THE 14TH-ORDER RUNGE-KUTTA METHOD FOR PREDICTING THE SPREAD OF A PANDEMIC IN CUBA

Disusun Guna Memenuhi Tugas Mata Kuliah Metode Numerik

Dosen Pengampu :

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Abstrak

Saat manusia menghadapi penyakit yang berpotensi menular, sebagian besar proses dalam masyarakat terpengaruh, jumlah tenaga kerja yang mampu melakukan tugas menurun, dan sistem perawatan kesehatan menjadi kewalahan oleh wabah penyakit mendadak. Pada tahun 2020, dunia menjadi korban Covid-19. Penyebarannya memiliki konsekuensi yang menghancurkan di banyak negara, mengubah kehidupan semua individu. Pengelolaan pandemi yang buruk secara global menyoroti kurangnya kesiapan untuk jenis bencana ini, yang mengarah pada upaya dan penelitian yang dilakukan untuk memfasilitasi pengelolaan penyakit ini. Salah satu upaya paling penting yang dilakukan untuk mengendalikan penyebaran virus menular ini adalah mencoba memprediksi perilakunya dan mengambil langkah-langkah untuk mengurangi kerusakan yang ditimbulkan. Dalam penelitian ini, metode Runge-Kutta orde 14 digunakan untuk memprediksi penyebaran virus. Metode ini dipilih karena kemampuannya untuk memberikan hasil yang lebih akurat dalam memecahkan persamaan diferensial non-linear yang menggambarkan dinamika penyebaran virus. Dengan menggunakan metode Runge-Kutta orde 14, model prediksi yang lebih akurat diharapkan dapat diperoleh, memungkinkan langkah-langkah mitigasi yang lebih efektif diambil berdasarkan data yang lebih dapat diandalkan. Penelitian ini akan memodelkan penyebaran virus di sebuah kota di Kuba, dengan mempertimbangkan karakteristik geografis dan demografis yang mempengaruhi perilaku virus.

Kata Kunci : *Pandemic in Cuba, SEIRS model, 14th-order Runge-Kutta method*.

1. **Pendahuluan**

Pemodelan matematika adalah proses untuk menggambarkan sistem atau masalah dunia nyata ke dalam bentuk pernyataan matematika. Hasil dari penerjemahan matematika tersebut dikenal sebagai model matematika. Terdapat berbagai macam model matematika yang digunakan untuk memecahkan masalah dunia nyata. Pada tahun 1927, Kermack dan McKendrick [1] menciptakan model SIR, yang memainkan peran penting dalam perkembangan matematika epidemiologi. Model SIR mengelompokkan individu menjadi tiga kategori: rentan (S), terinfeksi (I), dan sembuh (R). Seiring waktu, model SIR telah berkembang dan menghasilkan berbagai model lainnya yang disesuaikan dengan kondisi atau masalah spesifik. Model-model ini mempertimbangkan perbedaan risiko penyakit, struktur usia, pengaruh musiman, pengaruh spasial, serta beberapa model dengan penundaan waktu. Beberapa contohnya adalah model SEI, SEIS, SIRS, SEIR, SEIRS, SEIQR, dan masih banyak lagi [2].

Dalam makalah ini, dikembangkan model SEIR yang diajukan oleh Arif Fatahillah [3] yang membahas tentang kecanduan game online. Masalah yang dibahas dalam makalah ini adalah kasus penyebaran Covid-19 dari jurnal referensi pada [11], di mana individu yang telah sembuh (R) dapat kembali menjadi rentan setelah periode tertentu, sehingga dimodelkan dengan model SEIR. Selain model SEIR, terdapat juga beberapa model matematika lainnya yang mengasumsikan bahwa kesembuhan tidak bersifat permanen dan membentuk siklus, salah satunya adalah model VEISV untuk serangan virus jaringan [4]. Penelitian yang mengembangkan model SEIR telah dilakukan oleh beberapa peneliti [3][5][6][7][8] untuk mendapatkan solusi numerik dalam berbagai kasus, mulai dari penyebaran virus komputer, penyebaran penyakit menular, hingga perilaku merokok seseorang dan kasus kecanduan game online.

COVID-19 adalah penyakit menular yang disebabkan oleh virus SARS-CoV-2. Penyakit ini pertama kali teridentifikasi pada akhir Desember 2019 di Wuhan, Tiongkok, sebagai kluster pneumonia virus dengan penyebab yang tidak diketahui. COVID-19 dapat menyebar melalui tetesan kecil dari mulut atau hidung orang yang terinfeksi, terutama saat mereka batuk, bersin, berbicara, bernyanyi, atau bernapas. Menurut WHO, gejala COVID-19 dapat bervariasi dari ringan hingga berat dan

biasanya muncul 5-6 hari setelah terpapar virus, meskipun bisa berkisar dari 1-14 hari. Gejala umum yang paling sering dilaporkan meliputi:

1. Demam

2. Batuk kering

3. Kelelahan

Gejala yang kurang umum yang dapat mempengaruhi beberapa pasien meliputi:

1. Nyeri otot dan sendi

2. Sakit tenggorokan

3. Diare

4. Konjungtivitis (mata merah)

5. Sakit kepala

6. Kehilangan indra perasa atau penciuman

7. Ruam pada kulit atau perubahan warna pada jari tangan atau kaki

Model SEIR yang digunakan adalah sistem persamaan diferensial biasa (PDB) non-linier orde satu yang tidak dapat diselesaikan dengan metode analitik, sehingga memerlukan pendekatan numerik. Sistem persamaan diferensial biasa terdiri dari dua atau lebih persamaan diferensial dengan hanya satu variabel bebas. Salah satu metode numerik yang efektif adalah metode Runge-Kutta, yang lebih akurat dibandingkan metode Euler dan Heun. Kelebihan metode ini adalah akurasinya yang lebih tinggi karena memiliki pemenggalan yang kecil dalam pengintegrasian error. Error adalah selisih antara solusi eksak (solusi sebenarnya) dan solusi numerik. Metode Runge-Kutta dapat ditingkatkan ke orde yang lebih tinggi untuk mencapai efektivitas yang lebih besar. Beberapa penelitian sebelumnya telah mengembangkan metode Runge-Kutta, seperti metode Runge-Kutta orde empat untuk solusi numerik penyakit diabetes mellitus [7], metode Runge-Kutta orde delapan untuk model matematika penyebaran penyakit malaria [9], dan metode Runge-Kutta orde sembilan untuk model infeksi mycobacterium tuberculosis [10].

Metode Runge-Kutta mempunyai tiga sifat khas yaitu:

1. Metode Runge-Kutta adalah metode satu langkah: gunakan informasi yang tersedia pada titik sebelumnya, x_m, y_m, untuk memperoleh y_{m+1}

2. Metode Runge-Kutta sesuai dengan deret Taylor sampai dengan suku h^p, dimana p berbeda untuk metode berbeda dan disebut order metode tersebut,

3. Metode Runge-Kutta tidak memerlukan evaluasi setiap turunan $f(x, y)$,

tetapi hanya fungsi f itu sendiri.

Secara umum metode Runge-Kutta dapat dituliskan sebagai berikut :

$$y_{n+1} = y_n + h\sum_{i=1}^{m} b_i k_i \quad (1)$$

dimana,

$$k_i = f\left(x_n + c_i h, y_n + \sum_{j}^{i-1} a_{ij} k_j\right), i = 1,2,\ldots,m \quad (2)$$

Dengan asumsi :

$$c_i = \sum_{j=i}^{m} a_{ij}, dan \sum_{j=i}^{m} b_i = 1 \quad (3)$$

Nilai a, b, dan c dapat dituliskan dalam *butcer array* berikut ini :

$$
\begin{array}{c|ccccc}
0 & & & & & \\
c_2 & a_{21} & & & & \\
c_3 & a_{31} & a_{32} & & & \\
\vdots & \vdots & \vdots & \ddots & & \\
c_m & a_{m1} & a_{m2} & \cdots & a_{mm-1} & \\
\hline
& b_1 & b_2 & \cdots & b_{m-1} & b_m
\end{array}
$$

Makalah ini bertujuan untuk merumuskan dan mengembangkan model matematika yang berkaitan dengan penyebaran Covid-19 di Jepang. Penyelesaian model ini akan dilakukan dengan menerapkan metode Runge-Kutta orde 14. Tujuan dari penelitian ini adalah untuk memperdalam pemahaman dalam pemodelan matematika dan berkontribusi pada pengembangan pengetahuan baru dalam penggunaan metode Runge-Kutta orde 14 dalam pemodelan matematika.

2. Metode Penelitian

Metode penelitian berfungsi untuk mengumpulkan data yang akan dianalisis guna mencapai kesimpulan sesuai dengan tujuan penelitian. Dalam makalah ini, data yang digunakan berasal dari penelitian sebelumnya yang telah diaplikasikan oleh peneliti lain sebagaimana dicatat dalam referensi [11]. Data tersebut diaplikasikan untuk memodelkan penyebaran penyakit Covid-19 menggunakan model SEIR, dan efektivitas model ini akan dinilai dengan metode Runge-Kutta orde 14. Proses dimulai

dengan pembentukan dan pengembangan model SEIR, kemudian menetapkan nilai awal dan parameter berdasarkan data dari referensi [11]. Langkah berikutnya adalah merumuskan metode Runge-Kutta orde 14 dan mengimplementasikannya dalam program MATLAB. Setelah memasukkan nilai awal dan parameter, efektivitas model akan diukur melalui hasil grafik dan kesalahan yang dihasilkan. Penelitian ini akan diakhiri dengan kesimpulan berdasarkan analisis hasil yang diperoleh.

Metode penelitian ini bertujuan untuk memperoleh data yang akan dianalisis guna mencapai kesimpulan sesuai dengan tujuan penelitian. Dalam makalah ini, data yang digunakan adalah data yang telah digunakan oleh peneliti sebelumnya pada referensi [11]. Kami memodelkan penyebaran penyakit Covid-19 dalam model SEIR menggunakan metode Runge-Kutta orde 14 untuk menilai efektivitasnya berdasarkan data yang ada. Langkah pertama adalah membentuk dan mengembangkan model SEIR serta menentukan nilai awal dan parameter dari data penelitian sebelumnya pada referensi [11]. Selanjutnya, kami merumuskan metode Runge-Kutta orde 14 dan mengimplementasikannya dalam program MATLAB. Setelah nilai awal dan parameter dimasukkan, efektivitas model akan dianalisis melalui grafik hasil dan kesalahan yang dihasilkan. Penelitian ini akan diakhiri dengan kesimpulan berdasarkan analisis hasil yang diperoleh.

3. Hasil dan Pembahasan

Model SEIR yang dibentuk disesuaikan dengan kasus penyebaran Covid-19 dengan data yang sudah ada pada[11]. Model tipe SEIRS pada kasus penyebaran Covid-19 didefinisikan sebagai berikut :

- S *(Susceptible)* adalah individu rentan, merupakan individu yang belum terkena penyakit covid-19 atau sudah pernah terkena namun telah sembuh.
- E *(Exposed)* adalah individu terpapar, merupakan individu yang terkena penyakit covid-19.
- I *(Infected)* adalah individu yang terkena penyakit covid-19 dengan Kriteria sebagai berikut :
    1. Demam
    2. Batuk kering
    3. Kelelahan
- R *(Recovered)* adalah individu sembuh, merupakan individu terpapar atau individu terinfeksi yang sudah sembuh dari penyakit covid-19. Individu ini dapat rentan kembali karena penyebaran penyakit covid-19.

Berdasarkan definisi tersebut, kasus penyebaran penyakit covid-19 dimodelkan sebagai berikut :
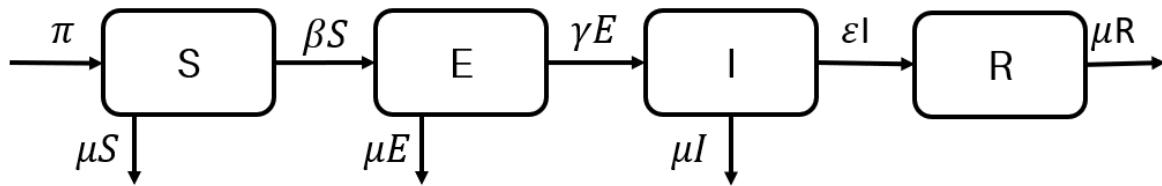
$$\frac{dS}{dt} = \pi - \mu S - \beta S$$

$$\frac{dE}{dt} = \beta S - \mu E - \gamma E$$

$$\frac{dI}{dt} = \gamma E - \mu I - \varepsilon I$$

$$\frac{dR}{dt} = \varepsilon I - \mu R$$

Nilai awal dan parameter diperoleh dari hasil penelitian pada [11]. Hasil penelitian tersebut yang kemudian dijadikan sebagai perbandingan kejadian sebenarnya dan solusi numerik. Berdasarkan penelitian pada [11] subjek dibagi menjadi 4 golongan yaitu rentan (S), terpapar (E), terinfeksi (I), dan sembuh namun rentan (R). Berdasarkan syarat model SEIR, dari hasil penelitian diperoleh nilai awal yaitu terdapat 5,7 Juta individu rentan (S), 390.629 individu terpapar (E), 193.945 individu terinfeksi (I), dan 192.643 individu sembuh. Pada makalah ini, pengelompokan individu SEIR menggunakan ketentuan dari penelitian pada [11].

Sehingga, didapatkan model matematika SEIRS pada kasus penyebaran penyakit pneumonia adalah sebagai berikut :

$$\frac{dS}{dt} = 30 - 9{,}2S - 110S$$

$$\frac{dE}{dt} = 110S - 9{,}2E - 330E$$

$$\frac{dI}{dt} = 330E - 9{,}2I - 63I$$

$$\frac{dR}{dt} = 63I - 9{,}2R$$

Tabel 1. Nilai awal

Nilai awal	Definisi	Nilai	Satuan
$S(0)$	Banyaknya individu rentan pada waktu $t = 0$	5.700.000	Indvidu
$E(0)$	Banyaknya individu terpapar pada waktu $t = 0$	390.629	Individu
$I(0)$	Banyaknya individu terinfeksi pada waktu $t = 0$	193.945	Individu
$R(0)$	Banyaknya individu sembuh pada waktu $t = 0$	192.643	Individu

Tabel 2. Parameter

Nilai awal	Definisi	Nilai	Satuan
μ	Tingkat kematian	9,2	Individu/hari
β	Laju perpindahan dari S ke E	110	Individu/hari
γ	Laju perpindahan dari E ke I	330	Individu/hari
ε	Laju perpindahan dari I ke R	63	Individu/hari
π	Laju Kelahiran	30	Individu/hari

Selanjutnya Metode Runge Kutta yang dihasilkan mempunyai sifat dan formulasi sebagai berikut :

$$\sum_{i=1}^{m} b_i = 1, m = 14 \quad (6)$$

$$\sum_{i=2}^{m} b_i c_i^p = \frac{1}{p+1}, p = 1,2,3,\dots, m-1 \quad (7)$$

$$\sum_{i=3}^{m-1} b_i \left(\sum_{j=2}^{i-1} c_j^q a_{ij} \right) = \frac{1}{(q+1)(q+2)}, q = 1,2,3,\dots, m-3 \quad (8)$$

$$y_{n+1} = y_n + \frac{h}{10000}(203k_1 + 1399k_2 - 777k_3 + 3879k_4 - 3770k_5$$
$$+ 5137k_6 - 1071k_7 - 1071k_8 + 5137k_9 - 3770k_{10}$$
$$+ 3879k_{11} - 777k_{12} + 1399k_{13} + 203k_{14}) \quad (9)$$

Dengan,

$$k_1 = f(x_n, y_n)$$
$$k_2 = f\left(x_n + \frac{h}{13}, y_n + \frac{h}{13}k_1\right)$$

$$k_3 = f\left(x_n + \frac{2h}{13}, y_n + \frac{2h}{13}k_2\right)$$

$$k_4 = f\left(x_n + \frac{3h}{13}, y_n + \frac{3h}{13}k_3\right)$$

$$k_5 = f\left(x_n + \frac{4h}{13}, y_n + \frac{4h}{13}k_4\right)$$

$$k_6 = f\left(x_n + \frac{5h}{13}, y_n + \frac{h}{1742}(33k_1 - 453k_3 + 1566k_4 - 476k_5)\right)$$

$$k_7 = f\left(x_n + \frac{6h}{13}, y_n + \frac{6h}{13}k_6\right)$$

$$k_8 = f\left(x_n + \frac{7h}{13}, y_n + \frac{7h}{13}k_7\right)$$

$$k_9 = f\left(x_n + \frac{8h}{13}, y_n + \frac{h}{702}(191k_2 - 122k_5 + 419k_6 + 79k_7 - 135k_8)\right)$$

$$k_{10} = f\left(x_n + \frac{9h}{13}, y_n + \frac{9h}{13}k_9\right)$$

$$k_{11} = f\left(x_n + \frac{10h}{13}, y_n + \frac{h}{1248}(-197k_4 + 1574k_9 - 417k_{10})\right)$$

$$k_{12} = f\left(x_n + \frac{11h}{13}, y_n + \frac{11h}{13}k_{10}\right)$$

$$k_{13} = f\left(x_n + \frac{12h}{13}, y_n + \frac{h}{2444}(-307k_3 + 2785k_{11} - 222k_{12})\right)$$

$$k_{14} = f\left(x_n + \frac{13h}{13}, y_n + \frac{h}{1118}(523k_6 + 595k_{13})\right)$$

Dengan membuat program MATLAB berdasarkan formulasi metode Runge-Kutta orde 14 yang terbentuk dan memasukkan model SEIRS pada kasus penyebaran penyakit covid-19, nilai awal dan parameter, maka diperoleh solusi numerik berupa grafik jumlah masing-masing individu dan grafik error pada metode Runge-Kutta orde 14.

Pada makalah ini digunakan ukuran langkah yang sama pada penelitian [11]. Dengan mengetahui solusi numerik dari suatu permasalahan, dapat ditentukan penyelesaian yang tepat. Pada penelitian milik Syafrudin side [7], hanya mencari solusi numerik dari penyakit diabetes millitus namun tidak menjelaskan efektivitas metode yang digunakan seperti pada penelitian [8][9]. Dapat diketahui pada setiap peningkatan orde, tingkat efektivitas juga semakin tinggi, karena nilai error semakin kecil.
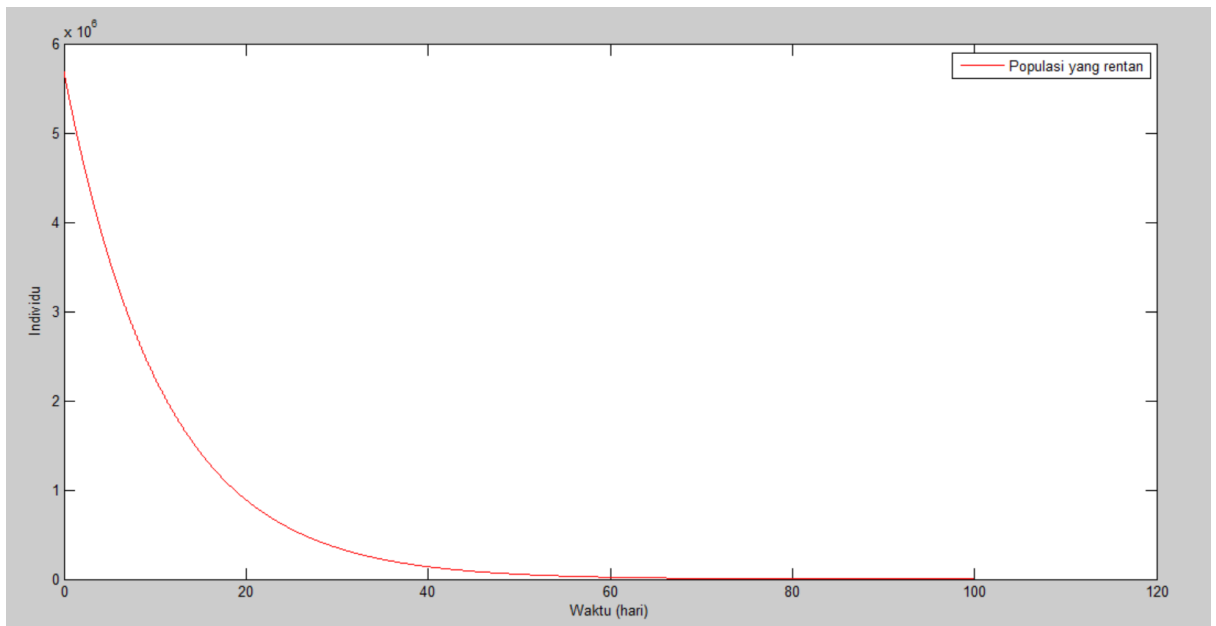
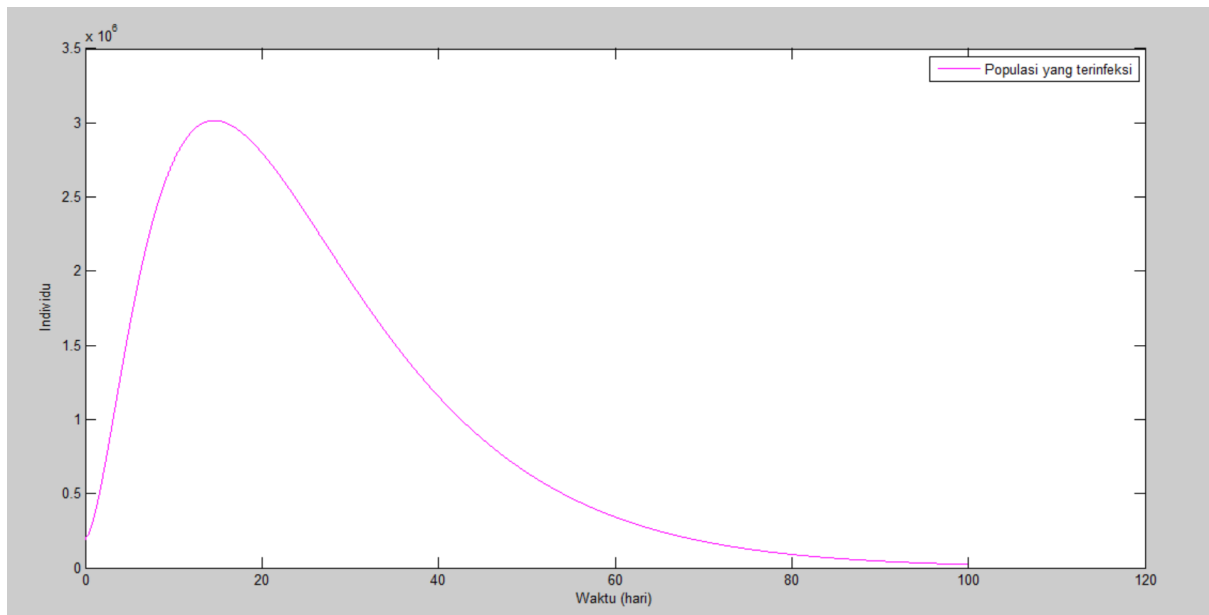**Gambar 1.** Grafik eksekusi RK14 pada Individu S dengan $h = 0.00001$

Gambar 1 merupakan grafik hasil eksekusi metode Runge-Kutta orde 14 pada individu rentan (S). Pada grafik tersebut terlihat bahwa individu rentan mengalami penurunan mulai hari pertama. Individu rentan turun secara eksponensial sampai mendekati nilai 0. Hal tersebut dikarenakan individu rentan akan terus berpindah menjadi individu bergejala dari waktu ke waktu secara perlahan.
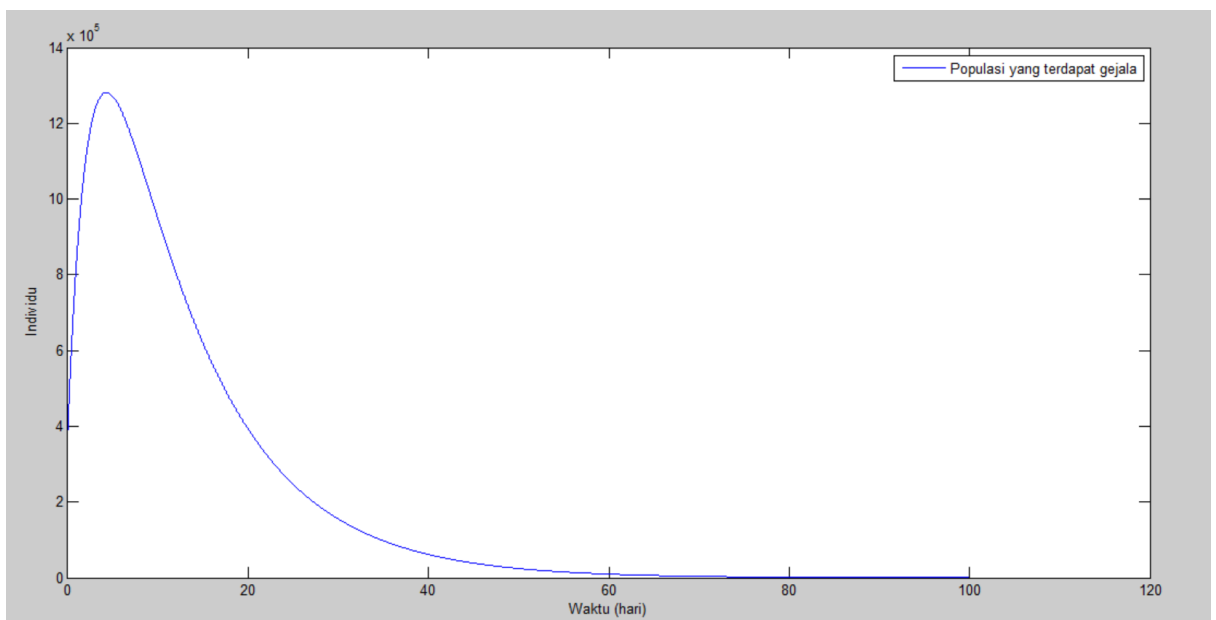
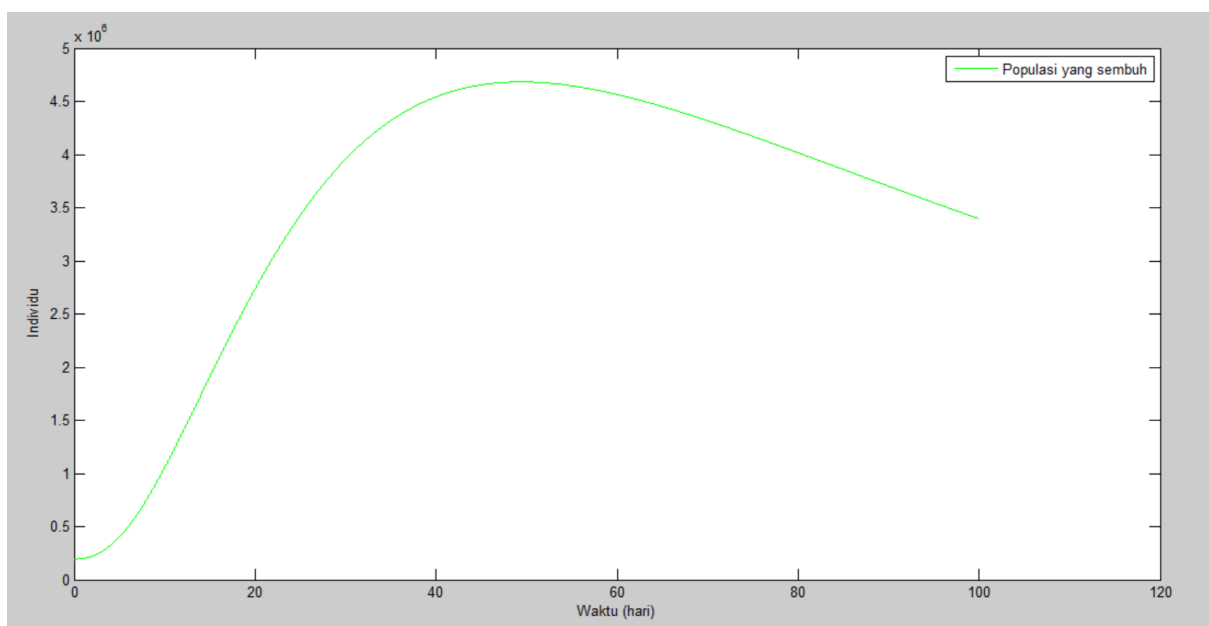**Gambar 2.** Grafik eksekusi RK14 pada Individu E dengan $h = 0.00001$

Gambar 2 merupakan hasil eksekusi program MATLAB pada individu bergejala (E). Gambar tersebut menunjukkan bahwa pada hari pertama grafik mengalami kenaikan yang disebabkan adanya perpindahan individu rentan menjadi bergejala lebih besar dibandingkan perpindahan individu bergejala menjadi individu

terinfeksi. Namun pada hari ke 12 sampai hari ke 100 orang yang bergejala mengalami penurunan yang lumayan dratis.

Gambar 3. Grafik eksekusi RK14 pada Individu I dengan $h = 0.00001$

Gambar 3 merupakan grafik eksekusi MATLAB pada individu terinfeksi (I). Gambar tersebut menunjukkan grafik mengalami kenaikan signifikan individu terinfeksi pada hari pertama sampai hari ke-15 yang disebabkan perpindahan dari individu bergejala. Individu terinfeksi pada dasarnya merupakan individu bergejala yang divalidasi oleh pihak kedokteran. Setelah hari ke-15 individu yang terinfeksi mengalami penurunan sampai mendekati 0 di hari ke-100.

Gambar 4. Grafik eksekusi RK14 pada Individu R dengan $h = 0.00001$

Gambar 4 merupakan grafik hasil eksekusi program MATLAB pada individu

sehat. Grafik menunjukkan kenaikan dari hari pertama sampai hari ke-45 dan sedikit melandai setelahnya yang diperoleh dari perpindahan individu terinfeksi yang perlahan sembuh.

4. **Kesimpulan**

Berdasarkan hasil pemodelan yang dilakukan, simpulan yang dihasilkan adalah kasus penyebaran penyakit covid-19 dapat dibentuk kedalam model SEIR dengan asumsi bahwa individu tidak akan mengalami siklus dimana terjadi kesembuhan permanen. Dapat dilihat bahwa penyebaran penyakit covid-19 sangat cepat, sehingga diperlukan vaksinasi dari pihak pemerintah.

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Agent-based simulation and SEIR models for predicting the spread of a pandemic in Cuba

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Abstract

When humanity faces a potentially contagious disease, most processes of society are affected, the workforce capable of performing tasks decreases, and healthcare systems become overwhelmed by sudden disease outbreaks. In 2020, the world fell victim to Covid-19. Its spread had devastating consequences in many countries, changing the lives of all individuals. The poor management of the pandemic on a global scale highlighted the lack of preparedness for this type of catastrophe, leading to efforts and research being conducted to facilitate the management of this disease. One of the most important endeavors undertaken to control the spread of the infectious virus was to attempt to predict its behavior and take measures to mitigate the damage caused. Pandemic control models, such as the SEIR model, were employed to create predictions, but the results proved to be imprecise due to the lack of infection data. Furthermore, a highly contagious virus that is transmitted by people behaves in a very erratic manner, making it more challenging to develop rigid prediction methods. It was determined that geographic and demographic characteristics greatly influenced the virus's behavior. Agent-Based Simulation was used to model processes and environments with unique characteristics while allowing for individual interaction. In this work, Agent-Based Simulation is employed to model the spread of a virus that affects individuals in a city in Cuba.

Keywords: Agent-Based Simulation; SEIR Model; City Simulation; Infectious virus

1. Introduction

In late 2019, cases of a new coronavirus were detected in Wuhan, China, officially named Covid-19, causing atypical pneumonia. In response to this outbreak, the Chinese government and provincial authorities in Hubei took measures to prevent the spread of the disease. Scientists began investigating and making contributions to better understand the virus and its behavior, aiming to improve control and contribute to future research [1].

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Initially, statistical methods that proved to be of little utility were used to comprehend the phenomenon. However, mathematical models such as the susceptible-exposed-infectious-recovered (SEIR) model were later employed, widely used for simulating the spread and contagion of diseases. Throughout the pandemic, several variants of this model have emerged to adapt to specific characteristics [1, 2, 3]. While these models operate on a large scale, they have limitations in terms of data accuracy and the number of variables that can be included [1].

It is important to note that these models are general and require adaptation by specialists to suit specific contexts. For instance, in a country where quarantines and vaccination campaigns are implemented, new states must be incorporated into the SEIR model to reflect the particular situation. In the case of Cuba, the government has implemented measures based on studies and predictions to prevent virus transmission, such as school closures, quarantines, mask usage, remote work, and enhanced cleaning protocols [4].

In situations that call for important decision-making, it is crucial to rely on the support of models or simulations that provide a better understanding of the system. Simulations hold high value as they recreate real-life scenarios and allow evaluation of how individual behaviors influence the system's evolution, considering its specificities. In this case, simulation based on intelligent agents proves particularly useful as these agents simulate human behavior more realistically. Furthermore, it enables the definition of specific factors related to the environment and individuals, such as population density, aging, and individual contagion risk factors. It is also possible to incorporate an infectious virus into the model, which directly interacts with the agents, ensuring appropriate adaptation to the Cuban context [4].The objective of this work is to develop an agent-based simulation model capable of predicting the spread of a virus in Cuba using the SEIR model.

2. Covid-19, Past Pandemics, and Future Pandemics

In December 2019, a new respiratory virus was identified in Wuhan, China, known as SARS-CoV-2, which causes the coronavirus disease (COVID-19). The global spread of this virus led to the declaration of a pandemic by the World Health Organization in March 2020. The pandemic has had a devastating impact in terms of loss of lives, economic repercussions, increased poverty, and changes in our way of life [5]. The globalization of the pandemic has caused economic havoc in economies worldwide, pushing many into recession. Unlike previous economic crises triggered by excessive debt and insolvency of financial institutions, this recession was caused by an infectious disease, resulting in reduced consumption and production, increased household debt, and income inequality [10]. In addition to the economic impacts, the pandemic has affected the mental health of many individuals due to movement restrictions and widespread quarantine. The rise in anxiety, depression, substance use, and exacerbation of pre-existing mental health problems are among the implications [9]. Everyday life has undergone significant changes, with the widespread adoption of remote work, distance education, and an increase in e-commerce. Adaptations have also been made in healthcare systems to cope with the demand generated by COVID-19 [11]. COVID-19 has surpassed the six previous epidemics of the 21st century in terms of its global reach and social consequences. Unlike previous epidemics, COVID-19 has also had widespread and complex environmental impacts. Here is a summary of the key characteristics of previous epidemics [12]:

- Severe Acute Respiratory Syndrome (SARS) occurred in 2003 and had a limited impact on local and regional economies, with around 8,000 infections and a 10% mortality rate.
- Swine flu (H1N1 influenza virus) became a pandemic in 2009 due to global mobility and had an estimated fatality rate of 0.4%.
- Middle East Respiratory Syndrome (MERS) was first identified in Saudi Arabia and Jordan in 2012 and is considered a zoonotic pathogen primarily transmitted by dromedary camels.
- Ebola virus has caused outbreaks in sub-Saharan Africa since 1976, with geographically limited but high epidemic and pandemic potential.
- Zika fever spread from Brazil to 29 countries in the Americas in 2015, with a major outbreak affecting hundreds of thousands of people. However, the WHO declared the end of the outbreak in November 2016.
- Avian influenza has been reported in various countries since 1997, with a higher frequency in China in 2016.

These examples highlight the magnitude and unique characteristics of COVID-19 compared to previous epidemics. To effectively address pandemics, a comprehensive and coordinated global approach is required. Key strategies include early detection and response, strengthening healthcare systems, fostering research and development, promoting international cooperation, and engaging in proactive planning. These strategies are essential for reducing the impact of pandemics on society and the global economy [7, 8]. These strategies, among others, are fundamental for effectively addressing pandemics and reducing their impact on society and the global economy.

3. SEIR Models and Agent-Based Simulation

SEIR models and agent-based simulation are two commonly used approaches in studying the spread and control of infectious diseases. Pandemic control models are mathematical tools that utilize information about the mechanisms of disease transmission and its parameters to explore different scenarios and determine preventive actions [14]. One of the most widely used models is the SEIR model, SEIR models, named after their compartments for susceptible (S), exposed (E), infected (I), and recovered (R) individuals, provide a mathematical framework for analyzing the dynamics of disease transmission [13]. These models consider factors such as the rate of infection, incubation period, and recovery rate to simulate the progression of an outbreak and evaluate the effectiveness of different intervention strategies. SEIR models have been extensively applied in understanding the spread of various diseases, including COVID-19, and informing public health interventions [1, 2, 3, 15, 16].

On the other hand, agent-based simulation takes a more individual-centered approach by modeling the behavior and interactions of individual agents within a population . Each agent represents an individual with specific attributes, such as age, location, and social connections, and follows predefined rules and behaviors. By simulating the interactions between agents and their environment, agent-based models can capture the complex dynamics of disease transmission, including spatial patterns, social interactions, and behavioral changes. This approach is particularly useful in studying the impact of individual-level decisions and interventions on the overall spread of a disease [17].

Both SEIR models and agent-based simulation have their strengths and limitations. SEIR models are useful for understanding the overall dynamics of disease transmission and assessing the impact of population-level interventions. Agent-based simulation, on the other hand, allows for a more detailed analysis of individual behaviors and the effects of localized interventions [18]. Combining these approaches can provide a more comprehensive understanding of disease spread and support evidence-based decision-making in public health. In conclusion, SEIR models and agent-based simulation are valuable tools in the study of infectious disease control. They offer complementary insights into the dynamics of disease transmission and the effectiveness of intervention strategies, ultimately contributing to more effective public health responses [19, 20].

3.1. Modified SEIR models

To simulate the behavior of a virus in a population, models extracted from different studies presented in [1, 15] were analyzed. Table 1a) and Table 1b) display the variables present in these models.

In Fig. 1a), model M1 is presented, a modified SEIR model that takes into account individuals immune to the disease and in quarantine. Additionally, the deceased state is included compared to the classical

a) State variables in mathematical models		b) Rate variables in mathematical models	
Name	**Description**	**Name**	**Description**
NS	Not susceptible, immunity to the virus	α	Protection rate
S	Susceptible	$\beta(t)$	Infection rate
E	Exposed, possesses the virus but not infectious	$\beta'(t)$	Asymptomatic infection rate
A	Asymptomatic and infectious	γ	Progression rate
I	Symptomatic and infectious	δ	Quarantine time k
Q	In quarantine and infectious	λ	Recovery rate
R	Recovered from symptomatic progression	λ'	Asymptomatic recovery rate
R'	Recovered from asymptomatic progression	k	Death rate
D	Deceased	ρ	De-immunization rate

Table 1: Variables in the Modified SEIR models

SEIR model. In Fig. 1b), model M2 is presented, another modified SEIR model that considers infectious asymptomatic individuals with their own infection rate, assuming they become symptomatic. Similar to M2, model M3 shown in Fig. 1c) allows asymptomatic individuals to recover without becoming symptomatic, and these cases will go unreported. Model M3 is also similar to M2 in that it allows recovered individuals to become susceptible to the disease again, see Fig. 1d).

(a) M1 variant of the SEIR model (b) M2 variant of the SEIR model

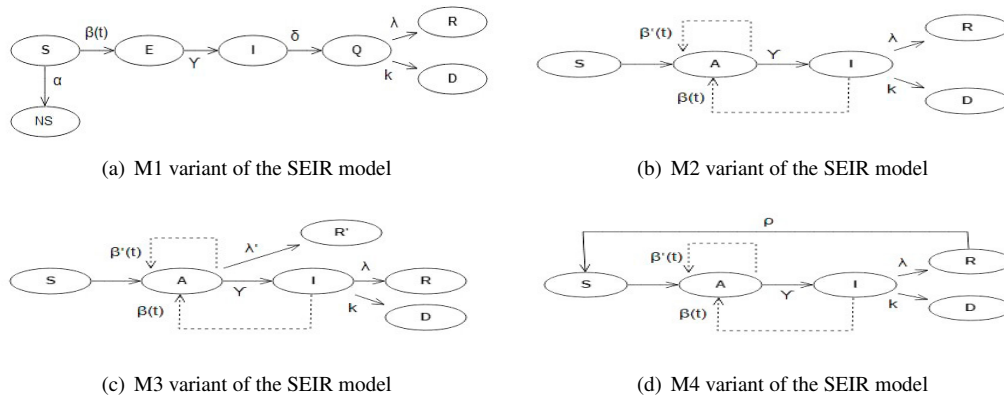(c) M3 variant of the SEIR model (d) M4 variant of the SEIR model

Fig. 1: SEIR Models: variants

4. Simulation Model Proposal

For the proposal, GAMA was used as the development platform due to the facilities it provides for modeling infections, in addition to meeting all the requirements [21]. This platform has been used to create agent-based simulation tools for virus propagation in cities using SEIR reference models [20].

4.1. Simulation Model Proposal

4.1.1. Geographic Scenario and Layered Structure

To avoid computational overload and enable a better understanding of the simulation environment, a fragment of Havana was selected, this fragment encompasses major roadways such as Avenida de los Presidentes, Avenida 23, and Carlos III. It was specifically chosen because it includes a significant number of residential buildings and representations of important building types for the simulation model, such as hospitals, schools, parks, and workplaces. The simulation map consists of multiple layers created using the QGIS tool [22]. The layers that compose the map include the road network, buildings (residential, workplace, hospital, market, park, school), satellite view, boundaries, and bus stops.

4.1.2. Restrictive Policies

To compare different scenarios and the impact of restrictive policies on the virus behavior, four different simulations were developed using the same map. These simulations can be executed in the simulation tool from their respective models. The simulations are as follows: All_Allowed (all actions and movements of agents (people) are allowed); Schools_Closed (schools are closed); Workplaces_Closed (workplaces, schools, and non-park recreational buildings are closed. Hospitals, markets, and parks remain open); Full_Lockdown (visits and park attendance are prohibited. People only leave their homes for hospital visits or to go to the markets. Public transportation is eliminated.)

4.1.3. Simulation Parameters

At the beginning of the simulation, 4 important parameters must be configured: the number of people participating in the simulation, the number of days to simulate, the initial percentage of people infected with the virus, and the file path containing the virus information (Virus parameter information). In addition to the initial simulation parameters, there are other parameters that affect the course of the simulation and can be modified at any time. The *Disinfection quality* parameter allows selecting one of 4 predefined values,
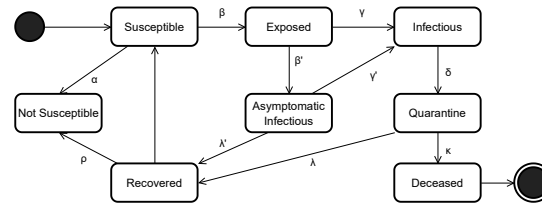
Fig. 2: State Transition Diagram

which regulates the quality of disinfection for individuals, buildings, and city roads, significantly impacting the spread of the virus. Lastly, the *Required face mask use* parameter mandates the use of face masks by individuals in the simulation, reducing the transmitted viral load by approximately 90%.

4.1.4. Movement Model

To implement the movement of agents throughout the city, each person has a daily schedule that controls their activities. To achieve a realistic approach, the activities in each person's schedule depend on their age. Several age groups were defined based on age ranges, and the percentage distribution of these groups in the population was extracted from real data from the Anuario demográfico de Cuba 2020 [23]. The Table 2 displays the age distribution.

Age Group	Age Range	Population %
Child	5 to 12	9.6
Adolescent	13 to 19	7.36
Young Adult	20 to 39	20.72
Adult	40 to 59	31.8
Elderly	60+	21.7

Table 2: Age Distribution in the Population

4.1.5. Contagion Model

In Fig. 2, the State Transition Diagram shows the variant of the SEIR model used in the project after analyzing the previously presented modified SEIR models. It illustrates the different states that individuals go through in the simulation and their transitions. The states and coefficients are explained in 3.1. In the simulation, real data from the SEIR model is used to simulate the spread of the virus. According to a study [24], the average incubation period of the virus (from acquisition to symptom manifestation and contagion) is 4 to 5 days, although it can range from 2 to 7 days. The duration of the infection (from symptom onset to recovery) is usually 7 to 8 days, but it can be longer in severe cases (10 to 12 days) or critical cases (15 or more days). In a study on immunity to the Covid-19 virus [25], several groups of vaccinated, recovered, and susceptible individuals (a total of 5.7 million people) were examined after exposure to the virus. It was found that only 10% of those who had recovered from the disease in the past 4 months experienced reinfection, while the rest exhibited immunity. However, this immunity diminishes over time, as for those infected more than 12 months ago, the reinfection rate increased to 30%. According to the June 2021 report in Cuba [26] (prior to the vaccination campaign), a total of 193,945 confirmed cases and 1,302 deaths were recorded, resulting in a mortality rate of 0.67% and a recovery rate of 99.33%. These data are used in the simulation to control the transition between states of individuals and model the spread and behavior of the virus. In SEIR models, the infection rate of individuals (the probability of each person contracting the virus) is typically calculated as a static value based on previously accumulated data. However, in the simulation environment, it is handled differently. Infectious individuals spread viral load in the places they visit, which is then absorbed by susceptible individuals. When their exposure reaches a threshold, they become infected and fully exposed to the virus. According to a study by the Center for Demographic Studies in Cuba [27], both sex and age are factors that affect the infection rate and mortality in individuals. Men are more prone to die from the disease, and there is also an increased mortality rate in older age groups [1].

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[1] It is important to note that the data used for the study dates back to 2020 when Cuba had not yet experienced the peak of the epidemic. However, the proportion of differences in mortality rates among age groups remains valid.

5. Experimental Design

To evaluate the spread of the infectious virus and the overall system, experiments were conducted to test the software with different configurations and analyze their results. Table 3 provides the data used for these experiments. Five key experiments were conducted:

- Experiment 1- Default simulation parameters were used to observe the behavior of a virus similar to the Omicron variant of Covid-19 in a city without restrictions.
- Experiment 2- Using the same virus, its behavior was examined in a city under quarantine.
- Experiment 3- Mandatory mask usage and constant disinfection of streets and buildings were implemented in the city, while activities remained unrestricted.
- Experiment 4- The behavior of a potentially infectious virus was tested in a city under quarantine.
- Experiment 5- The behavior of a potentially infectious virus was tested in a city under quarantine, with mandatory use of face masks and high-frequency disinfection.

Experiment	1	2	3	4	5
Scenario	All_Allowed	Full_Lockdown	All_Allowed	Full_Lockdown	Full_Lockdown
Number of people	500	500	500	500	500
Days to simulate	20	20	20	20	20
Initial percentage of infectious people	0.5	0.5	0.5	0.5	0.5
Face masks	No	No	Yes	No	Yes
Disinfection quality	Normal	Normal	High	Normal	High
Virus infection radius	2m	2m	2m	100m	100m
Virus transmission rate	Medium	Medium	Medium	Very High	Very High
Virus fatality probability	Low	Low	Low	High	High

Table 3: Experiment Details

5.1. Experiment Results

Below, in Table 4, the experiment results are presented, along with the values of certain attributes that may be useful for analysis.

Experiment	1	2	3	4	5
Total Infections	527	52	0	313	2
Deaths	13	2	1	110	1
Location with Most Infections	Homes - 49%	Homes - 90%	-	Homes - 49%	Homes - 100%
Second Location with Most Infections	Streets (Outdoor) - 28%	Hospitals - 6%	-	Streets (Outdoor) - 48%	-
Activity with Most Infections	Stay at home	Stay at home	-	Stay at home	Stay at home
Second Activity with Most Infections	Study	Work (Only hospitals or markets)	-	Shopping	-
Basic Reproduction Number (R0)	4	0.95	0	2.3	0.4
Percentage of Susceptible Population Exposed to the Virus	110%	10%	0%	80%	0.4%
Susceptible Individuals at the End of the Simulation	9	390	459	162	436
Immune Individuals at the End of the Simulation	445	98	40	210	62
Epidemic Peak	Day 5	Day 1	-	Day 7	Day 1

Table 4: Experiment Results

5.1.1. Results Evaluation

The evaluation of the results reveals several key findings. Firstly, the absence of infections in Experiment 3 stands out. This can be attributed to the consistent use of face masks from the beginning of the simulation and the rigorous cleaning and disinfection of buildings and streets. This particular experiment demonstrates that in a controlled environment of 500 individuals, with an initial infectious population of approximately 0.5% (around 3 people), rapid containment of the disease is achievable when everyone practices good hygiene and consistently wears face masks.

Furthermore, Experiment 1 and Experiment 2 highlight the effectiveness of implementing a strict full lockdown. Experiment 2 showed a significant 90.1% reduction in confirmed cases compared to Experiment

1. By imposing strict restrictions on people's movement within the city, gatherings are minimized, thereby impeding the spread and transmission of the virus. In Experiment 2, only around 10

An important metric worth noting is the basic reproduction number, which indicates the average number of people infected by a single infected individual throughout the infectious period. If this number surpasses 1 at any point, it signifies the potential for exponential spread, potentially leading to a pandemic. In Experiment 1, the highest value observed for this variable was 4, indicating the occurrence of pandemic outbreaks where each infected person infected, on average, 4 others. Conversely, Experiment 2 did not exceed a value of 0.95, indicating that even during the peak of the disease, there were individuals who did not transmit the virus to others. Throughout the lockdown period, the disease remained under control.

However, it should be noted that a full lockdown alone is not sufficient. Experiment 4 demonstrated a significant increase in infections during the lockdown period when a highly contagious virus was introduced. Despite the lockdown measures, individuals were required to leave their homes to purchase essential items, resulting in potential exposure and subsequent transmission of the virus. As indicated by the results, approximately 97% of the infections occurred within households and on the streets, with the riskiest activities being shopping and remaining at home.

Upon analyzing the experiments, it becomes evident that Experiment 3 and Experiment 5 yield superior qualitative results. The latter exhibited a remarkable 99.3% reduction in cases compared to Experiment 4, where a highly infectious virus was introduced. Therefore, the implementation of face masks and rigorous disinfection measures emerge as crucial factors in mitigating the spread of an infectious virus within a Cuban city.

5.1.2. Other approaches, limitations, and future work

In the field of agent-based simulation, many systems have been developed to model virus contagion and its impact in countries such as Ukraine [19] and Vietnam [20], or for more general purposes, adapting to different circumstances [6]. Additionally, the source code of the COMOKIT modeling toolkit [20] is available, an open-source simulation tool developed on the GAMA platform to predict the behavior of Covid-19 in Vietnam. This tool offers a wide range of experiments to model various situations, including total and partial quarantine, and it also aims to be studied and applied in other contagion and spread models [20], serving as a basis for the current work. However, the tool does not take into account factors such as public transportation or people's movement within a city. Considering the above, to date, there is no agent-based simulation model developed to adapt to the situation in Cuba, as proposed in this work. While this study effectively used agent-based simulation and the SEIR model to analyze virus spread in a Cuban city, data accuracy, and availability may be limitations. Future work should focus on improving data quality. Additionally, future research can explore incorporating real-time data and machine learning for more dynamic and adaptive pandemic response models.

6. Conclusion

In this work, agent-based simulation and the SEIR model were employed to analyze the spread of a virus in a city in Cuba. Factors such as population density, aging, and individual risk factors for contagion were considered, allowing for a realistic representation of the virus spread in the Cuban context. Additionally, variations of the SEIR model were explored, including considerations for immune individuals, individuals in quarantine, and fatalities, as well as asymptomatic progression and the possibility of reinfection in recovered individuals.

The experimental analysis conducted using this simulation provided valuable insights into virus propagation and facilitated the evaluation of different intervention measures, such as quarantines, vaccination campaigns, and mask usage. The obtained results helped to understand the impact of these interventions and guide decision-making to control the disease.

In summary, this study demonstrated the utility of agent-based simulation and the SEIR model in predicting virus spread in a city in Cuba. These approaches can be utilized in future studies and in the planning of public health strategies to address pandemics and contagious disease outbreaks. It underscores the importance of employing models and simulations in managing contagious diseases, as they provide a more comprehensive understanding of disease propagation and support evidence-based decision-making. Furthermore, it emphasizes the need for a global and coordinated response to pandemics, including early detection and response strategies, strengthening healthcare systems, research and development, international cooperation, and proactive planning to mitigate the impact of pandemics on society and the global economy.

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