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Research paper

Coupling and synchronization of hiv/aids fisher folk metapopulations

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Abstract

The study of epidemiology is often done with an assumption that the population is homogeneously mixed, and the disease dynamics is uniform. However, this is not always true, and cultural beliefs and economic activities significantly contribute to segregation not necessarily in spatial dimension but on the way of life. In this study, the dynamics of HIV/AIDS is studied in four distinct fisher-folk population patches, both individually and under all-to-all diffusive coupling. It was found that, the dynamics of each patch is periodic, and there exist an attracting invariant stable synchronization manifold. The manifold of the coupled system displayed robustness under small perturbation, even with a small coupling strength of $k \ll 1$. This guarantees uniformity of long term metapopulation disease dynamics.

Keywords: *Metapopulation; Synchronization; All-To-All Coupling; Invariant Manifold; Stability; Robustness; Perturbation.*

1. Introduction

Epidemiology is the study and analysis of the patterns, causes and effects of health and disease conditions in a defined population. It is the cornerstone of public health and shapes policy decisions and evidence based practice by identifying risk factors for the disease and targets the preventive health care. One of the main areas of epidemiological study is the disease surveillance which monitors the spread of a disease by establishing patterns of progression of the pandemic. The goal of the surveillance is to predict, observe and minimize the harm caused by the epidemic to the population.

Contributions of mathematics in epidemiology is capture in modeling and simulation, which is seen to be a virtual laboratory, enabling the analysis and monitoring of the variations of various parameters which are impossible or would take ages in real life situation.

In this paper, we focus on the study of the interactions of small subpopulations, which are distinct in HIV/AIDS dynamics and spatially separated. The study aims at investigating the synergic effect of coupling and possibility of synchronization. This will give vital effects of perturbation dynamics in terms of controlling the disease prevalence through intervention strategies including treatment, public health education and prevention.

Many population models assume that the individuals mix homogeneously implying that all individuals in the population are equally likely to encounter each other. In reality however, many populations are structured in space and are interconnected by human travel. The population may therefore be sub-divided into spatially separated sub-populations also known as the population patches. These population patches are connected to each other by movement of individuals. Moreover, each patch has its own dynamics which are influenced by both immigration and emigration of individuals. Such a distinct group of sub-population is known as a metapopulation [1].

Metapopulation dynamics is therefore defined as the study of fragmented population who's population dynamics occurs at two distinct levels; namely, within patch and between patch dynamics. Fisher folk subpopulations are spatially separated, but interact within Lake Victoria and its environs. These interactions are due to population interfaces in the same fish markets and fishing grounds.

In general, synchronization of coupled systems means that dynamic patterns which previously were different begin to behave in the same way and simultaneously so that the difference in their dynamics is zero, and the knowledge of one leads to the prediction of the other.

In this paper, the systems we consider are four population patches of Kisumu, Homabay, Siaya and Busia, all around Lake Victoria. The coupling under study is all-to-all configuration, which is more suitable due to common fishing and market grounds to all.

Consider the population dynamics of each subpopulation and denote their disease prognostic behaviour by

$$\dot{z}_i(t) = g_i(z_i) \tag{1}$$

Where z_i $i = 1,2,3,4$ represents the four subpopulation patches of Kisumu (1), Homabay (2), Siaya (3) and Busia (4), $z = (S, I, T, A,)$ is a 4 dimensional vector representing 4 distinct disease compartments; namely, Susceptible (S)m Infective (I), Treated (T) and AIDS (A)

class, and g(z) represents the dynamics of each patch, which are here assumed to be homogeneous, and each has periodic solution. Coupling therefore means connection of the four similar oscillators, whose dynamics are each described by a SITA model.
All – to – all coupling configuration of the four oscillators is defined as;

$$\dot{z}(t) = A(k)z + G(z) \tag{2}$$

Where $z = (z_1, z_2, z_3, z_4)$ and $G(z) = \left(g_1(z_1), g_2(z_2), g_3(z_3), g_4(z_4)\right)$ and A(k) is the coupling configuration matrix with coupling strength k. The coupling configuration matrix for all-to-all coupling is defined here as;

$$A(k) = k\Delta \otimes I_n \tag{3}$$

Where $\otimes$ is the kronecker product, and the coupling matrix Δ is defined as;

$$\Delta = \begin{pmatrix} -(n-1) & 1 & 1 & 1 & \dots & 1 \\ 1 & -(n-1) & 1 & 1 & \dots & 1 \\ 1 & 1 & -(n-1) & 1 & \dots & 1 \\ 1 & 1 & 1 & -(n-1) & \dots & 1 \\ \vdots & \vdots & \vdots & \vdots & \ddots & \vdots \\ 1 & 1 & 1 & 1 & \dots & -(n-1) \end{pmatrix} \tag{4}$$

In our case of 4 spatially distinct subpopulations patches, $n = 4$ and the disease dynamics of each oscillator is represented by the SITA model defined by

$$\frac{dS}{dt} = \lambda S - c\beta\phi SI - \mu S \tag{5a}$$

$$\frac{dI}{dt} = c\beta\phi SI - (\mu + \tau + \omega)I \tag{5b}$$

$$\frac{dT}{dt} = \tau I - (\sigma + \delta)T + \rho A \tag{5c}$$

$$\frac{dA}{dt} = \delta T - (\xi + \sigma + \rho)A + \omega I \tag{5d}$$

Where: β is the force of infection, with β_v being the vector folk infection rate, λ is the natural recruitment rate to the susceptible group. λ_v is the corresponding recruitment rate to the vector folk group, μ natural death rate. It is here assumed to be equal in all compartments, θ is the modification parameter accounting for the difference in the infection rate by the infected class. ψ is the modification parameter accounting for the difference in the infection rate by the treated class, ϕ is the modification parameter accounting for the difference in the infection rate by the AIDS class, τ is the rate at which infected class seek treatment, δ is the proportion of those under treatment, who will not be cured and therefore progress to AIDS class, ω is the rate at which people with AIDS seek treatment. ω_v is the corresponding rate for vector folk class, ρ is the recovery rate from AIDS status, back to treatment class. Note that treatment for HIV is a life-long process and therefore the AIDS class includes People Living With HIV AIDS (PLWHA), ω is the rate at which infected individuals progress to AIDS class without seeking treatment, and η is the accelerated death rate due to opportunistic diseases or AIDS.

2. Literature review

Mathematical modeling of infectious diseases and analytic techniques have given great insights into the study of the evolution and control of epidemics [2]. The occurrence of most epidemics is seasonal and therefore periodic. Infectious diseases can be therefore be modeled as biological oscillators using differential equations [3-6]. Many interesting dynamics occur in the study of oscillators, but most interesting phenomena, physically significant is the stability and robustness of oscillators under perturbation [7]. In this regard, the epidemic focused in this study is HIV/AIDS. The World Health Organization (WHO) report of 2004 states that, AIDS was discovered in 1981 and has become one of the leading causes of death, globally, affecting mostly impoverished people already. This is done with an attempt to shed light to a close to four decades problem since it was first reported and labeled as AIDS [8]. According to [9], HIV/AIDS had killed an estimate of 25 million people globally. It was estimated that over 33 million people were living with HIV, most of whom are unaware of their HIV status, and as a result, unknowingly contribute to the spread of the infection [10]. The epidemic has disproportionately affected people residing in areas of the world that have fewer resources to combat the disease. The [10] further estimated that there were 2.7 million people who were newly infected with HIV in 2007 and greater than 95% of these new infections occurred among persons residing in Low and Middle Income Countries. Sub-Saharan Africa accounts for an estimated 22 million cases of HIV/AIDS and has an estimated prevalence of 5% in adults ages 15-49. In these Low and Middle Income Countries, [10] says that the HIV/AIDS epidemic has often over-burdened the under-resourced health care infrastructure. In Kenya for example, the worst affected community is the fisherfolk as compared to the other populations [11-15]. Surveys conducted since 1992 in ten low or middle-income countries in Africa, Asia and Latin America revealed that HIV/AIDS prevalence among fishers or fishing communities are between 4 and 14 times higher than the National average prevalence rate for adults aged 15-49 [16, 17]. These considerable rates of HIV/AIDS infection place fisher folks among groups that are more usually identified as being at high risk [12, 18-20]. It is for this reason that this study focuses on dynamics of HIV/AIDS among the fisherfolk community around Lake Victoria Kenya, as a problem of coupled metapopulation patches, stability and robustness under small disease parameter perturbation.

3. Methods and analysis

In this section, the methods used in the analysis of the model are presented, and are discussed under the sections hereunder.

3.1. All-to-all coupling topology

Diffusive coupling is an arrangement, where oscillators are allowed to influence each other [7]. In terms of the biological oscillators under study, the periodic dynamics of HIV/AIDS pandemic in four distinct population patches around Lake Victoria are interacting through people entering and leaving each patch, together with interacting in the markets and common fishing grounds. The interaction referred to her is the relationship which leads to sexual intercourse. The level of interaction which leads to sexual relationship, significant to cause transfer of disease is here considered. All-to-all coupling, also called global coupling is represented geometrically as in Figure 1 below [21]. Each terminal point represents an oscillator, while the arrows joining the oscillators represent bidirectional coupling where oscillators are allowed to influence each other simultaneously.

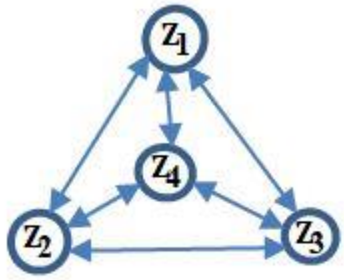

Fig. 1: All-To-All Coupling Configuration.

Each oscillator is represented by a system of ordinary differential equations, denoting a dissipative system of four variables, described by a set of four differential equations in equation (5), each describing the dynamics of Susceptible, Infective, Treated and AIDS cases. Using the notation of $z_i, i = 1, 2, 3, 4$ (Kisumu, Siaya, Homabay and Busia) to represent the fours oscilators, we derive the coupled system of oscillators given in equation (2) is represented in detail by

$$\begin{pmatrix} \dot{z_1}(t) \\ \dot{z_2}(t) \\ \dot{z_3}(t) \\ \dot{z_4}(t) \end{pmatrix} = k \begin{pmatrix} -3 & 1 & 1 & 1 \\ 1 & -3 & 1 & 1 \\ 1 & 1 & -3 & 1 \\ 1 & 1 & 1 & -3 \end{pmatrix} \otimes (I_4) \begin{pmatrix} z_1 \\ z_2 \\ z_3 \\ z_4 \end{pmatrix} + \begin{pmatrix} g_1(z_1) \\ g_2(z_2) \\ g_3(z_3) \\ g_4(z_4) \end{pmatrix} \tag{6}$$

Where I_4 is a 4 –dimensional identity matrix, $k\Delta \otimes I_4 = k \begin{pmatrix} -3I_4 & I_4 & I_4 & I_4 \\ I_4 & -3I_4 & I_4 & I_4 \\ I_4 & I_4 & -3I_4 & I_4 \\ I_4 & I_4 & I_4 & -3I_4 \end{pmatrix}$ and each $z_i, i = 1, 2, 3, 4$ is defined by equation (5a-d) as; $\dot{z_1}(t) = \begin{pmatrix} \dot{S}_i(t) \\ \dot{I}_i(t) \\ \dot{T}_i(t) \\ \dot{A}_i(t) \end{pmatrix} = \begin{pmatrix} \lambda S_i - c\beta\phi S_i I_i - \mu S_i \\ c\beta\phi S_i I_i - (\mu + \tau + \omega) I_i \\ \tau I_i - (\mu + \delta) T_i + \rho A_i \\ \delta T_i - (\xi + \sigma + \rho) A_i + \omega I_i \end{pmatrix}$

Where the subscripts $i = 1, 2, 3, 4$ represents the subpopulations in Kisumu, Homabay, Siaya and Busia respectively. In compact vector form, equation (6) is expressed equivalent to equation (2) as;

$$\dot{z} = k(\Delta \otimes I_4)z + G(z) \tag{7}$$

Where z and $G(z)$ are defined in equation (2) above. The coupled system (7) is said to be synchronized, if there exist a manifold

$\mathcal{M} \coloneqq \{z \in \mathbb{R}^{nd} : z_i = z_j \neq 0, i, j = 1, 2, 3, 4, i \neq j\}$

That is, there exist an invariant attractor $\mathcal{A}_k \forall\, k > 0$ invariant under the flow defined by equation (5) which contains the ω- limit set of the oscillator, so that the difference $z_i(t) - z_j(t) \to 0$ as $t \to \infty, \forall\, i, j$.

3.2. Construction of synchronization manifold

Synchronization manifold $\mathcal{M} \coloneqq (z \in \mathbb{R}^{nd} : z_i = z_j \neq 0, i, j = 1, 2, 3, \ldots, n-1\}$ is guaranteed since we are coupling identical oscillators, and thus the diagonal is invariant [22]. Our task is therefor to show that one of the eigenvalue of the coupling topology matrix Δ is $\lambda_0 = 0$ and the corresponding generalized eigenvector spans the diagonal in $\mathbb{R}^{nd}$ while the other eigenvalues $\lambda_s, s = 1, 2, .., n-2$ are bounded to the left side of the imaginary axis.

Consider our specific case where $n = 4$ and $d = 4$, then, the eigenvalues of the coupling matrix $\sigma(\Delta)$ are; $\lambda_0 = 0$ and $\lambda_s = -4, s = 1, 2, 3$, with the corresponding generalized eigenvectors as; $v_0 \coloneqq (1, 1, 1, 1) \in \mathbb{R}^4$ which spans the diagonal and the other eigenvectors are; $v_i \coloneqq [(-1,1,0,0), (-1,0,1,0), (-1,0,0,1)]$. These can be expressed as, $v_0 = e$ and $v_i = (0, 1,0,0)$ with 1 in the i^{th} position.

In order to determine the existence of a global attractor, (the diagonal or synchronization manifold) in a bounded set $U \in \mathbb{R}^{nd}$, we require a transformation, that splits the system into transverse flow and tangential flow to the manifold. Consider the transformation defined in [7] below.

$$z = ye + \tilde{e}w, \qquad w = (w_1, w_2, \dots, w_{n-1})^T, w \in \mathbb{R}^{nd-d}, y \in \mathbb{R}^d \tag{8}$$

$$\begin{aligned} w_j &= z_j - z_{j+1} \quad, 1 \le j \le n-1, \\ y &= \frac{1}{n}\sum_{j=1}^{n} z_j, \end{aligned} \tag{9}$$

Where e_j is the j^{th} column of an $n \times n$ identity matrix and $\tilde{e} = \sum_i^j \left(e_i - \frac{j}{n}e\right)$, with $\tilde{e} = (\tilde{e}_1, \tilde{e}_2, \dots, \tilde{e}_{n-1})$. The set $e, \tilde{e}_j$ is an orthogonal basis for $\mathbb{R}^n$.
Using transformation (9) in equation (7), we obtain

$$\begin{aligned} \dot{w} &= k(\Delta_1 \otimes I_d)w + F(w, y) \\ \dot{y} &= \frac{1}{n}\sum_{j=1}^{n} g(z_j) \end{aligned} \tag{10}$$

where $F(w, y) = (F_1(w, y), F_2(w, y), F_3(w, y))$ with $F_i(w, y) = g(z_i) - g(z_{i+1}), 1 \le i \le n-1$ and the matrix Δ_1 is given by $\Delta_1 = -knI_n \otimes I_d$.
The first equation in (9) describes the dynamics transverse to the synchronization manifold, and the second equation in (9) describes the dynamics tangential to the synchronization manifold.

3.3. Stability of the synchronization manifold

Synchronization means the deviations $z_i - z_j,\ \ i \ne j, i, j = 1, 2, 3, 4$ as $t \to \infty$ dies out, that means the solution of the first equation in (9) is expected to be exponentially stable, the property that $w = 0$ [23]. We are interested in local synchronization, and thus we consider the fundamental matrix solution $\Phi(t; z_0), z_0 \in \mathcal{M}$ of the linearization of equation (7) about $\mathcal{M}$ defined as $\dot{z} = A\big(z(t; z_0)\big)z$.
Let

$$\Phi(t; z_0) = \Phi_c(t; z_0) \oplus \Phi_s(t; z_0);$$

be the invariant splitting where $\Phi_c(t; z_0)$ and $\Phi_s(t; z_0)$ are restrictions of $\Phi(t; z_0)$ of the tangent bundle vector $T_{z_0}\mathcal{M}$ to the manifold at z_0 and N_{z_0} bundle of vectors normal to the manifold at z_0.
Linearizing equation (10) along the solution $\big(0, y_0(t)\big)$ on the manifold $\mathcal{M}$ yields

$$\begin{pmatrix} \dot{w} \\ \dot{y} \end{pmatrix} = \begin{pmatrix} k(\Delta_1 \otimes I_4 + I_3 \otimes D_z g(y_0(t)) & 0 \\ 0 & D_z g\big(y_0(t)\big) \end{pmatrix} \begin{pmatrix} w \\ y \end{pmatrix} \tag{11}$$

Whose solution is of the form

$$\begin{aligned} w(t) = \Phi_s(t; z_0) &\approx e^{(k\lambda_\zeta + \lambda_i)t}, \quad \zeta, i = 1, 2, 3 \\ y(t) = \Phi_c(t; t_0) &\approx e^{\lambda t} \end{aligned} \tag{12}$$

The invariant manifold $\mathcal{M}$ is attracting and stable if the maximum of $k\big(\lambda_\zeta + \lambda_i\big)$ is less than zero. In our case, $max\big(\lambda_\zeta\big) = -4k$ and $max(\lambda_i) = 1.6361$, thus the generalized Lyapunov exponent

$$\alpha(z_0) = max\big(k\lambda_\zeta + \lambda_i\big) = -4k + 1.6361$$

Giving the optimal coupling strength $k_0 = 0.409025$. The condition for robustness of synchronization manifold using Lyapunov exponents requires that for $\alpha(z_0) < 0$, we require (for persistence) that $\beta(z_0) < 1$, that is

$$\beta(z_0) \coloneqq \lim_{t\to\infty} sup \frac{ln\|\Phi_s(t, z_0)\|}{ln\, m\big(\Phi_c(t, z_0)\big)} < 1$$

From calculation, we obtained $\beta(z_0) = 0.1993 < 1$ as required.

4. Numerical solutions and graphical representation

4.1. Coupled oscillators

All-to-All coupling configuration described in equation (6) in section 3.1 is presented for four oscillators ($n = 4$) each of dimension four ($d = 4$), making a system of sixteen ordinary differential equations. The choice of $\dot{z}(t) = g\big(z(t)\big)$ is defined in equation (5a–d) for Kisumu (k), Homabay (h), Siaya (s) and Busia (b) as;

$$\dot{z}_k(t) = \begin{bmatrix} \dot{S}_k = & \lambda S_k - c\beta\phi S_k I_k - \mu S_k \\ \dot{I}_k = & c\beta\phi S_k I_k - (\mu + \tau + \omega) I_k \\ \dot{T}_k = & \tau I_k - (\sigma + \delta) T_k + \rho A_k \\ \dot{A}_k = & \delta T_k - (\xi + \sigma + \rho) A_k + \omega I_k \end{bmatrix} \tag{13a}$$

$$\dot{z}_h(t) = \begin{bmatrix} \dot{S_h} = & \lambda S_h - c\beta\phi S_h I_h - \mu S_h \\ \dot{I_h} = & c\beta\phi S_h I_h - (\mu + \tau + \omega) I_h \\ \dot{T_h} = & \tau I_h - (\sigma + \delta) T_h + \rho A_h \\ \dot{A_h} = & \delta T_h - (\xi + \sigma + \rho) A_h + \omega I_h \end{bmatrix} \quad (13b)$$

$$\dot{z}_s(t) = \begin{bmatrix} \dot{S_s} = & \lambda S_s - c\beta\phi S_s I_s - \mu S_s \\ \dot{I_s} = & c\beta\phi S_k I_k - (\mu + \tau + \omega) I_s \\ \dot{T_s} = & \tau I_s - (\sigma + \delta) T_s + \rho A_s \\ \dot{A_s} = & \delta T_s - (\xi + \sigma + \rho) A_s + \omega I_s \end{bmatrix} \quad (13c)$$

$$\dot{z}_b(t) = \begin{bmatrix} \dot{S_b} = & \lambda S_b - c\beta\phi S_b I_b - \mu S_b \\ \dot{I_b} = & c\beta\phi S_b I_b - (\mu + \tau + \omega) I_b \\ \dot{T_b} = & \tau I_b - (\sigma + \delta) T_b + \rho A_b \\ \dot{A_b} = & \delta T_b - (\xi + \sigma + \rho) A_b + \omega I_b \end{bmatrix} \quad (13d)$$

Coupling equation (14a-d) as described in equation (6), and transforming to a form similar to equation (10), yields the system which satisfies the criteria for synchronization and persistence.

4.2. Simulation and graphical presentation

In order to graphically the dynamics of HIV/AIDS in the four patches, namely Kisumu, Busia, Siaya and Homabay, the following data collected from the study area are presented in Table 1 below.

Table 1: Parameter Values from Data Collected from Siaya, Kisumu, Homabay and Busia

No	Symbol	Description	Value
1	λ	Recruitment rate of normal community	0.01385
2	μ	Natural death rate	0.00124
3	β	Probability of infectivity given sufficient contact	0.00033
4	ϕ	Modification parameter describing sexual interaction probability	0.00177
5	c	Contact rate of susceptible with infective, sufficient to transmit HIV	0.18624
6	τ	Progression rate of Treatment class to HIV patients	0.24
7	σ	Progression rate of HIV patients to AIDS status	0.023
8	η	Accelerated death rate due to HIV/AIDS	0.00124
9	δ	Accelerated death rate due to HIV infection, while on treatment	0.00496
10	ρ	Rate of seeking treatment by AIDS class	0.00354
11	ω	Direct progression to AIDS class from the time of infection	0.003218
12	p	Perturbation multiplier	0.01
13	k	Coupling strength	[0 , 1]
14	ξ	Accelerated death rate due to full blown AIDS status	0.00321

The fourth order numerical integration inbuilt in MATLAB is used to simulate the model in equation (13a – d) and plot trajectories with initial conditions $(S_0, I_0, T_0, A_0) = (300, 0.1, 0.01, 0.01)$. The dynamics of system (13a – d) are shown in the figure(s) below. Figure 2 below and subsequent figures will have (a) Top left – shows the orbit where we pick the initial conditions, (b) Top right – shows the invariant manifold or the diagonal, (c) Bottom left – shows the four graphs representing the dynamics of each class of disease dynamics, and (d) Bottom right – shows the differences of each oscillator versus time.

Clearly, the first graph (a) shows existence or periodic orbit, which is the characteristic of an oscillator. This is evidenced in all the four equations of the SITA model. Notice the smooth diagonal and absence of deviations from the synchronization manifold as depicted in figure (b) and (d) respectively.

4.3. Perturbation and coupling strength

In biological oscillators under study, perturbation is considered here as the small changes that arise due to changes in the intensity of interaction, for example changes in market forces, shift of fish populations, change in tidal waves, among others which contributes to more or less interaction of the fisher folk in the four population patches. Now adding a small perturbation of $p \ll 1$ to uncoupled system $(k = 0)$ yields the system (15) below.

$$\begin{aligned} \dot{S_i} &= \lambda S_i - c\beta\phi S_i I_i - \mu S_i + k\big(-3S_i + \textstyle\sum_j S_j\big) + p(a_{i1})S_i \\ \dot{I_i} &= c\beta\phi S_i I_i - (\mu + \tau + \omega) I_i + k\big(-3I_i + \textstyle\sum_j I_j\big) + p(a_{i2}) I_i \\ \dot{T_i} &= \tau I_i - (\sigma + \delta) T_i + \rho A_i + k\big(-3T_i + \textstyle\sum_j T_j\big) + p(a_{i3}) T_i \\ \dot{A_i} &= \delta T_i - (\xi + \sigma + \rho) A_i + \omega I_i + k\big(-3A_i + \textstyle\sum_j A_j\big) + p(a_{i4}) A_i \end{aligned} \quad (14)$$

Where the index $i = k, s, b, h$ denotes the metapopulations of Kisumu, Siaya, Busia and Homabay, while the elements a_{ij} $i = k, s, b, h;\ j = 1,2,3,4$ represents various vlues of perturbation parameter $a_{ij} \in \mathbb{R}$. Equation (14) is equivalent to

$$\dot{Z_i} = k(\Delta \otimes I_4) Z_i + G(Z_i) + p(Z_i)$$

Simulations are run with various values of the coupling strength $k \geq 0$ for the purpose of achieving the threshold coupling strength which eliminates all deviations from the diagonal.

With small perturbation, we notice loss of synchronization manifold (the diagonal) and deviations in the dynamics as shown in Figure 3 (a, b, d). As the coupling strength is increased gradually, it is found that the chaotic behavior is lost and synchronization is achieved again. This is achieved at $k \geq 1.1137$ as seen in Figure 4 below.

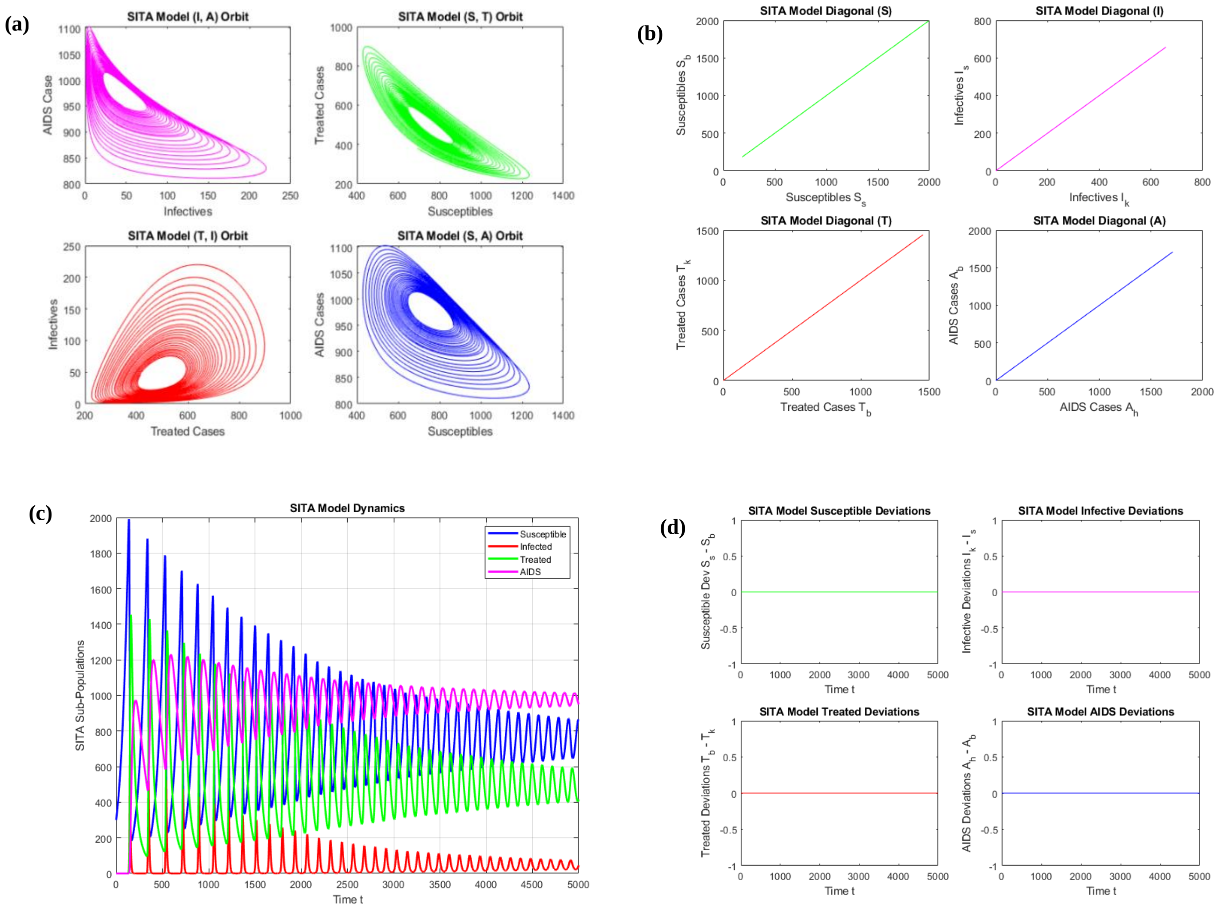

Fig. 2: HIV/AIDS Interaction Dynamics of Coupled Oscillators with $K = 0, P = 0$.

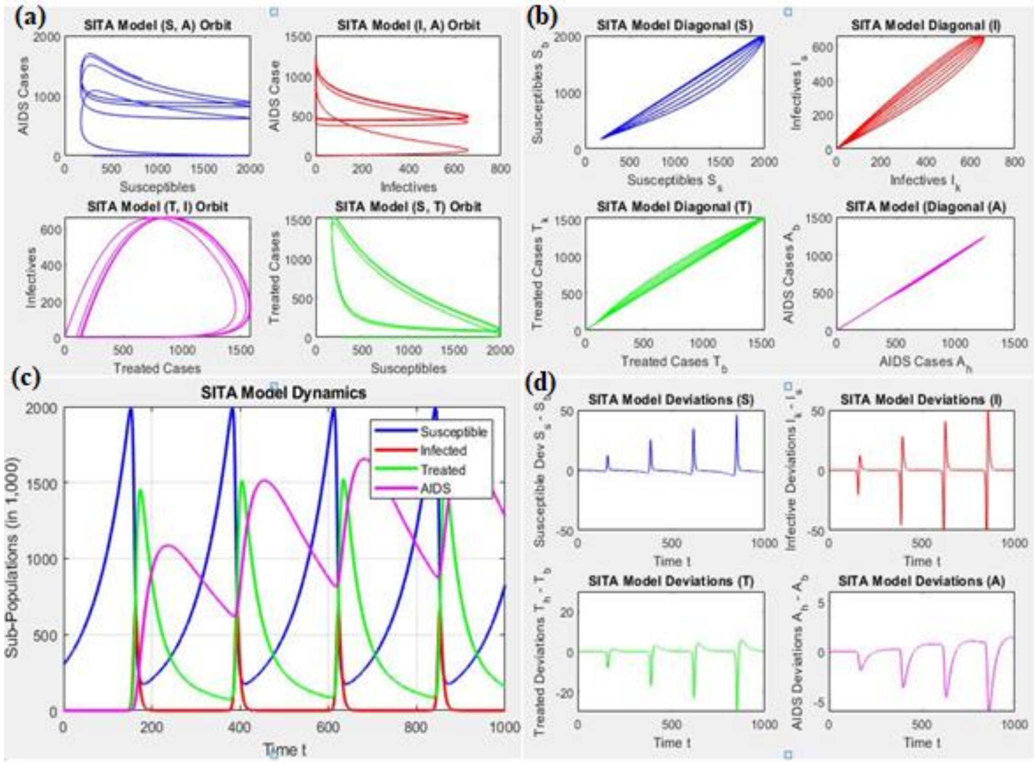

Fig. 3: HIV/AIDS Interaction Dynamics of Coupled Oscillators with $K = 0, P = 1$.

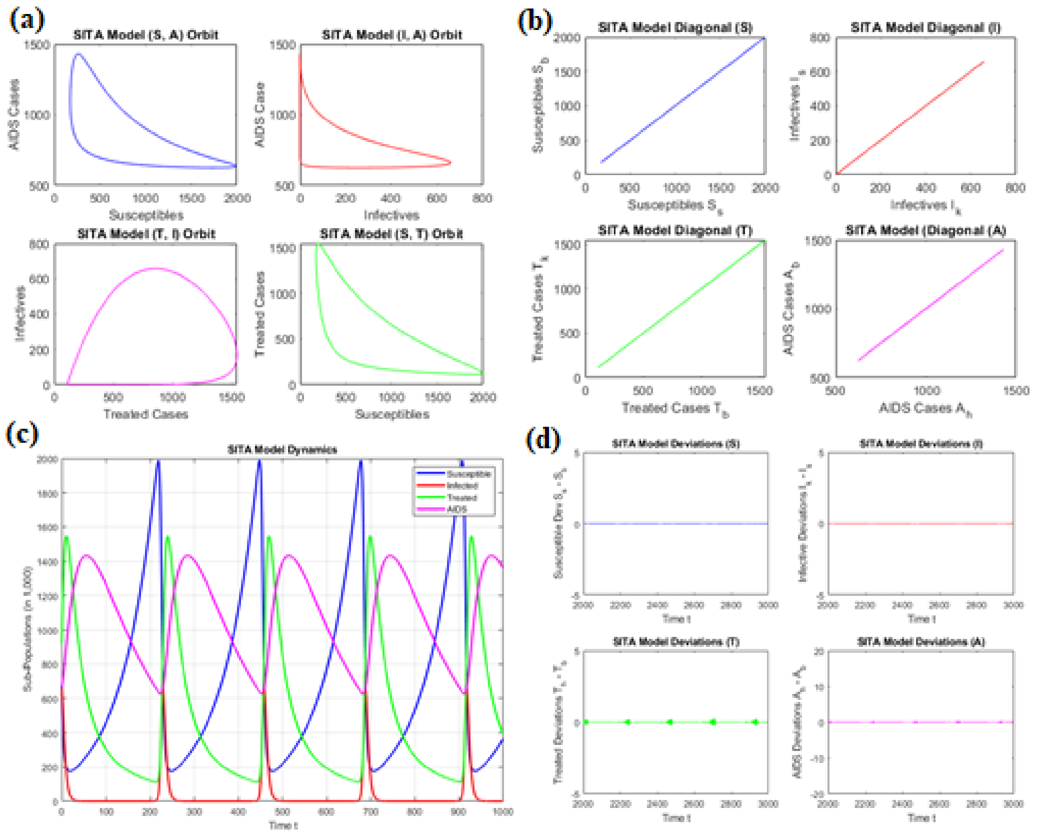

Fig. 4: HIV/AIDS Interaction Dynamics of Coupled Oscillators with $K = 1.1137, P \neq 0$.

5. Conclusion and recommendation

From the analysis above, it is noted that coupled oscillators have a tendency of being synchronized, and a small perturbation gives rise to chaotic behavior, which can be levelled off by increasing the coupling strength to $k = 1.1137$. This can be interpreted as 11% interaction of individuals across the metapopulations. It is recommended that a measure of the amount of chaotic deviations is expressed in terms of the coupling strength to assess the percentage of interaction.

References

[1] Jesse, M., et al., A fully coupled, mechanistic model for infectious disease dynamics in a metapopulation: movement and epidemic duration. Journal of theoretical biology, 2008. 254(2): p. 331-338.
[2] Allen, L.J., et al., Mathematical epidemiology. Vol. 1945. 2008: Springer.
[3] Olsen, L.F., G.L. Truty, and W.M. Schaffer, Oscillations and chaos in epidemics: a nonlinear dynamic study of six childhood diseases in Copenhagen, Denmark. Theoretical population biology, 1988. 33(3): p. 344-370.
[4] Murray, J.D., Mathematical biology: I. An introduction. Vol. 17. 2007: Springer Science & Business Media.
[5] Keeling, M.J. and P. Rohani, Modeling infectious diseases in humans and animals. 2011: Princeton University Press.
[6] Strogatz, S., H and R. Mirollo, E, Synchronization of Pulse-Coupled Biological Oscillators. SIAM J APPL MATHS, 1990. 8(6): p. 1645 - 1662.
[7] Wasike, A.A. and K. Rotich, Synchronization and persistence in Diffusively Coupled Lattice Oscillators. 2007.
[8] Control, C.f.D. and Prevention, Epidemiology of HIV/AIDS--united states, 1981-2005. MMWR. Morbidity and mortality weekly report, 2006. 55(21): p. 589-592.
[9] Abu-Radded, L., Dual infection with HIV and malaria fuels the spread of both diseases in sub-Saharan Africa. Science, 2007. 315(5812): p. 598.
[10] WHO, W.H.O., 2008 Report on the Global AIDS Epidemic. 2008: World Health Organization.
[11] Kissling, E., et al., Fisherfolk are among groups most at risk of HIV: cross-country analysis of prevalence and numbers infected. Aids, 2005. 19(17): p. 1939-1946.
[12] Olowosegun, T., et al., Sexuality and HIV/AIDS among Fisher folks in Kainji Lake Basin. Global Journal of Medical Research Diseases, 2013. 13(2): p. 4-18.
[13] Tanzarn, N. and C. Bishop-Sambrook, The dynamics of HIV/AIDS in small-scale fishing communities in Uganda. Rome, Italy: HIV/AIDS Programme, Food and Agriculture Organization (FAO) of the United Nations, 2003.
[14] Kamali, A., et al., Heterogeneity of HIV incidence: a comparative analysis between fishing communities and in a neighbouring rural general population, Uganda, and implications for HIV control. Sexually transmitted infections, 2016. 92(6): p. 447-454.
[15] Woodhead, A.J., et al., Health in fishing communities: A global perspective. Fish and Fisheries, 2018. 19(5): p. 839-852.
[16] Béné, C. and S. Merten, Women and fish-for-sex: transactional sex, HIV/AIDS and gender in African fisheries. World development, 2008. 36(5): p. 875-899.
[17] Huang, M. HIV/AIDS among fishers: vulnerability of their partners. in Global symposium on women in fisheries. 2002. ICLARM-WorldFish Center.
[18] Duwal, S., et al., Vulnerability of fishing communities to HIV/AIDS and impact on fish productivity in Nigeria. IOSR-JAVS, 2015. 8(2): p. 52-9.
[19] Allison, E.H. and J.A. Seeley, HIV and AIDS among fisherfolk: a threat to ‘responsible fisheries'? Fish and fisheries, 2004. 5(3): p. 215-234.
[20] Awuonda, M., The Voices of Dunga: Critical Study of Lake Victoria Fisherfolk and Their Perspectives on Fishery Management, Globalisation and Environmental Crises on Their Livelihoods and Local Institutions. 2003: Swedish University of Agricultural Science.
[21] Heagy, J., T. Carroll, and L. Pecora, Synchronous chaos in coupled oscillator systems. Physical Review E, 1994. 50(3): p. 1874.

[22] Sun, J., E.M. Bollt, and T. Nishikawa, Constructing generalized synchronization manifolds by manifold equation. SIAM Journal on Applied Dynamical Systems, 2009. 8(1): p. 202-221.
[23] Josic, K., Synchronization of chaotic systems and invariant manifolds. Nonlinearity, 2000. 13(4): p. 1321.