

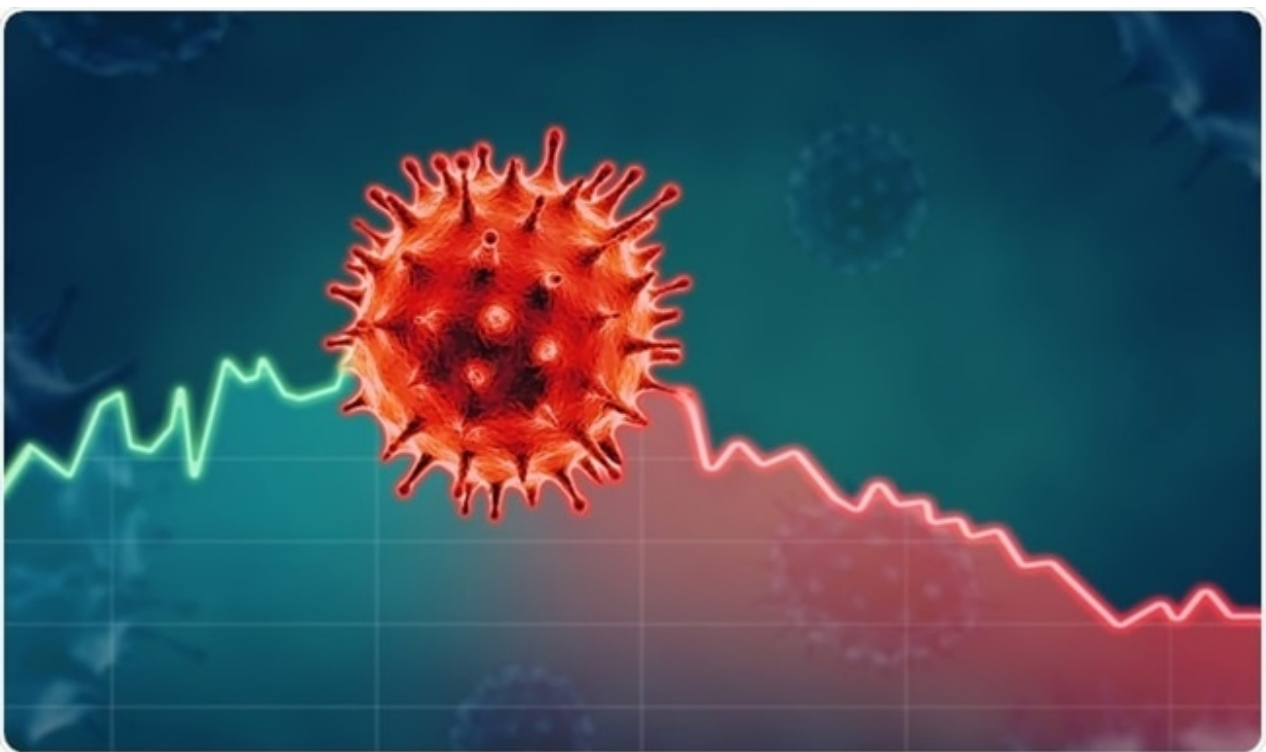
# Reproduction number of COVID-19 and how it relates to public health measures



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A new study published on the preprint server [\*medRxiv\*](#)\* in May 2020 reports the use of a dynamic SEIR model to identify variations in the reproductive number of SARS-CoV-2 over time, using machine learning techniques. This could help to model and predict the outcomes of various public health solutions.



*Study: [The reproduction number of COVID-19 and its correlation with public health interventions](#). Image Credit: Fikretow / Shutterstock*

## The reproductive number

The reproductive number has become the most discussed term in the current COVID-19 pandemic. This number, represented as  $R_0$ , refers to the number of new infections that one infected individual can cause in a susceptible population. It has been used to justify and explain why lockdowns, social distancing, and other mitigation strategies are needed to keep the case count and death toll low in this pandemic.

If the  $R_0$  is above 1, each infection breeds more, and the outbreak will continue to grow. When it falls below 1, the outbreak will continue but at a lower death rate, since less than 1 infected case follows the resolution of an earlier case by death or recovery.

Due to changes in the country, culture, type of calculation, and outbreak stage, the  $R_0$  has been reported with highly differing magnitudes. Even though it is important, it seems complicated to arrive at a precise, calculated value due to data limitations and reporting inaccuracies. Moreover, direct observation of  $R_0$  seems impossible.

The first reported  $R_0$  was from Wuhan, at 2.2, as a result of direct contact tracing. This became suspect due to the volume of cases, leading to the breakdown of healthcare systems and inadequate testing facilities at that stage, as well as evolving case definitions. Even today, model choice, starting conditions, and other assumptions shape the final calculation, which has led to a wide range of  $R_0$  values from 2.2–3.6 to 4.1–6.5.

## The SEIR model

The current study uses the SEIR model. This is a compartment model, common in epidemiological studies. It shows how the disease progresses through interactions between 4 compartments, namely, susceptible, exposed, infectious, and recovered. It is based on three parameters, the rates at which susceptible people become exposed ( $\beta$ ), the exposed become infectious ( $\alpha$ ), and the infectious become recovered ( $\gamma$ ). The last two are inversely associated with the latent period and the infectious period, respectively.

The latent period is the time in which an exposed individual is not yet infectious, and the infectious period is the duration when an infected person can infect others. These may differ from 2-6 days and 3-18 days.

This model captures the most crucial aspect of an epidemiological model, that is, the transition from susceptible to exposed state. This will change with the size of the susceptible and infectious populations and the rate of contact between them, as well as being inversely proportional to the contact period.

## The lockdown debate

Within 45 days from the first reported COVID-19 case in Europe, on January 24, 2020, the pandemic had affected all the 27 countries of the European Union, resulting in an EU-wide lockdown of all external borders. Within the next two weeks, many local travel restrictions and lockdowns followed, with a 95% decline in air travel between EU countries. This sparked immense disagreement based primarily on a lack of consensus as to how this would succeed in reducing the number of new cases.

## **Finding the dynamic reproduction number**

The current study aimed at finding correlations between lockdowns and changing outbreak conditions. It uses a dynamic SEIR model to reflect changing contact rates under lockdown parameters. The model allows calculation of the precise  $R_0$  in different conditions and the time delay between any public health measure and its effect on the outbreak spread. This latter is an essential parameter in deciding how to relax lockdowns in a phased manner, as well as to provide risk estimates with each course of action.

$R(t)$ , the effective reproductive number, is an important parameter in this model as it reflects the change in  $R_0$  (the basic reproduction number) with time and mitigation strategies. The  $R_0$  across Europe is 4.5, being highest in Spain, France, and Germany at nearly 6.0, and the lowest in Estonia, Slovenia, and Malta at around 1.4.

The current effective reproductive number  $R_t$  is much lower, with a mean EU value of 0.72, being highest in Slovakia, Sweden, and Bulgaria at around 1.1 and lowest in Austria, Cyprus, and France at about 0.3. The relative reduction in reproduction number is most substantial in Sweden, Hungary, and Denmark, ranging from 0.58 to 0.44.

The time delay from air travel restrictions to the reduction in effective reproductive number ranges from 1 day in France and Luxembourg to 30 days in Malta, with an EU mean of 13 days.

The SEIR model shows that herd immunity is reached at about 78% infection if the reproductive number is 4.5.

## Advantages of the dynamic SEIR model

The dynamic model used here allows for a changing contact rate, thus helping to predict temporary stable states which are away from the final herd immunity equilibrium. These can show massive and rapid changes once travel restrictions and social distancing regulations are relaxed, but can be studied with this model.

The changing effective reproductive number can also measure the strength of public health measures to help shape policies to contain the pandemic.

It also throws much light on the effect of public health interventions, especially travel restrictions, where France reacted the fastest and Sweden the least. The time delay to any observable effect on the transmission curve is also least in France, at one day, and slowest in Sweden, at 21 days.

Machine learning is also exploited by the researchers to evaluate the enormous volume of data from the pandemic and examine trends and correlations. This has yielded the effective reproduction number in the EU, for instance. This is higher than the number quoted by the World Health Organization (WHO) based on an early contact tracing study in Wuhan, at 2.2 but comparable to the currently cited figure of 5.7 for the Wuhan epidemic.

## Exiting the lockdown

The researchers postulated three sets of conditions; one in which the current reproductive number  $R_t$  is constant at the effective reproductive number  $R(t)$ ; and the other two reflecting the effect of a change from  $R_t$  to the basic reproduction number  $R_0$  for that country, either over one month or over 3 months.

Sweden has not enforced mandatory lockdown, and its reproductive number is still above 1, among the few countries in Europe which are in a similar situation. However, the Swedish situation will probably not change if the current moderate recommendations are removed, unlike the projected steep spike in some other countries like Austria after the removal of lockdown. The difference lies in the individual's willingness to take responsibility for one's health.

“The researchers conclude, “Our dynamic model provides the flexibility to simulate the effects and timelines of various outbreak control and exit strategies to inform political decision making and identify solutions that minimize the impact of COVID-19 on global health.”

## \*Important Notice

*medRxiv* publishes preliminary scientific reports that are not peer-reviewed and, therefore, should not be regarded as conclusive, guide clinical practice/health-related behavior, or treated as established information.

### Journal reference:

- Linka, K. et al. (2020). The Reproduction Number Of COVID-19 And Its Correlation With Public Health Interventions. *medRxiv* preprint doi: <http://medrxiv.org/cgi/content/short/2020.05.01.20088047>



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