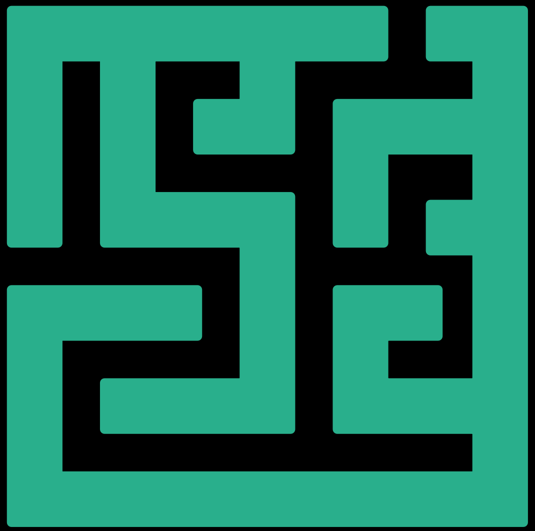
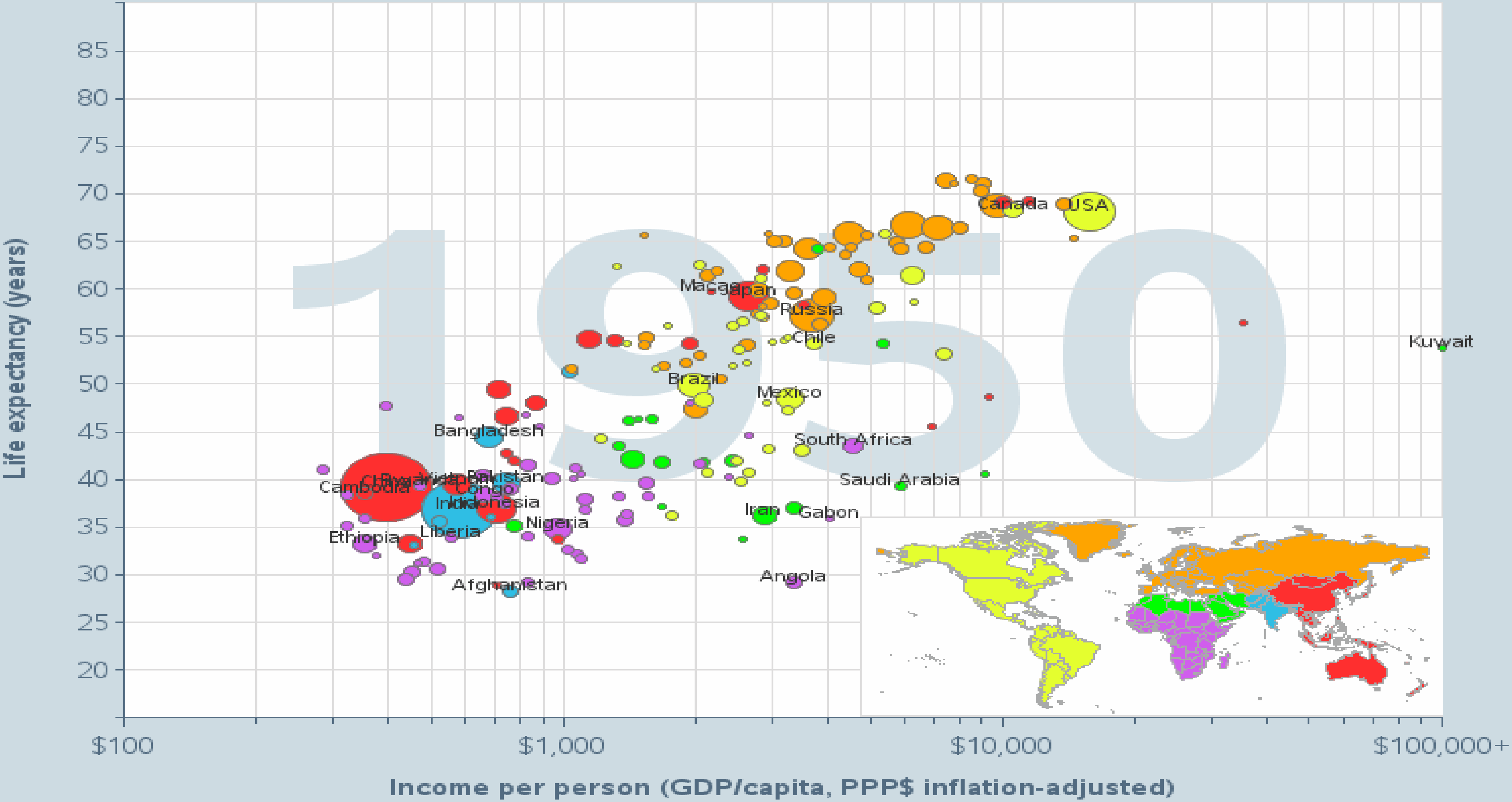
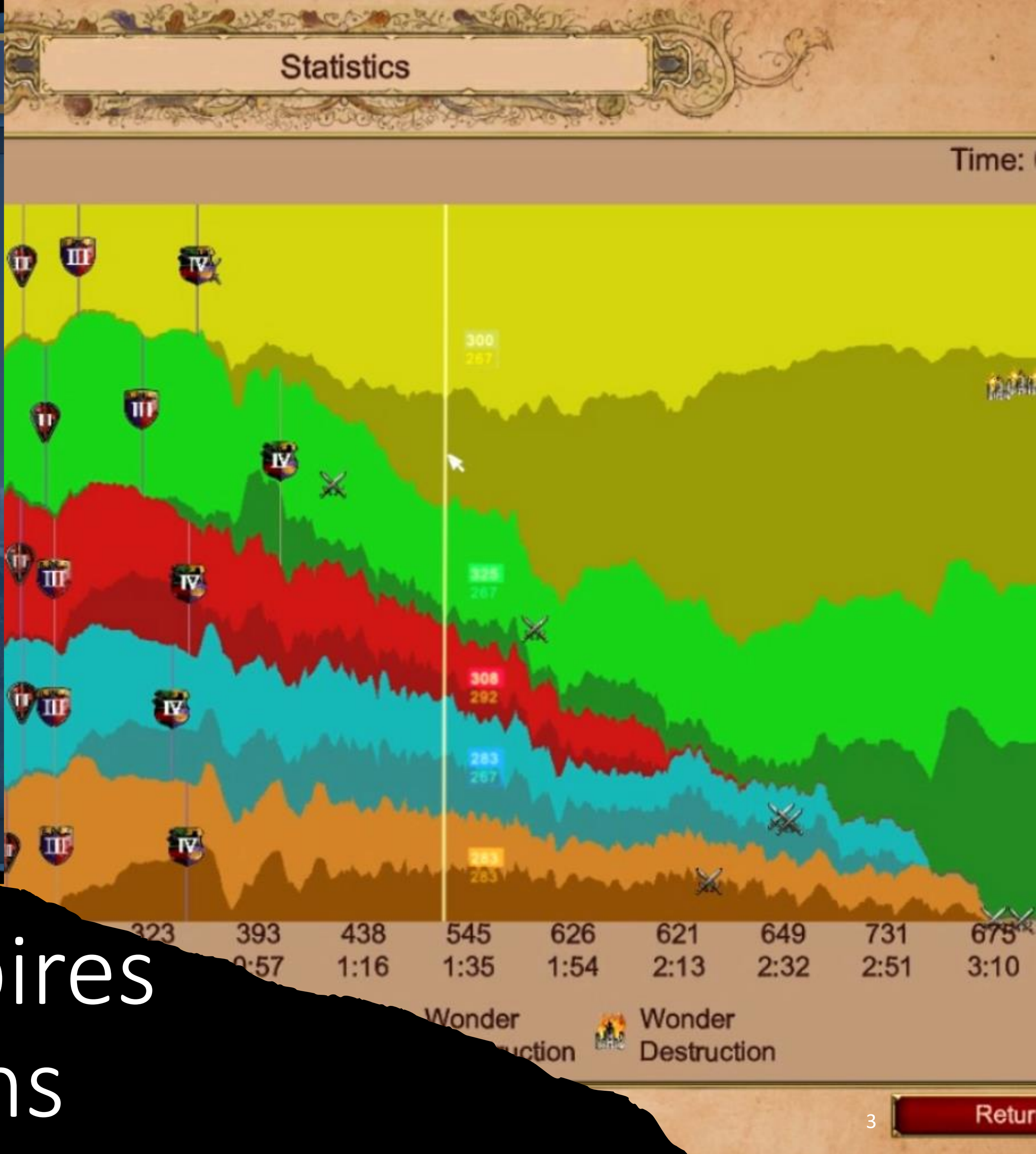
Echoes of the Spanish Lady: **Navigating the Maze of Epidemic Models**

A Look at the 1918 Flu Epidemic Models

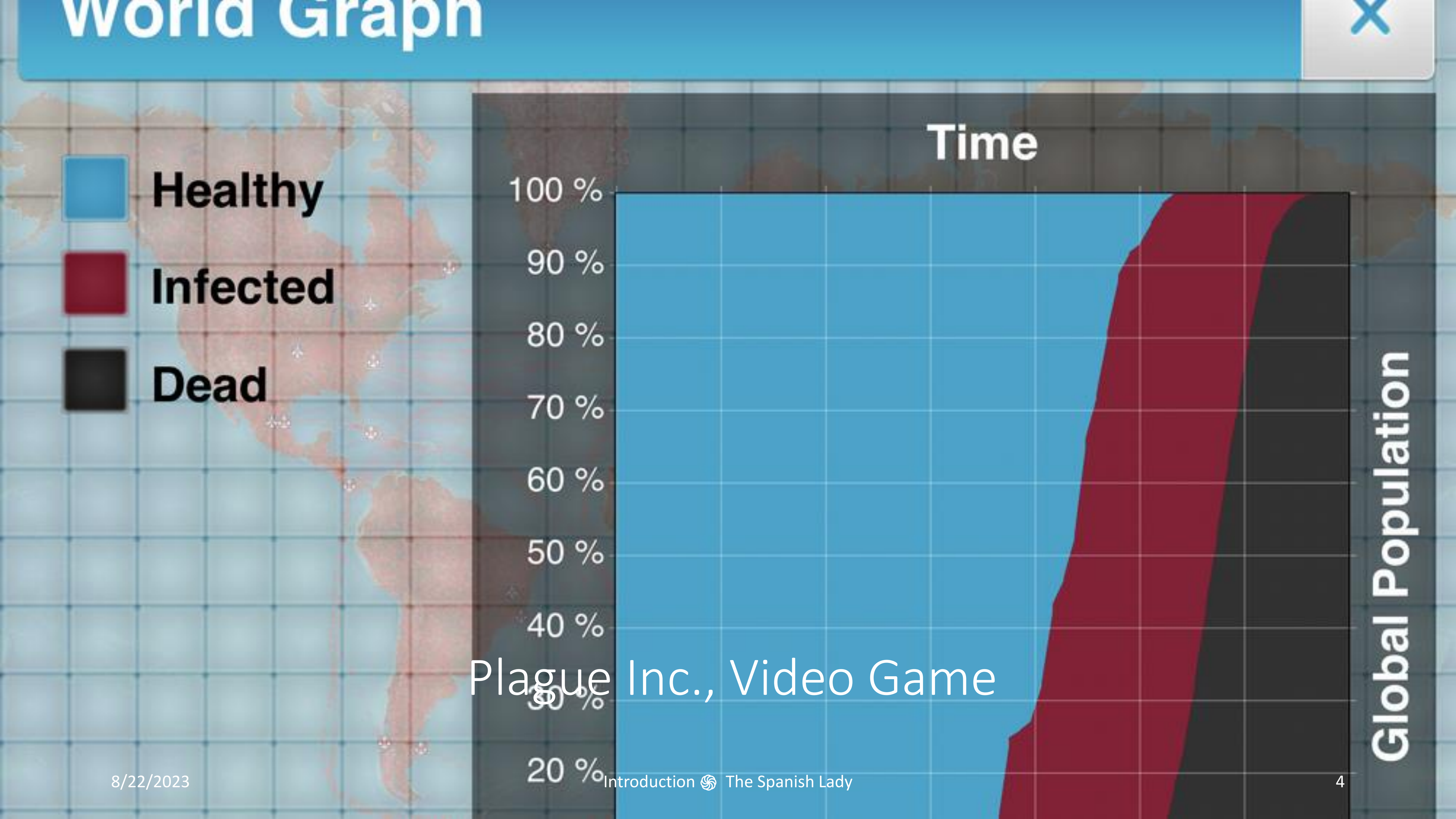


Wealth & Health of Nations





Civilization & Age of Empires Game Over Screen Graphs



Plague Inc., Video Game

Project Development

Computational Science Project Schedule

Week of June 7

- Defining the project scope and goals.
  - Clarity and feasibility of the project scope and goals.
  - Completeness of the project proposal

For June 21

- Literature review and research on existing methods
  - Breadth and depth of the literature review
  - Relevance of the literature to the project
  - Evidence of understanding the existing methods

For June 30

- Developing the computational method/algorithm:
  - Quality and completeness of the implementation
  - Evidence of testing and debugging of the method/algorithm
  - Evidence of understanding and implementation of the method/algorithm

Future Goals and Objectives

July 14

- Testing and optimization of the method/algorithm:
  - Evidence of understanding and implementation of optimization techniques
  - Evidence of testing and debugging of the optimization techniques
  - Scalability and computational efficiency of the method.

July 28

- Verification and validation of the method/algorithm:
  - Evidence of understanding and implementation of verification and validation techniques
  - Evidence of testing and debugging of the optimization techniques
  - Quality and completeness of the results

August 11

- Final Report/Presentation Preparation
  - Clarity and organization of the final report/presentation
  - Quality and completeness of the visual aids
  - Effectiveness of the delivery

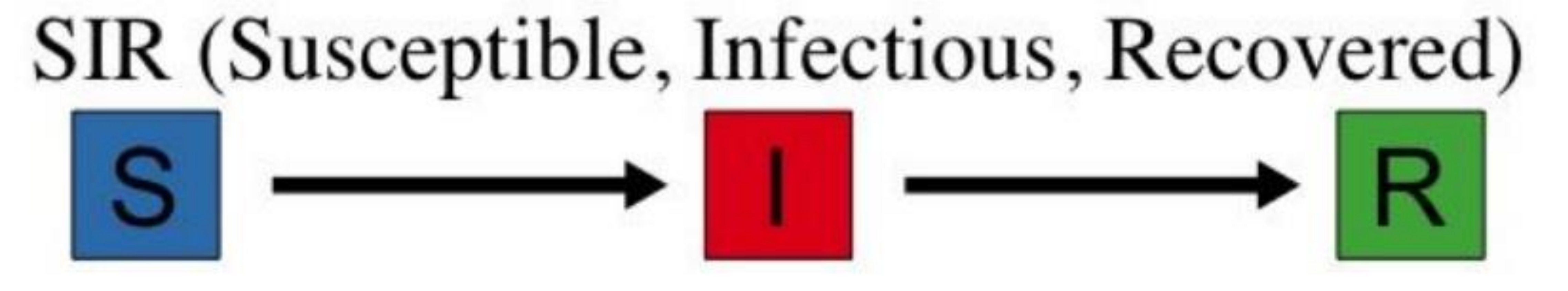
Introduction

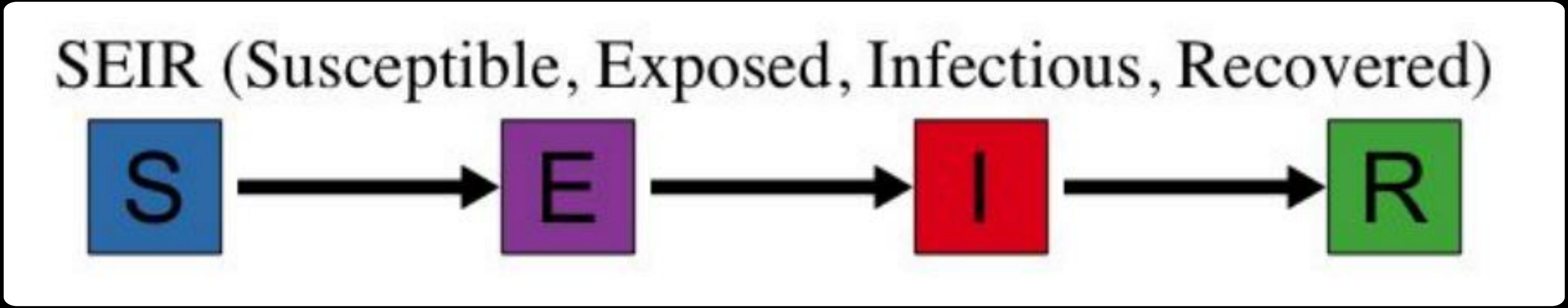
MATHEMATICAL MODELING OF INFECTIOUS DISEASES

KERMACK-MCKENDRICK MODEL

CELLULAR AUTOMATA AND MARKOV CHAINS

Basic SIR Model





The Corrupted Blood Incident

9/13/2005, World of Warcraft

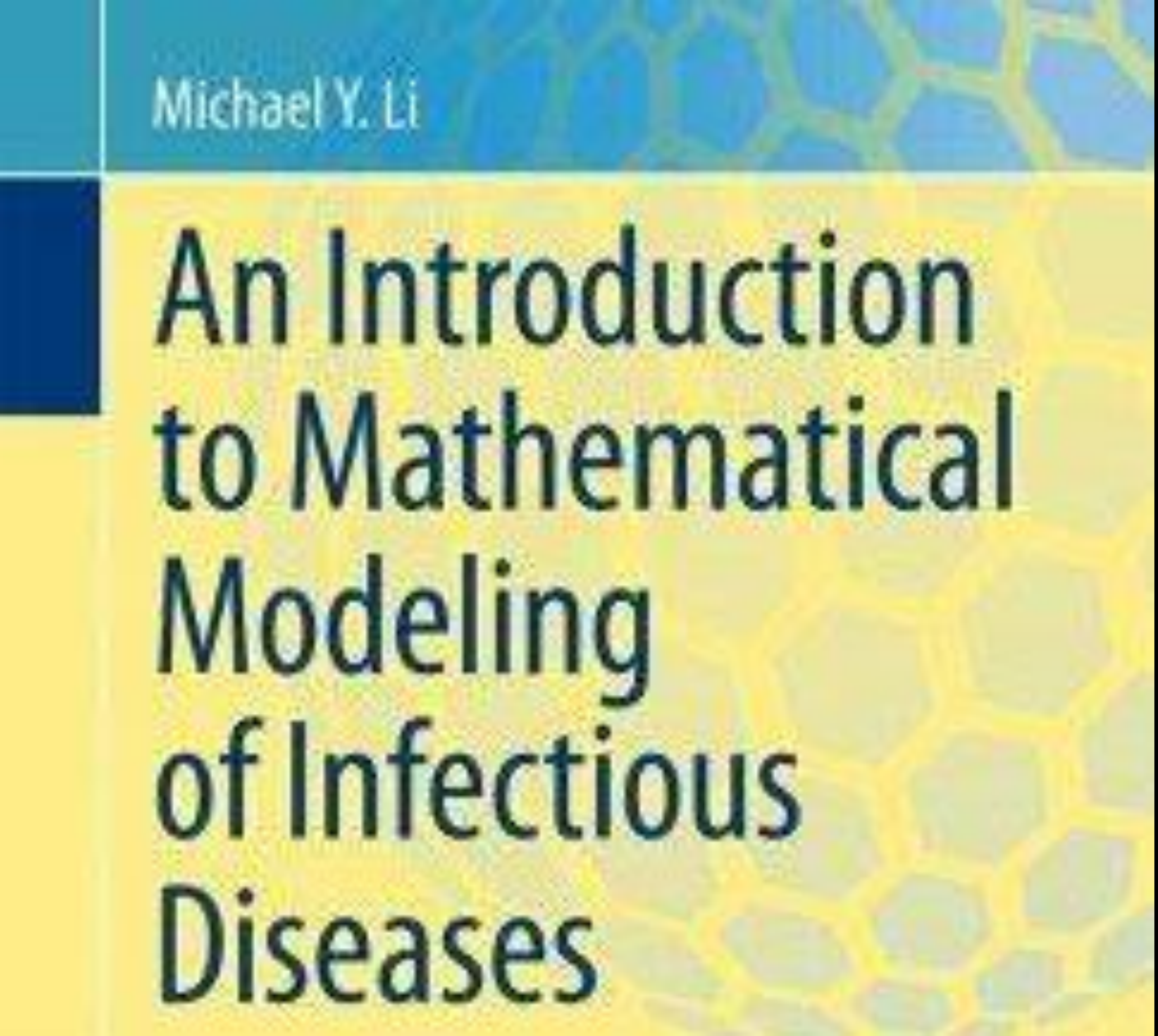
Release of new content: Blood God “Hakkar the Soulflayer“ for high level Avatars, during battle, Hakkar cast the spell “corrupted blood“ (CB) on random Avatars

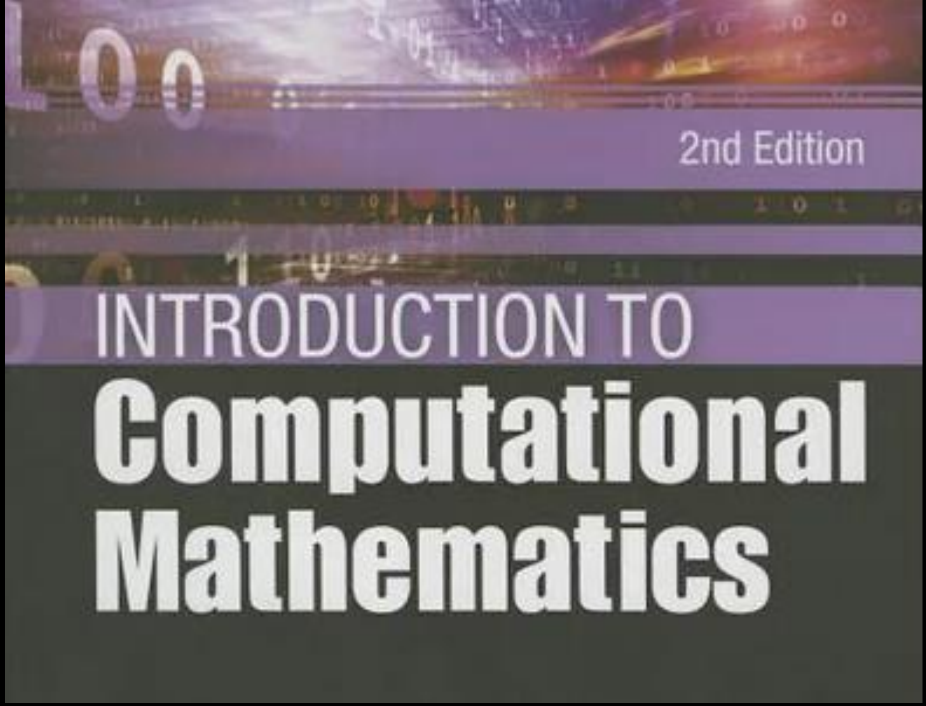
Corrupted Blood hit with severe damage: once plus additional damage over time; duration 10 seconds

Spread from Avatar to Avatar: INFECTIOUS

CB was never meant to leave Zul‘Gurub, but infected Avatars could teleport to cities

Hunters could dismiss their pets and call them back, <u>still infected</u> in cities


Michael Y. Li
An Introduction to Mathematical Modeling of Infectious Diseases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INTRODUCTION TO
Computational Mathematics


Numerical
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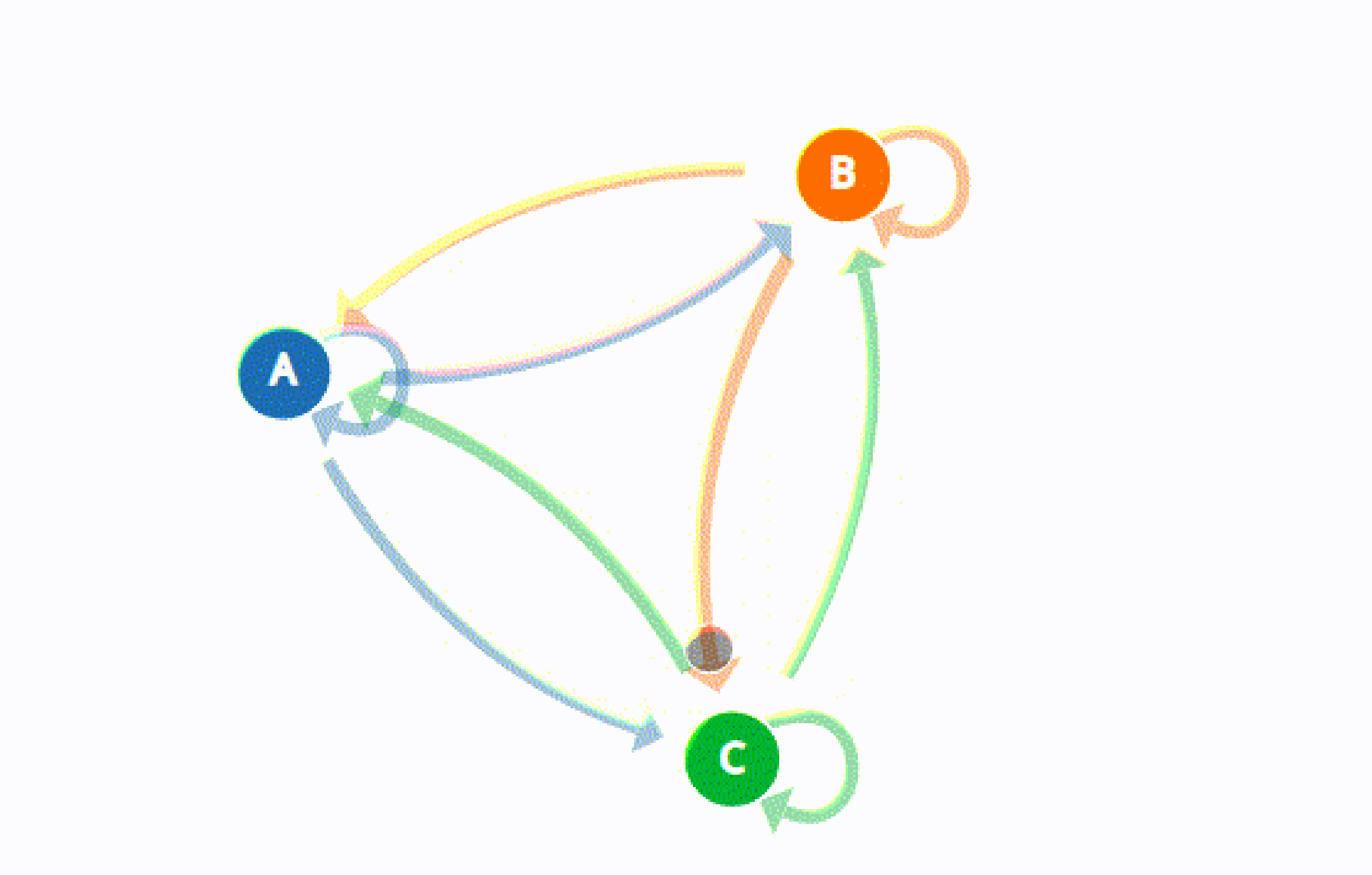
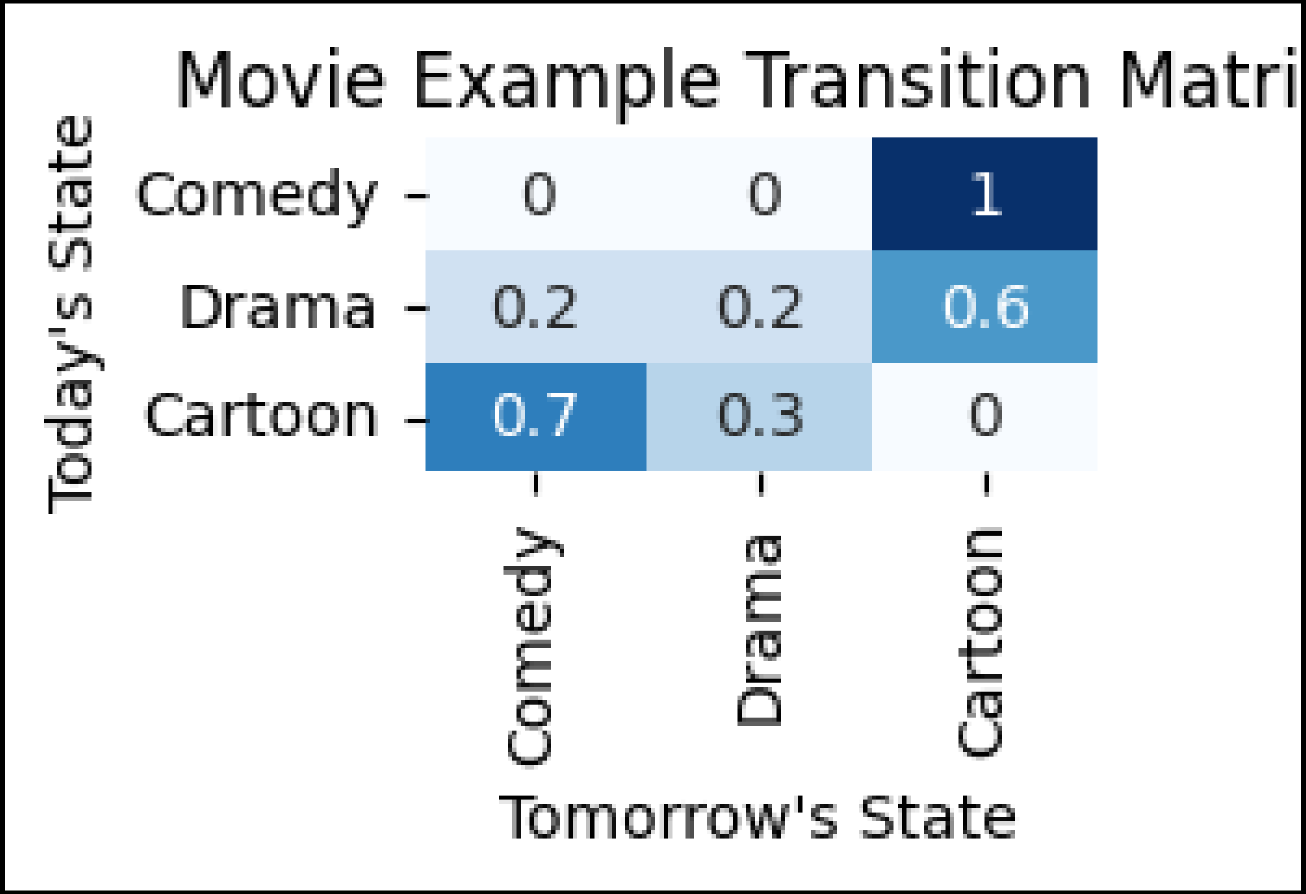
A Practical Techniques Approach for Industry

Markov Chain Example & Walk



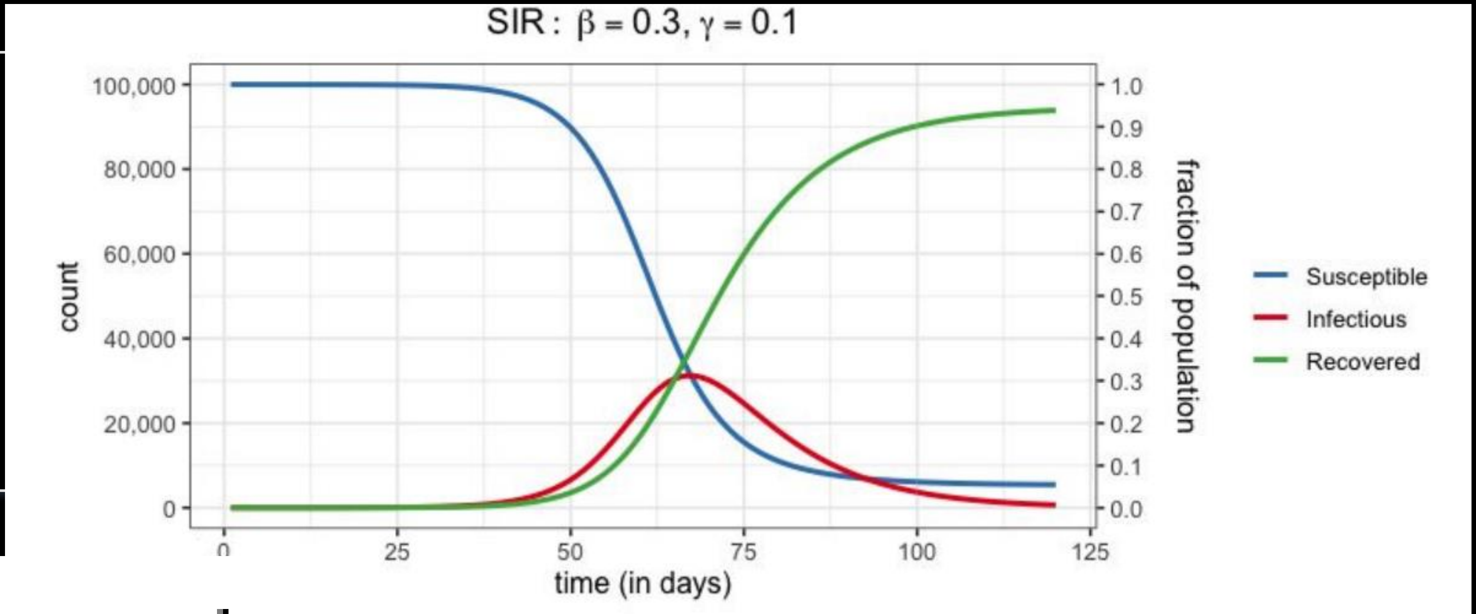
Markov Chain Example and SIR Example

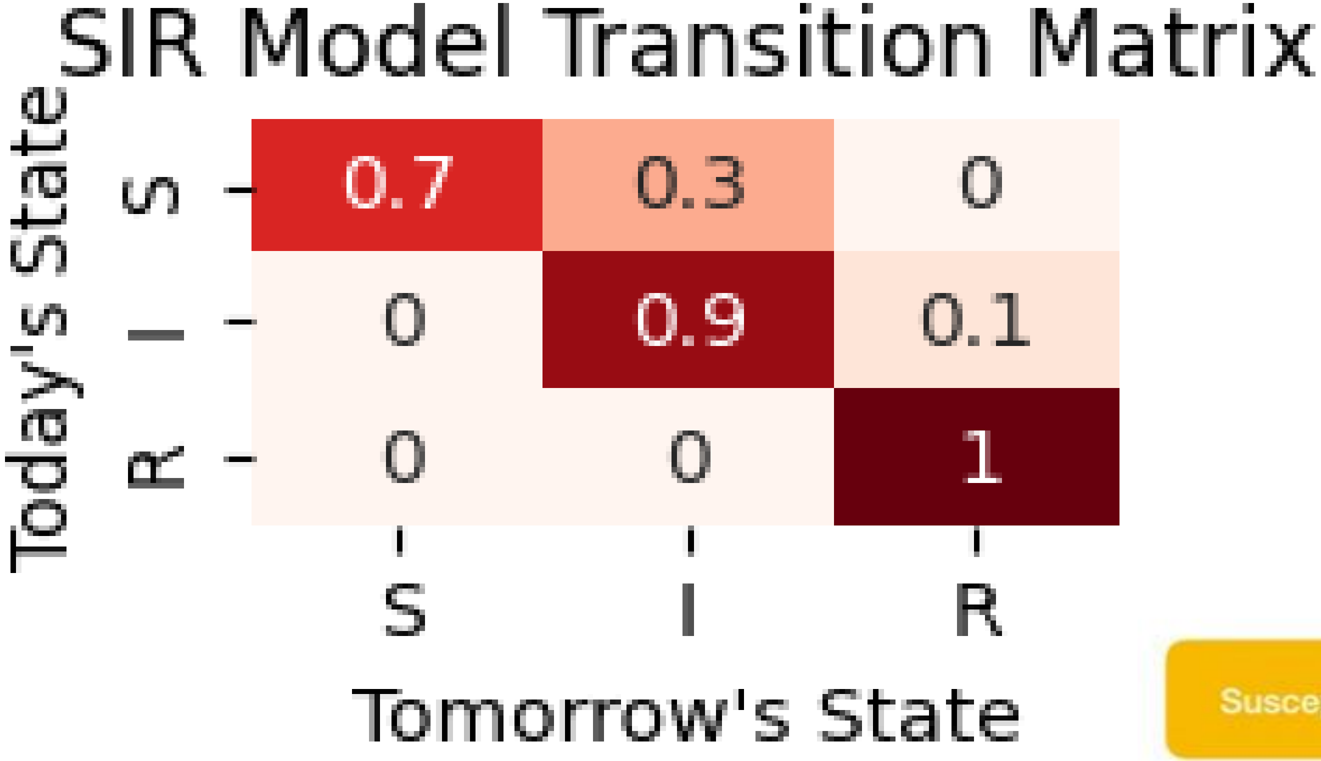
- If we watch a comedy today 100% we watch a comedy tomorrow.
- If we watch a drama today, 20% chance tomorrow we watch comdey, 20% another drama and 60% Cartoon
- If we watch cartoon today, 70% catroon tomorrow and 30% drama tomorrow.



SIR Example over Time

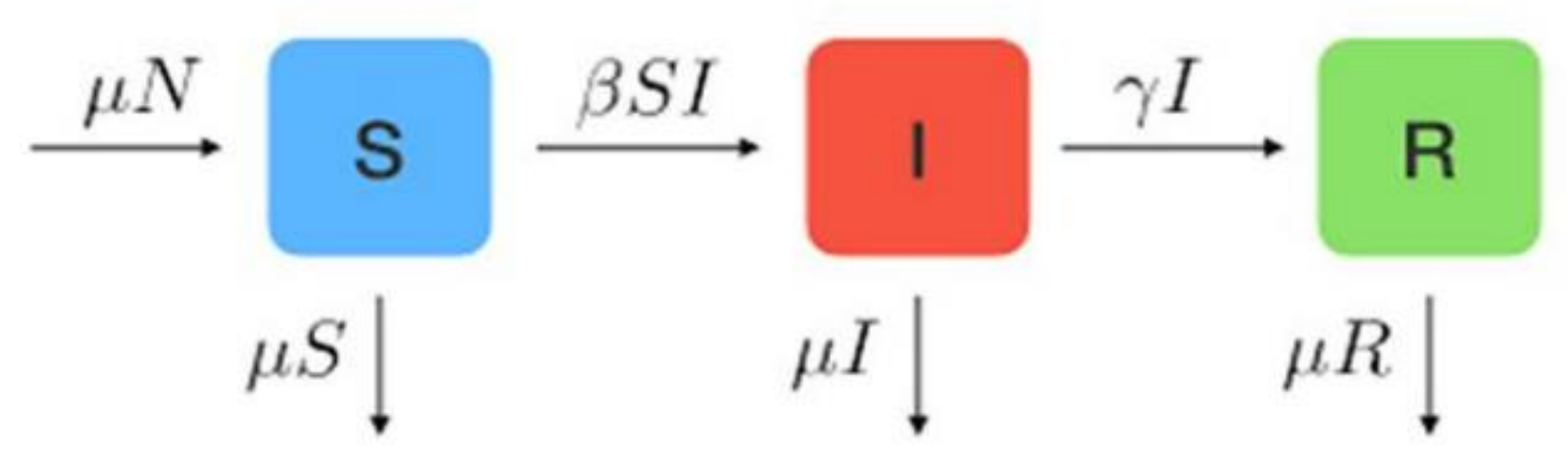
Syphilis, simplified to 30% β and 10% γ

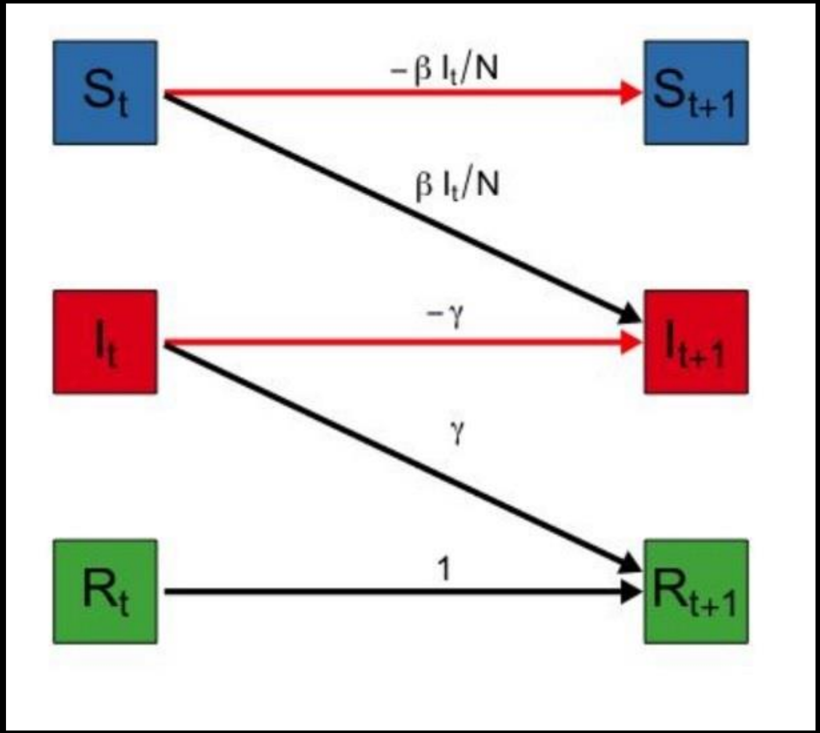




Graphical representation on the SIR model (Susceptible, Infectious and Recovered) above, and below their structure and dynamics in flow charts.

Differential Equations Model of SIR Transformations





Background & Project Focus

Leveraging cellular automata for simulating epidemic models, specifically the SIR (Susceptible, Infected, Recovered) model. Demonstrate the effectiveness of cellular automata in simulating the SIR models, showcasing an alternative to traditional methods.

The goal is to compare the efficiency and accuracy of these models with traditional techniques like Markov Chains, to develop more efficient and practical tools for simulating disease spread and understand the balance between model refinement and overfitting.

Explore the practicality and applicability of these simulation tools beyond academic research, such as their use in public health planning or game development.

Simulation & Data Analysis

The simulation uses cellular automata to model the spread of an infectious disease based on SIR models.

We represent the population as a 2D grid, each cell corresponds to an individual and its state: Susceptible, Infected, or Recovered.

The initial state of each cell is randomly assigned to reflect a realistic distribution of population states at the spread of a disease.

By assigning different portions of the grid to multiple processes, we aim to enhance computational efficiency.

The simulation rules apply for each time-step.

The state will evolve based on these rules, and the aggregate state of the population will be captured and analyzed.

As the SIR and SEIR models involve ordinary differential equations, numerical integration methods are used for their solution

Ultimately, we aim to generate a rich dataset that provides insight into the temporal dynamics of disease spread and the comparative efficiency and accuracy of SIR model when implemented.

Programming & Development

1. **Setting Up the Simulation Environment**
2. **Implementing SIR Models**
3. **Running the Simulation**
4. **Data Analysis and Model Refinement**
5. **Machine Learning Integration**

Real World Implications

UNFORESEEN VIRALITY

MERS HUMIDIFIER SPREAD 2015

KILLING BLACK CATS DURING PLAGUE

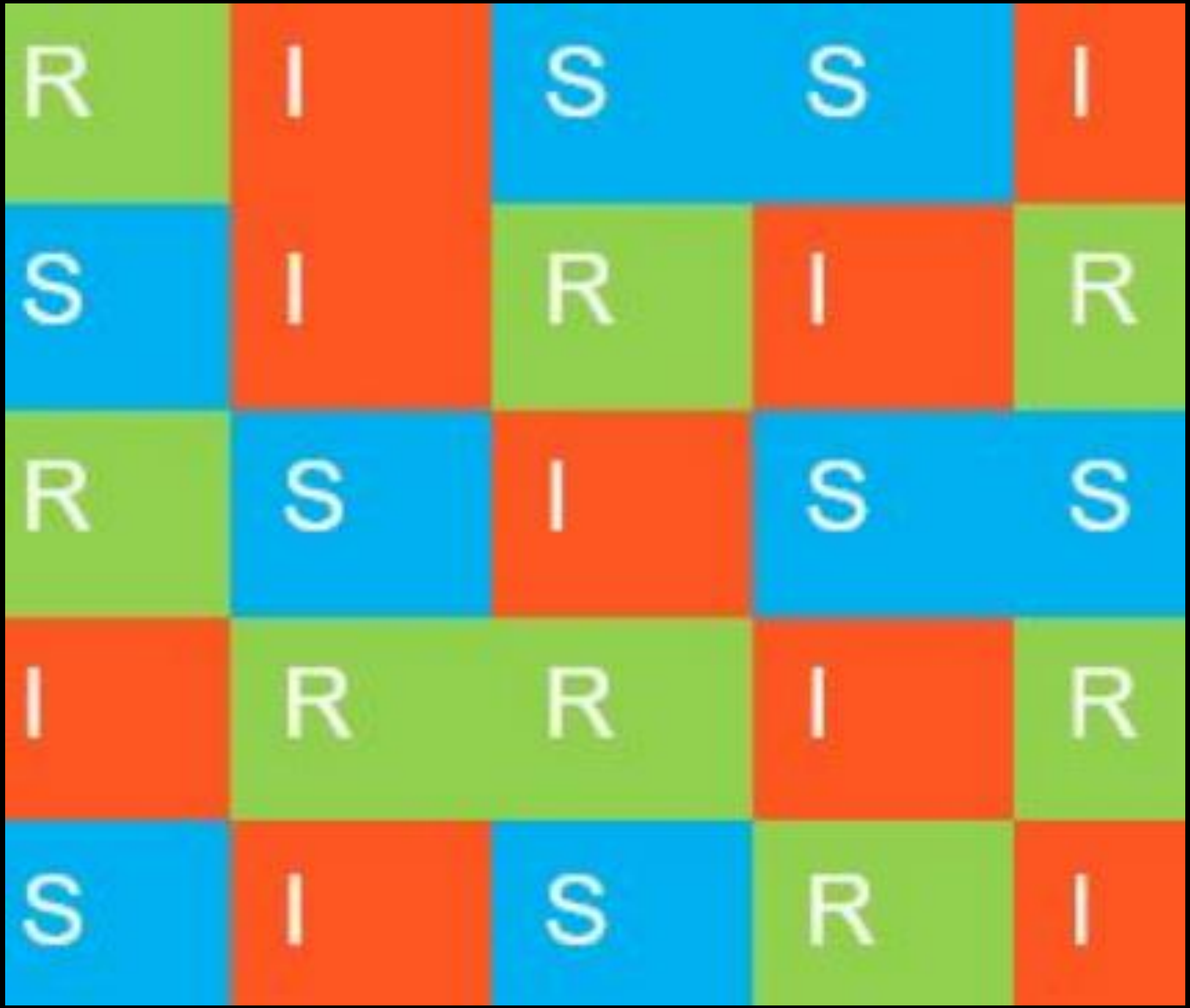
DISINFORMATION

Oversimplified Model

Cellular Automata Method

(simple,forced probability)

Can this method also produce similar graphs to traditional computational methods?



Data Sets

Data **Modelling Infectious Diseases in Virtual Realities**

Adapted from presentation at a video game conference in 2011 [22] in paper.

Florian Burckhardt MSc Epidemiology

	Measles	Syphilis	Norovirus	Corrupted Blood
Incubation period	10 days	1-3 weeks	10 hours	0 sec
Duration of infectiousness	8 days	1 year	2-4 days	10 sec
Transmission probability p	95%	30%	high	100%
Immunity	yes, lifelong	weak	only against subtype	no
Mode of Transmission	Droplet (airborne)	Sexually	Fecal-Oral, droplet, fomite	magic (droplet like)

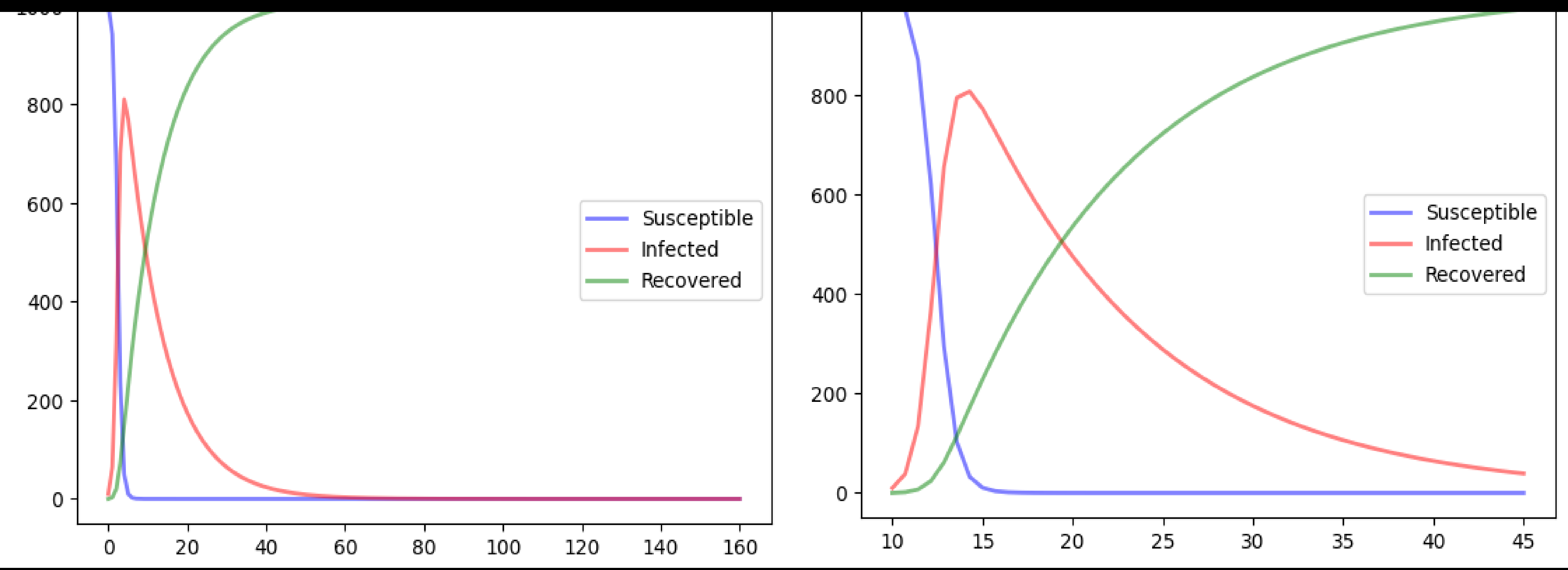
Disease	R_0
Measles	15 to 20
Foot and Mouth Disease	Initially 8.4 (Reduced to 1.3 with Animal Movement Restrictions)
Influenza	< 3
Smallpox	3 or 4
HIV	Between 2 and 12 (with condoms, $<< 1$)
Corrupted Blood	D x c x p = 10 sec x c x 1 50 (city: 5 contacts per second countryside: one every 20s)

Results

This approach allows to refine the parameters of our model iteratively to improve its predictive accuracy while preventing overfitting.

Because this is a fictional disease, it can be matched against known diseases in various ways, depend on what future metrics we would find interesting.

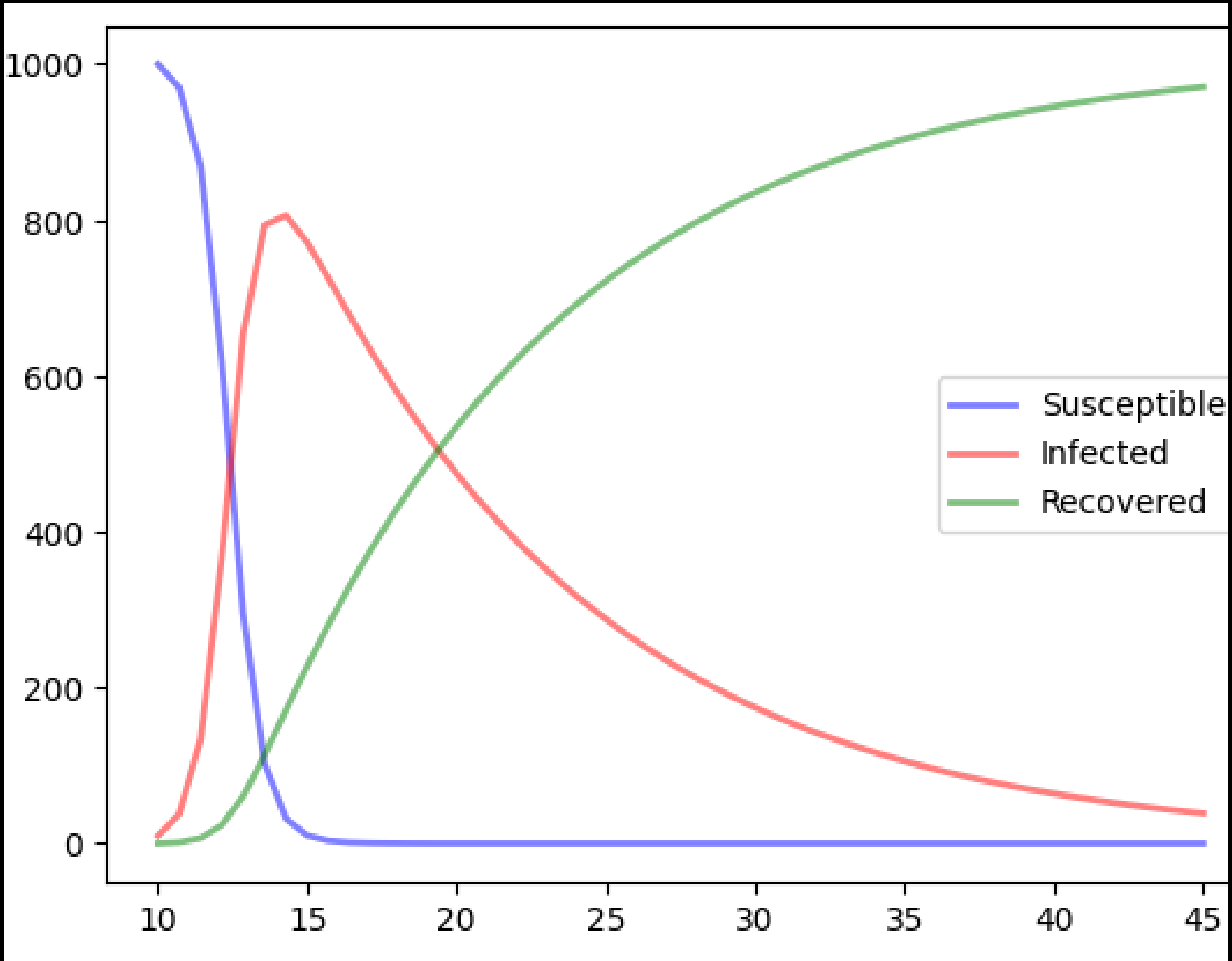
Susceptible Infected Recovered over Time using Cellular Automata on Corrupted Blood



Analysis

This serves as a baseline for proof-of-concept that this method can produce results in the neighborhood of more traditional methods.

In terms of data analysis, we introduce the concept of an 'error function' that assesses the difference between the simulated data and real-world observations.



Future Work

- To test the model results against T. Torku et al's COVID-19 Machine Learning Algorithm Models
- To run these samples on different disease models (for example, SEIR, vaccinated/unvaccinated)
- To model other social phenomena and compare with "End Game Graphs"
- Establish a groundwork for future research, such as the inclusion of more complex factors in epidemic models (like vaccination rates) and the potential for a reverse-engineering approach to model selection

Acknowledgements

- Research Advisor & Team

- Team meets weekly to support each other on nuances of research, presentation, and communication techniques

- A collaborative group with diverse backgrounds serves to facilitate developing proficiency and mastery of research skills