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## Simple discrete SIS criss-cross model of tuberculosis in heterogeneous population of homeless and non-homeless people

**Abstract** In this paper we propose a discrete criss-cross model of tuberculosis (TB) transmission in a heterogeneous population, which consists of two different subpopulations: homeless and non-homeless people. This criss-cross model is based on the simple continuous SIS model with bilinear transmission function and constant inflow into both subpopulations considered previously by us.

We make preliminary stability analysis. We show that to control the spread of the infectious disease in a heterogeneous population it is not enough to consider the dynamics of the disease in each subpopulation separately. This result is consistent with the result for continuous model. We also fit the model to epidemic data from Warmian-Masurian Province of Poland.

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### 1. Introduction

In this paper we propose a simple discrete SIS criss-cross model of tuberculosis (TB) epidemic in a heterogeneous population. This work is based on our previous papers [1] and [2] in which we have followed the ideas of [5], where the continuous criss-cross model of the dynamics of TB epidemic was proposed. The model took into account the effects of conducting programs of Active Case Finding (ACF) in the community of homeless people. As a consequence of applying ACF, the incidence of TB declined not only among homeless individuals, but also among the whole population in the region. In [2] the mathematical analysis of this model was presented. In this model, due to its Malthusian background, there can be situations when the population grows boundlessly or goes extinct. Because of that behaviour, the model has

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been modified and analysis of its modification is presented in [1]. We showed there that the dynamics of epidemic in a heterogeneous population is different than the dynamics of epidemic in a homogeneous population.

Both of the models analyzed in [1] and [2] are continuous. For these models we made simulations in order to compare the model dynamics with real data. However, the real data we base on has a discrete nature – the sizes of each group of the population correspond to the defined moment during the year. Furthermore, the programs of ACF correspond to detecting an infected person in a particular moment of time. For these reasons, it seems to be more justified to consider discrete models instead of continuous ones. The discretized model should be relied on this kind of discretization method, which expresses the real phenomenon in the possibly best way. Nevertheless, the discretization methods of this type can often lead to a model having complex form. In our case, the analysis of continuous models presented in [1] and [2], especially stability analysis, was complicated. That is why, it is reasonable to investigate the model based upon possibly the simplest type of discretization. Thus, we discretized the model from [1] with the use of the explicit (forward) Euler discretization. This discretization is widely applied in mathematical epidemiological modeling, c.f. [3, 4, 6] and the references therein.

Having proposed discretized version of the model presented in [1] we then focus on basic properties of solutions and make preliminary stability analysis. The results are complemented with the numerical simulations. Our work is applied to model the dynamics of TB in the population of homeless and non-homeless people. However, it should be marked that the model is much more general and could be used in the case of other diseases and other subpopulations within a heterogeneous population.

## 2. Modeling of epidemic dynamics in a homogeneous population

Firstly, let us introduce the following component SIS model which describes dynamics of epidemic in a homogeneous population. As usual in this type of models, we divide the whole population into the subpopulations of susceptible (S) and infected (I) people. Here the homogeneous population means the population in which we cannot differ individuals in regard of the risk of developing the particular disease. We would like to focus on the model based on the mass-action law, cf. [1]. Hence consider the following system of two differential equations

$$\begin{aligned}\dot{S} &= C - \beta SI + \gamma I - \mu S, \\ \dot{I} &= \beta SI - (\alpha + \gamma + \mu)I,\end{aligned}\tag{1}$$

where  $C$  is a constant inflow into the population,  $\beta$  is a transmission coefficient,  $\gamma$  stands for recovery rate,  $\mu$  is a natural death coefficient and  $\alpha$  reflects disease-related death. We assume that the coefficients are fixed and positive.

Following [1] we change the variables:

$$\tau = \gamma t, \quad x = \beta S, \quad y = \beta I,$$

and denote  $k = 1 + \alpha + \mu$ , obtaining

$$\begin{aligned} x' &= C - xy + y - \mu x, \\ y' &= xy - ky, \end{aligned} \tag{2}$$

where the meaning of the variables and parameters is the same as in (1). Note that the variables  $x, y$  are functions of  $\tau$  now, and  $k > 1$ .

Let us discretize System (2) with the use of the explicit Euler method. We then get

$$\begin{aligned} x_{n+1} &= x_n + h(C - x_n y_n + y_n - \mu x_n), \\ y_{n+1} &= y_n + h(x_n y_n - k y_n), \end{aligned} \tag{3}$$

where  $h$  is a step size of discretization method. Note that we can choose  $h > 0$  as small as necessary for System (3) to have adequate properties.

**2.1. Basic properties** Let us present some basic properties of System (3).

First, note that the basic reproduction number  $\mathcal{R}_0 = \frac{C}{\mu k}$  for both models (2) and (3) is the same, since while computing  $\mathcal{R}_0$ , we do not consider whether the model is continuous or discrete.

Next, we estimate the whole population size reflected by the variable  $w_n := x_n + y_n$ , assuming non-negativity of subpopulation sizes. Note that if we add both equations of (3) by sides, we get

$$w_{n+1} = w_n + h(C - \mu w_n - \alpha y_n) \leq w_n + h(C - \mu w_n).$$

Solving the above inequality, with the assumption  $h < \frac{1}{\mu}$ , we have

$$x_n, y_n \leq w_n \leq (1 - h\mu)^n w_0 + (1 - (1 - h\mu)^n) \frac{C}{\mu} \tag{4}$$

for all  $n \geq 0$ , and then we can state that  $w_n \leq w_0 + \frac{C}{\mu}$  for every  $n \geq 0$ , which means that the population is upper bounded. Moreover, using (4) we easily see that

**COROLLARY 2.1** *If*

$$h < \frac{1}{\mu} \tag{5}$$

*and  $w_0 \leq \frac{C}{\mu}$ , then  $w_n \leq \frac{C}{\mu}$  for every  $n \geq 0$ .*

System (3) is a discrete dynamical system described by the function

$$H(x, y) = \begin{pmatrix} F(x, y) \\ G(x, y) \end{pmatrix} = \begin{pmatrix} x + h(C - xy + y - \mu x) \\ y + hy(x - k) \end{pmatrix},$$

that is the orbit of an arbitrary point  $(x_0, y_0)$ , indicated by  $\mathcal{O}$ , has the form  $\mathcal{O} = ((x_0, y_0), H(x_0, y_0), H^2(x_0, y_0), \dots)$ . Due to the meaning of the variables  $x$  and  $y$  we must have  $F^n(x, y) \geq 0$  and  $G^n(x, y) \geq 0$  for nonnegative  $x$  and  $y$ . Moreover, basing on Corollary 2.1, we focus on the set

$$\Omega = \left\{ (x, y) \in \mathbb{R}^2 \quad x + y \leq \frac{C}{\mu} \right\},$$

which we require to be invariant for System (3). Hence, in the following we check under which assumptions this set has the desired property. Therefore, we focus on nonnegativity of solution of System (3) in  $\Omega$ .

- Looking for nonnegativity of the second variable, we easily see that  $G(x, y) = y(1 - kh) + hxy$  is nonnegative/positive for nonnegative/positive  $x$  and  $y$  under the assumption  $1 - kh > 0$ .

Hence in the following we assume that

$$h < \frac{1}{k}, \tag{6}$$

and this is obvious that if  $h$  satisfies Inequality (6), then it also satisfies Inequality (5), as  $k > \mu$ . This means that if  $x_0, y_0 \geq 0$ , then  $y_n \geq 0$  for any  $n$ .

- Looking for nonnegativity of the first variable we need to check minimal value of the function  $F(x, y)$  in the set  $\Omega$ . Calculating partial derivatives of  $F(x, y)$ , we get

$$\frac{\partial F}{\partial x} = 1 - h\mu - hy, \quad \frac{\partial F}{\partial y} = h(1 - x).$$

If we equate these derivatives to zero, then the solution of the following set of equations is  $(\bar{x}, \bar{y}) = \left(1, \frac{1-h\mu}{h}\right)$ .

In order to avoid extreme points of the function  $F(x, y)$  inside  $\Omega$ , the condition  $\frac{C}{\mu} - \bar{x} < \bar{y}$  has to be fulfilled. This inequality can be written as  $\frac{C}{\mu} - 1 < \frac{1}{h} - \mu$ . Note that, due to the meaning of the parameters  $C$  and  $\mu$ , we have  $C \gg \mu$ , that is  $\frac{C}{\mu} > 1$ . Hence, the above inequality is equivalent to

$$h < \frac{1}{\frac{C}{\mu} - 1 + \mu}. \tag{7}$$

Assuming (7) the point at which  $F$  can has extremal value lies outside  $\Omega$ , so we need to check values on the boundaries of this set. We have

- $F(0, y) = hy + hC > 0$  for any  $y \geq 0$ ;
- $F(x, 0) = x(1 - h\mu) + hC > 0$  for any  $x \geq 0$  under Assumption (6);
- $F\left(x, \frac{C}{\mu} - x\right) = f(x)$ , where

$$f(x) = x(1 - h\mu) + hC + h(1 - x) \left( \frac{C}{\mu} - x \right).$$

We see that  $f$  is a quadratic function of  $x$ :

$$f(x) = hx^2 + x \left( 1 - h \left( \frac{C}{\mu} + \mu + 1 \right) \right) + hC + h\frac{C}{\mu},$$

and it is obvious that  $f(x) > 0$  for  $x \geq 0$  if the condition

$$h < \frac{1}{\frac{C}{\mu} + \mu + 1} \quad (8)$$

holds. Note that Inequality (8) is stronger than (7).

We can sum up the analysis above as follows.

**COROLLARY 2.2** *If*

$$h < \min \left( \frac{1}{k}, \frac{1}{\frac{C}{\mu} + \mu + 1} \right) \quad (9)$$

*and  $(x_0, y_0) \in \Omega$ , then solutions  $(x_n, y_n)$  of System (3) remain in  $\Omega$  for any  $n$ .*

Let us look at Inequality (9) in the context of the basic reproduction number  $\mathcal{R}_0$ . Note that if  $\mathcal{R}_0 > 1$ , then  $\frac{C}{\mu} > k$ , that is  $\frac{C}{\mu} + \mu + 1 > k$ . Hence, in the situation of the spread of epidemic Inequality (9) is equivalent to  $h < \frac{1}{\frac{C}{\mu} + \mu + 1}$ .

**2.2. Local stability** Let us now focus on the local stability analysis. There are two stationary states of System (3):

- $E_d = (x_d, y_d) = \left( \frac{C}{\mu}, 0 \right)$  always existing,
- $E_e = (x_e, y_e) = \left( k, \frac{C - \mu k}{k - 1} \right)$  existing under the condition  $C > \mu k$ , which is equivalent to  $\mathcal{R}_0 > 1$ .

Note that System (3) has the same stationary states as (2) (cf. [1]).

Now, we investigate conditions of local stability of these stationary states. Let  $M$  denotes a Jacobian matrix for System (3). This matrix has the form

$$M(x, y) = \begin{pmatrix} 1 - h(y + \mu) & h(1 - x) \\ hy & 1 + h(x - k) \end{pmatrix}.$$

We start with the stability analysis of the disease-free state  $E_d$ . The Jacobian matrix for this state reads

$$M(E_d) = \begin{pmatrix} 1 - h\mu & h(1 - x_d) \\ 0 & 1 + h(x_d - k) \end{pmatrix}.$$

Recall that the conditions for stability of  $E_d$  are  $|\lambda_i| < 1$ ,  $i = 1, 2$ . We see that  $\lambda_1 = 1 - h\mu$  satisfies these inequalities under Assumption (5). On the other hand,  $\lambda_2 = 1 - hk + hx_d$  is positive under Assumption (9), while  $\lambda_2 < 1$  iff  $x_d < k$ , that is  $\mathcal{R}_0 < 1$ . More precisely, we can conclude that

**COROLLARY 2.3** *If Inequality (9) is satisfied, then the disease-free stationary state  $E_d$  is*

- a sink for  $\mathcal{R}_0 < 1$ ,
- non-hyperbolic for  $\mathcal{R}_0 = 1$ ,
- a saddle for  $\mathcal{R}_0 > 1$ .

Now we focus on the local stability of the endemic state  $E_e$ . We make the analysis under the existence condition  $\mathcal{R}_0 > 1$ . The Jacobian matrix for this state reads

$$M(E_e) = \begin{pmatrix} 1 - h(y_e + \mu) & h(1 - x_e) \\ hy_e & 1 \end{pmatrix},$$

yielding characteristic polynomial of the form

$$\mathcal{P}(\lambda) = \lambda^2 + \lambda \left( h \frac{C - \mu}{k - 1} - 2 \right) + 1 - h \frac{C - \mu}{k - 1} + h^2(C - \mu k).$$

The eigenvalues of the matrix  $M(E_e)$  have the form

$$\lambda_{1,2} = 1 - h \frac{(C - \mu) \pm \sqrt{\delta}}{2(k - 1)}$$

where  $\delta = (C - \mu)^2 - 4(C - \mu k)(k - 1)^2$ .

1. Assume that  $\delta \geq 0$ . Then we have two real eigenvalues  $\lambda_1 \geq \lambda_2$  and to get stability we only need to check the inequalities  $-1 < \lambda_2$  and  $\lambda_1 < 1$ . On the other hand, for  $E_e$  to be unstable it is enough that  $\lambda_1 < -1$ . It is easy to see that:

$\lambda_1 < 1$  for  $\mathcal{R}_0 > 1$ , that is whenever  $E_e$  exists;

$\lambda_2 > -1$  for  $h < \frac{4(k-1)}{C-\mu+\sqrt{\delta}}$ ;

$\lambda_1 < -1$  for  $h > \frac{4(k-1)}{C-\mu-\sqrt{\delta}}$ .

2. Assume that  $\delta < 0$ , that is we have complex eigenvalues. Note that  $|\lambda_1| = |\lambda_2| =: \lambda$  and  $\lambda_1 \lambda_2 = |\lambda|^2 = 1 - h \frac{C-\mu}{k-1} + h^2(C - \mu k)$ . It is obvious that  $|\lambda| < 1$  for  $h < \frac{C-\mu}{(k-1)(C-\mu k)}$ .

Let  $h_1 = \frac{4(k-1)}{C-\mu+\sqrt{\delta}}$ ,  $h_2 = \frac{4(k-1)}{C-\mu-\sqrt{\delta}}$  and  $h_3 = \frac{C-\mu}{(k-1)(C-\mu k)}$ . Hence we obtain the following corollary.

**COROLLARY 2.4** *If  $\mathcal{R}_0 > 1$ , then the endemic stationary state  $E_e$  exists and is*

- a sink for  $\delta \geq 0$  and  $h < h_1$  or  $\delta < 0$  and  $h < h_3$ ,
- a source for  $\delta \geq 0$  and  $h > h_2$  or  $\delta < 0$  and  $h > h_3$ ,
- non-hyperbolic if  $\delta \geq 0$  and  $h = h_1$ ,  $h = h_2$  or  $\delta < 0$  and  $h = h_3$ ,
- a saddle if  $\delta \geq 0$  and  $h_1 < h < h_2$ .

**3. Model for a heterogeneous population** In this section we consider a population consisting of two subpopulations with different risk of developing TB: non-homeless and homeless people, as in [5]. In this case the illness is transmitted not only among one subpopulation, but also between individuals of different subpopulations, and that is why we use the criss-cross model. Similarly like in the two-dimensional case, each subpopulation is divided into two groups of susceptible and infected people. Continuous model describing the dynamics of TB epidemic considered by us in [1] reads

$$\begin{aligned}
 \dot{S}_1 &= C_1 - \beta_{11}S_1I_1 - \beta_{12}S_1I_2 + \gamma_1I_1 - \mu_1S_1, \\
 \dot{I}_1 &= \beta_{11}S_1I_1 + \beta_{12}S_1I_2 - (\gamma_1 + \alpha_1 + \mu_1)I_1, \\
 \dot{S}_2 &= C_2 - \beta_{22}S_2I_2 - \beta_{21}S_2I_1 + \gamma_2I_2 - \mu_2S_2, \\
 \dot{I}_2 &= \beta_{22}S_2I_2 + \beta_{21}S_2I_1 - (\gamma_2 + \alpha_2 + \mu_2)I_2,
 \end{aligned} \tag{10}$$

where:

- $\beta_{ij}$ ,  $i, j = 1, 2$ , are transmission coefficients between specific groups in a heterogeneous population; here we assume that these coefficients are fixed;
- $\alpha_i$ ,  $i = 1, 2$ , reflect disease-related death rates for the non-homeless and homeless individuals, accordingly;
- $\gamma_i$ ,  $i = 1, 2$ , are recovery coefficients for the given subpopulation;
- $\mu_i$ ,  $i = 1, 2$ , stand for natural death rates for each subpopulation;
- $C_i$ ,  $i = 1, 2$ , reflect a constant inflow of humans into the given subpopulation; here they are numbers of newborn and net migrating individuals.

The values of the parameters are positive. Note that we do not consider explicit exchange of people between the groups of non-homeless and homeless individuals as even without such exchange the model has complex form.

After making scaling analogous to those for System (1) (for more details cf. [1]), and making discretization with the use of explicit Euler method, we get

$$\begin{aligned}x_{n+1}^{(1)} &= x_n^{(1)} + h \left( C_1 - x_n^{(1)} y_n^{(1)} - \beta_1 x_n^{(1)} y_n^{(2)} + y_n^{(1)} - \mu_1 x_n^{(1)} \right), \\y_{n+1}^{(1)} &= y_n^{(1)} + h \left( x_n^{(1)} y_n^{(1)} + \beta_1 x_n^{(1)} y_n^{(2)} - k_1 y_n^{(1)} \right), \\x_{n+1}^{(2)} &= x_n^{(2)} + h \left( C_2 - x_n^{(2)} y_n^{(2)} - \beta_2 x_n^{(2)} y_n^{(1)} + \eta_2 y_n^{(2)} - \mu_2 x_n^{(2)} \right), \\y_{n+1}^{(2)} &= y_n^{(2)} + h \left( x_n^{(2)} y_n^{(2)} + \beta_2 x_n^{(2)} y_n^{(1)} - k_2 y_n^{(2)} \right),\end{aligned}\tag{11}$$

where  $x_n^{(i)}$  and  $y_n^{(i)}$  are the sizes of the groups within  $i$ th subpopulation at the  $n$ th step,  $i = 1, 2$ ,  $h$  is a step size of the discretization method, and  $k_i \eta_i + \alpha_i + \mu_i$ ,  $i = 1, 2$ ,  $\eta_1 = 1$ ,  $\eta_2 = \frac{\gamma_2}{\gamma_1}$ . Note that  $k_i > \eta_i > 0$ .

Analogously to the two-dimensional case, we can estimate the size of each subpopulation denoted by  $w_n^{(i)} = x_n^{(i)} + y_n^{(i)}$ ,  $i = 1, 2$ . Adding by sides the first and second equation of (11) or the third and fourth equation of (11), we get

$$w_{n+1}^{(i)} = w_n^{(i)} + h \left( C_i - \mu_i w_n^{(i)} - \alpha_i y_n^{(i)} \right) \leq w_n^{(i)} + h \left( C_i - \mu_i w_n^{(i)} \right), \quad i = 1, 2.$$

Using the same reasoning like for System (3), we get that if

$$h < \frac{1}{\mu_i}, \quad i = 1, 2,\tag{12}$$

than  $w_n^{(i)} \leq w_0^{(i)} + \frac{C_i}{\mu_i}$  for every  $n \geq 0$ , meaning that each subpopulation is upper bounded and so is the whole population. Moreover, we can state that if Inequality (12) holds and  $w_0^{(i)} \leq \frac{C_i}{\mu_i}$ , then  $w_n^{(i)} < \frac{C_i}{\mu_i}$  for every  $n \geq 0$ .

Now, we rewrite System (11) in the form of discrete dynamical system defining the function

$$F(x_1, y_1, x_2, y_2) = \begin{pmatrix} F_1(x_1, y_1, x_2, y_2) \\ F_2(x_1, y_1, x_2, y_2) \\ F_3(x_1, y_1, x_2, y_2) \\ F_4(x_1, y_1, x_2, y_2) \end{pmatrix} =$$

$$\begin{pmatrix} x_1 + h(C_1 - x_1 y_1 - \beta_1 x_1 y_2 + y_1 - \mu_1 x_1) \\ y_1 + h(x_1 y_1 + \beta_1 x_1 y_2 - k_1 y_1) \\ x_2 + h(C_2 - x_2 y_2 - \beta_2 x_2 y_1 + \eta_2 y_2 - \mu_2 x_2) \\ y_2 + h(x_2 y_2 + \beta_2 x_2 y_1 - k_2 y_2) \end{pmatrix},$$

for which we have  $(x_{n+1}^{(1)}, y_{n+1}^{(1)}, x_{n+1}^{(2)}, y_{n+1}^{(2)}) = F(x_n^{(1)}, y_n^{(1)}, x_n^{(2)}, y_n^{(2)})$ .

**3.1. Local stability** In this section we perform local stability analysis under Assumption (12). Because of using the explicit Euler discretization

method, stationary states of System (11) are the same as in the continuous case and these states exist under the same conditions. The results of stationary state analysis obtained for the continuous model were presented in [1]. We summarize them below.

REMARK 3.1 System (11) has two stationary states:

- disease-free state  $E_1 = (\tilde{x}_1, 0, \tilde{x}_2, 0)$ , where  $\tilde{x}_i = \frac{C_i}{\mu_i}$ , existing if  $C_i > 0$ ,  $i = 1, 2$ ;
- positive (endemic) state  $E_2 = (\hat{x}_1, \hat{y}_1, \hat{x}_2, \hat{y}_2)$ , which exists if at least one of the following conditions hold:
  1.  $C_1 \geq \mu_1 k_1$ ;
  2.  $C_2 \geq \mu_2 k_2$ ;
  3.  $C_i < \mu_i k_i$ , for  $i = 1, 2$ , and  $(\mu_1 k_1 - C_1)(\mu_2 k_2 - C_2) \leq \beta_1 \beta_2 C_1 C_2$ .

Jacobian matrix of System (11), denoted by  $J$ , reads

$$J(x_1, y_1, x_2, y_2) = \begin{pmatrix} 1 - h(y_1 + \beta_1 y_2 - \mu_1) & h(1 - x_1) & 0 & -h\beta_1 x_1 \\ h(y_1 + \beta_1 y_2) & 1 + h(x_1 - k_1) & 0 & h\beta_1 x_1 \\ 0 & -h\beta_2 x_2 & 1 - h(y_2 + \beta_2 y_1 - \mu_2) & h(\eta_2 - x_2) \\ 0 & h\beta_2 x_2 & h(y_2 + \beta_2 y_1) & 1 + h(x_2 - k_2) \end{pmatrix}.$$

Let us now study the local stability of the disease-free state  $E_1$ . The Jacobian matrix for  $E_1$  reads

$$J_1(\tilde{x}_1, 0, \tilde{x}_2, 0) = \begin{pmatrix} 1 - h\mu_1 & h(1 - \tilde{x}_1) & 0 & -h\beta_1 \tilde{x}_1 \\ 0 & 1 + h(\tilde{x}_1 - k_1) & 0 & h\beta_1 \tilde{x}_1 \\ 0 & -h\beta_2 \tilde{x}_2 & 1 - h\mu_2 & h(\eta_2 - \tilde{x}_2) \\ 0 & h\beta_2 \tilde{x}_2 & 0 & 1 + h(\tilde{x}_2 - k_2) \end{pmatrix}.$$

The characteristic polynomial of  $J_1$  reads:

$$P_1(\lambda) = (1 - h\mu_1 - \lambda)(1 - h\mu_2 - \lambda)P_2(\lambda),$$

where

$$P_2(\lambda) = (1 - h(\tilde{x}_1 - k_1) - \lambda)(1 - h(\tilde{x}_2 - k_2) - \lambda) - h^2 \beta_1 \beta_2 \tilde{x}_1 \tilde{x}_2.$$

The eigenvalues of the matrix  $J_1$  have the form:  $\lambda_1 = 1 - h\mu_1$ ,  $\lambda_2 = 1 - h\mu_2$  and

$$\lambda_{3,4} = \frac{1}{2} \left( 2 - h \left( k_1 - \frac{C_1}{\mu_1} + k_2 - \frac{C_2}{\mu_2} \right) \pm h\sqrt{\theta} \right),$$

where  $\theta = \left( k_1 - \frac{C_1}{\mu_1} - k_2 + \frac{C_2}{\mu_2} \right)^2 + 4\beta_1 \beta_2 \frac{C_1 C_2}{\mu_1 \mu_2}$ , and  $h^2 \theta$  is a discriminant of  $P_2$ .

For local stability of  $E_1$  we require  $|\lambda_i| < 1$ ,  $i = 1, 2, 3, 4$ . Since Inequalities (12) hold, we have  $|\lambda_{1,2}| < 1$ . After considering the conditions for  $\lambda_{3,4}$ , we can state that the stationary state  $E_1$  is locally stable if the following inequalities

$$C_i < \mu_i k_i, \quad i = 1, 2, \quad (13a)$$

$$\beta_1 \beta_2 C_1 C_2 < (\mu_1 k_1 - C_1) (\mu_2 k_2 - C_2), \quad (13b)$$

$$h < \frac{4}{k_1 - \frac{C_1}{\mu_1} + k_2 - \frac{C_2}{\mu_2} + \sqrt{\theta}}, \quad (13c)$$

hold. It is worth noting that Conditions (13a) and (13b) are the conditions of stability of  $E_1$  in a model being a continuous version of (11); cf. [1]. In our case, discretization of the continuous model with the use of explicit Euler method requires additional condition, that is (13c) for the step size.

The local stability conditions for the endemic state  $E_2$  are hard to express explicitly, that is why we omit them in this paper.

**4. Numerical simulations** Here we illustrate the dynamics of System (11) for the parameters which we fitted to the data from Warmian-Masurian province of Poland. The simulations were conducted with Matlab software. The actual epidemic data and the numerical results of model simulations were compared in order to get the best-fitted parameters, which are presented in Table 1.

Table 1: Parameters for the model described by System (11)

Name	Definition	Value
$C_1$	Constant inflow of humans into the subpopulation of the non-homeless	11000
$C_2$	Constant inflow of humans into the subpopulation of the homeless	60
$\alpha_1, \alpha_2$	Disease-related death rates	0.09
$\gamma_1, \gamma_2$	Recovery coefficients	0.9
$\mu_1, \mu_2$	Natural death rate	0.009
$\beta_{11}$	Transmission coefficient	$6.0420 \cdot 10^{-7}$ (estimated)
$\beta_{12}$	Transmission coefficient	$6.2377 \cdot 10^{-6}$ (estimated)
$\beta_{21}$	Transmission coefficient	$1.9013 \cdot 10^{-6}$ (estimated)
$\beta_{22}$	Transmission coefficient	$5.0115 \cdot 10^{-4}$ (estimated)

Demographic data used in the simulations were obtained from statistical yearbooks. The numbers of homeless people were provided by the Regional Center for Social Policy, Office of the Marshall of the Warmian-Masurian province in the city of Olsztyn in Poland. The epidemic data used for the study were anonymized by the Independent Public Tuberculosis and Lung

Diseases Unit in Olsztyn, Poland, and only numerical results were used. The values of the parameters  $C_1$ ,  $C_2$ ,  $\alpha_1$ ,  $\alpha_2$ ,  $\gamma_1$ ,  $\gamma_2$ ,  $\mu_1$  and  $\mu_2$ , are taken from Central Statistical Office of Poland. A best-fit technique was used to estimate the values of the transmission coefficients  $\beta_{ij}$ ,  $i, j = 1, 2$ . All data are fully available without any restrictions. Comparison between the actual data and simulated values is illustrated in Fig. 1.

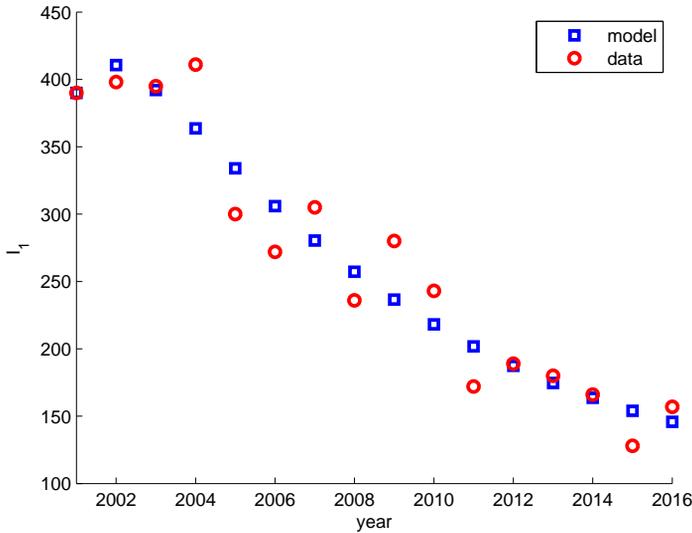


Figure 1: Tuberculosis in the Warmian-Mazurian province over the years 2001–2016 (number of infected non-homeless individuals). Comparison between the actual data and the model.

**5. Summary** Studying stability for homogeneous population we have shown that the sufficient conditions guaranteeing disease elimination are  $C < k\mu$  and  $0 < h < \min\left(\frac{1}{k}, \frac{1}{\frac{C}{\mu} + \mu + 1}\right)$ . However, these conditions do not guarantee that the disease will not spread in the heterogeneous population. If conditions  $C_i < \mu_i k_i$  and  $0 < h < \min\left(\frac{1}{k_i}, \frac{1}{\frac{C_i}{\mu_i} + \mu_i + 1}\right)$ ,  $i = 1, 2$  hold, but at least one of conditions (13b) or (13c) does not hold, the disease can still spread. Thus, our analysis suggests that disease transmission from one subpopulation to another may significantly influence the spread of the disease in a general population. Even if the basic reproduction number for one subpopulation is less than one and ensures that the infection cannot maintain itself in the corresponding isolated subpopulation, the disease can be transmitted from one subpopulation to another and TB can invade the heterogeneous mixed population. It means that to control the spread of the illness in a heterogeneous population it is not enough to consider the dynamics of the disease in each

subpopulation separately. In order to eliminate the infection it is required to consider a criss-cross dynamics of the disease spread.

In this article we have formulated a mathematical discrete model describing the dynamics of tuberculosis epidemic in heterogeneous population. The population is divided into two subpopulations regarding different risk of developing TB: homeless and non-homeless people. This paper is motivated by our previous work, cf. [1], [2] and [5], where we investigated continuous models.

What is important is the fact that some properties of solutions and stationary states of the system discretized with the explicit Euler method are analogous to those for the continuous system [1], especially boundedness of solutions and the existence of stationary states. However, the precise conditions for local stability of stationary states are more complicated than those for continuous case. For discrete models the additional conditions for step size of discretization method are needed.

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## Dyskretny krzyżowy model rozprzestrzeniania się gruźlicy w niejednorodnej populacji bezdomnych i niebezdomnych

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**Streszczenie** Zaproponowany został dyskretny krzyżowy model rozprzestrzeniania się gruźlicy w niejednorodnej populacji składającej się z bezdomnych i niebezdomnych. Model ten oparty jest na prostym modelu typu SIS z dwuliniową funkcją transmisji i stałym napływem w obu populacjach. Przeprowadzona została wstępna analiza stabilności stanów stacjonarnych. Pokazano, że aby kontrolować rozprzestrzenianie się choroby zakaźnej w niejednorodnej populacji nie jest wystarczające rozważanie dynamiki choroby w każdej podpopulacji oddzielnie. Parametry modelu zostały dopasowane do danych z województwa warmińsko-mazurskiego.

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