Global Connecting Orbits of a SEIRS Epidemic Model with Nonlinear Incidence Rate and Nonpermanent Immunity

P.S. Douris and M.P. Markakis

Abstract— In the present paper some aspects of the global dynamical behavior of a new SEIRS epidemic model with nonlinear incidence rate, non-permanent immunity and an additional epidemic-induced death rate are presented. More specifically, a point-to-point homoclinic connecting orbit to an endemic saddle equilibrium is numerically located, as a bifurcation with respect to the active parameter. Moreover, we compute members of the families of different types of heteroclinic connecting orbits. The physical meaning of these orbits in relation to the physical system is also discussed.

Index Terms— Epidemic models; Homoclinic connection; Limit cycles; Heteroclinic connection

I. INTRODUCTION

Modeling real world epidemics can be a challenging and complex task and its usefulness is undisputable, because the more realistic the modeling is, the more it can contribute to a better understanding of the physical phenomenon itself. Furthermore, a realistic enough model must exhibit global dynamics, which can be considered as good approximations of the evolution of the associated real-world system. The properties and aspects of the global dynamic behavior of the system can help someone decide whether a system constitutes an accurate model of the physical problem of interest. There are several publications in the field, such as [1], [2], for example.

Here, following our previous work [3] and the relevant references therein, we present some features concerning the global dynamics of a new SEIRS epidemic model. We also discuss the reflection of the mathematical results obtained herein on the real-world system, as well as the physical phenomena, the global asymptotic connections of which can be considered as stylized representations.

In [3], the SEIRS model was treated with respect to stability, as well as local bifurcation analysis, resulting in bifurcation portraits throughout the associated regions of the

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parameter space. Moreover, limit cycles generated by Hopf bifurcation of an endemic fixed point were obtained. In the present work we investigate the existence of homoclinic and heteroclinic orbits connecting invariant sets of the system. Then, we locate these orbits by means of standard numerical methods in combination with high order boundary conditions or the classical projection ones. Thus, a point-topoint (P2P) homoclinic orbit at an endemic equilibrium is derived. In addition, representative samples of families of point-to-cycle (P2C), as well as of different types of P2P heteroclinic connections are obtained.

The paper has the following structure: In Section II, a brief but necessary review of the local stability analysis from [3] with a few additions is made, so that the reader can follow the present work more smoothly. In Section III, the procedure regarding the computation of a homoclinic connecting orbit to a saddle-node endemic equilibrium is presented and the homoclinic orbit is obtained. Furthermore, some comments regarding its physical meaning and practical usefulness are made. In Section IV, various heteroclinic connections are presented together with comments on their topological configurations and practical meaning. Finally, in the last Section a summary of the analysis carried out together with the corresponding results is made.

II. OVERVIEW OF STABILITY ANALYSIS

The proposed SEIRS epidemic model, is structured by the following equations:

$$\dot{x} = r + \varepsilon - (r + \varepsilon)x - \varepsilon w - \varepsilon y + \alpha xy - \beta x^{m} y^{s}$$

$$\dot{w} = -(r + \sigma)w + \alpha wy + \beta x^{m} y^{s}$$

$$\dot{y} = \sigma w - (r + \gamma + \alpha)y + \alpha y^{2}$$
(1)

where x stands for the population of susceptible individuals normalized with respect to the total population, w denotes the normalized exposed (incubating) individuals and y denotes the normalized population of infective individuals. Furthermore, r denotes the birth rate, d denotes the physical death rate, ε denotes the rate of loss of immunity, σ denotes the rate of incubation, α is the additional death rate due to the epidemic, γ denotes the recovery rate, $\beta \in (0,1)$ and m,s are positive constants with s > 1. Equations (1) were extracted from a four-dimensional SEIRS model, by elimination of the fourth equation

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M. P. Markakis is with the Department of Electrical & Computer Engineering, University of Patras, GR 26504 GREECE (corresponding author, phone: 302610962782; e-mail: <u>markakis@upatras.gr</u>).

P. S. Douris is with the Department of Electrical & Computer Engineering, University of Patras, GR 26504 GREECE (e-mail: pandouris@ece.upatras.gr).

concerning the recovered individuals, as well as by substituting the nonlinear term $\beta x^m y^s$ for the incidence rate per infective individual. In general, both the nonlinear incidence rate and the additional death rate solely due to the disease lead to a more realistic modelling, since they offer a deeper insight into the actual relation between the different compartments of populations involved in the epidemic cycle. The specifics of the SEIRS epidemic model under consideration are briefly presented in Appendix A.

The system exhibits two types of equilibria. The first is a disease-free one, be it $\Sigma_0(1,0,0)$, the eigenvalues of which are found equal to

$$(\lambda_1, \lambda_2, \lambda_3) = (-r - \varepsilon, -r - \sigma, -r - \gamma - \alpha) \quad (2)$$

hence, it is asymptotically stable, while the second one, $\Sigma_1(x^0, w^0, y^0)$, represents an endemic fixed point corresponding to persistence of the disease. The coordinates of Σ_1 are presented in Appendix A. This equilibrium always has a pair of complex conjugate eigenvalues together with a negative one. Moreover, in [3], by appropriate stability analysis we determine the active parameter β and investigate the parameter space (γ, σ, β) (the other parameters being fixed) with respect to the existence and stability of the endemic equilibrium. In particular, by increasing the real exponents s or m (especially s) we conclude to regions with no endemic equilibrium in the whole range (0,1) for β . We also locate the *critical* regions, where it is proved that the sign change of the real part of the complex eigenvalues (as β varies) gives rise to supercritical Hopf bifurcations. Some aspects of the stability analysis associative to Σ_1 are briefly presented in Appendix A.

Furthermore, apart from the aforementioned fixed point, there exists a second endemic one in small regions of the parameter space, let it be denoted by Σ_2 , which is normally a saddle-node with one positive and two negative eigenvalues. When this equilibrium is continued numerically with respect to β (by increasing β), it gradually moves towards the disease-free one and finally it coincides with the latter. This endemic equilibrium also undergoes a limit point (fold) bifurcation when continued with respect to *s*. For instance, for

 $(\gamma, \sigma, r, \varepsilon, \alpha, \beta, m, s) = (0.042, 0.5, 10^{-4}, 10^{-3}, 10^{-4}, 0.1336..., 0.5, 1.2)$ the endemic equilibrium Σ_2 has coordinates (0.714394, 0.000613, 0.007269) and the quadratic coefficient has been computed to be $\theta^* \approx 3.24...10^{-3}$.

III. P2P HOMOCLINIC CONNECTING ORBIT

The system exhibits a relatively rich global dynamical behavior, in the sense that it possesses heterogeneous and topologically different connecting orbits. In the present Section the numerical location of a P2P homoclinic orbit is presented and the physical meaning of it together with its practical importance and usefulness are discussed.

P2P homoclinic connecting orbits are considered

separatrices in the state space in 2D conservative ODEs, since they divide the phase space into qualitatively different regions of motion; one region of periodic solutions and one of non-periodic ones, respectively. In that sense, homoclinic orbits can be perceived as the limit of periodic solutions, the fundamental period of which tends to infinity, while the orbit itself remains bounded. In other words, a P2P homoclinic orbit can be considered as a limit cycle, the value of the fundamental period of which is "very high". So, the last (the one with the highest period) limit cycle is used as an initial approximation of the homoclinic orbit.

Moreover, regarding the main algorithm associated with the numerical location of the P2P homoclinic orbit, there is well-known software and numerous techniques. The most famous ones are AUTO86 (see [4]) and MATCONT, (see [5], [6]), which use the method of orthogonal collocation on finite elements and the widely used technique of projection boundary conditions (BC from now on). The latter, as well as the method of eigenvectors (See [7]) are first order approximations, so the application of them presupposes good initial data for the reliable computation of the orbits of interest and this is becoming harder and harder to achieve as the number of state variables together with the number of active parameters increase.

Assuming that we are interested in the determination of a connecting orbit for the general system

$$\dot{q} = f(q; a), \ q \in \mathbb{R}^n, \ a \in \mathbb{R}^p, \ f: \mathbb{R}^{n+p} \to \mathbb{R}^n$$
(3)

where $q = (q_1, ..., q_n)^T$ is the vector of state variables and *a* a vector of system parameters. Let the required number of control parameters, for which the P2P homoclinic orbit under determination constitutes an isolated and structurally stable phenomenon of the system be *p*, that is the number of parameters, for which the connecting orbit is stabilized. Then this number is given by means of the following relation (See [8])

$$p = n + 1 - n_{-u} - n_{-c} - n_{+s} - n_{+c} \quad (4)$$

where *n* is the dimension of state variables of the system of interest, n_{-u} denotes the dimension of the unstable manifold of the invariant set, M_{-} , from which the connecting orbit leaves asymptotically $(a(\gamma) \subset M_{-})$, where "a" denotes the homonymous limit set and $\gamma = \{(q(t), a) : t \in \mathbb{R}\}$ is the connecting orbit of interest), n_{+s} denotes the dimension of the stable manifold of the invariant set, M_{+} , to which the connecting orbit arrives asymptotically (i.e. $\omega(\gamma) \subset M_{+}$, where " ω " denotes the homonymous limit set), while n_{-c} , n_{+c} are the dimensions of the respective center manifolds.

In the case where the numerical location of a homoclinic connecting orbit at a hyperbolic saddle equilibrium is sought, then $n_{-c} = n_{+c} = 0$ and $n_{+u} = n - n_{+s}$, so according to (4) we have

$$p = n_{+u} - n_{-u} + 1 \quad (5)$$

or p=1, since $n_{+u} = n_{-u}$, so one control parameter is needed and β has been chosen for this purpose; this is a global bifurcation in the phase space. Regarding the numerical location of the P2P homoclinic connecting orbit, first of all we locate a limit cycle bifurcating from the endemic fixed point Σ_1 through a supercritical Hopf bifurcation, by using a custom algorithm of orthogonal collocation on finite elements with an integral phase condition. Then, by means of a method of sequential continuation based on a custom algorithm of multiple shooting with an integral phase condition with active parameter β , the limit cycle is numerically continued with respect to its fundamental period up to an adequately high value. To this purpose, the original system (3) is transformed to ($q(t) = u[\tau(t)]$)

$$\dot{u} = T_n f(u; \alpha), \quad u = u(\tau) \quad (6)$$

where the time scaling $\tau = t/T_p$ maps the independent variable of time from $[0,T_p]$ to [0,1], where T_p denotes the fundamental period. This transformation makes the numerical continuation easier, as the variable of the fundamental period appears explicitly as a system variable. The aforementioned family of numerically continued limit cycles is presented in Figure 1.



Fig. 1 Numerically continued limit cycles starting from a supercritical Hopf bifurcation around the fixed point Σ_1 for $(\gamma, \sigma, r, \varepsilon, \alpha, m, s) = (0.042, 0.5, 10^{-4}, 10^{-3}, 10^{-4}, 0.5, 1.2)$ and β the active parameter.

A. High order BC

We briefly present a technique for the determination of high order BC used for the numerical location of asymptotically connecting orbits, which involve fixed points. This technique is based on a combination of the multiple scales approximation method and that of successive approximations. The idea for this comes from Deprit and Henrard [9], Bennett [10] and the relevant references therein. In addition, Hassard [11] presented the idea to use high order BC instead of the projection ones. It should be noted that the projection method converges exponentially by increasing the truncation interval. However, this can increase the computational time (mainly in ordinary PCs with low to moderate CPU power). So, the use of high order BC can be proved useful in cases like that. Let us now consider a dynamical differential system of the form (3), possessing a number of fixed points and let $q^0 = (q_1^0, q_2^0, ..., q_n^0)^T$ be the fixed point associated with the P2P homoclinic orbit. Then, after setting

$$\xi_i = q_i - q_i^0, \quad i = 1, ..., n$$
 (7)

we expand the right-hand side of (3) in a Taylor series and keep terms up to the fourth order, which is the desired order of approximation here. Thus, we get

$$\dot{\xi}_i = h_i(\xi_1, ..., \xi_n; a), \quad i = 1, ..., n$$
 (8)

with h_i polynomial functions of $\xi_1, ..., \xi_n$, of order less than or equal to four. We further assume that $\xi_i(t)$, i = 1, ..., ncan be approximated (up to the order of interest) by expanding in positive powers of a small orbital parameter, denoted as ε , as

$$\xi_{i}(t) \approx \sum_{j=1}^{k} \varepsilon^{j} \xi_{i,j}(t) \quad (9)$$

with k the desired order of approximation. Then, substitution of (9) in (8) and equation of the terms of the same order results in k linear (with respect to the variables $(\xi_{i,j}, i=1,...,n \text{ corresponding to the } j$ -order, j=1,...,k) scale order systems.

Additionally, assuming the hyperbolicity of the fixed point of interest (i.e. no eigenvalue associated with it has a real part equal to zero), the respective systems are solved successively. Regarding the solutions of a specific order, all the integration constants which are not associated with the manifold of interest (the high order approximation of which is constructed) and the integration constants associated with the homogeneous part of the respective second and higher order systems are set equal to zero. Then, the resulting expressions are substituted into the higher order systems. Thus, the final high order approximation up to the desired order, k, is obtained by means of the n summations of (9). For instance, regarding the scale order approximations of the outgoing (incoming) solution vector associated with the unstable (stable) manifold of the fixed point, by taking into account the solutions of the respective systems, the homogeneous part of the solution is removed $(j \ge 2, j = 1, ..., k)$ and the integration constants corresponding to the eigenvalues with negative (positive) real part are set equal to zero. The aforementioned solution procedure can be performed with the aid of a symbolic computational package, such as Mathematica or Maplesoft Maple (which offers direct integration with Mathworks Matlab), as the calculations can be lengthy even for low dimensional systems. Finally, high order BC are defined in the following form:

$$C_{i,0}\left[q_{i}\left(\tau=0\right)-\xi_{i}^{out}\right]^{2}+C_{i,1}\left[q_{i}\left(\tau=1\right)-\xi_{i}^{in}\right]^{2}=0, \quad i=1,...,n$$
(10)

where $(C_{i,0}, C_{i,1})$ are positive weighting coefficients (set equal to 1 for the location of the connecting orbits in this work) and $(\xi_i^{out}, \xi_i^{in})$ have been evaluated by use of (9).

Eqns. (10) are differentiable, so the standard iterative

correcting methods of Jacobian-based solvers can be used during the solution procedure. Optimization techniques and algorithms can be used, as well (See [12], for example). In this work the system of nonlinear algebraic equations corresponding to the original system of nonlinear differential equations is solved using optimization methods, such as a Conjugate Gradient Steihaug's method [13], instead of Newton-type ones. The use of optimization methods leads to a faster convergence of the associated system of nonlinear algebraic equations (for the same increment of the primary continuation parameter). The aforementioned method is used for the numerical location of the connecting orbits of interest, as well.

B. Scale order approximations and location of P2P connecting orbits

First of all, regarding a fixed point (x_0, w_0, y_0) of the system, we set

$$\xi = x - x_0, \quad \eta = w - w_0, \quad \zeta = y - y_0.$$
 (11)

Then, an expansion of the right-hand sides of (1) around the equilibrium of interest in a Taylor series, where terms up to the fourth order are kept (so that fourth order BC are extracted) results in

$$\begin{split} \xi &= h_{100}\xi + h_{010}\eta + h_{001}\zeta + h_{200}\xi^2 + h_{002}\eta^2 + h_{101}\xi\zeta + h_{300}\xi^3 + h_{003}\zeta^3 \\ &+ h_{201}\xi^2\zeta + h_{102}\xi\zeta^2 + h_{400}\xi^4 + h_{004}\zeta^4 + h_{301}\xi^3\zeta + h_{103}\xi\zeta^3 + h_{202}\xi^2\zeta^2 \\ \dot{\eta} &= q_{100}\xi + q_{010}\eta + q_{001}\zeta + q_{200}\xi^2 + q_{002}\zeta^2 + q_{101}\xi\zeta + q_{011}\eta\zeta \\ &+ q_{300}\xi^3 + q_{003}\zeta^3 + q_{201}\xi^2\zeta + q_{102}\xi\zeta^2 + q_{400}\xi^4 + q_{004}\zeta^4 \\ &+ q_{301}\xi^3\zeta + q_{103}\xi\zeta^3 + q_{202}\xi^2\zeta^2 \\ \dot{\zeta} &= l_{010}\eta + l_{001}\zeta + l_{002}\zeta^2 \end{split}$$
(12)

where

$$\begin{split} h_{100} &= \alpha y_0 - r - \varepsilon - \beta m x_0^{m-1} y_0^s, \\ h_{010} &= -\varepsilon, \ h_{001} = \alpha x_0 - \varepsilon - \beta s x_0^m y_0^{s-1}, \\ h_{200} &= -\frac{\beta m (m-1)}{2} x_0^{m-2} y_0^s \\ h_{002} &= -\frac{\beta s (s-1)}{2} x_0^m y_0^{s-2}, \ h_{101} = \alpha - \beta m s x_0^{m-1} y_0^{s-1}, \\ h_{300} &= -\frac{\beta m (m-1) (m-2)}{6} x_0^{m-3} y_0^s, \\ h_{003} &= -\frac{\beta s (s-1) (s-2)}{6} x_0^m y_0^{s-3}, \\ h_{201} &= -\frac{\beta m (m-1) s}{2} x_0^{m-2} y_0^{s-1}, \\ h_{102} &= -\frac{\beta m (m-1) s}{2} x_0^{m-1} y_0^{s-2}, \\ h_{400} &= -\frac{\beta m (m-1) (m-2) (m-3)}{24} x_0^{m-4} y_0^s, \\ h_{004} &= -\frac{\beta s (s-1) (s-2) (s-3)}{24} x_0^m y_0^{s-4}, \end{split}$$

$$\begin{aligned} h_{301} &= -\frac{\beta m (m-1)(m-2)s}{6} x_0^{m-3} y_0^{s-1}, \\ h_{103} &= -\frac{\beta m s (s-1)(s-2)}{6} x_0^{m-1} y_0^{s-3}, \\ h_{202} &= -\frac{\beta m s (m-1)(s-1)}{4} x_0^{m-2} y_0^{s-2}, \\ q_{100} &= \beta m x_0^{m-1} y_0^s, \ q_{010} &= \alpha y_0 - r - \sigma, \\ q_{001} &= \alpha w_0 + \beta s x_0^m y_0^{s-1}, \ q_{200} &= -h_{200}, \ q_{002} &= -h_{002}, \\ q_{101} &= \beta m s x_0^{m-1} y_0^{s-1}, \ q_{011} &= \alpha, \\ q_{300} &= -h_{300}, \ q_{003} &= -h_{003}, \ q_{201} &= -h_{201}, \ q_{102} &= -h_{102}, \\ q_{400} &= -h_{400}, \ q_{004} &= -h_{004}, \\ q_{301} &= -h_{301}, \ q_{103} &= -h_{103}, \ q_{202} &= -h_{202}, \\ l_{010} &= \sigma, \ l_{001} &= 2\alpha y_0 - r - \gamma - \alpha, \ l_{002} &= \alpha. \end{aligned}$$

Then, if (x_0, w_0, y_0) represent the coordinates of Σ_2 , by substituting (9) in (12) with k = 4, $(\xi_1, \xi_2, \xi_3) = (\xi, \eta, \zeta)$ and (ξ_j, η_j, ζ_j) , j = 1, 2, 3, 4 denoting the successive approximations of the state variables, we obtain the following scale order systems:

1st order of approximation

$$\dot{\xi}_{1} = h_{100}\xi_{1} + h_{010}\eta_{1} + h_{001}\zeta_{1}$$

$$\dot{\eta}_{1} = q_{100}\xi_{1} + q_{010}\eta_{1} + q_{001}\zeta_{1} \quad (13)$$

$$\dot{\zeta}_{1} = l_{010}\eta_{1} + l_{001}\zeta_{1}$$

2nd order of approximation

$$\begin{aligned} \dot{\xi}_{2} &= h_{100}\xi_{2} + h_{010}\eta_{2} + h_{001}\zeta_{2} + h_{200}\xi_{1}^{2} + h_{002}\zeta_{1}^{2} + h_{101}\xi_{1}\zeta_{1} \\ \dot{\eta}_{2} &= q_{100}\xi_{2} + q_{010}\eta_{2} + q_{001}\zeta_{2} + q_{200}\xi_{1}^{2} + q_{002}\zeta_{1}^{2} + q_{101}\xi_{1}\zeta_{1} + q_{011}\eta_{1}\zeta_{1} \\ \dot{\zeta}_{2} &= l_{010}\eta_{2} + l_{001}\zeta_{2} + l_{002}\zeta_{1}^{2} \end{aligned}$$

$$(14)$$

3rd order of approximation

$$\begin{aligned} \dot{\xi}_{3} &= h_{100}\xi_{3} + h_{010}\eta_{3} + h_{001}\zeta_{3} + 2h_{200}\xi_{1}\xi_{2} + 2h_{002}\zeta_{1}\zeta_{2} \\ &+ h_{101}\left(\xi_{2}\zeta_{1} + \xi_{1}\zeta_{2}\right) + h_{300}\xi_{1}^{3} + h_{003}\zeta_{1}^{3} + h_{201}\xi_{1}^{2}\zeta_{1} + h_{102}\xi_{1}\zeta_{1}^{2} \\ \dot{\eta}_{3} &= q_{100}\xi_{3} + q_{010}\eta_{3} + q_{001}\zeta_{3} + 2q_{200}\xi_{1}\xi_{2} + 2q_{002}\zeta_{1}\zeta_{2} \\ &+ q_{101}\left(\xi_{2}\zeta_{1} + \xi_{1}\zeta_{2}\right) + q_{011}\left(\eta_{2}\zeta_{1} + \eta_{1}\zeta_{2}\right) + q_{300}\xi_{1}^{3} + q_{003}\zeta_{1}^{3} \\ &+ q_{201}\xi_{1}^{2}\zeta_{1} + q_{102}\xi_{1}\zeta_{2}^{2} \\ \dot{\zeta}_{3} &= l_{010}\eta_{3} + l_{001}\zeta_{3} + 2l_{002}\zeta_{1}\zeta_{2} \\ \end{aligned}$$
(15)

$$\begin{split} \dot{\xi}_{4} &= h_{100}\xi_{4} + h_{010}\eta_{4} + h_{001}\zeta_{4} + h_{200}\left(2\xi_{1}\xi_{3} + \xi_{2}^{-2}\right) + h_{002}\left(2\zeta_{1}\zeta_{3} + \zeta_{2}^{-2}\right) \\ &+ h_{101}\left(\xi_{1}\zeta_{3} + \xi_{2}\zeta_{2} + \xi_{3}\zeta_{1}\right) + 3h_{300}\xi_{1}^{-2}\xi_{2} + 3h_{003}\zeta_{1}^{-2}\zeta_{2} \\ &+ h_{201}\left(2\xi_{1}\xi_{2}\zeta_{1} + \xi_{1}^{-2}\zeta_{2}\right) + h_{102}\left(2\xi_{1}\zeta_{1}\zeta_{2} + \xi_{2}\zeta_{1}^{-2}\right) + h_{400}\xi_{1}^{-4} \\ &+ h_{004}\zeta_{1}^{-4} + h_{301}\xi_{1}^{-3}\zeta_{1} + h_{103}\xi_{1}\zeta_{1}^{-3} + h_{202}\xi_{1}^{-2}\zeta_{1}^{-2} \\ \dot{\eta}_{4} &= q_{100}\xi_{4} + q_{010}\eta_{4} + q_{001}\zeta_{4} + q_{200}\left(2\xi_{1}\xi_{3} + \xi_{2}^{-2}\right) + q_{002}\left(2\zeta_{1}\zeta_{3} + \zeta_{2}^{-2}\right) \\ &+ q_{101}\left(\xi_{1}\zeta_{3} + \xi_{2}\zeta_{2} + \xi_{3}\zeta_{1}\right) + q_{011}\left(\eta_{1}\zeta_{3} + \eta_{2}\zeta_{2} + \eta_{3}\zeta_{1}\right) + 3q_{300}\xi_{1}^{-2}\xi_{2} \\ &+ 3q_{003}\zeta_{1}^{-2}\zeta_{2} + q_{201}\left(2\xi_{1}\xi_{2}\zeta_{1} + \xi_{1}^{-2}\zeta_{2}\right) + q_{102}\left(2\xi_{1}\zeta_{1}\zeta_{2} + \xi_{2}\zeta_{1}^{-2}\right) \\ &+ q_{400}\xi_{1}^{-4} + q_{004}\zeta_{1}^{-4} + q_{301}\xi_{1}^{-3}\zeta_{1} + q_{103}\xi_{1}\zeta_{1}^{-3} + q_{202}\xi_{1}^{-2}\zeta_{1}^{-2} \end{split}$$

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(16)

Then, with the aid of Maplesoft Mapple and via the procedure described in Section III-A, we arrive at the fourth order approximations of both the outgoing (locally asymptotically unstable) vector solution and the incoming (locally asymptotically stable) one. The effectiveness of high order BC implemented compared to the classic first order ones, often encountered in bibliography, is presented in Figure 2.



Fig. 2 Comparison between the high order BC and the classic first order ones around the fixed point associated with the homoclinic connecting orbit under determination for $(\gamma, \sigma, r, \varepsilon, \alpha, m, s) = (0.042, 0.5, 10^{-4}, 10^{-3}, 10^{-4}, 1, 1)$ and β is the control parameter.

More specifically, if the exact solution (of the asymptotically connecting orbit) was known, then by starting from a point which lies inside the unstable (stable) manifold of the equilibrium) associated with the connecting orbit and proceeding backwards (forward) in time, the orbit would asymptotically approach the invariant set. However, the exact solution is not known, so an approximation of the boundary conditions is sought. With the aid of the aforementioned technique reliable approximations of these conditions can be constructed. In principle, the higher the approximation order is, the closer the approximate orbit will be to the exact solution, and hence to the invariant set, when a backward (forward) integration is carried out in case of the outgoing (incoming) (part of the) orbit. Of course, inevitably the orbit will deviate from the invariant set, due to the approximation.

The infinite time horizon $(-\infty, +\infty)$ associated with the asymptotic orbit of interest is truncated to $[T_-, T_+]$, so that by setting $\tau = t / (T_+ - T_-)$, (3) becomes $(q(t) = \psi[\tau(t)])$, see [8])

$$\dot{\psi} = (T_{+} - T_{-}) f(\psi; \alpha), \quad \psi = \psi(\tau) \quad (17)$$

Moreover, by choosing a symmetric time interval we have $T = -T_{-} = T_{+}$. Thus equation (17), together with an integral phase condition constitute a truncated version of the boundary value problem, which is solved in order to locate the homoclinic point-to-point orbit of interest. Through the

normalization introduced above, the independent variable of time is scaled to [0, 1] and the system is reduced to

$$\dot{\psi} = 2Tf(\psi;\alpha), \quad \tau \in [0,1] \quad (18)$$

By means of the method of orthogonal collocation on finite elements combined with the aforementioned fourth order BC, derived from (10), the homoclinic connecting (i.e. orbit interest of at the fixed point $\Sigma_2(0.99760..., 5.156 \cdot 10^{-6}, 6.109 \cdot 10^{-5}))$ has been computed inside the truncated. symmetric time interval [-12000, 12000], which has been determined using the well-known Beyn's method for [8] $(\gamma, \varepsilon, \sigma, r, \alpha, m, s) = (0.042, 10^{-3}, 0.5, 10^{-4}, 10^{-4}, 0.5, 1.2)$ and $\beta_h \approx 0.2805305...$ The respective algorithm has been implemented in Mathworks Matlab and the P2P homoclinic connecting orbit is presented in Figure 3.

Point-to-point homoclinic orbit (SEIRS)



Fig. 3 P2P homoclinic connecting orbit at the equilibrium $\Sigma_2(0.99760..., 5.156 \cdot 10^{-6}, 6.109 \cdot 10^{-5})$ computed inside the truncated time interval [-12000, 12000], determined with Beyn's method [8] for

 $(\gamma, \sigma, r, \varepsilon, \alpha, m, s) = (0.042, 0.5, 10^{-4}, 10^{-3}, 10^{-4}, 0.5, 1.2),$ $\beta_h \approx 0.2805305...$ by means of a custom multiple shooting method with high order BC and an integral phase condition.

The physical meaning of the P2P homoclinic orbit presented above is closely associated with the fact that it can be considered as a limit cycle bounded in phase space with infinite period, as noted above. In that sense, this type of connecting orbit is a stylized mathematical representation of the "largest" possible epidemic cycle of the real-world system (i.e. the evolution of the population dynamics of the corresponding epidemic). Furthermore, from a practical point of view, the point-to-point homoclinic orbit can be useful for the management of the epidemic and treatment of the associated populations, as well as for the prediction and forecasting of required resources needed, so that both a sensible demand and general planning are carried out before the outspread of the epidemic. More specifically, on the one hand, in case the periods of the corresponding epidemic cycles are underestimated, this could lead to the

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underestimation of the resources required, which might, in turn, result in exposing the populations' lives at risk. On the other hand, in case of overestimation, valuable resources might be wasted with an evident economic loss, as a consequence.

The P2P homoclinic orbits for different sets of values of the system parameters and therefore for different types of epidemics, can be obtained by carrying out a numerical continuation of the computed homoclinic orbit. Also, by inspecting the corresponding variations of the phases of the associated epidemic and the general features of it, sensitivity analyses can be carried out, as well, in order to determine the robustness of the occurring phenomenon with respect to the system parameters of interest.

Additionally, the critical value of β , β_h , for which the P2P homoclinic connecting orbit occurs denotes the "limiting value" closely associated with the nonlinear incidence rate, for which epidemic cycles occur/do not occur, that is for $\beta < \beta_h$ no epidemic cycles appear and the orbit moves to the disease-free equilibrium, Σ_0 , asymptotically thus forming a heteroclinic P2P connection between Σ_1 and Σ_0 . Last, the occurrence of a P2P homoclinic orbit at a "nearly disease-free" (in the sense that only a few people are exposed and most people are susceptible and recovered) endemic equilibrium might answer the question why some epidemics, which are considered "extinct", appear again after a long time, with the "right trigger".

IV. HETEROCLINIC CONNECTING ORBITS

The system (1) exhibits both P2C heteroclinic connecting orbits and P2P heteroclinic ones. In the present Section some topological aspects of these types of connections are presented and representative members of the corresponding phase portrait are numerically located and presented. Practical usefulness and physical meaning are discussed, as well.

Here, the numerical location of the connecting orbit can be also posed in the form of a boundary value problem. However, in the case of a homoclinic point-to-point connection, the only invariant set involved is an equilibrium, while in the case of a heteroclinic point-topoint connection the initial point of the trajectory must lie in the unstable manifold of the a-limit point (fixed point) and the final point must lie in the stable manifold of the ω -limit point. Furthermore, in the case of a point-to-cycle heteroclinic connection the initial point of the trajectory must lie in the unstable manifold of the a-limit point (fixed point) and the final point must lie in the center-stable manifold of a limit cycle (ω -limit cycle).

A. P2C heteroclinic connecting orbits

This type of heteroclinic orbit connects the endemic saddle equilibrium Σ_2 to a stable limit cycle emerging through a supercritical bifurcation of the unstable endemic equilibrium Σ_1 . Then, taking into consideration (4) and

counting the dimensions of both the fixed point Σ_2 , for which $n_{-u} = 1$, $n_{-s} = 2$, $n_{-c} = 0$ and the limit cycle, for which $n_{+s} = 2$, $n_{+c} = 1$ we conclude that p = 0. So, the P2C heteroclinic orbits appearing in this system is a codimension zero phenomenon, hence they persist with no free parameters and they do not constitute bifurcations in phase space. Thus, there are infinitely many P2C heteroclinic connections in the phase space. This fact suggests that this model is realistic, since if there was a unique heteroclinic connection (i.e. a P2C heteroclinic bifurcation), that would mean that the only possible outbreak would be for one specific disease.

In order to locate these orbits numerically, the original system is transformed to (18) and a custom multiple shooting algorithm with projection BC, implemented in Matlab, has been used. A sample of the family of heteroclinic orbits from Σ_2 to a limit cycle is presented in Figure 4.



Fig. 4 P2C heteroclinic connecting orbits from $\Sigma_2(0.9983..., 0.0000037, 0.000044)$ to a stable limit cycles bifurcating from a supercritical Hopf bifurcation associated with the endemic equilibrium Σ_1 for

 $(\gamma, \sigma, r, \varepsilon, a, \beta, m, s) = (0.042, 0.5, 10^{-4}, 10^{-3}, 10^{-4}, 0.3135, 0.5, 1.2)$

These orbits connect two heterogeneous invariant sets, be them a saddle-node endemic equilibrium and a stable limit cycle. The stability of the limit cycles, expresses the persistence of the epidemic. Also, for a different value of β there is a "way", by which the associated epidemic cycle, with its own features, sets in. Thus, as far as the physical meaning is concerned, the P2C connecting orbits could be a connection between an outbreak and an epidemic cycle (associated with Σ_1). In addition, the limit cycles involved in the P2C connections do not exist for $\beta > \beta_{cr}$ (according to the obtained direction and stability of the Hopf bifurcation (see [3])), so by taking into consideration and analyzing the properties of these heteroclinic connections, it could be possible to obstruct the onset of the epidemic, i.e "send the orbit" to the disease-free equilibrium (ideally) by effectively changing (at least) one system parameter. However, there is also the choice of leading the trajectory to the endemic equilibrium Σ_1 , as this situation is easier to handle than the epidemic cycle, because the portions of the populations remain constant.

B. P2P heteroclinic connecting orbits

Now, we deal with P2P heteroclinic asymptotically connecting orbits between pairs of equilibria of the SEIRS system. We also focus on some topological features, as well as on the physical meaning of these orbits.

At first, we have a P2P heteroclinic connecting orbit from the saddle-node endemic fixed point Σ_2 to the stable node disease-free equilibrium, $\boldsymbol{\Sigma}_{\scriptscriptstyle 0}$. By counting the dimensions of both the fixed points Σ_2 and Σ_0 , for which $n_{-u} = 1, n_{-s} = 2, n_{-c} = 0$ and $n_{+s} = 3, n_{+c} = 0$, respectively, by means of (4) we conclude that p = 0. Thus no bifurcation occurs in phase portrait, since this heteroclinic orbit persists with no free parameters (codimension zero) and hence, as in the P2C case, infinite connections of this type exist. This result is physically meaningful, since there should always exist a "possibility" for an epidemic to occur and another one for it to be eradicated. In other words, in case there were specific parameter values of β for which the P2P connection could be performed, this would mean that in the rest cases the epidemic would not be possible to be eradicated.

As far as the numerical location of the aforementioned type of connecting orbit is concerned, the original system is transformed to (18) and a custom algorithm of orthogonal collocation on finite elements together with the high order BC obtained from (10), implemented in Matlab, have been used. A sample of the P2P heteroclinic orbits of this type is presented in Figure 5.



Fig. 5 P2P heteroclinic connecting orbit from the endemic "near-disease-free" equilibrium

 $\Sigma_2(0.9983..., 0.0000034, 0.000041)$ to the disease-free one Σ_0 , for

$$(\gamma, \sigma, r, \varepsilon, a, \beta, m, s) = (0.042, 0.5, 10^{-4}, 10^{-3}, 10^{-4}, 0.3185, 0.5, 1.2)$$

Next, we present a P2P heteroclinic connecting orbit leaving asymptotically in time from the saddle endemic equilibrium Σ_2 and reaching the stable (in this case) endemic fixed point Σ_1 , asymptotically in time, as well. Similarly to the previous cases, by considering the dimensions of both the fixed points Σ_2 and Σ_1 , for which $n_{-u} = 1$, $n_{-s} = 2$, $n_{-c} = 0$ and $n_{+s} = 3$, $n_{+c} = 0$, respectively, via Eqn. (4) we also obtain p = 0. Thus we also deal with a codimension zero phenomenon, where no bifurcation occurs in phase portrait, giving rise to a family of infinite orbits of this type.

Regarding the physical meaning of this P2P connection, we would like to mention that it might model the case, where starting from an outbreak the epidemic tends to a relatively unchanged condition, where all the populations involved remain more or less constant, while disequilibrium periodic fluctuations are absent. This is what happens in cases where the incubation rate is low (for the same values of all the rest system parameters), while in cases where this parameter attains higher values, the corresponding situations tend to be associated with periodic behavior. Some examples of diseases with similar behavior and respective data can be found in [14] and the associated references within. A sample of these P2P heteroclinic connections is shown in Figure 6. The specific orbit has been numerically located with the aid of a custom algorithm of orthogonal collocation on finite elements together with the high order BC given by (10).



Fig. 6 P2P heteroclinic connecting orbit from the endemic "near-disease-free" equilibrium

Σ₂(0.99897..., 0.0000022, 0.000026) (E_{ndf}) to the endemic equilibrium Σ₁(0.065465..., 0.00200..., 0.02375...) (E_H) for (γ, σ, r, ε, a, β, m, s) = (0.042, 0.5, 10⁻⁴, 10⁻³, 10⁻⁴, 0.3485, 0.5, 1.2)

Moreover, regarding the P2C and P2P heteroclinic orbits, presented so far, all starting from Σ_2 , we would like to comment on the sensitivity of the "path" the flow will follow, with respect to the initial conditions. In other words, a small perturbation near Σ_2 , of the corresponding to a specific disease portions of the population, can either

eradicate it or might turn it to an epidemic.

Yet another type of a P2P heteroclinic connecting orbit which occurs in the phase space, is the one that connects the endemic fixed point Σ_1 to the disease-free one, Σ_0 . Taking into account the dimensions of both the fixed points Σ_1 and Σ_0 , be them $n_{-u} = 2$, $n_{-s} = 1$, $n_{-c} = 0$ and $n_{+s} = 3$, $n_{+c} = 0$, respectively, by using Eqn. (4) we conclude that p = -1. So, this case concerns a somewhat different situation. Specifically, if $\Pi_u(\Sigma_1)$ denotes the unstable manifold associated with Σ_1 and $\Pi_s(\Sigma_0)$ stands for the stable manifold associated with Σ_0 , then the separatrix $\Pi_{\mu}(\Sigma_1) \cap \Pi_{\kappa}(\Sigma_0)$ has dimension $n_{-\mu} + n_{+\kappa} - n = 2$. Thus, combining with the above result we conclude to that one further condition needs to be introduced for parameterizing this kind of P2P orbits. In other words, there are multiple "routes" connecting the two aforementioned equilibria and a family of infinitely many orbits of this type is also generated in the phase space. In Figure 7, a numerically located member of this family is shown, obtained similarly to the previous cases of P2P heteroclinic connections.



Fig. 7 P2P heteroclinic connecting orbit from the endemic equilibrium $\Sigma_1(0.25561..., 0.001597..., 0.01892...)$ to the disease-free one, Σ_0 for

 $(\gamma, \sigma, r, \varepsilon, a, \beta, m, s) = (0.042, 0.5, 10^{-4}, 10^{-3}, 10^{-4}, 0.3185..., 0.9, 1.2)$

In terms of the physical meaning, these P2P heteroclinic orbits describe the possible ways, by which the epidemic vanishes starting from Σ_1 . We would like to stress that it is Σ_1 that comprises the most typical situation of a "wellestablished" epidemic, whereas Σ_2 is closer to the diseasefree situation. Also, for a model to be considered realistic, there should exist connections between every single endemic equilibrium and the disease-free one, as it is always possible for an epidemic to cease. Moreover, the fact that a restriction needs to be imposed in order to select a specific heteroclinic orbit of this type offers the possibility to take into consideration possible conditions that are (or must be) met during the transition to the disease-free state.

V. CONCLUSION-DISCUSSION

Throughout the present work asymptotically connecting orbits and their properties have been presented. These orbits have been numerically located either by means of a custom algorithm of multiple shooting or using a custom algorithm of orthogonal collocation on finite elements. Also, depending on the specific case, either the classical projection boundary conditions or the high order boundary conditions, defined via (10), have been employed. More specifically, the following types of connecting orbits have been numerically located:

A point-to-point homoclinic connecting orbit at the saddle-node endemic equilibrium Σ_2 . The respective procedure starts from the continuation of the stable limit cycles generated through a supercritical Hopf bifurcation of the saddle-focus endemic equilibrium Σ_1 .

A point-to-cycle heteroclinic connecting orbit from the saddle-node endemic equilibrium Σ_2 to a stable limit cycle emerged through the Hopf bifurcation of the saddle-focus endemic fixed point Σ_1 .

A point-to-point heteroclinic connecting orbit from the saddle-node endemic fixed point Σ_2 to the stable node disease-free equilibrium Σ_0 .

A point-to-point heteroclinic connection leaving from Σ_2 and reaching Σ_1 .

A point-to-point heteroclinic orbit, which connects Σ_1 to Σ_0 .

The homoclinic connection is manifested as a bifurcation in the phase space (codimension one), while infinitely many heteroclinic orbits of the above types exist, as they constitute a codimension zero phenomenon and hence no bifurcation occurs. Some topological properties of the orbits under consideration such as the structural stability have been discussed briefly together with their physical meaning, usefulness and relation to the physical background of the system. Also, arguments regarding the global behavior of the differential system in accordance with the physical properties of a disease have been presented.

APPENDIX A

The governing equations of the SEIRS epidemic model are the following:

$$\dot{S} = rN - dS + \varepsilon R - h(S, I)I$$

$$\dot{E} = -(d + \sigma)E + h(S, I)I$$

$$\dot{I} = -(\gamma + d + \alpha)I + \sigma E$$

$$\dot{R} = \gamma I - (d + \varepsilon)R$$
(A-1)

and

$$\dot{N} = rN - dN - \alpha I \quad (A-2)$$

where S, E, I, R, N denote the number of susceptible, exposed (incubating), infective, recovered individuals and the total population, respectively, while h(S, I) represents the incidence rate per infective individual. The various parameters involved are defined in Section II. Then by normalizing with respect to the total population N (= S + E + I + R) which is considered constant and taking into account Eqn. (A-2), the system becomes:

$$\dot{x} = r - rx + \varepsilon z + \alpha xy - \overline{h}(x, y) y$$

$$\dot{w} = -(r + \sigma) w + \alpha wy + \overline{h}(x, y) y$$

$$\dot{y} = \sigma w - (r + \gamma + \alpha) y + \alpha y^{2}$$

$$\dot{z} = \gamma y - (r + \varepsilon) z + \alpha y z$$

(A-3)

where

$$x = S/N, w = E/N, y = I/N, z = R/N,$$
 (A-4)
 $x + w + y + z = 1$

Then, by eliminating z = 1 - x - w - y and setting $\overline{h}(x, y) = \beta x^m y^{s-1}$ with β, m positive constants and s > 1, Eqns. (A-3) take the final form (1).

Furthermore, through tedious algebraic manipulations (see [3], Appendix A), the coordinates of Σ_1 are obtained in implicit form as

$$x^{0} = \frac{1}{\sigma(\alpha y^{0} - \kappa_{0})} \left[\alpha^{2} (y^{0})^{3} - \alpha \kappa_{4} (y^{0})^{2} + (\kappa_{3} + \sigma \varepsilon) y^{0} - \sigma \kappa_{0} \right]$$
(A-5)
$$\beta \sigma (x^{0})^{m} (y^{0})^{s-1} = \alpha^{2} (y^{0})^{2} - \alpha (\kappa_{4} - \varepsilon) y^{0} + \kappa_{3} - \varepsilon \kappa_{2}$$
(A-6)
$$w^{0} = \frac{1}{\sigma} \left[-\alpha (y^{0})^{2} + \kappa_{2} y^{0} \right]$$
(A-7)

where

$$\kappa_0 = r + \varepsilon, \ \kappa_1 = r + \varepsilon + \sigma, \ \kappa_2 = r + \gamma + \alpha, \kappa_3 = \kappa_1 \kappa_2, \ \kappa_4 = \kappa_1 + \kappa_2$$
(A-8)

That is, for specific values of the involved parameters, at first we solve numerically (A-6) with respect to y^0 and then x^0 and w^0 are obtained by use of (A-5) and (A-7), respectively.

Additionally, via the associated characteristic equation and the Routh-Hurwitz necessary and sufficient stability conditions, the critical (the real part of the complex eigenvalues becomes zero) value y_{cr}^0 is evaluated numerically (see [3]). Thus, by means of (A-5) and (A-7), x_{cr}^0 and w_{cr}^0 are also extracted and finally, under certain restrictions (see also [3]), (A-6) furnishes β_{cr} , namely

$$\beta_{cr} = \frac{\alpha^2 \left(y_{cr}^0\right)^2 - \alpha \left(\kappa_4 - \varepsilon\right) y_{cr}^0 + \kappa_3 - \varepsilon \kappa_2}{\sigma \left(x_{cr}^0\right)^m \left(y_{cr}^0\right)^{s-1}} \quad (A-9)$$

with $0 < \beta_{cr} < 1$, $0 < x_{cr}^0 < 1$, $0 < y_{cr}^0 < 1$. We always get zero or at most one critical value and thus, by considering (γ, σ, β) as the varying parameters and β as the active parameter, a *critical surface* $\beta_{cr} = \beta_{cr}(\gamma, \sigma)$ is generated in the parameter space (γ, σ, β) , over the respective *critical region* (γ, σ) (where critical values of β are derived). Moreover, as mentioned above (Section II), at these critical points $(\gamma, \sigma, \beta_{cr})$, stable limit cycles are emerged from the endemic fixed point Σ_1 .

Description of algorithm of orthogonal collocation on finite elements

The well-known algorithm of orthogonal collocation on finite elements with Lagrange polynomials of maximal degree m, defined by user, has been implemented. The algorithm has been used for the solution of the systems of differential equations and the approximation of the orbits of interest. For the numerical location of a point-to-point homoclinic orbit which satisfies the following differential system

$$\dot{x} = f(x; a), x \in \mathbb{R}^n, a \in \mathbb{R}, f : \mathbb{R}^{n+1} \to \mathbb{R}^n$$
 (B-1)

where $x = (x_1, ..., x_n)^T$ is the vector of state variables and *a* denotes a system parameter, the infinite time horizon $(-\infty, +\infty)$ is truncated to $[T_-, T_+]$. Then, setting $\tau = t / (T_+ - T_-)$, (B-1) becomes

$$\dot{y} = (T_{+} - T_{-})f(y;\alpha), \quad y = y(\tau) \quad (B-2)$$

For the sake of simplicity, a symmetrically truncated time interval is chosen, that is $T_+ = -T_- = T$. Thus, via the appropriate normalization, the independent (time) variable is scaled to [0, 1] and the system becomes

$$\dot{y} = 2Tf(y;\alpha)$$
 (B-3)

Then, choosing the maximal degree of the basis polynomials used, the time interval is subdivided into N-1 subintervals (the so-called "elements") denoted as $[\tau_i, \tau_{i+1}], i = 1, ..., N-1$. Thus, the solution of the system of differential equations is approximated by a weighted sum of the basis polynomials as

$$y_i(\tau) = \sum_{l=0}^m c_{i,l} P_{i,l}(\tau), \quad i = 1, ..., N-1, \quad y_i \in \mathbb{R}^n \quad (B-4)$$

within every subinterval, where $P_{i,l}(\tau)$ are the basis polynomials of degree l, while the coefficients $c_{i,l}$ need to be determined. The positions of the collocation points, $\tau_{i,j}$, j = 1,...,m are chosen to be the translated roots of the original Legendre polynomial of degree m. So, after substituting (B-4) in (B-3) we arrive at the discretized differential system, being a system of nonlinear algebraic collocation equations, which are required to be exact at the collocation points. Thus, the following nm(N-1) equations (n is the number of state variables) must hold

$$\left. \frac{dy_i}{d\tau} \right|_{\tau_{i,i}} = 2Tf \left[y_i \left(\tau_{i,j} \right) \right] \quad (B-5)$$

for i = 1, ..., N - 1, j = 1, ..., m; τ is the scaled independent time variable. Then, by setting

$$y_{i,j} = y_i(\tau_{i,j}), \quad i = 1, ..., N-1, \quad j = 1, ..., m$$

and requiring that the solution be continuous within the entire time interval we get the associated n(N-2) matching conditions

$$y_{i-1,m} = y_{i,0}, \quad i = 2, .., N-1$$
 (B-6)

APPENDIX B

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where $y_{i,0} = y_i(\tau_i)$, i = 1,.., N - 1. The discrete counterparts of the boundary conditions used for the location of limit cycles are the following *n* equations

$$y_{1,0} = y_{N-1,m}$$
 (B-7)

Finally, the discrete counterpart of an integral type phase condition is utilized for both limit cycles and homoclinic orbits; the continuous form of this condition is

$$\int_0^1 \dot{\hat{y}}(\tau)^T \left[y(\tau) - \hat{y}(\tau) \right] d\tau = 0 \quad (B-8)$$

where the approximation $\dot{\hat{y}}(\tau) \approx f(y(\tau))$ is used. Note that for the location of limit cycles, by the time normalization $\tau = t/T_p$, mapping $[0, T_p]$ to [0,1], with T_p the fundamental period of the limit cycle, the original system (B-1) is transformed to

$$\dot{y} = T_p f(y; \alpha), \quad y = y(\tau) \quad (B-9)$$

Also, (B-5) becomes

$$\frac{dy_i}{d\tau}\Big|_{\tau_{i,j}} = T_p f \Big[y_i \Big(\tau_{i,j}\Big) \Big] \quad (B-10)$$

Thus, the period appears explicitly as a system parameter (this is useful for the numerical continuation performed). Then, using the Gauss-Legendre quadrature, the discrete counterpart of the integral phase condition (B-8) becomes

$$\sum_{i=1}^{N-1} \sum_{j=0}^{m} \omega_{i,j} \left\langle y_{i,j} - \hat{y}_{i,j}, \dot{v}_{i,j} \right\rangle = 0 \quad (B-11)$$

where $\omega_{i,j}$ are the Gauss-Legendre quadrature coefficientsweights, $\dot{v}_{i,j}$, $\hat{y}_{i,j}$ denote the values of the derivatives and the points of the computed orbit at a previous step, respectively; $y_{i,j}$ are the points under determination. So, counting up the number of the unknowns and the number of the equations for the case of limit cycle location, we deduce that the problem is well-posed, as these numbers are equal.

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