

Bayesian Sir Modeling in the Case of Undocumented Infectious Individuals of COVID 19

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Abstract

Covid 19 that began in the end of 2019 has spread rapidly across continents in a short of time. This event makes most countries do not report and record the disease properly. There is considerable number of undocumented infectious individuals that should be considered when we want to estimate the Susceptible, Infectious, and Removal (SIR) parameters and to predict the future cases. The covid 19 data obtained from City of Surabaya were analyzed using Bayesian SIR modeling by BaySIR package in RStudio. The estimated and predicted medians of SIR compartment tend to decrease over time. The estimated and predicted medians of effective reproduction number tend to decrease over time. The results depend on the assumptions of SIR model to use such as the dynamic of covid 19, local government policies, and individual behavior in the community.

Keywords: Covid 19 Undocumented individuals • Bay SIR • Infectious Disease

Introduction

Covid 19 is an infectious disease phenomenon in the 21st century. It began in the end of 2019 in Wuhan province, China [1]. It has spread out across continents in a short of time. It affects individuals in the developing countries as well as the developed countries. It shakes socio-economic-political-psychological order in most countries. The occurrence of covid 19 that is so fast makes most countries lack of medical infrastructures in the hospitals as well as health infrastructures in the public health facilities. Lack of ventilators in the hospitals enhances death among severe cases. Lack of public health personnel who promote better health behaviors and perform mass screening in the community enhances asymptomatic cases. These cases make high undocumented cases. They are not reported officially so that they cannot be controlled properly.

Over years epidemiological experts implement Susceptible, Infectious, and Recovery (SIR) Compartment Model in understanding the dynamics of infectious diseases. Yang et al. [2] used SIR model as basis for estimating effective reproduction number of pandemic for pandemic influenza H1N1. This model is categorized as deterministic model in closed epidemic. It holds assumption of closed population in which there is no emigration as well as immigration, birth and death do not change [3]. In fact, the development of infectious diseases is dynamic and changes across time [4]. Change of health behaviors of individuals in the community as well as change of health policies affects the course of infectious diseases. Hence, deterministic model of SIR cannot accommodate these conditions. Besides an infectious disease is a random process, it needs probabilistic model to understand its progression.

Theoretical Frame-Work

Classical SIR Model

Kermack and MacKendrick [5] began their works concerning the difficulty of

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finding a causal factor that accounted for epidemic of a disease in the population. When an infected individual was introduced into a population, more or less susceptible to the disease in question. Disease spreading occurred when an infectious individual contacted unaffected one. Finally, an infected individual was removed from the number of infected individuals by recovery or by death. These stories inspired them to develop concepts of Susceptible, Infectious, and Removal compartments as part of SIR model.

According to Zhou and Ji [4]; Bjørnstad et al. [3], a population is divided into three compartments based on SIR model. First of all, susceptible individuals (S) are those who do not have the disease but they may be infected. Second, infectious individuals (I) are those who have the disease and they may infect the susceptible individuals. Third, recovered/removed individuals are those who had the disease, however, they are removed from the possibility of being reinfected or spreading the disease. They are removed due to several reasons such as recovery with immunity against reinfection, quarantine and isolation from the rest of the population, and death. Moreover, the SIR model can be expressed as differential system equations as follows.

$$\begin{aligned}dS_t/dt &= -\beta NS_t I_t \\dI_t/dt &= \beta NS_t I_t - \alpha I_t \\dR_t/dt &= \alpha I_t\end{aligned}\tag{1}$$

Transmission rate of the disease is denoted by β , while removal rate is denoted by α . When an infectious individual is doing effective contact with β individuals per unit time, then I infectious individuals result to a rate of new infections $(\beta S=N) \cdot I$. This is the explanation of the first part of equation (1). Moreover, the infectious individuals leave the infectious compartment at a rate of αI . This is the explanation of the third part of equation (1). Hence, the explanation of second part of equation follows immediately the explanations of first and second parts.

According to Zhou and Ji [4], to make easy to compute S, I, and R at given time t , we use a discrete-time approximation of equation (1) as follows.

$$\begin{aligned}S_t &= S_{t-1} - \beta S_{t-1} I_{t-1} / N \\I_t &= (1 - \alpha) I_{t-1} + \beta S_{t-1} I_{t-1} / N \\R_t &= R_{t-1} + \alpha I_{t-1}\end{aligned}\tag{2}$$

Stochastic sir model

When the spreading of a disease is not deterministic, then Classical SIR Model is not recommended. The spreading of a disease is a random process. Disease transmission among individuals is more random than deterministic, it is called

naturally stochastic. According to Zhang and Wang [6] when the diseases are massive such as in cases of avian influenza and SARS, stochastic differential equation is better option than SIR classical equation to understand the dynamics of the diseases.

Suppose $\{V_t: t \geq 0\}$ is a stochastic process. According to Zhou and Ji [4] it can be shown that $\{V_t: t \geq 0\}$ is a Markov process with transitional probabilities as follows.

Infection:

$$[V_{t+\delta} = (s - 1, i + 1, r) | V_t (s, i, r)] = \beta si\delta N + (\delta) \tag{3}$$

Removal:

$$[V_{t+\delta} = (s, i - 1, r + 1) | V_t (s, i, r)] = \alpha i\delta + (\delta) \tag{4}$$

in which δ is small increment in time.

State-space sir model

There is other model for modeling the uncertainty of epidemic process. According to Zhou and Ji [4] this is called State-space SIR Model. This model contains two components, for the epidemic process it is called Evolution Model, while for the data it is called Observation Model. Moreover, they can be presented as follows.

Evolution Model:

$$V_t \sim [V_t | f(V_{t-1}, \beta, \alpha)]$$

Observation Model:

$$\tilde{I}_t \sim p(\tilde{I}_t | I_t, \lambda)$$

For $t=1, 2,$

When we solve equation (1) at time t , with initial value of V_{t-1} at time $t-1$, and parameters β, α , it is assumed that V_t is to be centered at $f(\cdot)$ with variance, κ , then we obtained $f(V_{t-1}, \beta, \alpha)$ as part of evolution model. Moreover, \tilde{I}_t , in the observation model is the number of patients as the disease reports by health providers. It is assumed as proxy of true number of infectious individuals, I_t . Furthermore, \tilde{I}_t is assumed to be centered at I_t with variance, λ . Compared to Stochastic SIR Model in equation (3), State-space SIR Model is better in flexibility and manageable computation.

Model for the Epidemic Process

This model is better than other models when a number of infectious individuals is undocumented by health facilities [4]. We begin with closed population that is assumed to be no emigration, no immigration, no nature births and deaths. Moreover, we divide this population into four compartments as follows. First, susceptible individuals (S) who do not have disease, but they are susceptible to it. Second, undocumented infectious individuals (UI) who have disease and are capable to infect susceptible individuals. They include asymptomatic individuals, untested individuals. Since, they are undetected as infectious individuals then they are not reported by health facilities. Third, documented infectious individuals (DI) who are confirmed to have disease and capable to infect susceptible individuals. Hence, they documented officially. Fourth, removed individuals (R) who are removed from infectious ones because they do not have possibility to be reinfected or to spread the disease. According to Zhou and Ji [4] this model can be summarized in equations as follows.

$$\begin{aligned} S_t &= S_{t-1} - \beta_{t-1} S_{t-1} (I^u + I^d) N, \\ t-1 \quad t-1 \\ &= (1-\alpha) + \beta_{t-1} S_{t-1} (I^u + I^d) N - B_{t-1}, \\ t \quad t-1 \\ &= (1-\alpha) + B_{t-1}, \\ t \quad t-1 \\ &= R_{t-1} + (I^u + I^d), \end{aligned} \tag{4}$$

$t-1 \quad t-1$
 $t-1$
 $t-1$

For $t=1, 2, \dots, T$. When we add I^u and B_{t-1} to model lineation (2) we obtain model mentioned in equation (4) in which the first addition represents undocumented infection, while the second addition represents observed daily new cases.

Model for the Observed Data

In this model, the observed data represent the daily new confirmed Covid-19 cases,

B_t . According to Zhou and Ji it is assumed that in day t , the UI individuals who have been removed are diagnosed as disease with diagnosis rate of γ_t . Hence we have new confirmed Covid-19 cases, $B = (1 - \alpha)$. The value of γ_t is between 0 and 1. Usually we use log transformation of γ_t , $\tilde{\gamma}_t = \log(\gamma_t) \triangleq [\gamma_t = (1 - \gamma_t)]$. Zhou and Ji (2020) recommend using BaySIR package in R to choose other transformation such as probit, complementary log-log.

We use prior transformation of γ_t , as follows.

$$\tilde{\gamma}_t \sim (y^T, \eta, \sigma^2) \tag{5}$$

In which y_t is vector of covariates those are related to the diagnosis rate, η and σ^2 . They are respectively regression coefficient and variance term. Moreover, random fluctuations of confirmed case counts and report errors are captured by this variance term. Furthermore, sampling model for the daily new confirmed Covid -19 cases,

B_t is presented as follows.

$$\begin{aligned} \log(B_t | I^u, \alpha) &\sim (y^T, \eta, \sigma^2) \\ (1-\alpha) I^u & \\ t \end{aligned} \tag{6}$$

When we are doing simulation studies and real data analyses, it is better we use a simple choice of $y_t = 1$ in which we assume that the mean diagnosis rate is constant. Other covariates can be included to y_t such as the number of tests. However, it is difficult to detect the effect of these covariates.

Inference

Posterior Sampling

According to Zhou and Ji (2020) all model parameters and hyper parameters are

Presented as $\theta = \{I^u, \beta, \alpha, \mu, \sigma_\beta, \rho, \eta, \sigma^2\}$. Moreover, $\beta = (\beta_1, \dots, \beta_T)$ and $B =$

$$\begin{aligned} 0 \gamma 0 1 T \\ (B_0, B_1, \dots, B_T) \text{ is the vector of daily increments in confirmed cases. Then the joint posterior distribution of } \theta \text{ is presented as follows.} \\ (\theta | B, I^d) \propto [\prod_t (\tilde{\gamma}_t | y^T, \eta, \sigma^2)] \cdot \pi^*(\theta) \end{aligned} \tag{7}$$

$0 \quad t = 0 \quad t$
In which $(\cdot | \mu, \sigma^2)$ is the density function of a normal distribution with mean, μ And variance, σ^2 , and $\pi^*(\theta)$ is the prior density of θ .

Markov chain Monte Carlo (MCMC) algorithm is used to simulate from the posterior distribution and implement posterior inference. When the conditional posterior distribution of a parameter is not available in closed form, we use Metropolis-Hastings steps. Since among the model parameters show strong correlation, the regular Gibbs sampler is not very efficient in application.

Predictive Inference

Besides we estimate epidemiological parameters we also predict future observation. This prediction can be achieved by sampling from its posterior predictive distribution.

According to Zhou and Ji, $B^* = (B_{T+1}, T+T^*)$ is vector of daily confirmed cases for future days $t = T + 1, \dots, T + T^*$. Then the posterior predictive distribution of B^* is presented as follows.

$$\pi(B^*|B, I^D) = \int \pi(B^*|\theta, B, I^D) \cdot (\theta|B, I^D) d\theta \tag{8}$$

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Sampling from equation (8) involves computing

$$\pi(\tilde{\beta}^*|B, I^D) = \int \pi(\tilde{\beta}^*|\tilde{\beta}) \cdot (\tilde{\beta}|B, I^D) d\tilde{\beta} \text{ for } \tilde{\beta}^* = (\tilde{\beta}_1, \dots, \tilde{\beta}_*)$$

00T+1 T+T

$$\tilde{\beta}^* | \tilde{\beta} \sim [X^* \mu + C^* C^{-1} (\tilde{\beta} - X \mu), C^{**} - C^* C^{-1} C^*]$$

In which $X = (x_0, \dots, x_T)^T$, $X^* = (x_{T+1}, \dots, x_{T+T^*})^T$, C^* is a $T^* \times (T + 1)$ matrix with the (i, j) th entry being $C(T + 1, j - 1)$, and C^{**} is a $T^* \times T^*$ matrix with the (i, j) th entry being $C(T + 1, T + j)$. This is based on a GP prediction rule (Zhou and Ji, 2020).

Methods and Materials

Data for estimation and prediction of SIR parameters are obtained from JatimTanggap Covid 19 under Regional Government of East Java Province, Indonesia. They can be accessed easily through <http://infocovid19.jatimprov.go.id/>. Then we select data of City of Surabaya. According to rule of thumb, Day $t=0$ is selected when the 100th case of covid 19 was confirmed positive officially. Hence, $t=0$ occurred in 12 April 2020. In this time, total number of positive cases was 180. Then $I_{D_0}=180$. Moreover, the new cases start from $t=1, T$, in which $t=1$ occurred in 13 April 2020. Current time T occurred in 22 April 2020. Population of City of Surabaya is estimated as $N=2,928,042$. The data of new cases from $t=1$ until $T=10$ were stored in excel format `assubcty 030820.xlsx`

The data were analyzed using Bay SIR Package in R Studio. The command for estimation and prediction is presented as follows.

```
> library(readxl)
> subcty030820 <- read_excel("E:/VARIOUS COVID 19/BAYESIAN SIR 110720/PAPER FOR JOURNAL PUBLIC270720/DEFINITEDATA 030820/subcty030820.xlsx")
> View(subcty030820)
> library(BaySIR)
> bsby=subcty030820$Newcases
> idosby=c(180)
> Nsby=2928042
> surabaya=BaySIR_MCMC(B=bsby,I_D_0 =idosby, N=Nsby)
```

- [1] "BaySIR: Posterior simulation started. Date: Mon Aug 03 06:03:39 2020."
- [1] "BaySIR: Burn-in started (20000 iterations). Date: Mon Aug 03 06:03:39 20 20."
- [1] "BaySIR: Burn-in finished. Date: Mon Aug 03 06:03:58 2020."
- [1] "BaySIR: MCMC started (1000 iterations, 30 thin). Date: Mon Aug 03 06:03:58 2020."
- [1] "BaySIR: MCMC 20.00 % finished. Date: Mon Aug 03 06:04:042020."
- [1] "BaySIR: MCMC 40.00 % finished. Date: Mon Aug 03 06:04:092020."
- [1] "BaySIR: MCMC 60.00 % finished. Date: Mon Aug 03 06:04:152020."

- [1] "BaySIR: MCMC 80.00 % finished. Date: Mon Aug 03 06:04:212020."
- [1] "BaySIR: MCMC 100.00 % finished. Date: Mon Aug 03 06:04:27 2020."
- [1] "BaySIR: MCMC finished. Date: Mon Aug 03 06:04:27 2020."

```
> surabayapred=BaySIR_predict(T_pred = 10,MCMC_spls =surabaya$MCMC_spls,B=bs by,I_D_0 =idosby,N=Nsby)
```

The outputs of estimation includes estimated medians and their 95% confidence intervals for susceptible individuals (S), Undocumented infectious individuals (UI), Documented infectious individuals(DI),Undocumented removal individuals(UR), Documented removal individuals(DR), β and γ , and effective reproduction number from $t=1$ to $t=10$. Furthermore, the outputs of prediction include medians and their 95% confidence intervals of susceptible individuals (S), Undocumented infectious individuals (UI), Documented infectious individuals (DI), Undocumented removal individuals (UR), Documented removal individuals (DR), β and γ , and effective reproduction number from $t=11$ to $t=20$.

Results and Discussions

In time $t=1$ among 2,928,042 individuals of City of Surabaya, the number of them to be susceptible has estimated median equal to 2,927,452. This number includes 99.98% of the number of individuals in this City. Then at $t=2$ to $t=10$ the estimated median of susceptible individuals stand to decrease. The decrease of this number may result in the increased number of infectious individuals when they do not protect themselves against the transmission of corona virus from individuals who are confirmed as covid 19. Hence, they should protect themselves with masks, physical distance, and hand washing with soap (Table 1a & 1b).

In time $t=11$ until $t=20$ the estimated median of predicted individuals who are susceptible is stable to be 2,927,224 (99,97%). We hope this number does

Table 1a. Estimated median of susceptible individuals.

	Susceptible individuals (S)		
	Median and 95% CI		
	50%	2.50%	97.50%
[1]	2927452	2926761	2927663
[2]	2927330	2926490	2927569
[3]	2927280	2926371	2927530
[4]	2927251	2926319	2927516
[5]	2927235	2926263	2927513
[6]	2927226	2926237	2927508
[7]	2927224	2926223	2927506
[8]	2927224	2926216	2927506
[9]	2927224	2926212	2927506
[10]	2927224	42926205	2927506

Table 1b. Predicted median of susceptible individuals.

	Predicted susceptible individuals (S)		
	Median and 95% CI		
	50%	2.50%	97.50%
[11]	2927224	2926205	2927506
[12]	2927224	2926205	2927506
[13]	2927224	2926205	2927506
[14]	2927224	2926204	2927506
[15]	2927224	2926179	2927506
[16]	2927224	2926179	2927506
[17]	2927224	2926164	2927506
[18]	2927224	2926164	2927506
[19]	2927224	2926164	2927506
[20]	2927224	2926164	2927506

not decrease rapidly that may result in the increased number of infectious individuals. They should protect themselves by obeying there commendation of WHO. In this case, the roles of public health officers are important to assure individuals in the community keep in healthy conditions.

Figure 1 shows that individuals who are susceptible tend to decrease rapidly from time t=1 through t=5, then they decrease slowly until t=10. Moreover, individuals who are predicted after time t=10 tend to decrease steadily until t=20 (Table 2a).

Not all infectious individuals are recorded properly. In the beginning of Covid 19 for pandemic, most individuals and most health officers do not know well about this new disease, they lack of knowledge about signs and symptoms of covid 19, and lack of diagnostic test of covid 19. Hence, among infectious individuals are not detected and recorded properly. These individuals are classified as undocumented infectious individuals. Table 2a shows the estimated median of undocumented infectious individuals at time t=1 is 410 or about 14/100,000 population of City of Surabaya. This number tends to decrease from time t=2 to t=10 along with the increased capability of health officers to identify covid 19 and the increase number of diagnostic equipment to confirm covid 19.

Table 2b shows the median of undocumented infectious individuals is predicted to decreases in time t=11 compared to the number of those individuals in time t=10. At time t=11 the number is 108 then the number decrease to be 6 in time t=20. We hope the government, in this case Mayor, provides more skilled health officers in tracing the suspected cases and more diagnostic equipments in confirming diagnosis.

Table 3a shows that in time t=1 the estimated median of documented infectious individuals is 180. This number increase until time t=3. Then this number tends to decrease until t=10 to be 174. We hope most of the decreased number

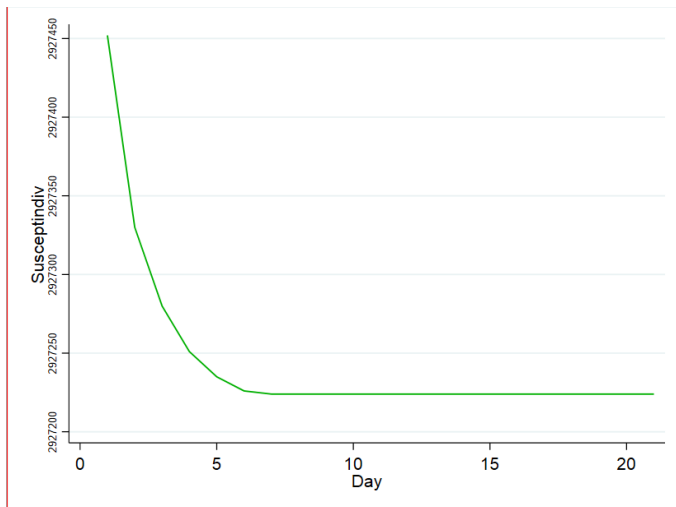


Figure 1. Estimated and predicted medians of susceptible individuals.

Table 2a. Estimated median of infectious individuals (Undocumented).

	Undocumented infectious individuals (UI)		
	Median and 95% CI		
	50%	2.50%	97.50%
[1]	410.1712	198.8732	1100.71
[2]	404.8147	186.92624	1176.8179
[3]	382.4987	174.29798	1143.5070
[4]	349.973	148.45346	1051.9764
[5]	307.8181	123.61531	963.0059
[6]	276.4882	109.41512	868.9782
[7]	244.5549	95.29002	793.9612
[8]	199.3867	65.89653	698.3371
[9]	149.1806	29.92635	599.8908
[10]	132.444	7.26.01899	543.1475

Table 2b. Predicted median of infectious individuals (Undocumented).

	Predicted undocumented infectious individuals (UI)		
	Median and 95% CI		
	50%	2.50%	97.50%
[11]	108.5803	12.5028	481.8343
[12]	80.87049	5.362555	414.7237
[13]	59.56823	2.538908	345.2095
[14]	43.81917	1.613641	294.9577
[15]	33.38643	0.83414	255.9212
[16]	25.83135	0.387106	217.4886
[17]	19.39332	0.188681	183.0044
[18]	14.33488	0.111751	157.4255
[19]	10.92303	0.061338	130.9515
[20]	8.096605	0.024105	102.0197

Table 3a. Estimated median of infectious individuals (Documented).

	Documented infectious individuals (DI)		
	Median and 95% CI		
	50%	2.50%	97.50%
[1]	180	180	180
[2]	243.3441	241.1453	245.5907
[3]	244.771	239.8667	249.8377
[4]	238.0421	230.7433	245.6739
[5]	228.048	218.7276	237.9128
[6]	205.1452	194.1708	216.9023
[7]	186.7434	174.5956	199.9239
[8]	186.3511	173.3971	200.5877
[9]	195.0017	181.3441	210.1872
[10]	174.707	6.160.326	3.190.8583

of these individuals to be individuals who recover from Covid 19. The better services in hospitals with better hospital facilities in curing covid 19, more documented infectious individuals recover from covid 19.

Table 3b shows the median of documented infectious individuals in time t=11 is predicted to be 166. The number is lower than the number of them in time t=10 is 174 (see Table 3a). This number tends to decrease from time t=12 to t=20.

Figure 2 shows that the median of undocumented individuals who are removed tend to decrease rapidly from time t=1 through t=10. Moreover, they are predicted to decrease after t=10 until t=20. Median of documented individuals who are removed tend to decrease gradually from time t=1 to t=10. Furthermore, they are predicted to decrease after t=10 until t=20. Rapid decrease of undocumented individuals is probably due to the better procedures for controlling covid19.

Table 4a shows that in time t=1 the estimated median of undocumented removal individuals is zero. Then this number tends to increase from t=2 to t=10. We hope that the increased number of removal individuals although they are undocumented, most of them recover from covid 19. However, we have to be careful to these individuals when they are reinfected that may result in the increased number of undocumented infectious individuals.

Table 4b shows that the median of removal individuals who are undocumented are predicted to decrease from time t=11 to t=20. Since they are undocumented, they may recover from covid 19 or they may be reinfected. We hope reinvested individuals tend to decrease along with the epidemic process.

Table 5a shows that the estimated median of removal individuals who are documented tend to increase from time t=1 to t=10. Better hospital personnel and equipments, cooperative covid 19 patients who are cured result in more recovery individuals and more removal individuals.

Table 3b. Predicted median of infectious individuals(Documented).

	Documented infectious individuals (DI)		
	Median and 95% CI		
	50%	2.50%	97.50%
[11]	166.6296	151.8603	183.3989
[12]	157.9524	137.6446	268.3583
[13]	149.2876	124.9809	275.991
[14]	140.184	112.5795	286.6097
[15]	129.8799	100.6954	266.2253
[16]	120.3933	91.20503	258.56
[17]	110.8115	80.46201	240.5977
[18]	101.4668	71.55932	216.6888
[19]	92.63593	63.45797	208.2658
[20]	84.08013	56.57627	186.2496

Table 4b. Predicted median of removal individuals(Undocumented).

	Predicted undocumented removal individuals (UR)		
	Median and 95% CI		
	50%	2.50%	97.50%
[11]	320.1539	128.4747	979.6944
[12]	331.0145	130.0944	1038.151
[13]	339.9535	130.5118	1076.886
[14]	347.6551	131.5584	1117.653
[15]	353.2465	132.4409	1153.07
[16]	357.2541	132.8494	1177.367
[17]	359.2325	133.0027	1197.582
[18]	362.0456	133.1125	1214.334
[19]	363.304	133.1928	1224.724
[20]	364.4554	133.2432	1233.735

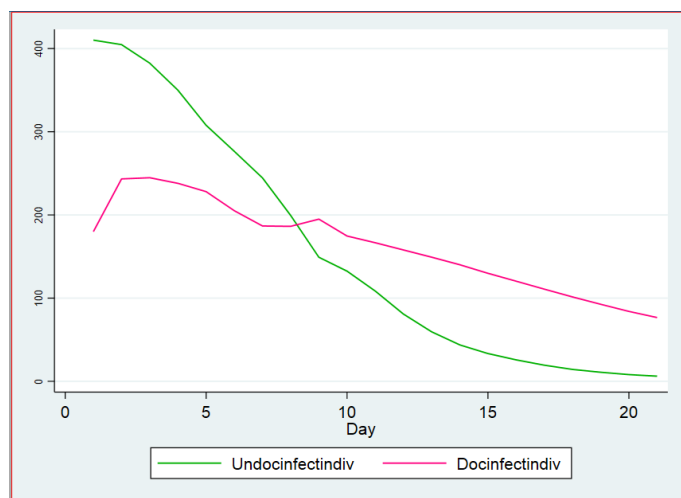


Figure 2. Estimated and predicted individuals who are infected.

Table 4a. Estimated median of removal individuals(Undocumented).

	Undocumented removal individuals (UR)		
	Median and 95% CI		
	50%	2.50%	97.50%
[1]	0	0	0
[2]	45.28501	21.03076	120.0935
[3]	89.71011	42.0695	256.5184
[4]	130.8489	62.64227	383.8074
[5]	169.4246	78.45925	496.6681
[6]	202.3032	91.33008	595.6239
[7]	233.5011	102.6664	690.9623
[8]	261.645	113.6496	787.9171
[9]	284.9611	120.3172	864.3829
[10]	303.7546	125.8539	925.5424

Table 5b shows that the median of removal individuals who are documented are predicted to increase from time $t = 11$ to $t = 20$. Assuming covid 19 patients receive better curing with better procedures. These conditions are maintained a long time $t = 1$ through $t = 20$.

Figure 3 shows that the estimated median of removal individuals who are undocumented tend to increase curvilinear from time $t = 1$ to $t = 10$. Moreover, this number is predicted to increase after time $t = 10$ to $t = 20$. The estimated median of removal individuals who are documented tend to increase linearly from time $t = 1$ to $t = 10$. Furthermore, this number is predicted to increase linearly after $t = 10$ to $t = 20$. We expect those who are removed from infectious compartment are individuals who recover from covid 19. It will happen if the treatment procedures are implemented properly.

Table 5a. Estimated median of removal individuals(Documented).

	Documented removal individuals (DR)		
	Median and 95% CI		
	50%	2.50%	97.50%
[1]	0	0	0
[2]	19.65593	17.40925	21.85468
[3]	46.22901	41.16232	51.13331
[4]	72.95791	65.32614	80.25669
[5]	98.95202	89.08724	108.2724
[6]	123.8548	112.0977	134.8292
[7]	146.2566	133.0761	158.4044
[8]	166.6489	152.4123	179.6029
[9]	186.9983	171.8128	200.6559
[10]	208.2925	192.1417	222.6738

Table 5b. Predicted data of removal individuals(Documented).

	Predicted documented removal individuals (DR)		
	Median and 95% CI		
	50%	2.50%	97.50%
[11]	227.3704	210.6011	242.1397
[12]	245.5663	228.3391	260.5778
[13]	263.1811	245.5739	281.5666
[14]	279.8271	261.6625	304.908
[15]	295.2463	276.2026	333.2632
[16]	309.3713	288.9481	361.9054
[17]	322.5876	300.6876	386.8173
[18]	334.3426	311.7083	408.9982
[19]	345.0103	321.6472	436.7071
[20]	355.0513	330.7993	461.9513

Table 6 shows that the median of new cases is predicted to decrease from time $t = 11$ to $t = 20$. In time $t = 17$ through $t = 20$ it is predicted no new case anymore. Assuming local government of City of Surabaya is doing better testing, contact tracing, and treatment, while individuals of this City are doing better prevention through using masks/face shields, washing hand with soaps more often, and keeping physical/social distance. Otherwise, new cases will be predicted to increase.

Table 7a shows that the estimated median of transmission rate tends to decrease from time $t = 1$ to $t = 10$. This occurs when the path from susceptible compartment (S) to infectious compartment (I) is cut. Susceptible individuals in S keep away from suspected and positive cases by physical/social distance, using masks, washing hands with soap, then the path will be cut, hence ,transmission rate tends to decrease. Otherwise, transmission rate will increase.

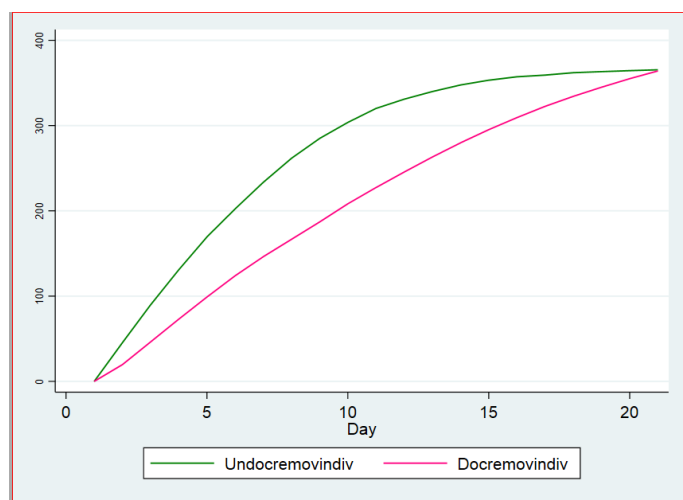


Figure 3. Estimated and predicted individuals who are removed.

Table 6. Predicted median of new cases.

	Predicted number of new cases (B)		
	Median and 95% CI		
	50%	2.50%	97.50%
[11]	6.371493	0.294303	124.7697
[12]	5.047099	0.189942	67.40418
[13]	3.473061	0.132681	59.4303
[14]	2.583275	0.07517	34.46808
[15]	1.873045	0.044087	34.42954
[16]	1.299923	0.014416	25.4757
[17]	0.976023	0.014426	20.39217
[18]	0.841563	0.006496	15.6601
[19]	0.594792	0.003743	13.09946
[20]	0.474509	0.001277	9.822414

Table 7a. Estimated median of transmission rate.

	Transmission rate (β)		
	Median and 95% CI		
	50%	2.50%	97.50%
[1]	2.04E-01	8.92E-02	0.443079
[2]	7.13E-02	1.78E-02	0.203424
[3]	2.63E-02	1.93E-03	0.130759
[4]	9.70E-03	2.17E-04	0.092862
[5]	3.57E-03	2.37E-05	0.062584
[6]	1.28E-03	2.31E-06	0.046432
[7]	4.68E-04	2.33E-07	0.033118
[8]	1.76E-04	1.98E-08	0.02529
[9]	6.19E-05	2.43E-09	0.019682
[10]	2.25E+00	5 2.169744e-1	0 0.01439943

Table 7b shows that the median of transmission rate is predicted to decrease from time $t=11$ to $t=20$. Assuming local government along with individuals in city of Surabaya hand in hand in implementing good prevention procedures in order to cut the path from susceptible compartment to Infectious compartment. Otherwise, transmission rate will be predicted to increase.

Table 7 shows that the estimated median of diagnosis rate tends to decrease from time $t=1$ to $t=10$. This rate represents how large individuals who are tested by PCR to be diagnosed as covid19. The number of individuals to be tested by PCR depends on the fund that is allocated by local government for providing PCR. Local government is targeting certain number of individuals to be tested by PCR. Let say local government allocates 100 individuals/day to be tested

Table 7b. Predicted median of transmission rate.

	Predicted transmission rate (β)		
	Median and 95% CI		
	50%	2.50%	97.50%
[11]	8.22E-06	2.40E-11	0.011532
[12]	2.98E-06	3.07E-12	0.009185
[13]	1.05E-06	3.00E-13	0.007469
[14]	3.84E-07	2.76E-14	0.00482
[15]	1.39E-07	2.55E-15	0.00354
[16]	5.19E-08	2.14E-16	0.002426
[17]	1.85E-08	2.31E-17	0.001862
[18]	6.61E-09	2.44E-18	0.001559
[19]	2.67E-09	2.11E-19	0.001185
[20]	9.65E-10	2.34E-20	0.000801

Table 7. Estimated median of diagnosis rate.

	Diagnosis rate (γ)		
	Median and 95% CI		
	50%	2.50%	97.50%
[1]	0.228245	0.084666	0.467889
[2]	0.077498	0.026671	0.166508
[3]	0.058481	0.019667	0.127843
[4]	0.051428	0.017054	0.121083
[5]	0.007314	0.002334	0.018145
[6]	0.016277	0.005158	0.040874
[7]	0.092019	0.02837	0.235173
[8]	0.164216	0.046466	0.492607
[9]	0.007512	0.001878	0.037691
[10]	0.09316756	6 0.02280642	8 0.47677557

Table 8a. Estimated median of effective reproduction number.

	Effective reproduction number (R_{eff})		
	Median and 95% CI		
	50%	2.50%	97.50%
[1]	1.86895	8.01E-01	4.054896
[2]	0.653938	1.65E-01	1.887191
[3]	0.240844	1.70E-02	1.194
[4]	0.087793	2.01E-03	0.839635
[5]	0.032756	2.12E-04	0.573822
[6]	0.011623	2.20E-05	0.415424
[7]	0.004346	2.22E-06	0.301748
[8]	0.001604	1.84E-07	0.231623
[9]	0.000576	2.18E-08	0.178469
[10]	0.000204478	7 1.945144e-0	9 0.1320187

by PCR. It is assumed that the decreased diagnosis rate results in decreased number of positive cases.

Table 8a shows that the estimated median of effective reproduction number tends to decrease from time $t=1$ to $t=10$. This number is used by local government to evaluate how good the program of controlling covid 19. Assuming that the local government has done well concerning the three principle programs such as suspect testing, contact tracing, and covid 19 treatment; while individuals in the City have done well concerning prevention program such as using masks, washing hands with soaps, and doing physical/social distances then effective reproduction number decreases. Otherwise it increases. An example effective reproduction number $int=3$ is 0.24 or roughly $\frac{1}{4}$. It means four infected cases will produce one new case. Effective reproduction number in $t=10$ is 0.0002. It means 10,000 infected cases will produce two new cases. Local government should make judgment with small number of effective reproduction number to make new normal order.

Table 8a. Estimated median of effective reproduction number.

	Predicted effective reproduction number (Reff)		
	Median and 95% CI		
	50%	2.50%	97.50%
[11]	7.48E-05	2.21E-10	0.100629
[12]	2.69E-05	2.88E-11	0.079083
[13]	9.54E-06	2.56E-12	0.067055
[14]	3.39E-06	2.54E-13	0.041293
[15]	1.25E-06	2.25E-14	0.032096
[16]	4.84E-07	2.10E-15	0.022236
[17]	1.60E-07	2.26E-16	0.017352
[18]	6.06E-08	2.08E-17	0.015347
[19]	2.44E-08	1.83E-18	0.011217
[20]	8.54E-09	1.90E-19	0.007889

Table 8b shows that the median of effective reproduction number is predicted to decrease from time $t=11$ to $t=20$. In Table 8 as we have already discussed that effective reproduction number tends to decrease because the local government is assumed to follow the rule for controlling covid 19. If we assume that the local government still keeps the rule or does better, then we predict that effective reproduction number will decrease lower than time $t=1$ through $t=10$.

Conclusion and Recommendation

The estimated median of number of individuals in susceptible, infectious, and removal compartment tend to decrease as well as the number of individuals to be predicted.

The decrease of undocumented infectious and removal individuals covaries with the decrease of documented infectious and removal individuals respectively.

The median of number of new cases is predicted to increase.

Both estimated median of transmission rate and diagnosis rate tend to decrease, this decrease covaries each other. The estimated medians of effective reproduction number tend to decrease as well as the median of one

to be predicted. Quality of the model in this study depends on the assumptions to be used. It is assumed that local government of City of Surabaya keeps the rules of covid 19 control measures by testing, contact tracing and covid 19 treatments, while individuals in this City keep the rules of covid 19 prevention by using masks, washing hands with soaps, and implementing physical/social distances. As long as the definitive vaccine against covid 19 has not yet been given to individuals for prevention measure, the government is recommended to intensify testing, contact tracing, and treating covid19 patients properly, while individuals in the community intensify preventive actions by using masks, washing hands, and implementing physical/social distances properly.

References

1. Qifang Bi, Yongsheng Wu, Shujiang Mei and Chenfei Ye, et al. "Epidemiology and Transmission of COVID-19 in Shenzhen China: Analysis of 391 cases and 1,286 of their close contacts." *Med Rxiv Preprint* (2020)
2. Fen Yang, Lingling Yuan, Xuhui Tan and Cunrui Huang, et al. "Bayesian estimation of the effective reproduction number for pandemic influenza A H1N1 in Guangdong Province China." *Annals of Epidemiology* (2013) 23:301-306.
3. Ottar N Bjørnstad, Katriona Shea, Martin Krzywinski and Naomi Altman. "Modeling infectious epidemics." *Nature Methods* (2020)17:453-456.
4. Tianjian Zhou, Yuan Ji. "Semi parametric Bayesian Inference For The Transmission Dynamics Of Covid-19 With A State-Space model." (2020).
5. William Ogilvy Kermack and AG Mc Kendrick. "A Contribution to the Mathematical Theory of Epidemics." *Proc R Soc Lond* (1927)115:700-721.
6. Xianghu Zhang, Ke Wang. "Stochastic SIR model with jumps." *Appl Math Lett* (2013) 26: 867-874.

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