Convolution-based Machine Learning To Attenuate Covid-19's Infections in Large Cities

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***Abstract*—In this paper a nonlinear mathematical model based at convolution theory and translated in terms of Machine Learning philosophy is presented. In essence, peaks functions are assumed as the pattern of rate of infections at large cities. In this manner, once the free parameters of theses patterns are identified then one proceeds to engage to the well-known Mitchell's criteria in order to construct the algorithm that would yield the best estimates as to carry out social intervention as well as to predict dates about the main characteristics of infection's distributions. The distributions are modeled by the Dirac-Delta function whose spike property is used to make the numerical convolutions. In this manner the parameters of Dirac-Delta function's argument are interpreted as the model parameters that determine the dates of social regulation such as quarantine as well as the possible date of end of first wave and potential periods of the beginning of a second one. The theoretical and computational approach is illustrated with a case of outbreak depending on free parameters simulating the implementation of new rules to detain the infections.**

I. Introduction

Recently, the apparition of Corona Virus Disease (Covid-19 in short) [1] has triggered the alarms of global public health operators as to apply the more robust schemes of recovering and surveillance. Although to date, the first wave of pandemic is in most countries reaching its end, it is rather natural to ask about what we have learned from world-wide datasets [2]. In fact, as seen at all surveillance systems in all affected countries, the understanding of data would exhibit imminent differences among them because the multicultural manifestations of societies as to face the arrival of a pandemic, as well as the level of resilience of them for recovering as soon as the conditions have been applied. These resilience implies the containment against the fast spread of strain in all cities either middle or large [3]. In this paper, attention is paid on theoretical and computational study of Covid-19 pandemics. As seen for example from data ranging between March and September, the presence of well-defined peaks and strong stochastic fluctuations, reinforce the hypothesis that in more cases (countries) the dynamics of spread and subsequent infections by Covid-19 appears to be strongly [4] related to randomness, fact that becomes a fundamental argument that states that diseases would follow a random pattern as consequence of the confluence of various variables [5].

Thus, this paper suggests the introduction of peaked-profiles in a mathematical mechanism of convolution that involves the Dirac-Delta function. The fact for using these function is because their spike property that makes them a strong candidate to model the intervention aimed to reduce the increasing of infections in a certain period [6].

Commonly in pandemic epochs one expects a firm set of roles coming from the epidemiology such as: **Role of the Epidemiology**

- Identify the strain and its main properties.
- Estimate possible impact on people.
- Identify the strength of the public health services [7][8].
- Take decisions to opt the correct pharmacology.

Under the assumption that the behavior of outbreak is to some extent dictated by randomness, a quasi-realistic computational-mathematical model would have the following properties:

- Estimate Probabilities of the velocity for virus spreading
- Adjudicate a value for all possible scenarios before decision
- Determine with high precision the resources to be used in the first weeks
- Estimate the before and after the implementation of the algorithm.

In this manner one expects that any universal algorithm based on the policy of Machine Learning [9] is able to yield estimates that based on the Tom Mitchell's [10] criteria given by (1) Task, (2) Performance and (3) Experience, establish a support to extract the parameters of dynamics of infections. Therefore, once the system parameters have been extracted, all of them are related to definitions entirely belonging to Epidemiology [11]. Special attention is paid on the impact of such parameters on the accumulation of infections for both short and large periods.

In concrete, this paper employs the convolution together to a nonlinear Dirac-Delta function $\delta[G(\alpha,\tau)]\delta[G(\alpha,\tau)]$ whose integration can be written as:

$$\mathbf{N}(t) = \sum_{\ell}^{L} \int_{(\ell-1)t}^{\ell t} d\tau \sum_{q}^{Q} \mathbf{B}_q(\beta\tau)\delta[G(\alpha,\tau)], \quad (1)$$

with $\mathbf{B}(\beta\tau)$ a peaked distribution and β, α the dynamics parameters. This paper is structured as follows: In second section, the mathematical machinery is presented whereas in third section the Mitchell's criteria are implemented. In fourth section the theoretical scenarios are confronted to their realistic pairs from official data. Finally the conclusion of paper is drawn.

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II. The Mathematical Approach

Consider the beginning of an outbreak dictated by a time-depending distribution inspired from Eq.(1) given by $\mathbf{B}(\tau, u)$, then one can argue that exists an operation of convolution given by:

$$\mathbf{B}(\tau) = \int du \mathbf{B}(\tau, u)\mathbf{H}(u). \tag{2}$$

When $\mathbf{B}(\tau, u)$ as well as $\mathbf{H}(u)$ depends on free parameters, then Eq.(2) acquires the form as:

$$\mathbf{B}(\tau, \alpha, \beta) = \int du \mathbf{B}(\tau, u, \alpha)\mathbf{H}(u, \beta). \tag{3}$$

Of course the function $\mathbf{H}(u, \beta)$ is not unique and contains a infinite sum of weighted function in the form as:

$$\mathbf{H}(u, \beta) = \sum_{q}^{Q} \beta_q \mathbf{h}_q(u), \tag{4}$$

by which when it is inserted in Eq.(3) one obtains that:

$$\mathbf{B}(\tau, \alpha, \beta_q) = \sum_{q}^{Q} \beta_q \int du \mathbf{B}(\tau, u, \alpha)\mathbf{h}_q(u), \tag{5}$$

thus while $\int du \mathbf{B}(\tau, u, \alpha)\mathbf{h}_q(u)$=$\mathbf{b}_q(\tau, \alpha)$ then Eq.(5) is reduced to:

$$\mathbf{B}(\tau, \alpha, \beta_q) = \sum_{q}^{Q} \beta_q \mathbf{b}_q(\tau, \alpha). \tag{6}$$

In this manner one can give a naive interpretation to Eq.(6): the beginning might be actually the succession of various "beginnings". In praxis, experience tells that usually $Q = 2$, denoting a truncated system. In terms of Epidemiology, these beginnings are restricted to two waves of pandemic, so that the entire process of outbreak and infections. Thus one expects that previous to the outbreak event, the strain has moved randomly in space and time triggering a multiple infection in a large city. In this manner this is mathematically translated as:

$$\mathbf{B}(\tau, \alpha, \beta_q) = \beta_0 \mathbf{b}_0(\tau, \alpha) + \beta_1 \mathbf{b}_1(\tau, \alpha) + \beta_2 \mathbf{b}_2(\tau, \alpha), \tag{7}$$

that states that any pandemic can be perceived as a chain of events by the which one calls waves [12]. In this manner one associates each period as:

$$\mathbf{B}(\tau, \alpha, \beta_q) == \begin{cases} \beta_0 \mathbf{b}_0(\tau, \alpha) & \mathrm{Pseudo-stability} \\ \beta_1 \mathbf{b}_1(\tau, \alpha) & \mathrm{Firstwave} \\ \beta_2 \mathbf{b}_2(\tau, \alpha) & \mathrm{Secondwave}, \end{cases}$$

with the β_q playing the role as amplitude of waves that is seen from the epidemiological angle as the peaks of the number of infections. Furthermore the definition of "Pseudo-stability" refers to the time where the strain has arrived to a large city although not any critic variable emerges, the infections are done randomly. One potential scenario is that of $\beta_1 > \beta_2 > \beta_0$, denoting that the first wave has more impact the a second one. Thus, one expects that the rate of infections distribution displays peaked morphologies as consequence of the random displacement of strain by producing a fast accumulation of infections in the shortest times [13]. In this way one requires the implementation of a set of functions that models the effect of the rapid interventions [14]. Therefore it is plausible to postulate the well-known Dirac-Delta that operates in a convolution operation as

$$\mathbf{b}_q(\tau, \alpha) = \int \delta(s - \tau)\mathbf{b}_q(s, \alpha) ds, \tag{8}$$

that by following the definition of Eq.(6) then one arrives to:

$$\mathbf{B}(\tau, \alpha, \beta_q) = \sum_{q}^{Q} \beta_q \int \delta(s - \tau)\mathbf{b}_q(s, \alpha) ds. \tag{9}$$

However, the more general case contemplates that instead sa linear formulation of Dirac-Delta function's argument it acquires an universal formulation given by the change: $s - \tau \to \mathbf{D}(s, \tau)$ so that Eq.(9) can be written as:

$$\mathbf{B}(\tau, \alpha, \beta_q) = \sum_{q}^{Q} \beta_q \int \delta[\mathbf{D}(s, \tau)]\mathbf{b}_q(s, \alpha) ds. \tag{10}$$

Clearly emerges the question: What is the mechanism to solve the Dirac-Delta integration as written in Eq.(8) when an universal function or also polynomial is involved? As given in [15] there is a procedure to evaluate integration of this type. Nevertheless in praxis one can assign in the *adhoc* manner a polynomial that aims to fit real data and therefore to make an approximation that engages the morphology of the infections distribution.

A. The Spike Property of Dirac-Delta Function

The well-known Dirac-Delta function exhibits notable applications in various disciplines and fields through its main property that is connected to Eq.(8) $f(t) = \int f(\tau)\delta(t - \tau) dt$. As explained above ans stated in Eq.(10) the logic extension demands to define another interesting property that is well-known as the spike property in the sense that Eq.(8) can be written as: $\delta[f(\tau)] = \delta\left[\prod_{i=1}^{N}(\tau - a_i)\right] = \sum_{i=1}^{N} \frac{\delta(\tau - a_i)}{\frac{df(\tau)}{d\tau}|_{\tau = a_i}}$ where one can formulate the general definition for $f(\tau) = (\tau - a_1)(\tau - a_2)...(\tau - a_{N-1})(\tau - a_N)$ denoting a function whose zeros are as follows: $a_1, a_2, ..., a_{N-1}, a_N$. For instance $f(t) = \int f(\tau)\delta(t^2 - \tau^2) dt \approx f(t)/2t$ that makes us to argument in the case that $\delta(t^m - \tau^n)$ the resulting convolution gets the form $f(t)/t^{n-1}$, thereby demonstrating that the resulting integration depends on $1/t^{n-1}$. It is also possible express $f(\tau)$ as $f(t, \tau)$ thereby suggesting to rewrite (1) in a most general manner

$$\delta[f(t, \tau)] = \begin{cases} \delta\left[\prod_{i=1}^{M}(t - \tau - a_i)\right] & \mathrm{simple} \\ \delta\left[\prod_{j=1}^{N}(\gamma_j t - \rho_j \tau - a_j)\right] & \mathrm{multi-parameter} \end{cases} \tag{11}$$

where the terminology "multi-parameter" express the fact that the argument contains γ_j, ρ_j and a_j free parameters in clear contrast to the "simple" case that only one sees that a_j turns out to be the unique set of parameters.

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III. The Machine Learning Modeling

A. The Tom Mitchell's Criteria

The science of Machine Learning gives offers multiple paths to solve complex problems. In this paper, the interest of using this technology is essentially the requirement of implement intelligent systems that can encompass the human decisions with a minimal cost and minimal risk. Clearly this is in accordance with the view of Epidemiology that in pandemic epochs has as main end to keep a solid resilience as to as fast recovering due to the consequences that appear during and after the strain has entered to a city. In its book, Tom Mitchell defines that any universal system can be perceived as one that satisfies the following characteristics:

- **All system has a task** that reflects the fact that the system justifies its existence. This translated in terms of Epidemiology express that once a pandemic has initialized and the strain is identified, the the system or public health operator has as main target to minimize the spread of virus in people as well as to recover the ones that have been infected.
- **All system has a performance to tackle down the task** Once the task is defined then the system requires to design a robust strategy to successfully surpass the different phases that the task would exhibit. This performance usually employs computational methodologies in order to seek an accurate solution without a substantial bias in both the quantitative results and the interpretation of them. In the territory of Epidemiology one can see that the performance targets to reduce the number of infections at time and to assess the capabilities of the health centers in order to provide medical assistance to the confirmed infections. In parallel, local official might also to suggest social regulation such as quarantine, curfew and promote rules of distancing among people. In this manner, the whole performance is seen as the decision to apply rules and therefore one would expect their consequences.
- **All system acquires experience** Once the performance has been applied and the system is able to evaluate whether this application was successful or failed, then there is a chance to reconfigure the mechanisms that have lead to solve the task. Here is manifested the probabilities of success of fail. Thus, in pandemic epochs, it is desired that the imposed rules should exhibit notable differences with respect to before and after. For example, given a number of infected N along a period, then after the social rules one would expect that a fraction M with $M < N$ for a subsequent period.

In this manner one can associate a mathematical model that encompasses these criteria whose end is that of reducing the number of infections in the shortest periods without affecting the ordinary mechanisms that sustain the societies. Therefore one can construct a formalism targeting the minimization of infections through concrete strategies that involve clear objectives with a minimal cost.

B. The Machine Learning Formalism

Eq.(10) appears as a strong candidate for modeling the Mitchell's criteria. In this manner one can tentatively to provide a meaning to each of the ingredients of Eq.(10). To accomplish this one can to formulate the Mitchell's criteria as a convolution operation such as:

$$\mathcal{E}(t) = \int du\mathcal{T}(s)\mathcal{P}(s,t)ds \tag{12}$$

by which the function $\mathcal{P}(s,t)$ recognized as performance plays the role as kernel or the mathematical function that transfer its variable t through the convolution with the task $\mathcal{T}(s)$ to the experience $\mathcal{E}(t)$. Of course one might to expect that either the task or performance are depending of a finite number of free parameters by which the experience is depending up. In other words the following scenario is also contemplated:

$$\mathcal{E}(t,a,b) = \int du\mathcal{T}(s,a)\mathcal{P}(s,t,b)ds \tag{13}$$

by which reads as the both task and performance are depending on the free parameters a and b respectively. Furthermore, more than a limited problem, one might to expect a multi-parameter problem in the sense as:

$$\mathcal{E}_{\mathbf{MN}}(t,a,b) = \sum_m^M \sum_n^N \int du\mathcal{T}(s,a_m)\mathcal{P}(s,t,b_n)ds. \tag{14}$$

Clearly one can ask about those scenarios that are strongly restricted to the available valued of M and N, so that one has a truncate double sum. From it the emerges the definition of error of Machine Learning method calculated from the degree of truncation or number of free parameters and it can be written as:

$$\mathbf{E} = \frac{\mathcal{E}_{\mathbf{(M+1)(N+1)}}(t,a_{m+1},b_{n+1})}{\mathcal{E}_{\mathbf{MN}}(t,a_m,b_n) + \mathcal{E}_{\mathbf{(M+1)(N+1)}}(t,a_{m+1},b_{n+1})}. \tag{15}$$

In Fig.1 the product of task and performance as function of time for a short period, is illustrated. For this exercise the random distributions through Gaussian profiles were employed. It was plotted as bivariate distributions. As stated above the usage of the product of task and performance that is in essence proportional to the number of infection under the theory of Tom Mitchell, the darkness areas would denote the peaks of the infections distributions.

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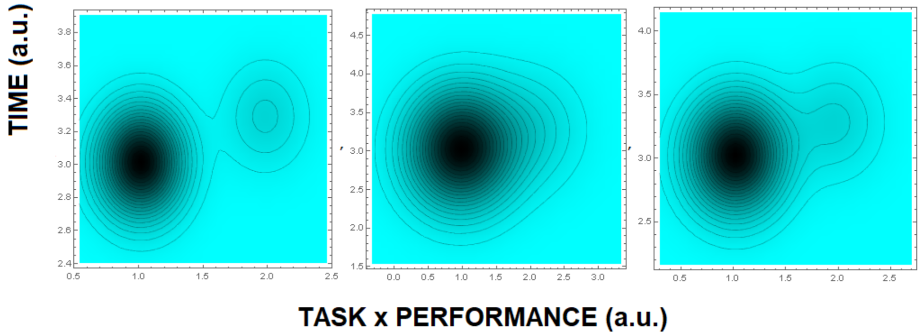

Fig.0 Illustration in the bivariate distribution of random behavior of the product between task and performance as function of time. For up to three values of bivariate 0.22 (left), 0.51 (middle) and 0.30 (right).

IV. Applications and Simulations

Consider Eq.(14). This can be projected onto a territory entirely dictated by epidemiological rules such as the beginning and prevalence of any outbreak due to the unexpected arrival of any strain. In this manner one can associate to Eq.(14) its meaning in the ongoing Covid-19 for example. In this manner by knowing the "spike" property of Dirac-Delta function, it is feasible to associate that the zeros of these function would denote the minimal number of infections. Clearly in the case when these functions contain in their argument any polynomial, the zeros of polynomial gives rise to the **dips** of the Dirac-Delta distributions. Therefore one has that:

$$\mathbf{N}(t) = \int \mathbf{P}_n(t,u)\mathcal{D}[\mathbf{F}(t,u,\beta_m)] \tag{16}$$

with $\mathcal{D}(t,u,\beta_m)$ the Dirac-Delta function. Thus it is assumed that the free parameters β_m are perceived as the ones that define the phases of pandemic. These phases can be explained in terms of risk's probabilities.

A. Experience as Probability of Risk

As seen in [20] there is a solid theoretical background that defines a probability distribution through the Dirac-Delta function. Thus one can also adjudicate to the operation of convolution the meaning of probability. Of course detailed specifications are beyond the scope of this study. Nevertheless one can consider the unnormalized probability given by:

$$\mathbf{N}(t) = \int \mathbf{J}_n(t,u)\mathcal{D}[\mathbf{F}(t,u,\beta_m)] \tag{17}$$

with $\mathbf{J}_n(t,u)$ the integer-order Bessel function. The choice of these polynomials is based on their oscillatory property that to some extent applies to the evolution of a pandemic that exhibits ups and downs.

In Fig.1 are plotted the probability distributions from the convolution given by:

$$P(t) = \int_{\infty}^{\infty} |J_q(x)|^2 \delta(tx - x + \beta_1 t - \beta_2)dx \tag{18}$$

where the zeros of Dirac-Delta are transferred to the square of Dirac-Delta function. As seen there, plots are done for

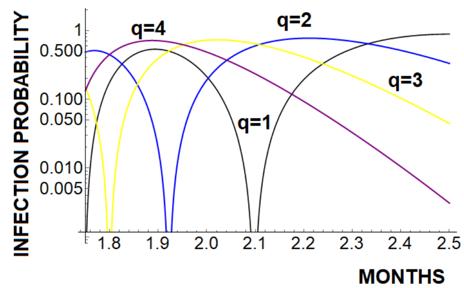

Fig. 1. Probability of infections normalized to 1, as function of months.

q ranging between 1 and 4. One can see there the effect of the convolution with the Dirac-Delta functions as seen at the shifting of the zeros of the Bessel functions. While the infection probability is function of months, one can see that $q = 1$ the probability acquires its maximum value at around 2.1 months. In that scenario dictated by the first order, the probability falls down for subsequent months. The case of $q = 2$ exhibits a dip in 1.9 months. It is actually beyond the dip that appears for 1.8 months. At this range the case of $q = 4$ only exhibits a slow fast reaching until the 2.5 months after the initialized the pandemic.

B. Task: the End and Beginning of Waves

In contrast to Eq.(18) by which the argument of Dirac-Delta function does not depends on the integer number q. It is argued that since the zeros of the argument are dictated by the polynomial form, then the implementation of the integer number q inside the argument would yield a morphology that to some extent is entirely dictated by these integers. Thus under the scenario that the following convolution with a Dirac-Delta function depending on up to three variables u, x and q the following operations are proposed:

$$P(u) = \int_{\infty}^{\infty} |J_q(x)|^2 \delta(ux - xq + 3uq - 10q)dx \tag{19}$$

$$P(u) = \int_{\infty}^{\infty} |J_q(x)|^2 \delta(ux - xq + 3qu^3 - 10q)dx \tag{20}$$

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whose distributions are plotted at Fig.2 (Up) and (Down). One can see in Up panel the apparition of case for $q = 4$ that is interpreted as the first and second wave respectively. In contrast to the case for $q = 1, 2$ and 4 whose distributions do not display dips in this range, one can argue that the Bessel function $J_4(x)$ encompasses well the ongoing scenario of pandemic. **The apparition of a dip in 6.5 month is associated to the modification of task in order to expect changes on the infections number. This change is perceived as the end of first wave.** In Fig.(3) the simulation of Eq.(20) is

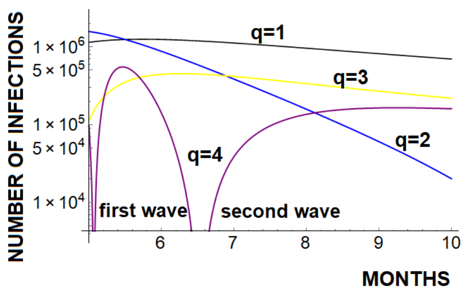

Fig. 2. Simulation of Eq.(19) displaying the different distributions to exception of $q = 4$ where a dip is seen defining the end of first wave as well as the beginning of second wave.

displayed. One can see that the Dirac-Delta argument converts nonlinear as seen in the change $3qu \to 3qu^3$. The resulting distributions display the confluence of dips for the cases of $q = 1, 2$ and 4, while $q = 3$ is not attained to the main morphology of distributions. While in this plot the number of infections is done as function of years, the dip appears at 0.22 years or equivalent to 2.6 months that it is not in agreement to Up panel. In fact the reason of this **under the context of Machine Learning is that of the implementation of a fully nonlinear task that should be adjusted as well to a nonlinear behavior of infections.**

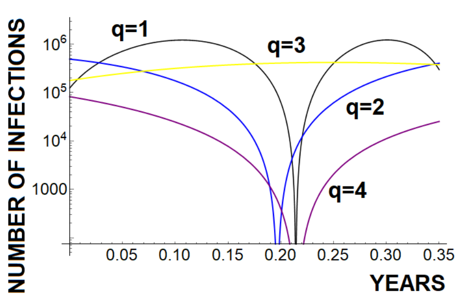

Fig. 3. Simulation of Eq.(20) with a fully nonlinear argument dictated by u^3 featuring the confluence of the orders $q = 1, 2$ and 4. The system is forced to confluence at a certain time after the implementation of nonlinear actions.

V. Conclusion

In this paper, the criteria of Tom Mitchell inside the context of Machine Learning has been used to model pandemics like the ongoing Covid-19 that appears to date to exhibit a first and second wave. The Dirac-Delta formulation appears to be encompassed to the behavior of pandemic that presents a first as well as a second wave. The implementation of nonlinear rules as seen in the argument of Eq.(20) is in concordance to a nonlinear or random behavior of strain. Nonlinear argument also reflects the fact of complex actions to be taken in order to minimize the number of infections and therefore to end the first wave.

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