20948	0.008600
Y05	5 a 9 años	24408	16467	22584	0.0003000
Y10	10 a 14 años	23916	18200	24221	0.0003000
Y15	15 a 19 años	21697	17117	26839	0.0007000
Y20	20 a 24 años	20956	17983	27167	0.0011840

Y25	25 a 29 años	18737	15600	23238	0.0015392
Y30	30 a 34 años	19724	14299	22911	0.0018944
Y35	35 a 39 años	19724	15600	22584	0.0024864
Y40	40 a 44 años	17998	16033	25203	0.0033152
Y45	45 a 49 años	15533	13867	22911	0.0066666
Y50	50 a 54 años	13560	15600	22257	0.0097560
Y55	55 a 59 años	9615	11917	17674	0.0144714
Y60	60 a 64 años	6904	8881	16039	0.0217884
Y65	65 a 69 años	4191	7584	11457	0.0258020
Y70	70 a 74 años	2958	4984	8183	0.0377720
Y75	75 a 79 años	1973	3683	5891	0.0578550
Y80	80 a 84 años	1233	2384	4255	0.0843220
Y85	85 años y más	986	2166	2946	0.1795500

- Two socio-economic strata were considered: poor and non-poor shows the number of inhabitants of each stratum per city.

Table 18. Socio-Economic Strata Population – Distribution by Region

Socio-Economic Strata	Altamira	Madero	Tampico
poor	129,438	81,249	125,359
non-poor	117,111	135,415	201,949

For verification purposes of the simulation model, March 24/2020 is considered as the beginning of the COVID-19 epidemic in TMA; the following table presents the initial conditions for that day (inhabitants by epidemiological state).

Table 19. Epidemic Initial Conditions in TMA

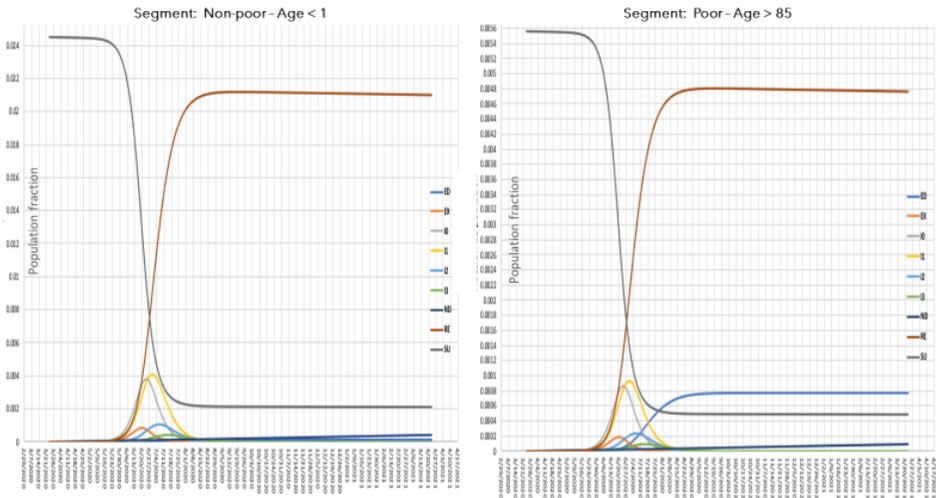
Region	SU	EX	I0	I1	I2	I3	ED	ND	RE
Tampico	327307	0	0	0	1	0	0	0	0
Madero	216662	0	0	0	2	0	0	0	0
Altamira	246548	0	0	0	1	0	0	0	0

The detailed configuration of parameters, the result and the analysis of those of the experiments is reported in the working paper “SEIMR/R-S. General Epidemic Simulation Model Multi-Infected States - Multi Socio-Demographics Segments - Multi-Region Mobility. Validation Case: Metropolitan Area: Tampico, Ciudad Madero and Altamira” available in <http://www.doanalytics.net/Documents/DW-2B-ITCM-SEIMR-R-S-Epidemic-Model-Case-TMA.pdf>.

The following graphs are examples extracted from that document.

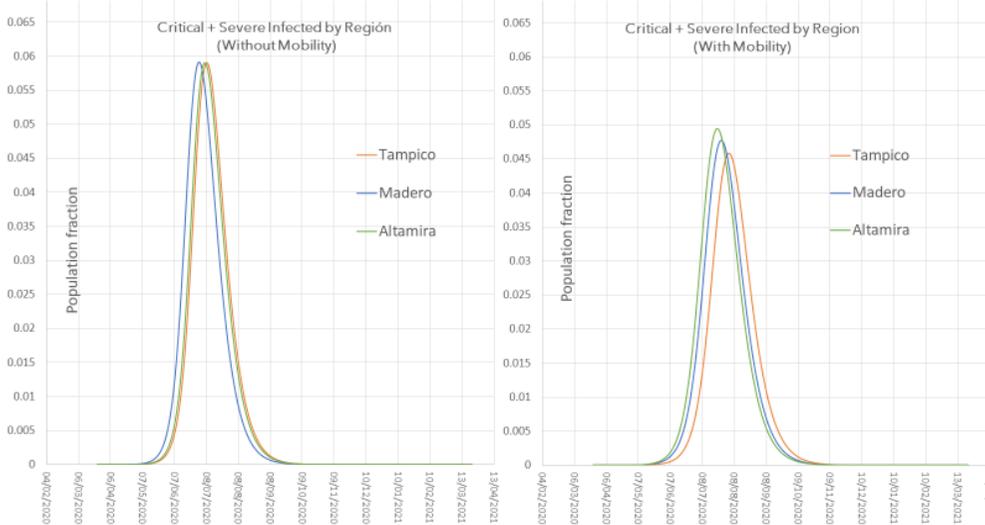
■ **Impact sociodemographic segments (without mobility):**

Figure 11. Example: Aggregate Results for Metropolitan Area (TMA) - Sociodemographic Segments



■ **Impact Mobility between regions:**

Figure 12. Example: Aggregate Results for Metropolitan Area (TMA) - Mobility



- <http://www.doanalytics.net/Documents/SEIMR-R-S-OPT-OPTEX-Implementation.pdf>
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