

Attacking the Covid-19 with the Ising-model and the Fermi-Dirac Distribution Function

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We employ a spin $S = 1/2$ Ising-like model and a Fermi-Dirac-like function to describe the spread of Covid-19. Our analysis, using the available official infections rate data reveals: *i*) that the epidemic curves, i.e., the number of reported cases *versus* time, is well-described by a Gaussian function; *ii*) that the temporal evolution of the cumulative number of infected people follows a distorted Fermi-Dirac-like distribution function; *iii*) the key role played by the quarantine in the prevention of the spread of Covid-19 in terms of an *interacting* parameter, which emulates the contact between infected and non-infected people. An analysis of the epidemic curves for Ebola, SARS, and Influenza A/H1N1 is also presented and described by a Gaussian function as well. Our findings demonstrate the universal character of well-established concepts in condensed matter Physics and their applications in different areas. Although initially proposed for describing magnetic systems, over the last decades the Ising-model ¹ has been revealed as an appropriate tool to describe several phenomena. Indeed, this includes the supercooled phase of water ², the vicinity of the Mott critical end point ³⁻⁵, magnetic field-induced

quantum critical points ⁶, econophysics ⁷, democratic elections ^{8,9}, as well as the spread of diseases ^{10–13}, just to mention a few examples. In the particular case of epidemics, every hour counts and there is an urge in predicting the temporal evolution of the disease aiming to find the best way to deal with it and to establish a proper control of its spread. Recently, the pandemic Covid-19 (Coronavirus disease) has been rapidly spreading all over the world, being needless to mention the impact of it in our lives in a broad context, see, e.g., Refs. ^{14–19}. It has been proposed that such a quick spread of Covid-19 in human beings is associated with a spike protein, which in turn has a site that is triggered by an enzyme called furin. The latter lies dangling on the surface of the virus, leading thus to the infection of human cells unfortunately much more easily ²⁰. Therefore, there is an urgency of an appropriate mathematical description of the spread of Covid-19. This is particularly true aiming to support the health government agencies all over the world to maximize the effectiveness of medical support strategy in such a global crisis. To this end, here we make use of the celebrated Ising-model ¹ and of a Fermi-Dirac-like function ²¹. We demonstrate the close relation between the number of people following the proposed quarantine and the spread of Covid-19. Although it is quite obvious that the more people respect the quarantine the lower will be the number of infected people, a proper quantitative description is still lacking.

The model

We consider that the *interaction* (contact) $\delta\varepsilon$ between infected and non-infected people can be associated with the magnetic interaction between nearest-neighbour magnetic moments in the well-established Ising-model ^{2,5,22,23}. Hence, analogously to the case of the Ising-model for magnetism

with spin $S = 1/2$, we assume that the number of infected people $p_i = +1/2$ is N^+ , while the number of non-infected people $p_i = -1/2$ is labelled by N^- , being $(N^+ + N^-) = N$ where N is the total number of considered habitants. In other words, infected and non-infected people can be identified considering a $S = 1/2$ Ising-like variable $p_i = +1/2, -1/2$, so that we write $N^+ = \sum_{i=1}^N 2 \left(p_i + \frac{1}{2}\right) p_i$, and $N^- = \sum_{i=1}^N 2 \left(p_i - \frac{1}{2}\right) p_i$. Yet, we consider that two people who are infected by Covid-19 have no effect on each other, so that in this case the interaction $\delta\varepsilon = 0$ and, otherwise, $\delta\varepsilon \neq 0$. In the same way, a non-infected person has no effect in another non-infected person. Essentially, in our approach $\delta\varepsilon$ quantifies, at some extent, the key role played by the quarantine in the spread of Covid-19. Following a similar mathematical treatment reported by us elsewhere, cf. Ref.⁵, we write a function for the total population C_T taking into account the contact between non-infected and infected people, which is emulated by $\delta\varepsilon$:

$$C_T = C_h - 4\delta\varepsilon \sum_{i \neq j=1}^N \left[\left(\frac{1}{2} + p_i\right) \left(\frac{1}{2} - p_j\right) + \left(\frac{1}{2} - p_i\right) \left(\frac{1}{2} + p_j\right) \right] p_i p_j, \quad (1)$$

where C_h is the total number of healthy people before the spread of the virus and p_j refers to a neighbour person of p_i . Note that the second term of the right side of Eq. 1 will always be negative for $p_i = +1/2$ and $p_j = -1/2$ and vice-versa. Furthermore, Eq. 1 indicates that, when $\delta\varepsilon \neq 0$, i.e., infected people interact with healthy people, C_h is decreased. Evidently the total number of the population remains constant. In order to determine a proper mathematical expression for $\delta\varepsilon$, one must take into account the number of isolated people n in quarantine. Here, we propose that the contact between infected and non-infected people can be described considering $\delta\varepsilon \propto n^{-1/2}$, with $1 < n < N$. As a matter of fact, we have tried different power-laws for $\delta\varepsilon$ in terms of n , but it turns out that $\delta\varepsilon \propto n^{-1/2}$ provides an appropriate fit for the data set. This is a reasonable

assumption, since as $n \rightarrow 0$, $\delta\varepsilon \rightarrow \infty$, i.e., the lower the number of isolated people in quarantine the higher will be the contact between them and, consequently, the number of infected people will be enhanced. Note that Eq. 1 does not incorporate any time evolution. It turns out that upon analyzing already officially reported epidemic curves^{24,25}, their typical time evolution in terms of the new cases *per* day follows an initial rapid increase of the number of infected people, which is usually assumed to be exponential, achieving a maximum value, which is followed by a drop. Essentially, in qualitative terms, the typical shape of epidemic curves is more or less the one of a simple Gaussian function. For the sake of completeness, we recall the mathematical expression for the Gaussian function:

$$y(t) = y_0 + \frac{A}{w\sqrt{\frac{\pi}{2}}} e^{-2\frac{(t-t_c)^2}{w^2}}, \quad (2)$$

where y_0 is related with an initial value, A is a normalization constant associated with the area under the curve, t is the time, t_c is the value of t associated with the maximum value of $y(t)$, and $w = 2\sigma$, where σ is the standard deviation. Hence, following a similar analysis employed by the authors of Ref.⁸, we make use here of a simple Gaussian function to describe the spread of Covid-19. In our analysis, the interaction between infected and non-infected people is incorporated in the Gaussian function by summing up $n^{1/2} \propto \delta\varepsilon^{-1}$ in t_c and w into the Gaussian function. We emphasize that in our analysis, we have summed up $\delta\varepsilon^{-1}$, as previously described, based on the argument that when the number of people n in quarantine is increased, the contact between infected and non-infected people is reduced and, as a consequence, $\delta\varepsilon^{-1}$ is increased. This gives rise to a broadening of the Gaussian distribution function, so that w is increased and its maximum is reduced. We stress that our analysis on $\delta\varepsilon$ in the Gaussian function was only possible due to the

Ising-like model that we have introduced previously, within which $\delta\varepsilon$ has its genesis. Given the relatively large amount of available data for China and the achievement of a proper control of the spread of Covid-19 in its territory, we propose a simple model ²⁶ assuming a maximum number of possible infected people labelled by P ; considering $I(t)$ the number of infected people in time t and, as consequence, $[P - I(t)]$ is the number of people that can be infected. Note that $[\frac{P-I(t)}{P}]$ corresponds to the percentage of the population that will be infected. Also, we consider that the number of people that can be infected by $I(t)$ in a time interval Δt is $[\frac{P-I(t)}{P}] n^* \Delta t$, where n^* quantifies how many times an infected person interacts with a non-infected person. The number of infected people in a time $(t + \Delta t)$ minus the number of infected people at t is proportional to the number of people of the population that can be infected by the already existent infected people at a given time t . Hence, it is straightforward to write:

$$\frac{I(t + \Delta t) - I(t)}{\Delta t} = K \left\{ \left[\frac{P - I(t)}{P} \right] n^* I(t) \right\}, \quad (3)$$

where K is a non-universal proportionality constant. Upon taking the limit when $\Delta t \rightarrow 0$ in both sides of Eq. 3, we achieve the following differential equation:

$$\frac{dI}{dt} = C \left(\frac{P - I}{P} \right) I, \quad (4)$$

where $C = Kn^*$ quantifies the frequency of infection. Making the integration in both sides of Eq. 4, we have:

$$I(t) = \frac{P}{me^{-Ct} + 1}, \quad (5)$$

where m is a non-universal integration constant. Equation 5 has some reminiscence of the well-known Fermi-Dirac (FD) distribution function. It provides a robust description for the evolution

of the number of infected people $I(t)$ over time, saturating at P . The data set for Covid-19 here discussed are available in Ref.²⁷ and were taken until the date of the submission of this manuscript. It is worth mentioning that we have focused our analysis in countries presenting a more advanced picture of the Covid-19 spread, such as South Korea and China²⁷.

Data analysis and discussion

Aiming to demonstrate the validity of our analysis, we start recalling the data set for Ebola, SARS, and Influenza A/H1N1. Their epidemic curves, depicted in Fig. 1, can be described by a fitting

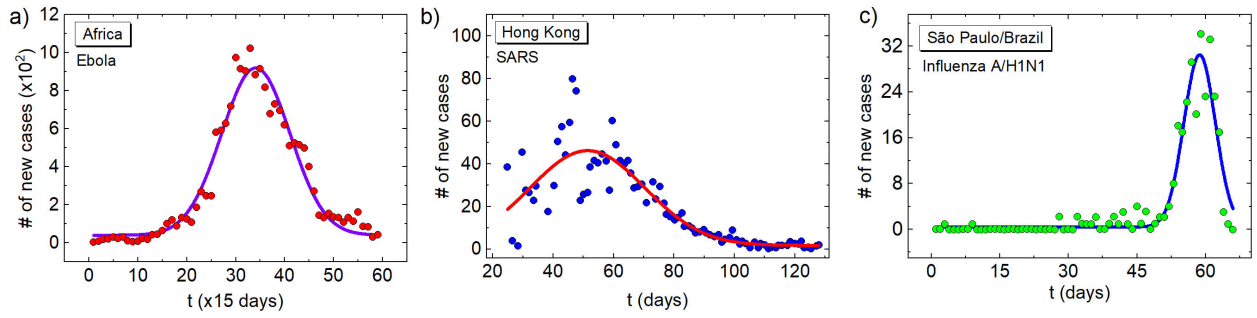


Figure 1: Number of new cases *versus* time in days for: a) Ebola²⁸, b) SARS²⁹, and c) Influenza A/H1N1³⁰. The solid lines in all panels represent the Gaussian fitting of the data set for each case. Details in the main text.

employing a Gaussian function. Table 1 shows the parameters obtained in the fitting for the various epidemics (Fig. 1) and their respective standard deviations. At this point, it is worth emphasizing that the Gaussian fitting for the epidemic curves must be performed carefully, since the low density [see, e.g., Fig. 1 b)] of available data can give rise to a non-intrinsic behavior. In other words, it is clear that it is not possible to make a forecast of an epidemic curve by only employing the data set associated with the initial growth of the epidemic curve. Now, we focus on the analysis of

the spread of Covid-19. We start with the available data set for Covid-19 in South Korea, see Fig. 2 a). The number of people joining the quarantine is directly associated with the previously defined *interaction* (contact) $\delta\varepsilon$ between infected and non-infected people. As discussed, in a hypothetical situation where no one joins the quarantine $n \rightarrow 0$ and so $\delta\varepsilon \rightarrow \infty$, which means that everyone interacts freely with each other. This would be the worst case at all. It has been broadly discussed that upon increasing the number of infected people in quarantine, the maximum in the epidemic curve associated with the number of new cases is not only lowered, but it is also shifted, indicating that the spread of Covid-19 will be more contained. The latter corresponds to the desired situation in terms of controlling the spread, since the health government agencies will have more time to manage the situation. Note that our analysis based on the Ising-like model incorporates such feature, already discussed in the media, see, e.g., Ref.³¹. We demonstrate such a situation employing the data set available for South Korea, assuming an hypothetical finite $\delta\varepsilon$ incorporated in the Gaussian function employed in the analysis, cf. depicted in the inset of Fig. 2 a). More specifically, when $\delta\varepsilon$ is lowered the maximum number of infected people is decreased and its position in time is increased, making thus the disease spread more controllable. Such decrease in $\delta\varepsilon$ represents more people joining the quarantine and avoiding contact with each other. Now, we treat the available data set of the spread of Covid-19 in China in terms of the FD-like distribution function. As depicted in Fig. 2 b), the number of accumulated infected people *versus* elapsed time saturated after roughly 60 days since the outbreak of Covid-19. In other words, for large values of t the ratio $I(t)/P \rightarrow 1$. Equation 5 fits nicely such data set, cf. Fig. 2 b). In the following, we

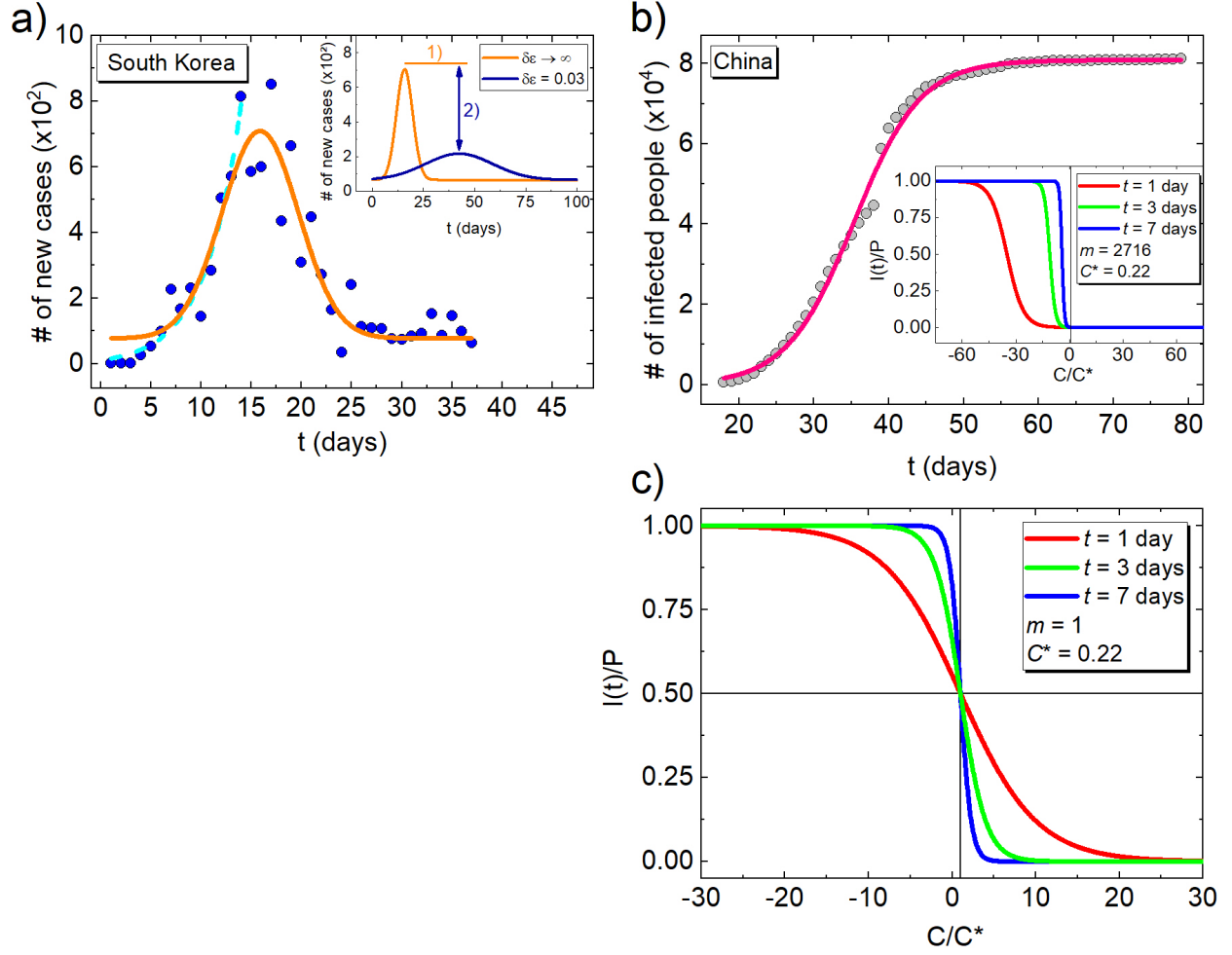


Figure 2: **a)** Number of new cases *versus* time (in days) for Covid-19 in South Korea, fitted with a Gaussian (orange color solid line) and exponential (dashed cyan line) functions. **Inset:** corresponding Gaussian fit for $\delta\varepsilon \rightarrow \infty$ (orange color solid line) and $\delta\varepsilon = 0.03$ (navy blue solid line); 1) delimitates the maximum number of new cases for $\delta\varepsilon \rightarrow \infty$ and 2) the reduction of the number of new cases when the number of people in quarantine is increased ³¹. **b)** Accumulative number of infected people *versus* time (in days) of Covid-19 for China and the correspondent fitting (pink solid line) employing Eq. 5. **Inset:** $I(t)/P$ *versus* C/C^* with $m = 2716$ and $C^* = 0.22$ for 1 day (red solid line), 3 days (green solid line), and 7 days (blue solid line). **c)** $I(t)/P$ *versus* C/C^* with $m = 1$ and $C^* = 0.22$ for 1 day (red solid line), 3 days (green solid line), and 7 days (blue solid line). Details in the main text. Data set available in Ref. ²⁷.

discuss the similarity between Eq. 5 and the FD distribution function. Rearranging Eq. 5, we have:

$$\frac{I(t)}{P} = \frac{1}{me^{(C-C^*)t} + 1}, \quad (6)$$

being C^* a constant introduced to play the role of the Fermi energy in the electron gas ²¹. Note that $I(t)/P \leq 1$ and, for $m = 1$ we have exactly the same form of the FD distribution function $f(E, T)$ ²¹, where E and T refer, respectively, to the energy and temperature. In the present case, C plays a role analogous to the energy for the Fermi gas, while t is analogous to Boltzmann factor $\beta = 1/k_B T$, where k_B is Boltzmann constant. Indeed, the time evolution of the Covid-19 spread has a similar significance than T for the FD distribution function for the Fermi gas. The behavior of $I(t)/P$ as a function of C/C^* is shown in the inset of Fig. 2 b) for several values of t . Considering that in our fit using Eq. 5 for the spread of Covid-19 in China [inset of Fig. 2 b)] we have obtained $m = 2716$, it becomes clear that we are dealing with a distorted variation of the FD function where $m = 1$, cf. Fig. 2 c). Hence, at some extent, we are faced with a behavior analogous to the distorted FD distribution for electrons in the picture of Landau Fermi-liquid ^{32,33}. Also, we emphasize that the ratio $I(t)/P$ gives us the probability of a person being infected in a certain time t in a similar way that $f(E, T)$ dictates the probability of a state with energy E being occupied at a certain temperature T . We anticipate that the spread of Covid-19 for other countries, not discussed in the present work given the lack of available data, should follow the same behavior as here discussed for South Korea and China. The position of the maximum in the epidemic curve, described by a Gaussian function, as well as $I(t)$, will be a reflex of the policies taken by the health government agencies by a particular country. Last but not least, this work was written during our period of quarantine.

Conclusions and perspectives

We have used a $S = 1/2$ Ising-like model and a Fermi-Dirac-like distribution function to describe the Covid-19 spread. Our analysis reveal that a Gaussian function suffices to describe the epidemic curves. The temporal evolution of the number of infected people has some resemblance with a distorted Fermi-Dirac-like distribution function found in the picture of Landau Fermi-liquid. The quarantine plays a crucial role in the amendment of Covid-19 spread. The present work highlights the universal character of fundamental concepts in condensed matter Physics and their possible applications to other subject areas. We hope that the governmental health agencies can have benefits from it.

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Author contributions

MdeS, LS wrote the paper with contributions from ACS and IFM. LS and IFM participated in some of the discussions and generated the figures. All authors revised the manuscript. MdeS conceived and supervised the whole project.

Additional Information

Competing Interests: The authors declare no competing interests.

Disease	y_0	A	w	t_c	σ
Ebola	41	15418	13.98	34.08	6.99
SARS	2	2122	38.08	51.39	19.04
Influenza A (H1N1)	0.42	260	6.89	58.69	3.44
Covid-19 (South Korea)	78	6055	7.65	15.89	3.82

Table 1: Gaussian fitting parameters for several epidemics [see Fig. 1 and Fig. 2 a)]. The lack of available full data set compromises the accuracy of the fittings. Details in the main text.