Predicting the Incident Cases of Emerging Infectious Disease Using a Bayesian Probability Model — China, February 2020

Yewu Zhang¹; Xiaofeng Wang¹; Yanfei Li¹; Siyu Wu¹; Ming Wan¹; Xuemei Su¹; Shigui Yang³; Hanjiang Lai⁴; Zhongwei Jia²; Jiaqi Ma^{1,#}

Summary

What is already known about this topic?

The exact number of incident cases of emerging infectious diseases on a daily basis is of great importance to the disease control and prevention, but it is not directly available from the current surveillance system in time.

What is added by this report?

In this study, a Bayesian statistical method was proposed to estimate the posterior parameters of the gamma probability distribution of the lag time between the onset date and the reporting time based on the surveillance data. And then the posterior parameters and corresponding cumulative gamma probability distribution were used to predict the actual number of new incident cases and the number of unreported cases per day. The proposed method was used for predicting COVID-19 incident cases from February 5 to February 26, 2020. The final results show that Bayesian probability model predictions based on data reported by February 28, 2020 are very close to those actually reported a month later.

What are the implications for public health practice?

This research provides a Bayesian statistical approach for early estimation of the actual number of cases of incidence based on surveillance data, which is of great value in the prevention and control practice of epidemics.

On January 20, 2020, the Chinese State Council added the latest coronavirus disease (COVID-19) to the Category B list of nationally notifiable diseases under Category A management (1-2). This means that if a case is diagnosed with COVID-19, it must be reported by the physician to the National Notifiable Disease Reporting System (NNDRS) within two hours. However, new cases reported every day from the surveillance system often contain cases that had onset on or before the reporting date, indicating a lag between onset and diagnosis. A more accurate assessment of incidence will allow public health professionals to better assess ongoing outbreaks, the pattern and scale of further epidemics, and the effectiveness of current prevention and control strategies, etc. (3). However, in the case of an emerging infectious diseases, such as COVID-19, the precise distribution of lag time between the dates of onset and the reporting times at the early stage of transmission was not known due to lack of historical data. Furthermore, all statistical incidence counts of each day are censored or truncated, i.e. up to the last reporting date, making it more difficult to estimate the precise distribution of delayed onset-reporting times. In this study, a Bayesian statistical method was proposed to estimate the exact probability distribution of the lag time between the onset date and the reporting time, and then to predict the actual number of new incident cases and the number of unreported cases per day.

All data for this study were obtained from NNDRS. The dataset for all suspected and confirmed cases of COVID-19 was downloaded from NNDRS around 24:00 on March 26, 2020, and the difference between date of onset and report time was used to calculate the lag time for each case. The lag time was assumed to follow the same probability distribution over a certain timeframe if the case diagnostic criteria, diagnostic methods, and other factors related to case reporting remained relatively stable. For this reason, new cases with onset dates between February 5 and February 28 were chosen for this analysis, and a training dataset (data reported as February 28 at 24:00) and a validation dataset (data reported as March 25 at 24:00) were built. Based on the distributions of time delays for other infectious diseases, particularly influenza cases in the last few years and the empirical distribution of time delays for all COVID-19 cases in NNDRS, the gamma probability distribution was selected to be validated with high priority in this study.

At first, the lag times were transformed using the base-2 logarithm. A random variable X that is gammadistributed with parameters α and β is denoted as follows:

$$X \sim \Gamma(\alpha, \beta) \equiv Gamma(\alpha, \beta).$$
(1)

Where α is a shape parameter and β is a scale parameter, also called a rate parameter. Its corresponding probability density function is as follows:

$$f(x;\alpha,\beta) = \frac{\beta^{\alpha} x^{\alpha-1} e^{-\beta x}}{\Gamma(\alpha)} \quad \text{for } x > 0 \quad \alpha,\beta > 0$$
 (2)

In our study, the logarithms of lag times were assumed to follow the truncated gamma distribution.

$$log_2(lagtime[i]) \sim \Gamma(\alpha, \beta) T(0, index[i]) \equiv Gamma(\alpha, \beta) T(0, index[i])$$
(3)

 $\alpha \sim uniform (9.0, 15) \tag{4}$

$$\beta \sim uniform(3.5, 6.5) \tag{5}$$

Where the α and β are the parameters to be estimated for the gamma distribution, the prior distributions of both parameters were set to follow the uniform distributions, *lagtime*[*i*] is the logarithm of the lag time of the i-th case, T stands for the truncated distribution, and *index*[*i*] is the logarithm of the time interval from the start date of the i-th case to the end of the study time frame (24:00 on February 28) of the training dataset.

The cumulative reported rate was calculated using the posterior parameters of gamma distribution estimated from the above-mentioned steps and the gamma cumulative distribution as follows.

$$rate[n] = F(n; \alpha, \beta) = \int_0^n f(u; \alpha, \beta) du$$
(6)

Where F and f are the gamma cumulative probability function and gamma probability density function, respectively. The number of unreported incident cases was assumed to follow the negative binomial distribution. The number of cases of incidence for each day were estimated as follows.

$$NR(n) \sim dnegbin(rate[n], reported[n])$$
 (7)

$$NN(n) = NR[n] + reported[n]$$
(8)

Where *n* is the number of days from date of onset to the 24:00 on February 28, the dnegbin is the negative binomial distribution, the rate[n] is the cumulative probability of reporting of *n* days, the *reported*[*n*] is the numbers of reported cases of n days calculated from the training data samples, and the NR[n] is the number of unreported cases, and the NN[n] is the predicted total number of cases. Since the number of new cases reported within two days was almost zero, we estimated the real incident cases from February 5 to February 26, 2020.

The validation data included all the cases with onset dates between February 5 and February 28, which were reported until 24:00 on March 26. The logarithm of the lag times in the validation dataset were fitted with gamma and other probability distribution models. The parameters of gamma probability distribution were estimated in both the training dataset using Bayesian Markov chain Monte Carlo (MCMC) method with truncated distribution and in the validation dataset using maximum likelihood method, respectively. The parameters of gamma probability distribution from training were used to estimate unreported and total number of incident cases every day. The estimated number of unreported and total incident cases were compared with the actual reported ones in the validation dataset. All statistical analyses were performed in R statistical software (version 4.0.3; The R Foundation for Statistical Computing, Vienna, Austria) (4), where Bayesian statistics were performed using the rjages (5) and runjags (6) packages, and general probability distribution fitting was performed using the fitdistrplus (7) package.

As of 24:00 on March 26, there were 24,551 cases in the validation dataset with onset dates between February 5 and February 28. The median lag time was 4.92 days, with 25 and 75 percentile values of 3.41 and 8.43 days, respectively. Gamma distribution was found to be the best fitted model compared to other probabilistic distribution models based on either the Akaike information criterion (AIC) or the Bayesian information criterion (BIC) values. The shape and rate parameters of the gamma distribution of the validation dataset were 8.56 and 3.54, respectively (Table 1).

The gamma probability distribution curves obtained for the two different methods as mentioned above are shown in Figure 1.

For the number of cases with an onset date between February 5 and February 26, the model predicted that there would be 2,112 unreported cases, while the actual reporting resulted in 1,665 newly reported cases as of March 26. The number of unreported cases predicted by the Bayesian model was 26.84% higher than the actual number of reported cases, with a ratio of 1:0.7881.

The model's prediction of the total number of incident cases per day and its trend from February 5 to February 26 were generally consistent with the actual incidence data reported as of March 26. However, the model's predictions after February 21 were significantly higher than the actual data reported as shown in Figure 2 and Table 2.

TABLE 1. The results of probability distribution fittings of the logarithm of the lagtimes based on validation dataset.

Distribution	LogLikelihood	Akaike information criterion(AIC)	Bayesian information criterion (BIC)
Gamma	-29,206.3	58,416.6	58,432.8
Burr	-29,705.1	59,416.3	59,440.6
Weibull	-29,757.8	59,519.6	59,535.8
Normal	-30,102.4	60,208.7	60,224.9
Pareto	-46,263.8	92,531.6	92,547.8



FIGURE 1. Comparison of the curves of the two gamma probability distributions of lag time based on the training and validation datasets.



FIGURE 2. Comparison of the predicted number of COVID-19 incident cases by the Bayesian probability model and the number actually reported.

DISCUSSION

We attempted to estimate the actual number of incident cases during an outbreak of a new infectious disease. We assumed that the probability distribution of the lag time between the start date and the reporting time was relatively stable. Based on data from reported cases, the gamma probability distribution, and the Bayesian statistical method for truncated data, the parameters for the gamma probability distribution of lag times were inferred. Using the cumulative reporting rates calculated from the gamma probability distribution of lag time, the number of reported cases, the negative binomial distribution, the numbers of both unreported and total incident cases, and their 95% CI, were predicted. The results showed that the Bayesian probability model predictions based on data reported by February 28, 2020 were similar to those actually reported 1 month later.

The parameters of distributions for the lag reporting time were obtained using two different methods and datasets. The first was inferred from the truncated training dataset using the Bayesian MCMC-based parameter estimation method, and the second was estimated from the actual data reported 1 month later using the maximum likelihood estimation (MLE) method. It was found that both the parameters and the curve patterns of the two distribution models were consistent with the Kullback–Leibler divergence 0.048.

As for the number of unreported cases, the Bayesian model prediction was 26.84% higher than the actual reported number, but the absolute difference was only 1.82% of the total number of cases reported, i.e. $(2,112-1,665) / 24,551 \times 100\%$. The total number of incident cases reported by March 26 were within the 95% CI of total number of incident cases predicted by the model.

The number of actual daily reported cases was highly congruous with the predicted number of cases and associated trends between February 5 and 20. However, the model predicted an increase from February 20 to 23, and subsequent reports verified an anomalous increase in the number of cases on February 21 that could have changed the direction and magnitude of the model's predictions and partly explain why the model's predictions were higher than the actual reported number. In addition, the model forecast trend for the period of February 23–26 was consistent with the actual report, although the predictions were higher than the subsequent report.

Limitations in the application of this model may

TABLE 2. Comparison	of the	predicted	number	of	COVID-19	incident	cases	by	the	Bayesian	probability	model	and	the
number actually reporte	ed.													

Date of onset	Number of incident cases reported by February 28	Number of unreported cases and 95% CI predicted by model	Total number of incident cases and the 95% Cl predicted by model	Number of incident cases reported by March 26	Cases reported from February 29 to March 26
2020/2/5	2,529	24(15–34)	2,553(2,544–2,563)	2,559	30
2020/2/6	2,072	22(13–32)	2,094(2,085–2,104)	2,087	15
2020/2/7	2,007	25(16–36)	2,032(2,023-2,043)	2,036	29
2020/2/8	1,814	26(17–37)	1,840(1,831–1,851)	1,833	19
2020/2/9	1,438	24(15–35)	1,462(1,453–1,473)	1,453	15
2020/2/10	1,830	36(25–49)	1,866(1,855–1,879)	1,875	45
2020/2/11	1,343	31(21–43)	1,374(1,364–1,386)	1,366	23
2020/2/12	1,465	41(28–54)	1,506(1,493–1,519)	1,495	30
2020/2/13	1,265	42(30–56)	1,307(1,295–1,321)	1,313	48
2020/2/14	1,027	42(30–55)	1,069(1,057–1,082)	1,111	84
2020/2/15	816	41(29–54)	857(845–870)	868	52
2020/2/16	739	46(33–61)	785(772–800)	787	48
2020/2/17	642	50(37–65)	692(679–707)	893	251
2020/2/18	813	81(64–101)	894(877–914)	851	38
2020/2/19	616	81(63–100)	697(679–716)	684	68
2020/2/20	384	68(51–86)	452(435–470)	461	77
2020/2/21	365	89(70–111)	454(435–476)	570	205
2020/2/22	379	134(109–161)	513(488–540)	452	73
2020/2/23	371	201(167–238)	572(538–609)	445	74
2020/2/24	282	259(217–305)	541(499–587)	350	68
2020/2/25	181	335(277–398)	516(458–579)	347	166
2020/2/26	74	408(314–517)	482(388–591)	281	207
Total	22,452	2,106(1,641–2,628)	24,558(24,093–25,080)	24,117	1,665

arise primarily from the assumption that the lag time distribution from onset to report is relatively stable. This is difficult to achieve in the process of preventing and controlling new infectious diseases. In the case of COVID-19, for example, changes in diagnostic or reporting criteria, improvements in diagnostic techniques, and increased prevention and control efforts may change the interval between onset and reporting, e.g. the use of square-cabin hospitals and the widespread availability of nucleic acid testing have significantly reduced the lag time interval. Second, a small number of cases may have an impact on the stability of the model parameter estimates. Therefore, it is recommended to use national or province-wide pooled data for model parameter estimates at the early stages of an epidemic for new infectious diseases.

In conclusion, this study provides an early prediction method for the actual number of incident cases based on data from the surveillance report, which is of great importance to epidemic prevention and control personnel in estimating the actual occurrence of the epidemic, predicting trends, and assessing the effectiveness of prevention and control measures.

Fundings: This study was supported by grants from the Key Joint Project for Data Center of the National Natural Science Foundation of China and Guangdong Provincial Government (U1611264), The National Major Scientific and Technological Special Project for HIV/AIDS and Hepatitis В prevention 2017ZX10303401-005, (2013ZX10004218-006, 2018ZX10201002), and the National Key Research Development and Program of China (2016YFC1200703).

doi: 10.46234/ccdcw2020.267

[#] Corresponding author: Jiaqi Ma, majq@chinacdc.cn.

¹ Center for Public Health Surveillance and Information Service, Chinese Center for Disease Control and Prevention, Beijing, China; ² School of Public Health, Peking University, Beijing, China; ³ State Key Laboratory for Diagnosis and Treatment of Infectious Diseases, Collaborative Innovation Center for Diagnosis and Treatment of

Infectious Diseases, The First Affiliated Hospital, College of Medicine, Zhejiang University, Hangzhou, Zhejiang, China; ⁴ Sun Yat-sen University, Guangzhou, Guangdong, China.

Submitted: December 03, 2020; Accepted: December 22, 2020

REFERENCES

- The Novel Coronavirus Pneumonia Emergency Response Epidemiology Team. The epidemiological characteristics of an outbreak of 2019 novel coronavirus diseases (COVID-19) — China, 2020. China CDC Wkly 2020;2(8):113 – 22. http://dx.doi.org/10.46234/ccdcw2020.032.
- WHO-China Joint Mission Members. Report of the WHO-China joint mission on coronavirus disease 2019 (COVID-19). http://covid-19.

chinadaily.com.cn/a/202003/30/WS5e81bcc0a31012821728315f.html. [2020-12-1].

- Rothman KJ, Greenland S, Lash TL. Modern epidemiology. 3rd ed. Philadelphia: Lippincott Williams & Wilkins. 2008. http://opac.calis. edu.cn/opac/check.do.
- 4. R Core Team. R: a language and environment for statistical computing. Vienna, Austria: R Foundation for Statistical Computing. 2020.
- Plummer M. Bayesian graphical models using MCMC. https://cran.rproject.org/web/packages/rjags/rjags.pdf. [2020-12-1].
- 6. Denwood MJ. Runjags: an R package providing interface utilities, model templates, parallel computing methods and additional distributions for MCMC models in JAGS. J Stat Softw 2016;71(9):1 – 25. http://dx.doi.org/10.18637/jss.v071.i09.
- Delignette-Muller ML, Dutang C. fitdistrplus: an R package for fitting distributions. J Stat Softw 2015;64(4):1 – 34. http://dx.doi.org/10.18637/ jss.v064.i04.