Herd immunity for Covid-19 in homogenous populations

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Abstract

In this note we estimate herd immunity levels for the Covid-19 epidemic based upon a standard SEIR system that models the disease dynamics in homogeneous populations. The results obtained are indicative of values between 80% and 90% for unprotected, fully susceptible populations. Basic protective measures like hand hygiene and mask wearing may be effective to lower herd immunity estimates down to values between 50% and 60%.

Key words: Covid-19 outbreak, SARS-Cov-2 coronavirus, reproduction numbers, SEIR models, homogeneous populations, herd immunity against Covid-19

AMS Subject Classification: 92-08, 92-10 (primary), 92-04 (secondary)

Matlab code: A complete MATLAB SOURCE CODE to compute reproduction numbers of Covid-19 or other epidemics is freely available by clicking here: find_Rt.m

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Summary and Conclusions

Section 1. Introduction
Simple models, with fewer variables and parameters, have practical advantages like involving less complex missing data and parameter determination problems.

Section 2. Implementing the SEIR model
A critical part is the initialization problem, that is, a satisfactory determination of initial values for all the variables in the model. For the SEIR system considered, $S(t_0)$ and $D(t_0)$ are given (modulo some errors), but $E(t_0), I(t_0), R(t_0)$ are missing. They can be obtained at some later initial time $t_\ast = t_0 + p$ (with $p > 0$ depending on the initial guess for the missing data) by continuously fitting the model (that is, the parameters $\beta(t)$ and $r(t)$, in this case) to the available data at $t_0, t_0+1, ..., t_0+p$. Computations can then proceed from $t_\ast$ onwards; previous values for $E(t), I(t), R(t)$ and related quantities (e.g., transmission rates and reproduction numbers) are not generally reliable. For the Covid-19 examples examined, we found $10 < p < 20$.

Section 3. Herd Immunity for Covid-19
For Covid-19, we have found higher herd immunity levels than previously suggested: 80% to 90% of an (off-guard) homogenous population. As a general guide, basic protective measures like hand hygiene and mask wearing can be effective to reduce herd immunity numbers to between 50% and 70% of the population, depending on the transmissibility status that will hold in this case. As transmissibility may vary significantly across different regions, local analysis is advised.

Section 4. Closing Remarks
Herd immunity estimates depend on the model used, data quality and other factors, some of which hardly predictable. Results should always be viewed with caution. Ours indicate that herd immunity may be close to 90% in homogeneous populations, providing upperbounds for more realistic studies taking heterogeneity into account.
1. Introduction

There is now a well developed mathematical literature providing a rich variety of continuous or discrete models and techniques to investigate the dynamics of communicable diseases, see e.g. [4, 8, 14, 20, 21] and references therein. Among the many important concepts are reproduction numbers and herd immunity, which are related to the disease potential of developing significant outbreaks. Herd immunity is the state when an infected individual in a given population generates on average less than one secondary infection during his infectious period — or, in other words, the effective reproductive number $R_t$ is smaller than one [4, 8, 11, 26]. In this situation, an outbreak will not develop. This is achieved when a proportion $p > \hat{p} \in (0, 1)$ of the population in question is immune to the infectious agent, where $\hat{p}$ is the herd immunity threshold [11, 12, 13, 23, 26]. Immunization may be acquired by overcoming some previous natural infection or through vaccination. Estimating $\hat{p}$ is a very important problem in the study of infectious diseases.

Herd immunity for Covid-19 has been examined in a number of previous works, with $\hat{p}$ estimates typically lying between 60% and 85% for well-mixed, homogeneous populations [5, 12, 13, 17, 27]. These estimates depend on reliable values for the reproductive numbers involved and other assumptions, which cannot be guaranteed. For example, in [17] it is estimated that $\hat{p} \approx 81\%$ for Spain using data on the daily number of new COVID-19 cases and the exponential growth method [3, 8, 30] to estimate $R_t$, the effective reproduction number, along with estimations on the serial interval and some underlying assumptions [22]. Starting with the same data, we estimated $R_t$ from daily infected population totals computed by a careful implementation of a standard SEIR model (Section 2), then obtaining $80\% < \hat{p} < 90\%$ for the Spanish population, in the absence of protective measures (Section 3).

Our approach to estimate herd immunity threshold values for Covid-19 is based on carefully implementing some chosen deterministic model so as to yield reliable estimates of the information needed, such as transmission rates and reproductive ratios. We illustrate the typical procedures by considering, for simplicity, the basic SEIR system defined by the equations (1.1) below, where for convenience we have ignored effects like birth or migration rates, deaths by natural or other causes, and so forth. This model divides the entire population in question into four classes: the susceptible individuals (class $S$), those exposed (class $E$, formed by infected people who are still inactive, that is, not yet transmitting the disease), the active infected or infectious individuals (class $I$) and the removed ones. The latter class is formed by the people who have either recovered from the disease (class $R$) or have died from it (class $D$). In the simplest setting, the dynamics among the populations $S(t), E(t), I(t), R(t)$ and $D(t)$ are given by the differential equations
\[
\begin{align*}
\frac{dS}{dt} &= -\beta \frac{S(t)}{N} I(t), \\
\frac{dE}{dt} &= \beta \frac{S(t)}{N} I(t) - \delta E(t), \\
\frac{dI}{dt} &= \delta E(t) - (r + \gamma) I(t), \\
\frac{dR}{dt} &= \gamma I(t), \\
\frac{dD}{dt} &= r I(t),
\end{align*}
\] (1.1)

see e.g. [4, 10, 14, 21] for a detailed discussion of the various terms and their meanings. The parameters \(\beta\) (average transmission rate) and \(r\) (average lethality rate due to the disease) vary with \(t\) (time, here measured in days), but \(\delta\) and \(\gamma\) are positive constants given by

\[
\gamma = \frac{1}{T_t}, \quad \delta = \frac{1}{T_\ell},
\] (1.2)

where \(T_t\) denotes the average transmission time and \(T_\ell\) stands for the mean length of the latent period (the time taken to become infectious, once infected), which for Covid-19 are typically taken from 10 to 14 days and from 3 to 5 days, respectively [13, 16, 19, 25, 28, 29]. In (1.1), \(N\) denotes the full size of the susceptible population initially exposed, so that we have \(S(t_0) + E(t_0) + I(t_0) + R(t_0) + D(t_0) = N\), where \(t_0\) denotes the initial time. From (1.1), it follows the conservation law

\[
S(t) + E(t) + I(t) + R(t) + D(t) = N, \quad \forall \ t > t_0.
\] (1.3)

For the model (1.1) to be useful, not only the values of \(\beta(t)\) and \(r(t)\) must be obtained but also initial values for \(S(t), E(t), I(t), R(t)\) and \(D(t)\) must be provided. Typical available data inform the total number \(C(t_i)\) of cases reported up until some time moments \(t_i\) and the total number of deaths, \(D(t_i)\). As \(S(t_i) = N - C(t_i)\), by (1.3) we are given the sums \(E(t_i) + I(t_i) + R(t_i)\), but not the individual values \(E(t_i), I(t_i)\) and \(R(t_i)\). This difficulty is addressed in Section 2. A satisfactory solution is important for obtaining good estimates of reproduction numbers and herd immunity values.

With the model (1.1) then completed, and implementation issues resolved, we are in good position to estimate herd immunity levels (Section 3). Taking ten countries for illustration, we examine their situation in two different periods of the year 2020: before contention measures were applied and after the first 75 days of intervention, when the population was well aware of the value of simple protective measures like hand hygiene and mask wearing. A few closing remarks are given in Section 4.
2. Implementing the SEIR model

Having introduced the SEIR equations (1.1), we now describe an implementation of this model that is suitable for all our needs (and much more).

(i) assigning a value to the population parameter $N$

In the case of Covid-19, which was caused by a new virus (SARS-CoV-2), it is reasonable to assume that the entire population of the region under consideration is initially susceptible, which was done in the code. In any case, it turns out that the exact value of $N$ is not so important for the short range dynamics (which accounts for the applications studied in this paper) as it proves to be for long time simulations (Figures 1a and 1b).

![Reported New Cases predicted by SEIR: 2 scenarios](image)

**Fig. 1a:** Prediction by model (1.1) of the daily number of new cases of Covid-19 expected to be reported in Brazil between the initial time $t = t_0 = 60$ (April 25) and $t = 200$ (September 12), considering susceptible populations of $N = 20$ million (red curve) and $N = 50$ million (black curve). Note the appreciable difference between the predicted peak values (34 and 70 thousand, resp.) and their respective dates, June 6 and July 4. Actual data points are shown in blue. (Computed from data available at the official site [https://covid.saude.gov.br](https://covid.saude.gov.br))
Fig. 1b: Thirty day prediction by model (1.1) of the daily number of new cases of Covid-19 to be reported in Brazil between the initial time $t = t_0 = 60$ (04/25) and $t = 90$ (05/25), considering susceptible exposed populations of $N = 20$ million (red curve) and $N = 50$ million (black curve). Note the very close similarity of the two 30D predictions in spite of the appreciable difference in the values of $N$. Points shown in blue are the official values reported (cf. [https://covid.saude.gov.br/](https://covid.saude.gov.br/)).

(ii) generation of initial data $S(t_0), E(t_0), I(t_0), R(t_0), D(t_0)$

Initial values $S_0, E_0, I_0, R_0, D_0$ for the five variables are generated from a starting date $t_s$ on, which is taken so as to meet some minimum value chosen of total reported cases (namely, 100). Denoting by $C_r(t)$ the total amount of reported cases up to some time $t$, and letting $EIR(t)$ be the sum of the populations $E(t), I(t)$ and $R(t)$, we set

$$EIR(t_s) = f_c \cdot (C_r(t_s) - D(t_s)), \quad (2.1)$$

where $f_c \geq 1$ denotes a correction factor to account for likely underreportings on the official numbers given. (In (2.1), we have neglected possible underreportings on the number of deaths, which could of course be similarly accounted for if desired.) Again, this factor $f_c$ will not play an important role in this paper and could be safely ignored, but it should be carefully considered in the case of long time predictions. We have typically taken $f_c = 5$. Having estimated $EIR(t_s)$, we then set

$$E(t_s) = E_0(t_s) := a \cdot (1 - b) \cdot EIR(t_s), \quad (2.2a)$$

$$I(t_s) = I_0(t_s) := (1 - a) \cdot (1 - b) \cdot EIR(t_s), \quad (2.2b)$$
\[ R(t_s) = R_0(t_s) := b \cdot \text{EIR}(t_s), \quad (2.2c) \]

\[ S(t_s) = S_0(t_s) := N - \left( E(t_s) + I(t_s) + R(t_s) + D(t_s) \right), \quad (2.2d) \]

where \( a = T_i/(T_i + T_l) \) and \( b = 0.30 \). Although (2.2) above might seem reasonable, the expressions (2.2a)-(2.2c) are nevertheless arbitrary and will be probably in error. However, all the errors will eventually fade away (Figure 2) as we compute more values \( S_0(t_0), E_0(t_0), I_0(t_0), R_0(t_0), D_0(t_0) \) at later initial times \( t_0 = t_s + 1, \ldots, t_F \), where \( t_F \) stands for the final (i.e., most recent) day of reported data available. This can be done as follows. For each \( t_0 \), the solution of the equations (1.1) with the previously obtained initial data at \( t_0 - 1 \) is computed on the interval \( J(t_0) = [t_0-1, t_1] \), \( t_1 = \min \{ t_0-1 + d_0, t_F \} \), with constant parameters \( \beta = \beta_0(t_0-1), r = r_0(t_0-1) \) determined so that the computed values for \( C_r(t), D(t) \) best fit the reported data for these variables on \([t_0, t_1]\) in the sense of least squares \[21\]. (Here, \( d_0 \in [2, 10] \) is chosen according to the data regularity.) Once this solution \((S, E, I, R, D)\)(t) is obtained, we set \( S_0(t_0) := S(t_0), E_0(t_0) := E(t_0), I_0(t_0) := I(t_0), R_0(t_0) := R(t_0), D_0(t_0) := D(t_0) \) and move on to the next time level \( t_0 + 1 \), repeating the procedure until \( t_F \) is reached.

Fig. 2a: Self-correction in the initialization procedure (ii) to generate \( S_0(t_0), E_0(t_0), I_0(t_0) \) and \( R_0(t_0) \) for \( t_0 = t_s, t_s + 1, \ldots, t_F \), showing above the case of \( I_0(t_0)/N \) in France. At time \( t_s = 0 \), the day of 100 total cases reported (29/02/2020), four very different sets of values \( \{E_0(t_s), I_0(t_s), R_0(t_s)\} \) are considered: our standard choice (2.2a)-(2.2c), shown in red; \( E_0(t_s) = I_0(t_s) = 0.05 \times \text{EIR}(t_s), R_0(t_s) = 0.90 \times \text{EIR}(t_s) \), shown in blue; \( E_0(t_s) = \text{EIR}(t_s), I_0(t_s) = R_0(t_s) = 0 \), shown in green; and \( I_0(t_s) = \text{EIR}(t_s), E_0(t_s) = R_0(t_s) = 0 \), in black. For \( t_0 > t_s + 15 \), all four initializations produce essentially the same values for \( I_0(t_0) \).
Fig. 2b: Self-correction in the values of $R_t = I_0(t+3)/I_0(t-3)$ induced by the correction of $E_0(t_0)$, $I_0(t_0)$ and $R_0(t_0)$ exhibited in Fig. 2a, considering the same four initializations at $t_s = 0$.

(iii) computing the solution on some final interval $[t_0, T]$ (prediction phase)

Having completed the previous steps, we can address the possibility of prediction. Although this is not important for our present goals, it is included for completeness. Choosing an initial time $t_0 \in (t_s, t_F]$, we then take the initial values

$$S(t_0) = S_0(t_0), \ E(t_0) = E_0(t_0), \ I(t_0) = I_0(t_0), \ R(t_0) = R_0(t_0), \ D(t_0) = D_0(t_0).$$

In order to predict the values of the variables $S(t), E(t), I(t), R(t), D(t)$ for $t > t_0$, it is important to have good estimates for the evolution of the key parameters $\beta(t)$ and $r(t)$ beyond $t_0$. This may be a particularly computationally intensive part of the algorithm. Such estimates can be given in the form

$$\beta(t) = \beta_0 + a_\beta e^{-\lambda_\beta(t-t_0)} \quad (2.3a)$$
$$r(t) = r_0 + a_r e^{-\lambda_r(t-t_0)} \quad (2.3b)$$

where $\beta_0, a_\beta, \lambda_\beta, r_0, a_r, \lambda_r \in \mathbb{R}$ are determined so as to minimize the maximum size of weighted relative errors in the computed values for $C_r(t), D(t)$ as compared to the official data reported for these variables on some previous interval $[t_0-\tau_0, t_0]$ (weighted Chebyshev problem) for some chosen $\tau_0 > 0$ (usually, $20 \leq \tau_0 \leq 30$). This problem is solved iteratively starting with an initial guess obtained from the analysis of the previous values $\beta_0(t), r_0(t)$ computed in the step (ii) above. The result is illustrated in Figure 3 for the case of $\beta(t)$, with similar considerations for $r(t)$. 

8
Fig. 3: Estimation of future values of the transmission parameter $\beta(t)$ beyond the initial time $t_0 = 70$ (05/05/2020) for the outbreak of Covid-19 in Brazil, assuming the basic form (2.3a), after solving the Chebycheff problem (red curve). The data points in the interval $[40, 70]$, shown here in blue, are values of the function $\beta_0(t)$ computed in step (ii), which are used to obtain the first approximation to $\beta(t)$. Values of $\beta_0(t)$ previous to $t = 40$ (04/05/2020), shown in black, are disregarded. The golden points beyond $t_0 = 70$ are future values of $\beta_0(t)$, not available on 05/05/2020, displayed to allow comparison with the predicted values $\beta(t)$.

Once $\beta(t)$, $r(t)$ have been obtained, the equations (1.1) are finally solved (Figure 4).

Fig. 4: Computation of $C_r(t) = (E(t) + I(t) + R(t))/f_c + D(t)$ for $t > t_0 = 70$ (05/05/2020), with initial data $C_r(t_0) = (E_0(t_0) + I_0(t_0) + R_0(t_0))/f_c + D_0(t_0)$, after obtaining $\beta(t)$, $r(t)$ – see Fig. 3 for $\beta(t)$. The numerical solution of equations (1.1) is easily obtained by any method.
3. Herd Immunity Estimates for Covid-19

In this section we use the SEIR algorithm developed in Section 2 to estimate immunization levels for a given population that could protect it against a Covid-19 outbreak. Since the results depend strongly on the transmission rates that would likely be observed, two distinct scenarios are considered: the case of an unsuspecting population caught off guard against the disease, and a warned population that takes some protective measures. Whether or not an outbreak will happen can be answered by examining the values of reproduction numbers associated with the infected population. Summing up the second and third equations in (1.1), we have

\[
\frac{d\Pi}{dt} = \alpha(t) I(t), \quad \alpha(t) = \beta(t) \frac{S(t)}{N} - r(t) - \gamma, \tag{3.1}
\]

where \(\Pi(t) = E(t) + I(t)\) is the infected population at time \(t\), \(\gamma\) is given in (1.2) and \(\beta(t), r(t)\) are the transmission and lethality rates of the disease, which are obtained as described in Section 2. Whether or not \(\Pi(t)\) decreases depends on whether or not \(\alpha(t) < 0\), that is, on whether the corresponding reproduction number

\[
R_t = \frac{\beta \cdot S/N}{r + \gamma} \tag{3.2}
\]

is smaller than the threshold value 1 or not. Assuming that a fraction \(p\) of the population has been immunized, so that \(S/N = 1 - p\), the condition \(R_t < 1\) becomes

\[
p > \hat{p} := 1 - \frac{1}{R_t}, \quad R_t = \frac{\beta}{r + \gamma} \tag{3.3}
\]

(see e.g. [21], p. 217), and the problem then reduces to obtaining reliable estimates of the basic reproductive ratios \(R_t\) given in (3.3).

(i) the case of an unsuspecting population caught off guard: 80% < \(\hat{p}\) < 90%

That is, the population is not aware of the presence of any infected individuals, and contention or hygienic measures are not being observed. This was the case of most countries around the world in the first weeks of their 2020 covid-19 outbreak. We can then obtain the \(R_t\) values needed to estimate \(\hat{p}\) by looking at what happened there in the days before the application of intervention measures, neglecting the initial results as they are subject to initialization errors (Section 2). This is illustrated in Figure 5 below, where we assumed \(\gamma = 0.1\), i.e., a transmission period of 10 days, and \(\delta = 1/3\), that is, a latency period of 3 days, cf. (1.2).
Fig. 5a: Time history of the reproductive ratios $R_t$ defined by (3.3) in five European countries (France, Germany, Italy, Spain and UK) about the time of their first intervention measures against Covid-19 ($t = 0$), assuming $T_t = 10$ and $T_\ell = 3$. The initial dashed parts of the curves correspond to the initialization phase of the algorithm before self-correction (Section 2), with the values shown in these parts being disregarded.

Fig. 5b: Time history of the reproductive ratios $R_t$ defined by (3.3) in five American countries (Argentina, Brazil, Mexico, Uruguay and US) about the time of their first intervention measures against Covid-19 ($t = 0$), assuming again $T_t = 10$ and $T_\ell = 3$. As in Fig. 5a, the dashed parts correspond to the initialization phase of the algorithm before self-correction (Section 2), with the respective values disregarded. All computations based on covid data available for the 10 countries at worldometers/coronavirus.
Observing the numerical ranges of the ratios $R_t$ in the region $t \leq 0$, pictured in Figure 5, we obtain the results displayed in the second and third columns of Table 1. Larger transmission or latency periods yield larger $R_t$ values in this region, leading to larger estimates of herd immunity levels. For example, taking $T_t = 14$ and $T_\ell = 5$ we obtain, repeating the procedure, the results given in the last column of Table 1.

| Country       | $R_t$ range (Case I) | $\hat{p}$ range (Case I) | $\hat{p}$ range (Case II) |
|---------------|----------------------|---------------------------|---------------------------|
| Argentina     | 4.95 < $R_t$ < 5.55  | 79% < $\hat{p}$ < 82%    | 85% < $\hat{p}$ < 89%    |
| Brazil        | 6.26 < $R_t$ < 8.05  | 84% < $\hat{p}$ < 88%    | 90% < $\hat{p}$ < 93%    |
| France        | 3.82 < $R_t$ < 6.47  | 73% < $\hat{p}$ < 85%    | 83% < $\hat{p}$ < 91%    |
| Germany       | 5.65 < $R_t$ < 6.62  | 82% < $\hat{p}$ < 85%    | 89% < $\hat{p}$ < 92%    |
| Italy         | 3.80 < $R_t$ < 5.65  | 77% < $\hat{p}$ < 86%    | 86% < $\hat{p}$ < 92%    |
| Mexico        | 4.38 < $R_t$ < 6.91  | 73% < $\hat{p}$ < 83%    | 83% < $\hat{p}$ < 90%    |
| Spain         | 4.14 < $R_t$ < 5.81  | 76% < $\hat{p}$ < 83%    | 85% < $\hat{p}$ < 90%    |
| United Kingdom| 4.16 < $R_t$ < 5.48  | 75% < $\hat{p}$ < 82%    | 84% < $\hat{p}$ < 89%    |
| Uruguay       | 2.91 < $R_t$ < 4.72  | 65% < $\hat{p}$ < 79%    | 79% < $\hat{p}$ < 88%    |
| United States | 4.88 < $R_t$ < 7.71  | 79% < $\hat{p}$ < 88%    | 86% < $\hat{p}$ < 93%    |

Table 1: Estimates of herd immunity levels $\hat{p} = 1 - 1/R_t$ for Covid-19 in the early days of the epidemic, before the application of contention measures. Case I corresponds to average latency and transmission periods of 3 and 10 days, respectively, while Case II assumes longer periods of 5 and 14 days. Computation of transmission and lethality rates for each country uses the SEIR algorithm above and covid data available at worldometers/coronavirus.

The values obtained are suggestive of a basic range $80\% < \hat{p} < 90\%$ in case (i).

(ii) the case of a wary population observing basic measures: $50\% < \hat{p} < 60\%$

By basic measures we mean simple hygienic procedures like washing hands and wearing masks, and perhaps some occasional social distancing, adopted by the majority of the population. This behavior was observed in most countries after the removal or relaxing of stricter intervention rules like severe mobility restrictions, curfew or lockdown measures. Estimates for $R_t$ in such case can then be obtained by looking at what happened in the year 2020 to this indicator in various countries after the initial contention measures have been relaxed or removed and searching for the maximum values in this period (Figure 6). The results are shown in Table 2 and seem indicative of a basic range $50\% < \hat{p} < 60\%$ in this scenario.
**Fig. 6a:** Time history in 2020 of the reproductive numbers (3.3) in four European countries (France, Germany, Italy and UK) after 75 days ($t = 0$) following the first intervention measures, assuming $T_e = 3$ and $T_i = 10$, see (1.2). The levels 1.25, 1.43, 1.67, 2.00 and 2.50 (dashed lines) correspond to $\hat{p} = 20\%$, 30\%, 40\%, 50\% and 60\%. All computations based on covid data available for these countries at [worldometers/coronavirus](https://www.worldometers.info/coronavirus/).

**Fig. 6b:** Time history in 2020 of the reproductive numbers (3.3) in four American countries (Argentina, Brazil, Mexico and US) after 75 days ($t = 0$) following the first intervention measures, assuming again $T_e = 3$ and $T_i = 10$. The levels 1.25, 1.43, 1.67, 2.00 and 2.50 (dashed lines) correspond to $\hat{p} = 20\%$, 30\%, 40\%, 50\% and 60\%. All computations based on covid data available for these countries at [worldometers/coronavirus](https://www.worldometers.info/coronavirus/).
| Country       | $R_t$ (Case I) | $\hat{p}$ (Case I) | $R_t$ (Case II) | $\hat{p}$ (Case II) |
|--------------|---------------|--------------------|-----------------|----------------------|
| Argentina    | $R_t < 1.78$  | $\hat{p} < 44\%$  | $R_t < 2.19$    | $\hat{p} < 55\%$    |
| Brazil       | $R_t < 1.55$  | $\hat{p} < 36\%$  | $R_t < 1.83$    | $\hat{p} < 46\%$    |
| France       | $R_t < 1.96$  | $\hat{p} < 49\%$  | $R_t < 2.39$    | $\hat{p} < 58\%$    |
| Germany      | $R_t < 2.23$  | $\hat{p} < 56\%$  | $R_t < 2.83$    | $\hat{p} < 65\%$    |
| Italy        | $R_t < 2.53$  | $\hat{p} < 61\%$  | $R_t < 3.42$    | $\hat{p} < 71\%$    |
| Mexico       | $R_t < 1.72$  | $\hat{p} < 42\%$  | $R_t < 1.79$    | $\hat{p} < 45\%$    |
| Spain        | $R_t < 2.40$  | $\hat{p} < 59\%$  | $R_t < 2.99$    | $\hat{p} < 67\%$    |
| United Kingdom| $R_t < 2.02$ | $\hat{p} < 51\%$  | $R_t < 2.52$    | $\hat{p} < 61\%$    |
| Uruguay      | $R_t < 2.75$  | $\hat{p} < 64\%$  | $R_t < 3.04$    | $\hat{p} < 68\%$    |
| United States| $R_t < 1.82$  | $\hat{p} < 46\%$  | $R_t < 2.15$    | $\hat{p} < 54\%$    |

Table 2: Estimates of herd immunity levels $\hat{p} = 1 - 1/R_t$ for Covid-19 in ten countries in the period of 2020 following the 75th day after the application of the first intervention measures. Case I corresponds to average latency and transmission periods of 3 and 10 days, respectively, while Case II assumes longer periods of 5 and 14 days. All the computations are based on covid data for each country available at [worldometers/coronavirus](https://worldometers/coronavirus).

4. Closing Remarks

Estimates of herd immunity levels are dependent on the underlying mathematical model and its assumptions and limitations, data quality and reliability, limitations of the mathematical methods employed, and various factors that may be difficult to predict like changes in the pathogenic agent or in the population behavior. Thus, any results should be viewed with caution and interpreted as guidelines and not as definitive answers. Of course, the estimates obtained here are in no way different. Constant checking and updating in face of new experimental evidence is necessary.

For example, we have assumed that underreporting levels of new covid cases in each surveyed country remained essentially constant along 2020, so that their effects on reproduction numbers are negligible [7]. But this may not have been quite so. In fact, data quality is commonly a major difficulty in the study of an epidemic.

Still, it seems safe to say that herd immunity for Covid-19 could be close to 90%, at least for sufficiently homogeneous populations. Good hygienic practices and mask wearing can very likely reduce these values to 70% or lower, depending on the case. As transmission rates may vary significantly across regions, even in the same country, local analysis is advised. Finally, our estimates provide basic upperbounds for more realistic models and similar studies considering heterogeneous populations.
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