Simulation Analysis of Community Infectivity

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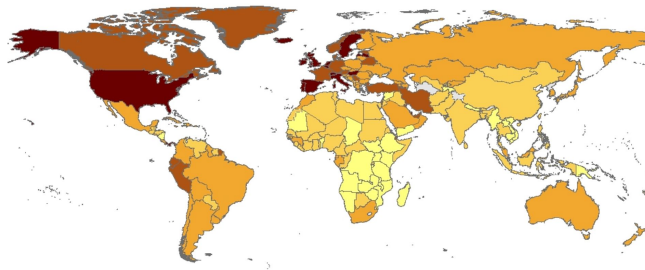
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Introduction

Coronavirus disease 2019 (COVID-19) is an infectious disease caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2).

Cumulative number of reported COVID-19 cases per 100 000

- < 1.0
- 1.0 - 9.9
- 10.0 - 99.9
- 100.0 - 199.9
- ≥ 200.0
- Countries and territories without cases reported

Date of production: 02/05/2020
The boundaries and names shown on this map do not imply official endorsement or acceptance by the European Union.

Introduction

In this project, we are going to do simulation and analyse the infectivity of community. Our work mainly focus on three parts:

- Introduce the traditional SEIR model in epidemiology;

- Improvement on basic SEIR to make our model closer to the reality :

  - Analyse SEIR under quarantine
  - Analyse SEIR under migration

- Do simulation and compare them with the real data.

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Baseline Method: SEIR

In this model, all the people are divided into five types:

- Susceptible(S) represents the people who are healthy but susceptible to the disease.
- The exposed(E) represents the people who are infected, but still under incubation periods.
- The infected(I) represents the infected people.
- The recovered(R) represents the recovered people, who are resistant to the disease.
- The deceased(D) represents the dead people because of this disease.
- If we use N to denote the number of living people, then $N = S + E + I + R$.

Also, there exists transitions between these four states.

Baseline Method: SEIR

- β represents the infection probability. E and I might infect S, thus some healthy people become E.
- σ represents the probability that E transmit to I.
- μ represents the death rate, γ is the recovered rate.
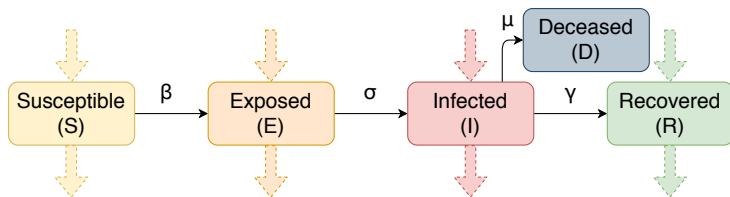
Formula Derivation

A person who carries the virus meets a healthy people with the probability $\frac{S}{N}$. And he infects the healthy person with the probability β.[1] So the infection rate is $\frac{S}{N}\beta_E E + \frac{S}{N}\beta_I I$.

$$\frac{dS}{dt} = -\frac{S}{N}(\beta_E E + \beta_I I)$$

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[1] Specifically, β_E and β_I represents the infection probability of the exposed(E) and the infected(I).

Formula Derivation

- $\dfrac{dS}{dt} = -\dfrac{S}{N}(\beta_E E + \beta_I I)$

- $\dfrac{dE}{dt} = \dfrac{S}{N}(\beta_E E + \beta_I I) - \sigma E$

- $\dfrac{dI}{dt} = \sigma E - (\mu + \gamma)I$
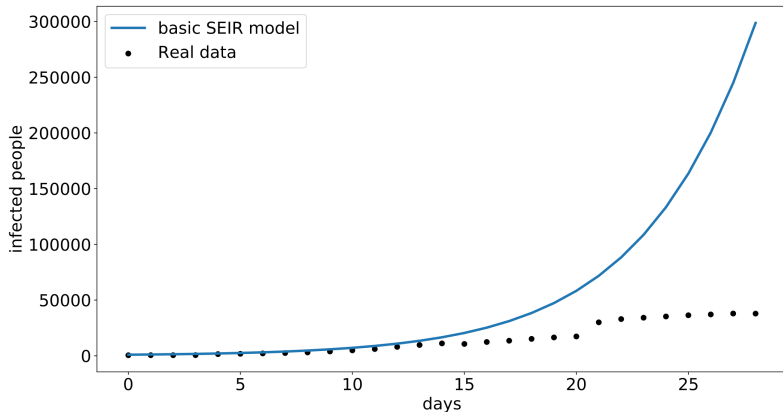
- $\dfrac{dR}{dt} = \gamma I$

Simulation

Figure: SEIR Simulation

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Contact Rate

Definition (Contact Rate)

It is defined as the total number of contacts per unit time of one person. We denote it as c.

The infection rate are $c\dfrac{S}{N}\beta_E E + c\dfrac{S}{N}\beta_I I$.

Quarantine

- There are three states that are newly introduced.

  - *SQ* represents the susceptible under quarantine.

  - *EQ* represents the exposed under quarantine.

  - *H* represents the people who get hospitalized.

Transition Between States

- q_S and q_E represents the portion of quarantine.
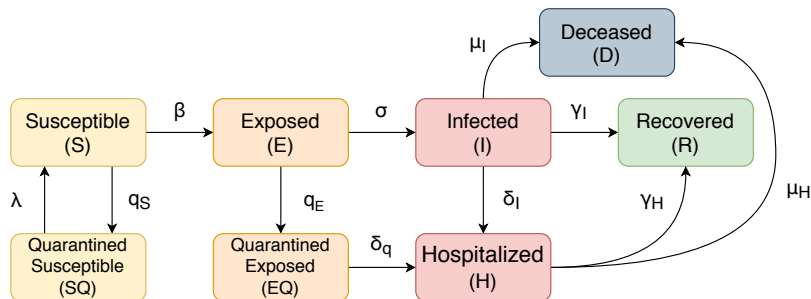- λ represents the rate of release from quarantine.

Figure: Modified model

Formula Derivation

- $\dfrac{dS}{dt} = -\dfrac{c \cdot S}{N}(\beta_E E + \beta_I I) + \lambda SQ - q_S S$

- $\dfrac{dE}{dt} = \dfrac{c \cdot S}{N}(\beta_E E + \beta_I I) - (\sigma + q_E)E$

- $\dfrac{dSQ}{dt} = q_S S - \lambda SQ, \quad \dfrac{dEQ}{dt} = q_E E - \delta_q EQ$

- $\dfrac{dI}{dt} = \sigma E - (\delta_I + \mu_I + \gamma_I)I, \quad \dfrac{dR}{dt} = \gamma_I I + \gamma_H H$

- $\dfrac{dH}{dt} = \delta_q EQ + \delta_I I - (\gamma_H + \mu_H)H$

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SEIR Under Quarantine

We use our model to approximate the transmission of COVID-19 in Wuhan since January 23, when the central government of China imposed a lockdown there.

The simulated number of hospitalized patients is compared with the real data.

SEIR quarantined model simulation without any jumps
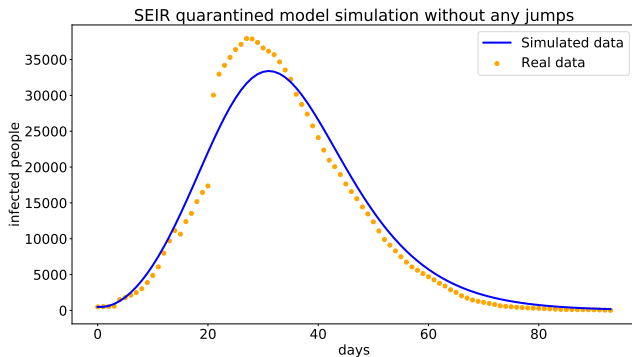
SEIR Under Quarantine

Parameter setting:

- Initial values of S, E, I, R: based on demography of Wuhan
- δ_i, q_E increase with time, approximated with a variant of softmax
- Other parameters: constant, based on previous studies about the decease
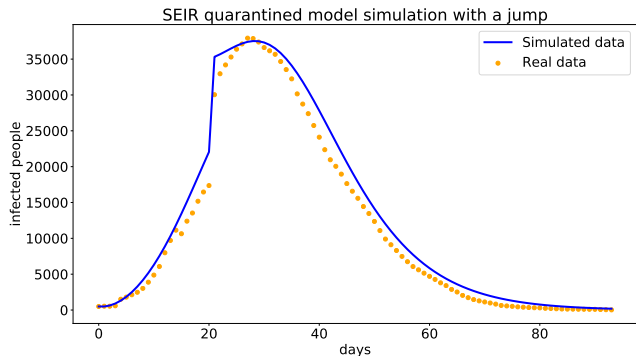
Contact Rate Change
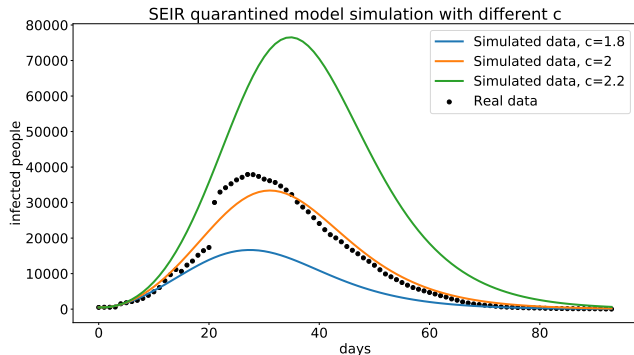
Control measures in Wuhan can change the contact rate *c*

Migration Data

We write code in Python to scrawl the migration flow between regions from January 15 to March 15.

	A	B	C	D	E	F	G	H	I	J	K	L
		省份	20200115	20200116	20200117	20200118	20200119	20200120	20200121	20200122	20200123	20200124
0		上海市	3.04	2.93	3.06	3.23	2.86	2.77	2.8	2.93	3.32	3.19
1		北京市	0	0	0	0	0	0	0	0	0	0
2		重庆市	0.74	0.78	0.81	0.82	0.71	0.78	0.84	0.93	1.1	1.23
3		天津市	7.46	7.27	7.88	8.36	7.92	7.45	7.52	7.33	6.61	6.16
4		内蒙古自治	3.79	3.44	3.19	3.24	2.88	3.24	3.14	3.05	2.79	2.48
5		广西壮族自	0.55	0.58	0.61	0.68	0.62	0.63	0.69	0.71	0.86	1.05
6		西藏自治区	0.04	0.04	0.05	0.04	0.03	0.04	0.03	0.02	0.03	0.03
7		新疆维吾尔	0.46	0.53	0.42	0.62	0.37	0.58	0.53	0.52	0.58	0.6
8		宁夏回族自	0.34	0.33	0.33	0.31	0.27	0.25	0.27	0.29	0.34	0.28
9		河北省	43.32	44.98	44.27	42.78	48.26	46.25	43.43	41.94	37.06	33.92
10		山西省	3.28	2.93	2.86	2.95	2.48	2.84	2.81	2.83	2.8	2.88
11		辽宁省	3.07	2.93	2.85	2.77	2.61	2.72	2.69	2.85	3.24	3.07
12		吉林省	1.25	1.11	1.13	1.17	1.03	1.09	1.27	1.42	1.6	1.62
13		黑龙江省	1.73	1.7	1.74	1.76	1.69	1.7	2.04	2.31	2.69	2.95
14		江苏省	3.36	3.35	3.43	3.88	3.29	3.3	3.13	3.11	3.76	3.53
15		浙江省	2.05	2.1	2.11	2.22	2.34	2.33	2.42	2.34	2.78	2.58
16		安徽省	1.47	1.43	1.44	1.42	1.23	1.34	1.68	1.87	2.1	2.31
17		福建省	0.92	0.95	0.95	1.06	0.97	0.88	1.04	1.13	1.22	1.23
18		江西省	0.71	0.73	0.74	0.77	0.67	0.77	0.77	0.82	0.89	1.02
19		山东省	6.37	6	5.94	5.85	5.17	5.73	5.81	5.41	5.42	5.63
20		河南省	4.19	3.78	3.86	3.71	3.4	3.52	3.97	4.06	4.42	5.13

北京 | 天津 | 广西壮族自治区 | 内蒙古自治区 | 宁夏回族自治区 | 新疆维吾尔自治区 | 西藏自治区 | 上海 ...

Figure: Fetched data of flow

SEIR with Migration

Simulation on cities. A is the place where the disease appears, and every day there are 1%, 0.5%, 0.25% percent of people moving from A to B, C, D separately.
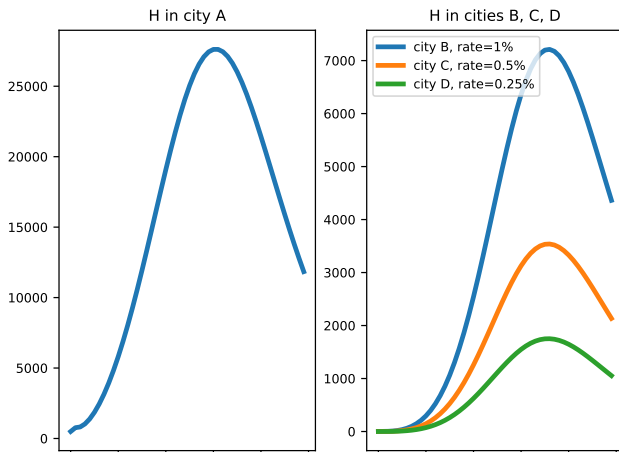
SEIR with Migration

Simulation on cities. A is the place where the disease appears, and every day there are 1%percent of people moving from A to B, C, D separately. B, C, D have different reaction time to take measures.
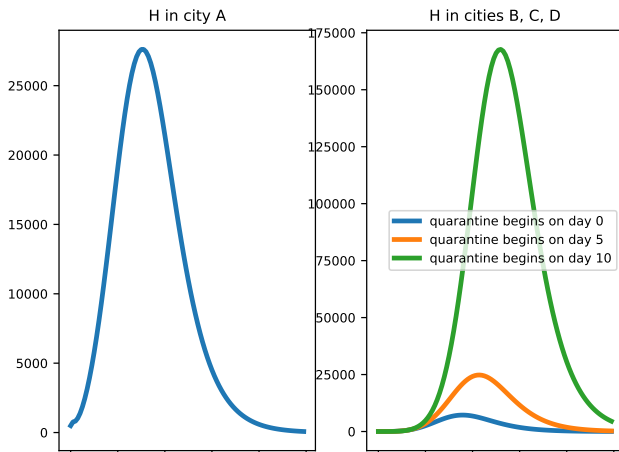
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Future Work

- Analyse and improve the two models based on flow graph.

- Do simulation and compare with the real migration statistics which we have extracted in the experiment.