ORIGINAL RESEARCH

Towards the global equilibrium of COVID-19: Statistical analysis of country-level data

Mark Last ⓘ

Department of Software and Information Systems Engineering, Ben-Gurion University of the Negev, Beer-Sheva, Israel

Correspondence
Mark Last, Ben-Gurion University of the Negev, Beer-Sheva 84105, Israel.
Email: mlast@bgu.ac.il

Abstract

In our study, we explore the COVID-19 dynamics to test whether the virus has reached its equilibrium point and to identify the main factors explaining the current R and case fatality rate (CFR) variability across countries. We present a retrospective study of publicly available country-level data from 50 countries having the highest number of confirmed COVID–19 cases at the end of September 2021. The mean values of country-level moving averages of R and CFR went down respectively from 1.118 and 6.3% on June 30, 2020 to 1.083 and 3.6% on September 30, 2020 and to 1.015 and 1.8% by September 30, 2021. In parallel, the 10%–90% inter-percentile range of R and CFR moving averages decreased, respectively, from 0.288 and 13.3% on June 30, 2020, to 0.151 and 7.7% on September 30, 2020, and to 0.107 and 3.3% by September 30, 2021. The slow decrease in the country-level moving averages of R, approaching the level of 1.0 and accompanied by repeated outbreaks ("waves") in various countries, may indicate that COVID-19 has reached its point of stable endemic equilibrium. A regression analysis implies that only a prohibitively high level of herd immunity (about 63%) may stop the endemic by reaching a stable disease-free equilibrium. It also appears that fully vaccinating about 70% of a country's population should be sufficient for bringing the CFR close to the level of the seasonal flu (about 0.1%). Thus, while the currently available vaccines prove to be effective in reducing the mortality from the existing COVID-19 variants, they are unlikely to stop the spread of the virus in the foreseeable future. It is noteworthy that government measures restricting people's behavior (such as lockdowns) were not found to have statistically significant effects in the analyzed data.

KEYWORDS
case fatality rate, COVID-19, endemic stability, herd immunity, reproduction number

1 | INTRODUCTION

The first case of COVID-19 was reported in the Chinese city of Wuhan in December 2019. According to the Humanitarian Data Exchange website,[1] on January 22, 2020, there were 557 confirmed cases of COVID-19 in 29 different countries. On the same date, the global number of reported COVID-19 victims has reached 17, all of them from the Hubei province in China. Due to extensive international travel, the virus has spread quickly around the world, exceeding one million cases in 254 countries and territories by the end of March 2020 and 100,000 deaths 8 days later. The continuous response of national and regional authorities to the pandemic varied significantly from the near-absolute closure of international borders (e.g., Australia and New Zealand) and repeated lockdowns (e.g., New York City and Israel) to focusing on the protection of high-risk populations only (e.g., Sweden). As the pandemic continued to spread, each period of a steady increase in either the local or global amount of COVID-19 cases and deaths was always followed by an opposite, decreasing trend, frequently assumed to be a result of various intervention measures. However, in many cases, another, often a deadlier "wave" took place sometime later. Starting from December 2020, many countries, in the hope of "winning the pandemic," launched massive vaccination campaigns. By the end of July 2021, 1.14 billion people (14.6% of the world population) were fully vaccinated, while the global number of confirmed COVID-19 cases approached 200 million with about 4.2 million victims in 251 different countries and territories. While the primary focus of health care systems was on COVID-19, some other infectious diseases emerged in several countries, for example, the Zika virus in India.[2]

Considering the widespread travel restrictions at the time of the pandemic, the COVID-19-related death toll in a given country depends mainly on the following two factors: the average value of the effective (time-varying) reproduction number R_{eff}, or R_t, which represents the average number of cases an infected person has generated in the country's population, and the average case fatality rate (CFR), calculated as a percentage of death outcomes out of all cases confirmed during a specific period. Thus, we focus our study on the comparative analysis of these two parameters at the country level.

In a completely susceptible population, the effective reproduction number, R_{eff}, equals to the basic reproduction number R_0. R_0 is defined as the average number of secondary infections an infected person will cause in an "immunologically naive" population before he or she is effectively removed from that population as a result of recovery, hospitalization, quarantine, and so on.[3] The population is expected to reach "herd immunity" when the proportion of nonsusceptible ("immunologically experienced") individuals exceeds $1 - 1/R_0$.[4] A direct measurement of R_0 requires identifying the exact source of each infection case, which is rarely possible. However, the basic reproduction number can be estimated from the epidemiological data using a mathematical model such as susceptible–exposed–infected–recovered (SEIR).[5] The authors of Linka et al.[6] used the SEIR model and the reported COVID-19 cases in each one

of the 27 European Union countries for projecting the effective reproduction number $R(t)$ and predicting the epidemic evolution from May 10 to June 20, 2020. They evaluated three possible scenarios for their prediction period: a constant value of the effective reproduction number $R(t)$, a slow return to the basic reproduction number R_0 within 3 months, and a fast return to R_0 within 1 month. Their study shows that the severe mobility restrictions on air travel, driving, walking, and transit, which were implemented across Europe during March–May 2020, were highly correlated with R_0 in most countries, resulting in a drastic reduction of the population-weighted mean of the basic reproduction number from 4.22 (confidence interval [CI]: 2.53–5.91) to 0.67 (CI: 0.49–0.85).

In our previous work,[7] we explored the overall evolution of the basic reproduction number in Israel, Greece, Italy, and Sweden between March and July 2020 using the relationship between the daily reproduction numbers R_t, the basic reproduction number $R_0(t)$, and the cumulative percentage of confirmed cases p_t, which is shown in Equation (1).

$$R_t = R_0(t)(1 - p_t). \tag{1}$$

The authors of Cao et al.[8] tried to identify the main factors affecting the case fatality rates in 209 countries and territories based on the COVID-19 data downloaded from the Our World in Data website[9] on July 2, 2020 (including 10,445,656 confirmed COVID-19 cases and 511,030 deaths). They found the average value of CFR to be about 2%–3% worldwide. The factors directly associated with country-level CFR included the population size and the proportion of female smokers, whereas the open testing policies, cardiovascular disease death rate, and diabetes prevalence had an inverse association with CFR. The association of CFR with the strictness of anti-COVID-19 measures was not found statistically significant, except for higher-income countries with active testing policies.

These and many other studies focused on analyzing the data that was available during the first months of the pandemic, also known as the COVID-19 "first wave." At the end of 2020, several COVID-19 vaccines became available for the adult population. Massive vaccination campaigns were launched across the globe in the hope of reaching "disease-free equilibrium," where the majority of the population is immunized by a vaccine providing a long-term immunity with high efficacy while providing "herd immunity" protection to those who cannot be immunized. Given the actual values of R_0 and vaccine efficacy VE, one can calculate the herd immunity threshold of vaccinated individuals f_v using Equation (2)[10]:

$$f_v = \frac{1}{\text{VE}}\left(1 - \frac{1}{R_0}\right). \tag{2}$$

According to a previous forecast,[10] eliminating COVID-19 in the United States using vaccination alone would require immunizing at least 70% of the United States population by a vaccine of nearly 70% efficacy against infection. Otherwise, the epidemic will persist in the state of *endemic equilibrium*. The goal of our study is to explore the actual situation of COVID-19 dynamics until September 30, 2021 in

50 countries having the highest absolute number of confirmed COVID-19 cases according to Ritchie et al.[9] It is noteworthy that the "Top-50" list includes only three African countries (Morocco, South Africa, and Tunisia), possibly as a result of under reporting COVID-19 cases in that continent.[11] Data variation within populous countries, such as the United States, is beyond the scope of this study.

2 | MATERIALS AND METHODS

2.1 | Country-level data extraction

To explore the differences between countries, we have extracted the following 180-day moving averages of country-level factors from the Our World in Data COVID-19 data set[9]:

- Average of Delta: Average share of analyzed SARS-CoV-2 sequences that were the Delta variant. This variable is not available for some low-middle-income countries (LMICs) due to insufficient genetic surveillance.[11,12]
- Average of total_cases_per_million: Average cumulative number of confirmed COVID-19 cases per one million people.
- Average of people_vaccinated_per_hundred: Average daily percentage of population vaccinated with any number of doses.
- Average of people_fully_vaccinated_per_hundred: Average daily percentage of fully vaccinated population.
- Average of total_boosters_per_hundred: Average daily percentage of population vaccinated with a booster dose.
- Average of stringency_index: The average daily value of the Government Response Stringency Index, a composite measure based on nine response indicators including school closures, workplace closures, and travel bans.
- Average of population_density: Number of people divided by country's area in square kilometers.
- Average of median_age: Median age of the country's population.
- Average of aged_65_older: Share of the population that is 65 years and older.
- Average of gdp_per_capita: Gross domestic product at purchasing power parity.
- Average of cardiovasc_death_rate: Annual number of deaths from the cardiovascular disease per 100,000 people.
- Average of diabetes_prevalence: Diabetes prevalence among people aged 20–79.
- Average of female_smokers: share of female smokers.
- Average of male_smokers: share of male smokers.
- Average of hospital_beds_per_thousand: Hospital beds per 1000 people. As indicated by Ghosh et al.,[13] in LMICs like India, this number can be significantly lower than in high-income countries, leading to an increased burn-out of healthcare workers during the pandemic.
- Average of life_expectancy: Life expectancy at birth in 2019.

- Average of human_development_index: A composite index measuring three basic aspects of human development—a long and healthy life, knowledge and a reasonable standard of living.

2.2 | Estimating R and CFR

Our estimations of the average R and CFR values in each country are based on the daily values of confirmed COVID-19 cases and deaths reported by the Our World in Data website.[9] The daily estimate of R on day t is calculated by Equation (3).

$$R = \frac{Cum\_C_t - Cum\_C_{t-w}}{Cum\_C_{t-g} - Cum\_C_{t-g-w}}, \quad (3)$$

where Cum_C_t is the cumulative number of confirmed cases on day t, $w = 7$ days is the size of the sliding window, and $g = 4$ days stands for the average duration of the COVID-19 generation period.[7]

The daily estimate of CFR on day t is calculated by Equation (4).

$$CFR = \frac{Cum\_D_t - Cum\_D_{t-w}}{Cum\_C_{t-d} - Cum\_C_{t-d-w}}, \quad (4)$$

where Cum_D_t is the cumulative number of deaths on day t and $d = 14$ days represents the average time between testing positive and death (based on the COVID-19 Data Repository published by the Israeli Ministry of Health[14]).

2.3 | Statistical analysis

For each country, we have calculated the daily moving averages of the reproduction number R using the pandas.DataFrame.rolling.mean () function with window = 180 days and min_periods (minimum number of observations in window required to have a value) = 30. The daily values of R were estimated from the first date when the total number of confirmed COVID-19 cases in the country has reached 1000 until September 30, 2021. The daily moving averages of the case fatality rate CFR were calculated using Equation (4), where the sliding window w was taken as the minimum between 180 days and the number of days since the date when the total number of COVID-19-related deaths in the country has reached 100. All missing values of country-level variables were imputed by the averages of the known values in the corresponding columns using the pandas.Data-Frame.fillna function with default settings.

Pearson product-moment correlation coefficients between country-level variables were calculated using the scipy.stats. pearsonr function. Highly correlated variable pairs (Pearson's $r \geq 0.60$, $p < 0.001$) were excluded from further regression analysis. For the remaining variables, we have applied the forward–backward feature selection procedure based on p value from the statsmodels.api.OLS function, which builds a multivariate linear regression model using the ordinary least squares (OLS) method. This stepwise variable selection procedure has two thresholds: threshold_in

< threshold_out. It starts with only the intercept and at each step, it adds the most significant variable to the model. The selected variable should have the lowest p-value, which does not exceed threshold_in. The procedure stops when no variable meets the threshold_in criterion. In addition, at each step, the algorithm recalculates the p-values of all existing model terms and removes the variables if their p-values exceed threshold_out. In our analysis, we set threshold_in to 0.05 and threshold_out to 0.10.

3 | RESULTS

3.1 | Descriptive statistics

The descriptive statistics of all data variables are shown in Figure 1. Figure 2 shows Pearson's correlation coefficients of all pairs of potentially predictive factors. No pairs of highly correlated variables (Pearson's $r \geq 0.60$, $p < 0.001$) were retained for further analysis.

3.2 | R and CFR evolution over time

Figures 3 and 4 show the evolution of the 180-day moving averages for the country-level values of R and CFR, respectively. While both of these parameters were highly unstable during the first months of the pandemic, their average values declined to much lower levels around July–October 2020 and remained stable since then. The differences of both parameters between various countries have decreased over time as well. The mean values of country-level moving averages of R and CFR went down from 1.118 and 6.3%, respectively, on June 30, 2020 to 1.083 and 3.6% on September 30, 2020 and to 1.015 and 1.8% by September 30, 2021. In parallel, the 10%–90%

inter-percentile range of R and CFR moving averages decreased from 0.288 and 13.3%, respectively, on June 30, 2020, to 0.151 and 7.7% on September 30, 2020, and to 0.107 and 3.3% by September 30, 2021.

3.3 | Country-level factors associated with R

After removing highly correlated variables, we have applied the forward–backward feature selection procedure with threshold_in = 0.05 and threshold_out = 0.10 to find a minimal set of factors significantly associated with the 180-day moving average of the reproduction number R calculated for each country on September 30, 2021. In the first feature selection step, the following variables had the lowest p-values (below 0.10):

- Average of Delta (p-value = 0.006, slope = 0.0010)
- Average of total_cases_per_million (p-value = 0.010, slope = −5.73e−07)

Consequently, the Average of Delta was selected as the first variable to be added to the regression model. According to this model, an increase of 1% in the Delta variant share is associated with an increase of 0.001 (95% CI: 0.000–0.002) in the average Reproduction Number R. A model based on the second significant factor (Average of total_cases_per_million) indicates that an increase of 1% in the total percentage of confirmed COVID-19 cases per country's population is associated with a decrease of 0.006 (95% CI: 0.001–0.011) in the average R. The effect of the Delta variant and confirmed cases on R is shown in Figures 5 and 6, respectively.

In the second step, only Average of total_cases_per_million had p-value below 0.05 (0.02 < 0.05, slope = −5.018e−07) and thus it was

	N	Mean	Std. Deviation	Skewness	Median	Min	Max
Moving Average of R (180 days)	50	1.02	0.06	1.44	1.01	0.87	1.24
Moving Average of CFR (180 days) in percent	50	1.79	1.48	1.90	1.49	0.20	7.68
Average of Delta	41	41.68	22.87	0.64	41.70	2.20	100.00
Average of total_cases_per_million	50	58269	35424	0.20	61009	1719	154460
Average of people_vaccinated_per_hundred	50	32.75	19.37	0.28	32.21	3.65	82.61
Average of people_fully_vaccinated_per_hundred	50	23.42	16.44	0.70	20.21	1.67	72.74
Average of total_boosters_per_hundred	12	3.68	4.87	1.40	0.66	0.03	15.12
Average of stringency_index	50	60.71	10.28	-0.11	61.13	41.68	77.30
Average of population_density	50	172.48	209.59	3.29	107.40	4.04	1265.04
Average of median_age	50	36.14	7.50	-0.21	36.85	20.00	48.20
Average of aged_65_older	50	12.52	6.55	0.15	11.55	1.14	27.05
Average of gdp_per_capita	49	24713	15920	0.67	23313	2443	67293
Average of cardiovasc_death_rate	50	228.46	123.10	0.83	195.50	79.00	540.00
Average of diabetes_prevalence	50	7.92	2.86	1.45	7.15	4.28	17.26
Average of female_smokers	48	15.03	11.03	0.26	14.75	0.80	37.70
Average of male_smokers	47	36.50	12.69	0.75	35.60	13.50	76.10
Average of hospital_beds_per_thousand	50	3.61	2.67	1.26	2.69	0.30	13.05
Average of life_expectancy	50	77.26	4.66	-0.55	77.02	64.13	84.63
Average of human_development_index	50	0.81	0.10	-0.55	0.82	0.56	0.96

FIGURE 1 Descriptive statistics

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
1	Average of Delta	1.00	-0.13	-0.07	-0.06	-0.11	-0.13	0.19	-0.05	-0.04	-0.07	0.04	0.07	-0.10	0.11	-0.11	-0.14	-0.18
2	Average of total_cases_per_million		1.00	0.57	0.57	0.14	-0.49	-0.18	0.42	0.47	0.46	-0.27	-0.11	0.62	-0.31	0.19	0.50	0.62
3	Average of people_vaccinated_per_hundred			1.00	0.96	0.17	-0.31	-0.15	0.54	0.49	0.80	-0.51	0.00	0.51	-0.37	0.16	0.73	0.77
4	Average of people_fully_vaccinated_per_hundred				1.00	0.25	-0.38	-0.12	0.50	0.45	0.78	-0.42	0.05	0.53	-0.26	0.16	0.69	0.74
5	Average of total_boosters_per_hundred					1.00	-0.05	0.07	-0.26	-0.20	-0.11	-0.05	0.12	-0.01	0.04	-0.16	0.04	-0.02
6	Average of stringency_index						1.00	0.17	-0.44	-0.46	-0.37	-0.02	0.14	-0.41	0.09	-0.44	-0.21	-0.46
7	Average of population_density							1.00	-0.13	-0.07	-0.11	-0.03	-0.02	-0.10	0.03	-0.11	-0.02	-0.22
8	Average of median_age								1.00	0.94	0.61	-0.30	-0.35	0.61	-0.12	0.67	0.73	0.78
9	Average of aged_65_older									1.00	0.56	-0.36	-0.48	0.69	-0.18	0.70	0.72	0.76
10	Average of gdp_per_capita										1.00	-0.49	-0.03	0.43	-0.35	0.34	0.72	0.87
11	Average of cardiovasc_death_rate											1.00	0.21	-0.27	0.54	0.02	-0.64	-0.50
12	Average of diabetes_prevalence												1.00	-0.27	0.00	-0.30	-0.20	-0.22
13	Average of female_smokers													1.00	-0.10	0.51	0.52	0.59
14	Average of male_smokers														1.00	0.07	-0.29	-0.30
15	Average of hospital_beds_per_thousand															1.00	0.35	0.52
16	Average of life_expectancy																1.00	0.84
17	Average of human_development_index																	1.00

FIGURE 2 Pearson's correlation coefficient

FIGURE 3 Moving average of R (180 days)

Case-based R (180 days Moving Average)

─◆─ Aver R   ─◆─ 10-th percentile   ─◆─ 90-th percentile

CFR (180 days Moving Average)

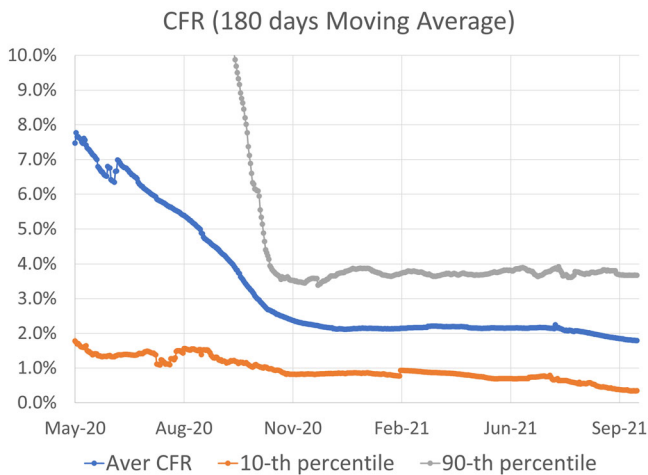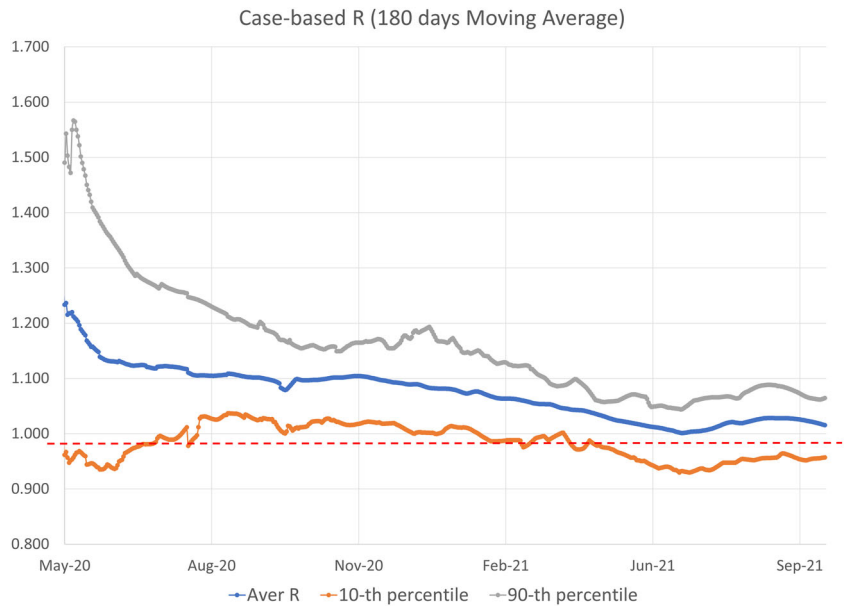─◆─ Aver CFR   ─◆─ 10-th percentile   ─◆─ 90-th percentile

FIGURE 4 Moving average of case fatality rate (CFR; 180 days)

selected as the second regression variable. No further variables were found statistically significant in the third step. The complete output of the resulting regression model is shown in Figure 7.

3.4 | Country-level factors associated with CFR

We have also applied the forward-backward feature selection procedure with threshold_in = 0.05 and threshold_out = 0.10 to find a minimal set of factors significantly associated with the 180-day moving average of the case fatality rate CFR calculated for each country on September 30, 2021. In the first step, only one variable, Average of people_fully_vaccinated_per_hundred, was found statistically significant (p value = 0.003, slope = −0.036) and added to the regression model. According to this model, an increase of 1% in the total percentage of fully vaccinated people per country's population

R vs Delta
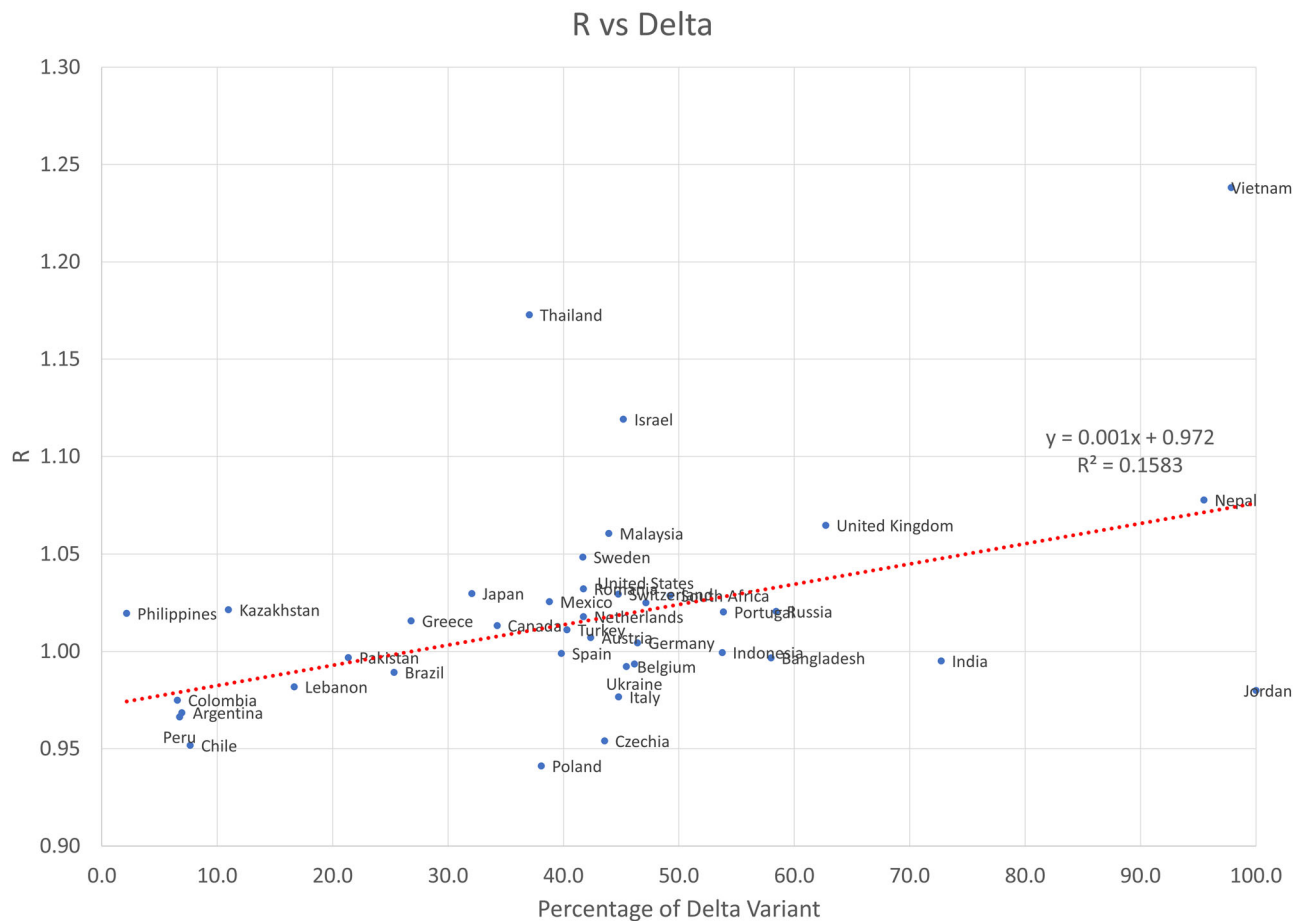
FIGURE 5 The effect of Delta variant on R

is associated with a decrease of 0.04% (95% CI: 0.01%–0.06%) in the average CFR. The effect of vaccination percentage on CFR is shown in Figure 8.

In the second step, no further variables were found statistically significant. The complete output of the resulting regression model is shown in Figure 9.

4 | DISCUSSION

4.1 | Global COVID-19 equilibrium

The increasingly low levels of the cross–country variance of R and CFR (see Figures 3 and 4), along with the average value of R approaching the value of 1.0, may indicate that the COVID-19 pandemic has reached its point of stable endemic equilibrium.[15] According to the mathematical model of COVID-19 presented in Ahmed et al.,[16] a stable endemic equilibrium is maintained as long as the basic reproduction number R_0 is greater than 1. In contrast, a stable disease-free equilibrium is achieved only when $R_0 < 1$. Though we do not have a direct way of estimating the current value of R_0 in each country, we may assume it to be close to the most recent peak in the effective reproduction number R. Considering the mean

difference of 0.22 between the average and the maximum country-level values of R during our period of interest (April–September 2021), we should be able to reach a stable disease-free equilibrium of COVID-19 only after the average R will go *globally* below 1.0 − 0.22 = 0.78.

What is the required percentage of infected and/or vaccinated population to make such an equilibrium possible? According to a regression model based on the Delta variant share and the number of confirmed cases (see Figure 7),

$$R = 1.006 + 0.0009 \text{ Average of delta} − 5.018E$$
$$− 07 × \text{Average of total\_cases}\_per\_\text{million}.$$

Assuming the maximum share of the Delta variant (100%), the requirement of $R = 0.78$ implies Average of total_cases_per_ million = (1.006 + 0.0009 × 100 − 0.78)/5.018E − 07 = 635000 per million = 63.5%, which is much higher than any country's current exposure to the virus of less than 22% and thus cannot be achieved globally in the foreseeable future. Moreover, reaching this level of natural herd immunity would require a prohibitively high cost in terms of human life. Thus, unfortunately, the regression model based on the data available at the end of September 2021 suggests that the endemic equilibrium of COVID-19 will maintain its stability as long as there will
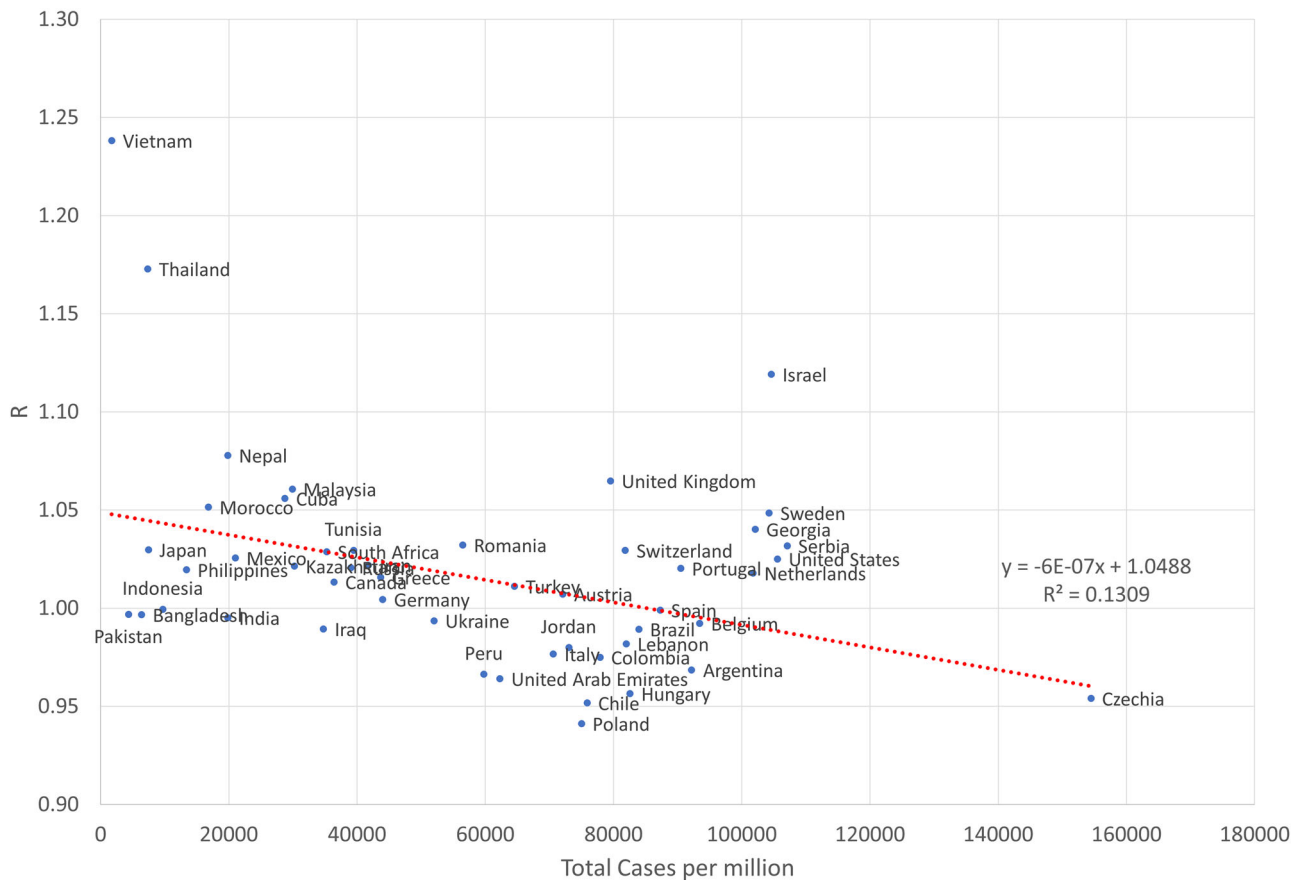
FIGURE 6   The effect of total confirmed cases on R

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                          OLS Regression Results
==============================================================================
Dep. Variable:              MA_R (180)   R-squared:                      0.246
Model:                             OLS   Adj. R-squared:                 0.214
Method:                  Least Squares   F-statistic:                    7.661
Date:                Sun, 03 Oct 2021   Prob (F-statistic):           0.00132
Time:                        11:35:26   Log-Likelihood:                80.618
No. Observations:                  50   AIC:                           -155.2
Df Residuals:                      47   BIC:                           -149.5
Df Model:                           2
Covariance Type:            nonrobust
==============================================================================
                                  coef    std err          t      P>|t|      [0.025      0.975]
------------------------------------------------------------------------------
const                           1.0060      0.021     47.801      0.000       0.964       1.048
Average of Delta                0.0009      0.000      2.677      0.010       0.000       0.002
Average of total_cases_per_million -5.018e-07  2.02e-07    -2.478      0.017   -9.09e-07   -9.44e-08
==============================================================================
Omnibus:                       10.428   Durbin-Watson:                  1.879
Prob(Omnibus):                  0.005   Jarque-Bera (JB):              13.428
Skew:                           0.687   Prob(JB):                     0.00121
Kurtosis:                       5.135   Cond. No.                    2.03e+05
==============================================================================
```

FIGURE 7   Ordinary least square (OLS) regression results—R
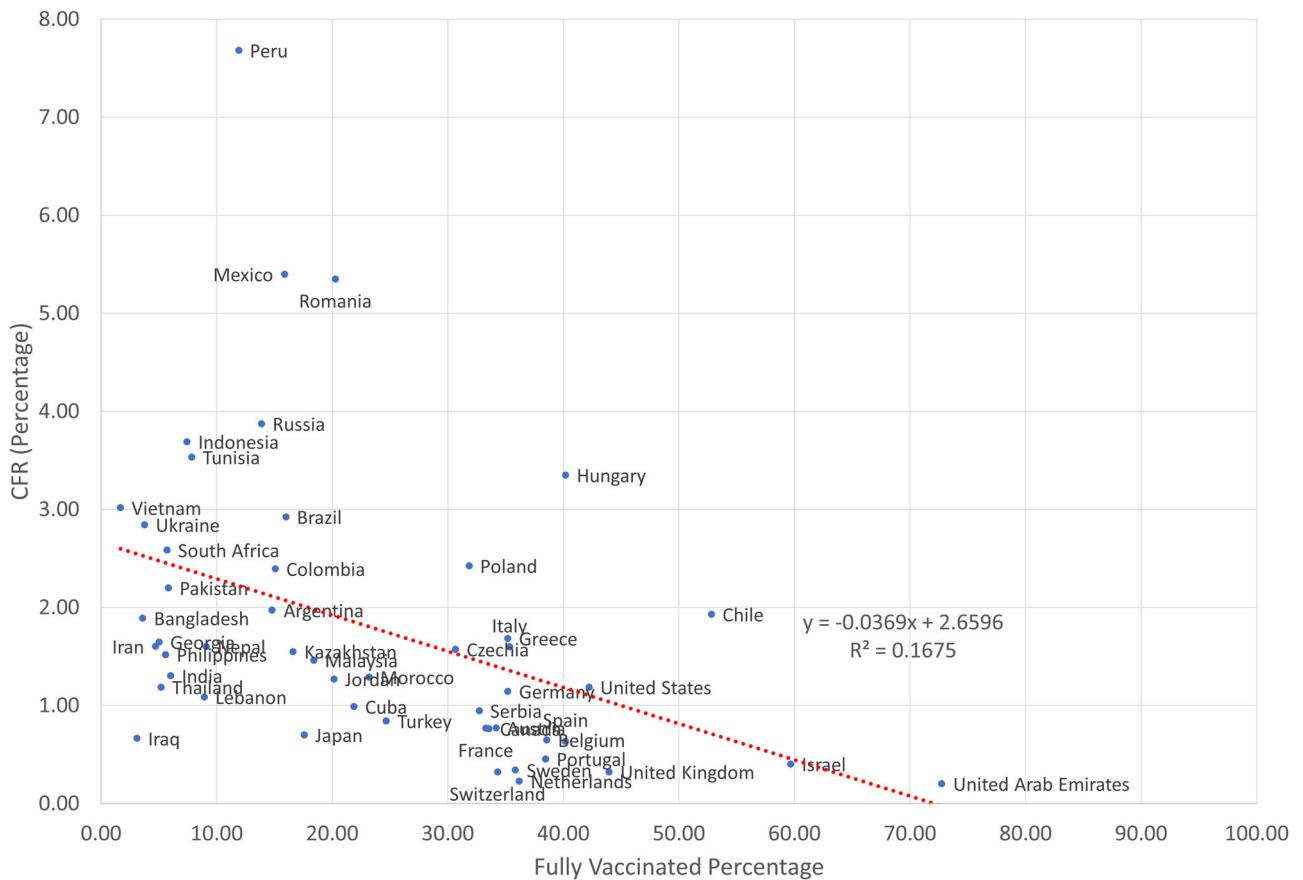
FIGURE 8 The effect of vaccination percentage on the case fatality rate (CFR)

```
                        OLS Regression Results
==============================================================================
Dep. Variable:             MA_CFR (180)   R-squared:                       0.167
Model:                              OLS   Adj. R-squared:                  0.150
Method:                   Least Squares   F-statistic:                     9.657
Date:                Sun, 03 Oct 2021     Prob (F-statistic):            0.00317
Time:                        11:35:26     Log-Likelihood:                -85.549
No. Observations:                  50     AIC:                             175.1
Df Residuals:                      48     BIC:                             178.9
Df Model:                           1
Covariance Type:            nonrobust
==================================================================================================
                                            coef    std err          t      P>|t|      [0.025      0.975]
--------------------------------------------------------------------------------------------------
const                                     2.6587      0.339      7.850      0.000       1.978       3.340
Average of people_fully_vaccinated_per_hundred  -0.0369   0.012     -3.108      0.003      -0.061      -0.013
==============================================================================
Omnibus:                       33.759   Durbin-Watson:                   2.190
Prob(Omnibus):                  0.000   Jarque-Bera (JB):               76.935
Skew:                           1.984   Prob(JB):                     1.97e-17
Kurtosis:                       7.603   Cond. No.                         50.0
==============================================================================
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FIGURE 9 Ordinary least square (OLS) regression results—case fatality rate

be no "game changer" in the form of either a vaccine more effective against infection or a less infectious virus mutation.

We may also estimate the average percentage of the fully vaccinated population, which should bring the CFR close to the level of the seasonal flu (about 0.1%). According to the regression model shown in Figure 9,

CFR = 2.6587 − 0.0369

Average of people_fully_vaccinated_per_hundred.

Setting CFR to 0.1 implies

Average of people_fully_vaccinated_per_hundred

= (2.6587 − 0.1)/0.0369 = 69%,

which is clearly a feasible number, already exceeded in several countries.[9] Thus, the currently available vaccines can be effective in reducing the mortality from the existing COVID-19 variants close to the level of the seasonal flu.

4.2 | Demographics and COVID-19

Our regression analysis has shown that the median age and the average density of a country's population are not statistically significantly associated with the average reproduction number. Contrary to Ahammed et al.,[17] we have also found no statistically significant associations of any demographic parameter with CFR.

4.3 | Economic development and stringency measures

Similar to the findings of Cao et al.,[8] the association of the Average of stringency_index with R and CFR was not found statistically significant. Thus, we could not identify any statistically significant effects of government measures restricting the people's behavior (such as lockdowns) on COVID-19 dynamics. The economic development factors (gdp_per_capita, hospital_beds_per_thousand, life_expectancy, and human_development_index) were removed from the regression analysis due to their high correlation with the median age.

4.4 | Limitations of this study

This retrospective study suffers from several limitations. First, the officially reported numbers of daily COVID-19 confirmed cases depend on the country-specific testing policy and usually underestimate the true number of carriers in the population. Second, the officially reported numbers of daily COVID-19 deaths in some

countries may include all deceased individuals who tested positive for COVID-19 (people who "died with coronavirus"), disregarding their actual cause of death, and exclude some victims (people who "died from coronavirus"), because they were not tested for COVID-19 before their death. Last but not least, the future dynamics of COVID-19 depend on the unknown characteristics of new variants, such as the Omicron, as well as short and long-term efficacy of currently developed vaccines, government decisions, public behavior, and other uncertainty factors.

5 | CONCLUSION

The continuous decrease in the country-level moving averages of R, down to the level of 1.0, accompanied by repeated outbreaks ("waves") in various countries, may indicate that COVID-19 has reached its point of stable endemic equilibrium. In our regression analysis, only the Delta variant share and the total percentage of confirmed cases were identified as statistically significant factors associated with the average values of R in different countries. According to the regression model shown in Figure 7, only a prohibitively high level of herd immunity (about 63%), associated with a tremendous cost in terms of human life, may naturally stop the endemic by reaching a stable disease-free equilibrium. On the other hand, the average percentage of the fully vaccinated population, which appears to be statistically significantly associated with country-specific CFR, can bring it close to the level of the seasonal flu (about 0.1%) after vaccinating more than 70% of a country's population. It is noteworthy that no statistically significant effect of vaccinations on R was found in our analysis. Thus, while the currently available vaccines prove to be effective in reducing mortality from the existing COVID-19 variants, they seem unlikely to stop the spread of the virus in the foreseeable future. In addition, the performed data analysis revealed no statistically significant effects of government measures restricting the people's behavior (such as lockdowns) on either R or the CFR.

AUTHOR CONTRIBUTION
Mark Last: conceptualization, data curation, formal analysis, investigation, methodology, resources, software, validation, visualization, and writing—original draft.

CONFLICT OF INTEREST
The author declares no conflict of interest.

TRANSPARENCY STATEMENT
The manuscript is an honest, accurate, and transparent account of the study being reported; no important aspects of the study have

been omitted; and any discrepancies from the study as planned (and, if relevant, registered) have been explained.

DATA AVAILABILITY STATEMENT

All data used in this study is publicly available at https://ourworldindata. org/ and cited in the article.

ORCID

Mark Last [ID] http://orcid.org/0000-0003-0748-7918

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