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REVIEW

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The basic reproduction number of SARS-CoV-2 in Wuhan is about to die out, how about the rest of the World?

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Summary

The virologically confirmed cases of a new coronavirus disease (COVID-19) in the world are rapidly increasing, leading epidemiologists and mathematicians to construct transmission models that aim to predict the future course of the current pandemic. The transmissibility of a virus is measured by the basic reproduction number (R_0), which measures the average number of new cases generated per typical infectious case. This review highlights the articles reporting rigorous estimates and determinants of COVID-19 R_0 for the most affected areas. Moreover, the mean of all estimated R_0 with median and interquartile range is calculated. According to these articles, the basic reproduction number of the virus epicentre Wuhan has now declined below the important threshold value of 1.0 since the disease emerged. Ongoing modelling will inform the transmission rates seen in the new epicentres outside of China, including Italy, Iran and South Korea.

KEYWORDS

the basic reproduction number (R_0), COVID-19, pandemic, SARA-CoV-2

1 | INTRODUCTION

The appearance of a new infectious disease is always a complex phenomenon, especially if it becomes pandemic. Globally, infections by SARS-CoV-2 that causes COVID-19 are rapidly growing, and they extended very fast with transmission chains throughout the world since the first case was detected in the Chinese city of Wuhan in December 2019. Imported cases and secondary cases have been reported in more than 1 436 198 confirmed cases globally.[1] On 11 March 2020, the World Health Organization (WHO) declared COVID-19 a pandemic and called for governments to take urgent actions to change the course of the outbreak.[2]

An infectious disease outbreak can be characterised by its basic reproductive number, known as R_0, which represents the average number of secondary infections generated by each infected person. If R_0 is equal to 1 or less, this indicates that the number of secondary cases will decrease over time and, eventually, the outbreak will peter out. If it is higher than one, the outbreak is expected to increasingly transmit infection to secondary cases, indicating the need to use control measures to limit its extension.

As governments and WHO work together to treat infected people and control the spread of the hitherto unknown SARS-CoV-2, several mathematical modelling groups in the China, United Kingdom, Europe and United States have rushed to estimate the basic reproduction number and predict the spread of SARS-CoV-2 infections and cases of COVID-19 disease. These groups used different approaches as illustrated in Table 1 with estimates hovering between 0.32 and 6.47 in Tables 2 and 3. These differences are not surprising, as there is uncertainty about many of the factors go into estimating R_0, such as different methods for modelling, different variables considered, and various estimation procedures.

In this review, we summarise the basic reproduction number R_0 of multiple published articles for pandemic COVID-19. Screening from 1 January 2020 to 6 April 2020, yielded 50 articles which estimated the basic reproduction number for COVID-19. Most of these studies concern China, some of them are from Italy, Iran, South Korea, Singapore, Japan, Israel and Brazil.

Initially, the WHO estimated the basic reproduction number for COVID-19 between 1.4 and 2.5, as declared in the statement regarding the outbreak of SARS-CoV-2, dated 23 January 2020.[52]

TABLE 1 Description of R_0 estimation methods with list of used abbreviations

ID	Methods	Method description with its abbreviation
1	SIR model[3-9]	It is a compartmental model in epidemiology that divides an infectious disease into three parts: **S**usceptible-**I**nfectious-**R**emoved (**SIR**), which is represented as a dynamical system in mathematics.
2	SEIR model[10-15]	**S**usceptible-**E**xposed-**I**nfectious-**R**emoved (**SEIR**) model which is another type of compartmental model which differs from SIR model by adding exposed part that represents the delay time of infected by virus and apparing symptoms (latency period).
3	MSIR model[16]	**M**aternally derived immunity-**S**usceptible-**I**nfectious-**R**emoved (**MSIR**) compartmental model that babies got protection from maternal antibodies.
4	MSEIR model[16]	It is the same as the model MSIR by joining Exposed component and becoming **M**aternally derived immunity-**S**usceptible-**E**xposed-**I**nfectious-**R**emoved (**MSEIR**).
5	SEIHR model[17,18]	Entering the Hospitalized class to SEIR model to obtain: **S**usceptible-**E**xposed-**I**nfectious-**H**ospitalized-**R**emoved (**SEIHR**).
6	SEIAR model[19]	A modified SEIR model with another movement class of compartmental model known as Asymptomatic, to get: **S**usceptible-**E**xposed-**I**nfectious-**A**symptomatic-**R**emoved (**SEIAR**).
7	SEQR model[20]	Incorporating the quarantine policy to a mathematical model and obtaining **S**usceptible-**E**xposed-**Q**uarantined-**R**emoved (**SEQR**) model.
8	SIRD model[21]	It is the SIR model that addresses the removed class with recovered and dead class to be **S**usceptible-**I**nfectious-**R**ecovered-**D**ead (**SIRD**) model.
9	SUQC model[22]	In this model, the infectious class of transmission model is separeted as un-quanrantined, quarantined and confirmed infected. The model is named **S**usceptible-**U**nquanrantined-**Q**uarantined-**C**onfirmed (**SUQC**) model.
10	SIQR model[23]	Its modified SIR model with considering quarantine, Susceptible-Infectious-Quarantined-Recovered (SIQR).
11	S $E_1E_2I_1I_2$HR time-dependent model[24]	It is a mathematical model focusing on the effects of medical resourceson transmission of COVID-19, stands for susceptible S (t), pre-stage exposed E_1(t), post-stage exposed E_2(t), infected with mild symptoms I_1(t), infected with serious symptoms I_2(t), hospitalized H(t) and recovered R(t) individuals.
12	SIDARTHE model[25]	It is a mathematical model that designed to show transsimssion between different stages in infectious disease. The abbrevation refers to: **S**usceptible-**I**nfected -**D**iagnosed-**A**iling-**R**ecognised-**T**hreatened-**H**ealed-**E**xtinct (**SIDARTHE**) model. In this model, being infected is dividing into 5 types as: undetected asymptomatic infected, detected asymptomatic infected, undetected symptomatic infected, detected symptomatic infected, and infected with detected life-threatening symptoms; whereas the removed class in compartmental model is classfied into recovered and dead.
13	Exponential growth[9,26-31]	It is a model that varies exponentially with the time by a specific rate.
14	Generalized growth model[32]	It is the growth model with two parameters: (r) represents the growth rate parameter with (p) that is the scaling growth rate parameter. Whenever $P = 1$, the generalized growth model returns to exponential growth and if $0 < P < 1$, then it is sub-exponential (polynomial) growth.
15	Logistic growth model[33]	It is a mathematical model that starts exponentially but it gets stabilized due to the capacity of population.
16	Bayesian estimation method[34]	It is a paramter estimation method that deals with paramters as random variables in a statistical model.
17	Fudan-CCDC model[12]	Developed model for the growth rate and CCDC stands for **C**hinese **C**enter for **D**isease **C**ontrol.
18	Least square based method[35]	It is a procedure to best fit data in statistics.
19	MCMC method[36]	**M**arkov **C**hain **M**onte **C**arlo (**MCMC**) method. In this technique, the posterior distribution of a desired parameter can be found.
20	Maximum Likelihood Estimation[30,37]	It is a method used to estimate parameters with knowing their distributions.
21	Phenomenological modelling[33]	Statistical method for modelling.

Additionally, several articles aimed to more precisely estimate the COVID-19 R_0. A review written by Liu et al[53] compared 12 published articles from the first January to the seventh of February 2020 which estimated for the R_0 for COVID-19 a range of values between 1.5 and 6.68.The authors of the review evaluated the mean and median of R_0 estimated by the 12 articles and they calculated a final mean and median value of R_0 for COVID-19 of 3.28 and 2.79, respectively, with an interquartile range (IQR) of 1.16. Zhao and Chen[22] developed a

TABLE 2 The basic reproduction number (R_0) from the published articles in Wuhan

ID	Researcher	Date	Location	Methods	Ro Est.	Ro (%95 CI)
1	Imai[38]	18 January 2020	Wuhan	Epidemic trajectories	2.60	(1.50-3.50)
2	Li et al[39]	22 January 2020	Wuhan	Exponential growth	2.20	(1.40-3.90)
3	Majumder et al[33]	26 January 2020	Wuhan	Phenomenological modelling	2.55	(2.00-3.10)
4	Park et al[40]	24 February 2020	Wuhan		2.20	
5	Read et al[11]	1-22 January 2020	Wuhan	SEIR	3.11	(2.39-4.13)
6	Shao et al[12]	16-February-20	Wuhan	SEIR model and Gamma distribution	3.12	
7	Shao et al[12]	16 February 20	Wuhan	Fudan-CCDC model	3.32	
8	Tuite et al[29]	24 January 20	Wuhan	Disease transmission model	2.30	
9	WHO[2]	22 January 20	Wuhan		1.95	(1.40-2.50)
10	Wu et al[41]	25 January 20	Wuhan	Markov Chain Monte Carlo methods	2.68	(2.47-2.86)
11	Zhang et al[19]	27 January 2020-10 February 2020	Wuhan	SEIAR model	2.88	
12	Zhao & Chen[22]	Before 30 January 2020	Wuhan	SUQC Model (Stage I)	4.70	
13	Zhao & Chen[22]	After 30 January 2020	Wuhan	SUQC Model (Stage II)	0.75	
14	Zhao & Chen[22]	After 13 Feb 2020	Wuhan	SUQC Model (Stage III)	0.47	
15	Wang et al[24]	23 January 2020	Wuhan	$SE_1E_2I_1I_2HR$ time-dependent model	2.71	

Susceptible, Un-quanrantined infected, quarantined infected, confirmed infected (SUQC) model to characterise the dynamics of COVID-19; suggesting that this model was more suitable for analysis and prediction than adopting existing epidemic models. Using daily confirmed cases, they applied the SUQC model to analyse the outbreak of COVID-19 in Wuhan, Hubei (excluding Wuhan), China (excluding Hubei) and four first-tier cities of China (only Wuhan considered in Table 1). They found that the reproduction number $R_0 > 1$ for all mentioned regions except Beijing, before 30 January 2020, was defined as stage I, $R_0 < 1$ for all regions after 30 January known as stage II, R_0 even smaller after 13th February called stage III. The article by Kucharski and colleagues[54] combined mathematical modelling with multiple datasets to calculate the median daily reproduction number in Wuhan, within 2 weeks of introducing travel restrictions; this crucial number began at 2.35 and declined to 1.05 throughout December 2019 and January 2020.

In order to understand a measure of transmissibility of the new disease, a lot of preprints and papers were published in the last months (Table 3), modelling various mathematical and statistical techniques, considering different compartment models in epidemiology and analysing its evolution in some countries. In this paper, we highlight the articles' estimates of COVID-19 R_0, explore the assumptions of the preditive methods of R_0 and illustare values of R_0 in differing geographic regions.

2 | METHODS

Along with reviewing articles and presenting their computing basic reproduction numbers, the mean; dividing the total of values by their number, of all R_0 that calculated by participating finding of it in each. The median, anothor measure of central is found for ungrouped ordering data which returns to the middle number among the whole values by Microsoft Excel 2010. A measure of variability, finally, named the interquartile range (IQR); is computed by dividing rank-ordered data into 4 parts and finding quarties as follows: Q_1 is the middle of first two parts and Q_3 is the middle of last two parts, while Q_2 is the median and it is the middle of all values as it is mentioned before. IQR, thus, is the difference between Q_3 and Q_1 also it found via Excel 2010.

LOESS method is utilised to sketch the curve of R_0 values in Wuhan with their range. LOESS stands for local regression; it is a nonparametric approach that fits multiple regressions in the local neighbourhood. LOESS can be particularly useful when the x-axis variables are bound within a range. It allows greater flexibility than traditional modelling tools because it can be used for situations in which we do not know which the parametric form of the regression surface is. A regression line (or curve) is fitted to the observations that fall within the window, the points closest to the centre of the window being weighted to have the most significant effect on the calculation of the regression line. It uses nearest neighbour algorithm. However, the predictor variable can just be indices from 1 to the number of observations in the absence of explanatory variables (as in Figure 1). A window of a specified width is placed over the data. The wider the window, the smoother the resulting loess curve. In other words, the size of the neighbourhood controls the degree of smoothing.[55]

The articles are estimated COVID-19 R_0 that were published from 1 January 2020 to 6 April 2020, searched in Science Direct, Google Scholar, PubMed, Scopus and MedRxiv, using the keywords "basic reprodation number," "R_0," "SARS-CoV-2," and "COVID-19," and yielded more than 60 articles. After screening relevancy, 50 studied met inclsion criteria, providing 103 R_0 estimaties. The reason for exclusion the rest of them due to have R_t, R_c and R_e instead of R_0 with couple of papers written in different languages. However, no research were excluded because of poor quality.

TABLE 3 The basic reproduction number (R_0) from the published articles

ID	Researcher	Date	Location	Methods	Ro Est.	Ro (%95 CI)
1	Anastassopoulou et al[21]	11-17 January 2020	Hubei, China	SIRD model	4.60	%90 CI (3.56-5.65)
2	Choi et al[17]	17 February 2020	Hubei, China	Deterministic mathematical model (SEIHR)	4.26	(4.24-4.29)
3	Choi et al[17]	17 February 2020	South Korea	Deterministic mathematical model (SEIHR)	0.55	(0.51-0.60)
4	Choi et al[17]	05 March 2020	NGP-South Korea	Deterministic mathematical model(SEIHR)	3.50	(3.47-3.54)
5	Di Lauro et al[42]	02 March 2020	World	Metapopulation model	2.50	
6	Hao[16]	17 February 2020	World	MSIR	1.50	
7	Hao[16]	17 February 2020	World	MSEIR	3.50	
8	Hellewell et al[43]	05 February 2020	World	Branching process model	2.50	(1.50–3.50)
9	Hossain et al[4]	13 March 2020	China	SIR (44 days quarantined)	1.40	
10	Hossain et al[4]	13 March 2020	China	SIR (24 days quarantine)	1.68	
11	Hossain et al[4]	13 March 2020	China	SIR (10 days quarantined)	2.92	
12	Imai et al[38]	18 January 2020	Wuhan	Computational modelling of potential epidemic trajectories	2.60	(1.50–3.50)
13	Jung et al[36]	08 December 2020	China	Developed exponential growth model and using MCMC techinqe.	2.10	(2.00-2.20)
14	Jung et al[36]	24 January 2020	China with exported cases	Developed exponential growth model and using MCMC techinqe.	3.20	(2.70-3.70)
15	Ku et al[7]	12 February 2020	Anhui, China	SIR after lockdown of Wuhan	3.89	(3.27-4.50)
16	Ku et al[7]	12 February 2020	Beijing, China	SIR after lockdown of Wuhan	3.30	(1.89-4.32)
17	Ku et al[7]	12 February 2020	Chongqing, China	SIR after lockdown of Wuhan	2.22	(1.26-3.14)
18	Ku et al[7]	12 February 2020	Fujian, China	SIR after lockdown of Wuhan	1.66	(0.72-2.87)
19	Ku et al[7]	12 February 2020	Gansu, China	SIR after lockdown of Wuhan	2.30	(1.02-3.96)
20	Ku et al[7]	12 February 2020	Henan, China	SIR after lockdown of Wuhan	3.70	(3.16-4.25)
21	Ku et al[7]	12 February 2020	Hubei, China	SIR after lockdown of Wuhan	4.65	(4.10-5.15)
22	Ku et al[7]	12 February 2020	Tianjin, China	SIR after lockdown of Wuhan	2.17	(1.23-3.54)
23	Ahmadi et al[44]	19 March 2020	Iran	Logistic growth model	4.70	
24	Kuniya[35]	15 January 2020-29 February 2020	Japan	Least-square-based method with Poisson noise	2.60	(2.40-2.80)
25	Lai et al[45]	11 February 2020	World		2.91	(2.24-3.58)
26	Li et al[39]	22 January 2020	Wuhan	Exponential growth	2.20	(1.40–3.90)
27	Lui et al[30]	22 January 2020	World	Exponential growth	2.90	(2.32-3.63)
28	Lui et al[30]	22 January 2020	World	Maximum Likelihood Estimation	2.92	(2.28-3.67)
29	Luo et al[13]	13 February 2020	China (except Hubei)	Develped SEIR model.	1.17	(1.15-1.16)
30	Luo et al[13]	13 February 2020	Hubei Province, China	Develped SEIR model.	1.49	(1.48-1.51)
31	Majumder et al[33]	26 January 2020	Wuhan	Phenomenological modeling	2.55	(2.00–3.10)
32	Meng et al[8]	12 February 2020	China (except Hubei)	Devloped SIR Model	2.81	(2.72-2.93)
33	Muniz-Rodriguez et al[32]	19-29 February 2020	Iran	Generalized growth model	3.60	(3.20-4.20)
34	Muniz-Rodriguez et al[32]	19-29 February 2020	Iran	Growth model with doubling times which is equal ln (2)/r where r is grwoth rate.	3.58	(1.29-8.46)
35	Park et al[40]	24 February 2020	Wuhan		2.20	
36	Read et al[11]	1-22 January 2020	Wuhan	SEIR	3.11	(2.39–4.13)
37	Remuzzi et al[27]	08 March 2020	Italy	Exponential growth	3.00	(2.76-3.25)
38	Riou et al[31]	18 January 2020	China	Computational modelling of potential epidemic trajectories	2.20	%90 CI (1.40-3.80)

TABLE 3 (Continued)

ID	Researcher	Date	Location	Methods	Ro Est.	Ro (%95 CI)
39	Rocklöv et al[14]	21 January 2020-19 February 2020	Diamond Princess Cruise Ship	SEIR Model	3.70	
40	Shao et al[12]	16 February 2020	Wuhan	SEIR model and Gamma distribution	3.12	
41	Shao et al[12]	16 February 2020	Hubei (without Wuhan)	SEIR model and Gamma distribution	3.01	
42	Shao et al[12]	16 February 2020	China (except Hubei)	SEIR model and Gamma distribution	3.04	
43	Shao et al[12]	16 February 2020	Beijing	SEIR model and Gamma distribution	3.25	
44	Shao et al[12]	16 February 2020	Shanghai	SEIR model and Gamma distribution	3.24	
45	Shao et al[12]	16 February 2020	Wuhan	Fudan-CCDC model	3.32	
46	Shao et al[12]	16 February 2020	Hubei (without Wuhan)	Fudan-CCDC model	3.37	
47	Shao et al[12]	16 February 2020	China (except Hubei)	Fudan-CCDC model	3.34	
48	Shao et al[12]	16 February 2020	Beijing	Fudan-CCDC model	3.27	
49	Shao et al[12]	16 February 2020	Shanghai	Fudan-CCDC model	3.31	
50	Shen et al[15]	12 December 2019	Hubei Province, China	By SEIR simulation	4.71	(4.50-4.92)
51	Shim et al[46]	26 February 2020	South Korea	Exponential growth	1.50	(1.40-1.60)
52	Sugishita et al[5]	14 January 2020-28 February 2020	Japan	SIR Model	2.50	(2.43-2.55)
53	Sugishita et al[5]	11 March 2020	Japan	%35 reduction of basic reproduction number (2.5), 0.65*2.5 = 1.625, by voluntary event cancellation	1.62	
54	Tang et al[10]	23 January 2020	China	SEIR Model	6.47	(5.71-7.23)
55	Tang et al[18]	03 February 2020	Shaanxi Province, China	Developed SEIHR Model	1.69	
56	Tapiwa et al[34]	14 January 2020-27 February 2020	Tianjin, China	Bayesian estimation method	1.59	(1.42-1.78)
57	Tapiwa et al[34]	21 January 2020-26 February 2020	Singapore	Bayesian estimation method	1.27	(1.19-1.36)
58	Traini et al[3]	20 February 2020-11 March 2020	Italy	SIR Model	3.40	
59	Tuite et al[29]	24 January 2020	Wuhan	Disease transmission model	2.30	
60	Wang & You et al[47]	17 January 2020-8 February 2020	Hubei, China	Exponential growth	3.49	(3.42-3.58)
61	Wang & You et al[47]	17 January 2020-8 February 2020	Hubei, China	Exponential growth (After including control measure)	2.95	(2.86-3.03)
62	Wang et al[48]	27 February 2020	China		2.75	(2.00-3.50)
63	WHO[2]	22 January 2020	Wuhan		1.95	(1.40–2.50)
64	Wu et al[41]	25 January 2020	Wuhan	Markov Chain Monte Carlo methods	2.68	(2.47–2.86)
65	Wu et al[9]	10 February 2020	Henan, China &China (without Hubei)	SIR Model	2.44	
66	Wu et al[9]	16 February 2020	Hubei, China	SIR Model	6.27	
67	Yang et al[49]	26 January 2020	China	Transmission model	3.77	(3.51-4.05)
68	Zhang et al[19]	27 January 2020-10 February 2020	Wuhan	SEIAR model	2.88	
69	Zhang et al[37]	16 February 2020	Diamond Princess cruise ship	Maximum Likelihood Estimation	2.28	(2.06-2.52)
70	Zhao & Chen[22]	Before 30 January 2020	Wuhan	SUQC Model (Stage I)	4.71	
71	Zhao & Chen[22]	After 30 January 2020	Wuhan	SUQC Model (Stage II)	0.75	
72	Zhao & Chen[22]	After 13 February 2020	Wuhan	SUQC Model (Stage II)	0.48	
73	Zhao & Chen[22]	Before 30 January 2020	Hubei (without Wuhan)	SUQC Model (Stage I)	5.93	

(Continues)

TABLE 3 (Continued)

ID	Researcher	Date	Location	Methods	Ro Est.	Ro (%95 CI)
74	Zhao & Chen[22]	After 30 January 2020	Hubei (without Wuhan)	SUQC Model (Stage II)	0.60	
75	Zhao & Chen[22]	Before 30 Jan 2020	China (excluding Hubei)	SUQC Model (Stage I)	1.52	
76	Zhao & Chen[22]	After 30 January 2020	China (excluding Hubei)	SUQC Model (Stage II)	0.57	
77	Zhao & Chen[22]	Before 30 January 2020	Beijing	SUQC Model (Stage I)	0.88	
78	Zhao & Chen[22]	After 30 January 2020	Beijing	SUQC Model (Stage II)	0.52	
79	Zhao & Chen[22]	Before 30 January 2020	Shanghai	SUQC Model (Stage I)	3.62	
80	Zhao & Chen[22]	After 30 Jan 2020	Shanghai	SUQC Model (Stage II)	0.51	
81	Zhao & Chen[22]	Before 30 January 2020	Guangzhou	SUQC Model (Stage I)	1.20	
82	Zhao & Chen[22]	After 30 Jan 2020	Guangzhou	SUQC Model (Stage II)	0.50	
83	Zhao & Chen[22]	Before 30 January 2020	Shenzhen	SUQC Model (Stage I)	5.93	
84	Zhao & Chen[22]	After 30 January 2020	Shenzhen	SUQC Model (Stage II)	0.53	
85	Zhao et al[50]	10-24 January 2020	China	Exponential growth	2.24	(1.96-2.55)
86	Zhao et al[50]	10–24 January 2020	China	Exponential growth	3.58	(2.89-4.39)
87	Zhuang et al[26]	31 January 20	Republic of Korea	Exponential growth	2.60	(2.30-2.90)
88	Zhuang et al[26]	05 February 2020	Republic of Korea	Exponential growth	3.20	(2.90-3.50)
89	Zhuang et al[26]	05 February 2020	Italy	Exponential growth	2.60	(2.30–2.90)
90	Zhuang et al[26]	10 February 2020	Italy	Exponential growth	3.30	(3.00-3.60)
91	Giordano et al[25]	20 February 2020-12 March 2020	Italy	SIDARTHE model	2.38	
92	Giordano et al[25]	16 March 2020	Italy	SIDARTHE model (Public health care)	1.66	
93	Hamidouche et al[51]	21 March 2020	Algeria	Mathematical model (Alg-COVID-19)	2.55	
94	Klausner et al[28]	21 February 2020-20 March 2020	Israel	Exponential Growth	2.19	
95	Sahafizadeh et al[6]	28 February 2020	Iran	SIR Model	4.86	
96	Sahafizadeh et al[6]	7 March 2020	Iran	SIR Model	4.5	
97	Sahafizadeh et al[6]	14 March 2020	Iran	SIR Model	4.29	
98	Sahafizadeh et al[6]	18 March 2020	Iran	SIR Model	2.10	
99	Tian et al[20]	prior to 23 January 2020	Anhui, China	SEQR model (Phase I)	2.97	
100	Tian et al[20]	23 January 2020-6 February 2020	Anhui, China	SEQR model (Phase II)	0.86	
101	Tian et al[20]	after 6 February 2020	Anhui, China	SEQR model (Phase III)	0.57	
102	Wang et al[24]	23 January 2020-6 March 2020	Wuhan	S E1E2I1I2HR time-dependent model	2.71	
103	Crokidakis, N[23]	26 February 2020	Brazil	SIQR model	5.25	

3 | RESULTS

As recently announced by WHO, the virus epicentre Wuhan and its surrounding Hubei province have not recorded new cases of COVID-19,[56] which shows the researchers' prediction on R_0 are on track (Figure 1 and Table 1). Figure 1 presents different estimated values of the R_0 in Wuhan city, Hubei province in China in the period between 12 December and 1 March 2020. It shows different

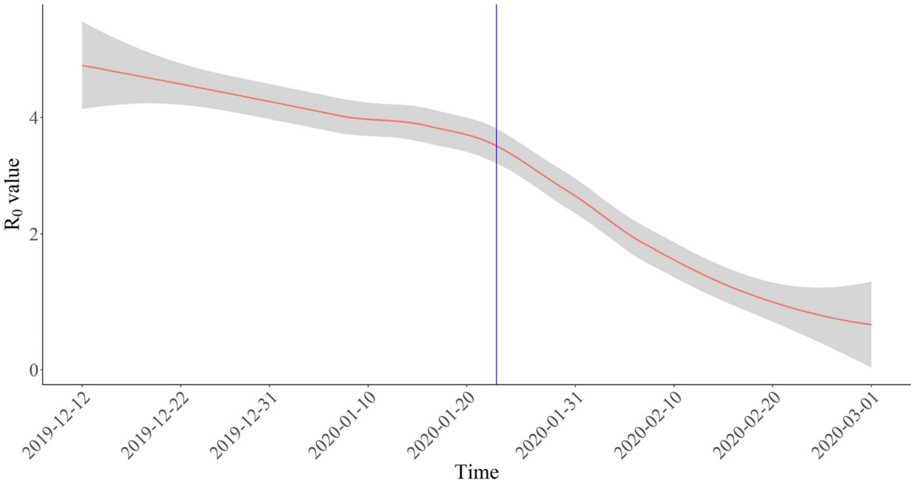

FIGURE 1 Smoothed curve showing the R_0 value in Wuhan city in the period from the 12th of December to the 1st of March 2020. The blue line marks travel restrictions starting on 23 January 2020, red line represents R_0, and grey shading represents 95% confidence intervals of the models estimate

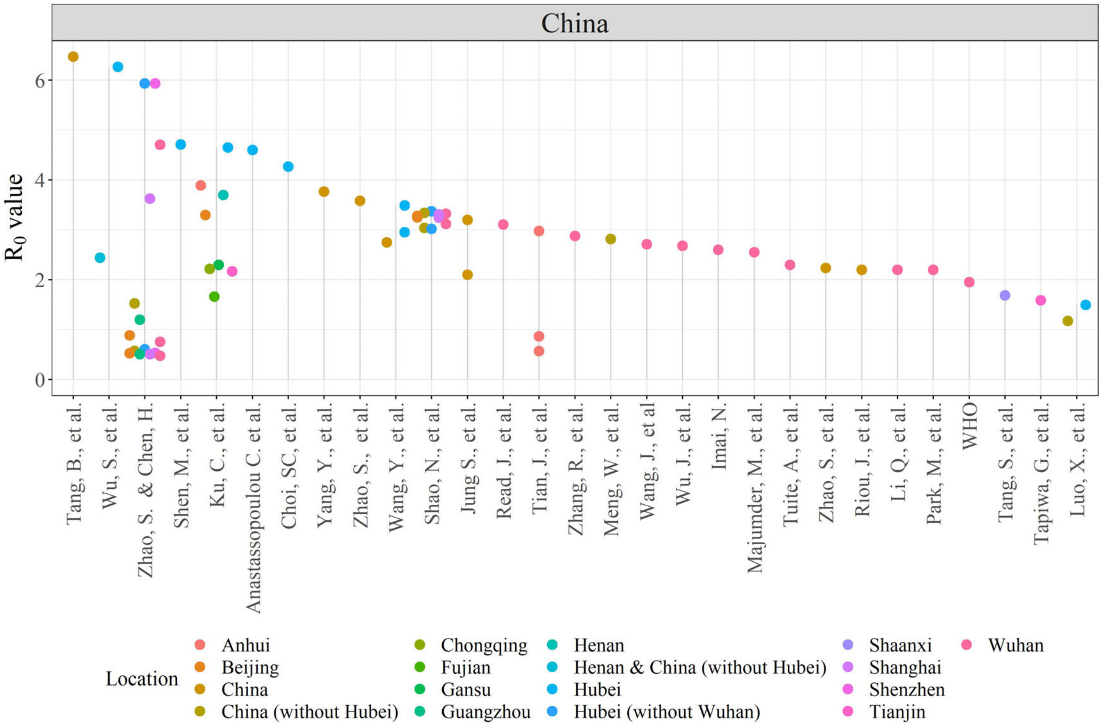

FIGURE 2 Dot chart showing the R_0 value estimated in the analysing papers coloured by location of interest in China

estimated values R_0 in Wuhan city through the papers reviewed sorted by chronological order; we can see how the reproduction rate smoothed with LOESS regression method shows a decreasing trend over time. It is worth noting that after the control measures were introduced in Wuhan on 23 January 2020,[52] shown by a vertical blue line in Figure 1, the R_0 started dropping down, based on the data in Table 1.

The dot chart in Figures 2 and 3 stratifies COVID-19 R_0 estimates in the period between the first of January to the 18th of March 2020 by authors in the analysed papers in Table 2. Figure 2 illustrates 68 R_0 values over 17 different regions in China. Tang et al[10] show the highest R_0 = 6.47 in China based on early outbreak data following the SEIR model, while Zhao and Chen[22] estimated the number to be 0.47, which is the lowest R_0 in the entire China through SUQC model, after 13 February 2020.

Figure 3 illustrates 35 R_0 values over 10 different countries. Brazil has the highest R_0 outside China, estimated more than 5.[23] In Iran, Muniz-Rodriguez et al[32] estimated a value of about 3.5. Zhuang et al,[26] Traini et al[3] and Remuzzi et al[27] estimated range of basic reproduction number from 2.6 to 3.4 in Italy. Kuniya[35] estimated R_0 to be 2.60 in Japan, Hamidouche et al[51] estimated R_0 to be 2.55 in Algeria, Klausner et al[28] estimatied R_0 to be 2.19 in Israel and Tapiwa et al,[34] estimated R_0 to be 1.27 in Singapore. Regarding the Republic of Korea, Choi et al[17] reported a value below 1 on 17 February 2020.

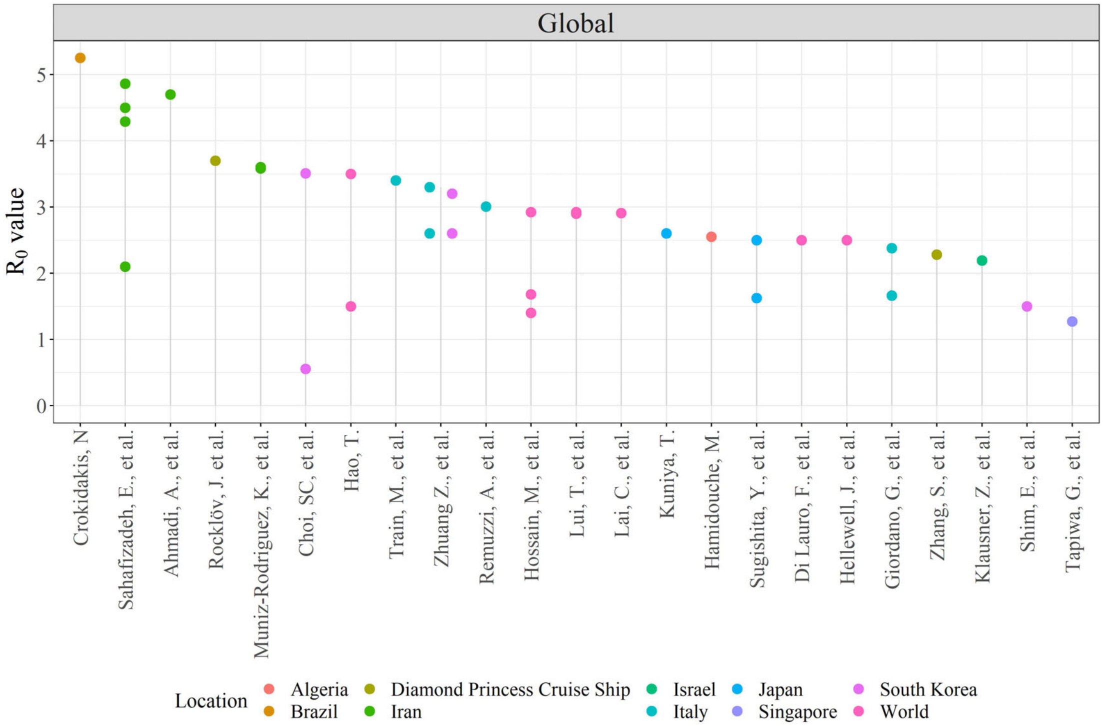

FIGURE 3 Dot chart showing the R_0 value estimated in the analysing papers coloured by location of interest in the global

With available articles regarding R_0 in Italy, Iran, South Korea, Singapore, Japan, Israel, Algeria, Brazil and China, we calculated the estimated mean R_0 = 2.71 for COVID-19, with median = 2.73 and interquartile range (IQR) = 1.73. This mean R_0 is very close to the upper boundary estimated by WHO but lower than the previous review by Liu et al.[53] However, the average R_0 between 2 and 3 seems to have stabilised in recent articles shown in Table 2.

As more results to mention, there are various methods utilised in estimating R_0 as listed in Table 1, some of them being special compartmental models which are mathematical models in epidemlogy, while others are statistical models and techniques; whereas some others are mix of mathematical and statistical approaches. More accurately, from 103 findings of R_0, 28 of them estimated it using statistical approaches, reported a range of 1.27 to 4.70 with an average 2.71, and 6 obtained of R_0 were found by mathematical models with statistics techniques estimated R_0 ranging from 3.01 to 4.71, with an average 3.39, the remaining 66 used mathematical models to estimate R_0 calculated a range from 0.47 to 6.47, with an average of 2.69.

4 | CONCLUSION

In the globalised world of today, the evolution of the outbreak and information on COVID-19 have become available at an unprecedented pace. Still, R_0 is not easy to calculate, especially there is much more to know about this new infection. The articles in Table 3, estimated different values of R_0, using results obtained from their respective models. The discrepancies observed among the studies of R_0 COVID-19 depend on a variety of assumptions in mathematical and statistical techniques, namely, the duration of contagiousness, the likelihood of infection per contact and the contact rate.[57] Due to variation in the assumptions and control strategies with time, the intervention measures, such as border control and quarantine in China, reduces R_0 from 2.92 to 1.40,[4] voluntary event cancellation in Japan reduced COVID-19 infectiousness by 35%,[5] social distancing and strict restriction on travelling in Iran during 4 weeks reduced from 4.86 to 2.1[6] and closing schools and remote working with some basic recommendations in Italy reduced R_0 from 2.38 to 1.66.[25] Moreover, the basic reproduction number is continuously modified during a pandemic by accurate assumptions introduced and becomes more reliable R_0 as more data and information come to light.

In this article, the potential transmission of the SARS-COV-2 virus results in COVID-19 that is expressible in basic reproduction number R_0 is summarised from 50 publishes with identifying their used approaches in finding it across the world. This review found that the estimated R_0 for COVID-19 in the case of Wuhan has decreased below the threshold of 1, and the estimated mean of R_0 is around 2.71 for COVID-19, with a median of 2.73 and IQR of 1.73. Our review coincides with a recent published article by Wang et al,[24] they estimated COVID-19 R_0 to be 2.71 in Wuhan. More reasonable match in their article showed that the epidemic gradually died out from calculating effective reproduction ratio, which is used to measure the daily reproduction number, started from 2.71 as of 23 January, has declined rapidly to below 1 since eighth February 2020 and dropped to 0.06 at 6 March 2020.

Along with new pandemic control measures introducing and treating procedures more mathematically desiged models are required to take account of all factors, in this point of view, the mathematical models are more recommended to be used. All in all, still R_0 is not easy to calculate especially there is much more to know about this novel virus.

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