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Structure of the Global Attractors in a Model for Ectoparasite-Borne Diseases

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***Abstract*—We delineate a mathematical model for the dynamics of the spread of ectoparasites and the diseases transmitted by them. We present how the dynamics of the system depends on the three reproduction numbers belonging to three of the four possible equilibria and give a complete characterization of the structure of the global attractor in each possible case depending on the reproduction numbers.**

***Keywords*-ectoparasites; global dynamics; global attractors**

I. Introduction

Ectoparasites (e.g. lice, fleas, mites) cause a serious problem in several parts in the world [2], [4]. Ectoparasite infestations are often connected to the lack of hygiene and poor economical conditions, however, their presence is increasing in developed countries as well.

The three louse species which transmit diseases are the head louse, the body louse and the pubic louse. These species are responsible for the spread of trench fever, epidemic typhus and relapsing fever. The flea species which most commonly affect humans are the cat, the rat and the human flea. Fleas transmit plague, murine typhus, fleaborne spotted rickettsiosis. The transmission of these diseases is different from that of other vector-borne diseases, as it is carried out through the human contact network, which means that the spread of the vectors themselves is similar to that of a disease.

In this paper we delineate a model for the dynamics of ectoparasite-borne diseases and we describe the structure of the global attractors in the different situations depending on the reproduction numbers. We assume the presence of one disease and one ectoparasite species which is a vector transmitting this particular disease.

The human population is divided into three compartments: susceptibles (i.e. those who can be infested by both infectious and non-infectous vectors, denoted by $S(t)$), those who are infected by non-infectious parasites (denoted by $T(t)$) and those who are infested by infectious vectors (denoted by $Q(t)$). We assume that someone infested by non-infectious vectors can transmit the parasites to susceptibles, while an individual infested by infectious vectors transmits both the parasites and the disease to susceptibles. An individual infested by infectious vectors transmits the infection to individuals infested by non-infectious vectors, i.e. a member of compartment T can move to compartment Q upon adequate contact with someone from compartment Q. We assume that a person is infected by the disease if and only he is infested by infectious parasites. We suppose that individuals infested by infected parasites transmit the disease at the same rate to susceptibles and to those who are infested by non-infected parasites. We denote this transmission rate by β_Q, and β_T denotes the transmission rate for non-infectious vectors (to susceptibles). The rate of disinfestation is denoted by μ for the infected compartment and by θ for the non-infected compartment. We denote by b the natural birth and death rates, and we assume the disease is not fatal, thus the population size is constant. In the model equations we use mass action incidence.

We have the following system of differential equations

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(with all the parameters assumed to be positive):

$$\begin{aligned} S'(t) &= -\beta_T S(t)T(t) - \beta_Q S(t)Q(t) \\ &\quad + \theta T(t) + \mu Q(t) + b - bS(t), \\ T'(t) &= \beta_T S(t)T(t) \\ &\quad - \beta_Q Q(t)T(t) - \theta T(t) - bT(t), \\ Q'(t) &= \beta_Q S(t)Q(t) \\ &\quad + \beta_Q Q(t)T(t) - \mu Q(t) - bQ(t). \end{aligned} \tag{1}$$

It can easily be seen that any solution with non-negative initial values remains non-negative for all forward time. We can suppose that

$$N(t) = S(t) + T(t) + Q(t) = 1$$

holds for the total population. The phase space of our system is $X := \{(S,T,Q) \in \mathbb{R}^3_+ : \ S+T+Q=1\}$.

II. Equilibria, Reproduction Numbers

By solving the algebraic equations

$$\begin{aligned} 0 &= -\beta_T S^*T^* - \beta_Q S^*Q^* + \theta T^* + \mu Q^* + b - bS^*, \\ 0 &= \beta_T S^*T^* - \beta_Q Q^*T^* - \theta T^* - bT^*, \\ 0 &= \beta_Q S^*Q^* + \beta_Q Q^*T^* - \mu Q^* - bQ^*, \end{aligned}$$

we can determine the four equilibria of system (1):

$$\begin{aligned} E_S &= (1,0,0), \\ E_T &= \left(\frac{b+\theta}{\beta_T}, 1 - \frac{b+\theta}{\beta_T}, 0\right), \\ E_Q &= \left(\frac{b+\mu}{\beta_Q}, 0, 1 - \frac{b+\mu}{\beta_Q}\right), \\ E_{QT} &= \left(\frac{\theta - \mu + \beta_Q}{\beta_T}, \frac{b+\mu}{\beta_Q} - \frac{\theta - \mu + \beta_Q}{\beta_T}, 1 - \frac{b+\mu}{\beta_Q}\right). \end{aligned}$$

Reproduction numbers have a clear biological interpretation. We can obtain them by multiplying the number of new infections and the average length of the infectious period of an infectious agent newly introduced into a population currently being in one of the equilibria.

By introducing an infested, non-infectious individual into a population in the equilibrium E_S, we obtain the reproduction number

$$R_1 = \frac{\beta_T}{b+\theta},$$

by introducing an infested and infectious individual into the same equilibrium we obtain the reproduction number

$$R_2 = \frac{\beta_Q}{b+\mu}.$$

Calculating the expected number of secondary infections caused by the introduction of an infectious infested individual into a population in the equilibrium E_T gives the same reproduction number R_2.

If we introduce a non-infectious infested individual into a population in the equilibrium E_Q, we obtain the reproduction number

$$R_3 = \frac{\beta_T(b+\mu)}{\beta_Q(\beta_Q - \mu + \theta)}.$$

The following lemma is taken from [3].

Lemma 2.1: The equilibrium E_S always exists. The equilibrium E_T exists if and only $R_1 > 1$. The equilibrium E_Q exists if and only if $R_2 > 1$. The equilibrium E_{QT} exists if and only if $R_2 > 1$ and $R_3 > 1$.

III. Structure of the Global Attractor

Here we recall the main result of [3].

Theorem 3.1: Let $X_Q := \{(S,T,0) \in \mathbb{R}^3_+ : \ S+T=1\}$ and $X_T := \{(S,0,Q) \in \mathbb{R}^3_+ : \ S+Q=1\}$ denote the extinction sets for Q and T, respectively. The four equilibria have the following global stability properties depending on the reproduction numbers:

(i) Equilibrium E_S is globally asymptotically stable if $R_1 \leq 1$ and $R_2 \leq 1$.

(ii) Equilibrium E_T is globally asymptotically stable on $X \setminus X_T$ if $R_1 > 1$ and $R_2 \leq 1$. On X_T, E_S is globally asymptotically stable.

(iii) If $R_2 > 1$, $R_3 \leq 1$ and $R_1 \leq 1$, then E_Q is globally asymptotically stable on $X \setminus X_Q$ and E_S is globally asymptotically stable on X_Q.

(iv) If $R_2 > 1$, $R_3 \leq 1$ and $R_1 > 1$, then E_Q is globally asymptotically stable on $X \setminus X_Q$ and E_T is globally asymptotically stable on X_Q.

(v) If $R_2 > 1$, $R_3 > 1$, then E_{QT} is globally asymptotically stable on $X \setminus (X_Q \cup X_T)$, E_T is globally asymptotically stable on X_Q and E_Q is globally asymptotically stable on X_T.

An equilibrium E is said to be globally asymptotically stable on a set Y if it is stable and for all $y \in Y$ the solution starting from y converges to E as $t \to \infty$. Following the notation of [1, 1.1.7], by Mt we denote the set consisting of the states at time t of the solutions started from all of the points $x \in M$.

Definition 3.2: Let $\mathcal{A} \in X$ be a compact invariant set. If $\mathcal{A}$ attracts each bounded subset of X, i.e. for any bounded subset $M \subset X$ and any neighbourhood U of $\mathcal{A}$ there exists a $T < \infty$ such that $Mt \subset U$ for all $t > T$, then $\mathcal{A}$ is called the *global attractor*.

Definition 3.3: The *ω-limit set* of a point $x \in X$, denoted by $\omega(x)$ consists of those elements y of X for which there exists a real sequence $\{t_n\}$ such that $t_n \nearrow \infty$ and $xt_n \to y$ as $n \to \infty$. The *α-limit set* is defined similarly with $t_n \searrow -\infty$.

In the following theorem we describe the structure of the global attractor for system (1) in the five cases listed in Theorem 3.1.

Theorem 3.4: The global attractor $\mathcal{A}$ for system (1) has the following structure:

(i) $\mathcal{A} = \{E_S\}$.

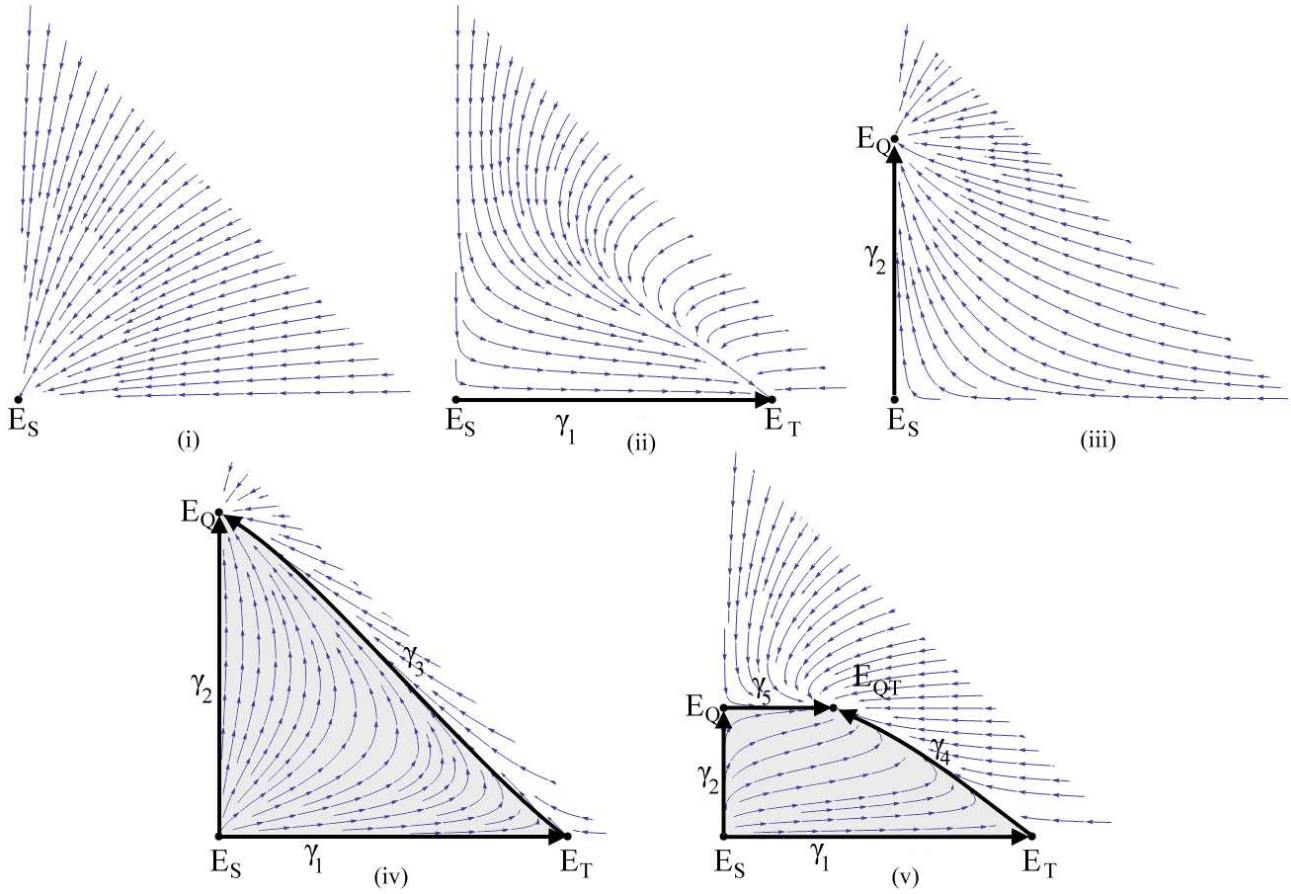

Fig. 1. Representation of the flow and the attractors on the TQ-plane.

(ii) $\mathcal{A} = \{E_S, E_T\} \cup \gamma_1$, where γ_1 is a connecting orbit from E_S to E_T, which is actually the segment between E_S and E_T in the extinction space X_Q.

(iii) $\mathcal{A} = \{E_S, E_Q\} \cup \gamma_2$, where γ_2 is a connecting orbit from E_S to E_Q, which is actually the segment between E_S and E_Q in the extinction space X_T.

(iv) $\mathcal{A} = \{E_S, E_T, E_Q\} \cup \gamma_1 \cup \gamma_2 \cup \gamma_3 \cup \mathcal{A}_1$, where γ_3 is a connecting orbit from E_T to E_Q, and $\mathcal{A}_1$ is the domain surrounded by $E_S, E_T, E_Q, \gamma_1, \gamma_2$ and γ_3 in the TQ-plane consisting of connecting orbits from E_S to E_Q.

(v) $\mathcal{A} = \{E_S, E_T, E_Q, E_{QT}\} \cup \gamma_1 \cup \gamma_2 \cup \gamma_4 \cup \gamma_5 \cup \mathcal{A}_2$, where γ_4 is a connecting orbit from E_T to E_{QT}, γ_5 is a connecting orbit from E_Q to E_{QT}, and $\mathcal{A}_2$ is the domain surrounded by $E_S, E_T, E_Q, E_{QT}, \gamma_1, \gamma_2, \gamma_4$ and γ_5 in the TQ-plane consisting of connecting orbits from E_S to E_{QT}.

Proof:

(i) As proved in Theorem 3.1, E_S is globally asymptotically stable in case (i), which means that the global attractor is the singleton E_S in this case.

For the proof of the remaining cases we reduce the system to two dimensions by substituting S with $1-T-Q$. We get the system

$$\begin{aligned} T'(t) &= \beta_T(1-T(t)-Q(t))T(t) \\ &\quad - \beta_Q Q(t)T(t) - \theta T(t) - bT(t), \\ Q'(t) &= \beta_Q(1-T(t)-Q(t))Q(t) \\ &\quad + \beta_Q Q(t)T(t) - \mu Q(t) - bQ(t) \end{aligned} \tag{2}$$

and the four equilibria

$$\begin{aligned} E_S &= (0,0), \\ E_T &= \left(1 - \frac{b+\theta}{\beta_T}, 0\right), \\ E_Q &= \left(0, 1 - \frac{b+\mu}{\beta_Q}\right), \\ E_{QT} &= \left(\frac{b+\mu}{\beta_Q} - \frac{\theta - \mu + \beta_Q}{\beta_T}, 1 - \frac{b+\mu}{\beta_Q}\right). \end{aligned}$$

By standard linearization, we calculate the eigenvalues and eigenvectors of the Jacobian of the linearized system in the four equilibria. The details of the calculations are straightforward thus omitted, here we only discuss the results and implications. The eigenvalues of the Jacobian

of the linearized equation around the equilibrium E_S are $\lambda_1 = -b-\theta+\beta_T = (b+\theta)(R_1-1)$ with corresponding eigenvector $(1,0)$ and $\lambda_2 = -b-\mu+\beta_Q = (b+\mu)(R_2-1)$ with corresponding eigenvector $(0,1)$. Linearizing at the equilibrium E_T, one finds the eigenvalues $\lambda_1 = b+\theta-\beta_T = (b+\theta)(1-R_1)$ with the eigenvector $(1,0)$ and $\lambda_2 = -b-\mu+\beta_Q = (b+\mu)(R_2-1)$ with the eigenvector

$$\left(\frac{(\beta_Q+\beta_T)(b+\theta-\beta_T)}{\beta_T(\beta_Q+\beta_T-2b-\theta-\mu)},1\right).$$

Linearization around the steady state E_Q gives the following eigenvalues of the Jacobian: $\lambda_1 = b+\mu-\beta_Q = (b+\mu)(1-R_2)$ with the eigenvector $(0,1)$ and $\lambda_2 = -\theta+\mu-\beta_Q+(b+\mu)\beta_T/\beta_Q = (R_3-1)\beta_T/(R_2R_3)$ with the eigenvector $(1,0)$. Finally, if we linearize the system around the equilibrium E_{QT}, we obtain the eigenvalues $\lambda_1 = b+\mu-\beta_Q = (b+\mu)(1-R_2)$ with corresponding eigenvector

$$\left(\frac{(\beta_Q+\beta_T)(\beta_Q(\beta_Q+\theta)-b\beta_T-\mu(\beta_Q+\beta_T))}{\beta_T(b(\beta_Q+\beta_T)-\beta_Q(2\beta_Q+\theta)+(2\beta_Q+\beta_T)\mu)},1\right)$$

and $\lambda_2 = \theta-\mu+\beta_Q-(b+\mu)\beta_T/\beta_Q = (1-R_3)\beta_T/(R_2R_3)$ with corresponding eigenvector $(1,0)$.

(ii) If $R_1 > 1$ and $R_2 < 1$ then E_S has the stable eigenvector $(0,1)$ and the unstable eigenvector $(1,0)$. This means that E_S has a one-dimensional stable manifold which coincides with the invariant extinction space X_T and a one-dimensional unstable manifold which coincides with the segment (E_S, E_T) of the extinction space X_Q, while both of the eigenvectors at E_T are stable. γ_1 is the connecting orbit from E_S to E_T lying in X_Q. If $R_2 = 1$ then the second eigenvalue at E_S is equal to zero. In this case, the equation for $Q'(t)$ takes the form

$$Q'(t) = -\beta_Q Q^2(t) < 0$$

on X_T, which means that all solutions started from X_T tend to E_S. Thus E_S has the same one-dimensional stable and unstable sets as in the case $R_2 \neq 1$. From Theorem 3.1 we know that all solutions started from $X \setminus X_T$ tend to E_T, thus E_T has a two-dimensional stable set.

(iii) If $R_1 < 1$, $R_2 > 1$ and $R_3 < 1$ then E_S has the stable eigenvector $(1,0)$, and the unstable eigenvector $(0,1)$, while $(0,1)$ and $(1,0)$ are both stable eigenvectors for E_Q. If $R_1 = 1$ then the equation for $T'(t)$ takes the form

$$T'(t) = -\beta_T T^2(t) < 0,$$

on the invariant extinction space X_Q. This means that all solutions on the center manifold belonging to the zero eigenvalue (which coincides with X_Q) tend to E_S. If $R_3 = 1$ then the Jacobian of the linearized system at E_Q has a zero eigenvalue with eigenvector $(1,0)$. The line

$$Q = 1 - \frac{b+\mu}{\beta_Q}$$

is invariant: if we substitute $1-(b+\mu)/\beta_Q$ into the equation for $Q'(t)$ we get $Q'(t) = 0$. This means that for $R_3 = 1$ the center manifold belonging to the zero eigenvalue coincides with this line. For $R_3 = 1$, the equation for $T'(t)$ has the form

$$T'(t) = -\beta_T T^2(t) < 0$$

on this line, which means that all solutions started from this line tend to the equilibrium E_Q. γ_2 is the connecting orbit from E_S to E_Q lying in X_T. This shows the statement of (iii).

(iv) In this case, the first eigenvector belonging to E_S loses its stability, while the same vector becomes a stable eigenvector for E_T. Thus, E_S has two unstable eigenvectors and E_T has the stable eigenvector $(1,0)$ and an unstable eigenvector. From Theorem 3.1 we know that any solution started from the one-dimensional unstable manifold of E_T tends to E_Q, from which the existence of a heteroclinic orbit γ_3 from E_T to E_Q follows. The situation for E_Q is the same as in case (iii). We have to show that $\mathcal{A}_1$ consists of heteroclinic orbits from E_S to E_Q. Let us take an arbitrary point $p \in \mathcal{A}_1$. From Theorem 3.1 we know that $\omega(p) = \{E_Q\}$. The negative limit set $\alpha(p)$ exists and is non-empty as the backward orbit is bounded by $\gamma_1 \cup \gamma_2 \cup \gamma_3$. From the Poincaré–Bendixson Theorem we know that $\alpha(p)$ can only be an equilibrium point (as there are no periodic orbits). We can exclude E_Q as it has a two-dimensional stable manifold. The unstable manifold of E_T coincides with X_Q, which is invariant and $\mathcal{A}_1 \cap X_Q = \emptyset$, thus $\alpha(p) = \{E_S\}$.

(v) In this case, again, E_S has two unstable eigenvectors and thus a two-dimensional unstable manifold. Similarly to the previous case, E_T has a stable and an unstable eigenvector, thus having a one-dimensional stable manifold and a one-dimensional unstable manifold. The eigenvector $(1,0)$ for E_Q is unstable, which means that E_Q has a one-dimensional stable manifold and a one-dimensional unstable manifold. E_{QT} has two stable eigenvectors and thus a two-dimensional stable manifold. From Theorem 3.1 we know that all solutions started from $X \setminus (X_T \cup X_Q)$ tend to E_{QT}, thus there exists a connecting orbit γ_4 from E_T to E_{QT} and a connecting orbit γ_5 from E_Q to E_{QT}. Similarly to case (iv) we can show that the domain $\mathcal{A}_2$ consists of connecting orbits from E_S to E_{QT}.

■

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IV. CONCLUSION

We described the global attractor in all possible cases. Depending on the three reproduction numbers, the global attractor might have the following structure:

- a singleton
- a one-dimensional set consisting of two equilibria and a connecting orbit
- a two-dimensional set consisting of three or four equlibria and connecting orbits between them.

The biological interpretation of our results is the following. The reproduction numbers R_i ($i = 1, 2, 3$) completely determine whether the infectious or the non-infectious parasites can invade a human population. This is mathematically expressed in the structure of the global attractors that we described. If $R_1 \leq 1$ and $R_2 \leq 1$, then the population is safe from any parasites. The implication for the control of the infection and infestation is that to eradicate the disease only, we have to decrease R_2 to be less than 1, which is possible by reducing β_Q or increasing μ. To eliminate all the parasites, besides decreasing R_2 we also have to decrease R_1 (possible by reducing β_T or increasing θ). Decreasing only R_1 is not enough for the elimination of the parasites. The reproduction number R_3 is a threshold parameter which shows whether all the parasites become infectious or both infectious and non-infectious parasites can be present in the population. The transmission rates β_Q and β_T can be effectively reduced by vigorous monitoring and isolation of infested individuals, while μ and θ can be increased by disinfestation treatment of individuals.

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