

COVID-19 Spread Analysis

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In this work we will see the effect of multiple policy parameters within our control and their effect on the spread of *COVID-19*. Specifically, we will concentrate our efforts on *Delhi* and *Andhra Pradesh*. Due to complexity of the problem we feel best to limit ourselves to specific regions than claim broad generalisations. We will conclude that states with better healthcare infrastructure will be able to tackle the spread, *Moderately* good healthcare systems will fail. We study the effect of better Law enforcement and Quarantine quality through our parameters *Quarantine Delay* and *Quarantine Ability*. Side effects of certain parameter changes lead to herd immunity and we show this via a live simulation.

Additional Key Words and Phrases: Datasets, Network Analysis, Random Network, Barabasi-Albert Model, COVID-19

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1 INTRODUCTION

Since December of 2019 *COVID-19* has had repercussion on a Global Scale affecting countries like *USA, Germany, Italy etc.* More Americans have died of *COVID-19* than the entirety of the Vietnam war. So the importance of studying the spread of this disease cannot be understated. We would like to highlight the **Macro** level effects of policy on the spread of diseases. While we do not undermine the need for *Micro* Policies. They can often miss certain key details about the behaviour of the disease, like importance of Emergency Mobile Healthcare and explaining Herd Immunity. In this paper(Section 4) we attempt to best **Quantify** qualitative parameters like **Law enforcement, Quality of Healthcare** and study its effect on spread of COVID-19. With this work we hope to propose directives and suggestions for future policy measures to curb the spread of the pathogen and limit loss of human life as much as possible.

2 RELATED WORK

[Fang et al. 2020] Used the parameterized susceptible-exposed-infectious-recovered model, and simulated the spread dynamics of coronavirus disease 2019 (COVID-19) outbreak and impact of different control measures, [Chinazzi et al. 2020] applied a global metapopulation disease transmission model to epidemiological data from China. They concluded that the travel quarantine introduced in

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Wuhan on 23 January 2020 only delayed epidemic progression by 3 to 5 days within China, but international travel restrictions did help to slow spread elsewhere in the world until mid-February. [Peng et al. 2020] proposed a generalized SEIR model to analyze this epidemic. Based on the public data of National Health Commission of China from Jan. 20th to Feb. 9th, 2020, authors reliably estimate key epidemic parameters and made predictions on the inflection point and possible ending time for 5 different regions (In China). [Singh and Adhikari 2020] used an age-structured SIR model with social contact matrices obtained from surveys and Bayesian imputation to study the progress of the COVID-19 epidemic in India. The basic reproductive ratio R_0 and its time-dependent generalization were computed based on case data, age distribution and social contact structure.

3 DATASET DESCRIPTION:

We used <https://api.covid19india.org/> api to fetch the dataset. Figure 1 shows structure of dataset. It had 141 rows, data of 47 days from March 14, 2020 to April 29, 2020. It contains 3 types of values for each state:

- (1) Confirmed: Number of patients tested positive on that particular date.
- (2) Recovered: Number of patients which were infected but declared as recovered on that particular date.
- (3) Deceased: Number of patients which had covid-19 and died on that particular date.

```
In [6]: df=pd.read_csv('state_wise_daily.csv')
df_conf=df[df['Status']=='Confirmed']
df_reco=df[df['Status']=='Recovered']
df_dece=df[df['Status']=='Deceased']
print(df)
```

	Date	Status	TT	AN	AP	AR	AS	BR	CH	CT	...	PY	PB	RJ	\
0	14-Mar-20	Confirmed	81	0	1	0	0	0	0	0	0	0	0	1	3
1	14-Mar-20	Recovered	9	0	0	0	0	0	0	0	0	0	0	0	0
2	14-Mar-20	Deceased	2	0	0	0	0	0	0	0	0	0	0	0	0
3	15-Mar-20	Confirmed	27	0	0	0	0	0	0	0	0	0	0	0	1
4	15-Mar-20	Recovered	4	0	0	0	0	0	0	0	0	0	0	0	2
...
136	28-Apr-20	Recovered	637	4	23	0	0	8	0	2	...	0	3	26	
137	28-Apr-20	Deceased	69	0	0	0	0	0	0	0	0	0	0	0	2
138	29-Apr-20	Confirmed	1762	0	73	0	0	37	12	0	...	0	33	74	
139	29-Apr-20	Recovered	690	0	29	0	2	0	0	0	0	0	0	0	44
140	29-Apr-20	Deceased	71	0	0	0	0	0	0	0	0	0	0	0	3
	SK	TN	TG	TR	UP	UT	WT								
0	0	1	1	0	12	0	0								
1	0	0	0	0	4	0	0								
2	0	0	0	0	0	0	0								
3	0	0	2	0	1	0	0								
4	0	0	1	0	0	0	0								
...								
136	0	54	42	0	63	1	4								
137	0	1	0	0	3	0	2								
138	0	184	7	0	81	1	28								
139	0	82	35	0	48	2	10								
140	0	2	0	0	5	0	0								

[141 rows x 40 columns]

Fig. 1. Dataset Description

4 METHODOLOGY

4.1 Possible States

- Susceptible: Healthy individuals who have not yet contacted the pathogen.
- Exposed: Contagious individuals who have contacted the pathogen and hence can infect others.
- Infected: Individuals who have been infected before, but have recovered from the disease, hence are not infectious.

4.2 Parameters

- **Transition Rate:** The probability of changing state after certain threshold criteria's are met.
- **Quarantine Delay:** How many people (in proportion) need to get infected before a Quarantine is set up.
- **Quarantine Ability:** How well does a Quarantine(once setup) do to curb the interaction of one node with its original neighbours.

4.3 Random Network Analysis:

First we tried to analyse the spread of virus by using random network model. We used SIS (Susceptible Infected Susceptible) model which assumes that after recovery people can get infected again. Covid-19 is a SIS kind of disease as people can get infected again. In random network model if:

β is the probability of transferring the disease.

$\langle k \rangle$ is average degree of the network.

i is the count of infected individuals

μ is the recovery rate

then the differential equation 1 gives us the rate at which people will get infected:

$$\frac{di}{dt} = \beta \langle k \rangle i(1 - i) - \mu i \quad (1)$$

Equation 2 is the solution of differential equation 1.

$$i = \left(1 - \frac{\mu}{\beta \langle k \rangle}\right) \frac{Ce^{(\beta \langle k \rangle - \mu)t}}{1 + Ce^{(\beta \langle k \rangle - \mu)t}} \quad (2)$$

where C has the value:

$$C = \frac{i_0}{1 - i_0 - \mu/\beta \langle k \rangle} \quad (3)$$

Where i_0 is the count of individuals infected initially. We tried to fit the spread of 4 different states using this random model.

4.3.1 Delhi: Figure 2 shows a graph between the count of infected individuals in Delhi vs days. The blue line shows the actual curve as plotted from the dataset. Orange line shows the curve obtained from equation 2. We took the value of $i_0 = 7$ initially infected individuals from the dataset. We took $\mu = 1/28$. We plotted curve for different values of $\beta \langle k \rangle$ and chose the curve which gave the best fit. We found out that the best fit corresponded to $\beta \langle k \rangle = 0.16$. We will use this $\beta \langle k \rangle$ value later to approximate the average degree of the network.

4.3.2 Maharashtra: Figure 3 shows a graph between the count of infected individuals in Maharashtra vs days. The blue line shows the actual curve as plotted from the dataset. Orange line shows the

```
In [84]: pop=2e7
i0=y[0]/pop
mu=1/28
beta=.16
plx=list()
c=i0/(1-i0-mu/beta)
for t in range(0,47):
    i=(1-mu/beta)*c*math.exp((beta-mu)*t)
    j=1+c*math.exp((beta-mu)*t)
    plx.append(i*pop/j)
plt.plot(range(0,47),active,plx)
```

```
Out[84]: [<matplotlib.lines.Line2D at 0x7fec6b210198>,
<matplotlib.lines.Line2D at 0x7fec6b2102e8>]
```

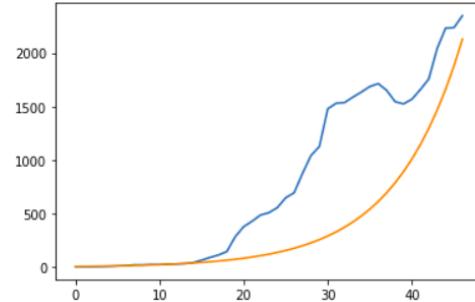


Fig. 2. Spread of Covid-19 in Delhi

curve obtained from equation 2. We took the value of $i_0 = 15$ initially infected individuals from the dataset. We took $\mu = 1/28$. We plotted curve for different values of $\beta \langle k \rangle$ and chose the curve which gave the best fit. We found out that the best fit corresponded to $\beta \langle k \rangle = 0.175$. We will use this $\beta \langle k \rangle$ value later to approximate the average degree of the network.

4.3.3 Andhra Pradesh: Figure 4 shows a graph between the count of infected individuals in Andhra Pradesh vs days. The blue line shows the actual curve as plotted from the dataset. Orange line shows the curve obtained from equation 2. We took the value of $i_0 = 1$ initially infected individuals from the dataset. We took $\mu = 1/28$. We plotted curve for different values of $\beta \langle k \rangle$ and chose the curve which gave the best fit. We found out that the best fit corresponded to $\beta \langle k \rangle = 0.185$. We will use this $\beta \langle k \rangle$ value later to approximate the average degree of the network.

4.3.4 Karnataka: Figure 5 shows a graph between the count of infected individuals vs days. The blue line shows the actual curve as plotted from the dataset. Orange line shows the curve obtained from equation 2. We took the value of $i_0 = 5$ initially infected individuals from the dataset. We took $\mu = 1/28$. We plotted curve for different values of $\beta \langle k \rangle$ and chose the curve which gave the best fit. We found out that the best fit corresponded to $\beta \langle k \rangle = 0.125$. We will use this $\beta \langle k \rangle$ value later to approximate the average degree of the network.

4.4 Generating a Representative Network

We can see that the random network model doesn't fit the curves properly and the reason is Real networks are not random. Random network model assumes any individual can have an edge with any

```
In [90]: pop=11e7
i0=active[0]/pop
mu=1/28
beta=.175
plx=list()
c=i0/(1-i0-mu/beta)
for t in range(0,47):
    i=(1-mu/beta)*c*math.exp((beta-mu)*t)
    j=1+c*math.exp((beta-mu)*t)
    plx.append(i*pop/j)
plt.plot(range(0,47),active,plx)
```

```
Out[90]: [<matplotlib.lines.Line2D at 0x7fec6afb3320>,
<matplotlib.lines.Line2D at 0x7fec6afb3470>]
```

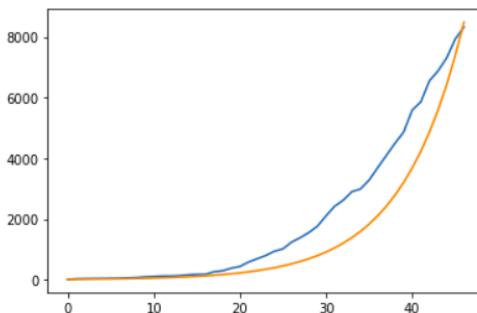


Fig. 3. Spread of Covid-19 in Maharashtra

```
In [114]: pop=5e7
i0=active[0]/pop
mu=1/28
beta=.185
plx=list()
c=i0/(1-i0-mu/beta)
for t in range(0,47):
    i=(1-mu/beta)*c*math.exp((beta-mu)*t)
    j=1+c*math.exp((beta-mu)*t)
    plx.append(i*pop/j)
plt.plot(range(0,47),active,plx)
```

```
Out[114]: [<matplotlib.lines.Line2D at 0x7fec6a7bac18>,
<matplotlib.lines.Line2D at 0x7fec6a7bad68>]
```

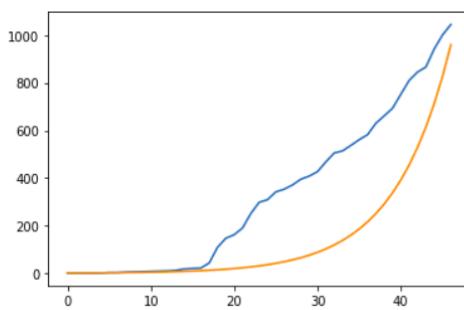


Fig. 4. Spread of Covid-19 in Andhra Pradesh

individual with same probability (Homogeneous Mixing). It also assumes all individuals have comparable degree so we can use $\langle k \rangle$ average degree as an approximation. Both of these assumptions are not true. We needed the exact degree distribution of the network. to

```
In [120]: pop=6.4e7
i0=active[0]/pop
mu=1/28
beta=.125
plx=list()
c=i0/(1-i0-mu/beta)
for t in range(0,47):
    i=(1-mu/beta)*c*math.exp((beta-mu)*t)
    j=1+c*math.exp((beta-mu)*t)
    plx.append(i*pop/j)
plt.plot(range(0,47),active,plx)
```

```
Out[120]: [<matplotlib.lines.Line2D at 0x7fec6a587630>,
<matplotlib.lines.Line2D at 0x7fec6a587780>]
```

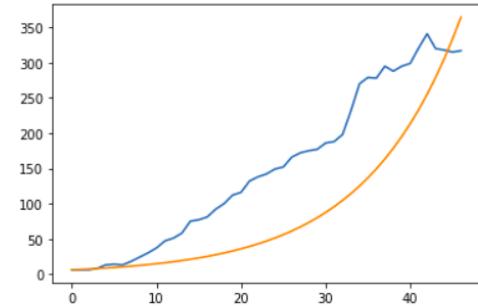


Fig. 5. Spread of Covid-19 in Karnataka

Table 1. Approximations

Real Parameter	Approximated parameter
Number of nodes	Population /100
Initial Degree in Barabasi-albert model	Population Density /100
ρ (Initial Population Infected)	Initially Infected / N
Quarantine start time	(Total Infected till March, 19) / N
Quarantine Effectiveness	$(3 - \beta < k >)/3$
Recovery Period	5 weeks

do the better analysis. We decided to use Barabasi-Albert model as it is closer to real network than random network. We used networkx to generate Barabasi- Albert graphs and did our analysis on those graphs. We wanted to model the spread of different states using those graphs but average population of states in India is of order 10^7 and we didn't have computational resources to work with that big model so we used some approximations and tried to model the situation in relatively smaller network. Table 1 shows the approximations used.

4.5 Implementing Parameters into the Network

Update in Transition Probability happens as follows:

- **Susceptible → Infected:** Once a node has more than 3 infected(or Exposed) neighbours, there is 90% chance of the node contracting it. This heuristic is inline with the common R_0 values of COVID – 19
- **Infected → Susceptible:** Once a node has been Infected for over 4 weeks(some simulations we set this to 5) there is a 90%

probability that the infected would be cured. This is in line with the average time a person takes to heal from *COVID-19*

- **Susceptible → Exposed** : If the threshold criteria for Infected are met, we can define a probability by which *S* goes to *E* instead of *I*. Thereafter, probability from *E* to *I* is much higher than *S* to *I*.

Simulating the effects of *imposing a Quarantine*,

- Once the enough number of nodes have reached the status *I* we induce a probability by which each node can effect its neighbours.Example, if said Probability was set to 10% then a node with 200 neighbours would on Average only effect 20 of its neighbours.
- We do **not** count nodes in state *E* since in reality they never show up in the system. They are silent carriers.

Quarantine ability is just the aforementioned probability.In our implementation the lower the value the better.0 would imply every node in the network is completely isolated.

4.6 SIS Model

We discuss different implementation and design aspects of our *SIS Model* in this section.

4.6.1 State Diagram. Refer to Figure 6 for the State diagram of *SIS Model*. C_{SI} are conditions that need to be met for the transitions to be possible.It can be trivial as just a Probability, or more involved with heuristics in place or a Probability Distribution over other Random Variables.Example, If we impose new Variable for *Healthcare* then the probabilities will be a function of this variable.

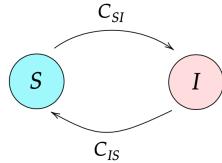


Fig. 6. State Diagram SIS Model

4.7 SIES Model

We add a new state for Exposed people, who carry the pathogen but do not get sick themselves. They do however play a role in spreading them. C_{SE} and C_{EI} follow the same rationale as above.

5 RESULTS

5.1 Delhi using S-I Model

We use the following parameters to simulate disease spread in New Delhi,

- (1) $\rho = (\frac{6}{19}) * 10^{-5}$
- (2) Transition Rate: 0.90
- (3) Quarantine Delay: $(\frac{12}{19}) * 10^{-5}$
- (4) Quarantine Ability: $(3 - \beta * k)/3$

As you can see if the ρ passes a certain margin you it is not possible to stop it till it peaks out a certain point.

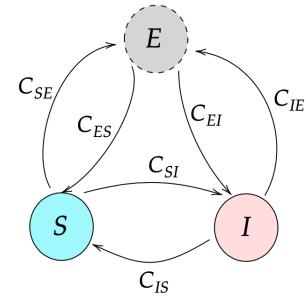


Fig. 7. State diagram for SIES MODEL

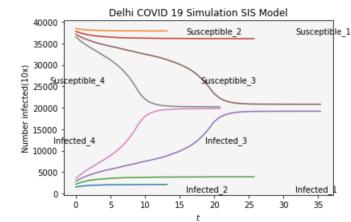


Fig. 8. Delhi SIS Model Results by varying initial ρ

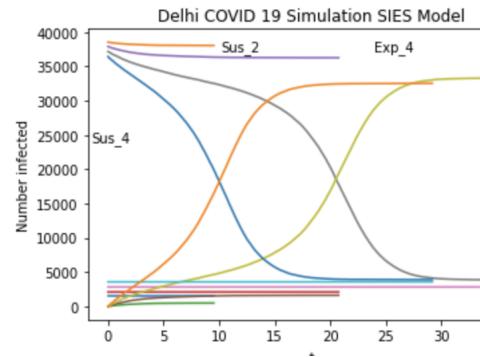


Fig. 9. Delhi SIES Model by varying values of ρ

5.2 Delhi using SI-E-S Model

When we add another state for exposed we see that the susceptible go down without the Infected going up.(Refer to Figure 9) Studying this trend would provide a good estimate for the number of people in the hidden state *E*.

This can provide valuable insight in determining the strength of the Quarantine etc.

5.3 The Role of Strong Quarantine and Good Law Enforcement

In this section we simulate a scenario where the Vaccine for *COVID-19* exists. However, we vary the level of access to this medication to varying degrees to see its effect on the spread.

5.3.1 The Role of a Good healthcare system. See Figure 10 and Figure 11. We have provided the spread at 2 different instances so that the rate of spread is more visible. **Purple dots** represent vaccinated people, **Blue dots** represent people who have recovered.

Comparing Figures 11 and 10 we can see that the disease spread has been contained.

5.3.2 The Role of a Bad healthcare system. See Figure 12 and 13. We have provided the spread at 2 different instances so that the rate of spread is more visible. **Purple dots** represent vaccinated people, **Blue dots** represent people who have recovered.

5.3.3 The Role of a Moderate healthcare system. Compared to Figure 12 Figure 15 shows that the disease spread is somewhat similar stressing over the need for a *Good healthcare system*, since there are no two ways about it.

5.4 Unexpected simulation of herd immunity

While running our simulations we noticed an interesting phenomenon occurring. **Purple dots** represent vaccinated people, **Blue dots** represent people who have recovered. Refer to Figures 16 and 17 and you will see that even after a long time has passed that specific section of the society remained unaffected by the disease spread.

6 CONCLUSIONS

So we can see that spread of *COVID -19* is going to be hugely dependent on our **Quarantine Ability** and **Quarantine Delay** if we are

late, no amount of policy changes can curb the spread of the disease. We have also seen a methodology to predict the *Silent Carriers* in the community which is key piece of Information. Then we have also considered the optimistic scenario where we have a vaccine for the disease but countries with a poor healthcare infrastructure will not be able to benefit from it. Moving forward investment in *Health Care* should be key for administrations. Lastly, we prove that a *Moderate Healthcare system* can leave room for herd immunity. However we would like to stress on the point that through multiple iterations of our simulations sometimes we do not see herd immunity taking place. So Governments should not bank on it too much. More research need to happen in this area.

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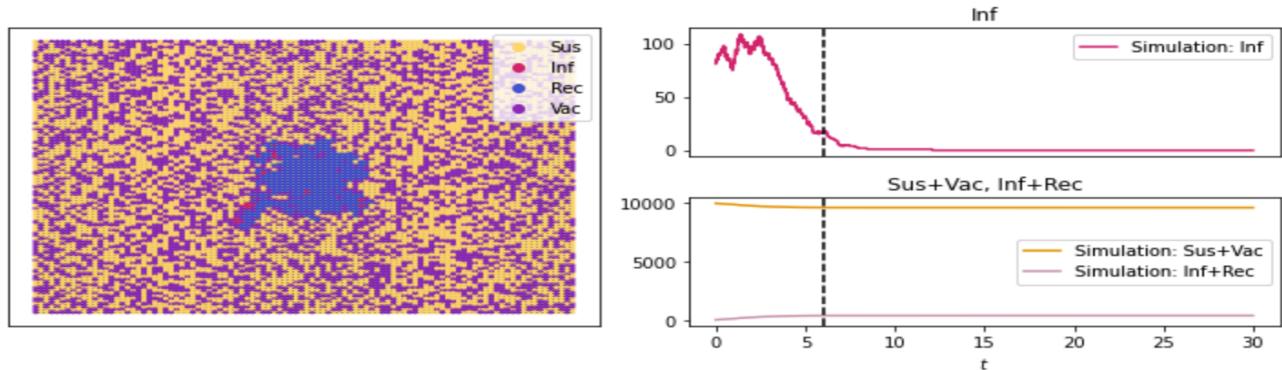


Fig. 10. Spread of Disease with Good healthcare system in place $t=6$

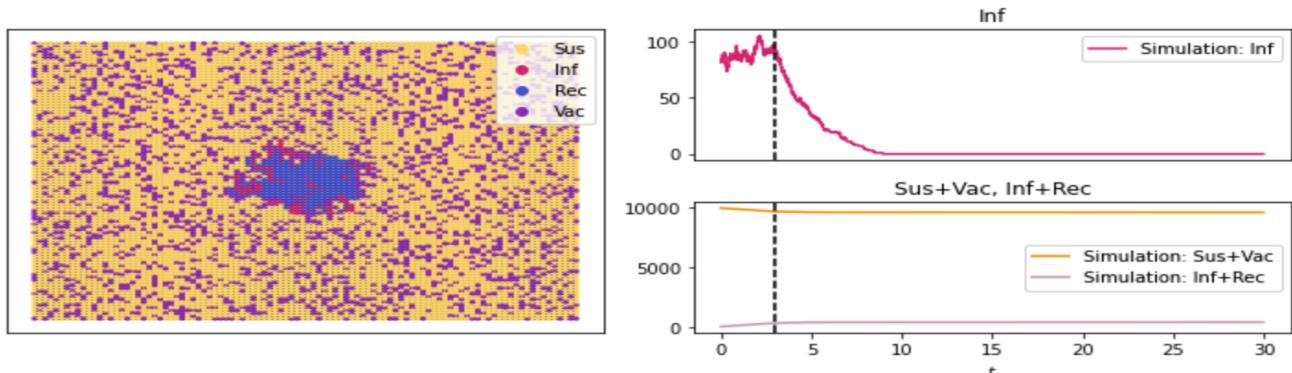


Fig. 11. Spread of Disease with Good healthcare system in place $t=3$

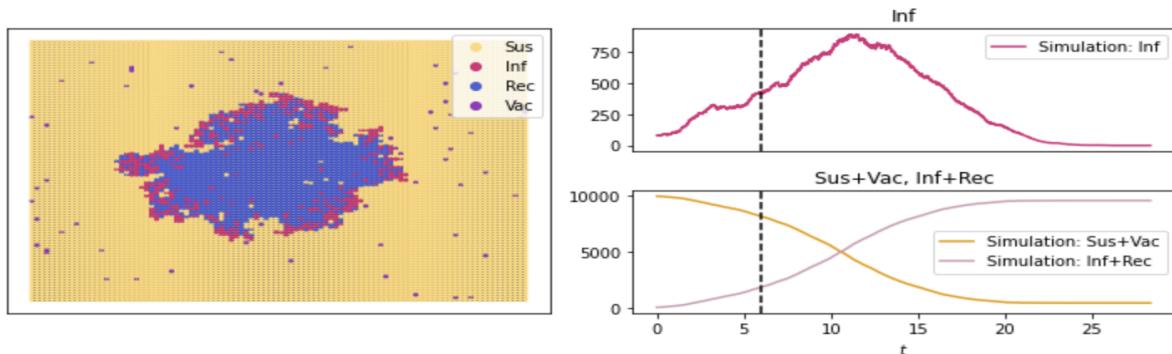
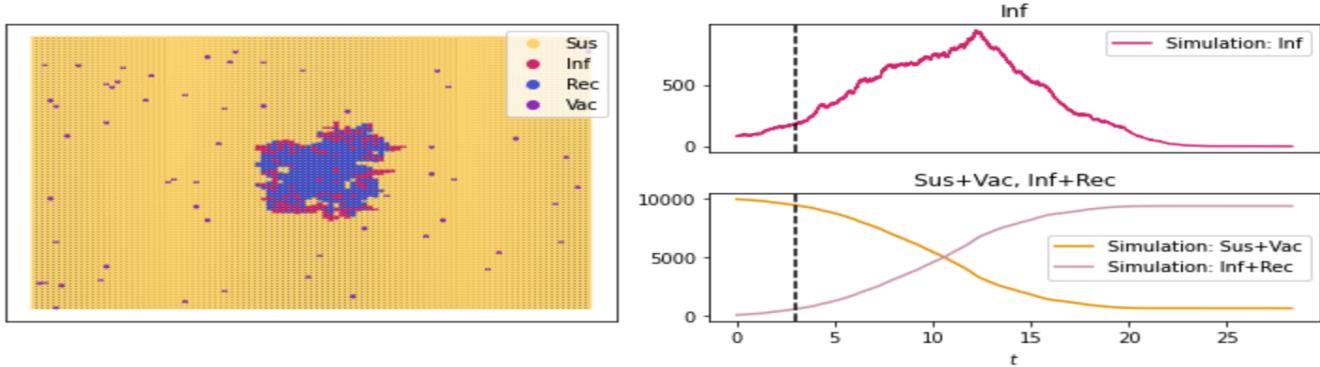
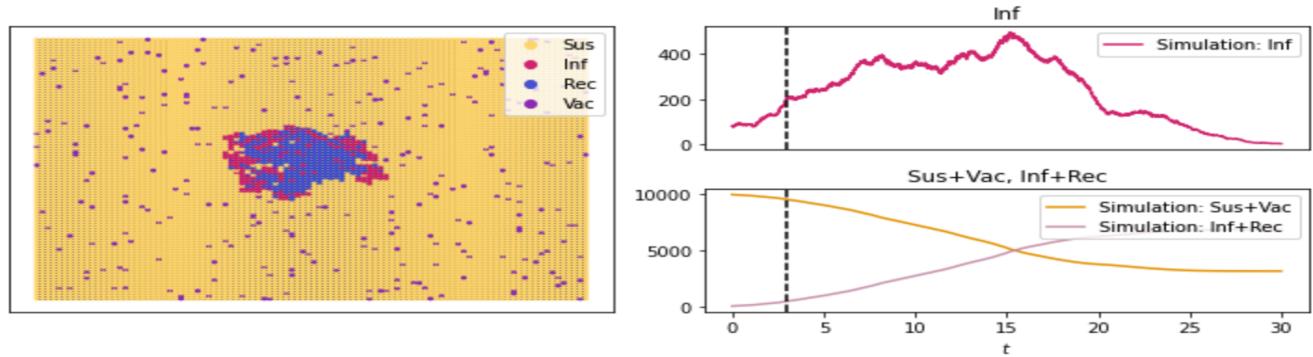
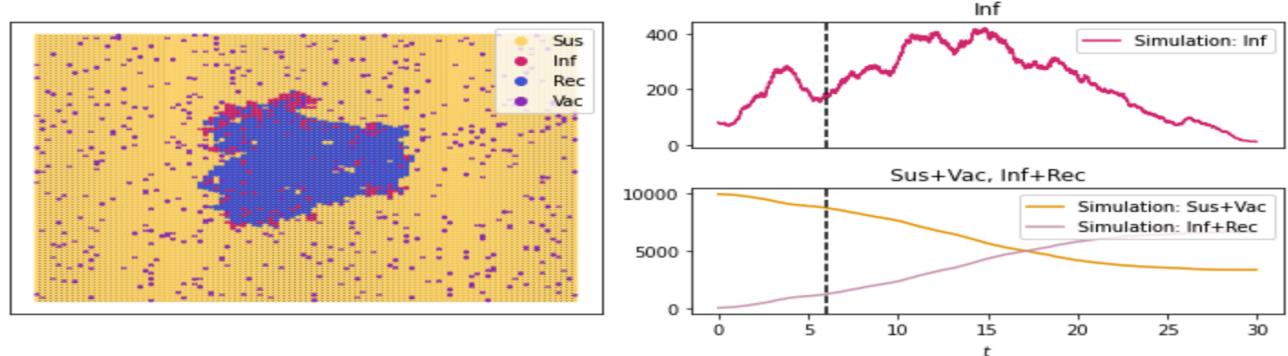


Fig. 12. Spread of Disease with Bad healthcare system in place $t=6$

Fig. 13. Spread of Disease with Bad healthcare system in place $t=3$ Fig. 14. Spread of Disease with Moderate healthcare system in place $t=3$ Fig. 15. Spread of Disease with Moderate healthcare system in place $t=6$

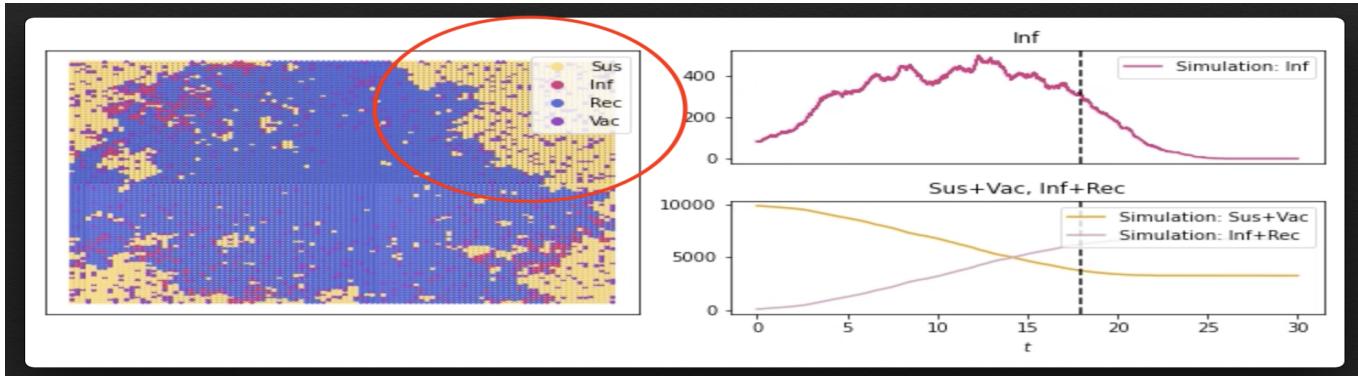


Fig. 16. Observing herd immunity $t=18$

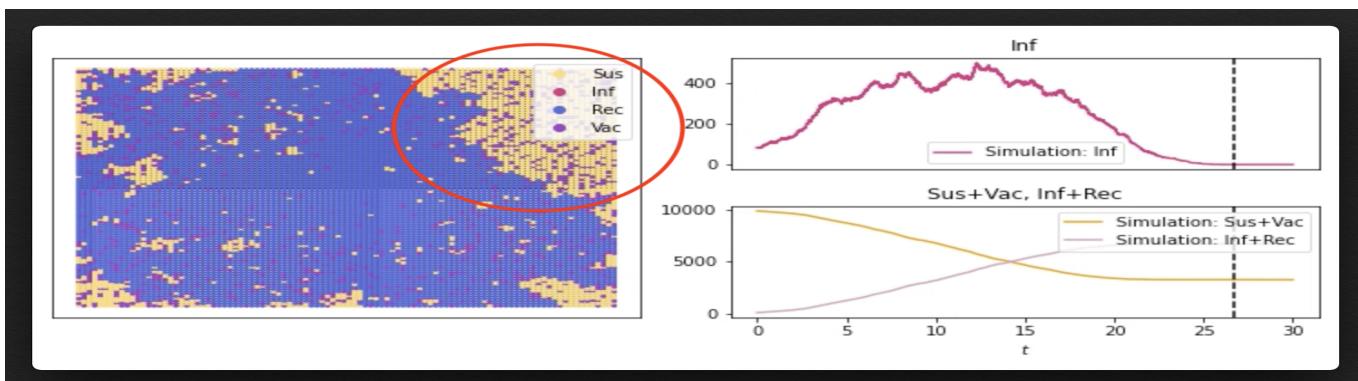


Fig. 17. Observing herd immunity $t=27$