



A knowledge transfer model for COVID-19 predicting and non-pharmaceutical intervention simulation

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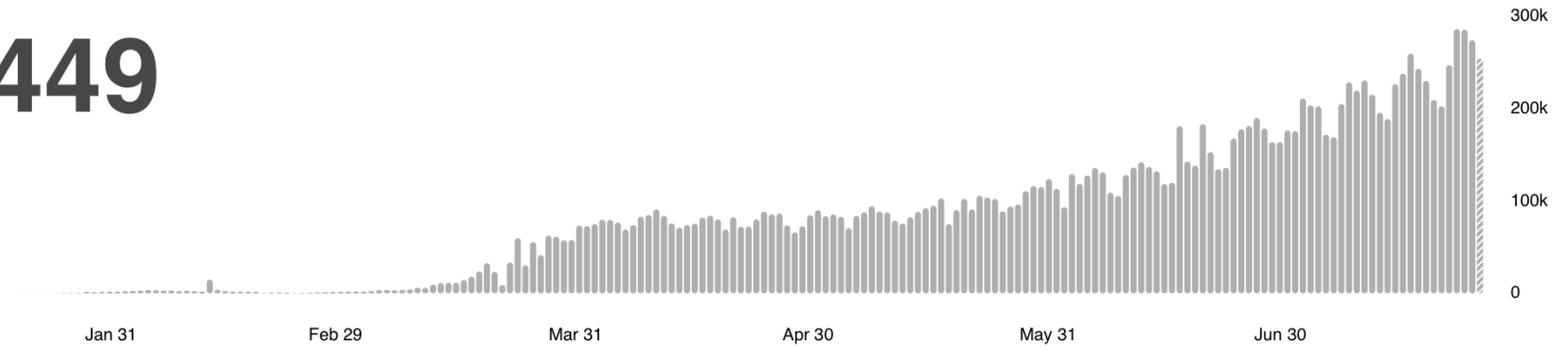


Background: COVID-19 and epidemic modelling

- COVID-19 has now spread globally

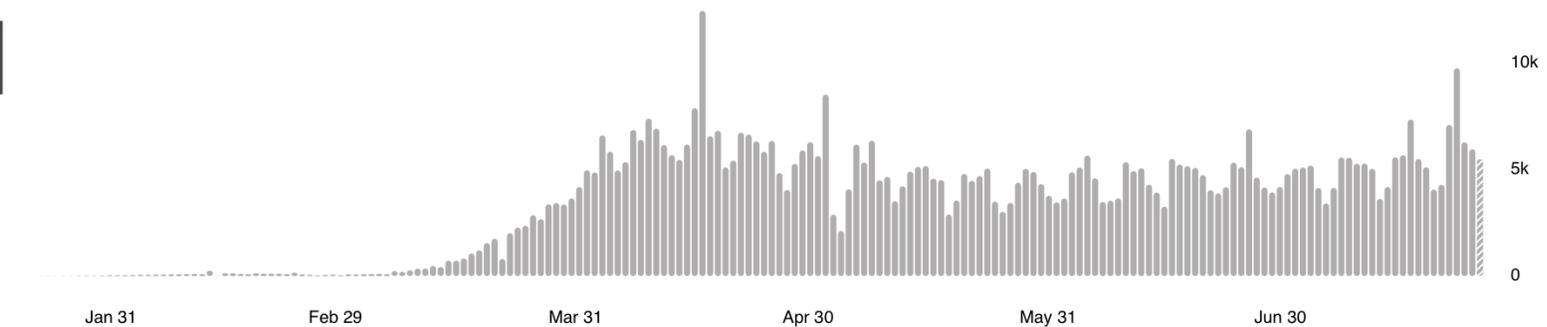
16,114,449

confirmed cases



646,641

deaths



Source: World Health Organization

▨ Data may be incomplete for the current day or week.

- Modelling the transmission of COVID-19 is at an urgent



Background: Basic SIR model

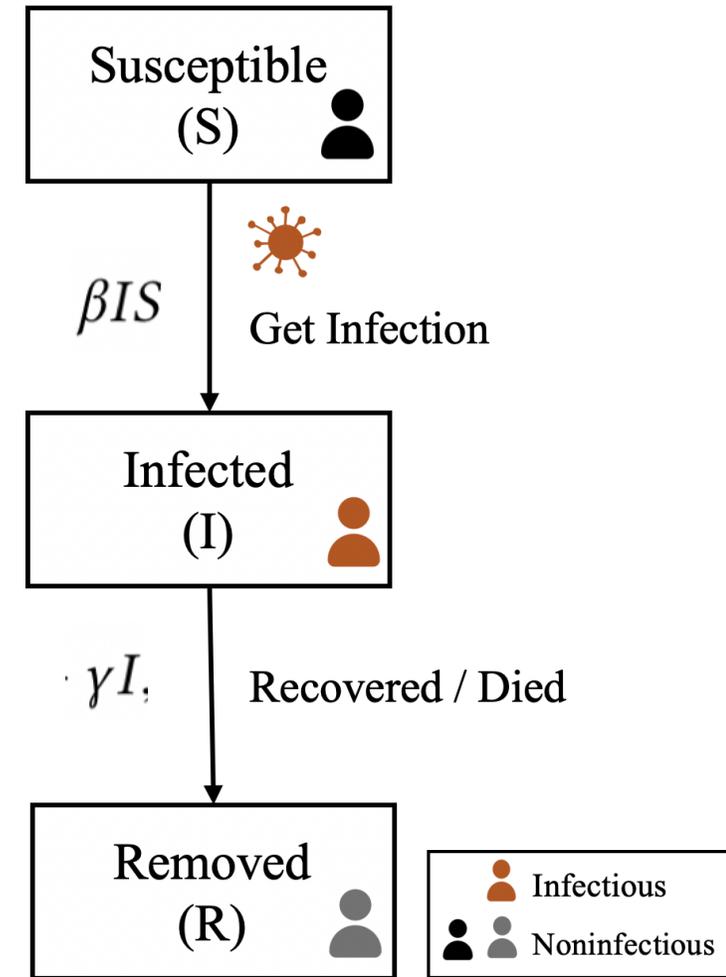
- The basic SIR model contains three compartments

$$\frac{dS}{dt} = -\beta IS,$$

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

$$\frac{dR}{dt} = \gamma I,$$

- SIR model has long been adopted in modelling and predicting the spread of epidemics



- Basic SIR model is not appropriate enough to capture the characteristics of COVID-19.
- The number of Susceptible population at initial (S_0) is needed to estimate.
- More expressive parameters are needed in model for simulation of different non-pharmaceutical interventions.



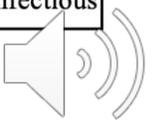
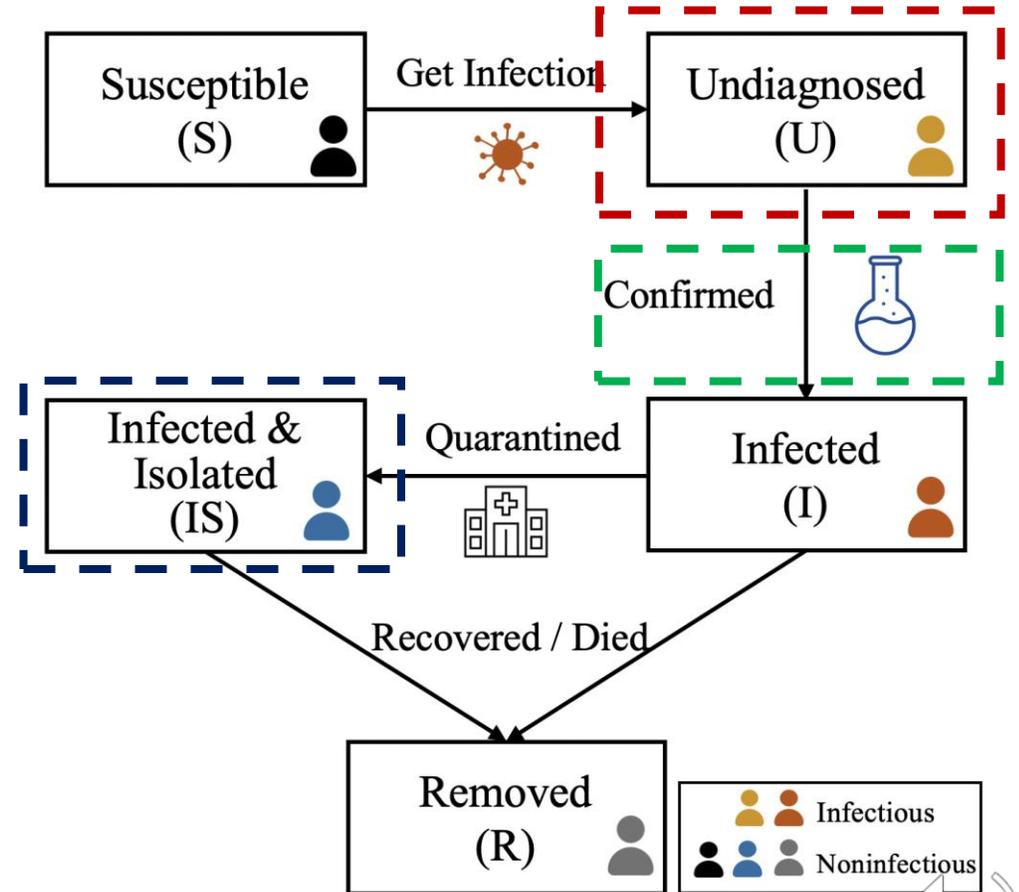
- Modification on basic SIR model by the characteristics of COVID-19
 - ✓ Injecting state of Undiagnosed (U)
 - ✓ Dividing state of I into infected (I) and infected-isolated (IS)
- Knowledge transferring
 - ✓ Introducing the R_t parameter for a rough estimate on the total number of infection as initial susceptible S_0 in the preliminary experiment
- Non-pharmaceutical intervention simulation
 - ✓ Parameters of models reveal the status of epidemics. Simulation on different intensities of interventions can be conducted by adjusting some parameters.



Our Solution – SUIR model

- The **Susceptible-Undiagnosed-Infected-Removed (SUIR)** model

$$\begin{aligned} \frac{dS}{dt} &= -\beta SI - \sigma \cdot S \cdot \max((U - \rho \cdot IS), 0), \\ \frac{dU}{dt} &= \beta SI + \sigma \cdot S \cdot \max((U - \rho \cdot IS), 0) - \epsilon \cdot U, \\ \frac{dI}{dt} &= (1 - \lambda) \epsilon \cdot U - \gamma \cdot I, \\ \frac{dIS}{dt} &= \lambda \epsilon \cdot U - \gamma \cdot IS, \\ \frac{dR}{dt} &= \gamma \cdot (I + IS), \end{aligned}$$



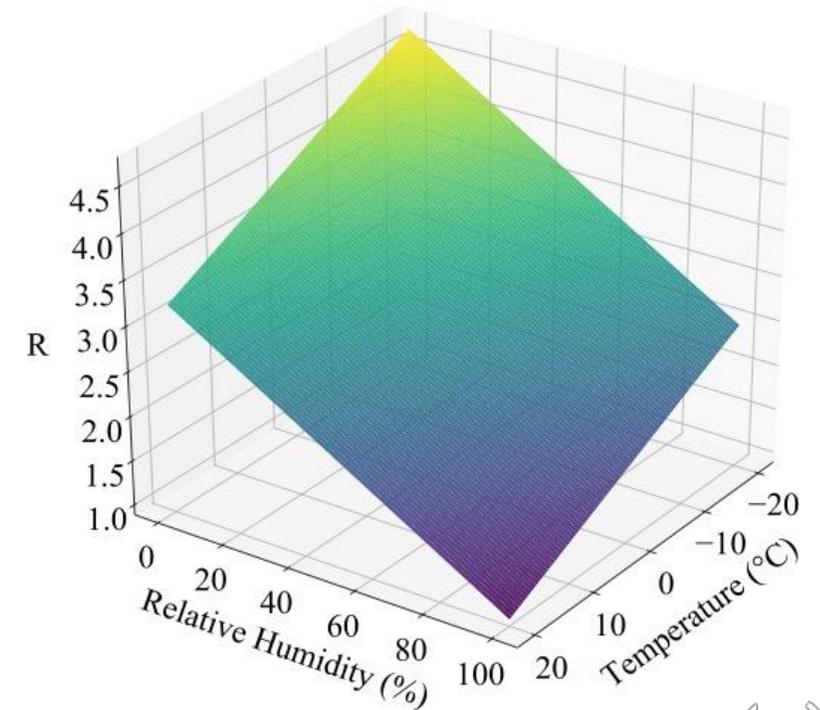
Estimation of Initial Susceptible – S_0

- R_t : Effective Reproduce Number
 - the average number of secondary cases of disease caused by a single infected individual
- The R_t is modelled as a function of temperature and relative humidity from historical data

- For SIR model, we have
$$R_t = \frac{\beta(t) \cdot M}{\gamma}$$

- A preliminary experiment on SIR model with R_t sequence is conducted for rough estimation of S_0

$$S_0 = I(T) + R(T)$$



Algorithm 1 : SUIR Model

Input: $\mathcal{R}(t)$, $(\beta_0, \sigma_0, \rho_0, \varepsilon_0, \lambda_0, \gamma_0)$, cumulative confirmed $\hat{C}(t)$, removal $\hat{R}(t)$, T

Output: $S(t)$, $U(t)$, $I(t)$, $IS(t)$, $R(t)$

- 1: **Initialization:** $\beta_0, \sigma_0, \rho_0, \varepsilon_0, \lambda_0, \gamma_0$
- 2: **Pretraining S_0 :** Apply $\mathcal{R}(t)$, γ on Eq. (1), (2), (3) and (7), obtain S_0 from Eq. (8)
- 3: **Estimation:**
- 4: Apply $(\beta_0, \sigma_0, \rho_0, \varepsilon_0, \lambda_0, \gamma_0)$ on Eq. (14)-(18), obtain $C(t)$ and $R(t)$ from Eq. (18) and (20)
- 5: Obtain MSE of $C(t)$ and $\hat{C}(t)$, $R(t)$ and $\hat{R}(t)$
- 6: Solve $(\beta, \sigma, \rho, \varepsilon, \lambda, \gamma)$ by using Nelder-Mead solver to minimize MSE
- 7: **Simulation:**
- 8: **for** $t = 1$ to T **do**
- 9: Apply $(\beta, \sigma, \rho, \varepsilon, \lambda, \gamma)$ on Eq. (14)-(18),
 update $S(t)$, $U(t)$, $I(t)$, $IS(t)$ and $R(t)$
- 10: **end for**

1. Estimate the initial susceptible population S_0 from R_t

2. Fit parameters from known epidemic data

3. Simulate / Predict using fitted parameters



Country	Model	T						
		1	2	3	4	5	6	7
Italy	SIR	0.94%	2.07%	3.13%	4.12%	4.88%	5.15%	5.02%
	SUIR	0.43%	1.01%	1.49%	1.90%	2.25%	2.55%	2.73%
US	SIR	2.07%	2.88%	3.06%	3.98%	4.80%	5.43%	6.83%
	SUIR	2.02%	2.64%	2.69%	2.59%	2.78%	5.06%	6.62%
Iran	SIR	5.00%	9.61%	13.56%	16.88%	19.72%	22.02%	23.90%
	SUIR	1.61%	3.09%	4.64%	6.08%	7.31%	8.20%	8.83%
UK	SIR	3.28%	5.66%	6.12%	6.31%	6.90%	7.06%	5.95%
	SUIR	2.96%	5.36%	5.09%	3.50%	2.86%	2.35%	2.63%
Spain	SIR	2.91%	5.74%	8.03%	9.53%	10.11%	10.07%	9.73%
	SUIR	1.72%	2.71%	3.20%	3.85%	4.10%	4.13%	4.15%
France	SIR	2.26%	4.38%	4.38%	4.74%	5.34%	9.26%	11.34%
	SUIR	1.50%	2.47%	2.57%	4.18%	5.29%	8.43%	9.55%
Germany	SIR	2.56%	4.51%	5.62%	6.13%	6.34%	5.90%	5.08%
	SUIR	1.88%	3.35%	4.00%	4.66%	5.05%	4.93%	4.50%

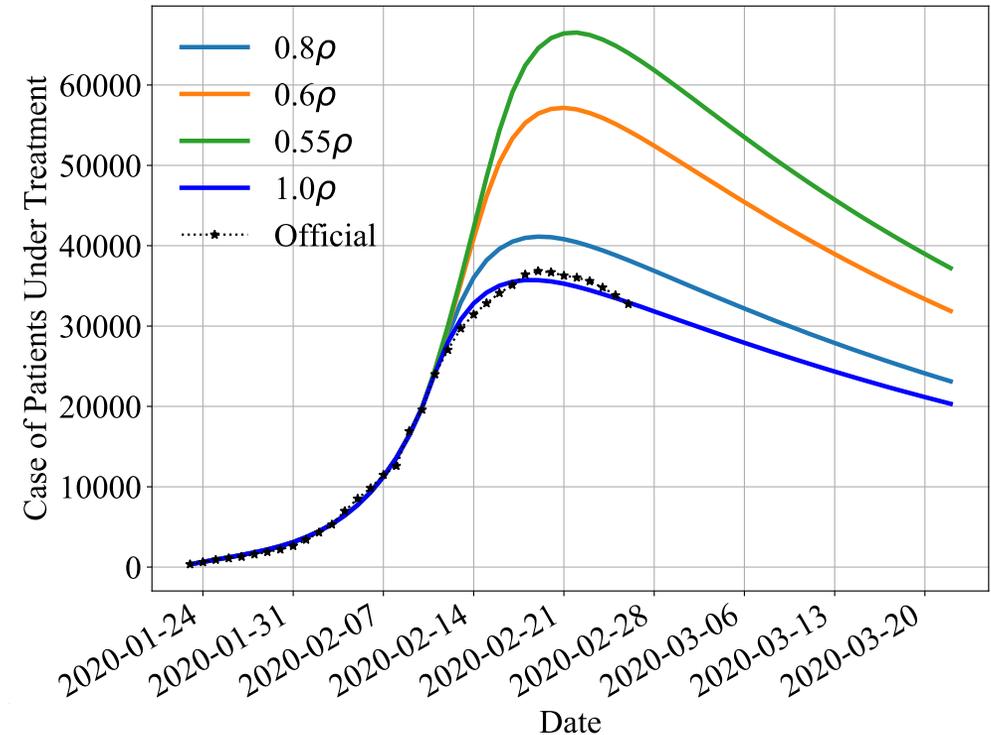
Prediction error of SIR and SUIR model after T days

On average, the SUIR model achieves a **38.4%** lower prediction error than SIR model



ρ : The average number of quarantined undiagnosed close-contacts per infected-isolated cases.

$$\begin{aligned}\frac{dS}{dt} &= -\beta SI - \sigma \cdot S \cdot \max((U - \rho \cdot IS), 0), \\ \frac{dU}{dt} &= \beta SI + \sigma \cdot S \cdot \max((U - \rho \cdot IS), 0) - \epsilon \cdot U, \\ \frac{dI}{dt} &= (1 - \lambda) \cdot \epsilon \cdot U - \gamma \cdot I, \\ \frac{dIS}{dt} &= \lambda \cdot \epsilon \cdot U - \gamma \cdot IS, \\ \frac{dR}{dt} &= \gamma \cdot (I + IS),\end{aligned}$$



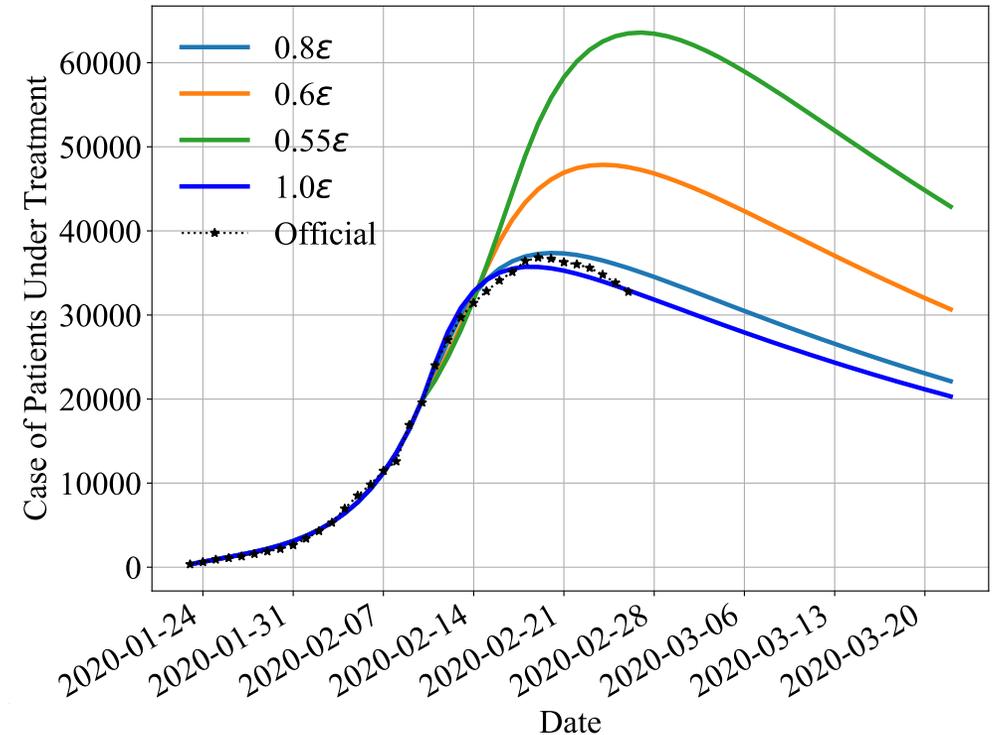
When the isolation ratio decreased to 0.55ρ ,

the peak number of patients in treatment reached more than **twice** the real value



ϵ : The probability of undiagnosed infection get confirmed.

$$\begin{aligned} \frac{dS}{dt} &= -\beta SI - \sigma \cdot S \cdot \max((U - \rho \cdot IS), 0), \\ \frac{dU}{dt} &= \beta SI + \sigma \cdot S \cdot \max((U - \rho \cdot IS), 0) - \epsilon U, \\ \frac{dI}{dt} &= (1 - \lambda) \epsilon U - \gamma \cdot I, \\ \frac{dIS}{dt} &= \lambda \epsilon U - \gamma \cdot IS, \\ \frac{dR}{dt} &= \gamma \cdot (I + IS), \end{aligned}$$



When the diagnose rate decreased to 0.55ϵ ,

the peak number of patients in treatment reached **1.8-fold increase** than real value



- We proposed the **SUIR model**, an epidemic transmission framework that offers effective prediction and intervention simulation of COVID-19.
- SUIR model incorporate **characteristics of COVID-19** into traditional model to achieve satisfying performance against SIR model.
- The utilization of **domain knowledge R_t** guarantees the appropriate estimation of initial susceptible population.



Thank You!

