Projection of Cumulative Coronavirus Disease 2019 (COVID-19) Case Growth with a Hierarchical Logistic Model

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ABSTRACT

Objective: To model cumulative coronavirus disease 2019 (COVID-19) case growth in various regions.

Methods: Publicly available time series data of cumulative COVID-19 cases form the John Hopkins University were used including reports up to 29 March 2020. A Bayesian hierarchical five-parameter logistic model was fit to observed data to estimate and project the cumulative number of cases in all regions and countries listed in the John Hopkins University dataset with at least one case. Projections for six regions (Hubei in China, South Korea, Germany, United States, Brazil, South Africa) were investigated in detail.

Findings: The proposed model approximated the observed numbers of COVID-19 cases very well and could be used to derive predictions. It provides information on the number of expected cases at the end of the current infection wave, on the time point when half of these cases are infected, and on the shape and pace of the long-term course of the epidemic. The average population model suggests that after two to three weeks of limited growth, a substantial case growth phase of five-to six weeks follows, before growth becomes limited again. Half of the expected number of cases is reported at about 40 days after the first documented case. However, regional variation of this course is considerable, as shown also by the six illustrative cases.

Conclusion: Although the model's predictive validity needs further confirmation, the presented approach is likely to offer valuable insights into understanding and managing COVID-19.

What was already known about the topic concerned

Projecting the number of cases affected by emerging infectious diseases like COVID-19 is challenging. Tradition epidemiological approaches, such as deterministic compartmental and stochastic transmission models, are increasingly used to predict COVID-19 case growth under certain circumstances. However, commonly these models allow confident conclusions only when it is known with sufficient certainty that the circumstances meet the modeling assumptions.

What new knowledge the manuscript contributes

A hierarchical logistic model is introduced to describe and predict the cumulative number of COVID-19 cases for each day after the first case was documented in every region with at least one case as of 29 March 2020. The presented model combines plausible theoretical assumptions with a data-driven approach and shows favorable properties both regarding accuracy and interpretability.

INTRODUCTION

The coronavirus disease 2019 (COVID-19) poses a global threat to public health. Obtaining valid epidemiological information on transmission dynamics, severity, susceptibility, and the effects of control measures has a high priority.[1,2] When knowledge on the epidemiological attributes of COVID-19 will have become available, powerful transmission models can be built, which are capable of providing valuable insights for health-care policy making.[3] For COVID-19, such models are being continuously developed and used to explain events retrospectively or to project the course events in a range of possible scenarios.[4–8]

In addition to modelling, day-to-day policy decision-making and public impression are guided by further sources of information. A major piece of data probably considered in most decisions and presented in almost every news broadcast is the country-level number of confirmed COVID-19 infections and deaths. These figures are publicly available on a daily basis, easy to communicate, and also recommended for surveillance by the World Health Organization.[9] Publicly available data have been shown to be able to provide epidemiological inferences of public health importance about the Middle East respiratory syndrome-related coronavirus.[10]

As long as epidemiological knowledge on COVID-19 is limited, traditional epidemiological modelling studies are obliged to make several assumptions (for example about the reproduction number and the incubation period of the infection). Thus, in countries, regions, and settings that are insufficiently covered by these assumptions or where it is unclear, which assumptions are reasonable, applicability of the model-based predictions remain largely uncertain. In addition, it is not always clear how the results of traditional modelling studies can be "expressed in the language of public health practice".[11(p35)]

In order to enrich existing modelling approaches, the objective of the present study was to create a descriptive mathematical model of the growth of the publicly reported cumulative number of confirmed COVID-19 cases in each region with at least one confirmed case as of 29 March 2020. In addition to description, the model was expected to be capable of providing predictions of the projected course of cumulative case numbers.

METHODS

Data source

Data on confirmed infections were abstracted from the 2019 Novel Coronavirus COVID-19 (2019-nCoV) Data Repository by Johns Hopkins University Center for Systems Science and Engineering (JHU CSSE).[12,13] In the repository, the number of confirmed infections are organized as time series data with daily records. For some countries, such as China, numbers for distinct provinces are reported, while for others, country-level data are provided. According to the JHU CSSE, the repository relies upon data from multiple sources, including the World Health Organization, the Chinese Center for Disease Control and Prevention, the Centers for Disease Control and Prevention, and the European Centre for Disease Prevention and Control.[13]

Data preprocessing

Data from the smallest possible geographical units defined by the JHU CSSE were used without change or aggregation (termed 'regions' in the following). Only regions with at least on confirmed case up to 29 March were considered. Instead of using calendar dates, time was scaled to start with the day of the first reported case in the database for each region, respectively. This means that day 1 can fall on different calendar dates for different countries. The reason for choosing this time scale was to unify the starting point for the cumulative case growth across different regions which may have been reached by COVID-19 several weeks apart.

Statistical model

The statistical approach was based on the three-parameter logistic model of self-limiting population growth, which has a long history in ecology.[14] The parameters of this model are the upper asymptote (the maximum size of the population), the inflection point (the point in time when growth begins to slow down), and the slope (the rapidity of reaching the upper asymptote) of the sigmoid logistic curve. Two parameters were added to the three-parameter model. First, modelling a lower asymptote was necessary to account for the fact that the first reported number of confirmed cases was more than one for several

regions. Second, an asymmetry parameter was introduced to be able to describe non-symmetrical developmental trajectories of case growth, which can be expected due to the presence of mitigation measures.[8] Among other applications, multi-parameter logistic models are frequently used in bioassay studies to analyze dose-response curves.[15,16]

Fitting the model to aggregated global data or to data from each region separately would be difficult, if possible at all, due to the low number of data points available for each analysis. Therefore, the model was formulated hierarchically, assuming that the parameters for each region stem from respective global distributions. The resulting random-effects model uses all available information effectively in a single framework but can still account for heterogeneity between regions.[17]

The applied hierarchical five-parameter logistic model was based on the five-parameter logistic equation reported in an overview by Gottschalk and Dunn[15] and defined the number of cumulative cases *Y* on day *t* in region *r* as:

$$Y_{tr} = \left(d_r + \frac{a_r - d_r}{\left(1+\left(\frac{t}{c_r}\right)^{b_r}\right)^{g_r}} \right) * e^{err_{tr}}, \text{ with}$$

$$\ln(a_r) \sim \text{dnorm}(theta_a, var_a),$$

$$b_r \sim \text{dnorm}(theta_b, var_b),$$

$$c_r \sim \text{dnorm}(theta_c, var_c),$$

$$\ln(d_r) \sim \text{dnorm}(theta_d, var_d),$$

$$g_r \sim \text{dnorm}(theta_g, var_g), \text{ and}$$

$$\ln(err_{tr}) \sim \text{dhalfnorm}(0, var_{err}),$$

where *a*, *b*, *c*, *d*, and *g* are the parameters of the logistic function, *err* is the error term, *ln* refers to the natural logarithm, *e* is Euler's number, *dnorm* refers to a normal distribution with mean *theta* and variance *var*, and *dhalfnorm* refers to a non-positive half-normal distribution. Due to model definition and restriction of the parameter space to reasonable values, *a*, *c*, *d*, and *g* were constrained to be positive,

and *b* was constrained to be negative.[15] The error term was assumed to follow a half-normal distribution because the true numbers can be higher, but not lower than the observed numbers.

Two additional parameters were calculated,[15] the time point of median infection *mi* as

$mi = c * \left(2^{1/g} - 1\right)^{1/b}$, and

the inflection point of the logistic curve *ip* as

$ip = c * (1/g)^{1/b}$.

A brief guidance to the interpretation of the model parameters is given in Table 1.

Table 1. Interpretation of model parameters

Abbreviation	Parameter	Interpretation
a	upper asymptote	maximum number of cases at the end of the infection wave, when further growth is negligible
b	slope	approximate growth rate or rapidity of reaching the maximum number of cases from the beginning of the exponential infection phase
c	position	approximate time point of the transition phase between the beginning of the exponential infection phase and the end of the infection wave
d	lower asymptote	number of cases at the beginning of the infection, here the first non-zero number in the dataset
g	asymmetry	parameter influencing the growth rate, accounting for possible improvement or worsening of the situation depending on the context
mi	median infection	time point, at which half of the expected maximum number of cases is infected
ip	inflection point	time point, at which the growth rate reaches its maximum and begins to slow down
theta	population mean	average of the respective parameter across regions that contributed data to the analysis
var	population variance	variance of the respective parameter across regions that contributed data to the analysis

Note: as the meaning of the parameters can strongly depend on the values of the other parameters and the characteristics of the analyzed data, the explanations should be considered approximate.

Assumptions

A major assumption of the model is that the form of the growth curve of the cumulative number of cases can be approximated by the five-parameter logistic curve described above. This has some theoretical plausibility due to resemblance to modelling self-limiting population growth in ecology and investigating pharmacological effects in receptors with multiple binding sites, but the presented approach should nevertheless be considered as empirical, descriptive, and data-driven to a substantial degree.

A second assumption refers to the normal distribution of the (logarithmic) parameters across regions (so called 'random-effects'). This is difficult to justify on a purely theoretical basis but has become common practice in the method of meta-analysis, aiming to combine findings from multiple studies on the same phenomenon.[17,18] In plain language, under consideration of the parameters of the logistic curve, the random-effects assumption reflects the belief that the course of events during COVID-19 is similar across different regions, although the regions may differ regarding the number of ultimately infected persons, the time and speed of the intensive case growth phase, as well as the timing and success of mitigation measures.

A consequence of the random-effects similarity assumption is that in case data are available only on a few time points for a region, information is borrowed from regions with more information on the estimated parameters. This equals to assuming the average case (adapted to the available data points) in case of missing information and enables prediction irrespective of the amount of available data, although uncertainty of predictions based on few data points is expected to be large.

Estimation

Computations were performed in a Bayesian framework due to the strengths of Bayesian approaches in case of substantial model complexity and presence of sparse data. Markov chain Monte Carlo sampling methods were utilized in *WinBUGS* version 1.4.3,[19] called from *R* version 3.6.1[20] with the package *R2WinBUGS*[21]. For estimation, the logarithm of both the number of cases and the logistic equation were used in order to being able to account for substantial variance in the scale of the case

numbers across regions, to simplify the modelling of the error term, and to improve convergence. The annotated *WinBUGS* code is provided in Supplement 1. Parameter estimates were given uninformative priors, and results were obtained from 60,000 iterations with a thinning rate of 60 after dropping 40,000 burn-in simulations. Three independent Markov chains were run with different starting values that were sampled randomly from a range of reasonable values derived from theoretical considerations and small-scale test runs. Convergence was checked visually and with Gelman and Rubin's convergence diagnostic.[22] Approximate global model fit was assessed by comparing the total standardized deviance with the number of data points. As a measure of uncertainty, 95% credible intervals were calculated for all parameters. Credible intervals describe the range of values within which a parameter falls with a 95% probability and correspond roughly to confidence intervals in frequentist statistics.

Region-specific analyses

In order to illustrate the application of the model, results from six geographically diverse regions are presented in detail: Hubei province in China, South Korea, Germany, United States, Brazil, and South Africa. These regions were selected a priori and thought to represent regions in different phases of the COVID-19 pandemic. The growth of the number of confirmed COVID-19 cases was modelled for 120 days from the first case, thus, it included both retrospective description and prospective prediction of the number of cases affected by COVID-19.

RESULTS

Data availability

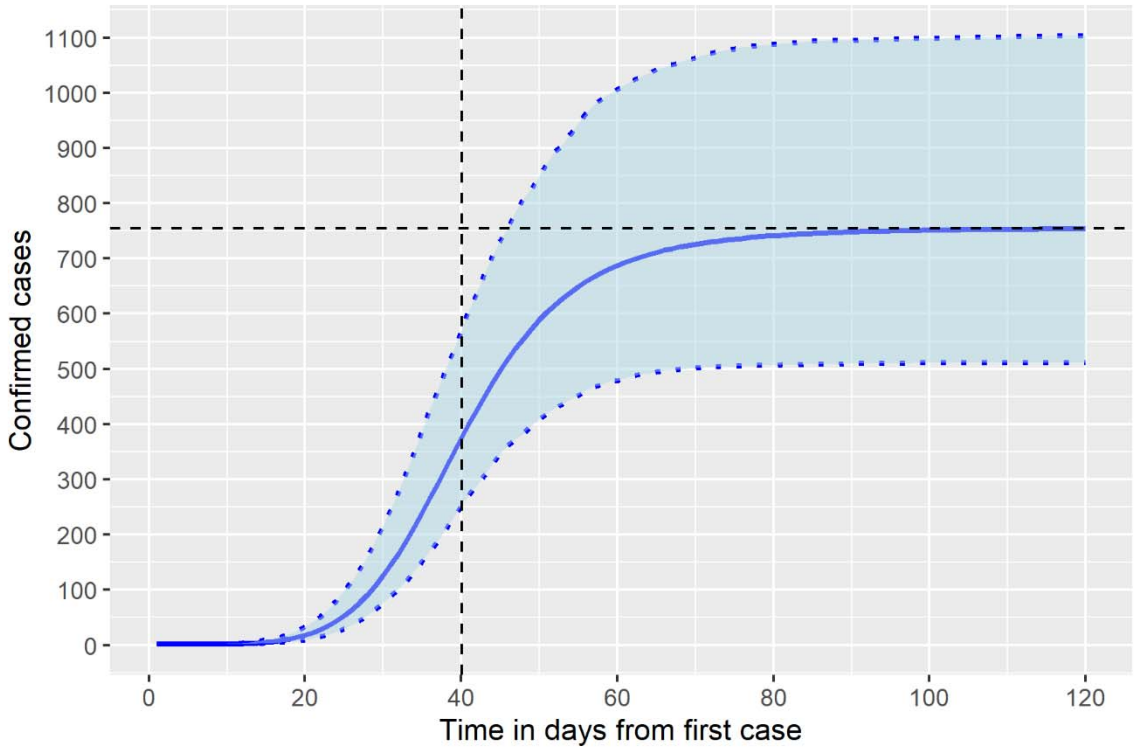
As of 30 March 2020, data on confirmed COVID-19 cases were listed from 253 regions in the JHU CSSE database. Two listed regions did not report any cases and were excluded from analysis (labelled as 'Canada, Diamond Princess' and 'Canada, Recovered', possibly erroneous entries). The first entry was from 22 January and the last from 29 March, resulting in maximum 68 days of observation,

although most regions reported the first conformed case after 22 January and therefore contributed less than 68 days of data. A total of 7901 data points form 251 regions (at average, 31.48 days per region) were included in the analysis.

Population findings

Globally, the model fit the data excellently (total residual deviance 7897.65, which is essentially identical to the number of data points). The population curve shows that it takes the disease an average of about 15 days after reporting the first case to enter a clearly noticeable growth phase and the maximum number of cases is reached approximately after 100 days, although uncertainty is considerable (Figure 1).

Figure 1. Estimated average population curve of COVID-19 case growth



Legend: The solid blue line shows the estimated mean number of cumulative cases. The blue dotted line shows the 95% credible interval of the estimates. The black horizontal dashed line shows the mean of the estimated number of total cases. The black vertical dashed line shows the estimated time point of mean infection, i.e., when half of the estimated number of total cases is infected.

Population parameters are listed in Table 2. The upper asymptote (parameter *a*) shows substantial variance across regions as expected due to various population sizes. The slope of the population curve (parameter *b*) is substantially different from one and varies widely across regions. Both the average median infection (parameter *mi*) and the average inflection point (parameter *ip*) indicate the highest growth rate at around 40±5 days after the first case, but the position of the curve on the time axis (parameter *c*, the major determinant of *mi* and *ip*) shows a very large variation across regions. The mean and variance of the lower asymptote (parameter *d*) indicates that for most, even if not for all, regions, the first reported number of cases is close to one. The asymmetry of the population curve (parameter *g*) is noticeable and varies considerably across regions.

Table 2. Population parameter estimates

Abbreviation	Parameter	Estimate	95% CI
theta.a	population mean of the upper asymptote	754.96	511.85 to 1106.55
var.(log)a	variance of the logarithmic upper asymptote	5.95	4.74 to 7.35
theta.b	population mean of the slope	-5.97	-6.67 to -5.33
var.b	variance of the slope	8.56	6.10 to 11.68
theta.c	population mean of the position	41.13	36.73 to 45.74
var.c	variance of the position	601.01	464.86 to 787.24
theta.d	population mean of the lower asymptote	1.64	1.53 to 1.75
var.(log)d	variance of the logarithmic lower asymptote	0.28	0.23 to 0.33
theta.g	population mean of the asymmetry coefficient	0.89	0.78 to 1.02
var.g	variance of the asymmetry coefficient	0.26	0.18 to 0.37
theta.mi	population mean of point of median infection	40.05	35.56 to 44.53
theta.ip	population mean of the inflection point	40.36	35.93 to 44.85

Note: see Table 1 for an explanation of the parameters; CI=credible interval

Case studies

The estimated case growth in province Hubei, China, presumably the origin of COVID-19, displays a rapid increase soon after the first reported case, with half of the expected number of approximately 69,400 cases infected after three weeks (Figure 2A). The projected numbers correspond well to the observed values, with the exception of the consequences of the substantial change in reporting

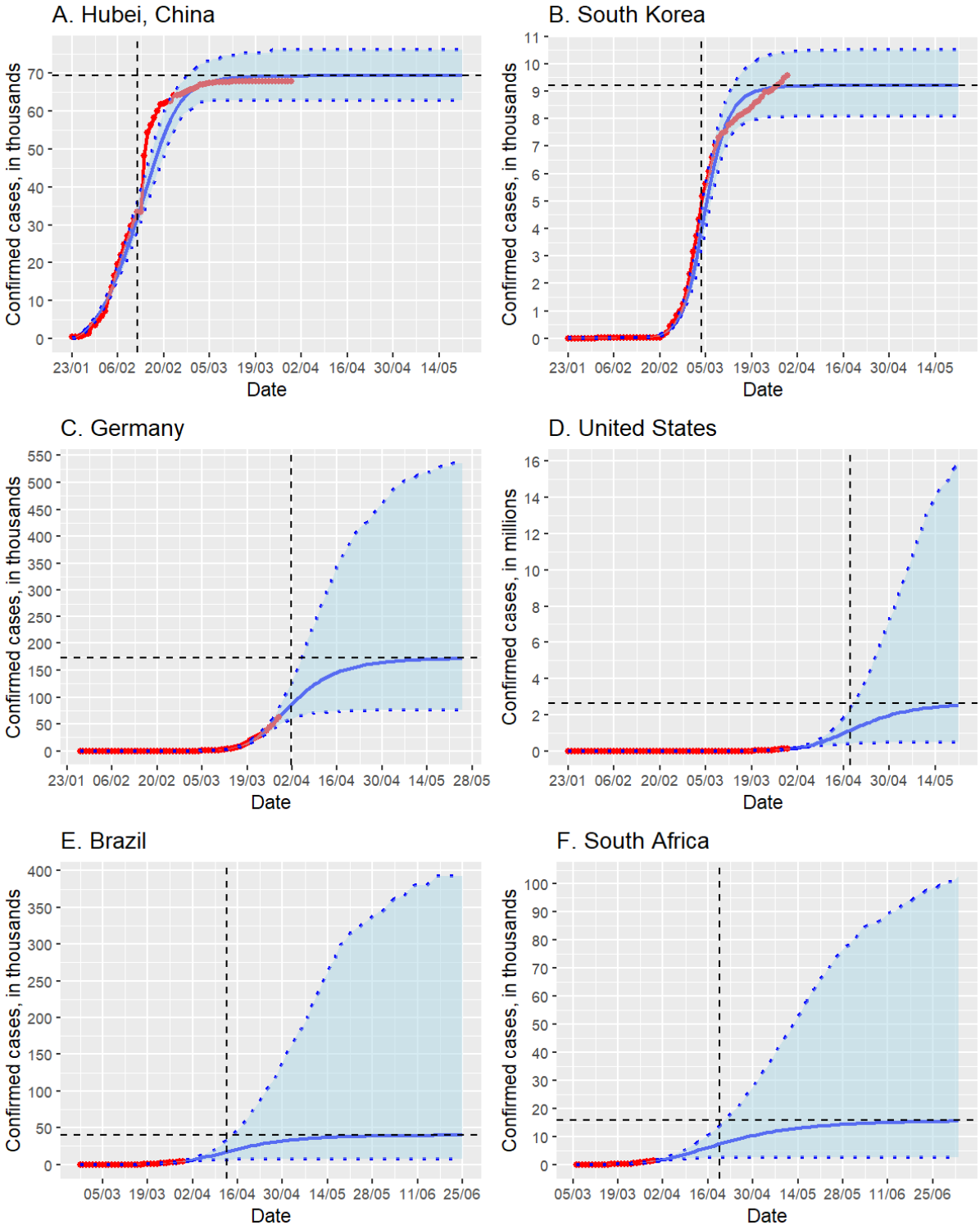
practices on 13 February 2020, from when clinically diagnosed infections were included in addition to laboratory-confirmed cases. But even under these circumstances, the credible interval of the projection encompasses the observed growth about one week later and on.

In South Korea, the estimated growth curve remained flat for about four weeks before rising steeply and reaching half of the expected number of 9,200 confirmed cases after six weeks (Figure 2B). The form of the average projected curve deviates from the observed trajectory of cases, but as of the end of March 2020, observations fall clearly within the credible interval.

In Germany, the initial phase of limited growth endured more than six weeks (Figure 2C). According to the model, half of the expected number of cases is likely to be confirmed after around nine and a half weeks (in the first days of April), and a total of 172,000 cases (with substantial uncertainty) are estimated to be reported approximately by the end of week sixteen. Model estimates agree very well with observed values so far.

The model estimates suggest that, as of the end of March 2020, the Unites States (Figure 2D), Brazil (Figure 2E), and South Africa (Figure (2F) are two to three weeks away from reaching the point of median infection. Due to the relatively early phase of the disease spread in these regions (according to the reported cases), the upper bound of the credible interval of the maximum number of expected cases is around six to nine times higher than the estimated mean, indicating a very high degree of uncertainty of the projections.

Figure 2. Estimated and observed COVID-19 case growth in six regions



Legend: The red points connected with a red solid line show the reported number of confirmed cases. The solid blue line shows the estimated mean number of cumulative cases. The blue dotted line shows the 95% credible interval of the estimates. The black horizontal dashed line shows the mean of the estimated number of total cases. The black vertical dashed line shows the estimated time point of mean infection, i.e., when half of the estimated number of total cases is infected.

Estimated parameters for each region are listed in Table 3 and can be used to plot the mean number of estimated cases for any time point using the five-parameter logistic formula[15].

Table 3. Parameters for each region

Region (country, province, area)	a	b	c	d	g	median infection	inflection point
Afghanistan	937.45	-5.63	51.4	1.05	1.03	52.45	52.31
Albania	719.13	-3.87	50.52	1.45	0.59	41.26	45.23
Algeria	2833.18	-6.64	62.82	1.08	0.57	55.24	57.99
Andorra	225.96	-10.9	17.88	1.05	2.15	19.56	19.2
Angola	130.92	-4.43	50.23	1.47	0.63	42.22	45.44
Antigua and Barbuda	396.98	-6.53	38.16	1.06	1.02	38.11	38.22
Argentina	5324.25	-6.08	55.63	1.14	0.59	48.79	51.25
Armenia	344.83	-7.01	18.17	1.06	1.75	20.19	19.73
Australia, Australian Capital Territory	1036.85	-5.29	33.85	1.15	0.87	32.77	33.21
Australia, New South Wales	11708.56	-8.84	73.19	3.79	1.37	77.16	76.21
Australia, Northern Territory	411.37	-6.19	40.2	1.05	1.08	41.01	40.87
Australia, Queensland	8057.25	-9.25	77.84	4.03	1.11	79.41	79.04
Australia, South Australia	5750.22	-8.87	78.64	1.98	1.14	80.56	80.1
Australia, Tasmania	728.22	-5.92	56.67	1.11	0.72	52.57	54.06
Australia, Victoria	10979.96	-9.39	80.92	3.29	1.21	83.51	82.87
Australia, Western Australia	3261.93	-6.2	50	2.1	0.85	48.62	49.18
Austria	68507.64	-7.01	56.02	2.56	0.68	51.9	53.33
Azerbaijan	1277.71	-5.84	59.1	3.47	0.61	51.8	54.44
Bahamas	144.12	-4.56	50.99	1.16	0.64	43.88	46.85
Bahrain	995.75	-5.48	62.23	1.33	0.33	40.99	49.88
Bangladesh	96.47	-5.19	22.04	2.66	1	21.7	21.91
Barbados	275.27	-4.16	46.69	1.54	0.61	39.16	42.29
Belarus	368.74	-4.65	44.33	1.1	0.75	41.3	42.53
Belgium	9016.66	-6.93	42.11	1.03	2.61	50.14	48.48
Belize	371.23	-6.26	49.64	1.5	0.98	48.72	49.25
Benin	71.49	-4.33	47.63	1.23	0.68	41.01	43.7
Bhutan	145.52	-5.83	56.82	1.07	0.94	56.3	56.63
Bolivia	372.35	-4.64	54.25	1.67	0.52	42.95	47.45
Bosnia and Herzegovina	2450.15	-5.6	47.71	2.13	0.71	44.1	45.47
Brazil	40236.59	-7.37	49.24	1.37	0.82	47.65	48.2
Brunei	105.37	-3.36	6.24	1.15	1.35	7.07	6.86
Bulgaria	933.22	-4.28	28.72	2.86	0.84	26.92	27.71
Burkina Faso	609.71	-4.73	22.91	1.39	1.01	23.18	23.19
Burma	213.89	-4.69	45.93	4.16	0.73	4197.62	355.83
Cabo Verde	70.38	-4.12	50.56	1.61	0.6	45.15	46.63
Cambodia	170.91	-12.99	54.81	1.03	1.8	58.19	57.43
Cameroon	302.45	-6.18	24.92	1.53	1.12	25.63	25.49
Canada, Alberta	4449.45	-5.76	50.54	1.36	0.58	43.54	46.11

Canada, British Columbia	11763.83	-9.02	84.47	2.64	0.98	84.53	84.57
Canada, Grand Princess	12.91	-7.32	5.91	1.82	1.11	5.87	5.9
Canada, Manitoba	386.29	-4.72	52.07	2.93	0.52	40.89	45.33
Canada, New Brunswick	491.34	-4.29	45.82	1.09	0.8	42.67	43.98
Canada, Newfoundland and Labrador	4089.51	-5.9	34.91	1.46	0.83	33.7	34.18
Canada, Northwest Territories	521.07	-7.13	47.94	1.12	1.11	48.46	48.46
Canada, Nova Scotia	1065.37	-4.71	48.08	3.46	0.54	38.63	42.34
Canada, Ontario	15553.19	-8.82	85.87	2.38	1.07	87.23	86.93
Canada, Prince Edward Island	420.9	-5.17	48.51	1.16	0.76	45.26	46.52
Canada, Quebec	57050.07	-8.05	48.55	1.33	0.95	48.5	48.57
Canada, Saskatchewan	1745.91	-4.94	42.24	1.71	0.71	38.15	39.72
Canada, Yukon	457.11	-6.44	45.53	3.06	0.98	44.15	44.86
Central African Republic	4.84	-7.18	15.72	1.12	1.04	14.52	15.12
Chad	101.48	-5.06	48.05	1.13	0.74	43.05	45.06
Chile	18059.36	-6.23	46.2	1.73	0.76	43.81	44.67
China, Anhui	1011.47	-4.8	17.08	1.21	0.59	14.21	15.25
China, Beijing	525.19	-3.23	26.37	2.12	0.51	17.96	21.11
China, Chongqing	590.03	-3.89	15.06	2.07	0.61	11.99	13.12
China, Fujian	309.35	-2.91	11.27	1.23	1.02	11.3	11.33
China, Gansu	129.4	-2.07	13.45	1.51	1.27	15.61	15.05
China, Guangdong	1394.41	-6.42	20.7	2.98	0.29	13.79	16.79
China, Guangxi	265.24	-3.29	15.59	1.42	0.73	13.07	14.01
China, Guizhou	148.46	-6.77	20.08	1.7	0.46	16.34	17.78
China, Hainan	173.31	-5.25	20.16	1.92	0.38	13.73	16.42
China, Hebei	330.51	-2.91	13.38	1.14	1.29	15	14.59
China, Heilongjiang	491.96	-6.56	21.58	1.65	0.38	16.39	18.48
China, Henan	1302.34	-3.65	13.3	3.12	0.99	13.15	13.25
China, Hong Kong	507.26	-7.99	93.74	2.35	0.23	63.35	77.36
China, Hubei	69366.25	-8.3	31.33	2.11	0.24	21.96	26.25
China, Hunan	1032.4	-5.25	16.05	1.99	0.51	12.79	14.01
China, Inner Mongolia	81.92	-3.6	18.12	1.29	0.57	13.31	15.19
China, Jiangsu	647.58	-4.37	16.44	1.23	0.67	14.17	14.96
China, Jiangxi	947.04	-6.06	17.9	1.6	0.45	14.21	15.62
China, Jilin	94.33	-6.79	18.84	1.57	0.39	14.51	16.25
China, Liaoning	128.05	-3.16	12.01	1.55	0.88	11.03	11.41
China, Macau	30.41	-1.07	49.6	1.21	1.24	88.96	75.21
China, Ningxia	77.58	-3.14	15.38	1.15	0.99	15.11	15.25
China, Qinghai	18.22	-3.66	8.02	1.2	0.8	6.92	7.36
China, Shaanxi	251.78	-4.22	14.77	1.71	0.58	11.58	12.78
China, Shandong	837.11	-2.36	17.28	1.42	1.08	18.07	17.89
China, Shanghai	375.39	-4.64	19.56	2.67	0.41	13.31	15.8
China, Shanxi	135.37	-3.46	11.34	1.11	1.17	12.01	11.86
China, Sichuan	553.53	-3.96	17.33	2.35	0.62	13.97	15.19
China, Tianjin	144.58	-4.88	22.52	2.25	0.43	15.83	18.54
China, Tibet	9.58	-8.25	79.5	1.05	1.36	1165.46	156.72
China, Xinjiang	78.75	-5.11	20.64	1.6	0.49	15.76	17.69
China, Yunnan	175.44	-3.46	10.58	1.24	0.99	10.47	10.54

China, Zhejiang	1228.03	-6.12	16.67	2.55	0.36	12.1	13.96
Colombia	3584.17	-5.4	35.14	1.09	0.85	34.01	34.5
Congo (Brazzaville)	101.4	-4.36	53.55	1.16	0.66	46.55	49.34
Congo (Kinshasa)	71.71	-6.4	12.99	1.41	1.06	13.11	13.11
Costa Rica	1709.75	-5.34	52.6	1.19	0.54	43.6	47
Cote d'Ivoire	3037.27	-6.03	37	1.08	0.88	36.17	36.52
Croatia	8248.09	-6.89	57.12	4.6	0.79	54.9	55.71
Cuba	2110.54	-5.5	41.23	3.18	0.8	39.13	39.99
Cyprus	957.74	-4.15	44.69	1.56	0.68	39.28	41.52
Czechia	17242.5	-6.41	48.9	3.5	0.65	44.34	45.98
Denmark	1861.45	-6.99	19.07	1.97	0.89	18.67	18.81
Denmark, Faroe Islands	154.2	-7.67	16.04	1.32	1.19	16.55	16.43
Denmark, Greenland	244.9	-4.72	49.95	1.15	0.69	44.5	46.58
Diamond Princess	732.54	-6.52	19.26	2.18	0.19	10.21	14.58
Djibouti	98.24	-6.4	19.35	1.1	1.08	19.31	19.4
Dominica	115.24	-5.54	29.36	1.27	0.79	25.38	27.01
Dominican Republic	17100.98	-7.53	47.09	1.63	0.92	46.73	46.9
Ecuador	2790.95	-8.63	24.82	10.58	1.2	25.62	25.43
Egypt	562.22	-6.54	30.97	1.05	1.87	35.11	34.17
El Salvador	858.91	-4.86	44.75	1.23	0.7	40.46	42.12
Equatorial Guinea	21.02	-4.82	18.27	1.14	0.95	15.4	16.56
Eritrea	992.89	-5.4	38.26	1.11	0.84	36.28	37.09
Estonia	879.46	-6.44	27.68	1.13	0.85	26.86	27.16
Eswatini	309.39	-5.67	40.35	1.08	0.92	39.17	39.66
Ethiopia	47.94	-3.81	29.48	1.14	0.84	25.88	27.56
Fiji	24.8	-5.39	28.63	1.15	0.84	25.21	26.63
Finland	2179.69	-9.52	56.11	1.04	1.4	59	58.31
France	72632.93	-8.95	61.6	6.66	1.56	66	64.97
France, French Guiana	159.02	-4.56	45.29	4.29	0.77	41.35	43.03
France, French Polynesia	42.58	-6.42	13.73	2.7	1.07	13.6	13.7
France, Guadeloupe	85.8	-4.32	7.36	1.17	1.15	7.72	7.65
France, Martinique	523.01	-4.54	39.07	1.77	0.86	37.9	38.5
France, Mayotte	896.46	-5.19	34.92	1.13	0.8	32.69	33.6
France, New Caledonia	164	-4.23	43.35	1.59	0.62	35.49	38.74
France, Reunion	2102.14	-5.69	47.73	1.28	0.58	41.06	43.54
France, Saint Barthelemy	88.02	-5.69	55.15	1.76	0.91	53.99	54.53
France, St Martin	150.5	-5.23	45.74	1.86	0.85	43.61	44.5
Gabon	7.52	-7.91	9.01	1.09	1.21	9.14	9.12
Gambia	145.4	-4.9	48.92	1.11	0.81	45.95	47.2
Georgia	265.42	-3.94	43.15	1.13	0.91	42.44	42.96
Germany	172469.22	-9.5	63.5	9.91	1.37	66.67	65.91
Ghana	3300.82	-5.29	39.8	4.26	0.78	37.5	38.39
Greece	4178.8	-5.05	47.22	1.92	0.77	44.51	45.6
Grenada	107.7	-7.55	20.23	1.11	1.14	19.67	19.93
Guatemala	76.46	-3.67	21.47	1.14	0.91	20.29	20.89
Guinea	1025.82	-5.85	46.34	1.08	0.93	45.96	46.21
Guinea-Bissau	485.86	-6.99	48.31	1.95	1.09	48.57	48.68
Guyana	7.66	-7.27	4.61	1.14	1.13	4.66	4.66
Haiti	144.14	-4.26	46.09	1.62	0.61	37.4	40.92

Holy See	493.96	-7.62	42.32	1.05	1.23	44.06	43.66
Honduras	1172.99	-5	47.48	1.7	0.72	43.37	44.96
Hungary	2685.56	-5.88	54.04	2	0.58	46.95	49.53
Iceland	4365.6	-5.73	56.78	1.13	0.55	48.02	51.35
India	3689.77	-7.2	63.54	2.45	1.49	68.71	67.49
Indonesia	6282.07	-5.21	40.21	1.76	0.9	39.87	40.14
Iran	44050.58	-5.04	33.53	2.47	0.8	31.8	32.4
Iraq	1348.82	-6.17	62.96	1.15	0.41	48.21	54.09
Ireland	22750.93	-6.65	54.34	1.19	0.67	50.07	51.58
Israel	24883.82	-7.68	64.2	1.18	0.66	59.34	61.01
Italy	107688.28	-5.01	40.52	2.33	2.81	52.42	49.93
Jamaica	84.59	-2.91	37.65	1.21	0.78	33.66	35.7
Japan	3378.05	-8.08	91.98	2.87	0.4	75.32	81.82
Jordan	196.51	-8.87	16.22	1.05	1.91	17.83	17.47
Kazakhstan	1373.96	-4.6	51.82	2.49	0.54	41.39	45.45
Kenya	562.88	-4.86	47.87	1.27	0.67	42.37	44.49
Korea, South	9205.68	-13.02	43.53	7.14	0.85	42.73	42.98
Kosovo	238.23	-3.15	40.03	1.91	0.42	Inf	Inf
Kuwait	482.97	-2.66	50.37	1.29	0.91	54.53	54.3
Kyrgyzstan	923.86	-4.46	41.84	1.98	0.63	35.46	37.98
Laos	212.94	-4.33	45.83	1.79	0.58	36.84	40.65
Latvia	1117.31	-5.01	33.47	1.07	1.01	34.44	34.31
Lebanon	1980.22	-5.24	56.99	1.08	0.8	54.35	55.43
Liberia	10.9	-4.05	39.87	1.29	0.68	32.59	35.81
Libya	2870.27	-7.24	16.21	1.11	1.14	16.5	16.46
Liechtenstein	59.85	-8.39	16.38	1.07	1.25	16.99	16.84
Lithuania	2593.93	-6.8	36.69	1.05	1.21	38.47	38.05
Luxembourg	3807.46	-7.26	28.36	1.13	1.05	28.83	28.74
Madagascar	357.16	-4.61	36.61	2.03	0.72	31.25	33.4
Malaysia	16605.2	-8.99	77.22	11.71	1.08	78.4	78.14
Maldives	27.3	-2.98	39.21	1.92	0.56	28.54	33.38
Mali	1237.38	-4.45	38.63	1.57	0.68	34.1	35.95
Malta	773.61	-4.38	39.96	2.49	0.77	36.96	38.19
Mauritania	172.05	-5.23	54.25	1.18	0.76	50.22	51.83
Mauritius	1294.73	-4.28	41.6	1.78	0.66	35.7	38.05
Mexico	4803.84	-6.49	40.67	3.98	1.02	41.12	41.07
Moldova	1997.8	-5.07	44.83	1.18	0.72	41.29	42.66
Monaco	228.84	-6.16	37.01	1.06	1.1	37.89	37.72
Mongolia	10.77	-8.26	9.08	1.08	1.35	9.48	9.39
Montenegro	753.06	-4.47	32.15	1.51	0.72	28.27	29.75
Morocco	4626.13	-6.43	45.91	1.3	0.85	44.54	45.08
Mozambique	125.26	-4.76	35.63	1.19	0.79	31.05	32.9
MS Zaandam	565.82	-6.59	45.48	1.93	1.06	50.44	47.69
Namibia	224.82	-4.93	50.2	1.93	0.75	45.93	47.6
Nepal	468.09	-11.51	81.01	1.02	1.88	87.14	85.78
Netherlands	49675.32	-6.54	52.17	1.18	0.6	46.27	48.37
Netherlands, Aruba	1551.66	-5.79	44.43	2.08	0.77	41.79	42.78
Netherlands, Curacao	69.87	-4.19	52.98	1.19	0.63	45.07	48.37

Netherlands, Sint Maarten	222.97	-4.84	49.28	1.19	0.69	44.16	46.19
New Zealand	11299.36	-7.78	48.36	2.21	1.01	48.79	48.73
Nicaragua	353.4	-5.36	47.07	1.46	0.82	43.89	45.21
Niger	712.45	-4.69	45.12	1.18	0.71	40.65	42.39
Nigeria	607.87	-7.55	36.52	1.17	1.22	37.97	37.63
North Macedonia	2733.24	-6.5	50.93	1.08	0.88	50.09	50.44
Norway	12395.72	-4.95	42.94	1.16	0.75	40.23	41.27
Oman	387.34	-6.11	68.52	2.5	0.42	52.68	58.96
Pakistan	2222.44	-8.3	28.44	3.54	1.04	28.71	28.66
Panama	5305.19	-5.41	49.25	1.25	0.51	39.97	43.43
Papua New Guinea	356.66	-7.64	54.16	1.07	1.19	55.61	55.36
Paraguay	354.91	-4.79	55.79	1.18	0.58	46.46	50.02
Peru	5407.45	-5.7	45.83	1.23	0.63	40.92	42.76
Philippines	1411.64	-9.37	51.61	2.46	1.93	56.58	55.48
Poland	12895.15	-5.66	49.43	1.22	0.67	44.92	46.55
Portugal	43766.88	-6.82	49.95	2.9	0.64	45.46	47.01
Qatar	533.57	-9.37	13.93	4.01	1.04	13.98	13.98
Romania	13783.17	-6.19	52.5	1.93	0.85	51.15	51.68
Russia	11172.4	-9.18	68.24	1.94	1.38	71.86	70.99
Rwanda	669.72	-4.28	46.41	1.16	0.67	40.31	42.71
Saint Kitts and Nevis	419.74	-6.86	48.15	1.96	1.11	48.72	48.78
Saint Lucia	468.45	-5.92	48.96	1.81	0.92	47.64	48.3
Saint Vincent and the Grenadines	257.52	-8.02	59.24	1.05	1.24	61.2	60.78
San Marino	329.79	-2.55	20.6	1.09	1.41	25.57	24.29
Saudi Arabia	9944	-6.29	49.37	1.17	0.68	45.37	46.85
Senegal	879.61	-5.09	43.3	2.55	0.92	42.57	42.94
Serbia	3504.02	-4.19	38	1.08	1	38.69	38.68
Seychelles	18.78	-3.64	36.63	1.64	0.65	29.94	33.04
Singapore	748.52	-8.57	93.3	1.53	0.23	64.96	78.09
Slovakia	439.36	-4	19.63	1.17	0.95	19.87	19.89
Slovenia	1202.2	-3.79	24.89	1.87	0.81	23.72	24.23
Somalia	1033.26	-6.52	42.61	1.07	1.02	42.88	42.91
South Africa	15893.99	-5.81	49.31	1.15	0.76	46.57	47.56
Spain	156055.04	-8.73	54.45	1.45	1.58	58.66	57.68
Sri Lanka	126.81	-17.28	50.35	1.03	2.35	53.57	52.91
Sudan	111.27	-4.86	54.85	1.17	0.73	50.05	51.93
Suriname	9.17	-7.27	9.73	1.09	1.17	9.82	9.83
Sweden	3329.69	-8.68	44.47	1.04	1.82	48.72	47.76
Switzerland	86174.51	-6.93	56.33	1.29	0.59	50.28	52.42
Syria	330.84	-5.04	40.91	1.15	0.79	36.94	38.5
Taiwan	213.48	-8.26	97.82	1.59	0.21	64.78	80.41
Tanzania	17.54	-4.47	9.81	1.18	0.92	8.89	9.27
Thailand	16216.94	-9.51	86.62	21.14	1.13	88.44	88.01
Timor-Leste	370.88	-7.44	51.25	1.08	1.16	52.42	52.23
Togo	25.56	-13.74	15.6	1.05	1.85	16.52	16.31
Trinidad and Tobago	144.07	-5.53	16.96	2.01	0.77	15.78	16.29
Tunisia	3115.09	-5.64	53.68	1.1	0.73	49.96	51.33
Turkey	52022.27	-6.71	26.03	1.45	0.89	25.59	25.77

Uganda	329.21	-4.72	29.84	1.16	0.84	26.44	27.84
Ukraine	6982.87	-7.27	40.4	1.06	1.04	40.96	40.86
United Arab Emirates	2110.77	-7.64	85.62	5.82	0.73	80.86	82.49
United Kingdom	179250.03	-9.55	74.22	4.63	1.08	75.33	75.07
United Kingdom, Anguilla	582.29	-6.68	46.39	1.91	1.04	45.93	46.31
United Kingdom, Bermuda	497.52	-4.73	46.66	1.72	0.64	40.31	42.82
United Kingdom, British Virgin Islands	577.97	-6.71	46.82	1.92	1.02	46.2	46.6
United Kingdom, Cayman Islands	81.65	-4.86	38.99	1.09	0.83	36.55	37.57
United Kingdom, Channel Islands	1428.48	-4.96	43.1	1.5	0.83	41.17	41.93
United Kingdom, Gibraltar	427.45	-6.09	33.97	1.05	1.25	35.77	35.36
United Kingdom, Isle of Man	32.16	-6.35	4.27	1.18	1.15	4.38	4.36
United Kingdom, Montserrat	582.38	-6.57	32.84	1.07	1.03	32.76	32.88
United Kingdom, Turks and Caicos Islands	617.06	-6.43	45.25	3.45	1	57.01	48.22
Uruguay	369.49	-3.78	12.32	2.53	1	11.94	12.14
US	2629030.61	-11.71	86.16	7.52	1.19	88.14	87.65
Uzbekistan	729.09	-3.47	41.97	1.24	0.77	38.1	39.88
Venezuela	306.92	-2.89	26.1	1.44	0.84	23.49	24.71
Vietnam	176.52	-8.41	96.62	1.92	0.25	69.08	81.5
West Bank and Gaza	192.39	-3.79	53.25	1.76	0.49	37.29	44.31
Zambia	1416.48	-5.91	30.66	1.88	0.95	30.28	30.49
Zimbabwe	243.76	-4.74	49.81	1.82	0.68	43.13	45.86

Note: the average number of cases *y* at day *t* after the first case can be estimated as $y(t)=d+((a-d)/(1+(t/c)^b)^g$, see text for further information.

DISCUSSION

Being able to monitor and predict the course of the COVID-19 pandemic in affected regions is essential for the development and implementation of effective countermeasures. Here, a model of cumulative case growth based on publicly reported data was used to identify trends which may be informative of the future trajectory of the disease. Having both theoretically plausible (mechanistic) and data-driven (empirical) components, the presented approach may be best categorized as a 'hybrid' model.[16]

At first glance, it might be surprising that the model provides predictions without considering explicitly which mitigation and control measures are taken by national and international institutions.

It seems to suggest a deterministic rather than a hypothetical future and thus appears to miss the flexibility of offering different scenarios. The projections can probably be best considered as the most likely course events, provided that the conditions remain sufficiently similar among regions. In a statistical sense, the model uses information from regions dealing with COVID-19 for a longer time period to inform predictions for regions that were reached by the disease later. Interestingly, this is quite the same strategy that public health decision-makers apply when they review and reflect on the experience made with COVID-19 in regions that were affected early. Thus, the mean estimates may be used as benchmarks for navigating the disease, a kind of beacon in heavy fog. At the same time, credible intervals around the point estimates are likely to encompass several possible courses of future events. Here, credible intervals may be seen less as a measure of statistical uncertainty due to randomness but rather as the bounds of different possible futures.

It is essential to point out the limitations of the model, which are strongly associated with its assumptions. First, the model does not intend to project the true number of infections. Both its input and its output relates to the reported number of confirmed infections, irrespective of the poproportion of unrecognized cases, which is likely to vary strongly across regions due to variable testing capacities and other factors. Second, predictions for regions that are extremely different from most other regions may be untrustworthy. Third, if the five-parameter logistic curve ceases to be able to approximate the cumulative case growth curve adequately, projections may be uninformative. This might be the case if abrupt changes in the conditions occur. For instance, the model may be of limited value if testing practices change radically (for example, if a country decides to test very broadly after a phase of narrowly focused testing), if case counting and reporting are restructured (as it was seen in the Hubei example), or if a new wave of infection is hitting. In summary, homogeneity of conditions both among regions and across different time points is likely to increase the accuracy of the projections. On the other hand, a substantial misfit between the model-based predictions and the observations may be considered an early indicator of extreme conditions or disruptive events which may go unnoticed otherwise.

The proposed model can be expanded to offer more flexibility. For example, one or more parameters can be manipulated artificially in simulation studies to model effects of health care policy measures. Furthermore, adding time-invariant covariates to explain parameters may reduce heterogeneity between regions and increase the precision of projections. For example, it may be hypothesized that the initial limited growth phase of the disease is longer in regions that were reached later by COVID-19 (an effect on parameter *c*) or that regions with larger economical resources may report more cases at average due to higher testing capacities (an effect on parameter *a*). Time-varying covariates may be used to model changes in testing practices, to model further infection waves, or to investigate the effects of mitigation measures.

Even if a thorough empirical evaluation of the proposed model will be possible only in the retrospect, the first impression presented here suggests that postulating a multi-parameter logistic trend in the cumulative number of COVID-19 cases that shares similarities across regions agrees well with publicly reported data. Thus, it may be informative for further research activities and support policy makers in monitoring and managing the disease.

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COMPETING INTERESTS

The author reports no competing interests.

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Supplement 1. Annotated WinBUGS code

```
# START
model{

  # loop through data points
  # n.data = number of data points
  for (i in 1:n.data){
    # likelihood with half-normally distributed errors
    # y = logarithmic number of cases
    y[i] ~ dnorm(mu[i], tau.e)I( ,mu[i])
      # hierarchical logistic model with parameters a, b, c, d, g
      # rid = region indicator
       mu[i] <- log(
      d[rid[i]]+
      (a[rid[i]]-d[rid[i]])/
      pow((1+(pow(time[i]/c[rid[i]], b[rid[i]]))), g[rid[i]]))
      # deviance contribution of each data point
      resdev[i] <- (y[i]-mu[i])*(y[i]-mu[i])*tau.e
    }

  # loop through regions
  # nr = number of regions
  for (k in 1:nr){
    # half-normal distributions for log(a), b, c, log(d), g
    log(a[k]) <- log.a[k]
    log.a[k] ~ dnorm(theta.a, tau.a)I(0, )
    b[k] ~ dnorm(theta.b, tau.b)I(, 0)
    c[k] ~ dnorm(theta.c, tau.c)I(0, )
    log(d[k]) <- log.d[k]
    log.d[k] ~ dnorm(theta.d, tau.d)I(0, )
    g[k] ~ dnorm(theta.g, tau.g)I(0, )
    # calculate median infection and inflection point
    mi[k] <- c[k]*pow((pow(2,(1/g[k]))-1),(1/b[k]))
    ip[k] <- c[k]*pow((1/g[k]),(1/b[k]))
    }

  # project values for selected regions
  # loop through selected regions
  # npreg = number of selected regions
  for (m in 1:npreg){
    # loop through time points
    # ptime = number of projected time points in days
    # pmu = projected values (logarithmic)
    for (t in 1:ptime){
      pmu[m,t] <- log(
      d[preg[m]]+
      (a[preg[m]]-d[preg[m]])/
      pow((1+(pow(t/c[preg[m]], b[preg[m]]))), g[preg[m]]))
      }
    }
```

```
# project population values
  # loop through time points
  for (t in 1:ptime){
    # popy = projected population values (logarithmic)
    popy[t] <- log(
    exp(theta.d)+
    (exp(theta.a)-exp(theta.d))/
    pow((1+(pow(t/theta.c, theta.b))), theta.g))
    }

  # calculate median infection and infection point for population
  popmi <- theta.c*pow((pow(2,(1/theta.g))-1),(1/theta.b))
  popip <- theta.c*pow((1/theta.g),(1/theta.b))

  # vague normal priors for population means
  theta.a ~ dnorm(0, 1.0E-4)
  theta.b ~ dnorm(0, 1.0E-4)
  theta.c ~ dnorm(0, 1.0E-4)
  theta.d ~ dnorm(0, 1.0E-4)
  theta.g ~ dnorm(0, 1.0E-4)

  # vague gamma priors for precision parameters
  tau.a ~ dgamma(0.001, 0.001)
  var.a <- 1/tau.a
  tau.b ~ dgamma(0.001, 0.001)
  var.b <- 1/tau.b
  tau.c ~ dgamma(0.001, 0.001)
  var.c <- 1/tau.c
  tau.d ~ dgamma(0.001, 0.001)
  var.d <- 1/tau.d
  tau.g ~ dgamma(0.001, 0.001)
  var.g <- 1/tau.g
  tau.e ~ dgamma(0.001, 0.001)
  var.e <- 1/tau.e

  # total residual deviance
  totresdev <- sum(resdev[])
  }
  # END
```