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A CONTINUOUS–TIME *SIS* CRISS-CROSS MODEL OF CO–INFECTION IN A HETEROGENEOUS POPULATION

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ABSTRACT

In a population we indicate two subpopulations, a low–risk (LS) and a high–risk (HS) subpopulation, that relate to the risk of getting infected. LS and HS have accordingly 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 mean a density of individuals from the given subpopulation that are infected by a pathogen of disease which we call disease A (DA). Similarly, we define J_i as a density of individuals suffering from disease B (DB). A 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 introduces transmission rates: $\beta_{11}, \beta_{22}, \beta_{12}, \beta_{21}$ reflecting transmission: among LS, among HS, from HS to LS and from LS to HS, respectively. Indicating four different rates means 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 differs 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 a 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 reads

$$\dot{S}_1 = C_1 - \beta_{11} S_1 I_1 - \beta_{12} S_1 I_2 + \gamma_1 I_1 - \mu_1 S_1 - \sigma_1 S_1 (J_1 + J_2) + g_1 J_1, \tag{1a}$$

$$\dot{I}_1 = \beta_{11} S_1 I_1 + \beta_{12} S_1 I_2 - (\gamma_1 + \alpha_1 + \mu_1) I_1 - \sigma_1 I_1 (J_1 + J_2) + g_1 K_1, \tag{1b}$$

$$\dot{J}_1 = \sigma_1 S_1 (J_1 + J_2) - (g_1 + a_1 + \mu_1) J_1 - \beta_{11} J_1 I_1 - \beta_{12} J_1 I_2 + \gamma_1 K_1, \tag{1c}$$

$$\dot{K}_1 = \sigma_1 I_1 (J_1 + J_2) + \beta_{11} J_1 I_1 + \beta_{12} J_1 I_2 - (g_1 + a_1 + \gamma_1 + \alpha_1 + \mu_1) K_1, \tag{1d}$$

$$\dot{S}_2 = C_2 - \beta_{22} S_2 I_2 - \beta_{21} S_2 I_1 + \gamma_2 I_2 - \mu_2 S_2 - \sigma_2 S_2 (J_1 + J_2) + g_2 J_2, \tag{1e}$$

$$\dot{I}_2 = \beta_{22} S_2 I_2 + \beta_{21} S_2 I_1 - (\gamma_2 + \alpha_2 + \mu_2) I_2 - \sigma_2 I_2 (J_1 + J_2) + g_2 K_2, \tag{1f}$$

$$\dot{J}_2 = \sigma_2 S_2 (J_1 + J_2) - (g_2 + a_2 + \mu_2) J_2 - \beta_{22} J_2 I_2 - \beta_{21} J_2 I_1 + \gamma_2 K_2, \tag{1g}$$

$$\dot{K}_2 = \sigma_2 I_2 (J_1 + J_2) + \beta_{22} J_2 I_2 + \beta_{21} J_2 I_1 - (g_2 + a_2 + \gamma_2 + \alpha_2 + \mu_2) K_2. \tag{1h}$$

Each parameter is fixed and positive. In particular, every parameter besides C_i is in the range $(0, 1)$. Figure 1 is a schematic drawing of the proposed model.

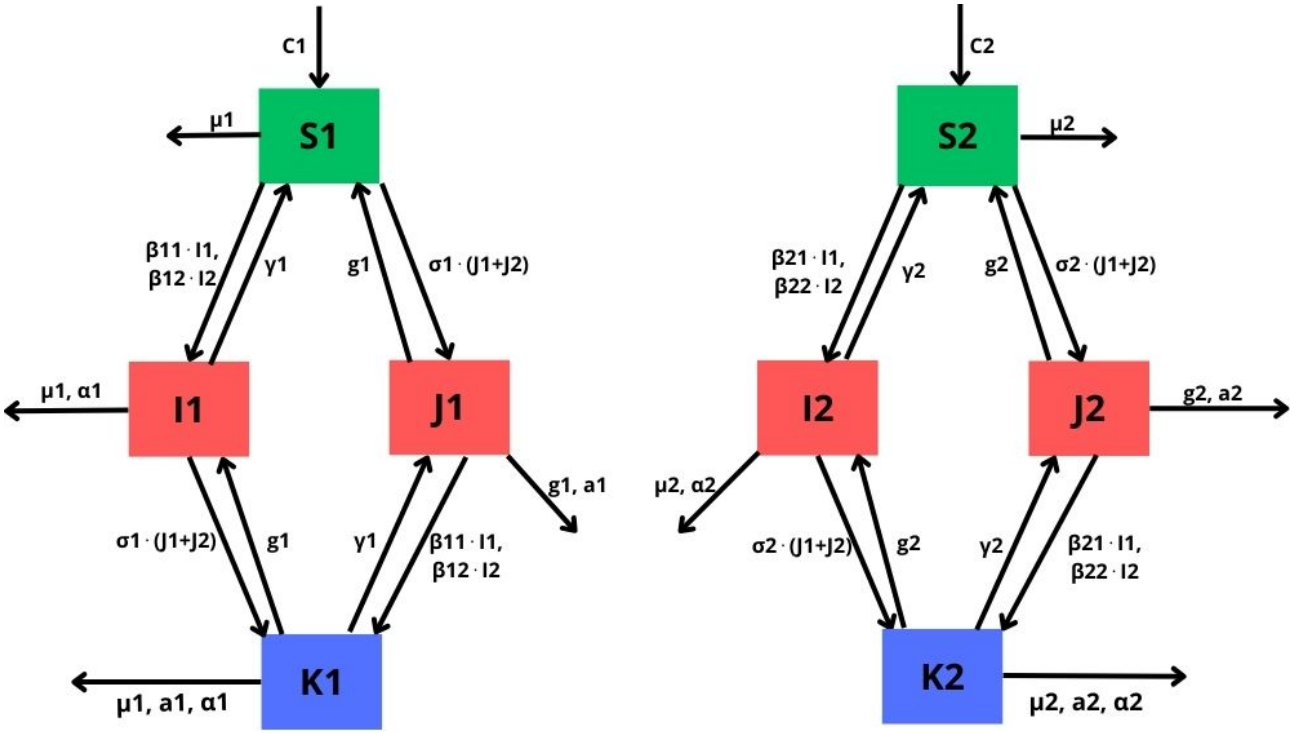

Figure 1. Possible movements between particular classes from system (1).

System (1) has four stationary states: disease–free (E_{df}), with sole DA or DB (E_A and E_B). We also suspect that there exists the endemic state (E_e), with two diseases present, exists, but we did not manage to prove it because of complicated computations. State E_{df} has the form

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

It exits 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 (1) we computed the basic reproduction number $\mathcal{R}_0$. This number can be written as

$$\mathcal{R}_0 = \max(\lambda_1, \lambda_2),$$

where

$$\lambda_1 = \tfrac{\sigma_1}{q_1}\widehat{S}_1 + \tfrac{\sigma_2}{q_2}\widehat{S}_2, \qquad q_i := g_i + a_i + \mu_i$$

and

$$\lambda_2 = \frac{1}{2k_1k_2}\left(k_2\beta_{11}\widehat{S}_1 + k_1\beta_{22}\widehat{S}_2 + \sqrt{(k_2\beta_{11}\widehat{S}_1 - k_1\beta_{22}\widehat{S}_2)^2 + 4k_1k_2\beta_{12}\beta_{21}\widehat{S}_1\widehat{S}_2}\right),$$

where $k_i := \gamma_i + \alpha_i + \mu_i$. Later we investigated the local stability of the stationary state. State E_{df} is locally stable if $\mathcal{R}_0 < 1$, what is expected. Analysis of the local stability for E_A and E_B provided the list of conditions. What is important is that the parameters from both diseases affect the local stability of both states.

REFERENCES

[1] M. Bodzioch, M. Choiński, and U. Foryś: *SIS criss-cross model of tuberculosis in heterogeneous population*, Discrete and Continuous Dynamical Systems – B **24** (2019), 2169–2188.