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Contents lists available at ScienceDirect

Journal of Infection and Public Health

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Original Research Article

Nonlinear dynamics for the spread of pathogenesis of COVID-19 pandemic



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ARTICLE INFO

Article history:

Received 20 May 2020

Received in revised form 23 March 2021

Accepted 6 April 2021

Keywords:

COVID-19

RNA genome

Phase space

Time domainic analysis

Lyapunov exponents

ABSTRACT

Coronaviruses did not invite attention at a global level and responsiveness until the series of 2003-SARS contagion followed by year-2012 MERS plus, most recently, 2019-nCoV eruptions. SARS-CoV & MERS-CoV are painstaking, extremely pathogenic. Also, very evidently, both have been communicated from bats to palm-civets & dromedary camels and further transferred ultimately to humans. No country has been deprived of this viral genomic contamination wherever populaces reside and are interconnected. This study aimed to develop a mathematical model for calculating the transmissibility of this viral genome. The analysis aids the study of the outbreak of this Virus towards the other parts of the continent and the world. The parameters such as population mobility, natural history, epidemiological characteristics, and the transmission mechanism towards viral spread when considered into crowd dynamism result in improved estimation. This article studies the impact of time on the amount of susceptible, exposed, the infected person taking into account asymptomatic and symptomatic ones; recovered i.e., removed from this model and the virus particles existing in the open surfaces. The transition from stable phase to attractor phase happens after 13 days i.e.; it takes nearly a fortnight for the spread to randomize among people.

Further, the pandemic transmission remains in the attractor phase for a very long time if no control measures are taken up. The attractor-source phase continues up to 385 days i.e., more than a year, and perhaps stabilizes on 386th day as per the Lyapunov exponent's analysis. The time series helps to know the period of the Virus's survival in the open sources i.e. markets, open spaces and various other carriers of the Virus if not quarantined or sanitized. The Virus cease to exist in around 60 days if it does not find any carrier or infect more places, people etc. The changes in LCEs of all variables as time progresses for around 400 days have been forecasted. It can be observed that phase trajectories indicate how the two variables interact with each other and affect the overall system's dynamics. It has been observed that for exposed and asymptotically infected ($y-z$), as exposed ones (y) change from 0 to 100 the value of asymptotically infected (z) increased upto around 58, at exposed ones ($y=100$), asymptotically infected (z) has two values as 58 and 10 i.e. follows bifurcation and as exposed ones (y) changes values upto 180, the value of asymptotically infected (z) decreases to 25 so for exposed ones (y) from 100 to 180, asymptotically infected (z) varies from 58 to 25 to 10 follows bifurcation. Also, phase structures of exposed-symptomatically infected ($y-u$), exposed-removed ($y-v$), exposed-virus in the reservoir ($y-w$), asymptotically infected-removed ($z-v$), symptomatically infected-removed ($u-v$) specifically depict bifurcations in various forms at different points. In case of symptomatically infected-virus in the reservoir ($z-w$), at *asymptotically infected* ($z=10$), the value of viruses in the reservoir ($w=50$), then as asymptotically infected (z) increases to upto around 60. At this point, removed ones (v) increase from 50 to 70 and asymptotically infected (z) decrease to 20 i.e., crosses the same value twice, which

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shows its limiting is known as limit cycle behavior and both the values tend to decrease towards zero. It shows a closed-loop limit cycle. Today, there has been no scientific revolution in the development of vaccination, nor has any antiviral treatment been successful, resulting in lack of its medication. Based on the phases, time series, and complexity analysis of the model's various parameters, it is studied to understand the variation in this pandemic's scenario.

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Introduction

The World Health Organization (WHO), on January 30, 2020, has announced 2019–2020 corona genomic-virus a public health emergency of international concern that can be abbreviated as PHEIC. The situation further worsened worldwide, which was declared pandemic on March 11, 2020. Till now, local transmission of this epidemic is being recording and increasing the count in countries including all of the WHO regions. The specific virus-gene is believed to be evolved through 7-month-old infant having been infected with bronchiolitis and conjunctivitis. The entire genomic sequencing indicates that this genomic viral is not recombinant; however, it was discovered that relatively more recent group-1 corona-genomic-virus. In-vitro-host cell array for HCoV-NL63 is prominent as this imitates on tertiary monkey-kidney LLC-MK2 cell-lining. The viral gene consists of distinctive features consisting of a distinctive N-terminal sliver within spike-protein. This article studies time series, phase dynamics with Lyapunov characteristics for the development of the COVID-19 originated in China. Today, there has been no scientific revolution in the development of vaccination, nor has any antiviral treatment been introduced, resulting in a lack of its medication. The best alternative left for mankind is to follow preventive measures such as no direct human interaction, self-quarantine, keeping the living area hygienic, and maintaining social distance. Based on the phases, time series, and complexity analysis of the model's various parameters, it is studied to understand the variation in this pandemic's scenario.

The Corona-genomic viruses - the genus of *Coronaviridae* species encased viruses along with sizeable plus-strand RNA-gene. Genomic RNA has a size 27–32 kb wrapped polyadenylated – three serologically distinctive assemblies for coronaviruses description. In every cluster, viruses pigeon-holed via their host-range & genomic sequencing. Corona was first found in mice, rats, chickens, turkeys, swine, dogs, cats, rabbits, horses, cattle & humans causing various severe diseases such as gastric-intestinal & respiratory-tract diseases. Three human-infecting *nCo-V* are known to be present: human-affecting coronavirus-229E (HCoV-229E), HCoV-OC43 & severe acute respiratory syndrome (SARS)-associated Coronavirus (SARS-CoV). These coronaviruses consist of many types of virus-genes that could infect different animal species in various other ways. The predominant diseases associated with these viruses are respiratory and gastric infections, however hepatic & neurological diseases also occurring. Human coronaviruses identified in the 1960s (including the prototype viruses HCoV-OC43 and HCoV-229E) are responsible for up to 30percent of respiratory tract disorders. Fig. 1 depicts the scenario of this viral taint affecting the host RNAs structure.

Coronaviruses (Co-Vs) are majorly identified through respiratory and gastrointestinal-tract infections plus are genetically categorized into four main genres: *Alpha coronavirus*, *Beta Coronaviruses*, *Gamma coronavirus*, and *Delta coronavirus*. The first two genera predominantly infect mammals, and the last two are primarily found in birds. Six different types of mankind-affecting viral infection is already studied and identified successfully. These include HCo-V-NL63 and HCo-V229E, which evolved through the

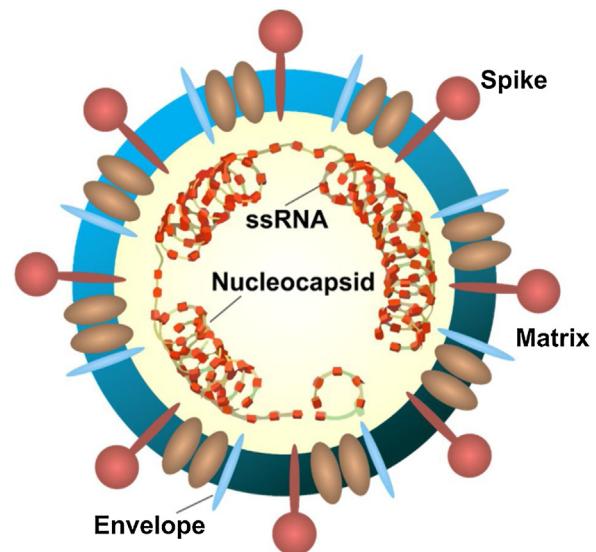


Fig. 1. Detailed diagram of COVID-19 affecting the host RNAs.

Alpha coronavirus genus; and HCo-V-OC43, HCo-VHKU1, severe acute respiratory syndrome coronavirus (SARS-Co-V), and Middle-East respiratory syndrome coronavirus (MERS-Co-V) belonging into *Beta coronavirus* genus (Fig. 2).

Their structure observed so far can be described as enveloped non-segmented positive-sense RNA-genomic viruses having a place in the clan of *Corona-viridae* majorly circulated in humans with other mammals. However, in most cases studied, individual-related coronavirus infections are mild, having identified two *Beta coronaviruses*: severe acute respiratory syndrome coronavirus (SARS-CoV) & Middle-East respiratory syndrome coronavirus (MERS-CoV).

Coronaviruses did not invite attention at a global level and responsiveness until the series of 2003-SARS contagion followed by year-2012 MERS plus, most recently, 2019-*nCoV* eruptions. SARS-CoV & MERS-CoV are painstaking, extremely pathogenic. Very evidently, both have been communicated from bats to palm-civets & dromedary camels and further transferred ultimately to humans. Novel Coronavirus (nCoV)–“2019 novel-coronavirus”/“2019-nCoV” coined directly from World Health Organization (WHO) is accountable for recent unknown viral genomic outburst that began early December 2019 in Wuhan City, Hubei Province, China. This outbreak is connected to the huge sea-food & animal husbandry souk. Today, more than thousands of human infections have been confirmed in China along with many others that traveled across the globe. No country has been deprived of this viral genomic contamination wherever populaces reside and is interconnected.

Chloroquine drug usages, action mechanisms and other characteristics from various diseases were studied for this pandemic treatment [1]. Estimating atmosphere pollutants through dynamic indicators, discussion of the meditating body complexity, statistical simulations towards dynamics of HIV, IoT-based wireless transmis-

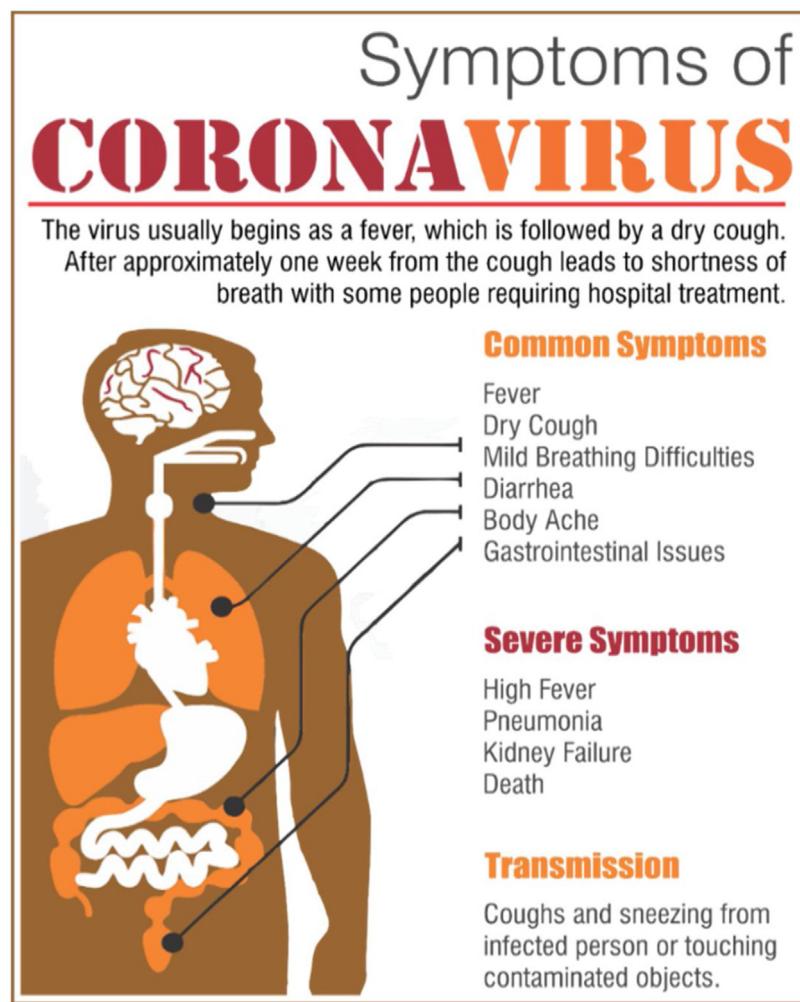


Fig. 2. Coronavirus, its symptoms and transmission as considered by CDCP/USA Today/WHO.

sions having malware spread were modeled and studied in detail [2–5]. The deliberation of human Corona due to spiked glycoprotein in the receptor-binding sites was studied [6]. Transformations of time series are explained for various analysis [7]. Transmissibility of novel Coronavirus based on the phases was modeled mathematically [8]. Dynamic modeling for transmissibility via hand, foot, and mouth is discussed [9]. Chloroquine for the 2019 SARS-CoV-2 analyzed [10]. An epidemiological model towards acute/chronic HCV infections is discussed to study global dynamical systems [11]. A study of the human respiratory tract for the isolation of a novel virus is done [12]. A detailed study of Coronavirus is explained [13]. Various small-molecule antiviral drugs such as Raltegravir, Indinavir, Tipranavir, Dolutegravir, and Etravirine were screened so as to investigate if these could serve as potential drugs for the treatment of COVID-19 [14]. Investigated the antiviral components in various natural sources to determine potential agents to develop alternative therapy for the future [15]. The conclusive study of observations from AIDS for the study of viral disease is explained [16]. An important study of coronaviruses in acute lower respiratory tract for infants is discussed [17]. Coronavirus in relation with pneumonia into the immuno-compromised patients discussed in detail [18]. Corona theorem for countably many functions discussed [19]. A detailed study of corona theorem and its application in spectral problems with Hilbert space is discussed [20].

WHO report on novel Coronavirus in Japan and MERS-CoV update has been surveyed [21,22]. Analysis of molecules that target severe acute respiratory syndrome human Coronavirus is stud-

ied [23]. The WHO reported Coronavirus updated on January 19, 2020, and discussed an outbreak of pneumonia with bats leading to Coronavirus. Necessary antibiotics to potently hamper the entry for Ebola virus, MERS-CoV & SARS-CoV into the humans and other mammals is discussed. WHO reported the status of the novel Coronavirus in China on January 12, 2020 [24–27].

None of the authors have studied the six-dimensional mathematical model for the spread of COVID-19 viral. In this paper, we studied the impact of time on the amount of susceptible; exposed; the infected person taking into account asymptomatic and symptomatic ones; recovered i.e., removed from this model and the virus particles existing in the open surfaces. Also, state-dynamics through time progression, phase-structure and Lyapunov characteristics have been analyzed. Further, the phase-trajectories, time series, and characteristics analysis of the model's various parameters need to be determined due to the unprecedented variation in this pandemic scenario. The LCEs transition from stability to attractor-limiting phase must be recorded for the spread to randomize among populaces. As it shows the number of days that would take for the pandemic to spread in the source phase with no control measures in place.

Modelling the pathogenesis of COVID-19 pandemic spread

The outburst of uncharacteristic pneumonia stated as severe-acute-respiratory-syndrome (SARS) was first recognized in Wuhan's markets, China fast spreading to the distant parts of the

COVID-19 TRANSMISSION MATHEMATICAL MODEL

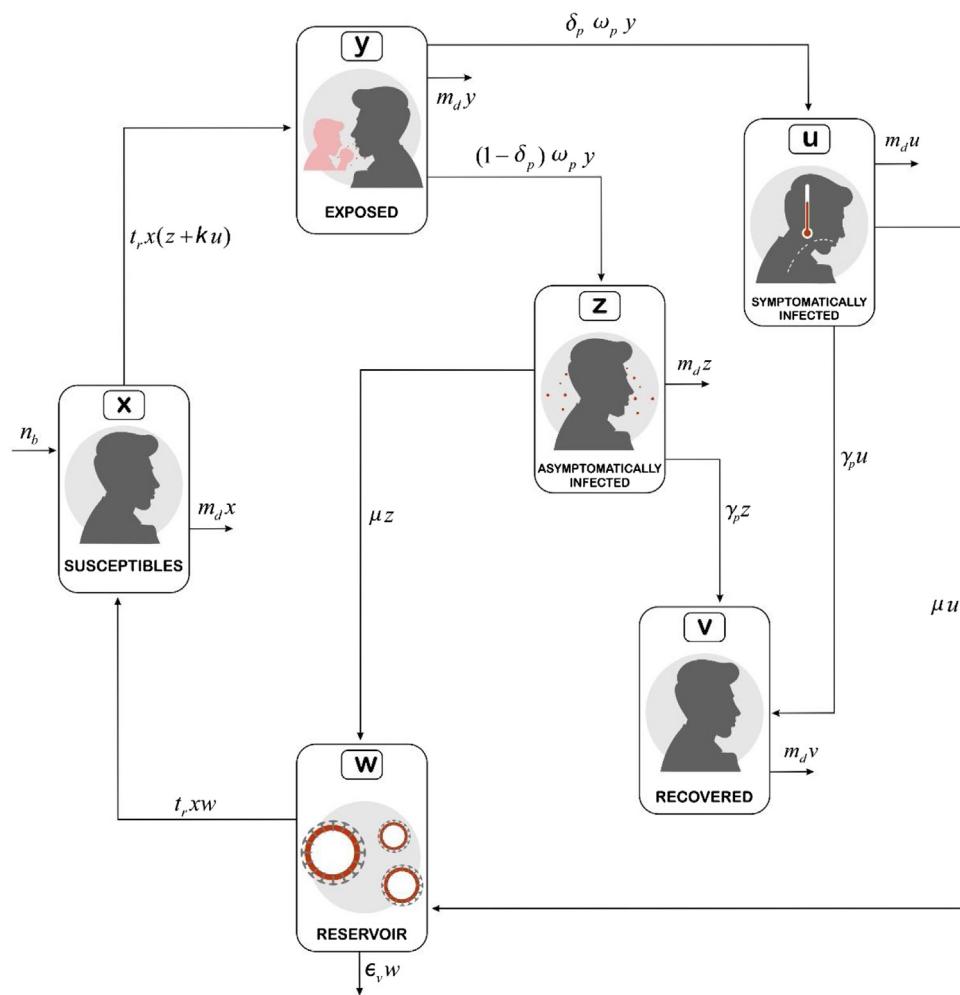


Fig. 3. Flowchart of COVID-19 transmission model.

world. This unknown viral brutality is such that the mortality ranges from 3 to 6 percent though a recent report recommends the rate could be extended from 43 to 55 percent in people aged more than 60 years. (SARS-Co-V) originated in bats further communicated unwaveringly towards homosapiens through market civets & dromedary camels. The spread of Virus is supposed to be analogical to the crowd dynamics extended biological viral spread model. Susceptible-Infected-Recovered (SIR) system is complex because of the nonlinear nature of the interactions that govern the real-world systems. The systems belong to some physical or biological sciences, which have to be analyzed using mathematical theories whose validation is drawn from computer simulations. After this, mathematical equations are developed which approximate the logic or rule that governs system behavior. Simulations of system flow through that of phase portraits, time series, and characteristics plots finally aid in determining the complexity of system evolution.

Let us consider x as the number of susceptible people (susceptible); y as the people that are not following preventive measures knowing and unknowingly (exposed ones); z as asymptotically infected people (infecteds-1); u as symptomatically infected people (infecteds-2); v as recovered/removed people (removed ones) and w as the virus genomics always present in the reservoir (Virus) which majorly depends on the lifetime of the virus survival. Then, assume

various parameters on which these variables depend, extending towards a detailed model.

Some of the presumptions necessary for this model design are:

A1: According to the variation in COVID-19 virus behavior, it is complicated to detect it without symptoms thus, latent period ($1/\omega_p$) and incubation period ($1/\omega_p$) are considered to be equal in terms of its spread.

A2: Birth rate accounts for both new lives and people moving into the cities, and death rates account for deaths and people moving out of the cities.

A3: As per various WHO reports, the average transmission or spread time of the Virus is deduced to be 4–5 days so transmission rate is $(1/5)$ i.e. 0.20.

A4: Susceptible will be exposed as soon as they contact the Virus in any form including the reservoir or the infected whether asymptotically or symptomatically.

A5: Virus in the reservoir includes all of the surviving viruses on various surfaces, open places/markets and people carrying the Virus.

A6: The proportion of infection rate of people for both: the ones with the symptoms and the ones without symptoms are taken to be the same i.e. $1/\delta_p$

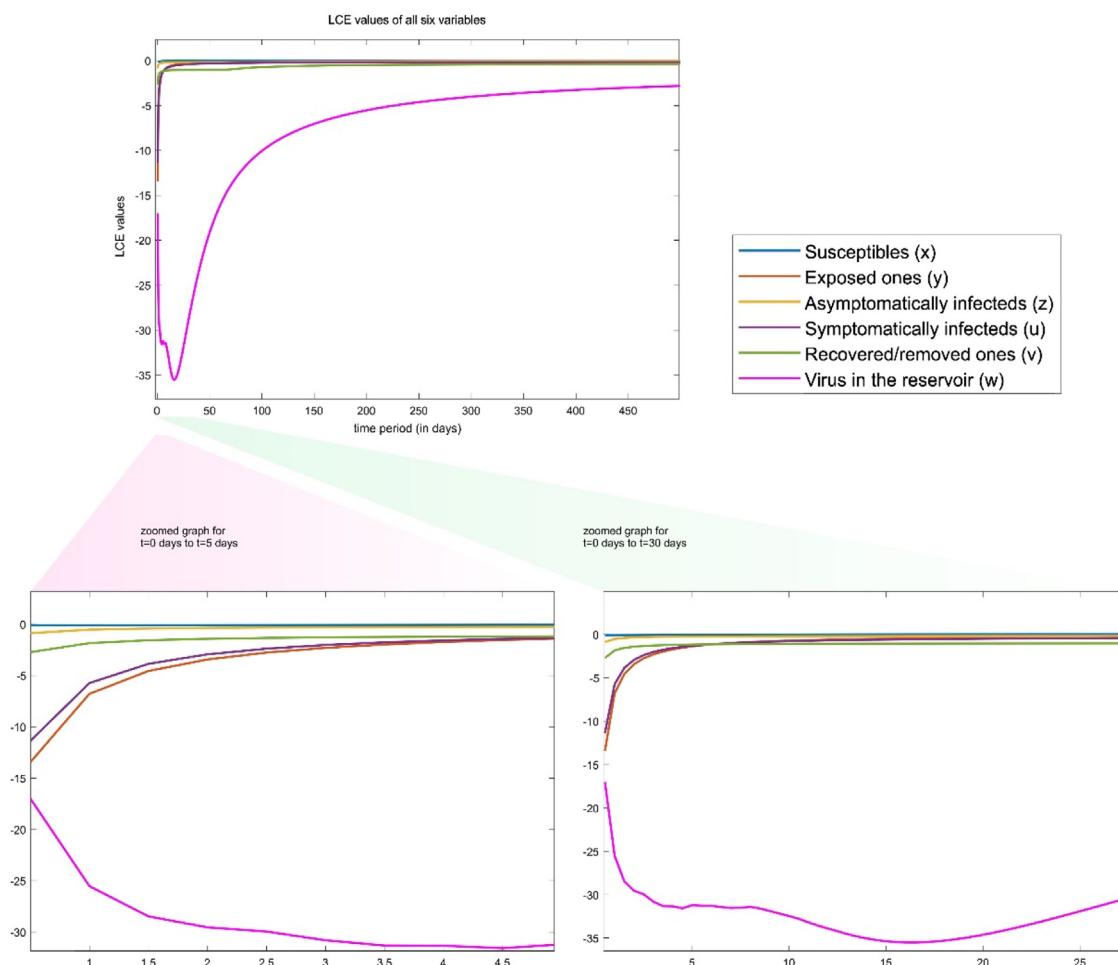


Fig. 4. LCE values of all six variables: x, y, z, u, v, w .

A7: All parameters taken are positive variables and constants as the study is based on people.

The flowchart of the transmission model designed mathematically is shown in Fig. 3. The model so developed is mathematically modelled as follows:

$$\begin{aligned}\dot{x} &= n_b - m_d x - t_r x \times w - t_r \times x \times (z + \kappa \times u) \\ \dot{y} &= t_r \times x \times (z + \kappa \times u) + t_r x \times w - (1 - \delta_p) \omega_p y - \delta_p \omega'_p y - m_d y \\ \dot{z} &= (1 - \delta_p) \omega_p y - (\gamma_p + m_d) \times z \\ \dot{u} &= \delta_p \omega'_p y - (\gamma_p + m_d) \times u \\ \dot{v} &= \gamma_p \times (z + u) - m_d v \\ \dot{w} &= \varepsilon_v (z + \mu \times u - w)\end{aligned}$$

where \dot{x} – rate of change susceptibles; \dot{y} – rate of change of exposed ones; \dot{z} – rate of change of asymptotically infected ones; \dot{u} – rate of change of symptomatically infected ones; \dot{v} – rate of change of recovered/removed ones; \dot{w} – rate of change of virus in the reservoir; n_b – birthrate of people; m_d – dirhrate of people; t_r – transmission rate from x to y ; κ – transmissibility of people from u to z ; μ – shedding coeffocoent from z & u to w ; δ_p – proportion of infection of people; $1/\omega_p$ – incubation period of people; $1/\omega'_p$ – latent period of people; $1/\gamma_p$ – infectious period of people; $1/\varepsilon_v$ – lifetime of virus.

The model with the above equations studies the dynamics of Coronavirus spread globally transmitted due to various peo-

ple of society and various other factors responsible for its local transmission in the communities' world over. This Virus with single-stranded RNAs has become a communicable disease with no or less symptoms like cold, cough, and fever. It is proving to be a pandemic for humankind, as stated by WHO.

The nonlinear techniques like Lyapunov exponents, phase trajectory & simulation are discussed through time progression to study the system evolution with time and change the parameter values. The methods applied are:

M1: Evaluation of Lyapunov characteristics determines the rate or speed at which the trajectories will diverge i.e. divergence rate guarantees speed at which this pandemic spread may lead to the chaotic situation.

M2: The stage at which limit-cycles begin and later turns into Chaos, can be detected through phase-trajectories of each variable plotted against every other variable in the 2D plane with all possible distinct combinations.

M3: Simulations through time progression will aid in a detailed study of virus structure dynamic evolution, and the randomness of the system can be controlled by designing the Lyapunov function.

Methodologies for the prediction of its spread

Simulation of time progression

In general, n -dimensional structure comprises equilibrium states & variable values at each instantaneous simulate stationary

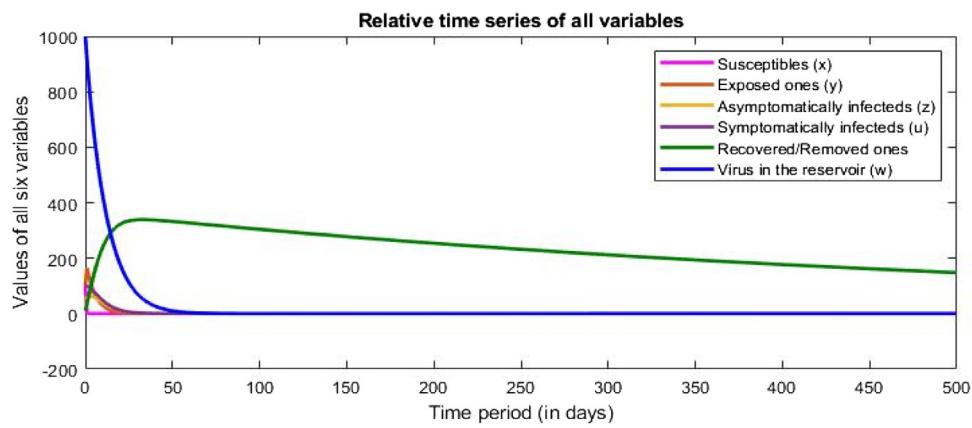


Fig. 5. Relative time series of all six variables: x, y, z, u, v, w for the time period considered.

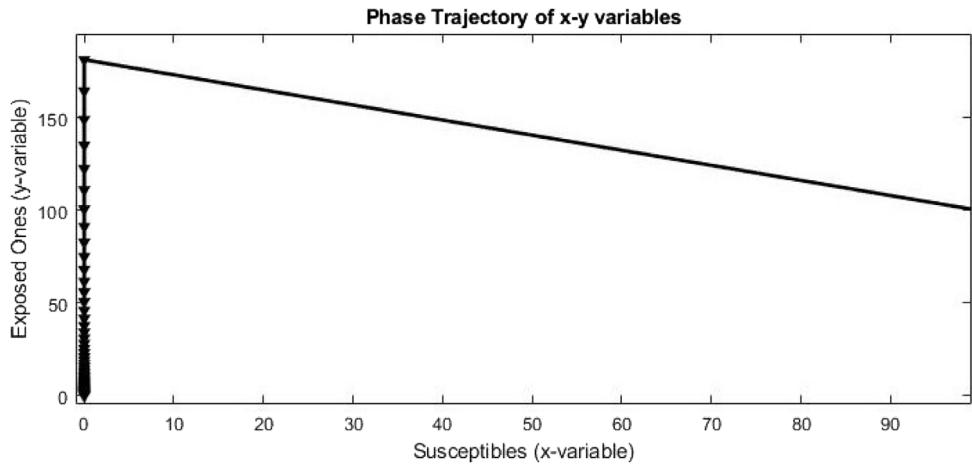


Fig. 6. Phase diagram of three variables: $x-y$.

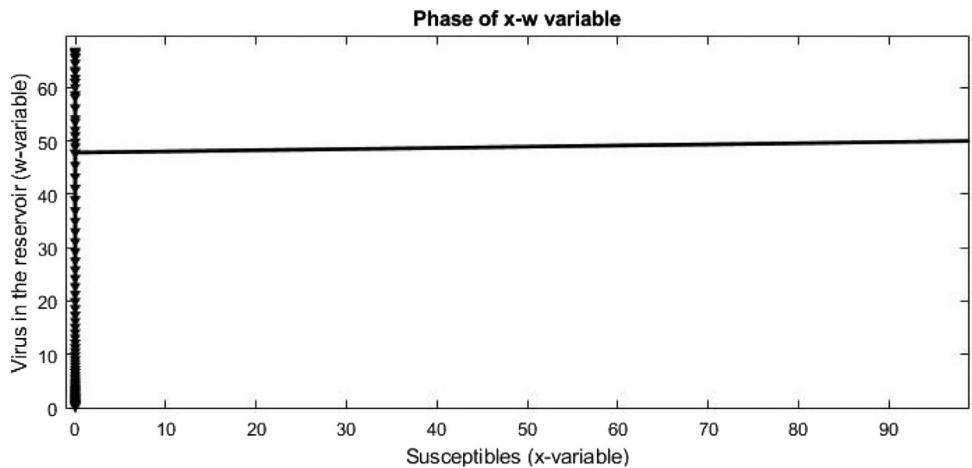
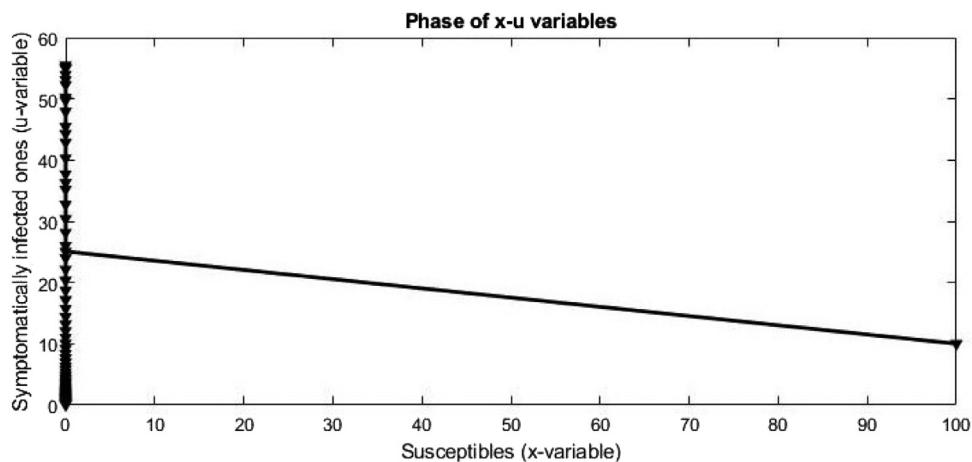
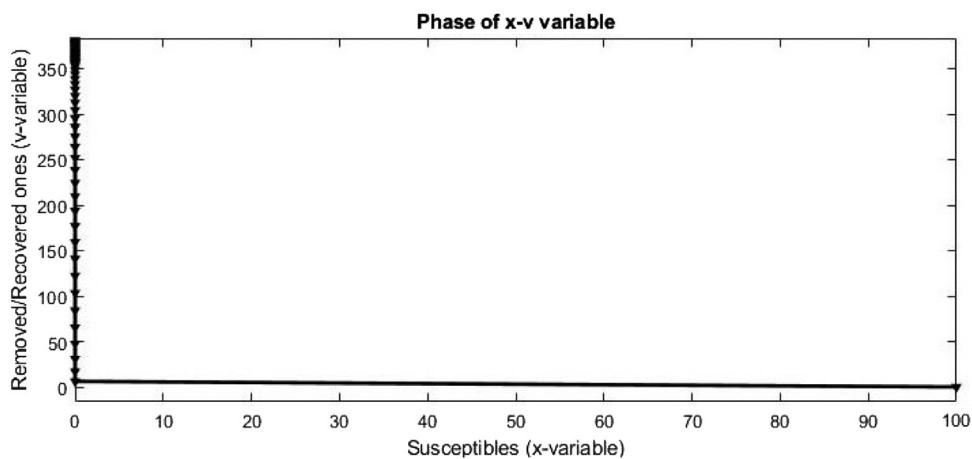
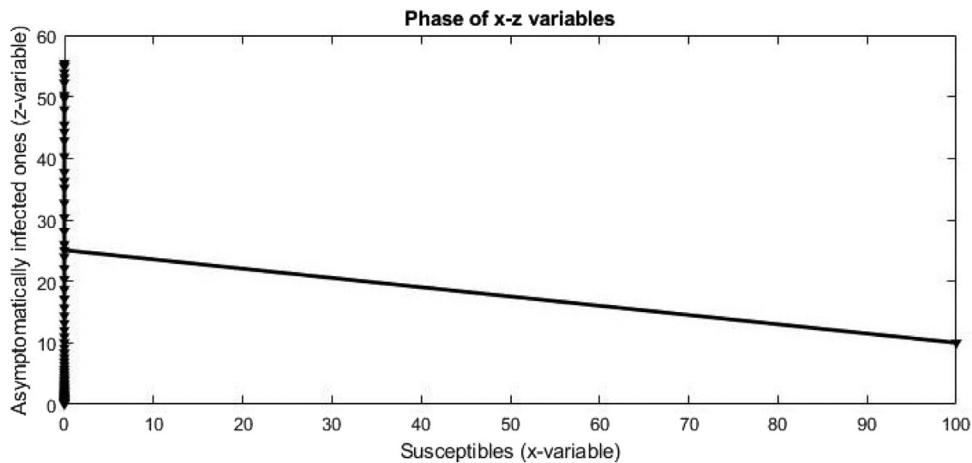


Fig. 7. Phase diagram of three variables: $x-w$.

points of the array of equilibrium. There are various techniques for scrutinizing these points/equilibrium points that the structure can possibly constitute as it evolves along with time. The steadiness of these conditions shifting via one-another with variations in the parameters of the structural organization. Evaluation of these points is required to understand conditions that could happen within this structure & the kind of consequences that it will result in. Inter-relations among these parameters and their critical val-

ues are also calculated in this analysis, which helps decipher the evolution of the system under study.

Simulations are essentially testing the complexity of that particular mechanism plus the parametrically-related different sensibilities. The successions of manual numerical-simulations along with different responses aid in attaining empathetic knowledge of the related mappings. Besides, these are computed for formal-simulations generating corresponding conclusions. Also, it

**Fig. 8.** Phase diagram of three variables: $x-u$.**Fig. 9.** Phase diagram of three variables: $x-v$.**Fig. 10.** Phase diagram of variables: $x-z$.

benefits in knowing the prospects of these forecasters based on the assumptions necessary to recruit. Simulations of systematic flow in phase portraits, time series, and plot decisively determine the complexity of structure advancement.

Time progression $\{x_t : \forall t \in T_p\}$ is the assemblage of random parameters customarily categorized viareal line: $T_p = R$ non-

negative real-line: $T_p = R^+$ integers: $T_p = Z$ positive integers: $T_p = Z^+$

Univariate time-progression analysis stands for exploring a unary ordered set having data, whereas multivariate time-progression involves innumerable sets having info for the time domains' analogous order. The probability quantity of the time

Table 1

Change in Lyapunov exponents' values for all six variables w.r.t. time.

Time (in days)	Susceptible (λ_1)	Exposed (λ_2)	Asymptomatically infected (λ_3)	Symptomatically infected (λ_4)	Removed ones (λ_5)	Virus in the reservoir (λ_6)	Behavior of LCEs
1	-0.088534	-6.778416	-0.520472	-5.727966	-1.836256	-88.740685	Since, all's are negative with $\sum_i \lambda_i < 0$; thus, the system is in a stable state
5	-0.056605	-1.377457	-0.243340	-1.305277	-1.166170	-92.147317	
10	-0.013025	-0.715883	-0.208767	-0.777638	-1.083187	-81.932111	
12	-0.001404	-0.613235	-0.203006	-0.686472	-1.069324	-77.538860	
13	0.002942	-0.574193	-0.200790	-0.650848	-1.063991	-75.373792	As ($\lambda_1 > 0$) & rest of the's are negative with $\sum_i \lambda_i < 0$; thus, the system behaves as an attractor, i.e., intermediate state
20	0.016467	-0.410406	-0.191483	-0.496308	-1.041595	-61.566354	
30	0.017131	-0.307195	-0.185722	-0.394750	-1.027730	-46.782336	
60	0.009635	-0.202354	-0.179961	-0.286615	-1.013872	-25.122143	
90	0.005898	-0.166146	-0.177739	-0.244788	-0.784220	-17.046580	
120	0.003977	-0.132817	-0.156055	-0.21536	-0.641936	-13.034772	
150	0.002822	-0.106323	-0.131070	-0.206958	-0.563277	-10.627548	
200	0.001667	-0.081088	-0.096672	-0.198744	-0.492441	-8.220080	
300	0.000510	-0.053267	-0.062064	-0.190569	-0.428071	-5.812387	
350	0.000180	-0.048928	-0.054293	-0.188237	-0.404902	-5.124653	
385	0.000001	-0.043802	-0.051940	-0.186958	-0.392313	-4.749520	
386	-0.000004	-0.043689	-0.051842	-0.186925	-0.391999	-4.739801	Since all's are negative with $\sum_i \lambda_i < 0$, thus the system is in a stable state
390	-0.000022	-0.043254	-0.051436	-0.186794	-0.390768	-4.701424	
400	-0.000067	-0.042283	-0.050323	-0.186478	-0.387848	-4.608837	

Table 2

Study of variations in all six variables on a daily basis.

Time (in days)	Susceptible(x)	Exposed(y)	Asymptomatically infected (z)	Symptomatically infected (u)	Removed ones (v)	Virus in the reservoir (w)
1	100	100	50	100	10	1000
5	0.000011	92.05711	61.73832	86.64717	118.0996	705.91050
10	0.000017	34.88560	43.47180	53.89697	224.19160	462.41946
12	0.000020	23.66507	35.32537	42.68363	253.80891	390.05034
13	0.000021	19.49160	31.57070	37.75255	266.16302	358.02001
20	0.000041	5.01612	12.94567	14.77185	318.38610	193.79900
30	0.000109	0.728023	3.036576	3.356467	338.0143	77.35208
60	0.001916	0.010771	0.029575	0.03130	327.04170	4.192560
90	0.01780	0.004950	0.003387	0.003395	309.94352	0.21665
120	0.05736	0.001193	0.000941	0.000939	293.6708	0.01290
150	0.10468	0.000207	0.0001720	0.0001717	278.23773	0.00108
200	0.18129	0.0000134	0.0000108	0.00001079	254.2911	0.000038
300	0.31613	0.00000026	0.00000015	0.00000015	212.4018	0.0000004
350	0.37498	0.00000017	0.00000011	0.00000012	194.1207	0.000000098
385	0.413145	0.00000018	-0.00000017	-0.00000017	182.2683	0.000000235
386	0.41420	0.00000027	-0.00000029	-0.00000029	181.9405	0.000000358
390	0.41840	0.00000015	-0.000000148	-0.00000015	180.6353	0.000000203
400	0.428778	0.000000261	-0.000000289	-0.000000289	177.4129	0.00000034

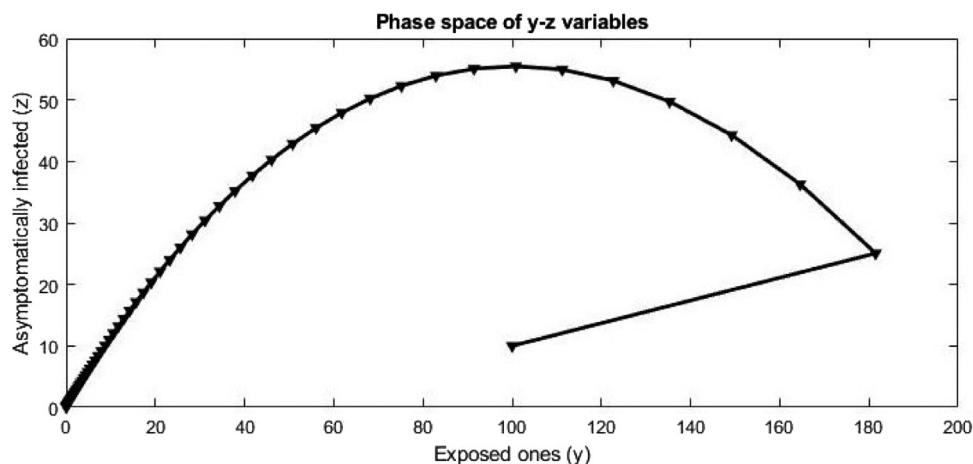
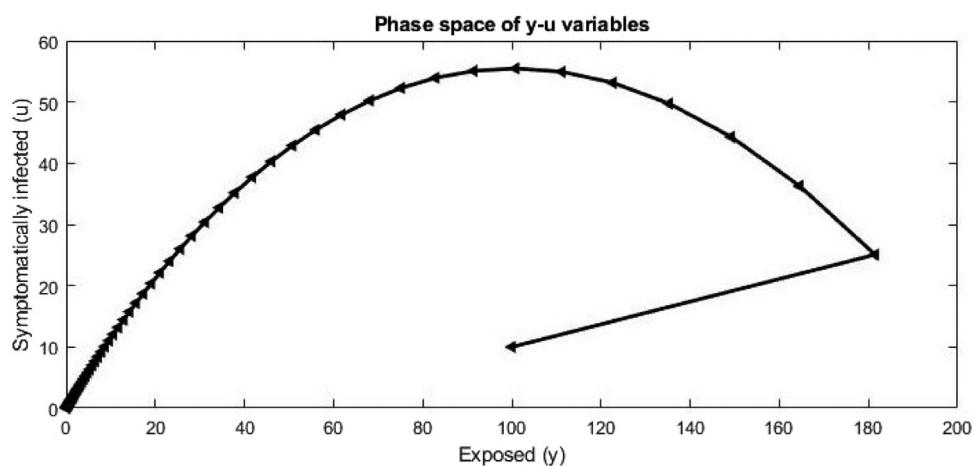
domain is defined by stipulating joint distribution in the unswerving behaviour for all finite-subsets $\{x_t : \forall t \in T_p\}$.

Phase-structure analytics

Inside a phase-space, all degrees-of-freedom (DOF) i.e., parameters of that particular system, are exemplified as the alignment of multi-dimensional space where one-dimensional system referred as the phase-line; two-dimensional exists as phase trajectory in the

plane. At each possible state of the system, there is a combination of standards of the system's considerations. The point is included in the multi-dimensional space. The system's evolved phase w.r.t. time traces the pathway through the phase-space trajectory for that particular system via n-dimensional space.

Mathematically, this structure trajectory referred through a manifold, M that should be finite/infinite-dimensional also, of every site: $q \in M$ in this structural space, momentum (p) of this system

**Fig. 11.** Phase diagram of variables: y - z .**Fig. 12.** Phase diagram of variables: y - u .

could acquire findings into cotangent-space: T_q^*M . Phase-structure is usually represented through cotangent-bundle:

$$T^*M := \{(q, p) : q \in M, p \in T_q^*M\},$$

That could be stemmed as canonical-symplectic-form as: $\omega := dp \wedge dq$.

Hamilton's equation of motion designates gesture as: $t \mapsto (q(t), p(t))$ for the structural organization in phase-trajectories through the-time functionalities into the formation of the Hamiltonian: $H : M \rightarrow \mathbb{R}$ (via Hamilton's equation of motion)

$$\frac{d}{dt}q(t) = \frac{\partial H}{\partial p}(q(t), p(t));$$

$$\frac{d}{dt}p(t) = -\frac{\partial H}{\partial q}(q(t), p(t)),$$

Unvaryingly in form of the symplectic version, ω as:

$$\dot{x}(t) = \nabla_{\omega}H(x(t)),$$

where, $x(t) := (q(t), p(t))$ is the trail of set-up in phase-space & ∇_{ω} is the symplectic-gradient, hence, $\omega(\cdot, \nabla_{\omega}H) = dH$.

Lyapunov characteristics (LCE)

The n th ordered difference/differential equalities structure fragmented into ' n ' single-ordered difference/differential equivalences after which utilizing:

$$f'(x_n) = 0$$

for n equations and n variables, n -dimensional stationary-points could be simulated having steadiness into n -dimensions of phase-structure determined through the Jacobian method on the basis of either related eigenvalues or its trace & determinant stationary point. Lyapunov exponents are equivalent to real parts of the Eigenvalues at those critical points.

If LCEs ≤ 0 , it means proximate initial-conditions that converge to one-another & delta small-errors decreasing throughout time interval.

At least one of the LCEs = +ve, then infinitesimally-proximate initial situations diverge from one- another exponentially, i.e. differences propagate with respect to time.

If trajectories diverge with time, then the condition is known as sensitive dependence on initial conditions which is coined as Chaos.

Algorithm for the computation of LCE:

Let $x_n = f_n(x_0); y_n = f_n(y_0)$.

Table 3

Behavior of variables in various phases.

Figure Nos.	Phase trajectories	Behaviour of variables
Fig. 6.	x-y	As susceptible (x) is zero exposed ones (y) are maximum upto 170 and as x changes from 0 to 100 the value of y decrease from 170 to around 100.
Fig. 7	x-w	As susceptible (x) is zero, viruses in the reservoir (w) is maximum nearly 67 and then there is sudden drop in the value of viruses i.e. 48 for $x = 1$, then gradually w increase from 48 to 51 with the value of susceptible from 2 towards 100
Fig. 8	x-u	As susceptible (x) is zero symptomatically infected (u) maximum i.e. around 55 and then sudden drop in the value of u i.e. 25 for $x = 1$, and then as x increases from 0 to 100 then the value of u decreases sharply from 25 to 10
Fig. 9	x-v	At susceptible (x) is 0, the value of removed ones (v) is 385, then sudden drop to 10 at $x = 1$ and as x varies from 5 to 1000, the v change from 10 to 0.
Fig. 10	x-z	At susceptible (x)=0, the value of asymptotically infected (z) is 55 and then drops to 25 at $x = 1$, further as x changes upto 100, value of z decreases to 10
Fig. 11	y-z	As exposed ones (y) changes from 0 to 100 the value of z is increasing upto 58, at exposed ones ($y = 100$), z has two values as 58 and 10 so following bifurcation and as y changes values upto 180, the value of z decreases to 25 so for y from 100 to 180, asymptotically infected (z) varies from 58 to 25 to 10 follows bifurcation
Fig. 12	y-u	As exposed ones (y) changes from 0 to 100 the value of symptomatically infected (u) is increasing upto 58, at $y = 100$, symptomatically infected (u) has two values as 58 and 10 so following bifurcation and as y changes values upto 180, the value of u decreases to 25 so for y from 100 to 180, symptomatically infected (u) varies from 58 to 25 to 10 follows bifurcation
Fig. 13	y-v	At exposed ones ($y = 0$), the value of removed ones (v) is 365 then it decreases sharply to 0 as y varies upto 180. At $y = 100$ to 180 bifurcation is observed the values of removed ones (v) are bifurcated with two values and $y = 180$ it is one value of v
Fig. 14	y-w	As exposed ones (y) changes from 0 to 60 the value of viruses in the reservoir (w) is changing maximum upto 67 and then start decreasing. At $y = 100$, the bifurcation starts and the value of w is varying from 60 to 50. Bifurcation remains from exposed ones $y = 100$ to 150 and then again unique behavior is observed for $y = 150$ to 180 with unique value of w as 50
Fig. 15	z-u	As asymptotically infected (z) varies from 0 to 55 the value of symptomatically infected (u) increases proportionately from 0 to 55.
Fig. 16	z-v	At asymptotically infected ($z = 0$) the value of removed ones (v) is around 365, then it gradually decreases. Bifurcation observed for z from 10 to 55 as the value of v decreases to zero
Fig. 17	z-w	As asymptotically infected ($z = 10$), the value of viruses in the reservoir ($w = 50$), then as z increases to upto around 60. At this point, v increases from 50 to 70 & z decrease to 20 i.e. crosses the same value twice which shows its limiting known as limit cycle behaviour and both the values tend to decrease towards zero. It shows a closed loop limit cycle
Fig. 18	u-v	At symptomatically infected ($u = 0$), the value of removed ones (v) = 365, then it gradually decreases. Bifurcation can be observed for u from 10 to around 55 as the value of v decreases towards zero
Fig. 19	u-w	As symptomatically infected ($u = 10$), the value of viruses in the reservoir ($w = 50$), then as u increases to upto around 60. At this point, v increase from 50 to 70 and u decrease to less than 20 i.e. crosses the same value twice which shows its limiting known as limit cycle behaviour and both the values tend to decrease towards zero. It shows a closed loop limit cycle
Fig. 20	v-w	At viruses in the reservoir ($w = 50$), the value of removed ones (v) = 0, then w increases maximum around 67, then the value of v = 200 (approx.), but then w decreases to zero as v increases to around 365, i.e. it crosses the same value 50 twice which shows its limiting known as limit cycle behaviour

Then, n th iteration of orbits of x_0 and y_0 under fare: $|x_0 - y_0| \ll 1$; $|x_n - y_n| \ll 1$.

Further, separation at n th iteration for one dimensional system can be given by:

$$|x_n - y_n| \approx \left(\prod_{t=0}^{n-1} |f'(t)| |x_0 - y_0| \right)$$

wherever $|x_0 - y_0| \ll 1$, $|x_n - y_n| \ll 1$, and $x_n = f_n(x_0)$, $y_n = f_n(y_0)$ respectively n th reiterations of revolutions for x_0 & y_0 under f .

Then, exponential departure rate $\log|f'(x)|$ of adjoining initial-equilibriums, averaged over all-inclusive trajectory, could be assumed as:

$$\lambda(x_0) = \lim_{n \rightarrow \infty} \frac{1}{n} \log \left(\prod_{t=0}^{n-1} |f'(x_t)| \right) \quad \text{where } \prod_{t=0}^{n-1} |f'(x_t)| \approx e^{\lambda(x_0)n}$$

for, $n \gg 1$.

$\lambda(x_0)$ defined as the LCE of orbit of x_0 .

Quantitatively, two paths in phase-structure along with initial partition, δx_0 diverging $|\delta x(t)| \approx e^{\lambda t} |\delta x(0)|$ whenever, $\lambda > 0$ is the Lyapunov exponent.

Let $\lambda_1, \lambda_2, \dots, \lambda_n$ be the Eigen-values of normalized equivalences: $\frac{du}{dt} = A(u^*)$ such that $m_1(t) = e^{\lambda_1 t}$ and $\tilde{\lambda}_i = \lim_{t \rightarrow \infty} \frac{1}{t} \ln |e^{\lambda_i t}| = Re[\lambda_i]$.

LCEs have the following characteristics:

1. Measures relative stabilizations of the dynamically evolving structures(s);
2. Generalizations of the eigenvalues of the steady-state and limit-cycle solution towards the so-called unsolvable differential equations;
3. Utmost direct-indicators & quantifiers for the determination of chaos/randomness;
4. The number of Lyapunov Exponents depends on the trajectories obtained through phase-structure.

Results and discussion

With the Corona spread model's equations, phase space diagram, time series, and Lyapunov characteristics have been simulated. Fig. 4 depicts the LCEs of all six variables i.e. susceptible, exposed, symptomatically infected, asymptotically infected, removed ones and the reservoir virus for the days of spread. It zooms into the situation at 5th day and then after a month, i.e. 30th day. It shows the initial trend in the changes in variables. Fig. 5 show the relative time series of all these six variables. Also, the relative time series of all six variables depict the statistical increase in recov-

Table 4

Various studies using different intelligent models for the widespread COVID-19 pandemic.

Year	Author	Description	Parameters	Results
Feb, 2020	Chen T-M, et al.	A mathematical model for simulating the phase-based transmissibility of a novel coronavirus	SEIR model with two more variables as a reservoir (seafood market) and asymptotic people	Simulation of Reproduction number, R_0 through the reservoir to the person transmission model
October, 2020	Indu P, et al.	Various drugs tested as main protease and RNA polymerase of SARS-CoV towards molecular docking and drug repurposing approach	FDA approved small-molecule antiviral drugs repurposed against the major viral proteins of SARS-CoV-2	The screened small-molecule antiviral drugs Raltegravir, Indinavir, Tipranavir, Dolutegravir, and Etravirine could be served as potential drugs for the treatment of COVID-19
Nov, 2020	Jansi RS, et al.	New emerging paradigms of viral diseases and paramount role of resources as antiviral agents	Major viral disease outbreaks such as Zika, Ebola, Chikungunya, Herpes, SARS etc. have been reviewed for their immune mechanism	Investigated the antiviral components in various natural sources to determine potential agents to develop alternative therapy for future
2021	Present study	Nonlinear Dynamics for the spread of Pathogenesis of COVID-19 Pandemic	Modeling of the factors related to COVID-19 transmission to minimize its spread	The attractor-source phase continues up to 385 days i.e., more than a year and perhaps stabilizes on the 386th day as per the Lyapunov exponent's analysis. Time series depicts the survival of the Virus on surfaces if not sanitized

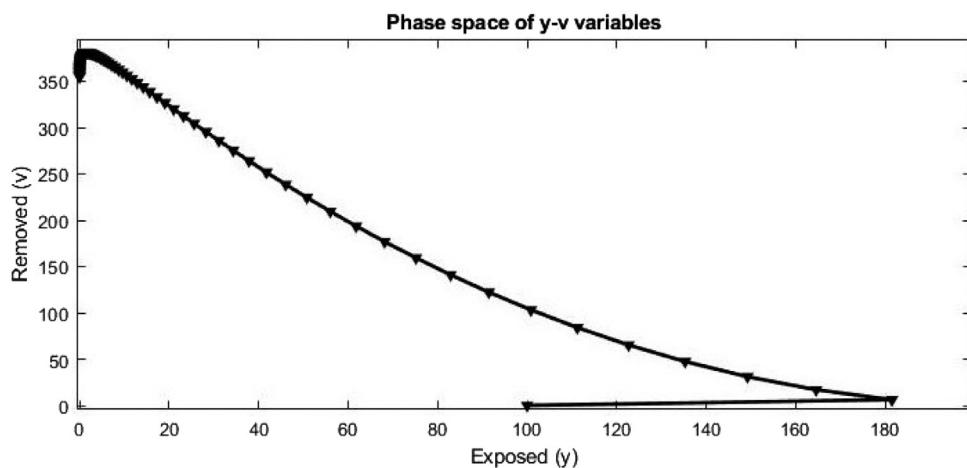


Fig. 13. Phase diagram of variables: $y-v$.

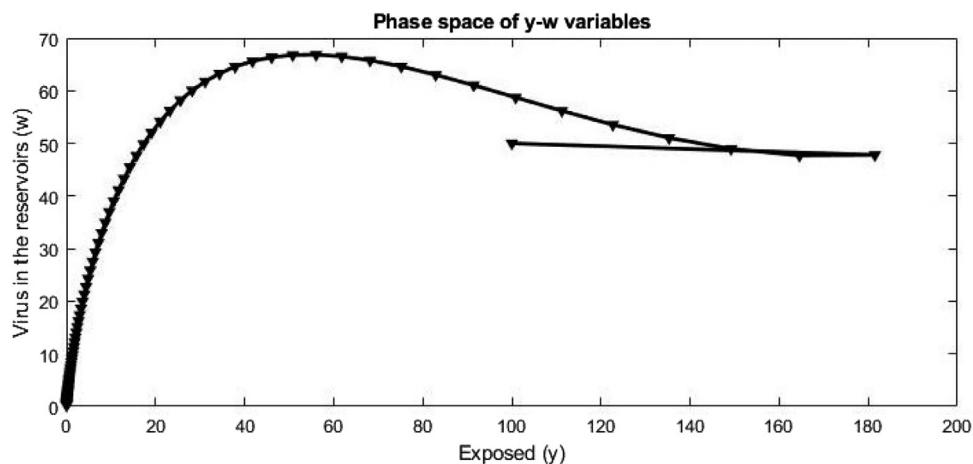
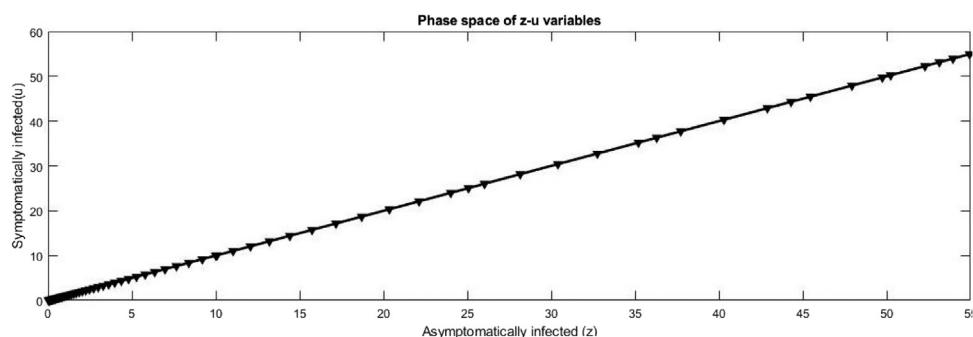
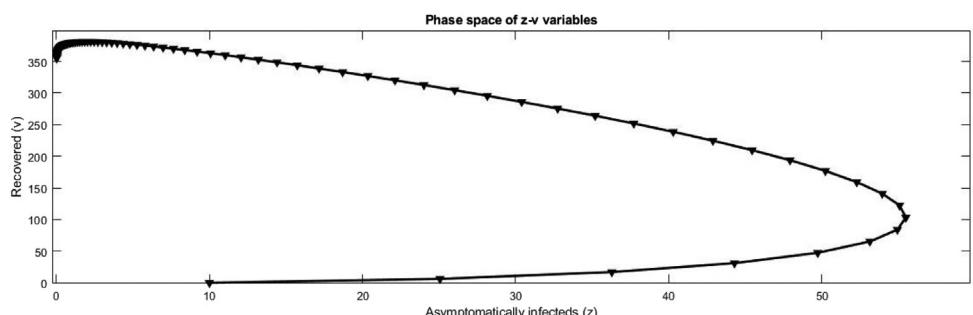
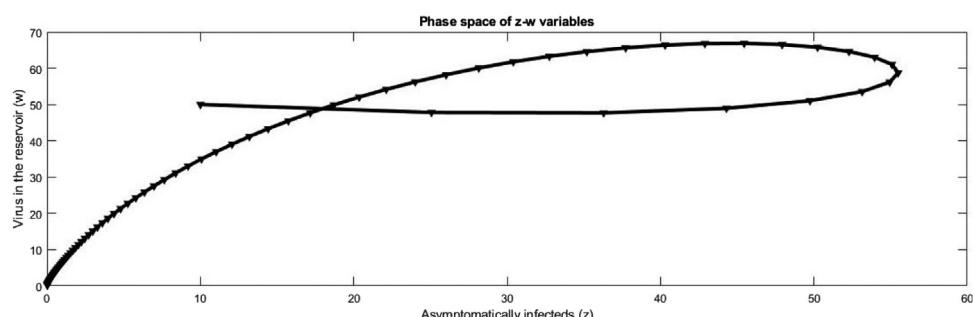
ered or removed ones and decrease in the Virus in the reservoir i.e., in the open surfaces, market places, etc.

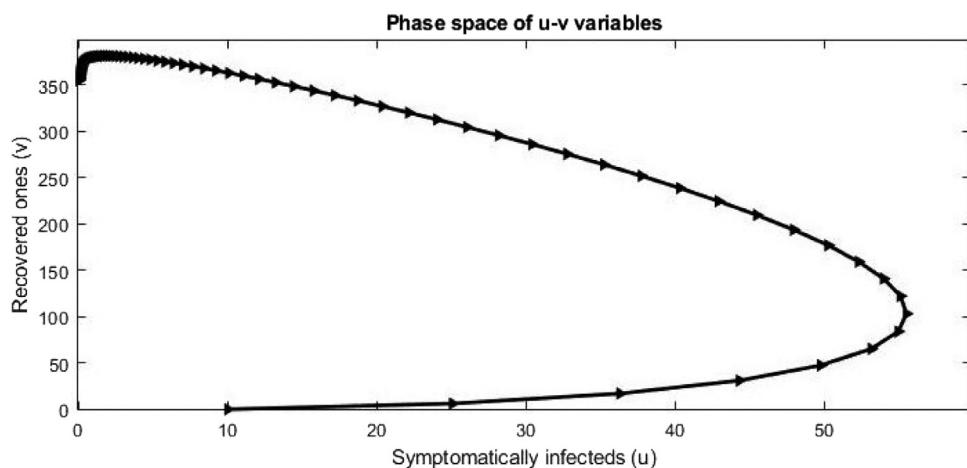
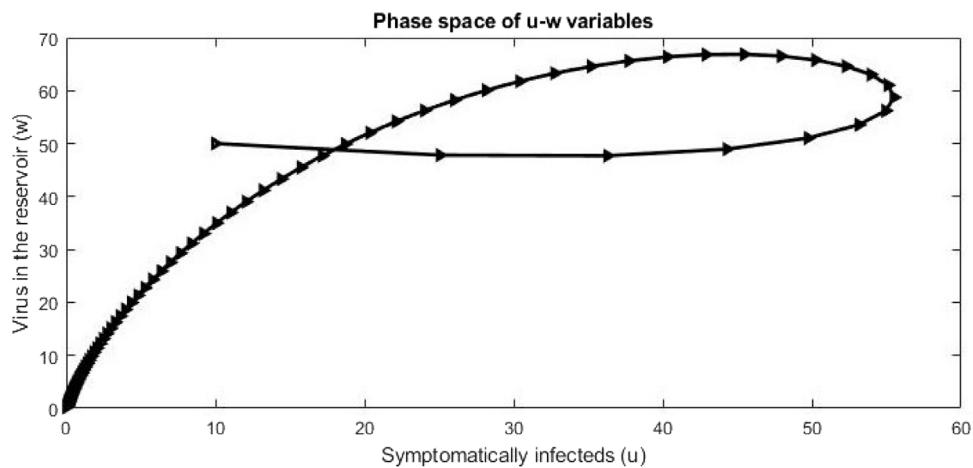
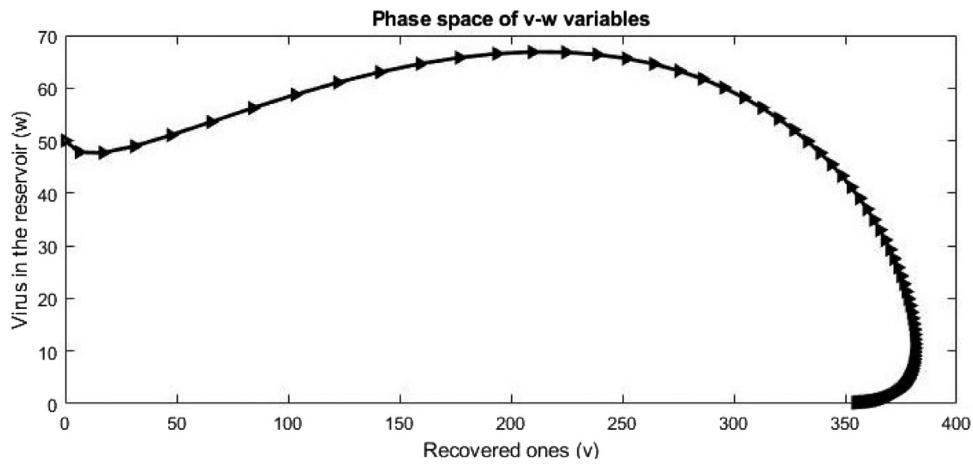
Phase structure of all six variables are very essential to be studied in detail. Thus, the phase diagram of all variables in perspective of other variables in the 2D plane in all combinations possible have been plotted and their trajectories have been observed from Figs. 6–20. The phase trajectories plot the variation of two related parameters out of the six parameters so as to describe the phenomena in detail. Susceptible and Exposed i.e. $x-y$ phase, depicts the rate at which susceptible transform into exposed ones with each passing day in Fig. 5. Exposed and asymptotically infected i.e., $y-z$ phase structure first increases then have a decreasing curve and tend to zero in Fig. 10. Similarly, all the phases provide a relative change in both variables as considered.

Table 1 forecasts the changes in LCEs of all variables as time progresses for around 400 days. As at day 5 & 10, all LCEs are negative, and their sum is less than zero, indicating a stable state. On day-13, LCE value (λ_1) corresponding to susceptible (x -variable) becomes positive, and all other variables are negative, and their sum also turns out to be negative, which depicts an attractor state. This behavior is further observed for a long time to reach stability in the system again. The system remains in this intermediate attrac-

tor phase for 385 days. On the 386th day, LCE values of susceptible behavior change from positive to negative again. It transforms the corona-based model from attractor phase to stable state. Thus, the estimation states that the pandemic spread can remain in a random state for 385 days at a stretch per the data and consider all factors in the mathematical-model design.

Table 2 tabulates the variation in variables for the period under consideration in this study. It can be observed that all the susceptible transform to either exposed or asymptotically infected on reaching day-5. After that, we observe the variation for 13 days of the first fortnight, where the changes are studied. The x , y , z , u variables have effectively reduced while removed ones denoted by v -variable have increased in this period. Also, z -variable has decreased in number quite evidently. After 60 days, i.e., two months period, it can be concluded that Virus in the open surfaces, i.e., w -variable reduces significantly. Hence, it can be concluded that Virus in the reservoir, i.e., open spaces, can almost annihilate if there are no carriers of this Virus, i.e., infected and no other contact that would spread this genomic Virus. Hence, the social distancing and subsequent lockdown of the infected areas, including cities, countries are important and necessary measures to be carried out. Also, it should be followed strictly. Then, it is recorded for around 400 days

**Fig. 14.** Phase diagram of three variables: $y-w$.**Fig. 15.** Phase diagram of three variables: $z-u$.**Fig. 16.** Phase diagram of three variables: $z-v$.**Fig. 17.** Phase diagram of three variables: $z-w$.

**Fig. 18.** Phase diagram of three variables: $u-v$.**Fig. 19.** Phase diagram of three variables: $u-w$.**Fig. 20.** Phase diagram of two variables: $v-w$.

in accordance with the Lyapunov characteristics (LCEs). The simultaneous changes in both the nonlinear techniques are observed and studied in detail.

Table 3 shows behavior of variables in various phases as simulated. It can be observed that phase trajectories indicate how the two variables interact with each other and affect the overall system's dynamics. It is observed that for exposed and asym-

tomatically infected ($y-z$), as exposed ones (y) change from 0 to 100 the value of asymptotically infected (z) increased upto around 58, at exposed ones ($y=100$, asymptotically infected (z) has two values as 58 and 10 i.e. follows bifurcation and as exposed ones (y) changes values upto 180, the value of asymptotically infected (z) decreases to 25 so for exposed ones (y) from 100 to 180, asymptotically infected (z) varies from

58 to 25 to 10 follows bifurcation. Similarly, phase structures of exposed-symptomatically infected ($y-u$), exposed-removed ($y-v$), exposed-virus in the reservoir ($y-w$), asymptomatically infected-removed ($z-v$), symptomatically infected-removed ($u-v$) specifically depict bifurcations in various forms at different points. In case of asymptomatically infected-virus in the reservoir ($z-w$), at asymptomatically infected ($z=10$), the value of viruses in the reservoir ($w=50$), then as asymptomatically infected (z) increases to upto around 60. At this point, removed ones (v) increase from 50 to 70 and asymptomatically infected (z) decrease to 20 i.e., crosses the same value twice, which shows its limiting is known as limit cycle behavior, and both the values tend to decrease towards zero. It shows a closed-loop limit cycle. Similar behavior can be inferences from symptomatically infected-virus phases in the reservoir ($u-w$) and removed ones-virus in the reservoir ($v-w$). Table 4 tabulates various studies using different models for the widespread COVID-19 pandemic.

Conclusions

The need of the hour to model the factors of COVID-19 transmission to minimize its spread and the extent to which it can be harmful. Since China is the first country to record and report such cases, so it is, in a way, the breeding place of this pandemic. Thus, it is necessary to understand the scenario, and from this study, we conclude that the transmission rate should be minimized as much as possible. Prevention measures should be followed at their best so that the Virus does not communicate to more people and to stop its breeding further.

As per the phase-trajectories, time series and characteristics analysis of the model's various parameters have been deliberated due to the unprecedent variation in the scenario of this pandemic. The LCEs transit from stability to attractor-limiting phase happens after 13 days i.e. takes nearly a fortnight for the spread to randomize among populaces. This pandemic transmission remains in the so-formed source phase for a very long time with no control measures. The attractor-source phase continues upto 385 days i.e. more than a year and perhaps stabilizes on 386th day as per the Lyapunov exponents analysis. The time series helps to know the period of the Virus's survival in the open sources i.e. markets, open spaces and various other carriers of the Virus if not quarantined or sanitized.

The Virus would cease to exist in around 60 days if it does not find any carrier or infect more places, people, civilizations etc. Hence, the social distancing and subsequent lockdown of the infected areas including cities, countries are important and necessary measure to be carried out and should be followed strictly. Further, there have been observations regarding bifurcation and limit cycles in general and in closed loops as evident through phase trajectories. Phase-structures of asymptomatically infected-virus in the reservoir ($z-w$), symptomatically infected-virus in the reservoir ($u-w$) and removed-virus in the reservoir ($v-w$) depict limit-cycles while exposed-asymptomatically infected ($y-z$), exposed-symptomatically infected ($y-u$), exposed-removed ($y-v$), exposed-virus in the reservoir ($y-w$), asymptomatically infected-removed ($z-v$), symptomatically infected-removed ($u-v$) represent bifurcations. If the situation is not controlled, this scenario might transform these bifurcations and limiting cycles into randomness. Hence, the social distancing and subsequent lockdown of the infected areas, including cities, countries are important and necessary measures to be carried out and should be followed strictly. The coronaviruses already identified might only be the tip of the iceberg having potentially more novel & severe zoonotic events expected to unfold.

No antiviral-genomic treatment for this pandemic has been proven to be effective. The six-dimensional model involving susceptible turning into exposed, then some of them becoming asymptomatic or symptomatic infected and further getting removed from this model helps determine the rate of transfer of Virus through various stages. Also, the Virus in the reservoir considers the viruses existing in the environment, which might be creating havoc in the future if not controlled or monitored. This article may be used as a base if more variables are required to be taken as per their effect on the pandemic spread. The outcomes of this study can provide efficient learning and understanding of the pathogenesis of COVID-19. Also, it may aid in improving clinical strategies against this pandemic. This would help biologists design and develop some clinical advancements within a period when the epidemic model shows the situation under control. This model provides the time domain where the virion characteristics change from stability to attractor phase. Also, the model simulation can be used to develop a better outcome for virus annihilation.

Funding

This work is not supported by any funding.

Competing interests

The author declares that they no conflict of interest. The author of this research acknowledge that they are not involved in any financial interest.

Ethical approval

Not required.

Acknowledgments

The corresponding author is thankful to Guru Gobind Singh Indraprastha University for providing financial support and research facilities. The authors declare no conflict of interest for the publication of this article. Dr. Mohammed Alshehri would like to thank Deanship of Scientific Research at Majmaah University for supporting this work under the Project No. R-2021-190.

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