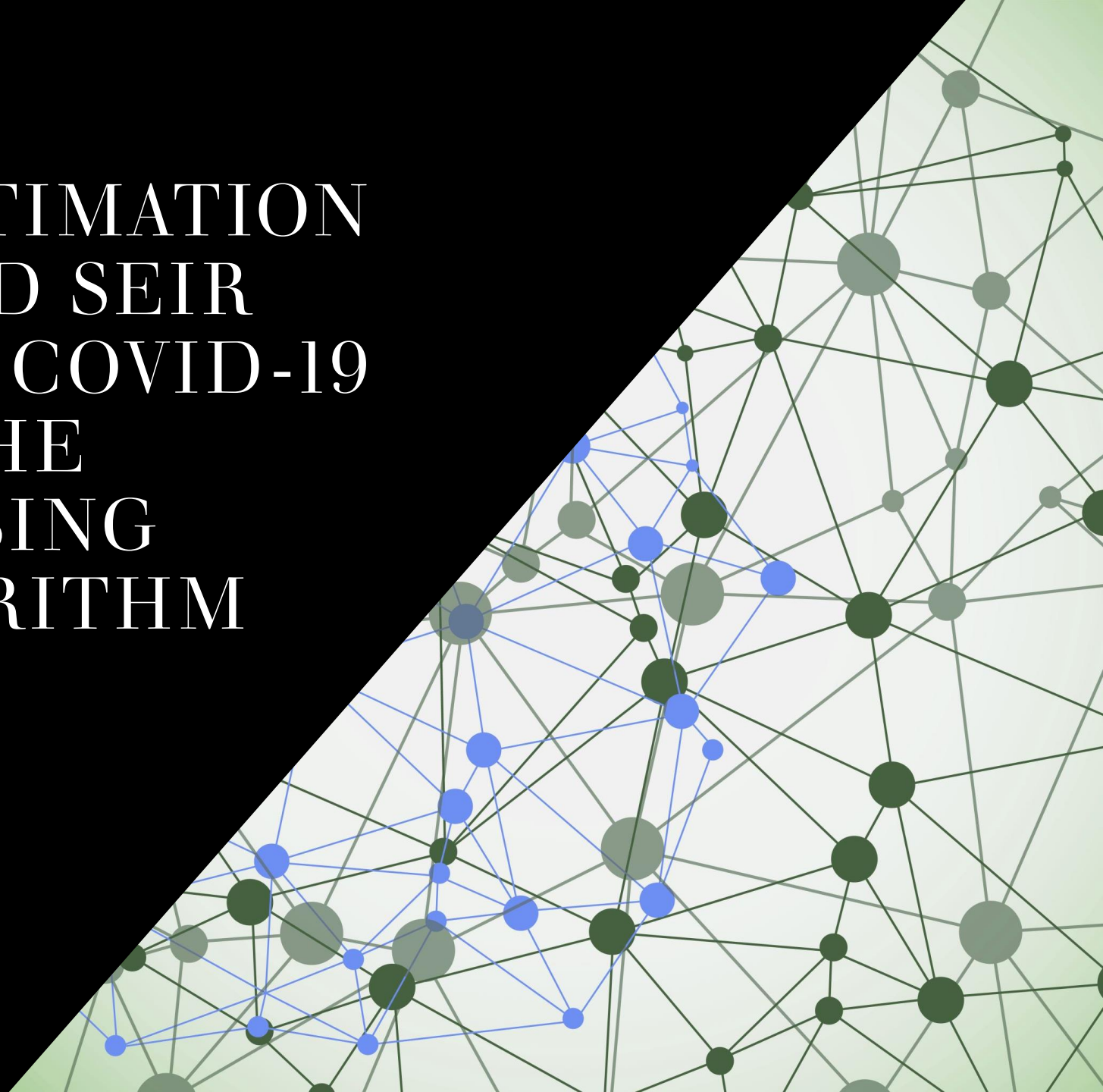


PARAMETER ESTIMATION FOR A MODIFIED SEIR MODEL OF THE COVID-19 DYNAMICS IN THE PHILIPPINES USING GENETIC ALGORITHM

Gabriel Lorenzo I. Santos

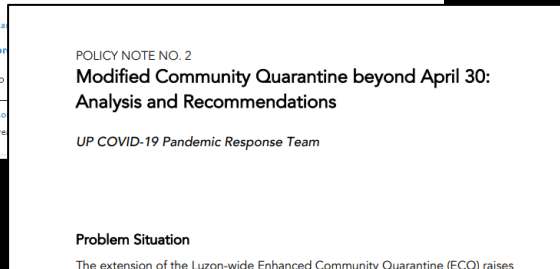
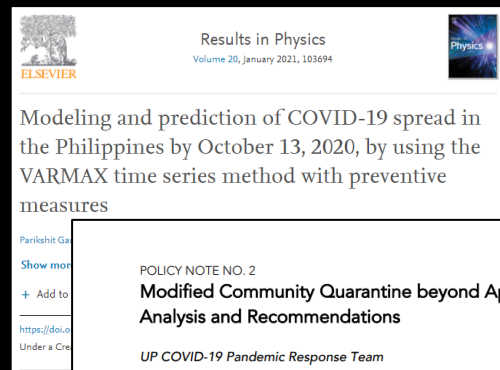
CS 280 Mini Project



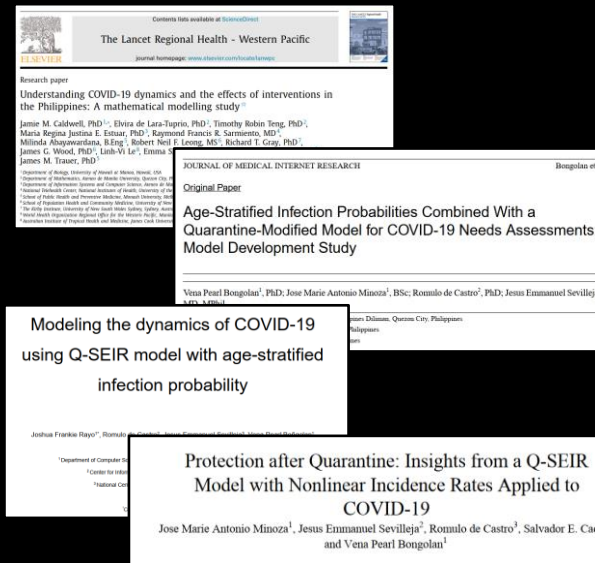
State of COVID-19 in the Philippines



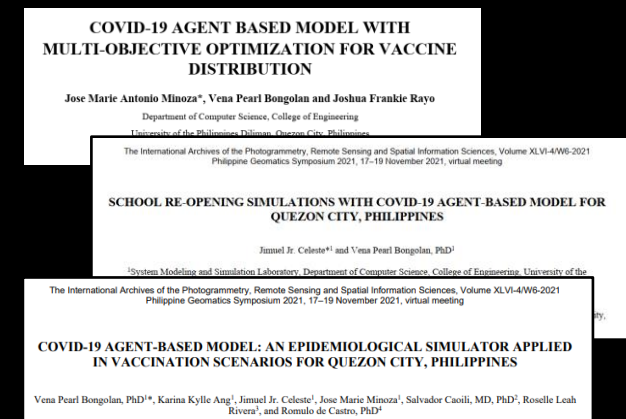
Research on COVID-19 in the Philippines



Time-series Analysis

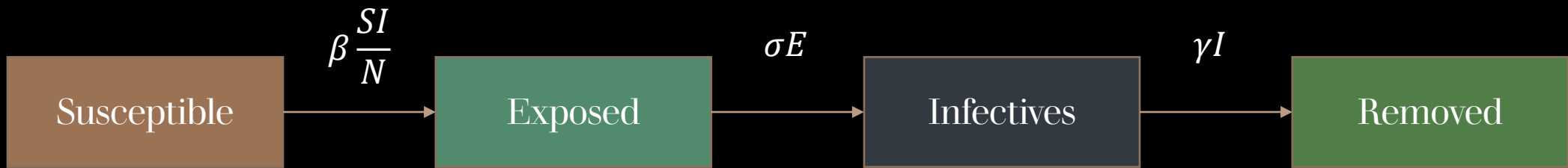


Compartmental Models



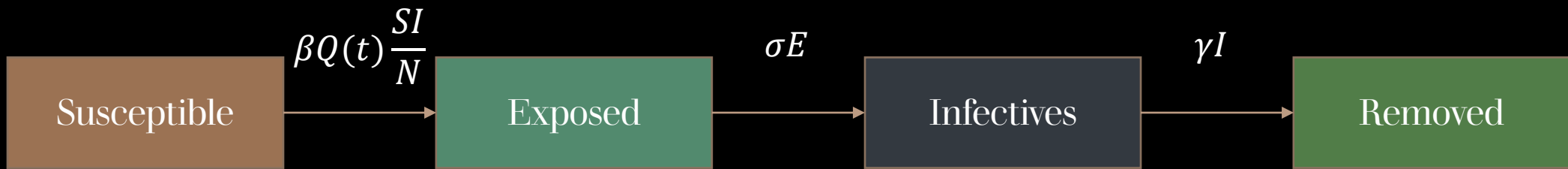
Agent-based Modeling

SEIR Model



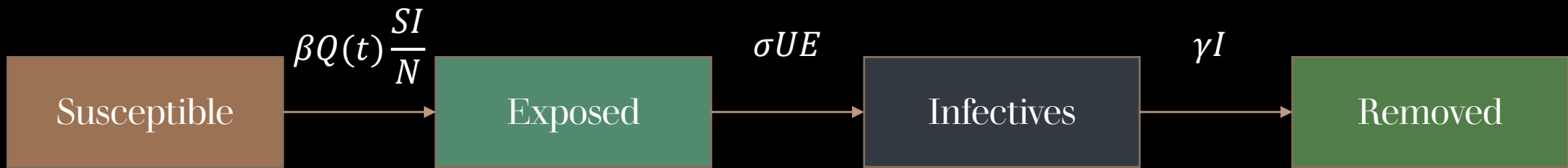
- Transmission rate (β), incubation period (σ), and recovery period (γ) are inherent properties of the virus.
 - All compartments are well-mixed and homogenous.
-

Q-SEIR Model (Bongolan, 2021a)



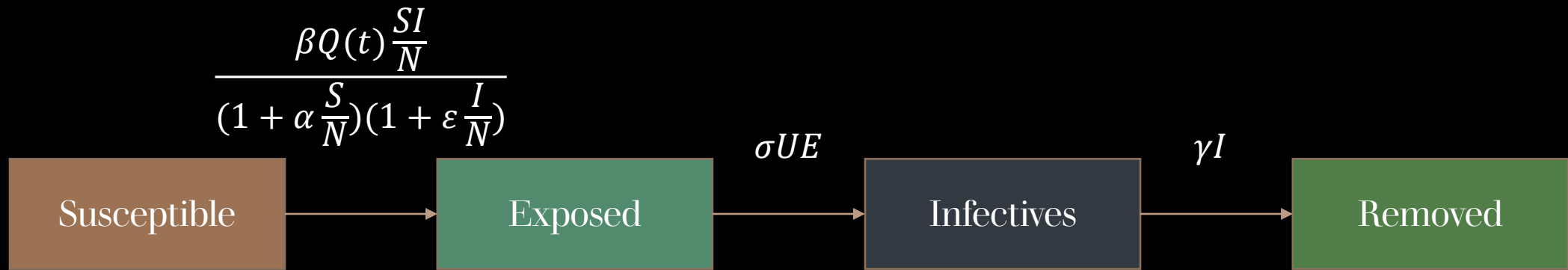
- Quarantine factor ($Q(t)$) controls the exposure between susceptible-infectious interactions.
 - $Q(t) = 0.2$: 80% success rate of quarantine
-

ASQ-SEIR Model (Rayo, 2020)



- Age-stratified Infection Probability ($0 < U \leq 1$) = relative proportion of infected cases by age group
-

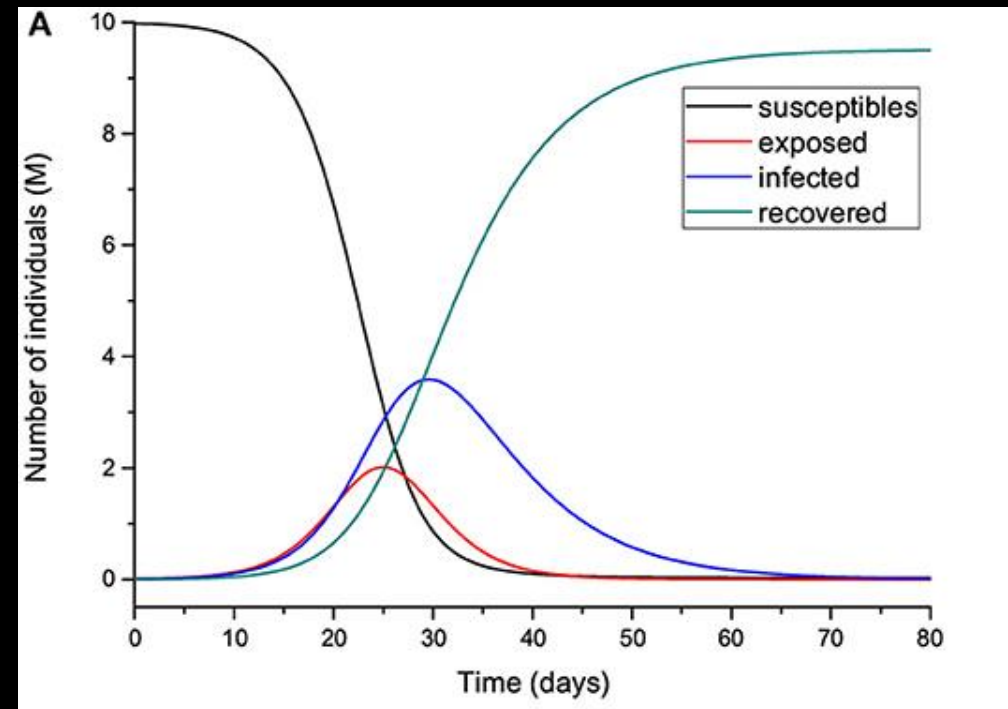
ASQ-SEIR-NLIR Model (Minoza, 2020)



- Behavioral (α) and disease-resistance (ε) factors are incorporated.
 - While β, σ, γ are properties of the virus, α, ε are properties of the S and I population.
-

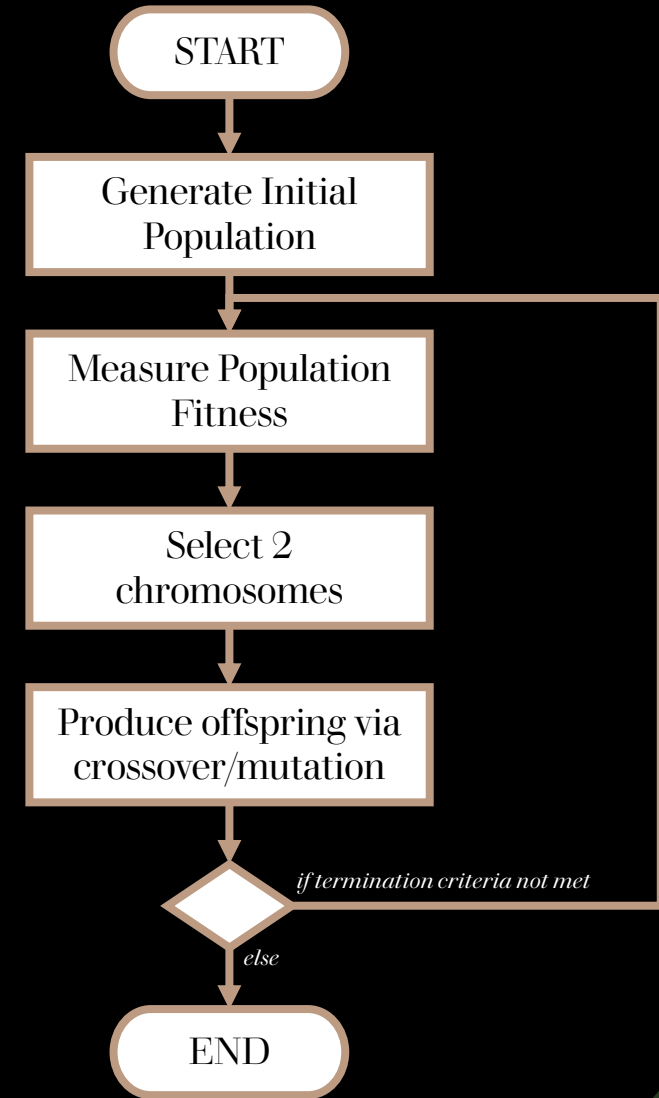
Governing ODEs of ASQ-SEIR-NLIR

$$\begin{aligned}\frac{dS}{dt} &= -\frac{\beta Q(t) \frac{SI}{N}}{(1 + \alpha \frac{S}{N})(1 + \varepsilon \frac{I}{N})} \\ \frac{dE}{dt} &= \frac{\beta Q(t) \frac{SI}{N}}{(1 + \alpha \frac{S}{N})(1 + \varepsilon \frac{I}{N})} - \sigma UE \\ \frac{dI}{dt} &= \sigma UE - \gamma I \\ \frac{dR}{dt} &= \gamma I\end{aligned}$$



Genetic Algorithm

- A heuristic search or optimization technique that belongs to a larger class of evolutionary algorithms
- Relies on the randomness in the crossover and mutation of the highest quality (fitness) candidate to maximize (or minimize) an objective



Chromosome (Individual) Representation

- Each chromosome (Ω) is composed of individual *gene*, which refers to a single piece of data.
- Binary representation is commonly used in GA. Here, floating point representation is used.
- Ranges are defined based on available literature and author's assessment.

β	σ	γ	Q	U	α	ε
[2, 3.2]	[0.13, 0.28]	[0.05, 0.33]	[0.2, 0.9]	(0, 1]	[0, 1]	[0, 0.7]

Fitness Function

- Measures the quality or “fitness” of the chromosome
 - $f(i) = \omega_c \|c_r - c_m^\Omega\|_{L_2} + \omega_r \|r_r - r_m^\Omega\|_{L_2}$
 - $c_r - c_m^\Omega$: difference between the reported cumulative active cases (c_r) and predicted cumulative active cases (c_m^Ω)
 - $r_r - r_m^\Omega$: difference between the reported removed cases (r_r) and predicted removed cases (r_m^Ω)
 - ω_c : weight of objective function for active cases
 - ω_r : weight of objective function for removed cases
 - Fitness Rank = 1 / Fitness Score = $1/f(i) \Rightarrow$ lower distance, higher rank, v.v.
-

Selection

- Get the top X chromosomes according to the fitness rank
 - Select 2 random chromosomes from the set of top chromosomes via Roulette Wheel
 - *Probabilities are computed by getting the relative rank of each chromosome.*
-

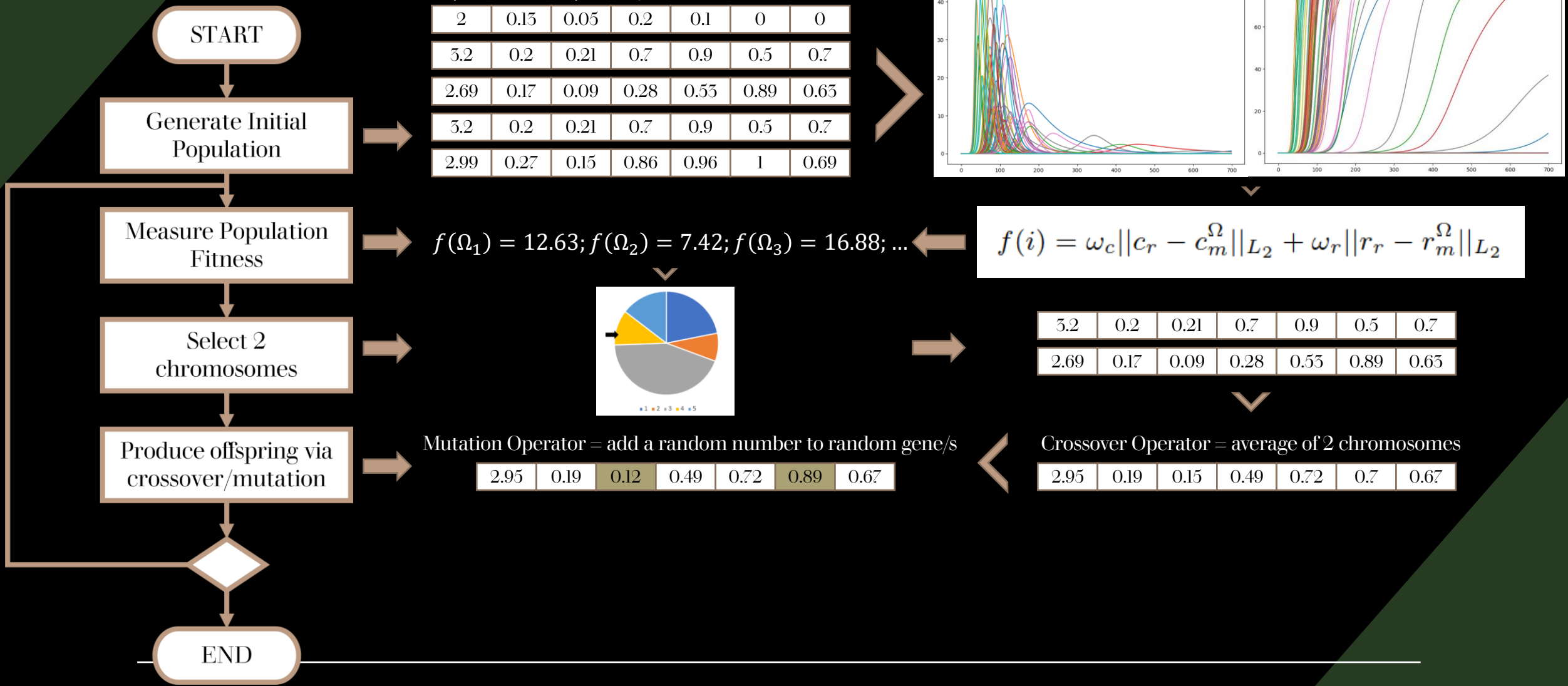
Crossover

- When the crossover threshold is met, the 2 chromosomes are crossed over.
 - Operator: average of the 2 parent chromosomes
 - Since it will produce 2 identical child chromosome, only 1 is forwarded for mutation.
 - If the crossover threshold is not met, the chromosome with the higher fitness rank is forwarded for mutation.
-

Mutation

- When the mutation threshold is met, the child chromosomes is mutated.
 - Randomly select gene/s to mutate
 1. *Assign a random score to each gene.*
 2. *If a gene meets the random threshold, that gene is mutated.*
 3. *If no gene meets the random threshold, then a random gene is mutated.*
 - The mutated chromosome is inserted back to the population.
 - If the crossover threshold is not met:
 - If there is a child chromosome, the child chromosome is inserted back to the population.
 - If there is no child chromosome, the parent with the higher fitness rank is inserted back to the population
-

GA Methodology

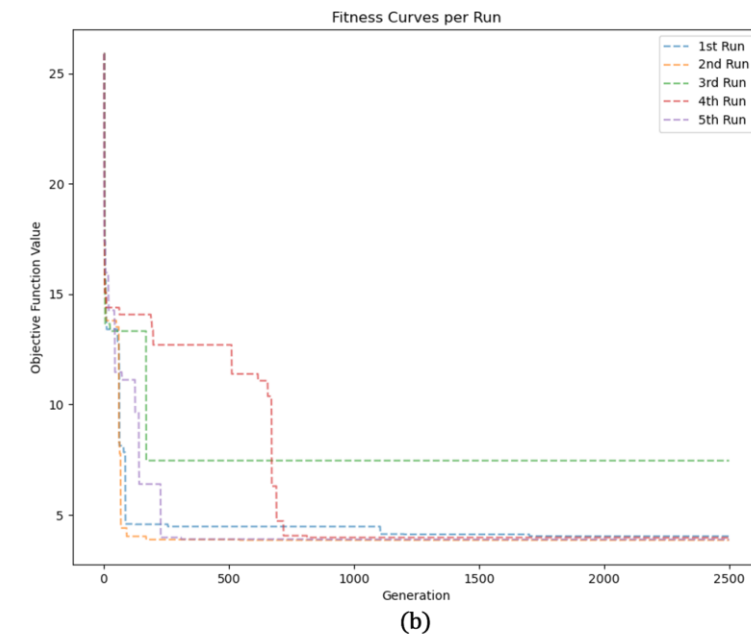
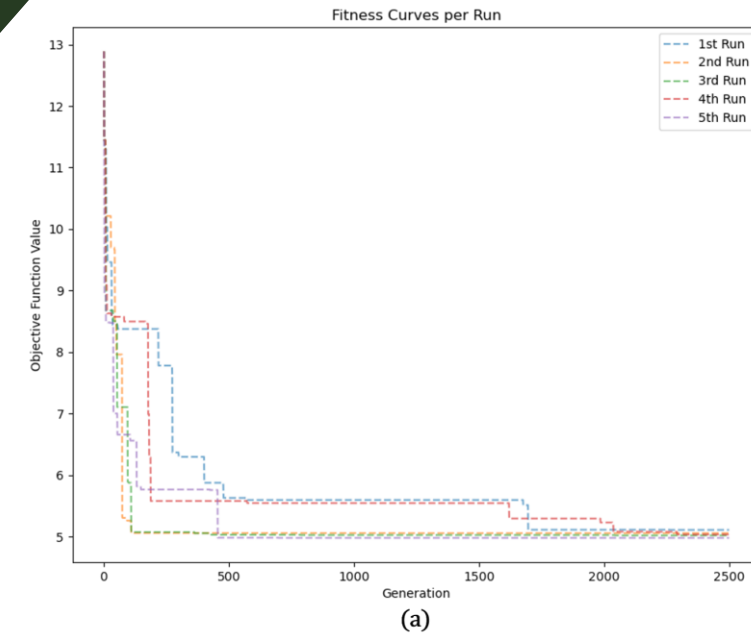


Experiment

- Population size = 70; Sample size (top chromosomes) = 5
 - Generations = 2,500
 - Runs = 5; Get the fittest chromosome for each run.
 - The final chromosome is the fittest among the 5 runs.
 - Regions of Interest: Philippines (country level) and Quezon City (city level)
-

FITNESS CURVES

RESULTS

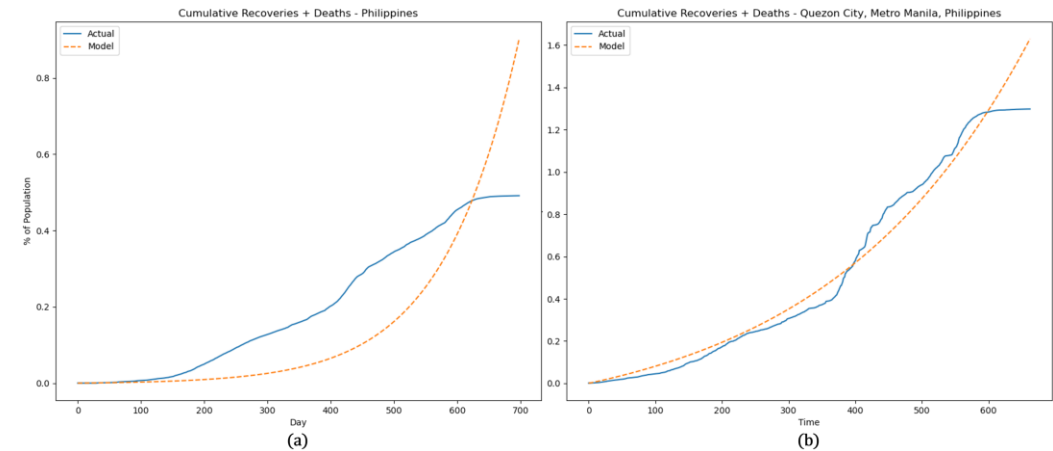
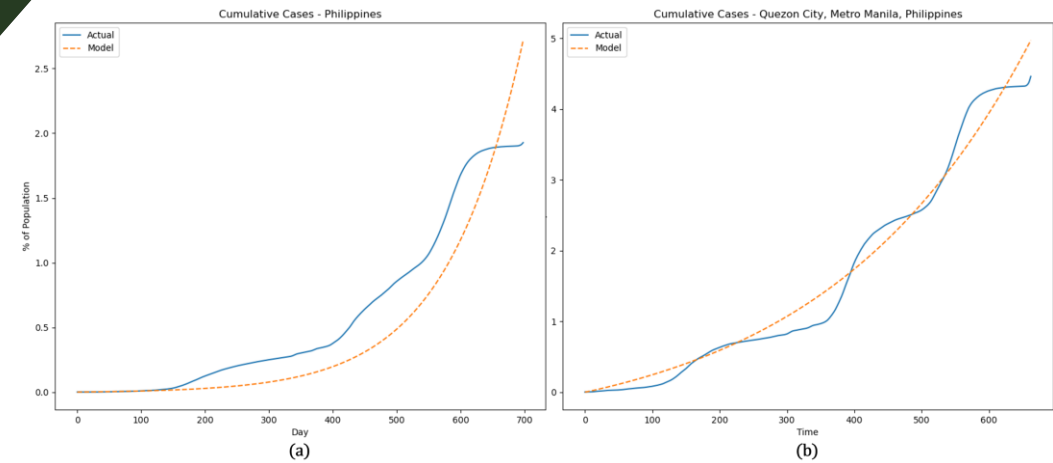


FITNESS CURVES

RESULTS

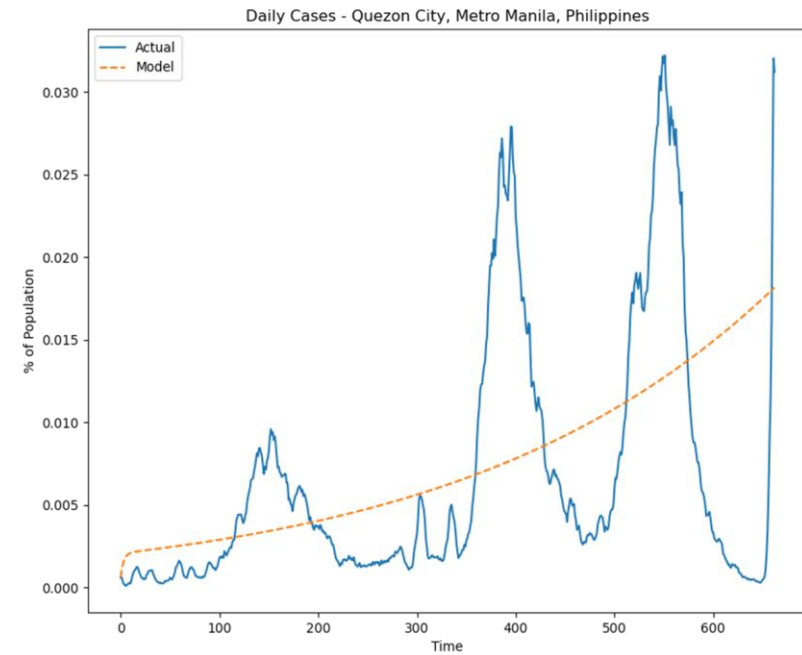
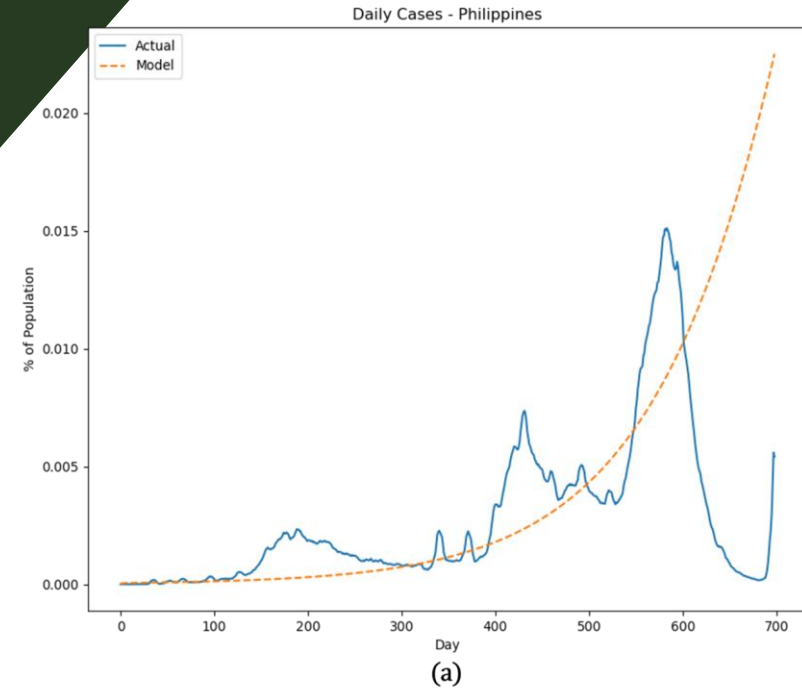
Country-level Fit = 4.978

City-level Fit = 3.857



TRAJECTORY

RESULTS



OPTIMAL PARAMETERS RESULTS

Insights:

- High resistance, low MHS compliance (PH & QC)
- Faster transmission in QC ($\beta Q_{QC} > \beta Q_{PH}$)
- $\sigma U_{PH} > \sigma U_{QC}$ == may be interpreted as more undetected cases in QC (needs validation)
- QC, same removal rate as PH

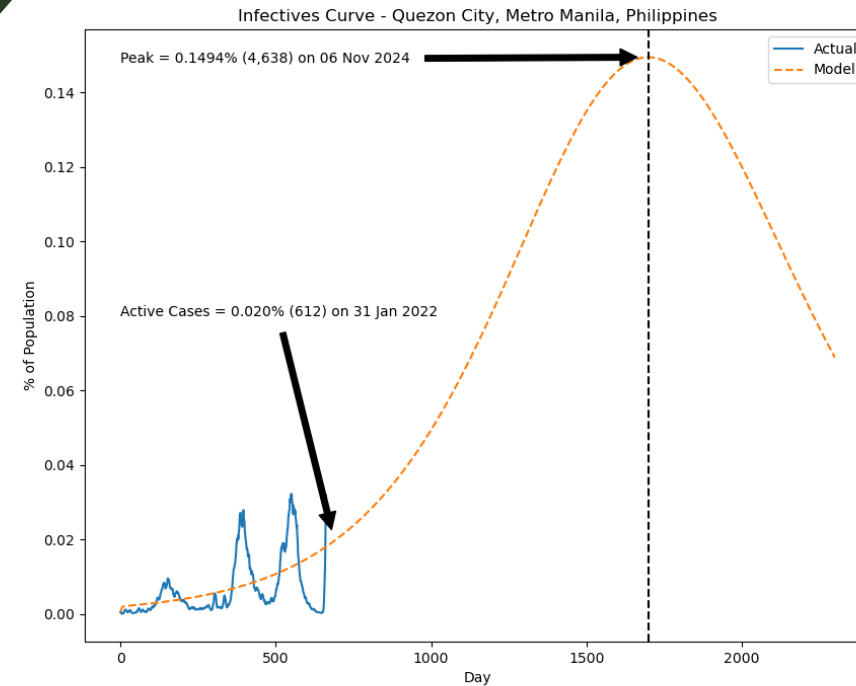
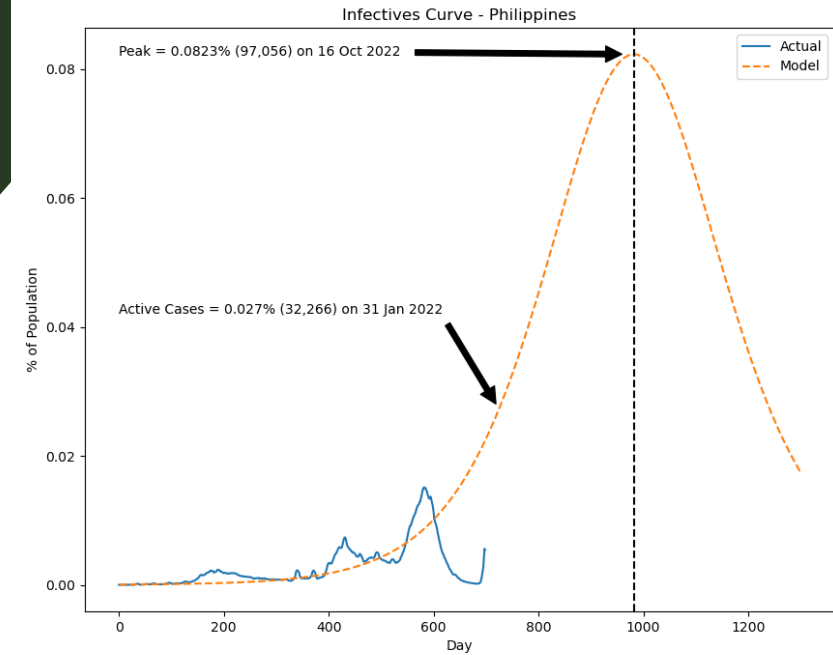
Optimal Parameter Values		
Parameter	Country	City
Transmission/Contact Rate (β)	2	3.12
Incubation Period (σ)	0.28	0.28
Removal Rate (γ)	0.33	0.33
Quarantine Factor (Q)	0.2	0.2
Age-Stratified Infection Probability (U)	1	0.03
Behavioral Factor (α)	0.13	0.36
Disease-resistance Factor (ϵ)	0.7	0.7

INFECTION PEAK

RESULTS

Insights:

- PH: 0.0823% of population by Oct 2022
- QC: 0.01494% of population by Nov 2024



Conclusion

- Use of genetic algorithm for parameter estimation
- Average trajectory of ASQ-SEIR-NLIR model produced by the GA parameters
- Dynamics described by the GA parameters

Future Work:

- Using time-based parameters to capture specific peaks
 - Using other types of fitness function
 - Modification of compartments to capture other population
-

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