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A network-based model to explore the role of testing in the epidemiological control of the COVID-19 pandemic

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- **Title:** A network-based model to explore the role of testing in the epidemiological control of the COVID-19 pandemic.

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Outline

INTRODUCTION

History

- Back in the 1990s, most epidemic models assumed **uniform or homogeneous mixing**.
- However there were some limitations of the homogeneous mixing in certain situations. Hence, **non-homogeneous mixing** was introduced.
- The non-homogeneous mixing is commonly used in case of disease outbreaks. This is called **Network epidemiology**
- Here links are used to model contact and nodes, to model actors. These 'actors' may be in one state at a time: **susceptible, infected, removed, or recovered.**

Situations

- A network epidemic is a process of widespread and rapid propagation of a contagion through a network.
- Some examples of this process are :-
  1. Spread of a disease among living organisms
  2. Spread of malicious software
  3. Spread of an idea, concept, news, or popular notion.

Models

- **SIR Model:** Susceptible, Infected and Recovered

Figure 1: SIR Model

SIR Model

$$\frac{dS}{dt} = -\beta SI$$

$$\frac{dI}{dt} = \beta SI - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$
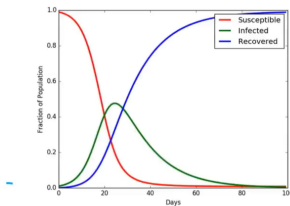
$$[\beta/\gamma] = R_0$$

Figure 2: SIR Model

SIS Model
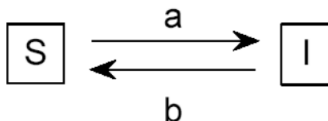
- **SIS Model:** Susceptible–Infected–Susceptible Epidemics

Figure 3: SIS Model

- Actors are in one of two states—infected or susceptible.
- Susceptibles become infected at rate a.
- Infecteds recover at rate b.

SEIR Model

Susceptible-Exposed-Infectious-Recovered Model

- E: Exposed (latent) humans
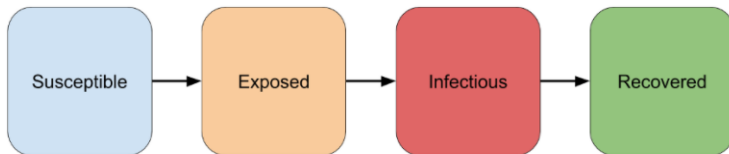- S: Susceptible humans
- I: Infectious humans
- R: Recovered humans

Figure 4: SEIR Model

Networks

- The presence of a relationship between individuals in a population is the issue of concern in the context of an epidemic.
- Networks can be defined in terms of how individuals are distributed in space (which may be geographical or social). They are :-
    1. Small-world Networks
    2. Spacial Networks
    3. Scale-free Networks

- The aim of this study was to determine how testing affects the spread of epidemics and the daily testing volume needed to control infectious diseases.
- Researchers have found that testing plays an important role in controlling the spread of infectious diseases.
- In order to analyze the covid data and study the role of testing on disease outbreaks,an epidemic transmission model was combined with a testing mechanism.

Method

1. Epidemic transmission model
- A network is composed of nodes and edges.
- The number of edges connected with a node is called the degree of the node.
- Power-law distribution - Indicates that vast majority of individuals have small degrees.
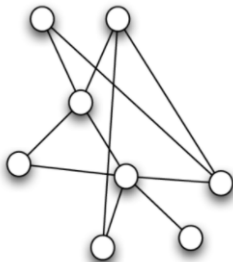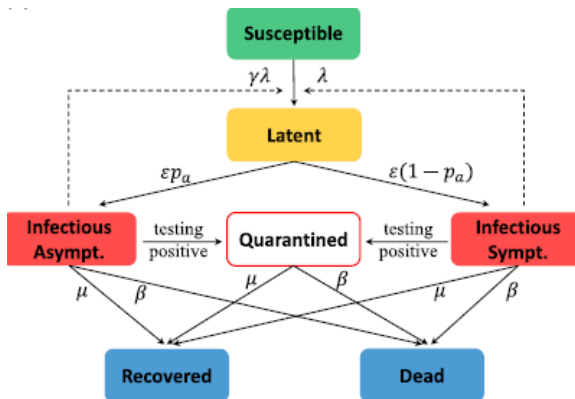

Figure 5: Epidemic transmission Model

Figure 6: Epidemic transmission Model

Methods

2. Testing mechanism

- The current time step is greater than T will the testing mechanism be introduced into the epidemic transmission model.
- The change in daily testing volume is

$$V = \max\left(V_{\text{inc}} \times (t - T), V_{\text{limit}}\right) \tag{1}$$

- where,
  V_{inc} is increase speed
  V_{limit} is upper bound of the daily testing volume.

Figure 7: Testing mechanism

Model Validation
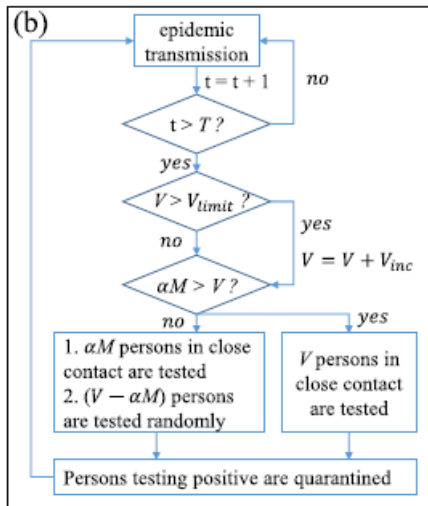
- To validate the model, they have compared a simulated data with the real world data.
- The testing-positive rate can represent the actual infection scale in the population to some extent.
- Basic reproduction number $R_0 = 2.6$
- Model is validated when (v_i, p_i) curve is consistent with (V_i, P_i) curve.

Results

- Barabasi-Albert (BA) scale-free networks were generated and used to describe the contact structure of population in real life
- Two indicators were considered: the peak value of infections, v_p, and the time when the peak arrives, t_p
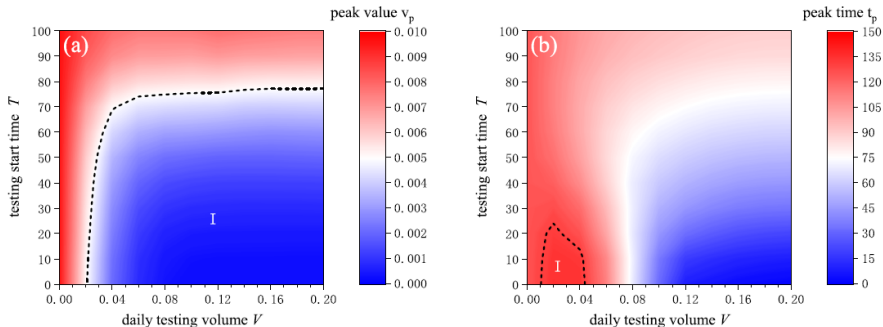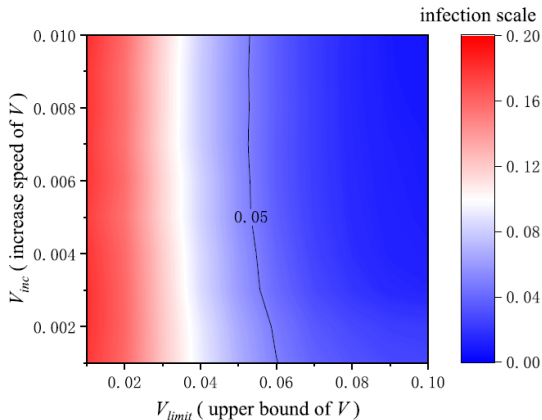
Results

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- Two indicators were considered: the peak value of infections, v_p, and the time when the peak arrives, t_p

Figure 8

Figure 9: The impact of changes in daily testing volume on infection scale.
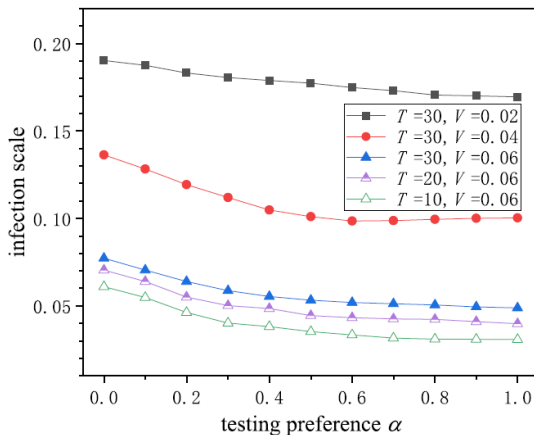
Results

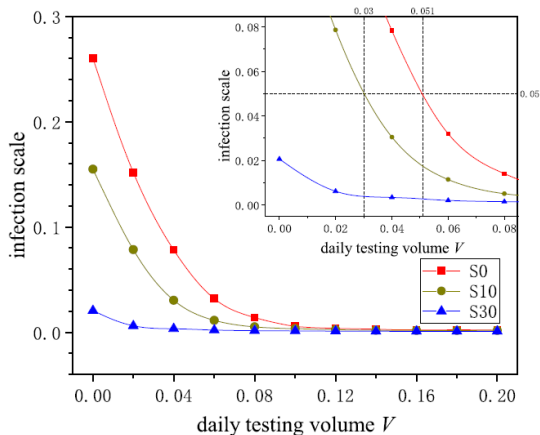Figure 10: The impact of testing preference on epidemic transmission

Figure 11: The effect of testing on epidemic transmission under different scenarios
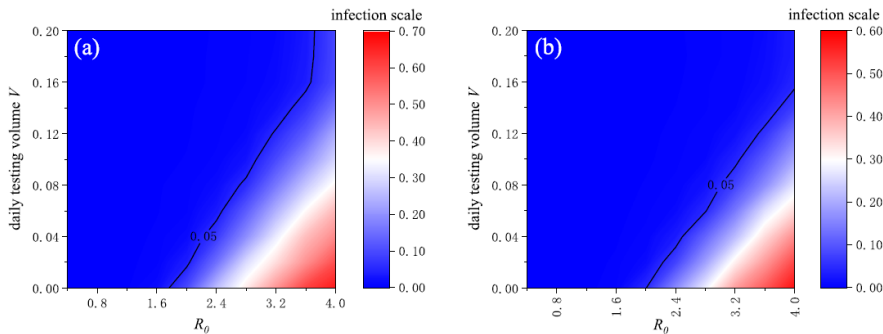
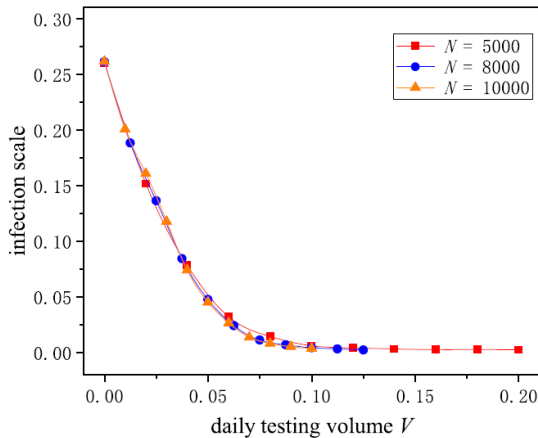Figure 12: The effect of basic reproductive number R0 and testing on infection scale under different scenarios

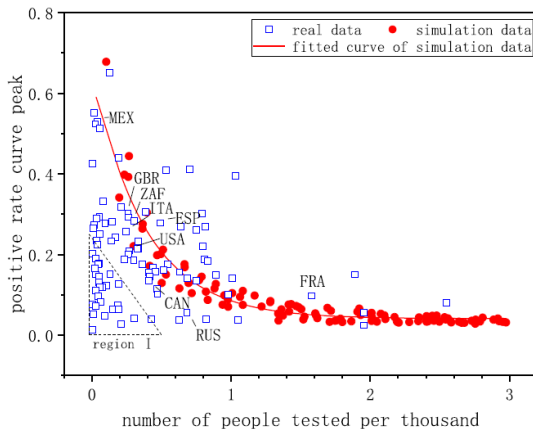# Results

Figure 13: The impact of network scale

Figure 14: The simulation data versus real data.

Conclusion

- Non-homogeneous mixing is preferred over homogeneous mixing in the context of disease outbreaks to account for the highly contagious individuals,proximity and frequency of contacts.
- It was discovered that early testing, increase in daily testing volume largely impacted the reduction in the infection scale.
- When the daily testing volume was large, testing preferences had little impact on the infection scale
- If the testing was combined with additional measures, the required daily testing volume to control the situation was reduced.

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THANK YOU