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COVID-19, a brief overview of virus reproductive emergent behavior

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Abstract: Researches were investigated from January to March, 2020, searching for empirical evidences and theoretical approaches at that time to determine a mathematical modeling for COVID-19 transmission for individual/community infection. It was found that despite traditional forms of transmission of the virus SARS-COV-2 through SIR model equations early detected on 2020, empirical evidences suggested the use of more dynamic mathematical modeling aspects for this equation in order to estimate the disease spreading patterns. The SIR equation modeling limitations were found as far as common epidemic preventive methods did not explain effectively the spreading patterns of disease transmission due to the virus association with the human emergent behavior in a complex network model.

Keywords: COVID-19, emergent phenomenon, epidemiology, mathematical modeling, biological high convergence phenomena.

1. Background

Not only for the urgency of detecting SARS-COV-2 epidemic spreading patterns among humans since December 2019 and early 2020 [1], due to the increasing number of infections and deaths [1], the importance of a mathematical epidemiologic framework remains for the public policies and healthcare infrastructure needs in order to estimate the disease patterns of transmission that is related to the potential damage within a pandemic scenario quickly affecting economics and survival of human individuals [2–6].

As COVID-19 epidemics continuously keep a growing pattern of infection since its beginning until July 2020, theoretical analysis was briefly performed to track the main transmission pattern of the virus reproductive behavior during the period from January to March, 2020. Latest empirical data retrieved from researches about COVID-19 transmission patterns were used to identify modeling patterns of SARS-COV-2 transmission based on SIR model equation and its derivatives for this period and how those models failed to find a pattern of transmission involving individual's actions or groups behaviors.

SARS-COV-2 was noted as expressing different patterns of transmission among humans [2–4]. This feature is being investigated not only by clinical trials/data [2–7], statistical tools [2,4,6–8] and medical interviews with the patients [2,3,5–7], but also through the mathematical point of view concerning the maximum possible rate of infection of the virus and human daily life [2,9,10] that keeps the dissemination with an increasing margin of probability/statistical outcomes.

This mini review also focused on the investigation of a specific theoretical framework understood as the high biological convergence phenomena (author conceptualization) between SARS-COV-2 and high random forms (nonlinear properties of biological interactions) this virus transmission patterns presents associated with human behavior from an strictly empirical point of view. Biological high convergence was defined as an uncontrolled biological association of rapid dissemination between organisms, presenting distinct possible causes of transmission and mainly important to say, expressing an emergent phenomena of transmission originated from the host individual to the groups behavior since early global outbreak.

Using the new definition of biological convergence phenomena, ecological consequences in global terms were briefly described as the limitations of SIR models. Also an important point was addressed and stressed to the individual level of infection, rather than community transmission since biological behavior of the infected organism represents the key aspect for the disease convergence towards high exponential growth curve. The

urgency for mathematical modeling of the virus transmission needs to be improved in many senses due to the presence of nonlinear behavior of the phenomena and exponential cumulative daily new cases behavior.

2. Empirical evidences

Based on researches from January to March, 2020, at that time it was pointed that the transmission nature of COVID-19 was caused by near human's proximity and interactions within a set of empirical given variables constituted by the most basic forms of social interactions such as cough, sneeze, hand shake, clothes, cups, general touching and general objects sharing behaviors [1,4,11]. This set of variables are the type of interactions that don't follow a specific pattern of expression among each of the samples (individual) [9] due to psychological nature of the event in terms of how hosts will behave in personal and communitarian behavior. In this sense, the pre-assumed forms of transmission at that time presented a limitation concerning the continuous form of observation (partially unpredictable) of human behavior. And being this feature a higher domain of probabilities distributions assuming distinct patterns of occurrence for symptoms (pre-asymptomatic, symptomatic, asymptomatic) [4,6,7] and mainly transmission [9–11], researches based on traditional SIR models on this period encountered important limitations regarding predictive analysis and SARS-COV-2 spreading patterns definition.

This feature of analysis was noted during January to March in the forms of transmission patterns based on traditional methods as standard [2,6,10–14]. These traditional approaches gave a false observation of the event and other unsuspected factors for transmission and modeling patterns that were not inferred [9,10,15–17] as mathematical counterproof predictions. In this sense, the high chances of transmission, statistical fluctuations, distinct SIR (mathematical modeling of infectious diseases) patterns formation of the epidemiological data observed for that period and until now demands more empirical and theoretical investigations concerning how the virus gets transmitted and how hosts behavior present an imperative convergence about virus dissemination. Several branches of knowledge are required to understand how lethal and damaging can be biological infections that are in a nonlinear scenario of epidemic spreading [9,10,13,14,17].

Based on the random nature of transmission patterns, the COVID-19 seen to continue the spreading of infection, standing beyond the predefined and known measures of epidemic prevention until now (July, 2020) and therefore demanding alternative scientific and mathematical hypothesis and further probabilistic and statistical frameworks definitions.

2.1. Virus reproductive emergent behavior event

Many diseases share in common the same forms of infection as COVID-19 [2], however, not only the causes of transmission are important issues to be considered, as the chemical and biological properties of transmission forms, but the human emergent behavior events [18–21] since it is in the main cause of virus community transmission patterns. All these mentioned parameters share a high convergent solutions (affinity) if observed with a nonlinear time series analysis [22–26], thus, possibly presenting high asymptotic stability for the dissemination network [24]. This was proved to be true by July 2020 where many researches pointed to the importance of preventive methods towards individual and community behavior [27]. In this sense, further researches in this field of knowledge are required in order to clarify time, space and coupling interactions of the virus towards human society's organizations.

The mathematical patterns of transmission might express an indeterminate pattern in its causation due to the number of variables that causes the transmission and the random variable's variance defined by each of the individual behavior's hosts infected by the virus [9,15]. At this point the concept of high biological convergence phenomena meets its definition and meaning, where not many diseases or organisms interaction find very closed interaction regarding one organism basic forms of expression being it the most effective way of spreading patterns of other organism reproduction. Not defined in science as a traditional occurrence, the previous models of epidemic infection [2,17,25] can be too discrete (SIR tendency to deterministic approaches) in terms of knowing the true nature of event causation and random expression, being this latter feature a continuous indefinite observation of the virus spreading pattern, that promotes an unresolvable distance between the established mathematical predictions during January to March and the empirical evidences found until July, 2020.

The mathematical modeling adopted by several researches that gives a glance of discretization methods, to obtain virus behavior through its hosts, might not present a new novel considering high degree of randomness in the individual scale of virus spreading, since it does not consider human behavior characteristics as the main role of the virus reproductive behavior. In this way, unpredictable spread of the infections might be noticed beyond the traditional methods boundaries [17].

It is suggested that the modeling patterns of transmission and infection in the spatial life course epidemiology need to be observed in the time-varying unresolved empirical data [17] through the human emergent behavior phenomenon [18], to track a high order non autonomous function of the virus infection towards human emergent behavior under the view of local limitations, just to mention a few, public health infrastructure/efficacy, public health policies and biological resistance/drug responsiveness. A theoretical approach for this suggestion was showed to be important during pandemics evolution due to fails in many researches to predict virus quantitative aspects of transmission per population ratio, thus generating high degree of uncertainly for future predictions based on SIR traditional approaches.

3. Evidences synthesis

These epidemiological factors, that is, forms of infection, biological- chemical affinities and human emergent behavior modeling patterns ensures to the preventive epidemic framework the need to consider any given number of infected individuals as potentially dangerous for the pandemic start and continuity (posterior waves of infection). This statement leads to the conclusion that no minimum range of infected individuals are parameters to consider the local epidemics as controlled as it is notably pre assumed in SIR models formulation, therefore, a post critical epidemics event should be treated as an alert phase, since new probabilistic outcomes are expected to generate the same non autonomous phase space of the origin where uncertainty prevails.

To conclude the previous paragraph statements, the analyzed mathematical framework of this mini review, points that the transmission patterns resemble the own host emergent behavior [18–21], and for this reason it assumes the infodemics domains of analysis in a multidimensional form, where the heteroskedasticity aspect, in which SIR models can not handle this feature by its main variables compartments. Therefore, the virus reproduction need to be quantified, as it is designed theoretically in this review, with a high order organization of the host individual/group/community behavior [17] in the outside scope of the strictly SIR models basis or at least a consistent modification of the basic compartments. The importance of this approach remains mainly in the public policy actions and media information campaign where these confounding variables stands beyond pre assumed forms of observation of empirical data concerning deterministic approaches of new daily infections. It means that more specific definitions, strategies and monitoring of human behavior are needed to estimate disease spreading patterns under the SIR models view point.

These statements lead also to the evidence observed [26] that not only 140 thousand (number of infected individuals during January to March), but even 20 contaminated individual hosts are at risk of keeping propagating the disease [24] due to convergence of epidemic factors and stability aspect of the biological atypical organism's interaction (biological convergence phenomena). Also being this interaction possibly modeled by an emergent phenomenon [28,29] of the host's behavior thus being this new mathematical model directly proportional to the virus reproductive formed patterns that is being observed since pandemic outbreak and therefore, outside the common mathematical SIR models approaches already performed by nowadays science.

The human emergent behavior phenomenon shares with the COVID-19 virus, the intrinsic relation between the nonlinear expression of forms of transmission plus human forms of socializing, resulting into a high convergence of infection with results pointing in the direction and the view that human most basic form of socializing is also a tool for the self-spreading pattern of transmission and infection [30] of COVID-19, being this virus reproductive behavior pattern the own human emergent phenomena behavior [18,19] itself in a very closed interaction.

Note that this review also take into account the digital behavior (infodemics) [31] that can also present high influential effect at virus transmission. Future researches need be carried out to integrate infodemics and life course epidemiology with a mathematical overview of the pandemic COVID-19, and also this represents

nowadays a very important tool for policy making in order to prevent fake news and false science information to take place within human behavior at individual or community scale.

This natural phenomenon of extreme convergence (host emergent phenomena behavior and virus reproductive patterns formation) might give us a new glance of biological organizations, towards rare extreme conditions where nature and/or human society can share uncontrolled biological association of rapid dissemination. This observation gives us also a view of about humanity capacity of organizing, preventing and determining extreme convergence phenomena with rapid preventive and corrective response towards new high convergent pathogens [25].

The more random forms of transmission, associated with human behavior, the more effective are the infection and spread of SARS-COV-2 virus among individuals. This feature is not observed in other type of epidemic diseases [14]. Non convergence solutions patterns for transmission of the virus need to be adopted through human behavior dimension by society as a whole, and this means not only the government through policy, health infrastructure and medical treatment, but all individuals behavior in a single manner [30].

4. Concluding remarks

COVID-19 dissemination was theoretically investigated during the period of January to March 2020 and it showed that virus reproductive patterns were wrongly investigated by that time, mainly because the virus spreading patterns are much closed with the human behavior in terms of expressing high randomness or emergent patterns formation. New empirical data need to be investigated regarding human behavior as the main nonlinear property of analysis to sustain SIR model predictive equations efficacy. Also new epidemiologic mathematical methods need to be further advanced towards new variables that influence virus reproductive patterns such as agent-based models and complex networks.

Also, considering these theoretical review findings, and extended with other branches of knowledge, this review brings the attention to adoption of new strategies to be used for policy makers and citizens in general, beyond the mathematical predictions already implemented worldwide as a counterproof of mathematical uncertainty existent in the actual SIR models used for predictive analysis.

The review also points out for the individual scale of prevention very well pointed in Lopes and McKay [32] that in its turns leads to the group and community dimension of human emergent behavior. This approach can be easily transferred by analogy to an infodemics analysis. This novel, since pandemic outbreak until now constituted the main center of the COVID-19 spreading pattern analysis for a local epidemic or pandemic simulation and new methods of control.

Conflicts of Interest: "The author declares no conflict of interest."

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