



Research article

A continuous-time SIS criss-cross model of co-infection in a heterogeneous population

Marcin Choiński*

Institute of Information Technology, Warsaw University of Life Sciences – SGGW,
Nowoursynowska 159 Street, building 34, 02-776 Warsaw, Poland

* **Correspondence:** Email: marcin_choinski@sggw.edu.pl.

Abstract: In this paper, we introduce and analyze a continuous-time model of co-infection dynamics in a heterogeneous population consisting of two subpopulations that differ in the risk of getting infected by individuals with two diseases. We assume that each parameter reflecting a given process for each subpopulation has different values, which makes the population completely heterogeneous. Such complexity and the population heterogeneity make our paper unique, reflecting co-infection dynamics. Moreover, we establish an epidemic spread for each disease not only in a sole subpopulation but also with criss-cross transmission, meaning between different subpopulations. The proposed system has a disease-free stationary state and two states reflecting the presence of one disease. We indicate conditions for their existence and local stability. The conditions for the local stability for states reflecting one disease have a complicated form, so we strengthened them so that they are more transparent. Investigation on the existence of a postulated endemic state corresponding to both disease's presence leads to a complex analysis, which is why we only provide an insight on this issue. Here, we also provide the basic reproduction number of our model and investigate properties of this number. The system has a universal structure; as such, it can be applied to investigate co-infection of different infectious diseases.

Keywords: co-infection; SIS model; local stability; population heterogeneity; dynamical systems

1. Introduction

There is a large number of papers with mathematical models of epidemic dynamics. These papers relate to both homogeneous and heterogeneous populations. By heterogeneous population we understand a population with at least two subpopulations that differ in the risk of getting infected. Because of convenience and lack of appropriate data, only two subpopulations are often distinguished. In recent papers [1] and [2], one can find exemplary models of epidemic spread in such populations with mathematical analysis.

Nowadays, the risk of co-infections is increasing worldwide, including co-infections with COVID-19 [3]. This increase is caused by, for example, increased people's mobility [4], drug resistance [5], impaired immunity after suffering from long COVID-19, and reduction of exposure to microbiota caused by home isolation during the COVID-19 pandemic [6]. Also, getting an infection raises the probability of simultaneous development of another illness [7]. Co-infection also boosts healthcare costs [8] and number of deaths [9]. It is therefore essential to put an effort into reducing co-infection cases. This reduction can be achieved by applying mathematical modeling. Thanks to mathematical models of co-infection spreading and their mathematical analysis, one can predict co-infections and implement proper therapeutic approaches. This is desirable since data concerning co-infections are less accessible than for single epidemics.

Generally, models of co-infection dynamics are based on models that describe the spread of a single epidemic. Hence, they have a more complex form and are, consequently, more difficult to analyze. However, one can find literature dealing with mathematical analysis of co-infection spread. A recent paper [10] conducted a systemic review of mathematical models. A model of general co-infection for an acute and a chronic disease was presented in [11]. The authors in [12] proposed and analyzed the model of COVID-19 and tuberculosis (*TB*) infection. The same type of epidemics, together with measuring impact on isolation, was investigated in [13]. Papers [14] and [15] provide mathematical models for the spread of SARS-CoV-2 with hepatitis B virus and SARS-CoV-2 with human T-cell lymphotropic virus type-I, respectively. The analysis of models concerning individuals suffering from COVID-19 and kidney disease was presented in a recent work [16]. An interesting approach is presented in [17], where the authors investigated the co-infection of airborne and vector-host diseases, namely COVID-19 and dengue.

Not only COVID-19 is investigated in co-infection modeling. Since *HIV* infection increases the probability of developing *TB* [18], papers related to the modeling of *TB* and *HIV* spread contribute significantly to the literature. Authors in [19] distinguish two *TB* infected classes: fast and slow latent. They also considered acute and chronic *HIV*-infected groups. A recent paper [20] focused on an analysis of a *TB/HIV* epidemic spread in Ethiopia, with two infected groups for each disease. Naturally, other co-infections are also analyzed in the literature. Authors in [21] investigated the epidemic of *HIV* and hepatitis C virus, whereas paper [22] dealt with co-infection of *TB* and pneumonia.

In each paper described above, authors assumed that there is only one class of people that are not infected with any disease; this means they are susceptible to both infections. This leads to situations where the probability of co-infection is raised only by encountering a single infection. That supposition implies no population heterogeneity for healthy individuals. Clearly, this case is not valid. Therefore, there is a need to include heterogeneity in a susceptible class. While modeling an epidemic of a single infection for a heterogeneous population, authors assume that values of parameters reflecting a given subpopulation are the same. This assumption actually leads to the case of a homogeneous population. To adequately describe the dynamics of infection, and consequently of co-infection, in a heterogeneous population, one must consider different values of parameters for each subpopulation. Such consideration makes the mathematical analysis of the model more difficult; thus, this approach is uncommon.

Our paper aims to construct and analyze the mathematical models of co-infection in a heterogeneous population consisting of two subpopulations. We assume that parameter values reflecting a given process in each subpopulation differ. This assumption and the heterogeneity in the population make our

paper novel among the literature considering the modeling of co-infections. In our model, we also introduce a case of a spread of each disease not only among one subpopulation but also between subpopulations. This introduction enables our system to be classified as a criss-cross model. We propose a system of ordinary differential equations that is a *SIS*-type (*susceptible–infected–susceptible*) model. In models of such type, there is no immunity after recovery and an individual becomes susceptible again. Including heterogeneity constrains computations. For this reason, we do not incorporate a recovered class to maintain explicit results of the analysis. Our model does not relate to particular diseases. Hence, one can apply the obtained results to different infections. Such applications include co-infections that combine sole airborne illnesses, such as *TB*, COVID-19, or influenza, sexually transmitted diseases, such as gonorrhea, *HIV*, and hepatitis *B*, or incorporate illnesses from both types.

This paper is a continuation of our work from [23] and [24], in which we investigated the criss-cross model of epidemic spread of a single disease for a heterogeneous population. In [23], we conducted the mathematical analysis of the model that was proposed in [25]. The aim of that analysis was to confirm, from a mathematical point of view, the medical hypothesis that stated that to control the epidemic spread in the heterogeneous population, one must consider criss-cross illness transmission. Investigating such spread in a single subpopulation does not provide complete insight into the epidemic dynamics. Because of the proposed model's unexpected properties, such as a possible unbounded population growth, we modified the system from [23] by assuming a constant inflow into each subpopulation. We analyzed that modified system in [24] and again obtained consistency with the medical hypothesis. Considering that the second disease in epidemic dynamics for a heterogeneous population is medically driven by an increasing number of co-infections worldwide and different scenarios regarding individuals' susceptibility can provide mathematical results that can help predict a co-infection course.

In [23] and [24], we focused on the stability analysis; we indicated stationary states appearing in the given systems and determined the conditions for their local stability. In this paper, we also apply this approach. The model presented herein relies on the system from [24].

The paper is organized as follows: In Section 2, we describe and introduce our model. Then we find stationary states of the system and describe conditions for their existence. The basic reproduction number of the model is computed in Section 4. The following section deals with local stability of the found stationary state. We summarize our results in Section 7.

2. Formulation of a model and its basic properties

Let us first describe the assumptions concerning the proposed model. In a population, we indicate two subpopulations, a low-risk (*LS*) and a high-risk (*HS*) subpopulation, relating to the risk of getting infected. *LS* and *HS* have, respectively, lower and higher susceptibility to each disease. For every variable and parameter, we assign a subscript i equal to 1 and 2 for *LS* and *HS* respectively. If i has no assigned value, then $i \in \{1, 2\}$. By S_1 and S_2 , we denote a density of healthy people in *LS* and *HS*, respectively. The variables I_i refer to the density of individuals from the given subpopulation that are infected by a pathogen of the disease that we call disease *A* (*DA*). Similarly, we define J_i as the density of individuals suffering from disease *B* (*DB*). The density of a group infected by pathogens from both diseases is denoted by K_i .

Migrating and newborn individuals join each subpopulation through S_i class with a recruitment rate C_i . A natural death rate for each subpopulation is equal to μ_i . For *DA*, we introduce the transmission

rates β_{11} , β_{22} , β_{12} and β_{21} , reflecting transmission among *LS*, among *HS*, from *HS* to *LS*, and from *LS* to *HS*, respectively. These four different rates mean that *DA* differs in spreading and contracting a pathogen. To get a preliminary insight on co-infection dynamics for the heterogeneous population, for *DB* we assume that individuals differ only in contracting a pathogen. For this reason, we take only two transmission coefficients for *DB*: σ_1 for *LS* and σ_2 for *HS*. By γ_i and g_i , we denote the recovery rate for *DA* and *DB*, respectively. The disease-mortality rate for *DA* and *DB* is depicted by α_i and a_i .

The proposed model of co-infection is

$$\dot{S}_1 = C_1 - \beta_{11}S_1I_1 - \beta_{12}S_1I_2 + \gamma_1I_1 - \mu_1S_1 - \sigma_1S_1(J_1 + J_2) + g_1J_1, \quad (2.1a)$$

$$\dot{I}_1 = \beta_{11}S_1I_1 + \beta_{12}S_1I_2 - (\gamma_1 + \alpha_1 + \mu_1)I_1 - \sigma_1I_1(J_1 + J_2) + g_1K_1, \quad (2.1b)$$

$$\dot{J}_1 = \sigma_1S_1(J_1 + J_2) - (g_1 + a_1 + \mu_1)J_1 - \beta_{11}J_1I_1 - \beta_{12}J_1I_2 + \gamma_1K_1, \quad (2.1c)$$

$$\dot{K}_1 = \sigma_1I_1(J_1 + J_2) + \beta_{11}J_1I_1 + \beta_{12}J_1I_2 - (g_1 + a_1 + \gamma_1 + \alpha_1 + \mu_1)K_1, \quad (2.1d)$$

$$\dot{S}_2 = C_2 - \beta_{22}S_2I_2 - \beta_{21}S_2I_1 + \gamma_2I_2 - \mu_2S_2 - \sigma_2S_2(J_1 + J_2) + g_2J_2, \quad (2.1e)$$

$$\dot{I}_2 = \beta_{22}S_2I_2 + \beta_{21}S_2I_1 - (\gamma_2 + \alpha_2 + \mu_2)I_2 - \sigma_2I_2(J_1 + J_2) + g_2K_2, \quad (2.1f)$$

$$\dot{J}_2 = \sigma_2S_2(J_1 + J_2) - (g_2 + a_2 + \mu_2)J_2 - \beta_{22}J_2I_2 - \beta_{21}J_2I_1 + \gamma_2K_2, \quad (2.1g)$$

$$\dot{K}_2 = \sigma_2I_2(J_1 + J_2) + \beta_{22}J_2I_2 + \beta_{21}J_2I_1 - (g_2 + a_2 + \gamma_2 + \alpha_2 + \mu_2)K_2. \quad (2.1h)$$

Each parameter is fixed and positive. In particular, every parameter besides C_i is in the range $(0, 1)$. If we assume that $\sigma_i, g_i, a_i = 0$, the above system would reduce to the system that we introduced and analyzed in [24].

Figure 1 is a schematic drawing of the proposed model.

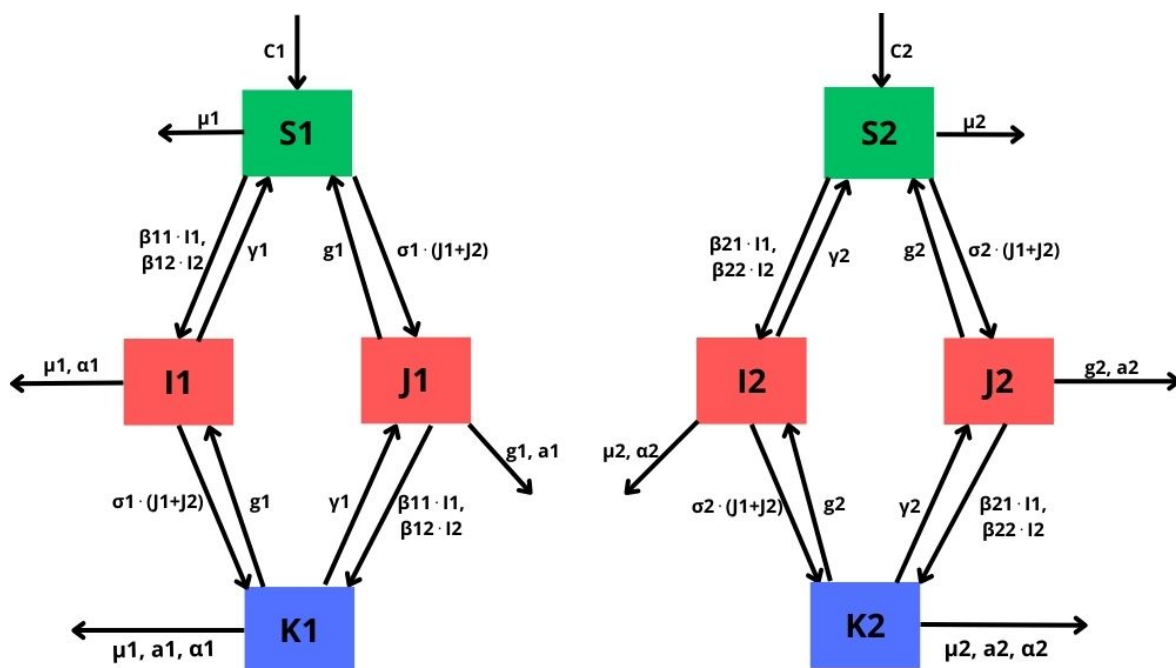


Figure 1. Possible movements between particular classes from system (2.1). The green rectangles correspond to non-infected classes, the red rectangles reflect groups with one infection, and the blue rectangles relate to co-infected classes. For the sake of transparency, subscripts are expressed as regular symbols.

In order to make the form of system (2.1) more transparent, we define:

$$k_i := \gamma_i + \alpha_i + \mu_i, \quad q_i := g_i + a_i + \mu_i, \quad r_i := g_i + a_i + \gamma_i + \alpha_i + \mu_i. \quad (2.2)$$

Now we indicate the basic properties of the model. The form of the right-hand side of system (2.1) implies that its solutions exist and are unique and positive for any positive initial condition. Let us introduce a variable $N_i := S_i + I_i + J_i + K_i$ that naturally means a density of the whole *HS* or *LS*. After adding both sides of Eqs (2.1a)–(2.1d) or Eqs (2.1e)–(2.1h), we get

$$\dot{N}_i = \dot{S}_i + \dot{I}_i + \dot{J}_i + \dot{K}_i = C_i - \mu_i N_i - \alpha_i I_i - a_i J_i - (\alpha_i + a_i) K_i. \quad (2.3)$$

See that we can estimate Eq (2.3) from above by the inequality

$$\dot{N}_i \leq C_i - \mu_i N_i, \quad (2.4)$$

which solution is

$$N_i(t) \leq \left(N_i(0) - \frac{C_i}{\mu_i} \right) e^{-\mu_i t} + \frac{C_i}{\mu_i}.$$

For $N_i(0) > \frac{C_i}{\mu_i}$, we observe a decrease of the population. Clearly, we have

$$S_i(t), I_i(t), J_i(t), K_i(t) \leq N_i(t) \leq N_i(0).$$

For $N_i(0) < \frac{C_i}{\mu_i}$, we have a limited growth of the population, since

$$S_i(t), I_i(t), J_i(t), K_i(t) \leq N_i(t) \leq -\tilde{C}e^{-\mu_i t} + \frac{C_i}{\mu_i} \leq \frac{C_i}{\mu_i},$$

where \tilde{C} is any positive constant.

Now we estimate Eq (2.3) by

$$\dot{N}_i \geq C_i - (\mu_i + \alpha_i + a_i) N_i. \quad (2.5)$$

Combining inequalities (2.4) and (2.5), we get

$$C_i - (\mu_i + \alpha_i + a_i) N_i \leq \dot{N}_i \leq C_i - \mu_i N_i,$$

which produces the invariant set

$$\Omega : \left\{ (S_1, I_1, J_1, K_1, S_2, I_2, J_2, K_2) : S_i + I_i + J_i + K_i \in \left[\frac{C_i}{\mu_i + \alpha_i + a_i}, \frac{C_i}{\mu_i} \right] \right\}.$$

This set attracts all solutions of system (2.1). We therefore conclude that the variables $S_i(t)$, $I_i(t)$, $J_i(t)$, and $K_i(t)$ are defined for every $t > 0$.

3. Stationary states

In this section, we indicate stationary states of system (2.1) and determine conditions for their existence.

3.1. Non-endemic stationary states

Firstly, we find stationary states that are not endemic, meaning that at least one of their coordinates equals zero.

We consider separated cases.

1) Firstly, let us assume that $I_i = J_i = K_i = 0$. We immediately get the form of the disease-free stationary state:

$$E_{df} = (\widehat{S}_1, 0, 0, 0, \widehat{S}_2, 0, 0, 0), \quad \text{where} \quad \widehat{S}_1 = \frac{C_1}{\mu_1}, \quad \widehat{S}_2 = \frac{C_2}{\mu_2}. \quad (3.1)$$

Clearly, this state always exists.

2) Now, consider the case $K_i = 0$. Without loss of generality, we take $K_1 = 0$. From Eq (2.1d) for any stationary state we have $0 = \sigma_1 I_1 (J_1 + J_2) + \beta_{11} J_1 I_1 + \beta_{12} J_1 I_2$, which implies

$$(I_1 = 0 \vee J_1 + J_2 = 0) \quad \wedge \quad (J_1 = 0 \vee I_1 = 0) \quad \wedge \quad (J_1 = 0 \vee I_2 = 0). \quad (3.2)$$

Let us consider the first alternative from (3.2).

a) We first take $I_1 = 0$. From Eq (2.1b), we have $\beta_{12} S_1 I_2 = 0$, which yields $S_1 = 0$ or $I_2 = 0$. If $S_1 = 0$, then Eq (2.1b) gives the contradiction $0 = C_1 + g_1 J_1$. If $I_2 = 0$, then from Eq (2.1h) we have $K_2 = 0$ and our system reduces to:

$$\begin{aligned} \dot{S}_i &= 0 = C_i - \mu_i S_i - \sigma_i S_i (J_1 + J_2) + g_i J_i, \\ \dot{J}_i &= 0 = \sigma_i S_i (J_1 + J_2) - q_i J_i. \end{aligned} \quad (3.3)$$

The above system's form suggests that there is a stationary state with present *DB* and absent *DA*. We will investigate the existence of such postulated state later. System (3.3) fulfills the case $I_1 = 0 \wedge I_1 = 0 \wedge I_2 = 0$ from (3.2).

Now, assume that $I_1 = 0 \wedge J_1 = 0 \wedge J_1 = 0$ holds. Then from Eq (2.1b), we get $\beta_{11} S_1 I_2 + g_1 K_1 = 0$. It provides $S_1 = 0$ or $I_2 = 0$. Case $S_1 = 0$ linked to Eq (2.1a) yields the contrary, $0 = C_1$, hence we must have $I_2 = 0$. Then from Eqs (2.1c) and (2.1h), we get $J_2 = 0$ and $K_2 = 0$, respectively. We obtain state E_{df} .

It is easy to check that the case $I_1 = 0 \wedge J_1 = 0 \wedge I_2 = 0$ gives E_{df} as well. The case $I_1 = 0 \wedge I_1 = 0 \wedge J_1 = 0$ is equivalent to $I_1 = 0 \wedge J_1 = 0 \wedge J_1 = 0$.

b) Now assume that $J_1 + J_2 = 0$. This assumption obviously provides $J_1 = 0$ and $J_2 = 0$. From Eq (2.1g), we get $\dot{J}_2 = \gamma_2 K_2$, giving $K_2 = 0$. We obtain the system

$$\begin{aligned} \dot{S}_i &= 0 = C_i - \beta_{ii} S_i I_i - \beta_{ij} S_i I_j + \gamma_i I_i - \mu_i S_i, \\ \dot{I}_i &= 0 = \beta_{ii} S_i I_i + \beta_{ij} S_i I_j - k_i I_i, \end{aligned} \quad (3.4)$$

where $j = 3 - i$. The above system fulfills condition $J_1 + J_2 = 0 \wedge J_1 = 0 \wedge J_1 = 0$, emerged from (3.2).

If we take $J_1 + J_2 = 0$ and simultaneously one of the cases $J_1 = 0 \wedge I_2 = 0$, $I_1 = 0 \wedge J_1 = 0$ or $I_1 = 0 \wedge I_2 = 0$, then we obtain E_{df} .

3) Now suppose that $I_1 = 0$. From Eq (2.1b), we get $0 = \beta_{12}S_1I_2 + g_1K_1$. From $S_1I_2 = 0$, we get $I_2 = 0$, which gives system (3.3). Choosing $K_1 = 0$ leads to system (3.4).

4) Consider $J_1 = 0$. Then Eq (2.1c) yields $0 = \sigma_1S_1J_2 + \gamma_1K_1$. Both cases $J_2 = 0$ and $K_1 = 0$ provide system (3.4).

5) Assuming $I_1 = 0 \wedge J_1 = 0$ leads to state E_{df} .

6) Supposing $I_1 = 0 \wedge K_1 = 0$ and $J_1 = 0 \wedge K_1 = 0$ results in systems (3.3) and (3.4), respectively.

Reasoning from points 1)–6) conducted for the variables with subscript 2 gives the same conclusions.

System (3.4) appears in our previous paper [24]. The solution of this system provides the endemic state $E^* = (S_1^*, I_1^*, S_2^*, I_2^*)$. This state is the projection of the state

$$E_A = (S_1^*, I_1^*, 0, 0, S_2^*, I_2^*, 0, 0), \quad S_i^*, I_i^* > 0, \quad (3.5)$$

onto the non-negative subspace $(S_1, I_1, S_2, I_2) \in \mathbb{R}^4$. State E_A reflects the presence of *DA* and the absence of *DB*. Observe that adding both sides of Eqs (2.1a)–(2.1b) and Eqs (2.1e)–(2.1f) for E_A yields $0 = C_i - \mu_i(I_i + S_i) - \alpha_i I_i$, providing

$$I_i = \frac{C_i - \mu_i S_i}{\mu_i + \alpha_i}. \quad (3.6)$$

Relying on results for state E^* from [24], we formulate conditions for the existence of state E_A .

Proposition 1. *In System (2.1), there exists the stationary state E_A defined in (3.5) that reflects the presence of disease A and the absence of disease B. This state exists if at least one of three cases holds:*

1) $\beta_{11}C_1 \geq \mu_1 k_1$;

2) $\beta_{22}C_2 \geq \mu_2 k_2$;

3) $\beta_{ii}C_i < \mu_i k_i$ and

$$(\mu_1 k_1 - \beta_{11}C_1)(\mu_2 k_2 - \beta_{22}C_2) \leq \beta_{12}\beta_{21}C_1C_2. \quad (3.7)$$

For E_A , we have

$$0 < S_i^* < \frac{k_i}{\beta_{ii}}, \quad \max\left(0, \frac{\beta_{ii}C_i - \mu_i k_i}{\mu_i + \alpha_i}\right) < I_i^* < \frac{\beta_{ii}C_i}{\mu_i + \alpha_i}.$$

Now we focus on system (3.3). Equation (2.3), being the sum of equations from this system, simplifies to $\dot{N}_i = 0 = C_i - \mu_i S_i - (\mu_i + a_i)J_i$, which gives

$$S_i = \frac{C_i - (\mu_i + a_i)J_i}{\mu_i}. \quad (3.8)$$

Computations concerning this system indicate the expected stationary state. Observe that the structure of system (3.3) is analogous to the structure of system (3.4). Based on this analogousness and Proposition 1, we formulate the following proposition concerning the other stationary state.

Proposition 2. *In System (2.1), there exists the stationary state*

$$E_B := (\bar{S}_1, 0, \bar{J}_1, 0, \bar{S}_2, 0, \bar{J}_2, 0), \quad \bar{S}_i, \bar{J}_i > 0, \quad (3.9)$$

with present disease B and absent disease A . This state exists if at least one of three cases holds:

- 1) $\sigma_1 C_1 \geq \mu_1 q_1$;
- 2) $\sigma_2 C_2 \geq \mu_2 q_2$;
- 3) $\sigma_i C_i < \mu_i q_i$ and

$$\frac{\sigma_1 C_1}{\mu_1 q_1} + \frac{\sigma_2 C_2}{\mu_2 q_2} \geq 1. \quad (3.10)$$

For E_B , we have

$$0 < \bar{S}_i < \frac{q_i}{\beta_{ii}}, \quad \max\left(0, \frac{\sigma_i C_i - \mu_i q_i}{\mu_i + a_i}\right) < \bar{I}_i < \frac{\sigma_i C_i}{\mu_i + a_i}.$$

3.2. The existence of the endemic stationary state

Now we investigate the endemic stationary state, reflecting the presence of both diseases A and B . Since it is difficult to obtain its explicit form, we limit our investigation to indicate some properties concerning its existence. Let us define $Z_i := I_i + J_i + K_i$. Obviously, variable Z_i is the density of individuals from the particular subpopulation infected by disease A , B , or both. Summing both sides of Eqs (2.1b)–(2.1d) gives

$$\dot{Z}_1 = \beta_{11} I_1 S_1 + \beta_{12} I_2 S_1 - g_1 J_1 - a_1 (J_1 + K_1) + \sigma_1 S_1 (J_1 + J_2) - \gamma_1 I_1 - \mu_1 Z_1 - \alpha_1 (I_1 + K_1).$$

From the above equation for the postulated endemic state, we have

$$S_1 = \frac{g_1 J_1 + a_1 (J_1 + K_1) + \gamma_1 I_1 + \mu_1 Z_1 + \alpha_1 (I_1 + K_1)}{\beta_{11} I_1 + \beta_{12} I_2 + \sigma_1 (J_1 + J_2)}. \quad (3.11)$$

Equation (2.3) and definition of N_1 for this state yield

$$S_1 = \frac{1}{\mu_1} \left(C_1 - \mu_1 (I_1 + J_1 + K_1) - \alpha_1 I_1 - a_1 J_1 - (\alpha_1 + a_1) K_1 \right). \quad (3.12)$$

Since $S_1 > 0$, one must fulfill

$$C_1 > \mu_1 (I_1 + J_1 + K_1) + \alpha_1 I_1 + a_1 J_1 + (\alpha_1 + a_1) K_1.$$

Combining reorganized Eqs (3.12) and (3.11), we get

$$\begin{aligned} & (C_1 - \mu_1 (I_1 + J_1) - \alpha_1 I_1 - a_1 J_1 - s_1 K_1) (\beta_{11} I_1 + \beta_{12} I_2 + \sigma_1 (J_1 + J_2)) \\ &= \mu_1 (k_1 I_1 + w_1 J_1 + s_1 K_1), \end{aligned} \quad (3.13)$$

where $s_1 := \alpha_1 + a_1 + \mu_1$ and $w_1 := g_1 + a_1 + \mu_1$.

From Eqs (2.1a)–(2.1d), we get the formula for coordinates S_1, I_1, J_1, K_1 :

$$S_1 = \frac{C_1 + g_1 J_1 + \gamma_1 I_1}{\beta_{11} I_1 + \beta_{12} I_2 + \mu_1 + \sigma_1 (J_1 + J_2)}, \quad (3.14a)$$

$$I_1 = \frac{\beta_{12} S_1 I_2 + g_1 K_1}{\sigma_1 (J_1 + J_2) + k_1 I_1 - \beta_{11} S_1}, \quad (3.14b)$$

$$J_1 = \frac{\sigma_1 S_1 J_2 + \gamma_1 K_1}{q_1 + \beta_{11} I_1 + \beta_{12} I_2 - \sigma_1 S_1} \quad (3.14c)$$

$$K_1 = \frac{\beta_{11} I_1 J_1 + \beta_{12} J_1 I_2 + \sigma_1 I_1 (J_1 + J_2)}{r_1}. \quad (3.14d)$$

Positivity of coordinates I_1 and J_1 yields inequalities:

$$S_1 < \frac{\sigma_1 (J_1 + J_2) + k_1 I_1}{\beta_{11}}, \quad S_1 < \frac{q_1 + \beta_{11} I_1 + \beta_{12} I_2}{\sigma_1}.$$

Combining the above dependences with condition (3.14a), we get

$$C_1 < \min \left(\frac{\sigma_1 (J_1 + J_2) + k_1 I_1}{\beta_{11}}, \frac{q_1 + \beta_{11} I_1 + \beta_{12} I_2}{\sigma_1} \right) (\sigma_1 (J_1 + J_2) + \mu_1 + \beta_{11} I_1 + \beta_{12} I_2) - \gamma_1 I_1 - g_1 J_1.$$

If we substitute Eq (3.14d) into the above inequality, we get

$$C_1 > \mu_1 (I_1 + J_1) + \alpha_1 I_1 + a_1 J_1 + \frac{\alpha_1 + a_1 + \mu_1}{r_1} (\beta_{11} I_1 J_1 + \beta_{12} J_1 I_2 + \sigma_1 I_1 (J_1 + J_2)).$$

Observe that the reasoning presented in this subsection can be applied to variables with subscript 2. This application provides another condition for the existence of the postulated endemic state.

4. The basic reproduction number

In this section, we find and investigate the basic reproduction number \mathcal{R}_0 of system (2.1). According to the definition from [26], \mathcal{R}_0 refers to the number of new infections produced by a single infectious individual in a population at a disease-free stationary state. To compute \mathcal{R}_0 , we will rely on the next generation method described in [26]. In this section, we provide a sketch of computations leading to the formula for \mathcal{R}_0 . We consider the subsystem of system (2.1), including the equations only for infected variables:

$$[\dot{I}_1, \dot{J}_1, \dot{K}_1, \dot{I}_2, \dot{J}_2, \dot{K}_2]^T = \mathcal{F} - \mathcal{V},$$

where vector \mathcal{F} concerns the terms related to new infections, and vector \mathcal{V} reflects the remaining processes. These vectors read

$$\mathcal{F} = \begin{bmatrix} \beta_{11} S_1 I_1 + \beta_{12} S_1 I_2 \\ \sigma_1 S_1 (J_1 + J_2) \\ \sigma_1 I_1 (J_1 + J_2) + \beta_{11} J_1 I_1 + \beta_{12} J_1 I_2 \\ \beta_{22} S_2 I_2 + \beta_{21} S_2 I_1 \\ \sigma_2 S_2 (J_1 + J_2) \\ b_2 I_2 (J_1 + J_2) + \beta_{22} J_2 I_2 + \beta_{12} J_2 I_1 \end{bmatrix}, \quad \mathcal{V} = \begin{bmatrix} k_1 I_1 + \sigma_1 I_1 (J_1 + J_2) - g_1 K_1 \\ q_1 J_1 + \beta_{11} J_1 I_1 + \beta_{12} J_1 I_2 - \gamma_1 K_1 \\ r_1 K_1 \\ k_2 I_2 + \sigma_2 I_2 (J_1 + J_2) - g_2 K_2 \\ q_2 J_2 + \beta_{22} J_2 I_2 + \beta_{21} J_2 I_1 - \gamma_2 K_2 \\ r_2 K_2 \end{bmatrix},$$

respectively. We construct matrices F and V that are the Jacobian matrices of \mathcal{F} and \mathcal{V} evaluated at E_{df} . These matrices have the form

$$F = \begin{bmatrix} \beta_{11}\widehat{S}_1 & \beta_{12}\widehat{S}_1 & 0 & 0 & 0 & 0 \\ \beta_{21}\widehat{S}_2 & \beta_{22}\widehat{S}_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & \sigma_1\widehat{S}_1 & \sigma_1\widehat{S}_1 & 0 & 0 \\ 0 & 0 & \sigma_2\widehat{S}_2 & \sigma_2\widehat{S}_2 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}, \quad V = \begin{bmatrix} k_1 & 0 & 0 & 0 & -g_1 & 0 \\ 0 & k_2 & 0 & 0 & 0 & -g_2 \\ 0 & 0 & q_1 & 0 & -\gamma_1 & 0 \\ 0 & 0 & 0 & q_2 & 0 & -\gamma_2 \\ 0 & 0 & 0 & 0 & r_1 & 0 \\ 0 & 0 & 0 & 0 & 0 & r_2 \end{bmatrix},$$

Then we compute FV^{-1} and obtain

$$FV^{-1} = \begin{bmatrix} \frac{\beta_{11}}{k_1}\widehat{S}_1 & \frac{\beta_{12}}{k_2}\widehat{S}_1 & 0 & 0 & \frac{g_1\beta_{11}}{k_1r_1}\widehat{S}_1 & \frac{g_2\beta_{12}}{k_2r_2}\widehat{S}_1 \\ \frac{\beta_{21}}{k_1}\widehat{S}_2 & \frac{\beta_{22}}{k_2}\widehat{S}_2 & 0 & 0 & \frac{g_1\beta_{21}}{k_1r_1}\widehat{S}_2 & \frac{g_2\beta_{22}}{k_2r_2}\widehat{S}_2 \\ 0 & 0 & \frac{\sigma_1}{q_1}\widehat{S}_1 & \frac{\sigma_1}{q_2}\widehat{S}_1 & \frac{\gamma_1\sigma_1}{q_1r_1}\widehat{S}_1 & \frac{\gamma_2\sigma_1}{q_2r_2}\widehat{S}_1 \\ 0 & 0 & \frac{\sigma_2}{q_1}\widehat{S}_2 & \frac{\sigma_2}{q_2}\widehat{S}_2 & \frac{\gamma_1\sigma_2}{q_1r_1}\widehat{S}_2 & \frac{\gamma_2\sigma_2}{q_2r_2}\widehat{S}_2 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}.$$

The basic reproduction number is the spectral radius of the matrix FV^{-1} . The eigenvalues of this read $\lambda_{1,2,3} = 0$, $\lambda_4 = \frac{\sigma_1}{q_1}\widehat{S}_1 + \frac{\sigma_2}{q_2}\widehat{S}_2$, and

$$\lambda_{5,6} = \frac{1}{2k_1k_2} \left(k_2\beta_{11}\widehat{S}_1 + k_1\beta_{22}\widehat{S}_2 \mp \sqrt{(k_2\beta_{11}\widehat{S}_1 - k_1\beta_{22}\widehat{S}_2)^2 + 4k_1k_2\beta_{12}\beta_{21}\widehat{S}_1\widehat{S}_2} \right)$$

We finally get

$$\mathcal{R}_0 = \max(\lambda_4, \lambda_6).$$

See that λ_4 consists of terms relying to only infection B , whereas λ_6 refers only to infection A .

Now we formulate the theorem relied on the dependence between λ_4 and λ_6 .

Theorem 4.1. $\mathcal{R}_0 = \lambda_4$ if

$$\widehat{S}_1\widehat{S}_2(\beta_{12}\beta_{21} - \beta_{11}\beta_{12}) < \widehat{S}_1\widehat{S}_2 \left(\frac{\sigma_1 u_2}{q_1} + \frac{\sigma_2 u_1}{q_2} \right) + \frac{\sigma_1 u_1}{q_1} \widehat{S}_1^2 + \frac{\sigma_2 u_2}{q_2} \widehat{S}_2^2, \quad (4.1)$$

where

$$u_i := k_{3-i} \left(\frac{k_i \sigma_i}{q_i} - \beta_{ii} \right), \quad (4.2)$$

and

$$\widehat{S}_1 \left(\frac{2\sigma_1}{q_1} - k_2\beta_{11} \right) + \widehat{S}_2 \left(\frac{2\sigma_2}{q_2} - k_1\beta_{22} \right) > 0. \quad (4.3)$$

Proof. Observe that $\lambda_4 > \lambda_6$ if

$$\sqrt{(k_2\beta_{11}\widehat{S}_1 - k_1\beta_{22}\widehat{S}_2)^2 + 4k_1k_2\beta_{12}\beta_{21}\widehat{S}_1\widehat{S}_2} < 2\lambda_4 k_1k_2 - k_2\beta_{11}\widehat{S}_1 - k_1\beta_{22}\widehat{S}_2. \quad (4.4)$$

Under fulfillment of

$$2\lambda_4 k_1 k_2 > k_2 \beta_{11} \widehat{S}_1 + k_1 \beta_{22} \widehat{S}_2 \quad (4.5)$$

we raise both sides of inequality (4.4) to the square and transform the result to

$$\widehat{S}_1 \widehat{S}_2 (\beta_{12} \beta_{21} - \beta_{11} \beta_{12}) < \lambda_4 (\lambda_4 - k_2 \beta_{11} \widehat{S}_1 - k_1 \beta_{22} \widehat{S}_2).$$

Using the definition of λ_4 in the above inequality and transforming the obtained expression, we get

$$\widehat{S}_1 \widehat{S}_2 (\beta_{12} \beta_{21} - \beta_{11} \beta_{12}) < \left(\frac{\sigma_1 \widehat{S}_1}{q_1} + \frac{\sigma_2 \widehat{S}_2}{q_2} \right) (\widehat{S}_1 u_1 + \widehat{S}_2 u_2), \quad (4.6)$$

where u_i is defined by Eq (4.2). We rewrite inequality (4.6) as inequality (4.1). Inequality (4.5) with the definition of λ_4 can be transformed into inequality (4.3).

Let us strengthen the assumptions from Theorem 4.1 so that we obtain more explicit ones. Suppose that $u_i > 0$, which can be written as

$$\beta_{ii} q_i < k_i \sigma_i. \quad (4.7)$$

Then condition

$$\frac{\sigma_1 u_2}{q_1} + \frac{\sigma_2 u_1}{q_2} > \beta_{12} \beta_{21} - \beta_{11} \beta_{12} \quad (4.8)$$

suffices fulfillment of inequality (4.1). Moreover, if

$$\beta_{ii} q_i < \frac{2\sigma_i}{k_{3-i}}, \quad (4.9)$$

then inequality (4.3) is always true. Combining inequalities (4.7) and (4.9) yields

$$\beta_{ii} q_i < \max \left(k_i \sigma_i, \frac{2\sigma_i}{k_{3-i}} \right). \quad (4.10)$$

We conclude that

Corollary 1. *If inequality (4.10), then $\mathcal{R}_0 = \lambda_4$.*

The above corollary confirms the obvious dependence that if the transmission of infection B , represented by σ_i , is sufficiently stronger than the transmission of infection A between different subpopulations, reflected by β_{ii} , then infection B plays a bigger role in the whole population.

Observe that if in inequality (4.3) we replace sign $>$ by sign $<$, then $\lambda_4 < \lambda_6$. It yields $\mathcal{R}_0 = \lambda_6$, which is the same as \mathcal{R}_0 for the system with one infection from [24].

From a medical point of view, the desirable situation is when $\mathcal{R}_0 < 1$. Let us check when this case holds. We formulate the theorem

Theorem 4.2. *For system (2.1) $\mathcal{R}_0 < 1$ if*

$$\frac{\sigma_1 \widehat{S}_1}{q_1} + \frac{\sigma_2 \widehat{S}_2}{q_2} < 1, \quad (4.11)$$

$$\widehat{S}_i < \frac{k_i}{\beta_{ii}} \quad (4.12)$$

and

$$\beta_{12} \beta_{21} \widehat{S}_1 \widehat{S}_2 < (\beta_{11} \widehat{S}_1 - k_1)(\beta_{22} \widehat{S}_2 - k_2). \quad (4.13)$$

Proof. Condition (4.11) is obvious from the definition of λ_4 . The part of the proof related to λ_6 is similar to the proof of Theorem 4.1. The inequality $\lambda_6 < 1$ can be transformed into

$$\sqrt{(k_2\beta_{11}\widehat{S}_1 - k_1\beta_{22}\widehat{S}_2)^2 + 4k_1k_2\beta_{12}\beta_{21}\widehat{S}_1\widehat{S}_2} < 2k_1k_2 - (k_2\beta_{11}\widehat{S}_1 + k_1\beta_{22}\widehat{S}_2). \quad (4.14)$$

Under condition

$$2 > \frac{\beta_{11}}{k_1}\widehat{S}_1 + \frac{\beta_{22}}{k_2}\widehat{S}_2 \quad (4.15)$$

multiplying both sides of inequality (4.14) yields

$$\beta_{12}\beta_{21}\widehat{S}_1\widehat{S}_2 < k_1k_2 - k_2\beta_{11}\widehat{S}_1 - k_1\beta_{22}\widehat{S}_2 + \beta_{11}\beta_{12}\widehat{S}_1\widehat{S}_2,$$

which can be written as inequality (4.13). The right-hand side of inequality (4.13) must be positive. It is true when $\widehat{S}_i > \frac{k_i}{\beta_{ii}}$ or (4.12). The first case is contrary to inequality (4.15). Hence, inequality (4.12) must hold, which is stronger than inequality (4.15).

It is easy to check that inequality (4.13) is opposite to inequality (3.7) from Proposition 1 discussing the existence of state E_A . Similarly, inequality (4.11) is opposite to inequality (3.10) from Proposition 2 providing conditions for the E_B existence.

5. Local stability of stationary states

Now we investigate the local stability of states E_{df} , E_A , and E_B . The Jacobian matrix of system (2.1) can be written as $J = \begin{pmatrix} M_1 & M_2 \end{pmatrix}$, where

$$M_1 = \begin{pmatrix} G_1 & -\beta_{11}S_1 + \gamma_1 & -\sigma_1S_1 + g_1 & 0 \\ F_1 & \beta_{11}S_1 - k_1 - \sigma_1(J_1 + J_2) & -\sigma_1I_1 & g_1 \\ \sigma_1(J_1 + J_2) & -\beta_{11}J_1 & \sigma_1S_1 - q_1 - F_1 & \gamma_1 \\ 0 & \sigma_1(J_1 + J_2) + \beta_{11}J_1 & \sigma_1I_1 + F_1 & -r_1 \\ 0 & -\beta_{21}S_2 & -\sigma_2S_2 & 0 \\ 0 & \beta_{21}S_2 & -\sigma_2I_2 & 0 \\ 0 & -\beta_{21}J_2 & -\sigma_2S_2 & 0 \\ 0 & \beta_{21}J_2 & \sigma_2I_2 & 0 \end{pmatrix},$$

and

$$M_2 = \begin{pmatrix} 0 & -\beta_{12}S_1 & -\sigma_1S_1 & 0 \\ 0 & \beta_{12}S_1 & -\sigma_1I_1 & 0 \\ 0 & -\beta_{12}J_1 & \sigma_1S_1 & 0 \\ 0 & \beta_{12}J_1 & \sigma_1I_1 & 0 \\ G_2 & -\beta_{22}S_2 + \gamma_2 & -\sigma_2S_2 + g_2 & 0 \\ F_2 & \beta_{22}S_2 - k_2 - \sigma_2(J_1 + J_2) & -\sigma_2I_2 & g_2 \\ \sigma_2(J_1 + J_2) & -\beta_{22}J_2 & \sigma_2S_2 - q_2 - F_2 & \gamma_2 \\ 0 & \sigma_2(J_1 + J_2) + \beta_{22}J_2 & \sigma_2I_2 + F_2 & -r_2 \end{pmatrix}$$

with

$$F_i := F_i(I_1, I_2) = \beta_{ii}I_i + \beta_{ij}I_j, \quad G_i := G_i(I_1, I_2, J_1, J_2) = -F_i - \mu_i - \sigma_i(J_1 + J_2), \quad j = 3 - i.$$

We start from the local stability of E_{df} .

Theorem 5.1. E_{df} is locally stable if $\mathcal{R}_0 < 1$.

Proof. The Jacobian matrix for state E_{df} reads

$$\begin{pmatrix} -\mu_1 & -\beta_{11}\widehat{S}_1 + \gamma_1 & -\sigma_1\widehat{S}_1 + g_1 & 0 & 0 & -\beta_{12}\widehat{S}_1 & -\sigma_1\widehat{S}_1 & 0 \\ 0 & \beta_{11}\widehat{S}_1 - k_1 & 0 & g_1 & 0 & \beta_{12}\widehat{S}_1 & 0 & 0 \\ 0 & 0 & \sigma_1\widehat{S}_1 - q_1 & \gamma_1 & 0 & 0 & \sigma_1\widehat{S}_1 & 0 \\ 0 & 0 & 0 & -r_1 & 0 & 0 & 0 & 0 \\ 0 & -\beta_{21}\widehat{S}_2 & -\sigma_2\widehat{S}_2 & 0 & -\mu_2 & -\beta_{22}\widehat{S}_2 + \gamma_2 & -\sigma_2\widehat{S}_2 + g_2 & 0 \\ 0 & \beta_{21}\widehat{S}_2 & 0 & 0 & 0 & \beta_{22}\widehat{S}_2 - k_2 & 0 & g_2 \\ 0 & 0 & -\sigma_2\widehat{S}_2 & 0 & 0 & 0 & \sigma_2\widehat{S}_2 - q_2 & \gamma_2 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -r_2 \end{pmatrix}.$$

Immediately, we get four negative eigenvalues: $-\mu_1, -\mu_2, -r_1, -r_2$. The remaining eigenvalues are the zeros of the characteristic polynomial of the matrix:

$$\begin{pmatrix} \beta_{11}\widehat{S}_1 - k_1 & 0 & \beta_{12}\widehat{S}_1 & 0 \\ 0 & \sigma_1\widehat{S}_1 - q_1 & 0 & \sigma_1\widehat{S}_1 \\ \beta_{21}\widehat{S}_2 & 0 & \beta_{22}\widehat{S}_2 - k_2 & 0 \\ 0 & -\sigma_2\widehat{S}_2 & 0 & \sigma_2\widehat{S}_2 - q_2 \end{pmatrix}.$$

This polynomial reads $P(\lambda) = P_1(\lambda)P_2(\lambda)$, where

$$P_1(\lambda) = \lambda^2 - (\beta_{11}\widehat{S}_1 - k_1 + \beta_{22}\widehat{S}_2 - k_2)\lambda + (\beta_{11}\widehat{S}_1 - k_1)(\beta_{22}\widehat{S}_2 - k_2) - \beta_{12}\beta_{21}\widehat{S}_1\widehat{S}_2,$$

$$P_2(\lambda) = \lambda^2 - (\sigma_1\widehat{S}_1 - q_1 + \sigma_2\widehat{S}_2 - q_2)\lambda + (\sigma_1\widehat{S}_1 - q_1)(\sigma_2\widehat{S}_2 - q_2) - \sigma_1\sigma_2\widehat{S}_1\widehat{S}_2.$$

It is easy to check that their discriminants are positive. The zeros of P_1 are negative if inequalities (4.12) and (4.13) hold. Analogously, P_2 has negative zeros if

$$\sigma_1\widehat{S}_1 - q_1 + \sigma_2\widehat{S}_2 - q_2 < 0 \quad (5.1)$$

and

$$(\sigma_1\widehat{S}_1 - q_1)(\sigma_2\widehat{S}_2 - q_2) > \sigma_1\sigma_2\widehat{S}_1\widehat{S}_2. \quad (5.2)$$

Inequality (5.2) can be transformed into inequality (4.11). According to Theorem 4.2, merging inequality (4.11)–(4.13) yields $\mathcal{R}_0 < 1$. Inequality (5.2) yields two exclusive possibilities: $\sigma_i\widehat{S}_i > q_i$ or

$$\sigma_i\widehat{S}_i < q_i. \quad (5.3)$$

The first case is contrary to inequality (5.1), whereas inequality (5.3), under condition (5.2), yields inequality (5.1). Hence, we replace inequality (5.1) by inequality (5.3). We rewrite inequality (5.3) as

$$\widehat{S}_i < \frac{q_i}{\sigma_i}.$$

Observe that the above inequality is weaker than inequality (4.11); hence, it is omitted in the thesis of Theorem 5.1.

Theorem 5.1 is in line with the analogical result from [24], where we also obtained the local stability of the given disease-free stationary for the basic reproduction number smaller than one.

5.1. Local stability of E_A

Now we provide a theorem guaranteeing the local stability of state E_A .

Theorem 5.2. E_A is locally stable if

$$\frac{\gamma_i}{\beta_{ii}} < S_i^* < \frac{k_i}{\beta_{ii}}, \quad (5.4)$$

$$(k_1 - \beta_{11}S_1^*)(k_2 - \beta_{22}S_2^*) > \beta_{12}\beta_{21}S_1^*S_2^*, \quad (5.5)$$

$$\beta_{ii}I_i^* + \beta_{ij}I_j^* + q_i > \sigma_i S_i, \quad j = 3 - i, \quad (5.6)$$

$$S_1^*S_2^* < \frac{r_1r_2}{\sigma_1\sigma_2}, \quad (5.7)$$

$$r_i(\beta_{ii}I_i^* + \beta_{ij}I_j^* - \sigma_i S_i^* + q_i) > \gamma_i(\beta_{ii}I_i^* + \beta_{ij}I_j^* + \sigma_i I_i^*), \quad (5.8)$$

$$\left(\frac{r_j}{\gamma_j}(\beta_{jj}I_j^* + \beta_{ji}I_i^* - \sigma_j S_j^* + q_j) - \beta_{jj}I_j^* - \beta_{ji}I_i^* - \sigma_j I_j^* \right) \cdot (\beta_{ii}I_i^* + \beta_{ij}I_j^* - \sigma_i S_i^* + q_i + r_i) > \sigma_i S_i^* \left(\frac{r_j \sigma_j}{\gamma_j} S_j^* + \sigma_j I_j^* \right), \quad j = 3 - i, \quad (5.9)$$

and

$$\prod_{m=1}^2 \left(r_m(\beta_{mm}I_m^* + \beta_{mj}I_j^* - \sigma_m S_m^* + q_m) - \gamma_m(\beta_{mm}I_m^* + \beta_{mj}I_j^* + \sigma_m I_m^*) \right) > \prod_{m=1}^2 (r_m \sigma_m S_m^* + \gamma_m \sigma_m I_m^*), \quad j = 3 - m. \quad (5.10)$$

Proof. Let us rearrange matrix $J(E_A)$ so that the characteristic polynomial of the new matrix remains the same. We get $M^* = \begin{pmatrix} M_1^* & M_2^* \\ 0 & M_3^* \end{pmatrix}$, where

$$M_1^* = \begin{pmatrix} -\beta_{11}I_1^* - \beta_{12}I_2^* - \mu_1 & -\beta_{11}S_1^* + \gamma_1 & 0 & -\beta_{12}S_1^* \\ \beta_{11}I_1^* + \beta_{12}I_2^* & \beta_{11}S_1^* - k_1 & 0 & \beta_{12}S_1^* \\ 0 & -\beta_{21}S_2^* & -\beta_{22}I_2^* - \beta_{21}I_1^* - \mu_2 & -\beta_{22}S_2^* + \gamma_2 \\ 0 & \beta_{21}S_2^* & \beta_{22}I_2^* + \beta_{21}I_1^* & \beta_{22}S_2^* - k_2 \end{pmatrix}$$

and

$$M_3^* = \begin{pmatrix} -\beta_{11}I_1^* - \beta_{12}I_2^* + \sigma_1 S_1^* - q_1 & \gamma_1 & \sigma_1 S_1^* & 0 \\ \beta_{11}I_1^* + \beta_{12}I_2^* + \sigma_1 I_1^* & -r_1 & \sigma_1 I_1^* & 0 \\ \sigma_2 S_2^* & 0 & -\beta_{22}I_2^* - \beta_{21}I_1^* + \sigma_2 S_2^* - q_2 & \gamma_2 \\ \sigma_2 I_2^* & 0 & \beta_{22}I_2^* + \beta_{21}I_1^* + \sigma_2 I_2^* & -r_2 \end{pmatrix}.$$

The form of $M_2^* \in M_4(\mathbb{R})$ is not needed for further computations.

We start by investigating matrix M_1^* . To simplify computations, we define auxiliary notations:

$$a_i = \beta_{ii}I_i^* + \beta_{ij}I_j^*, \quad u_i = \beta_{ii}S_i^* - \gamma_i, \quad t_i = k_i - \beta_{ii}S_i^*, \quad z_i = \beta_{ij}S_i^*, \quad \text{where } j = 3 - i. \quad (5.11)$$

Thanks to this simplification, matrix M_1^* reads

$$M_1^* = \begin{pmatrix} -a_1 - \mu_1 & -u_1 & 0 & -z_1 \\ a_1 & -t_1 & 0 & z_1 \\ 0 & -z_2 & -a_2 - \mu_2 & -u_2 \\ 0 & z_2 & a_2 & -t_2 \end{pmatrix}.$$

The characteristic polynomial of M_1^* has the form

$$P_1(\lambda) := \lambda^4 + c_3\lambda^3 + c_2\lambda^2 + c_1\lambda + c_0,$$

where

$$\begin{aligned} c_3 &= a_1 + a_2 + t_1 + t_2 + \mu_1 + \mu_2, \\ c_2 &= (a_1 + \mu_1)(a_2 + \mu_2) + (t_1 + t_2)(a_1 + a_2 + \mu_1 + \mu_2) + a_1u_1 + a_2u_2 + t_1t_2 - z_1z_2, \\ c_1 &= a_1a_2(t_1 + t_2 + u_1 + u_2) + \mu_1\mu_2(t_1 + t_2) + t_1t_2(a_1 + a_2) + a_1\mu_2(t_1 + t_2 + u_1) \\ &\quad + a_2\mu_1(t_1 + t_2 + u_2) + a_1u_1t_2 + a_2u_2t_1 + (\mu_1 + \mu_2)(t_1t_2 - z_1z_2), \\ c_0 &= a_1a_2(t_1 + u_1)(t_2 + u_2) + a_1t_2\mu_2(t_1 + u_1) + a_2t_1\mu_1(t_2 + u_2) + \mu_1\mu_2(t_1t_2 - z_1z_2). \end{aligned}$$

Observe that if

$$u_i > 0, \quad t_i > 0 \quad (5.12)$$

and

$$t_1t_2 - z_1z_2 > 0, \quad (5.13)$$

then each coefficient of P_1 is positive. Hence, from Descartes' rule of signs, we get that P_4 has real negative roots or complex roots with negative real parts. Substituting definition (5.11) into inequalities (5.12) and (5.13) provides inequalities (5.4) and (5.5), respectively.

Let us focus now on matrix M_3^* . After using notations:

$$\begin{aligned} t_i &= \beta_{ii}I_i^* + \beta_{ij}I_j^* - \sigma_iS_i^* + q_i, \quad a_i = \beta_{ii}I_i^* + \beta_{ij}I_j^* + \sigma_iI_i^*, \\ s_i &= \sigma_iS_i^*, \quad y_i = \sigma_iI_i^*, \quad \text{where } j = 3 - i, \end{aligned} \quad (5.14)$$

we rewrite M_3^* as

$$M_3^* = \begin{pmatrix} -t_1 & \gamma_1 & s_1 & 0 \\ a_1 & -r_1 & y_1 & 0 \\ s_2 & 0 & -t_2 & \gamma_2 \\ y_2 & 0 & a_2 & -r_2 \end{pmatrix}. \quad (5.15)$$

The characteristic polynomial of the matrix reads $P_3(\lambda) := \lambda^4 + c_3\lambda^3 + c_2\lambda^2 + c_1\lambda + c_0$, where

$$\begin{aligned} c_3 &= t_1 + t_2 + r_1 + r_2 > 0, \\ c_2 &= (r_1 + t_1)(r_2 + t_2) - s_1s_2 + r_1t_1 - \gamma_1a_1 + r_2t_2 - \gamma_2a_2, \\ c_1 &= \sum_{j=1}^2 \left((t_j + r_j)(t_{3-j}r_{3-j} - \gamma_{3-j}a_{3-j}) - s_j(r_{3-j}s_{3-j} + \gamma_{3-j}y_{3-j}) \right), \\ c_0 &= (\gamma_1a_1 - r_1t_1)(\gamma_2a_2 - r_2t_2) - (r_1s_1 + \gamma_1y_1)(r_2s_2 + \gamma_2y_2). \end{aligned}$$

Let us investigate the signs of the coefficients of polynomial P_3 . Observe that if inequality (5.6) holds, then $t_1, t_2 > 0$, which yields $c_3 > 0$. Conditions $r_1 r_2 > s_1 s_2$ and $r_i t_i > \gamma_i a_i$, which can be written as inequalities (5.7) and (5.8), respectively, yield $c_2 > 0$. See that $c_1 > 0$ if $(t_i + r_i)(t_j r_j - \gamma_j a_j) > s_i(r_j s_j + \gamma_j y_j)$ for $j = 3 - i$, which we transform to

$$(t_i + r_i) \left(\frac{r_j}{\gamma_j} t_j - a_j \right) > s_i \left(\frac{r_j}{\gamma_j} s_j + y_j \right).$$

Using expressions from (5.14), we rewrite the above inequality as inequality (5.9). Condition $c_0 > 0$ can be written as

$$\prod_{m=1}^2 (\gamma_m a_m - r_m t_m) > \prod_{m=1}^2 (r_m s_m + \gamma_m y_m)$$

With (5.14), the above inequality transforms into inequality (5.10).

Now let us strengthen conditions from Theorem 5.2 providing the local stability of E_A so that they have a more explicit form. Observe that the condition

$$S_i^* < \frac{q_i}{\sigma_i}. \quad (5.16)$$

yields fulfillment of inequality (5.6). Moreover, from definitions (2.2), clearly we have $r_i > q_i$. Hence, inequality (5.16) implies inequality (5.7).

Again relying on (2.2), we get $r_i > \gamma_i$. Instead of inequality (5.8), it is therefore enough to investigate the inequality

$$r_i(q_i - \sigma_i S_i^*) > \gamma_i \sigma_i I_i^*.$$

If inequality (5.16) holds, then the left-hand side of the above inequality is always positive. Using Eq (3.6), we transform this inequality into

$$S_i^* < \frac{r_i q_i - \frac{C_i \gamma_i \sigma_i}{\alpha_i + \mu_i}}{r_i \sigma_i - \frac{\gamma_i \sigma_i \mu_i}{\alpha_i + \mu_i}}. \quad (5.17)$$

From the definition of r_i , the denominator of the right-hand side of inequality (5.17) is positive if

$$(g_i + a_i + \alpha_i + \mu_i)(\mu_i + \alpha_i) + \gamma_i \alpha_i > 0,$$

which is always true. The positivity of the numerator of the right-hand side of inequality (5.17) is maintained if

$$C_i < \frac{r_i q_i (\mu_i + \alpha_i)}{\gamma_i \sigma_i}. \quad (5.18)$$

Now observe that since $r_i > \gamma_i$, inequality (5.9) can be, under fulfillment of inequality (5.16), strengthened to

$$(q_j - \sigma_j(S_j^* + I_j^*)) \cdot (\beta_{ii} I_i^* + \beta_{ij} I_j^* - \sigma_i S_i^* + q_i + r_i) > \sigma_i S_i^* \left(\frac{r_j \sigma_j}{\gamma_j} S_j^* + \sigma_j I_j^* \right). \quad (5.19)$$

If inequality (5.16) holds, then one must fulfill

$$S_i^* + I_i^* < \frac{q_i}{\sigma_i}. \quad (5.20)$$

so that inequality (5.19) makes sense. Using Eq (3.6), we transform inequality (5.20) into

$$S_i^* < \frac{q_i(\mu_i + \alpha_i) - C_i\sigma_i}{\sigma_i\alpha_i}, \quad (5.21)$$

which is reasonable if

$$C_i < \frac{q_i(\mu_i + \alpha_i)}{\sigma_i}. \quad (5.22)$$

Observe that inequality (5.22) is stricter than inequality (5.18). Rewriting inequality (5.19), we get

$$\begin{aligned} & (\beta_{ii}I_i^* + \beta_{ij}I_j^*)(q_j - \sigma_j(S_j^* + I_j^*)) + (q_i + r_i)q_j \\ & > \left(\frac{r_j}{\gamma_j} - 1\right)\sigma_1\sigma_2S_1^*S_2^* + (\sigma_iq_jS_i^* + (q_i + r_i)\sigma_j(S_j^* + I_j^*)). \end{aligned}$$

Using again Eq (3.6), we transform the above inequality into

$$\begin{aligned} & -\frac{\beta_{ij}\sigma_j\mu_j^2}{(\mu_j + \alpha_j)^2}(S_j^*)^2 - \frac{\beta_{ii}\mu_i}{\mu_i + \alpha_i} \cdot \frac{\sigma_j\mu_j}{\mu_j + \alpha_j}S_1^*S_2^* + \left(\frac{r_j}{\gamma_j} - 1\right)\sigma_1\sigma_2S_1^*S_2^* \\ & + \left(\frac{\beta_{ii}C_i}{\mu_i + \alpha_i} \cdot \frac{\beta_{ij}C_j}{\mu_j + \alpha_j}\right)\frac{\sigma_j\mu_j}{\mu_j + \alpha_j}S_j^* - \frac{\beta_{ij}\mu_j}{\mu_j + \alpha_j}\left(q_j - \frac{\sigma_jC_j}{\mu_j + \alpha_j}\right)S_j^* \\ & + \frac{\alpha_j(q_i + r_i)}{\mu_j + \alpha_j}S_j^* + \left(q_j - \frac{\sigma_jC_j}{\mu_j + \alpha_j}\right)\left(\frac{\beta_{ii}(C_i - \mu_iS_i^*)}{\mu_i + \alpha_i} + \frac{\beta_{ij}C_j}{\mu_j + \alpha_j}\right) \\ & + \sigma_iq_jS_i^* + \frac{(q_i + r_i)\sigma_jC_j}{\mu_j + \alpha_j} + (q_i + r_i)q_j > 0, \quad j = 3 - i. \end{aligned} \quad (5.23)$$

Now we use the dependence $r_i > \gamma_i$ and transform inequality (5.10) into

$$\prod_{m=1}^2 (r_m(q_m - \sigma_mS_m^*) - \gamma_m\sigma_mI_m^*) > \prod_{m=1}^2 (r_m\sigma_mS_m^* + \gamma_m\sigma_mI_m^*),$$

which can be simplified to

$$\frac{\sigma_1}{q_1}(S_1^* + I_1^*) + \frac{\sigma_2}{q_2}(S_2^* + I_2^*) < 1. \quad (5.24)$$

Clearly, inequality (5.24) is stricter than inequalities (5.16) and (5.21).

Using Eq (3.6), we rewrite inequality (5.24) as

$$\sum_{j=1}^2 \left(\frac{\sigma_j(S_j^*\alpha_j + C_j)}{q_j(\mu_j + \alpha_j)} \right) < 1. \quad (5.25)$$

We finally conclude that

Corollary 2. *If (5.4), (5.5), (5.17), (5.22), (5.23) and (5.25), then E_A is locally stable.*

Let us treat the left-hand side of inequality (5.23) as a quadratic trinomial $P(S_j^*)$. If inequality (5.22) holds, then the condition $C_i > \sigma_iS_i^*$ suffices for the constant of $P(S_j^*)$ to be positive. Hence, the form of $P(S_j^*)$ implies that inequality (5.23) is true for $0 < S_j^* < \mathcal{S}$, where \mathcal{S} is the positive zero of $P(S_j^*)$.

5.2. Local stability of E_B

Now we provide the theorem indicating the conditions for the local stability of state E_B :

Theorem 5.3. E_B is locally stable if

$$\bar{S}_i < \frac{k_i}{\beta_{ii}}, \quad (5.26)$$

$$\bar{S}_1 \bar{S}_2 < \frac{r_1 r_2}{\beta_{12} \beta_{21}}, \quad (5.27)$$

$$r_i(\sigma_i(\bar{J}_1 + \bar{J}_2) - \beta_{ii}\bar{S}_i + k_i) > g_i(\sigma_i(\bar{J}_1 + \bar{J}_2) + \beta_{ii}\bar{J}_i), \quad (5.28)$$

$$\begin{aligned} & \left(\frac{r_j}{g_j}(\sigma_j(\bar{J}_1 + \bar{J}_2) - \beta_{jj}\bar{S}_j + k_j) - \sigma_j(\bar{J}_1 + \bar{J}_2) - \beta_{jj}\bar{J}_j \right) \\ & \cdot (\sigma_i(\bar{J}_1 + \bar{J}_2) - \beta_{ii}\bar{S}_i + k_i + r_i) > \beta_{12}\beta_{21}\bar{S}_i \left(\frac{r_j}{g_j}\bar{S}_j + \bar{J}_j \right), \quad j = 3 - i, \end{aligned} \quad (5.29)$$

$$\begin{aligned} & \prod_{m=1}^2 \left(g_m(\sigma_m(\bar{J}_1 + \bar{J}_2) + \beta_{mm}\bar{J}_m) - r_m(\sigma_m(\bar{J}_1 + \bar{J}_2) - \beta_{mm}\bar{S}_m + k_m) \right) \\ & > \prod_{m=1}^2 \left(r_m\beta_{mj}\bar{S}_m + g_m\beta_{mj}\bar{J}_m \right), \quad j = 3 - m. \end{aligned} \quad (5.30)$$

Proof. Similarly as in the proof of Theorem 5.2, we transform matrix $J(E_B)$ into $M_B = \begin{pmatrix} \bar{M}_1 & \bar{M}_2 \\ 0 & \bar{M}_3 \end{pmatrix}$, where

$$\bar{M}_1 = \begin{pmatrix} -\mu_1 - \sigma_1(\bar{J}_1 + \bar{J}_2) & -\sigma_1\bar{S}_1 + g_1 & 0 & -\sigma_1\bar{S}_1 \\ \sigma_1(\bar{J}_1 + \bar{J}_2) & \sigma_1\bar{S}_1 - q_1 & 0 & \sigma_1\bar{S}_1 \\ 0 & -\sigma_2\bar{S}_2 & -\mu_2 - \sigma_2(\bar{J}_1 + \bar{J}_2) & -\sigma_2\bar{S}_2 + g_2 \\ 0 & \sigma_2\bar{S}_2 & \sigma_2(\bar{J}_1 + \bar{J}_2) & \sigma_2\bar{S}_2 - q_2 \end{pmatrix},$$

$$\bar{M}_3 = \begin{pmatrix} \beta_{11}\bar{S}_1 - k_1 - \sigma_1(\bar{J}_1 + \bar{J}_2) & g_1 & \beta_{12}\bar{S}_1 & 0 \\ \sigma_1(\bar{J}_1 + \bar{J}_2) + \beta_{11}\bar{J}_1 & -r_1 & \beta_{12}\bar{J}_1 & 0 \\ \beta_{21}\bar{S}_2 & 0 & \beta_{22}\bar{S}_2 - k_2 + \sigma_2(\bar{J}_1 + \bar{J}_2) & g_2 \\ \beta_{21}\bar{J}_2 & 0 & \sigma_2(\bar{J}_1 + \bar{J}_2) + \beta_{22}\bar{J}_2 & -r_2 \end{pmatrix}.$$

We start from matrix \bar{M}_1 . After using notations:

$$a_i = \sigma_i(\bar{J}_1 + \bar{J}_2), \quad s_i = \sigma_i\bar{S}_i, \quad t_i = q_i - \sigma_i\bar{S}_i, \quad (5.31)$$

we transform \bar{M}_1 to

$$\bar{M}_1 = \begin{pmatrix} -a_1 - \mu_1 & g_1 - s_1 & 0 & -s_1 \\ a_1 & -t_1 & 0 & s_1 \\ 0 & -s_2 & -a_2 - \mu_2 & g_2 - s_2 \\ 0 & s_2 & a_2 & -t_2 \end{pmatrix}.$$

The characteristic polynomial of matrix \bar{M}_1 reads $P_1(\lambda) = \lambda^4 + c_3\lambda^3 + c_2\lambda^2 + c_1\lambda + c_0$, where

$$\begin{aligned} c_3 &= a_1 + a_2 + t_1 + t_2 + \gamma_1 + \gamma_2, \\ c_2 &= t_1t_2 - s_1s_2 + a_1(s_1 - g_1) + a_2(s_2 - g_2) + (t_1 + t_2)(a_1 + \mu_1 + a_2 + \mu_2) + (a_1 + \mu_1)(a_2 + \mu_2), \\ c_1 &= a_1a_2(s_1 + s_2 - g_1 - g_2) + (\mu_1 + \mu_2)(t_1t_2 - s_1s_2) + a_1(t_2 + \mu_2)(s_1 - g_1) + a_2(t_1 + \mu_1)(s_2 - g_2), \\ &\quad + a_1t_1(t_2 + \mu_2) + a_2t_2(t_1 + \mu_1) + (a_1a_2 + \mu_1\mu_2)(t_1 + t_2) + a_1t_2\mu_2 + a_2t_1\mu_1, \\ c_0 &= (t_1t_2 - s_1s_2)(\mu_1\mu_2 + a_1a_2) + a_1t_2(a_2 + \mu_2)(s_2 - g_2) + t_1t_2(a_1\mu_2 + a_2\mu_1) \\ &\quad + a_2t_1(a_1 + \mu_1)(s_1 - g_1) + a_1a_2(s_1 - g_1)(s_2 - g_2) + a_1a_2s_1s_2. \end{aligned}$$

Observe that if

$$s_1 > g_1, \quad s_2 > g_2, \quad (5.32)$$

and

$$t_1t_2 > s_1s_2 \quad (5.33)$$

then $c_2, c_1, c_0 > 0$. Hence, from Descartes' rule of signs, we get that P_1 has real negative roots or complex roots with negative real parts.

Using definitions (5.31), we rewrite inequality (5.32) as inequality (5.6) and inequality (5.33) as

$$\frac{\sigma_1}{q_1}\bar{S}_1 + \frac{\sigma_2}{q_2}\bar{S}_2 < 1. \quad (5.34)$$

Now we focus on matrix \bar{M}_3 . With the use of expressions,

$$\begin{aligned} t_i &= \sigma_i(\bar{J}_1 + \bar{J}_2) - \beta_{ii}\bar{S}_i + k_i, \quad a_i = \sigma_i(\bar{J}_1 + \bar{J}_2) + \beta_{ii}\bar{J}_i, \\ s_i &= \beta_{ij}\bar{S}_i, \quad y_i = \beta_{ij}\bar{J}_i, \quad \text{where } j = 3 - i, \end{aligned} \quad (5.35)$$

we rewrite \bar{M}_3 as

$$\bar{M}_3 = \begin{pmatrix} -t_1 & g_1 & s_1 & 0 \\ a_1 & -r_1 & y_1 & 0 \\ s_2 & 0 & -t_2 & g_2 \\ y_2 & 0 & a_2 & -r_2 \end{pmatrix},$$

which has a similar form as matrix M_3^* from (5.15). This similarity allows us to apply reasoning for M_3^* to \bar{M}_3 . Analogically to conditions (5.6)–(5.10), we obtain inequalities (5.26)–(5.30).

Similarly as for Theorem 5.2, let us strengthen conditions from Theorem 5.3 providing the local stability of E_B . Since $r_i > g_i$, we replace inequality (5.28) by

$$r_i(k_i - \beta_{ii}\bar{S}_i) > g_i\beta_{ii}\bar{J}_i, \quad (5.36)$$

which obviously requires fulfillment of inequality (5.26). Using Eq (3.8), we express the above inequality as

$$\bar{S}_i < \frac{r_i(\mu_i + \alpha_i)k_i - C_i\beta_{ii}g_i}{\beta_{ii}((a_i + \gamma_i + \alpha_i + \mu_i)\mu_i + r_i\alpha_i)}, \quad (5.37)$$

under fulfillment of

$$C_i < \frac{r_i(\mu_i + \alpha_i)k_i}{\beta_{ii}g_i}. \quad (5.38)$$

Again using the dependence $r_i > g_i$, we simplify inequality (5.29) to

$$\left(\frac{r_j}{g_j}(k_j - \beta_{jj}\bar{S}_j) - \beta_{jj}\bar{J}_j\right)(\sigma_i(\bar{J}_1 + \bar{J}_2) - \beta_{ii}\bar{S}_i + k_i + r_i) > \beta_{12}\beta_{21}\bar{S}_i\left(\frac{r_j}{g_j}\bar{S}_j + \bar{J}_j\right), \quad j = 3 - i. \quad (5.39)$$

Since inequality (5.26) holds, it is enough that inequality (5.36) holds so that inequality (5.39) makes sense.

Inequality (5.30) can be strengthened by

$$\prod_{m=1}^2 (g_m\beta_{mm}J_m + r_m(\beta_{mm}\bar{S}_m - k_m)) > \prod_{m=1}^2 (r_m\beta_{mj}\bar{S}_m + g_m\beta_{mj}\bar{J}_m),$$

which can be expressed as

$$\begin{aligned} &(\beta_{11}\beta_{22} - \beta_{12}\beta_{21})(g_1\bar{J}_1 + r_1\bar{S}_1)(g_2\bar{J}_2 + r_2\bar{S}_2) \\ &+ \beta_{11}k_2r_2(r_1\bar{S}_1 - g_1\bar{J}_1) + \beta_{22}k_2r_1(r_2\bar{S}_2 - g_2\bar{J}_2) + r_1r_2k_1k_2 > 0. \end{aligned} \quad (5.40)$$

The above inequality is always true if

$$\beta_{11}\beta_{22} > \beta_{12}\beta_{21} \quad (5.41)$$

and

$$r_i\bar{S}_i > g_i\bar{J}_i. \quad (5.42)$$

Using Eq (3.8), we rewrite inequality (5.42) as

$$\bar{S}_i > \frac{C_i g_i}{\mu_i g_i + \mu_i r_i + \alpha_i r_i}. \quad (5.43)$$

Let us compare inequalities (5.26) and (5.27). Observe that $r_i > k_i$. Moreover, if inequality (5.41) holds, then inequality (5.26) is stronger than inequality (5.27).

Finally, we conclude that

Corollary 3. *If inequalities (5.26), (5.37), (5.38), (5.39), (5.40), (5.41), and (5.43) hold, then E_B is locally stable.*

6. Postulated local stability of the endemic state: numerical simulation

In Subsection 3.2, we provided only a slight analysis of the existence of the endemic stationary state E_E , with two diseases present. We are therefore not certain if this state exists. Furthermore, the complexity of the proper Jacobian matrix does not allow us to obtain the explicit conditions for local stability of such a postulated equilibrium. However, the conditions from Theorems 5.2 and 5.3 restrict a set of parameters' values guaranteeing the local stability of existing states E_A and E_B . Such restriction suggests that there should be ranges of the values for the E_E local stability under its existence. Indicating these ranges is difficult, even numerically, because of the system's intricacy. For this reason, for each parameter, we only give specific values that yield the desirable local stability. We rely on the values from [10] that concern *TB* and *COVID-19*. In our system, these diseases correspond to diseases *A* and *B*, respectively. Since paper [10] relates to co-infection dynamics in a homogeneous population,

we arbitrarily choose the values of incompatible parameters from our system. These values are chosen so that we reach the E_E local stability. In Table 1, one can find the taken numbers.

Table 1. The parameters' values providing the local stability of postulated state E_E . Each value has the unit day^{-1} . The values of C_1 , C_2 , β_{12} , β_{21} , β_{22} are indicated discretely, whereas the remaining numbers can be found in [10].

Symbol	Value
C_1	130
C_2	10
β_{11}	$2 \cdot 10^{-6}$
β_{12}	$8 \cdot 10^{-6}$
β_{21}	$3 \cdot 10^{-6}$
β_{22}	$6.5 \cdot 10^{-6}$
σ_1, σ_2	$5.5 \cdot 10^{-6}$
γ_1, γ_2	0.02
μ_1, μ_2	$\frac{1}{59.365}$
g_1, g_2	0.015
α_1, α_2	0.004
a_1, a_2	0.0018

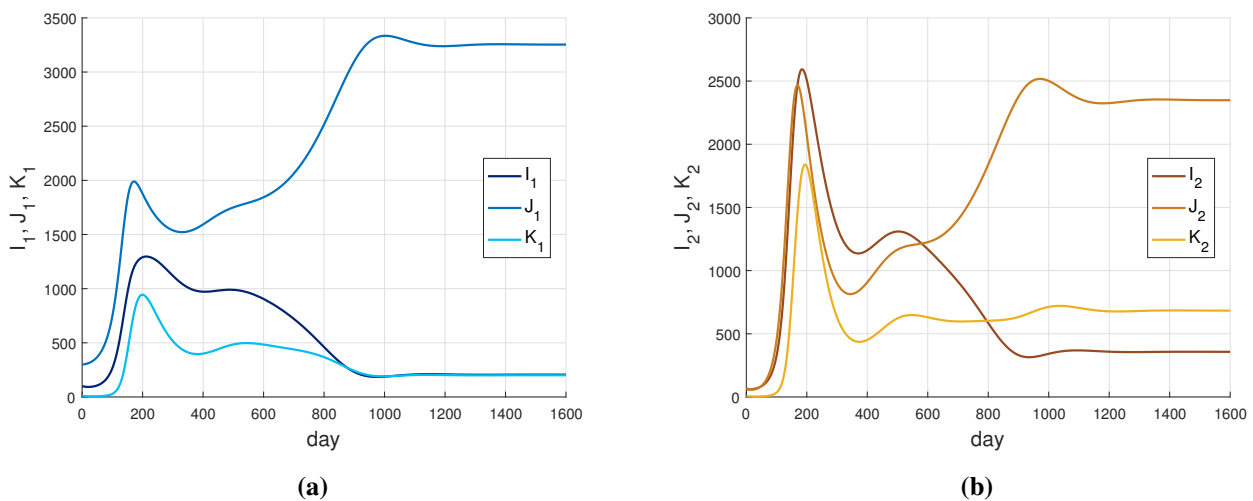


Figure 2. Dependence of the infected variables for the low-risk (a) and the high-risk (b) subpopulation of system 2.1 on time. Each curve for the particular variable has a different color. In Figure 2(a) the curves for variables J_1 and K_1 merge because of the similar values of these variables.

We illustrate the local stability of E_E on the plots showing the dependence of the system's solution on time for each particular variable. For the illustration, we use the Matlab software, which provides a built-in *ode45* function. This function numerically solves a given differential equation system for a specified initial condition [27]. For the simulation, we take the parameters' values from Table 1 and

the arbitrarily chosen initial condition

$$(S_1(0), I_1(0), J_1(0), K_1(0), S_2(0), I_2(0), J_2(0), K_2(0)) = (5000, 100, 300, 10, 500, 60, 70, 5).$$

Figures 2–3 depict the result of the simulation. For the figures' transparency, we show plots for the infected variables for each subpopulation and the non-infected variables in separate picture graphs. The obtained figures suggest the existence of the stationary state E_e that is locally stable for the parameter values from Table 1.

Now for the illustrated example of epidemic, we depict the relative sizes of the infections for time t that we define by ratios:

$$R_1(t) := \frac{I_1(t) + K_1(t)}{J_1(t) + K_1(t)}, \quad R_2(t) := \frac{I_2(t) + K_2(t)}{J_2(t) + K_2(t)}, \quad R(t) := \frac{I_1(t) + I_2(t) + K_1(t) + K_2(t)}{J_1(t) + J_2(t) + K_1(t) + K_2(t)}.$$

These ratios correspond to LS , HS , and the whole population, respectively, and in our case represent the number of TB -infected individuals relative to the number of COVID-infected ones. Figure 4 shows the dependence of the relative sizes on time.

For the last point of the simulation timescale, i.e., $\bar{t} = 1600$, we get $R_1(\bar{t}) = 0.1176$ and $R_2(\bar{t}) = 0.3432$. Plots from the figure suggest the convergence of each relative size. We therefore state that for the stabilized co-infection epidemic, for one TB -infected person, there are approximately nine and three COVID-infected people in LS and HS , respectively.

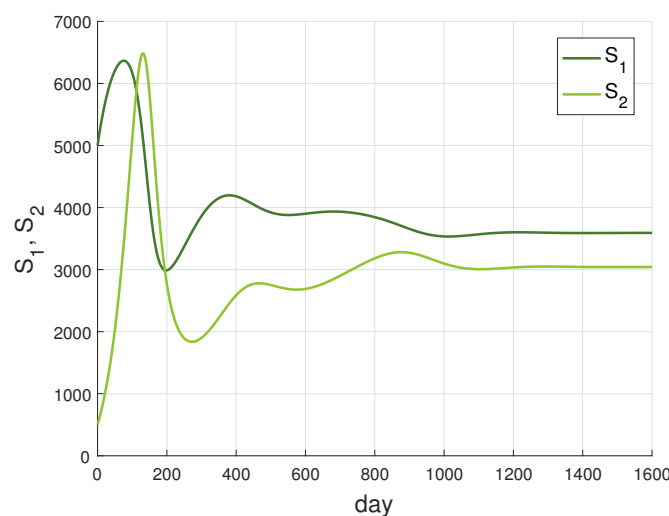


Figure 3. Dependence of the non-infected variables of system 2.1 on time.

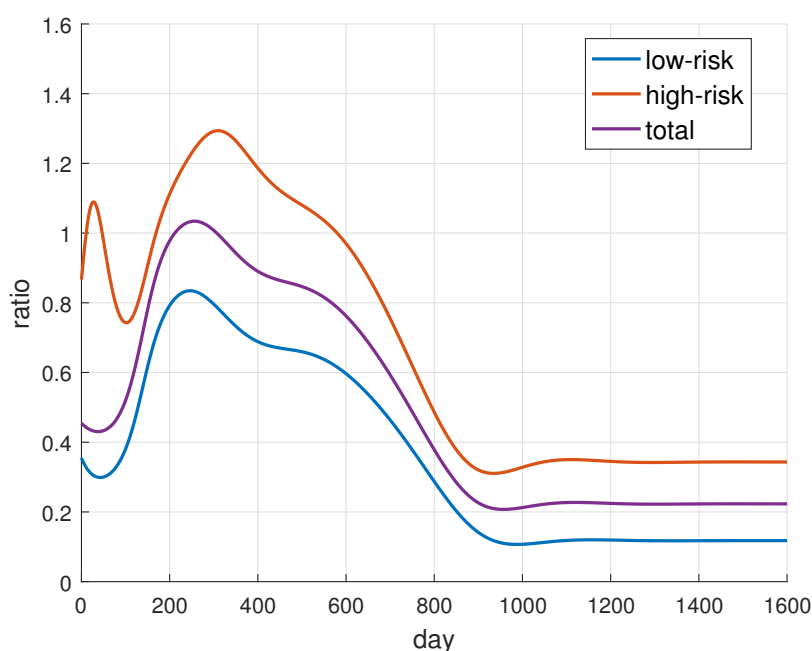


Figure 4. The relative sizes of the infections.

7. Conclusions

In this paper, we proposed and analyzed the continuous-time model (2.1) describing co-infection in a heterogeneous population, in which we distinguish two subpopulations. These subpopulations, low-risk LS and high-risk HS , differ in the risk of getting infected by any of two diseases, called disease A (DA) and disease B (DB). The values of the parameters for every subpopulation are different, which guarantees complete population heterogeneity. System (2.1) has three stationary states: disease-free (E_{df}), with sole DA or DB (E_A and E_B). We also suspect that the endemic state, with two diseases present, exists, but we did not manage to prove it because of complicated computations. State E_{df} exists unconditionally, while provided conditions determine the existence of E_A and E_B . For state E_e , we only gave insight into its existence because of the complexity of the computations. For system (2.1), we computed the basic reproduction number \mathcal{R}_0 . This number is the maximum of two terms, whose forms depend on parameters corresponding to the particular sole infection. Later, we investigated the local stability of the stationary state. State E_{df} is locally stable if $\mathcal{R}_0 < 1$, which is expected. Analysis of the local stability for E_A and E_B provided the list of conditions. Importantly, the parameters from both diseases affect the local stability of both states.

The proposed model expands the system from [24], where we investigated the epidemic dynamics of one disease in heterogeneous populations. In that system, there are only two stationary states: the disease-free state and the endemic state, which is a counterpart of state E_A of system (2.1). The results for their local stabilities are analogical to those for state E_{df} and E_A in this paper.

The next step of our work will be an analysis of the proposed model with some assumptions simplifying this form. We hope to obtain the endemic state of the simplified model and get explicit results concerning its local stability.

Use of AI tools declaration

The authors declare they have not used Artificial Intelligence (AI) tools in the creation of this article.

Conflict of interest

The author declares there is no conflict of interest.

References

1. L. Almeida, P. A. Bliman, G. Nadin, B. Perthame, N. Vauchelet, Final size and convergence rate for an epidemic in heterogeneous population, *Math. Models Methods Appl. Sci.*, **31** (2021), 1021–1051. <https://doi.org/10.1142/S0218202521500251>
2. G. Ellison, Implications of heterogeneous SIR models for analyses of COVID-19, *Rev. Econ. Design*, **28** (2024), 651–687. <https://doi.org/10.1007/s10058-024-00355-z>
3. X. Yan, K. Li, Z. Lei, J. Luo, Q. Wang, S. Wei, Prevalence and associated outcomes of coinfection between SARS-CoV-2 and influenza: a systematic review and meta-analysis, *Int. J. Infect. Dis.*, **136** (2023), 29–36. <https://doi.org/10.1016/j.ijid.2023.08.021>
4. J. Sandlund, P. Naucle, S. Dashti, A. Shokri, S. Eriksson, M. Hjertqvist, et al., Bacterial coinfections in travelers with malaria: rationale for antibiotic therapy, *J. Clin. Microbiol.*, **51** (2013), 15–21. <https://doi.org/10.1128/JCM.02149-12>
5. R. B. Birger, R. D. Kouyos, T. Cohen, E. C. Griffiths, S. Huijben, M. J. Mina, et al., The potential impact of coinfection on antimicrobial chemotherapy and drug resistance, *Trends Microbiol.*, **23** (2015), 537–544. <https://doi.org/10.1016/j.tim.2015.05.002>
6. J. Marcinkiewicz, Increase in the incidence of invasive bacterial infections following the COVID-19 pandemic: potential links with decreased herd trained immunity – a novel concept in medicine, *Pol. Arch. Intern. Med.*, **134** (2024), 16794. <https://doi.org/10.20452/pamw.16794>
7. A. Sophonsri, C. Kelsom, M. Lou, P. Nieberg, A. Wong-Beringer, Risk factors and outcome associated with coinfection with carbapenem-resistant *Klebsiella pneumoniae* and carbapenem-resistant *Pseudomonas aeruginosa* or *Acinetobacter baumannii*: a descriptive analysis, *Front. Cell. Infect. Microbiol.*, **13** (2023), 1231740. <https://doi.org/10.3389/fcimb.2023.1231740>
8. L. R. Idrus, N. Fitria, F. D. Purba, J. W. C. Alffenaar, M. J. Postma, Analysis of health-related quality of life and incurred costs among human immunodeficiency virus, tuberculosis, and tuberculosis/HIV coinfecting outpatients in Indonesia, *Value Health Reg. Issues*, **41** (2024), 32–40. <https://doi.org/10.1016/j.vhri.2023.10.010>
9. D. L. Silva, C. M. Lima, V. C. R. Magalhaes, L. M. Baltazar, N. T. A. Peres, R. B. Caligiorno, et al., Fungal and bacterial coinfections increase mortality of severely ill COVID-19 patients, *J. Hosp. Infect.*, **113** (2021), 145–154. <https://doi.org/10.1016/j.jhin.2021.04.001>
10. F. Inayaturohmat, N. Anggriani, A. K. Supriatna, M. H. A. Biswas, A systematic literature review of mathematical models for coinfections: tuberculosis, malaria, and HIV/AIDS, *J. Multidiscip. Healthcare*, **2024** (2024), 1091–1109. <https://doi.org/10.2147/JMDH.S446508>

11. J. Li, L. Wang, H. Zhao, Z. Ma, Dynamical behavior of an epidemic model with coinfection of two diseases, *Rocky Mt. J. Math.*, **38** (2008), 1457–1479. <https://doi.org/10.1216/RMJ-2008-38-5-1457>
12. K. G. Mekonen, L. L. Obsu, Mathematical modeling and analysis for the co-infection of COVID-19 and tuberculosis, *Heliyon*, **8** (2022). <https://doi.org/10.1016/j.heliyon.2022.e11195>
13. F. Inayaturohmat, N. Anggriani, A. K. Supriatna, A mathematical model of tuberculosis and COVID-19 coinfection with the effect of isolation and treatment, *Front. Appl. Math. Stat.*, **8** (2022), 958081. <https://doi.org/10.3389/fams.2022.958081>
14. A. Din, S. Amine, A. Allali, A stochastically perturbed co-infection epidemic model for COVID-19 and hepatitis B virus, *Nonlinear Dyn.*, **111** (2023), 1921–1945. <https://doi.org/10.1007/s11071-022-07899-1>
15. A. M. Elaiw, A. S. Shflot, A. D. Hobiny, Stability analysis of SARS-CoV-2/HTLV-I coinfection dynamics model, *Mathematics*, **8** (2022), 6136–6166. <https://doi.org/10.3934/math.2023310>
16. M. A. Hye, M. H. A. Biswas, M. F. Uddin, M. M. Rahman, A mathematical model for the transmission of co-infection with COVID-19 and kidney disease, *Sci. Rep.*, **14** (2024), 5680. <https://doi.org/10.1038/s41598-024-56399-2>
17. E. F. Obiajulu, A. Oname, S. C. Inyama, U. H. Diala, S. A. AlQahtani, M. S. Al-Rakhami, et al., Analysis of a non-integer order mathematical model for double strains of dengue and COVID-19 co-circulation using an efficient finite-difference method, *Sci. Rep.*, **13** (2023), 17787. <https://doi.org/10.1038/s41598-023-44825-w>
18. J. Bruchfeld, M. Correia-Neves, G. Kaellenius, Tuberculosis and HIV coinfection, *Cold Spring Harbor Perspect. Med.*, **4** (2015), a017871. <https://doi.org/10.1101/cshperspect.a017871>
19. S. W. Teklu, Y. F. Abebaw, B. B. Terefe, D. K. Mamo, HIV/AIDS and TB co-infection deterministic model bifurcation and optimal control analysis, *Inf. Med. Unlocked*, **41** (2023), 101328. <https://doi.org/10.1016/j.imu.2023.101328>
20. T. K. Ayele, E. F. Doungmo Goufo, S. Mugisha, Co-infection mathematical model for HIV/AIDS and tuberculosis with optimal control in Ethiopia, *PLoS One*, **19** (2024), e0312539. <https://doi.org/10.1371/journal.pone.0312539>
21. F. Dayan, N. Ahmed, A. Bariq, A. Akgül, M. Jawaz, M. Rafq, et al., Computational study of a co-infection model of HIV/AIDS and hepatitis C virus models, *Sci. Rep.*, **13** (2023), 21938. <https://doi.org/10.1038/s41598-023-48085-6>
22. R. I. Gweryina, C. E. Madubueze, V. P. Bajiya, F. E. Esla, Modeling and analysis of tuberculosis and pneumonia co-infection dynamics with cost-effective strategies, *Results Control Optim.*, **10** (2023), 100210. <https://doi.org/10.1016/j.rico.2023.100210>
23. M. Choiński, M. Bodzioch, U. Foryś, Simple criss-cross model of epidemic for heterogeneous populations, *Commun. Nonlinear Sci. Numer. Simul.*, **79** (2019), 104920. <https://doi.org/10.1016/j.cnsns.2019.104920>
24. M. Bodzioch, M. Choiński, U. Foryś, SIS criss-cross model of tuberculosis in heterogeneous population, *Discrete Contin. Dyn. Syst. - Ser. B*, **24** (2019), 2169–2188. <https://doi.org/10.3934/dcdsb.2019089>

25. J. Romaszko, A. Siemaszko, M. Bodzioch, A. Buciński, A. Doboszyńska, Active case finding among homeless people as a means of reducing the incidence of pulmonary tuberculosis in general population, *Adv. Exp. Med. Biol.*, **911** (2016), 67–76. https://doi.org/10.1007/5584_2016_225
26. P. van den Driessche, J. Watmough, Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission, *Math. Biosci.*, **180** (2002), 29–48. [https://doi.org/10.1016/S0025-5564\(02\)00108-6](https://doi.org/10.1016/S0025-5564(02)00108-6)
27. MathWorks, ode45, 2006. Available from: <https://www.mathworks.com/help/matlab/ref/ode45.html>. last access: 18th February, 2005.



AIMS Press

© 2025 the Author(s), licensee AIMS Press. This is an open access article distributed under the terms of the Creative Commons Attribution License (<https://creativecommons.org/licenses/by/4.0>)