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Research paper

Network synchronization, stability and rhythmic processes in a diffusive mean-field coupled SEIR model

Tina Verma, Arvind Kumar Gupta

Department of Mathematics, Indian Institute of Technology Ropar, Rupnagar, 140001, Punjab, India

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A B S T R A C T

Connectivity and rates of movement have profound effect on the persistence and extinction of infectious diseases. The emerging disease spread rapidly, due to the movement of infectious persons to some other regions, which has been witnessed in case of novel coronavirus disease 2019 (COVID-19). So, the networks and the epidemiology of directly transmitted infectious diseases are fundamentally linked. Motivated by the recent empirical evidence on the dispersal of infected individuals among the patches, we present the epidemic model SEIR (Susceptible-Exposed-Infected-Recovered) in which the population is divided into patches which form a network and the patches are connected through mean-field diffusive coupling. The corresponding unstable epidemiology classes will be synchronized and achieve stable state when the patches are coupled. Apart from synchronization and stability, the coupled model enables a range of rhythmic processes such as birhythmicity and rhythmogenesis which have not been investigated in epidemiology. The stability of Disease Free Equilibrium (or Endemic Equilibrium) is attained through cessation of oscillation mechanism namely Oscillation Death (OD) and Amplitude Death (AD). Corresponding to identical and non-identical epidemiology classes of patches, the different steady states are obtained and its transition is taking place through Hopf and transcritical bifurcation.

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1. Introduction

For last many years, several researchers of different fields are working on epidemic modeling which mainly consists of two components i.e., disease state model and its connectivity. The disease model describes the effect of infection over the population with respect to time and connectivity determines the contact and movement among the population. To clarify the dynamics of transmitting infectious diseases such as measles, mumps, West-Nile virus and Nipah virus so on, multi-patch epidemic models [1–3] have been studied in the literature of mathematical epidemiology. The mathematical epidemiology models are based on the compartments such as Susceptible(S), Exposed (E), Infected (I) and Recovered (R). The dispersal of population affects the dynamics of disease. The infectious disease brings misery and cause millions of death every year [4]. Significantly, recent example is COVID-19 [5,6] which has affected most of the countries. It was originated in China and spread in most of the countries through dispersal of infected ones. So, the dispersal of population plays an important role during the disease spread.

The dispersal among separated patches connects the corresponding epidemiology classes and generate rhythmic processes. Birhythmicity is an important concept in rhythmic process which is one of the dynamical feature of non linear
systems and studied in the fields of physics, chemistry and biology. It is an interesting demonstration of multi-stability that arises in many natural as well as human-made systems. Birhythmic oscillations which appear in living systems are the intracellular Ca2+ oscillations [7], glycolytic oscillations and enzymatic reactions [8–11], the circadian oscillation in Period (PER) and Timeless (TIM) proteins in Drosophila [12], the cyclic AMP signaling system of the slime mold Dictyostelium discoideum [13] and rhythm that arises in population dynamics [14]. Aside from living systems, many artificial systems also exhibit birhythmic oscillations (e.g., the wind-induced mechanical energy harvesting system [15,16]). Another important concept of rhythmic oscillation is rhythmogenesis which is the inverse of the amplitude death. The mechanism of rhythmogenesis has been studied in the respiratory center [17] and is used for defining the process of breath generation. The dispersal induced synchrony [18–20], brings rhythmic process in the compartment classes of the population when these spatial separated patches are connected through coupling for dispersal. In the same manner, dispersal induced stability [21] stabilizes all the oscillators (Susceptible, Exposed, Infected and Recovered) of the patches.

The effects of the coupling on the population usually depends on the nature of coupling, its strength and the dynamic behaviour of the compartment classes of the population. In the present work, mean-field diffusive coupling [22] is used for the connectivity of the patches. The dynamics of population in the patches can be easily modelled through differential equations. Generally, when the coupling is moderate and weak then the oscillators (S, E, I and R) of the patches oscillate in the synchronized manner. When the coupling is strong and high, these oscillators suppress or quench and drive each other to attain a fixed point [23]. The intriguing effects are AD (Amplitude Death) and OD (Oscillation Death) to deal with the cessation of oscillations [24]. AD is the suppression of oscillations in trivial homogenous steady state (HSS) whereas OD is formation of inhomogeneous steady state. On the other hand, coupling can regenerate the oscillations from steady state which is called rhythmogenesis [25]. So, rhythmogenesis is a coupling induced oscillation that takes the entire system from steady state to oscillatory state. From biology prospective of rhythm, birhythmicity is one more fascinating event [26]. The phenomenon of birhythmicity is defined as the coexistence of two stable limit cycles of different frequencies and amplitude which are separated by an unstable limit cycle. Since, dispersal plays an important role for transmission of disease thus birhythmicity and rhythmogenesis, which are induced by coupling, are not explored so it requires special attention.

The issues involved in the present paper are how the movement of an infected individual can effect the public at large and whether the effect would be same for identical epidemiology classes and non-identical epidemiology classes i.e., when all the parameters for each patch are same and different respectively.

We considered SEIR model in which the patches are connected using mean-field diffusive coupling for dispersal. After the study, it has been found that the state of synchronization of the patches and stability is obtained through the movement of infected individual. The effect of coupling is not same for identical and non-identical epidemiology classes. In identical epidemiology classes, the state of synchronization, birhythmicity and stability is obtained whereas in non-identical epidemiology classes, apart from these states, one new state rhythmogenesis is also obtained which is a novel effect involving generation of oscillations observed when two quiescent oscillators are coupled.

2. Model formulation

We consider a model in which the host population is divided into N patches which forms a network. In the network, each patch represent a node with bidirectional links M. Here M represents the total number of connections each node has with other nodes containing itself too. The subpopulation in each patch (or node) is divided into four epidemiology classes S, E, I and R. Here, each node represent a city or a town, a country, or a small domain such as neighborhoods, which belong respectively to the global domain of interest, which could in turn represent a part of a continent or even a whole continent etc. The interactions among the epidemiology compartments (namely S, E, I and R) within the patch and their associated migration among the patches are modeled using SEIR model. This model involves logistic growth [27], bilinear incidence rate [28], natural death rate [29], death due to disease [29], transmission rate from exposed to infected population and recovery rate.

Since the movement of the susceptible population will not change the dynamics significantly however the dynamics will change even if there is movement of a single infected person. So, we have considered the movement of the infected ones only. The mean-field coupling is used in the compartment class I. The dynamics in the ith patch of S, E, I and R using mean-field diffusive coupling is defined as follows:

\[
\frac{dS_i}{dt} = rS_i \left(1 - \frac{S_i}{R_i}\right) - \frac{\beta_iS_iI_i}{1 + \alpha_iS_i} - \mu_iS_i,
\]

\[
\frac{dE_i}{dt} = \frac{\beta_iS_iI_i}{1 + \alpha_iS_i} - (\mu_i + \sigma_i)E_i,
\]

\[
\frac{dI_i}{dt} = \sigma_iE_i - (\mu_i + \delta_i + \gamma_i)I_i + \epsilon(\theta I - I_i),
\]

\[
\frac{dR_i}{dt} = \gamma_iI_i - \mu_iR_i,
\]
where, \( i = 1, 2, \ldots N \) and \( \bar{I} = \frac{1}{M} \sum_{j=1}^{M} I_j \).

The parameters in the above equations are defined as follows: In the compartment class of \( S \), \( r \) is the growth rate of Susceptible with its carrying capacity \( K \) in the logistic growth and in the infection transmission, \( \beta_i \) is the transmission or contact rate and \( \alpha_i \) denotes the inhibitory effect whereas \( \mu_i \) is the natural death rate for all the compartment classes in the \( i^{th} \) patch. In the \( i^{th} \) patch of compartment class of \( E \), \( \sigma_i \) denotes the transmission rate from the exposed class to infected class. \( \delta_i \) and \( \gamma_i \) denote the death due to disease and recovery rate in the epidemiology class of \( I \) respectively. The intrinsic dynamics of the epidemiology classes in the \( i^{th} \) patch is expressed by the above mentioned parameters without their movement among the patches.

On the other hand, the movement of the epidemiology class \( I \) is described by the mean-field diffusive coupling. In the mean-field diffusive coupling, the parameters \( \varepsilon \) represent the dispersal rate i.e., coupling strength of compartment class \( I \). The parameter \( \theta \) describes the mean-field strength of compartment class \( I \).

The interpretations of mean-field diffusive coupling for the epidemic model are as follows: the immigration and emigration of the sub-population is described by the positive and negative terms of the mean-field coupling (\( \varepsilon \)). The parameters \( \varepsilon \) establish the strength of dispersal of \( I \) among the connected patches. The average distribution of the compartment class \( I \) among the connected patches is measured through the mean-field density \( \theta \), which lies between 0 and 1. The considered coupling induces the same qualitative and quantitative behavior as in ref. [30] with additional epidemiology class of Exposed population. In particular, the dispersion of infected ones will not take place among the selected patches when the value of \( \theta \) is 0. It causes that the diffusion out of \( I \) among the selected patches. The task of balancing the immigration in the \( i^{th} \) patch by the emigration from other selected patch will be done when the value of \( \theta \) is 1. The important and interesting epidemic relevance occur when \( 0 < \theta < 1 \) as the immigration and emigration of \( I \) will take place among the selected patches.

Furthermore, it has been considered that the new born population will be susceptible. It is further assumed that the infection is transmitted only when the susceptible population come in contact with infected population and the disease will be transmitted immediately upon contact.

A network of the epidemic model in which the population is divided into \( N \) patches is shown in Fig. 1. Here, the \( i^{th} \) patch is connected to \( j^{th} \) and \( k^{th} \) patch, so the value of the connection link i.e., \( M \) of \( i^{th} \) patch is 3. Since, mean-field diffusive coupling is used so migration will take place in all the patches including \( j^{th} \) and \( k^{th} \) patch but for the clarity purpose it has been shown only in \( i^{th} \) patch as the main motive of Fig. 1 is to show how the migration takes place. Here, the migration will take place only in the epidemiology class \( I \) whereas in [30] it is considered in all the epidemiology classes.

3. Existence of disease-free equilibrium and endemic equilibrium

Since, the governing equations of the model working for \( N \) patches so for simple calculation purpose and for better understanding, two patches have been taken into account. When the patches will be synchronized with identical epidemiology classes, then we have \( S_1 = S_2 = S \), \( E_1 = E_2 = E \), \( I_1 = I_2 = I \) and \( R_1 = R_2 = R \). The analytic solution of equilibrium points is obtained by equating the equations (1) – (4) to zero.

The trivial fixed point of the coupled SEIR model is \((0,0,0,0,0,0,0)\) and two of the non-trivial fixed points are \((S^0,0,0,0,S^0,0,0)\) and \((S^*,E^*,I^*,R^*,S^*,E^*,I^*,R^*)\). These two non-trivial fixed points \((S^0,0,0,0,S^0,0,0)\) and \((S^*,E^*,I^*,R^*,S^*,E^*,I^*,R^*)\) represent disease-free equilibrium (DFE) and endemic equilibrium (EE) respectively, where

\[
S^0 = K \left( 1 - \frac{\mu}{r} \right),
\]

\[
S^* = \frac{\sigma (\mu + \sigma)}{\alpha \sigma (\mu + \sigma) - \beta \sigma}.
\]
\[ E^* = \frac{\partial [\varphi (\mu + \sigma) [\alpha K (\mu - r)] - K \beta \sigma (\mu - r)]}{K \mu (\mu + \sigma) \vartheta - \beta \sigma} \]  
\[ \lambda \]  
\[ (\mu - r) \]  
\[ j_{\lambda 3} \]  
\[ j_{\lambda 4} \]  
\[ j_{\lambda 5} \]  
\[ j_{\lambda 6} \]  
\[ \lambda_{1,2} = -\mu; \]  
\[ \lambda_{3,4} = \mu - r; \]  
\[ \lambda_{5,6} = \frac{-1}{2v} \left( \frac{b_v}{v \sqrt{\pi} + \sqrt{2\pi} \left( \sigma^2 + \sigma^2 - 2\delta (\sigma - \gamma - \varepsilon) + (\gamma + \varepsilon)^2 \right) - 2\sigma (\gamma + \varepsilon - (2\beta - \alpha \gamma - \alpha \varepsilon) S_0)} \right); \]  
\[ \text{3.2. Linear stability analysis} \]  
\[ \text{The stability of the DFE and EE can also be verified by calculating the eigen values of the Jacobian matrix of the equations (1)-(4) at these points. The Jacobian of the coupled system of equations (1)-(4) at the DFE } \]


\[
\lambda_{7,8} = -\frac{1}{2\nu} \left( w - \varepsilon \theta \right) v \pm \sqrt{\nu \left[ \nu \left( \delta^2 + \sigma^2 - 2\delta (\sigma - \gamma) + (\gamma + \varepsilon - \varepsilon \theta)^2 + (\theta - 1) (\sigma + \delta) \right) - 2\sigma (\gamma + \alpha \gamma - 2\beta S_0) \right]}
\]

where, \( w = (2\mu + \delta + \sigma + \gamma + \varepsilon), \) \( \nu = (1 + \alpha S_0). \)

The eigen values of the proposed coupled system reduces to the uncoupled system if \( \varepsilon = 0 \) is substituted in the eigen values \( \lambda_3 \) and \( \lambda_8 \) i.e, when the system is uncoupled then \( \lambda_1, \lambda_3, \lambda_5 \) and \( \lambda_8 \) are the eigen values of the uncoupled system. The new eigen values \( \lambda_7 \) and \( \lambda_8 \) are obtained due to coupling of infected class in two patches.

The stability of DFE can be easily checked by substituting the values of the parameters in the obtained eigen values.

Similarly, the stability of EE can be checked after calculating the eigen values at EE point. Since, the calculations are very lengthy in case of EE, therefore it has been skipped. The equations are solved and stability is checked through the softwares Maple and Mathematica.

4. Results

The dynamics of the coupled SEIR model is studied in this section. The stability of the equilibrium points, obtained in Section 3, will be checked by substituting the values of the parameters in the reproduction number and eigen values. The two patches i.e., patch 1 and patch 2 are considered with the assumption that in the absence of dispersal, the sub-population of each individual patch shows oscillatory behavior. In absence of dispersal rate (\( \varepsilon_1 = \varepsilon_2 = 0 \)), the SEIR model exhibits the local dynamics. The dynamics of coupled SEIR model are identified when all the parameters are same and some of the parameters are different i.e.,identical and non-identical epidemiology classes respectively. The state of birhythmicity,synchronization, stability and rhythmogenesis is analyzed. The numerical bifurcation is done through Xppaut [33] and matcont [34] package.

4.1. Bistability, synchronization and birhythmicity in identical epidemiology classes

Firstly, identical epidemiology classes of two patches have been considered in which all the epidemiology classes will have same contact rate (\( \beta_i \)), inhibitory effect (\( \alpha_i \)), natural death rate (\( \mu_i \)), transmission rate from exposed to infectious (\( \sigma_i \)), death rate due to disease (\( \delta_i \)) and recovery rate (\( \gamma_i \)). In absence of the dispersal (\( \varepsilon = 0 \)), the epidemiology classes of both the patches will be independent and non-synchronized. It exhibits a limit cycle with the parameters \( r = 3, \) \( K = 20, \) \( \beta_1 = 1.25, \alpha_i = 0.8, \mu_i = 0.5, \delta_i = 0.1, \sigma_i = 0.96 \) and \( \gamma_i = 0.035 \) Vs. When the patches are coupled using mean-field diffusive coupling, the patches will come to synchronized state, will suppress each other and lead towards the equilibrium points through oscillation quenching mechanism i.e., amplitude death (AD) and oscillation death (OD). The new state birhythmicity is also observed which have not been studied in epidemiology.

Using one parameter bifurcation, the dynamics of the population of epidemiology classes is shown in Figs. 2(a)-2(d) for continuous variation in the coupling strength \( \varepsilon \). Here, the limit cycles are represented by the circles whereas blue circles indicate unstable limit cycle and green circles denote stable limit cycle. The black curves represent unstable steady state and red curves indicate stable steady state. The value of mean-field strength \( \theta \) is fixed as 0.9 and other parameters are same which are chosen to exhibit oscillatory state. In the presence of coupling, all the corresponding epidemiology classes from both the patches will be synchronized. When coupling strength is low, the population of epidemiology classes \( S, E, I \) and \( R \) will show oscillatory behavior and exhibits limit cycle. With more increment in coupling strength \( \varepsilon \), the population of epidemiology classes \( S, E, I \) and \( R \) quenches to oscillation death (OD).

Here, we have observed one state of OD i.e., OD1. The inhomogeneous steady state of OD1 is created through supercritical Hopf bifurcation HB1. Depending on the initial conditions, the population of the epidemiology classes from both the patches shows synchrony and stability induced by dispersal. From biological prospective, the inhomogeneous steady state OD represents endemic equilibrium in which the population of all the epidemiology classes co-exist with non-zero density. When coupling strength is high, there will be occurrence of two states of amplitude death i.e., AD1 and AD2. The state of AD1 is created through another supercritical Hopf Bifurcation HB3 which represents another endemic equilibrium state (EE). The state of AD2 is created through transcritical bifurcation (TB1) which represents disease-free equilibrium (DFE). Since, the state AD2 which represents DFE is coupling independent so it reaches to a constant value.

In the figures 2(a)-2(d), the bifurcation points HB, PB, TB and SNLC represent Hopf bifurcation, pitchfork bifurcation, transcritical bifurcation and saddle-node bifurcation of limit cycle respectively. In Figs. 2(a)-2(d), the green circles originating from HB3 indicates the perfect synchronized oscillation of the population of epidemiology classes \( S, E, I \) and \( R \).

The state of perfect synchronization is shown in Fig. 3(a) in which considered coupling strength \( \varepsilon \) is 0.5 and mean-field strength \( \theta \) is 0.9. In Figs. 2(a)-2(d), there exist one more stable limit cycle at HB1. When the coupling strength is decreased from HB1, the stable limit cycle loses its stability via saddle-node bifurcation of limit cycle (SNLC). There is also co-existence of two stable limit cycles between HB1 and SNLC for the value of \( \varepsilon = 0.59 \). This indicates birhythmic oscillation in coupled SEIR model. Each of the stable limit cycle acquires its own basin of attraction. Birhythmic oscillations are shown in Fig. 3(b) at \( \varepsilon = 0.59 \) using time series. Two different colors have been used to distinguish between these two time series of birhythmic oscillations. Using corresponding phase portrait, the co-existence of two stable limit cycles is shown in Fig. 3(c).
4.2. Bistability, synchronization, birhythmicity and rhythmogenesis in non-identical epidemiology classes

Since, the model has many parameters so, it is not possible to check the effect by changing all the parameters one by one and jointly. For this reason, in non-identical epidemiology classes of two patches, the contact rate ($\beta$) and inhibitory effect ($\alpha$) are considered different. These different parameters are $\beta_1 = 1.25$, $\beta_2 = 1.3$, $\alpha_1 = 0.5$ and $\alpha_2 = 0.2$, where as the other parameters are same as in identical case. Likewise identical epidemiology classes, here also the parameters are chosen in such a way that it remains in oscillatory state in absence of coupling. The dynamics of the the epidemiology classes of both the patches is shown in Figs. 5(a)-5(d) using one-parameter bifurcation diagram of $\varepsilon$.

Likewise identical epidemiology classes, here also the coupled epidemiology classes show synchrony, bistability and birhythmic oscillations. The oscillations are suppressed to inhomogeneous steady state. Two inhomogeneous steady states are observed in this case i.e., OD1 and OD2. The OD1 state and OD2 state are created through supercritical Hopf bifurcation and transcritical bifurcation which are named as HB1 and TB1 in the figures 5(a)-5(d), respectively. As in identical epidemiology classes, here also the birhythmicity occurs between HB1 and SNLC. Furthermore, when the coupling strength is increased then one more interesting feature takes place i.e., rhythmogenesis which is a new concept in epidemiology. The process of rhythmogenesis occur between the Hopf bifurcation points HB2 and HB3. Between these points, the oscillation are regenerated which were suppressed before. So, the mean-field coupling plays an important role to suppress and regen-
Fig. 3. (a) The synchronized solution for $\varepsilon = 0.5$. (b) Time series showing birhythmic oscillations for $\varepsilon = 0.59$. Two different colors are used to represent different time series of birhythmic oscillations. (c) Phase portrait with two co-existing limit cycles of the corresponding birhythmic oscillations.

Fig. 4. Two parameter bifurcation in 2D-plane of $\varepsilon$ and $\theta$.

erate the oscillations. When the coupling strength is stronger the regenerated oscillations suppress to homogeneous steady states AD1 and AD2. At HB1, the density of epidemiology class $S_2$ is nearly zero but $S_1$ has positive density. The states OD1, OD2 and AD1 represents the steady state of endemic equilibrium as all the epidemiology classes have non-zero density. Since, AD2 state is coupling independent so it is homogeneous steady state and represents disease-free equilibrium where only susceptible class has non-zero and constant density and other classes converges to zero. We have also observed period doubling bifurcation in coupled non-identical epidemiology classes. When the coupling strength is low, the period-doubling bifurcation is exhibiting by the epidemiology classes which is named as PD in the figures 5(a)-5(d).
Fig. 5. Non-identical epidemiology classes: (a), (b), (c), (d) One parameter bifurcation of $S_1, S_2, E_1, E_2, I_1, I_2$ and $R_1, R_2$ by varying coupling strength $\varepsilon$ for $\theta = 0.9$.

Fig. 6. (a) Time series showing birhythmic oscillations for $\varepsilon = 2.1$. Two different colors are used to represent different time series of birhythmic oscillations. (b) Phase portrait with two co-existing limit cycles of the corresponding birhythmic oscillations.

The birhythmic oscillations and co-existence of two stable limit cycles at coupling strength $\varepsilon = 2.1$ and mean-field density $\theta = 0.9$ are shown in Figs. 6(a) and 6(b) using time series analysis. Two different colors are used to indicate the birhythmicity.

Using two-parameter bifurcation diagram of $\varepsilon$ and $\theta$, the dynamics of the epidemiology classes is more clearer which has shown in Fig. 7. The epidemiology classes will be in oscillatory motion when the coupling strength is low and mean-field density is high. Between the curves $PD$ and $HB1$, the epidemiology classes will exhibit period doubling and birhythmicity.
which is observed by increasing the coupling strength $\varepsilon$. The epidemiology classes exhibit bistable states, which are inhomogeneous steady states, between Hopf bifurcation curves $HB1$ and $HB3$. When the coupling strength is increased more, the epidemiology classes tend to homogeneous steady states.

Further we investigate the sensitivity of the parameter values on the system dynamics. It is observed that the dynamics of the epidemiology classes will remain unaffected against small variations in all the model parameters. There will be no qualitatively change even when the difference between transmission rate of two epidemiology classes $(\beta_1 = 1.25, \beta_2 = 1.55)$ is same as the difference between inhibitory effect $(\alpha_1 = 0.5, \alpha_2 = 0.2)$ or same transmission rate i.e., $(\beta_1 = \beta_2 = 1.25)$ is considered. However, if $\alpha_1 \approx \alpha_2$ i.e. the difference between $\alpha_1$ and $\alpha_2$ is small then the dynamics of the population of non-identical epidemiology classes become similar to the case of identical epidemiology classes.

In order to find the interplay between the non-identical patches, the value of inhibitory parameter $\alpha_1$ and $\alpha_2$ was considered distinctly otherwise it will be the same as in identical epidemiology classes. Note that the different values considered for $\alpha_1$ and $\alpha_2$ also depends on other system parameters. Hence, it is reasonable to conclude that the change in inhibitory effect is more significant for the qualitative change in the dynamics as compared to other system parameters.

5. Conclusion

In this paper, we have studied the dynamics of an epidemic SEIR model in which the population is divided into patches. The four epidemiology classes $S$, $E$, $I$ and $R$ are considered in the patches and the patches are connected through mean-field diffusive coupling. The synchronization and stability for coupled epidemic model SEIR are explored using mean-field diffusive coupling. Different rhythmic processes have also been explored. The epidemiology classes of two distinct patches, which were uncoupled, behave independently and exhibits a limit cycle for the chosen parameters. The dynamics is studied when the epidemiology classes of two patches are identical and non-identical.

In case of identical epidemiology classes, contact rate, inhibitory effect, transmission rate from exposed class to infected class and recovery rate are considered same for epidemiology classes of two patches. When the patches of epidemiology classes are connected through mean-field diffusive coupling, the corresponding epidemiology classes of two patches will synchronize and follow same rhythm. Apart from this, we have observed the following:

- There is co-existence of two stable limit cycles between Hopf bifurcation ($HB1$) and saddle-node limit cycle ($SNLC$) where each stable limit cycle acquires its own basin of attraction. This indicates birhythmicity which has not been observed earlier in epidemiology.
- For higher coupling strength, the oscillations suppress and lead to inhomogeneous steady state $OD1$. Thereafter, $OD1$ converges to homogeneous steady state $AD1$ and then to $AD2$ through Hopf bifurcation and transcritical bifurcation respectively.
- The state $OD1$ and $AD1$ represent the steady state of endemic equilibrium whereas $AD2$ represents disease free equilibrium. The stability is verified through the reproduction number $R_0$ as well as through linear stability analysis.

In case of non-identical epidemiology classes, contact rate and inhibitory effect are considered different for epidemiology classes of two patches. Likewise identical epidemiology classes, the corresponding epidemiology classes of two patches will synchronize, follow same rhythm and birhythmicity occurs too. Moreover, we have analyzed the following results:

- Here, we have explored bistable inhomogeneous steady state $OD1$ and $OD2$ which are created through Hopf and transcritical bifurcation respectively. Furthermore, two homogeneous steady states are also observed i.e., $AD1$ and $AD2$.
- For low coupling strength, we have also explored period-doubling bifurcation. The states $OD1$, $OD2$ and $AD1$ represent steady state of endemic equilibrium and $AD2$ represents disease-free equilibrium.
• Here, the mean-field diffusive coupling acts as feedback for the interesting feature of rhythmicity i.e., rhythmogenesis is explored. In this feature, the oscillations which were suppressed are regenerated.

We have studied the impact of coupling on the dynamics of coupled SEIR model with mean-field diffusive coupling in which the movement of only infectious class is considered. Apart from dispersal of infectious class, one can study the dynamics by considering the dispersal of all the epidemiology classes. The population of epidemiology classes can disperse through different mechanism which will also be very interesting to study its dynamics. Here, we have not considered the death due to movement of infectious people. One can consider the death of infectious population and other difficulties due to movement. It will also be interesting to study the dynamics when the delay will be considered.

Credit author statement

Tina Verma: The implementation of the idea, analysis, and method.
Arvind Kumar Gupta: Proposed the idea, interpret the results and supervised the work.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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