# Cellular Automata for Air-Borne Infectious Diseases


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*In partial fulfilment of the requirements for the award of*

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*Of*



School of Digital Sciences

Kerala University of Digital Sciences, Innovation and Technology

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# BONAFIDE CERTIFICATE

This is to certify that the project report entitled "**Cellular Automata for Air-Borne Infectious Diseases"** submitted by **ALOK HAREENDRAN (223206), ANANDHU A S (223208), ANANDHU K A (223209), ANJANA S NAIR (223210), and ANN MARIA JOSMON (223211)** in partial fulfillment of the requirements for the award of **Master of Science in Data Analytics and Computational Science** is a bonafide record of the work carried out at "**Kerala University of Digital Sciences Innovation and Technology".**



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Head of Institution

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Vice Chancellor
DUK

# DECLARATION

We students of **MSc Data Analytics and Computational Science**, hereby declare that this report is substantially the result of our own work, except, where explicitly indicated in the text and has been carried out during the period **April 2023 – August 2023**.

Place: Trivandrum
Date:

# ACKNOWLEDGEMENT

We extend our heartfelt thanks to Dr. T K. Manoj Kumar, Professor, at the School of Digital Sciences, Digital University Kerala in Trivandrum, who served as our mentor and helped me to successfully complete my project.

We would also like to thank Prof. Saji Gopinath for creating a supportive environment, offering valuable guidance, and giving us access to educational resources.

Furthermore, we want to convey our gratitude to our friends and family for their unwavering support, inspiration, and assistance throughout the journey of completing this project.

# ABSTRACT

Airborne infectious diseases present significant challenges to public health, necessitating the development of effective modelling tools for understanding and mitigating their spread. This project explores the use of cellular automata to model the dynamics of airborne infectious diseases within populations.

The study incorporates parameters derived from relevant literature and conducts simulations to evaluate the impact of different intervention strategies, such as social distancing and lockdown measures. Results indicate that intervention timing and intensity play pivotal roles in disease containment. The model's reliability is affirmed through sensitivity analysis, highlighting its potential for informing public health strategies.

This study provides valuable insights into the best ways to control airborne infectious disease outbreaks.

# CONTENTS

# 1. INTRODUCTION

Airborne infectious diseases present global health challenges, characterized by their rapid and unpredictable spread. Accurate modelling and forecasting tools are crucial for understanding disease dynamics and evaluating intervention strategies. Cellular automata, a powerful tool, have emerged for simulating disease spread within populations. This report focuses on using cellular automata to model airborne infectious diseases and analyse different scenarios for disease control.

Diseases like influenza, COVID-19, and tuberculosis spread via respiratory droplets and aerosols, leading to complex transmission patterns. Cellular automata offer a novel approach by representing states of a country in cells, enabling detailed exploration of disease dynamics. Unlike traditional models, cellular automata capture individual interactions and intervention impacts simultaneously, aiding decision-making for effective public health strategies.

The study aims to simulate disease spread using cellular automata and evaluate intervention effectiveness. By considering infection probabilities, research provides insights into evolving transmission patterns under various conditions.

# 2. LITERATURE REVIEW

## Disease Modeling Techniques

Infectious disease modeling is vital for understanding disease dynamics and shaping public health strategies. Various techniques simulate disease spread:

1. Compartmental Models: These models (like SIR) divide populations into compartments based on disease status. They are simple but lack individual interactions and spatial consideration. They are great for a broad view.

2. Network Models: Representing individuals as nodes and interactions as edges, these models suit diseases spread through contacts. They are realistic but data-heavy and complex.

3. Agent-Based Models: These models simulate unique individuals, capturing spatial and temporal dynamics. They are complex but detail-rich, ideal for localized disease transmission.

## Cellular Automata in Disease Modeling

Cellular automata offer a unique approach by capturing interactions among agents in space and time. Cells with behavior rules simulate disease spread, accounting for density, movement, and interventions.

Previous research has demonstrated the utility of cellular automata in modeling diseases like malaria, including factors like vectors and human mobility. These studies have also examined the effects of interventions like vaccination campaigns.

## Gaps in the Literature

While earlier studies have made contributions, there are still gaps to address:

**.** Spatial Realism: Many models ignore spatial aspects, crucial for airborne diseases. Cellular automata can fill this gap with explicit spatial dynamics.

**.** Individual Interactions: Common models overlook individual interactions. Cellular automata embrace local interactions, movement, and diverse agent traits for a more authentic representation.

. Intervention Effects: Studies haven't fully explored intervention strategies. Cellular automata can assess their impact under various conditions.

This project addresses these gaps by employing cellular automata to study the spread of airborne diseases. Through intervention analysis, it enhances our knowledge and provides guidance for targeted public health measures.

# 3. METHODOLOGY

The computational model is based on a cellular automaton, within a two-dimensional grid.

Cellular Grid Definition

The study employs a two-dimensional cellular grid to represent the geographic area under investigation. Each cell within the grid represents a discrete state, and the entire grid encompasses the study region.

State Definitions

Each cell within the grid represents a specific state related to the infectious disease model. State definitions include:
Healthy (H): Cells with a healthy population.
Infected (I): Cells with individuals in the infected state.
Recovered (R): Cells with individuals recovered from the disease.

Grid Initialization

A grid of specified dimensions was initialized, and a fraction of cells were randomly marked as initially infected based on a predefined probability.

Grid Width: 100
Grid Height: 100

Transition Rules

The transition rules dictate how states change over time within the cellular automata framework. These rules are formulated based on known disease dynamics, including infection probabilities and recovery rates.
A Moore neighborhood was employed, considering all surrounding cells, to simulate interactions and disease transmission.

Time Steps

The model operates in discrete time steps, during which state transitions occur. The choice of time step duration is determined based on the disease's characteristics and the desired temporal granularity of the simulation. At each time step, the state of the

grid was visualized using a heatmap, with different colours representing healthy, infected, and recovered states.

Simulation Scenarios

The study explores a range of simulation scenarios to evaluate disease spread under different conditions. The following scenarios were simulated:

No Restrictions: Infection Probability = 0.95
Recovery Probability = 0.01

Wearing Mask & Social Distancing: Infection Probability = 0.8
Recovery Probability = 0.1

No School: Infection Probability = 0.67
Recovery Probability = 0.16

No Public Transport: Infection Probability = 0.58
Recovery Probability =0.2

No Private Vehicles Transport & Markets Closed: Infection Probability = 0.5
Recovery Probability = 0.24

Complete Lockdown: Infection Probability = 0.4
Recovery Probability = 0.28

These parameters for the air borne infectious disease, including infection probabilities and recovery rates are determined based on assumptions and insights from relevant literature, including research papers and journals in our field of study. Each scenario is executed separately to assess the effectiveness of various strategies in mitigating disease spread.

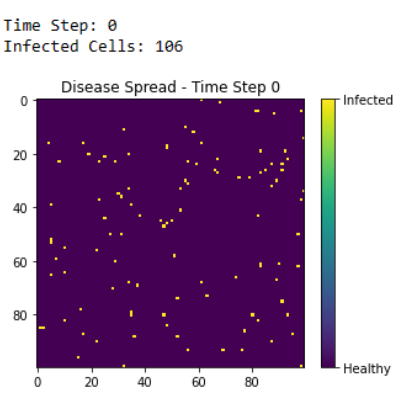
Model Implementation

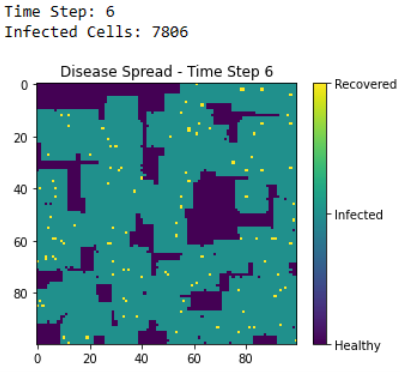
The cellular automata model is implemented using Python. Model outputs are generated, capturing the state of the system at each time step, enabling the visualization of disease spread over time.

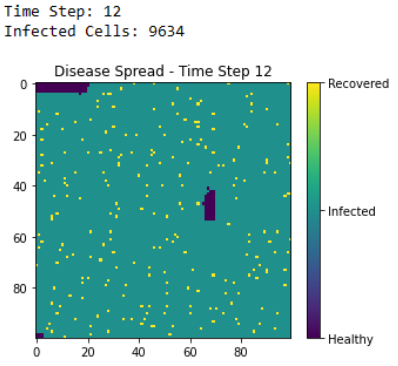
# 4. RESULTS

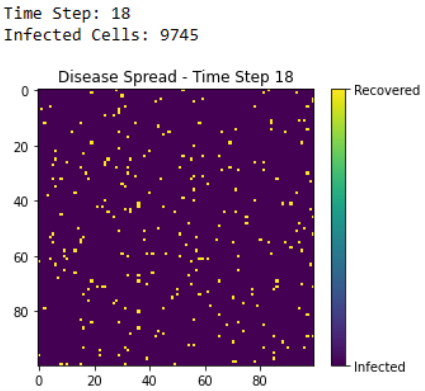
The results obtained from our cellular automaton simulations for modeling the spread of airborne infectious diseases under various scenarios:

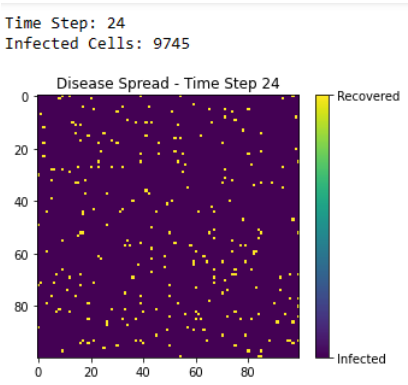
No Restrictions:



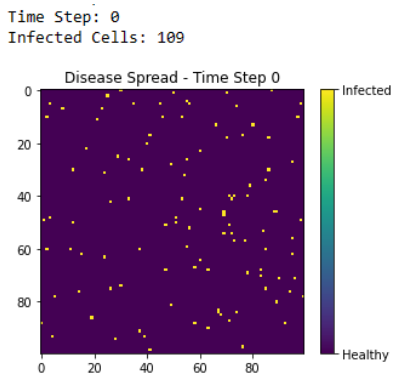



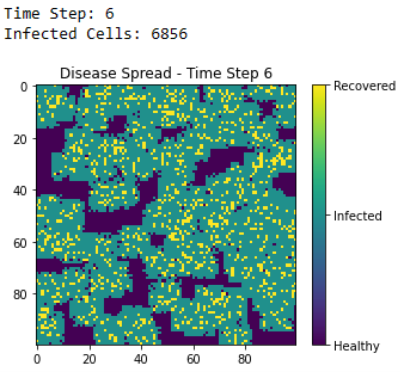



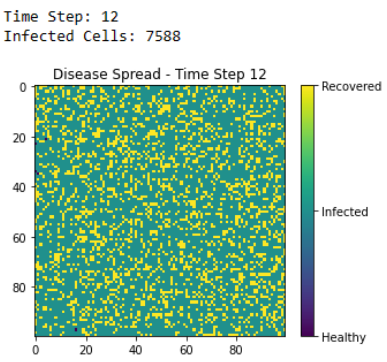



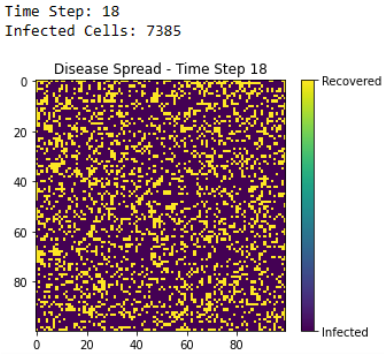



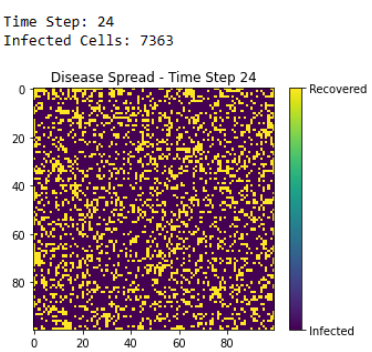

Wearing Mask & Social Distancing:



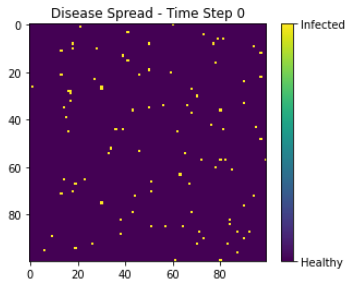



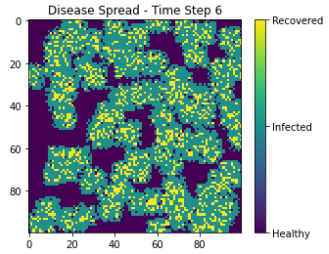



## No School:

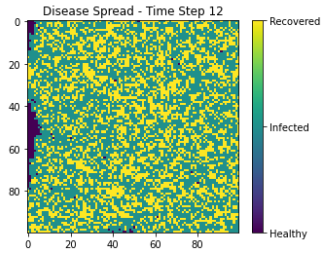
Time Step: 0
Infected Cells: 96



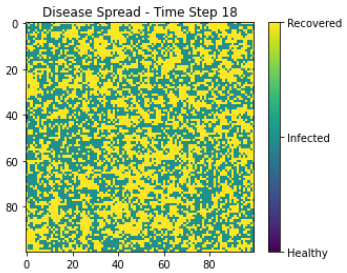

Time Step: 6
Infected Cells: 5465



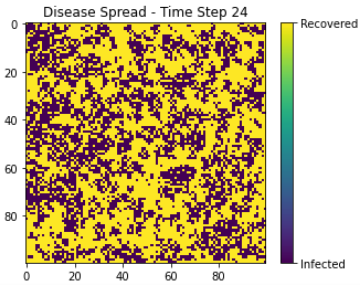

Time Step: 12
Infected Cells: 5966




Time Step: 18
Infected Cells: 5077

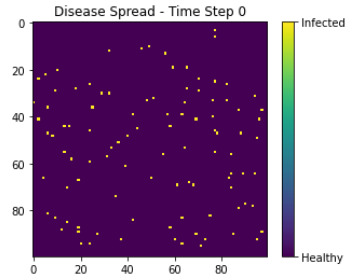



Time Step: 24
Infected Cells: 4127

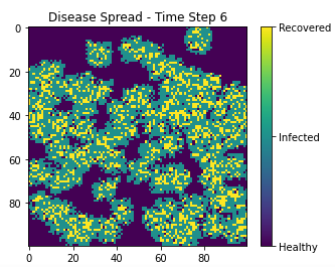



## No Public Transport:

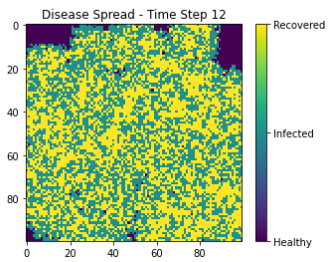
Time Step: 0
Infected Cells: 100



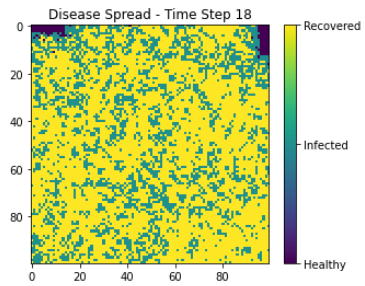

Time Step: 6
Infected Cells: 4734



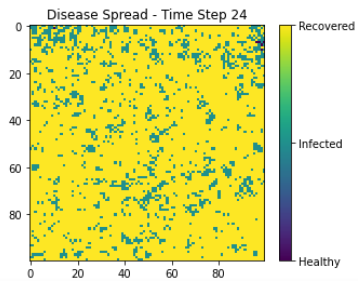

Time Step: 12
Infected Cells: 4583




Time Step: 18
Infected Cells: 2860

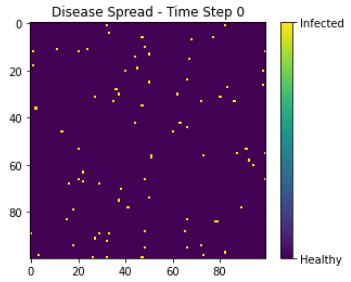



Time Step: 24
Infected Cells: 1422

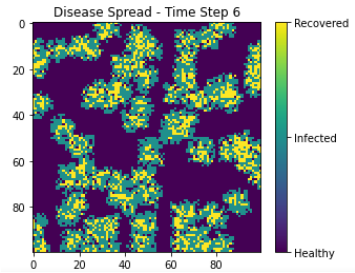


## No Private Vehicles Transport & Markets Closed:

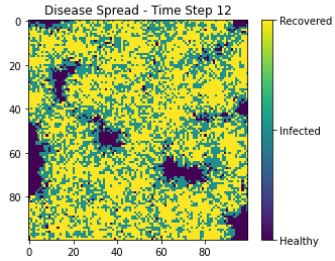
Time Step: 0
Infected Cells: 81



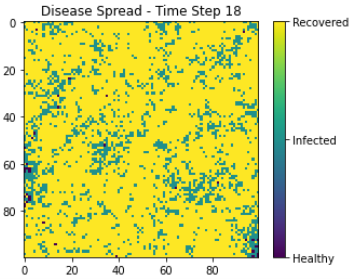

Time Step: 6
Infected Cells: 3331



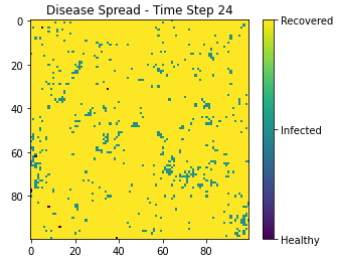

Time Step: 12
Infected Cells: 3816




Time Step: 18
Infected Cells: 1753

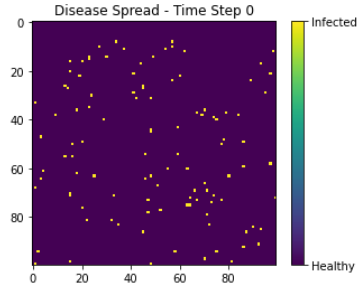



Time Step: 24
Infected Cells: 503

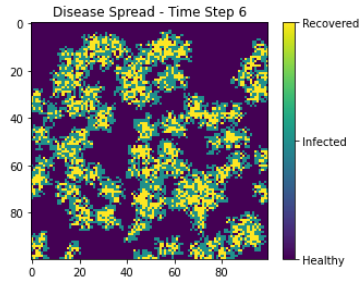



## Complete Lockdown:

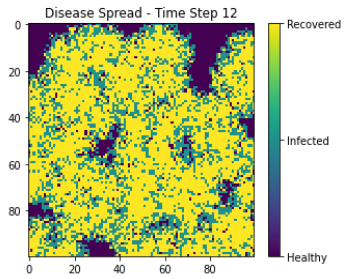
Time Step: 0
Infected Cells: 107



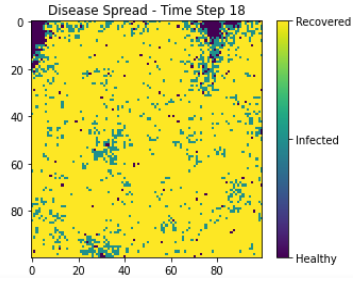

Time Step: 6
Infected Cells: 2762



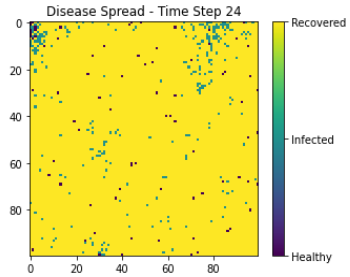

Time Step: 12
Infected Cells: 2719



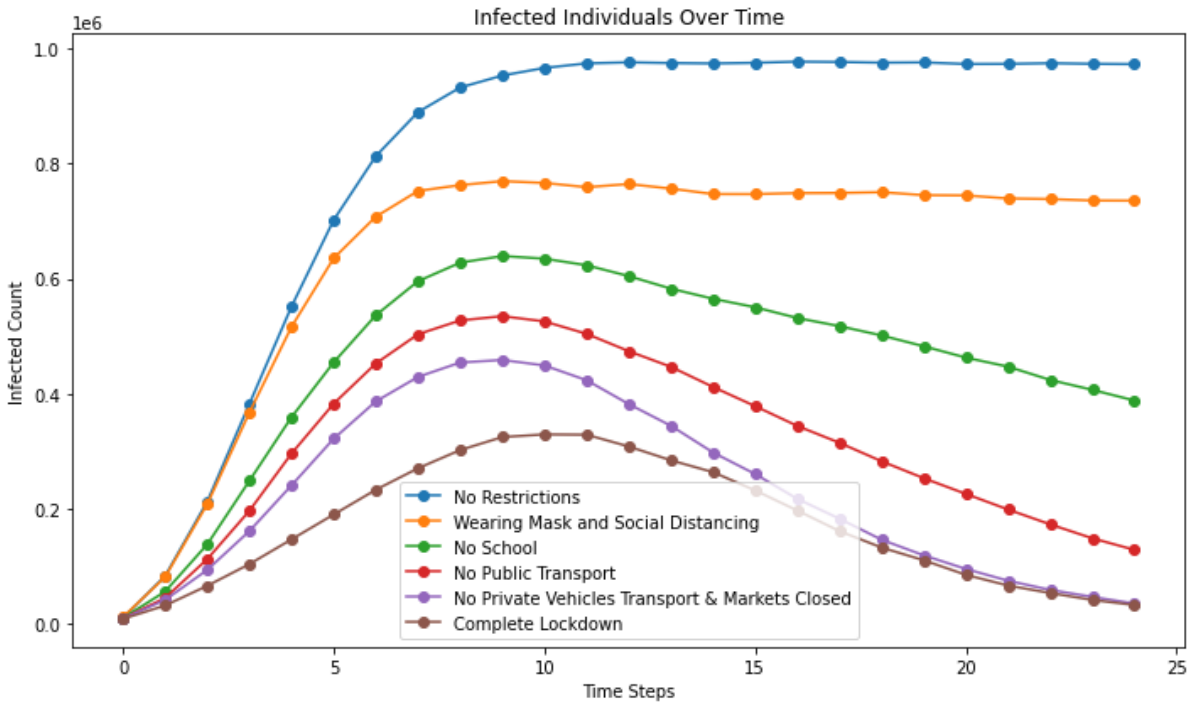

Time Step: 18
Infected Cells: 1075




Time Step: 24
Infected Cells: 268



The simulations were conducted under various scenarios to assess the impact of different intervention strategies on disease transmission dynamics.




In the absence of any restrictions, our model projected a rapid and widespread outbreak of the disease. The results indicate that without intervention, the disease can quickly overwhelm the healthcare system.

Under scenarios simulating partial interventions like social distancing and mask wearing, the rate of disease transmission exhibited a noticeable decline. It indicates the effectiveness of these measures in slowing the spread of the disease.

In the scenario representing a complete lockdown, with the lowest infection probability, our model demonstrated a significant reduction in disease transmission. This scenario highlights the importance of strict containment measures in preventing disease escalation.

# 5. CONCLUSION

Our simulations highlight two critical factors in the fight against airborne infectious diseases: the timing and strength of intervention measures. These insights offer valuable guidance for crafting effective public health strategies and better preparing for future outbreaks.

Firstly, our study underscores the immense importance of early intervention. Early action is crucial, as seen in the concept of "flattening the curve," which emphasizes the need for quick and decisive measures to prevent healthcare systems from becoming overwhelmed. Early interventions result in fewer infections and reduce healthcare burden.

Secondly, the intensity of interventions also plays a vital role. The intensity of interventions also matters. Strong measures, like complete lockdowns, can significantly reduce disease transmission rates, while milder interventions like social distancing and mask-wearing help to some extent. Preparedness and rapid response to emerging diseases are essential. Proactive planning and adaptable response frameworks are needed to address the changing nature of infectious diseases.

In summary, our research provides insights into disease dynamics and intervention strategies, emphasizing the importance of timely, well-coordinated interventions and preparedness to effectively control diseases in an era of evolving threats.

# 6. FUTURE SCOPE

Our study has limitations. Our disease model simplifies elements and does not take into account all the factors that influence disease transmission, such as human behavior and environmental conditions. Additionally, we did not investigate vaccine distribution or virus mutations, both of which hold significance in realworld scenarios.

In summary, our research provides valuable insights into combatting airborne diseases, but it does not encompass the entirety of the issue. Future studies should employ more comprehensive models, incorporate considerations for vaccine distribution and virus mutations, in order to gain a deeper understanding. This ongoing research is indispensable for effective planning and response to future outbreaks.

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