

Time evolution of the covid19 plague using the stochastic Langevin equation.

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Abstract.

We used the Langevin stochastic equation to show the contribution of stochastic effects in the time evolution of the covid19 plague. It was shown that stochastic effects play a predominant role at the beginning of the plague evolution and cannot be ignored for later times.

Key words: covid19 plague; time evolution; stochastic Langevin equation.

(1) Introduction.

Our paper was inspired by the work published by Enrico Fermi in 1949^[1] "On the Origin of the Cosmic Radiation". He showed how charged cosmic rays are accelerated by interstellar stochastically fluctuating electromagnetic fields, reaching extremely high kinetic energies $\varepsilon = mv^2/2$. Using subtle arguments, Fermi concluded that the energy variation per unit of time $d\varepsilon/dt$ was proportional to ε , that is, $d\varepsilon/dt \sim \varepsilon$. Thus showed that, after a time t expended by the charge trip in the interstellar space, its energy increases exponentially like $\varepsilon(t) = m_0 c^2 \exp(\theta t)$, where m_0 is rest mass of the charge, c the light velocity and θ is a constant.^[1]

The pandemic propagation of virus or bacterial infections depend on many factors like, for example, hygienic and economic conditions, genetic, transmission dynamics, climatic, geographic and immigrations. That is, the number of infections $n_i(t)$ per unit of time are functions of many variables and interrelations between them. So, mathematical predictions of the time evolution of a plague is extremely difficult. Many attempts have been done involving long analytic and numerical calculations.^[2-4] Some papers, for instance, have been written inspired by the Lotka -Volterra and nonlinear models of interacting populations.^[5-7]

Analyzing recent papers of Ciufolini and Paolozzi^[8] one can see, from their Figures 1 and 3, that the infected number $n_i(t)$ with the covid19 in China and Italy, initially seems to increase exponentially with t . Thus, we suspected that, as occurs with the cosmic rays, the temporal evolution

of $n_i(t)$ could also be governed, at the beginning, by stochastic laws. To investigate this we assumed that $n_i(t)$ could be described by the stochastic Langevin equation^[9,10] which has a factor $n_i(t)/dt \sim n_i(t)$, similar to $d\varepsilon/dt \sim \varepsilon$, obtained by Fermi.^[1]

(2) Stochastic Langevin equation.

Let us assume that the number of infected persons, per unit of time, $dn_i(t)/dt$, obeys the stochastic Langevin equation:^[9]

$$dn_i/dt = \lambda_i n_i + \xi(t) \quad (2.1),$$

where $\lambda_i = \text{constant}$ = gives the probability of infections per unit of time and $\xi(t)$ is a "noise function". Putting $n_i(t) = u_i(t)\exp(\lambda_i t)$, where $u_i(t)$ is a function to be determined and replacing $n_i(t)$ in the Eq.(2.1) we get

$$du_i(t)/dt = \exp(\lambda_i t)\xi(t) \quad (2.2).$$

Integrating Eq.(2.2):

$$u_i(t) = u_{i0} + \int_0^t \exp(\lambda_i t') dt' \quad (2.3),$$

where u_{i0} is a constant of integration. Consequently, with Eqs.(2.1) and (2.3) we obtain:

$$n_i(t) = n_{i0} \exp(\lambda_i t) + \exp(\lambda_i t) \int_0^t \xi(t') \exp(-\lambda_i t') dt' \quad (2.4),$$

where n_{i0} is the number of infected at $t = 0$. Averaging $n_i(t)$, given by Eq.(2.4), over all stochastic processes involved in the plague at a time t and taking into account that the average $\langle \xi(t) \rangle = 0$ we get,

$$\langle n_i(t) \rangle = \langle n_{i0} \rangle \exp(\lambda_i t) \quad (2.5),$$

where $\langle n_i(t) \rangle$ is the average number of infected and $\langle n_{i0} \rangle$ is the initial average number.

We do not intend to determine the complex infectious processes responsible for the probabilities λ_i . We only want, using Eq.(2.5), to obtain λ_i values able to explain the diagnosed cases $n_i(t)$.

According to Eq.(2.5), $\langle n_i(t) \rangle$ is proportional to $\langle n_{i0} \rangle$ and increases exponentially from $\langle n_{i0} \rangle$ up to infinite. However, as is known, in a population with N persons only N^+ persons would be infected by some kinds of virus or bacteria. From Figures 1 and 3 of Ciufolini and Paolozzi^[8] we see that $n_i(t)$ increases with t , from 0 up to a time t^* . For $t > t^*$, $n_i(t) =$

$N^* = \text{constant}$. In general, due to quarantines and lockouts $N^+ > N^*$.

In **Appendix** are seen figures published by Ciufolini and Paolozzi^[8] showing the diagnosed cases $n_i(t)$ of the covid19 plague in China and Italy, respectively. We have $N^* = 80.000$ for China and $N^* = 200.000$ for Italy.

Note that Eq.(2.5), $n_i(t)$ is proportional to the initial number of infected n_{i_0} . This means, for example, that if n_{i_0} sick immigrants enter a country the number of infections will be amplified by a factor n_{i_0} .

To simplify our calculations, putting $\langle n_{i_0} \rangle = 1$ and using Eq.(2.5), it was verified that for $\lambda_i = 0.37 \pm 0.01$ there is a fair agreement between our predictions and diagnosed cases in Italy^[8] in the interval $0 \leq t < 30$ days. Our predictions and the diagnosed cases are seen in **Figure 1**.

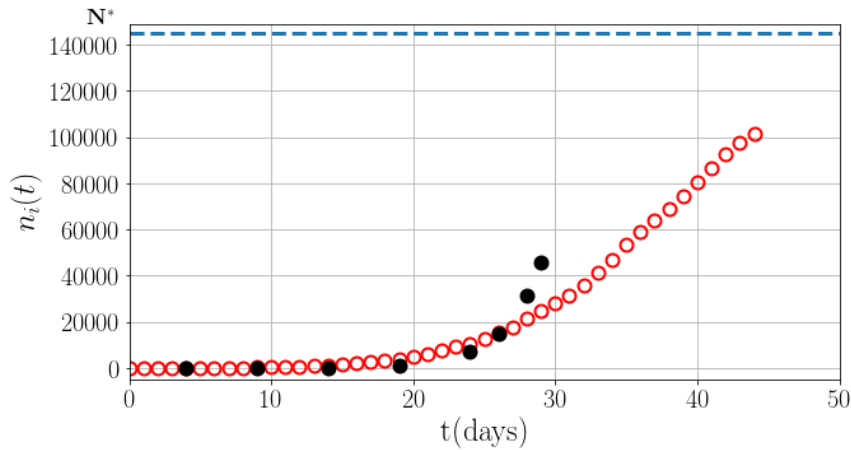


Figure 1. The diagnosed cases in Italy (red circles) and our predictions (black dots). There is a fair agreement only for $t < 30$ days.

From **Figure 1**, we note that only for $t < 30$ days there is a good agreement between our predictions and the diagnosed cases. For $t > 30$ days the $n_i(t)$ evolution cannot be only explained by the stochastic Langevin equation. For times $t > 30$ days, according to **Section 1**, mathematical predictions for $n_i(t)$ involve long analytic, nonlinear models of interacting populations and numerical calculations.^[2-4,5-7]

We were not able to perform a similar analysis for the $n_i(t)$ results for China because the $n_i(t)$ values for the initial times of the infection are not clearly shown in reference.^[8]

The number of deaths (fatalities) $n_d(t)$ can be estimated by $n_d(t) = P_d n_i(t)$ where P_d is the probability of deaths. These numbers, for China and Italy, are given by of Ciufolini and Paolozzi.^[8]

(3) CONCLUSIONS.

Langevin approach gives for Italy a fair description of the $n_i(t)$ evolution only for times $0 \leq t < 30$ days. That is, stochastic effects seem to be predominant for initial times. For $t > 30$ days only stochastic Langevin effects are not sufficient to describe $n_i(t)$. More complex, long analytic and numerical calculations^[2-4,5-7] must be used to describe $n_i(t)$.

As the plague propagation depends on the interaction between infected and non infected persons let us assume that the population is a gas composed by N^+ **white** molecules and by $n_i(t)$ **black** molecules. Collisions between molecules of the same color do not alter their colors. However, when a black molecule collides with a white one this molecule becomes black. Thus, as the time increases the number of black molecules ($n_i(t)$) increases and the number of white molecules (N^+) decreases. In this way, the infection probability per unit of time λ_i must decrease as time increases. Since for times $0 \leq t < 30$ days we have $N^+ \gg n_i$ the parameter λ_i can be taken constant, that is, $\lambda_i \approx \text{constant} = 0.37$.

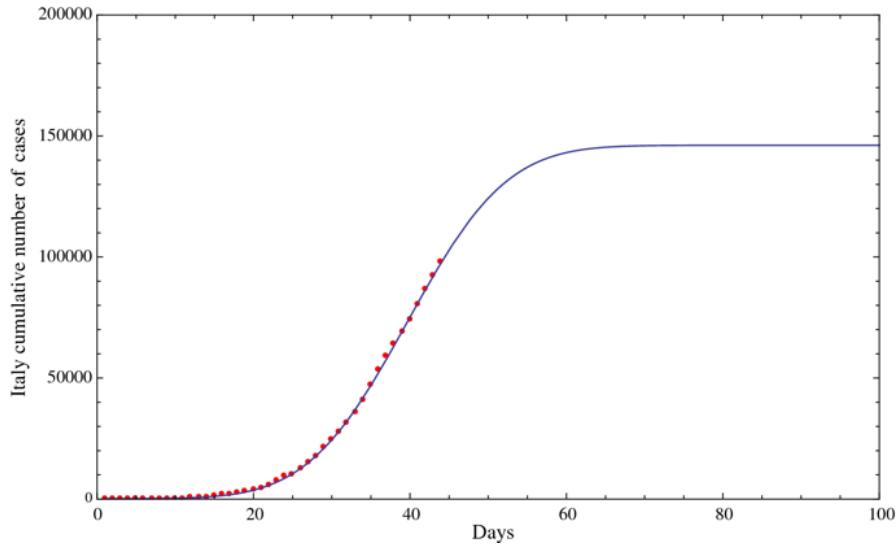
Finally, as interactions are stochastic we believe that stochastic effects would be important in the $n_i(t)$ evolution for all instants of time.^[2]

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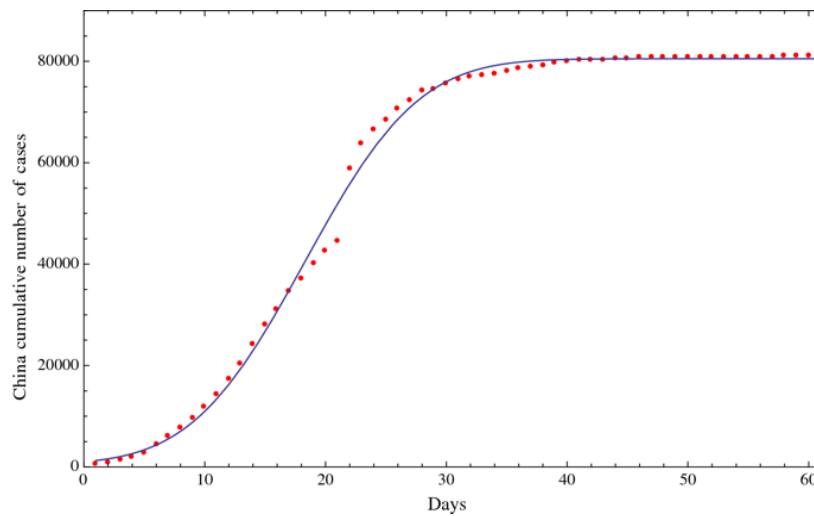
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APPENDIX. Figures showing the temporal evolution of the covid19 plague in Italy and China from the Ciufolini and Paolozzo paper^[8]



Italy(Figure 3 of reference 8)

The red dots are diagnosed cases. The continuous line was obtained by a best fit with the diagnosed cases and extending the curve up to the saturation value $N^* \approx 150.000$.



China(Figure 1 of reference 8).

The red dots are diagnosed cases and the continuous line was obtained by a best fit with the diagnosed cases. In this case $N^* \approx 80.000$.