Mathematical models of epidemics in closed populations and their visualization via web application PhaPl

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Abstract: Mathematical modeling of the spread of epidemics is one of the main problems in mathematical biology. In this paper, we will consider dynamical systems describing epidemics models, examine the stability of solution to the system in the neighborhood of equilibrium points, and construct phase portraits for its special cases with the help of PhaPl web application.

Key–Words: Mathematical modeling in biology, epidemics, nonlinear dynamical system, phase portrait, web application.

1 Introduction

In 1927, Anderson McKendrick and William Kermak published the first mathematical study on the issue of epidemiology. Mathematically, the dynamics of the epidemic process can be described by a system of differential equations, and solutions of the system characterize the dynamics of population changes in different groups.

In its original form, the Kermak-McKendrick theory divides an infected population into only two classes: susceptible and recovered. Years later, it was transformed into a susceptible-infected-recovered model. In subsequent works by other authors, other classes were introduced.

In this paper we consider two simple mathematical models of epidemics whose general case was considered in [1]. We discuss the problem of stability in the epidemic process in closed populations and provide visualization via PhaPl [2].

PhaPl is a software to study and plot phase portraits of autonomous systems of two differential equations on a plane. It automates all steps of the solution process: it finds equilibrium points, linearizes the system at each equilibrium point, finds eigenvalues and determines stability. It is easy to use and suitable for students and researchers. It has been deployed for teaching purposes at Moscow State University of Economics, Statistics, and Informatics (MESI), Lomonosov Moscow State University (MSU) since 2013, and in Plekhanov Russian University of Economics since 2016. Results were described in [3].

The new version of PhaPl was produced as a web application[2] with all computations performed on the client side. So it is easy to host PhaPl on almost any web server. And it is possible to download a local copy to use PhaPl offline. To provide these properties, a full stack of technologies in PhaPl was replaced by better options: SymPy is used to perform analytical research, MathJax is used for beautiful formulas, PyPy.js is used to run SymPy inside a web browser. PhaPl should work well in all web browsers with support for the canvas element of HTML5, thus covering desktop and mobile users. New technologies allowed the significant reduction of size of PhaPl. All components and PhaPl itself are Free and Open Source Software.

SymPy (cf. [4]) is a library for symbolic computations comparable to advanced computer algebra systems. It allows PhaPl to perform analytical calculations without applying numerical methods, while

the Euler method is used to plot phase portraits only. Nevertheless, PhaPl cannot guarantee a perfect solution, so a researcher should check the correctness of obtained results.

PhaPl chooses multiple random initial conditions to plot representative phase trajectories automatically. When the mouse pointer hovers a phase portrait in the user interface, an additional temporary trajectory is plotted using the position of the pointer as the initial condition. PhaPl allows one to study a system with given constant coefficients quickly, which might be helpful during research. Systems with parameters are not supported yet. PhaPl provides information not available in any other computer system to plot phase portraits: on phase portraits dedicated to a single equilibrium point, different colors are used for forthcoming and recessive parts of phase trajectories in relation to the equilibrium point.

All figures with phase portraits in this paper were obtained via PhaPl. Violet shows parts of phase trajectories where the trajectories go closer to the equilibrium point. Green marks the movement outwards from the equilibrium point. Light blue is used for the eigenvectors. Red triangles point to the equilibrium points. Respective equilibrium points may be out of sight, so there may be odd number of triangles. Red circles emphasize the equilibrium points within sight. Black triangles mark the axes when 0 is within sight. The axes are shown in violet, also there is grey grid for integer values. There may be one temporary trajectory shown in red and blue. Red is used for the part where time proceeds forward in relation to the initial condition. Blue is for the part of the temporary trajectory where time goes in reverse in relation to the initial condition.

In this paper, phase portraits are used to illustrate behaviour of trajectories of a system on a plane. For 2D system, the phase portrait shows trajectories of the system itself. It is said "plane (X, Y)" about a figure to tell that OX is the horizontal axis and OY is the vertical axis. For 3D system, a set of phase portraits is constructed relying on additional restrictions: we show special cases of the SEIRS model when one of the variables is a constant.

2 The SIRS model

We consider a model of epidemics in a population where individuals can only have one of the following three states: S (susceptible) is the number of healthy individuals that are susceptible to infection, I (infection) is the number of infected individuals and R (recover) is the number of recovered individuals who received immunity or died (cf. [5]).

This model is suitable only for a closed population. It is also called a box model: each individual belongs only in one "box": healthy, infected or recovered. From being healthy you can only go to infected, from infected only to sick/die and then you can again go to susceptible: $S \to I \to R \to S$.

A simpler version of such a model ($S \to I \to R$) is described in [6].

N is the number of individuals in the population, β is the parameter controlling how often a susceptible-infected contact results in a new exposure, γ_1 is the rate at which an infected individual recovers, γ_2 is the rate at which an recovered individual becomes susceptible.

This model is described by the following system of differential equations:

$$\begin{cases} \dot{S} = -\beta SI + \gamma_2 R, \\ \dot{I} = \beta SI - \gamma_1 I, \\ \dot{R} = \gamma_1 I - \gamma_2 R. \end{cases}$$

Since $S + I + R = N$, we obtain the following system of equations:

$$\begin{cases} \dot{S} = -\beta SI + \gamma_2 (N - S - I), \\ \dot{I} = \beta SI - \gamma_1 I. \end{cases}$$

This system has two equilibrium points: $M_1 = (N, 0)$ and $M_2 = \left(\frac{\gamma_1}{\beta}, \frac{\beta\gamma_2 N - \gamma_1\gamma_2}{\beta(\gamma_1+\gamma_2)}\right)$.

The first equilibrium point M_1 describes the situation in which there are no infected or recovered individuals.

We find the eigenvalues corresponding to this equilibrium point $\lambda_1 = \beta N - \gamma_1; \lambda_2 = -\gamma_2$. Since $\beta, \gamma_{1,2}, N$ are positive, λ_2 is negative. If $\beta N - \gamma_1 > 0$, than this equilibrium point is a saddle, otherwise, if $\beta N - \gamma_1 <, 0$ it is a stable node.

Now consider the second equilibrium point M_2. The corresponding eigenvalues are:

$$\begin{aligned} \lambda_{1,2} = & \frac{1}{2(\gamma_1+\gamma_2)} \cdot \Big(-\beta\gamma_2 N - \gamma_2^2 \\ & \pm \Big(\beta^2\gamma_2^2 N^2 \\ & \quad + \left(-2\beta\gamma_2^3 - 8\beta\gamma_1\gamma_2^2 - 4\beta\gamma_1^2\gamma_2\right) N \\ & \quad + \gamma_2^4 + 4\gamma_1\gamma_2^3 + 8\gamma_1^2\gamma_2^2 + 4\gamma_1^3\gamma_2 \Big)^{\frac{1}{2}} \Big). \end{aligned}$$

Since the real parts of both eigenvalues are negative, our equilibrium point is stable. Note that $\beta N - \gamma_1 > 0$, otherwise the equilibrium point would lie outside the part of the plane considered by us, since S and I are positive. Two different cases are possible here.

1. If the radicand is positive, then M_2 is a node. To give an example, we consider the case $\beta = 0.1$, $\gamma_1 = 5$, $\gamma_2 = 2$ and construct a phase portrait in the neighborhood of the equilibrium point (see figure 1).

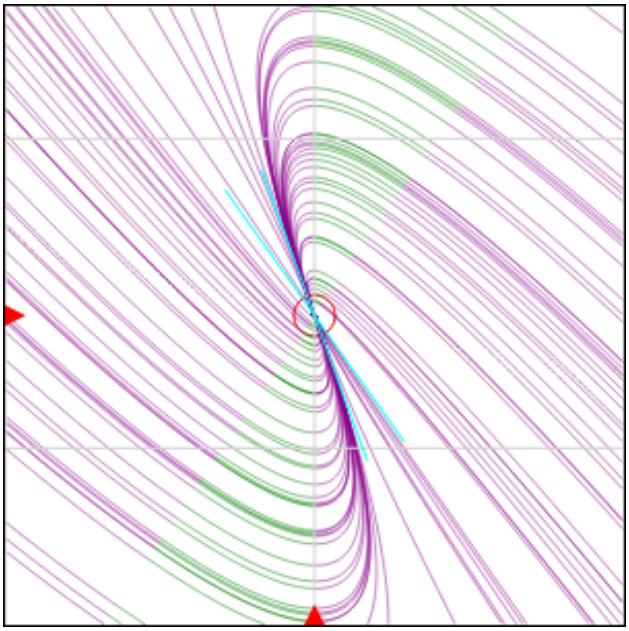

Figure 1: Example of stable node in SIRS model (the plane (S, I))

2. If the radicand is negative, then M_2 is a focus. As an example, we consider the case $\beta = 0.01$, $\gamma_1 = 5$, $\gamma_2 = 2$ and construct a phase portrait in the neighborhood of the equilibrium point (see figure 2).

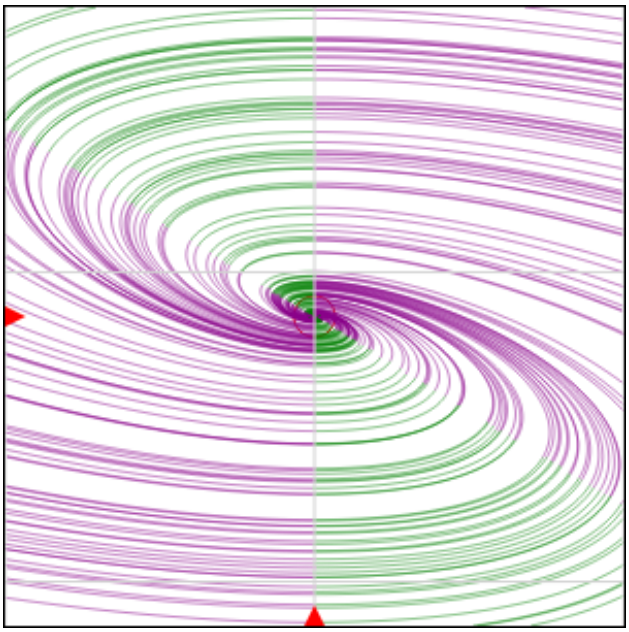

Figure 2: Example of stable focus in SIRS model (the plane (S, I))

3 The SEIRS model

It should be mentioned that many diseases have an incubation period, which means that sick individuals become infected only after some time. To describe this phenomenon we introduce an additional class E (exposed).

We introduce the infectivity function $A(\tau)$. It contains the information about the infectivity of an individual that was infected τ units of time ago. For example, if we assume that the probability of infection by contact is p, the average number of contacts per unit of time is c, and the individual is contagious at intervals of time from τ_1 to τ_2, then

$$A(\tau) = \begin{cases} cp & \text{if } \tau_1 \le \tau \le \tau_2, \\ 0 & \text{otherwise.} \end{cases}$$

We denote the number of new cases at time t by $i(t)$. Obviously, the equality $i(t) = -\dot{S}$ holds. Using Formula (6.2), [6], p.158, we describe i as

$$i(t) = \frac{S(t)}{N} \int_0^\infty A(\tau) i(t-\tau) d\tau.$$

The integral on the right hand side of the equation describes the average number of contacts that are leading to the transmission of infection at the time t. The contacts are random, so only $\frac{S(t)}{N}$ of them are with individuals that are healthy at the time t. We rewrite the equation in other terms:

$$\dot{S}(t) = \frac{S(t)}{N} \int_0^\infty A(\tau) \dot{S}(t-\tau) d\tau,$$

where N is the number of individuals in the population, β is the parameter controlling how often a susceptible-infected contact results in a new exposure, γ_1 is the rate at which an infected individual recovers, γ_2 is the rate at which an recovered individual becomes susceptible, θ is the rate at which an exposed person becomes infected,

$$A(\tau) = \beta N \frac{\theta(\gamma_1 + \gamma_2)}{\gamma_1 + \gamma_2 - \theta} \left(e^{-\theta\tau} - e^{-\gamma_1\tau} - e^{-\gamma_2\tau} \right).$$

Then the class E is calculated as

$$E(t) = -\frac{1}{\beta} \int_0^\infty A(\tau) \dot{S}(t-\tau) d\tau.$$

We change the limits of integration:

$$E(t) = -\frac{1}{\beta} \int_{-\infty}^t A(t-\tau) \dot{S}(\tau) d\tau.$$

We differentiate both sides of the equality:

$$\begin{aligned}\frac{d}{dt}E(t) &= -\frac{d}{dt}\frac{1}{\beta}\int\limits_{-\infty}^{t} A(t-\tau)\dot{S}(\tau)d\tau \\ &= -\frac{d}{dt}\frac{1}{\beta}\int\limits_{-\infty}^{t} \beta N\frac{\theta(\gamma_1+\gamma_2)}{\gamma_1+\gamma_2-\theta} \\ &\cdot\left(e^{-\theta(t-\tau)}-e^{-\gamma_1(t-\tau)}-e^{-\gamma_2(t-\tau)}\right) \\ &\cdot\dot{S}(\tau)d\tau \\ &= -\frac{1}{\beta}A(0)\dot{S}-0+\int\limits_{-\infty}^{t} N\frac{\theta(\gamma_1+\gamma_2)}{\gamma_1+\gamma_2-\theta} \\ &\cdot\left(-\theta e^{-\theta(t-\tau)}+\gamma_1 e^{-\gamma_1(t-\tau)}+\gamma_2 e^{-\gamma_2(t-\tau)}\right) \\ &\cdot\dot{S}(\tau)d\tau \\ &= -\frac{1}{\beta}A(0)\dot{S}+\int\limits_{-\infty}^{t} N\frac{\theta(\gamma_1+\gamma_2)}{\gamma_1+\gamma_2-\theta}\dot{S}(\tau) \\ &\cdot d\left(e^{-\theta(t-\tau)}-e^{-\gamma_1(t-\tau)}-e^{-\gamma_2(t-\tau)}\right) \\ &= -\frac{1}{\beta}A(0)\dot{S}+\left(N\frac{\theta(\gamma_1+\gamma_2)}{\gamma_1+\gamma_2-\theta}\dot{S}(\tau)\right. \\ &\cdot\left.\left(e^{-\theta(t-\tau)}-e^{-\gamma_1(t-\tau)}-e^{-\gamma_2(t-\tau)}\right)\right)\Bigg|_t^{\infty} \\ &+\int\limits_{-\infty}^{t} N\frac{\theta(\gamma_1+\gamma_2)}{\gamma_1+\gamma_2-\theta} \\ &\cdot\left(e^{-\theta(t-\tau)}-e^{-\gamma_1(t-\tau)}-e^{-\gamma_2(t-\tau)}\right)d\dot{S}(\tau).\end{aligned}$$

Thus, we obtain the following equation:

$$\frac{d}{dt}E(t)=\beta SI-\theta E.$$

Consequently:

$$\begin{cases}\dot{S}=-\beta SI+\gamma_2 R,\\ \dot{E}=\beta SI-\theta E,\\ \dot{I}=\theta E-\gamma_1 I,\\ \dot{R}=\gamma_1 I-\gamma_2 R.\end{cases}$$

Since $S+E+I+R=N$, we obtain the following system of equations:

$$\begin{cases}\dot{S}=-\beta SI+\gamma_2 R,\\ \dot{I}=\theta(N-S-I-R)-\gamma_1 I,\\ \dot{R}=\gamma_1 I-\gamma_2 R.\end{cases}$$

Equilibrium points of the system are the following:

1. $M_1=(N,0,0)$,
2. $M_2=(\frac{\gamma_1}{\beta},\frac{\gamma_2\theta(N\beta-\gamma_1)}{\beta(\gamma_1\theta+\gamma_1\gamma_2+\gamma_2\theta)},\frac{\gamma_1\theta(N\beta-\gamma_1)}{\beta(\gamma_1\theta+\gamma_1\gamma_2+\gamma_2\theta)})$.

As we have mentioned before, the first point M_1 describes the situation where there are no infected or recovered individuals.

We can reduce the system by the following substitutions:

$$\begin{cases}S_1=AS,\\ I_1=BI,\\ R_1=CR.\end{cases}$$

Since all functions are functions of t, we may introduce one more substitution: $t_1=Tt$.

$$\begin{cases}\frac{1}{T}A\dot{S_1}=-\beta ABS_1I_1+\gamma_2 CR_1,\\ \frac{1}{T}B\dot{I_1}=\theta(N-AS_1-BI_1-CR_1)-\gamma_1 BI_1,\\ \frac{1}{T}C\dot{R_1}=\gamma_1 BI_1-\gamma_2 CR_1.\end{cases}$$

We move T to the right hand side:

$$\begin{cases}\dot{S_1}=-\beta BTS_1I_1+\frac{\gamma_2 CT}{A}R_1,\\ \dot{I_1}=\frac{\theta NT}{B}-\frac{\theta AT}{B}S_1-\theta TI_1-\frac{\theta CT}{B}R_1-\gamma_1 BI_1,\\ \dot{R_1}=\frac{\gamma_1 BT}{C}I_1-\gamma_2 TR_1.\end{cases}$$

We perform the following change of variables:

$$\begin{cases}\gamma_1=1+\frac{B}{A},\\ \gamma_2=\frac{A}{CT},\\ \theta=\frac{B}{AT},\\ \beta=\frac{1}{BT}.\end{cases}$$

Thus, we obtain the following system:

$$\begin{cases}\dot{S_1}=-S_1I_1+R_1,\\ \dot{I_1}=\frac{N}{C}-\frac{A}{C}S_1-I_1-R_1,\\ \dot{R_1}=I_1-\frac{A}{C}R_1.\end{cases}$$

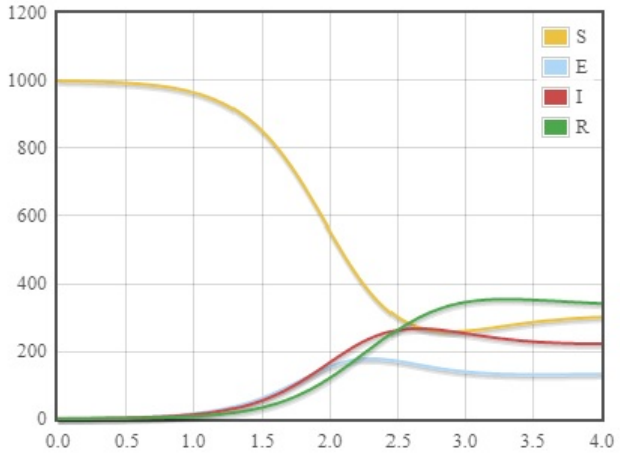

Figure 3: The evolution of the epidemic: the number of individuals of each class in time

We again reduce the system by the following substitutions:

$$\begin{cases} S_2 = S_1 - \dfrac{C}{A}, \\ I_2 = I_1 - \dfrac{(N-C)A}{(C+A)C}, \\ R_2 = R_1 - \dfrac{N-C}{C+A}, \\ N = C + 2A. \end{cases}$$

Then the system looks as follows:

$$\begin{cases} \dot{S}_2 = -\dfrac{A}{C}S_2 - \dfrac{C}{A}I_2 - S_2 I_2 + R_2, \\ \dot{I}_2 = -S_2 - I_2 - R_2, \\ \dot{R}_2 = I_2 - \dfrac{A}{C}R_2. \end{cases}$$

Hence, the linearization matrix of the autonomous system is as follows:

$$J = \begin{pmatrix} -\frac{A}{C} & -\frac{C}{A} & 1 \\ -1 & -1 & -1 \\ 0 & 1 & -\frac{A}{C} \end{pmatrix}.$$

Now we calculate the characteristic polynomial:

$$\begin{vmatrix} -\frac{A}{C} - \lambda & -\frac{C}{A} & 1 \\ -1 & -1 - \lambda & -1 \\ 0 & 1 & -\frac{A}{C} - \lambda \end{vmatrix} = 0.$$

So we have the following equation for eigenvalues:

$$\lambda^3 + \lambda^2\left(1 + \frac{2A}{C}\right) + \lambda\left(1 + \frac{A^2}{C^2} + \frac{2A}{C}\right) + \left(\frac{A^2}{C^2} + \frac{A}{C} - 2\right) = 0.$$

We use the *Lyapunov theorem on stability by the first approximation*:

If all the eigenvalues λ_i of the Jacobian J have negative real parts, then the zero solution of the initial system and the linearized system is asymptotically stable.

To find conditions which guarantee the negativity of the real parts of all eigenvalues of the resulting system, we use the Routh-Hurwitz criterion:

$$1 + \frac{2A}{C} > 0,$$
$$1 + \frac{A^2}{C^2} + \frac{2A}{C} > 0,$$
$$\frac{A^2}{C^2} + \frac{A}{C} - 2 > 0,$$
$$\begin{vmatrix} 1 + \frac{2A}{C} + \gamma_2 & 1 \\ \frac{A^2}{C^2} + \frac{A}{C} - 2 & 1 + \frac{A^2}{C^2} + \frac{2A}{C} \end{vmatrix} > 0.$$

As $A > 0$ and $C > 0$, we have to consider only the third condition:

$$\frac{A^2}{C^2} + \frac{A}{C} - 2 > 0.$$

That is $(A - C)(A + 2C) > 0$. As $A + 2C > 0$, the condition is the following:

$$A - C > 0,$$

where

$$A = -1 + \sqrt{\frac{\beta^2(1+\gamma_1)^2}{\gamma_2} + N},$$
$$C = \frac{A^2\beta(1+\gamma_1)}{\gamma_2}.$$

This gives us the following result.

Theorem 1 *If $A > C$ holds, then in the SEIRS model there exists an asymptotically stable equilibrium point.*

Now we show an example of such a point for $N = 1000$, $\beta = \frac{1}{100}$, $\gamma_1 = 5$, $\gamma_2 = 3$, $\theta = 2$, $S(0) = 999$, $I(0) = 1$.

Figure 3 shows the evolution of the epidemic over a period of time t.

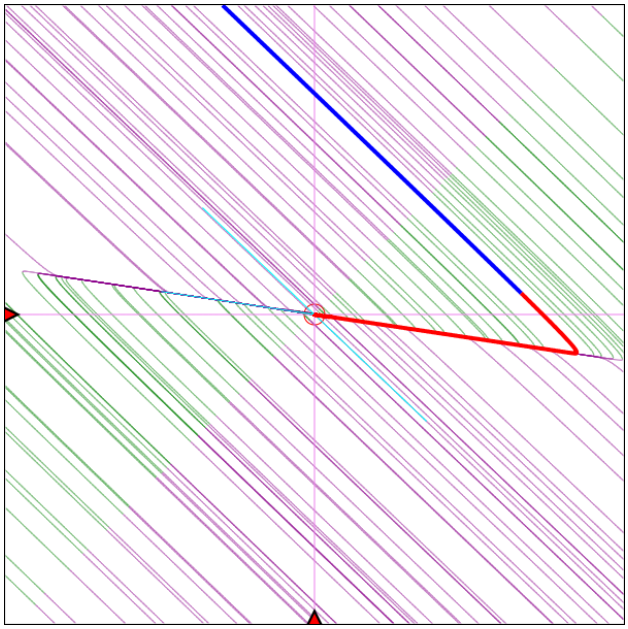

Figure 4: Saddle on the plane (S, I) with $R = const$

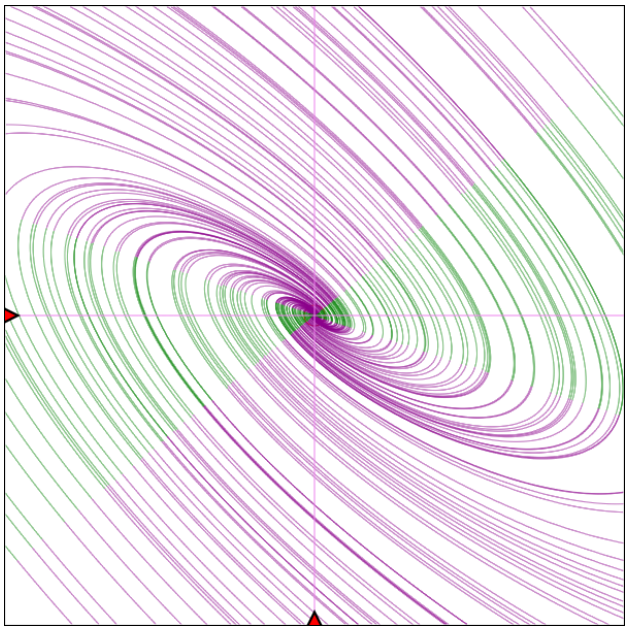

Figure 5: Stable focus on the plane (S, R) with $I = const$

To visualize the behavior of functions, we construct phase portraits for particular cases in which one of the functions (S, I or R) is a constant.

1. The plane (S, I) with $R = const$ ($\dot{R} = 0$) is shown on figure 4.

2. The plane (S, R) with $I = const$ ($\dot{I} = 0$) is shown on figure 5.

3. The plane (R, I) with $S = const$ ($\dot{S} = 0$) is shown on figure 6.

If $A < C$ then we have the following options.

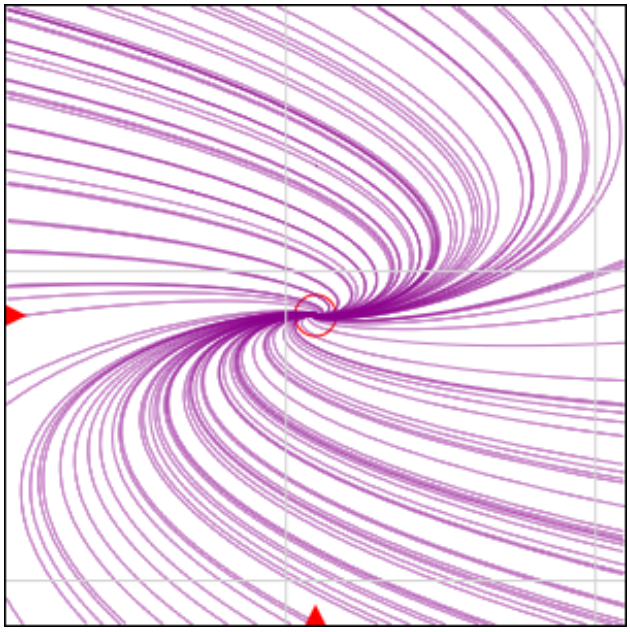

Figure 6: Stable focus on the plane (S, R) with $I = const$

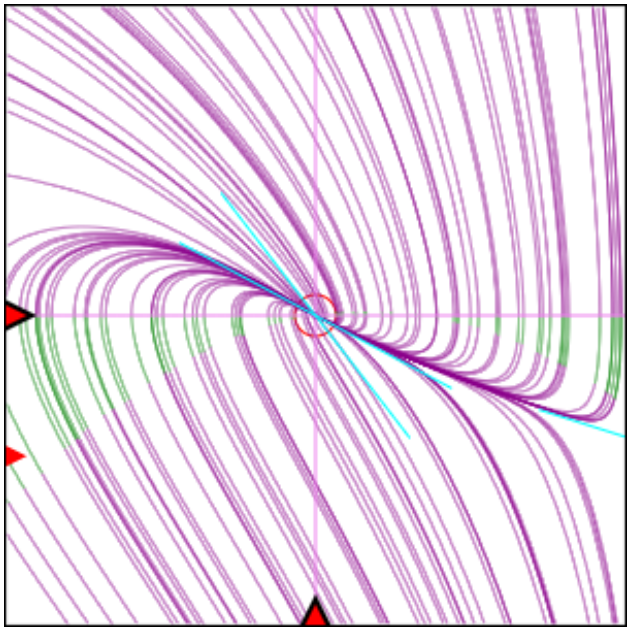

Figure 7: Stable node on the plane (S, I) with $R = const$ and $A < C$

1. If $\lambda_1 > 0, \lambda_{2,3} = x \pm iy, x > 0$, where $\lambda_1, x, y \in \mathbb{R}$, then the equilibrium point is an unstable node-focus.

Figure 7 shows a sample phase portrait on the plane (S, I) with $\dot{R} = 0$ in the neighborhood of the equilibrium point.

Figure 8 shows a sample phase portrait on the plane (S, R) with $\dot{I} = 0$ in the neighborhood of the equilibrium point.

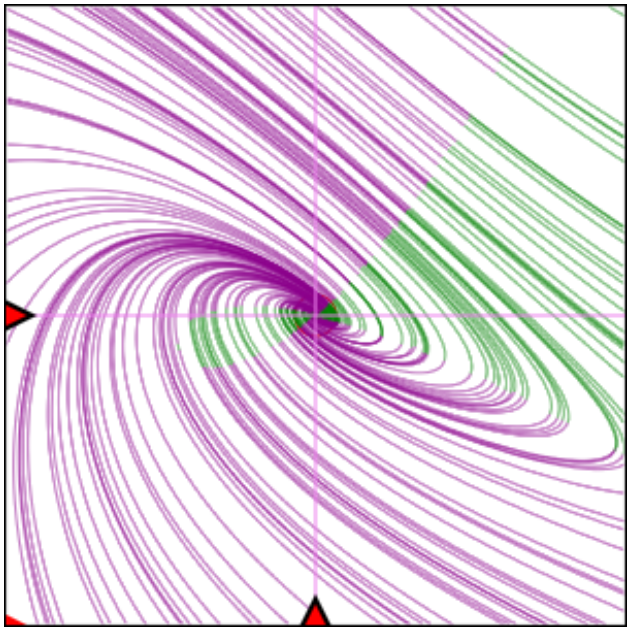

Figure 8: Stable focus on the plane (S, R) with $I = const$ and $A < C$

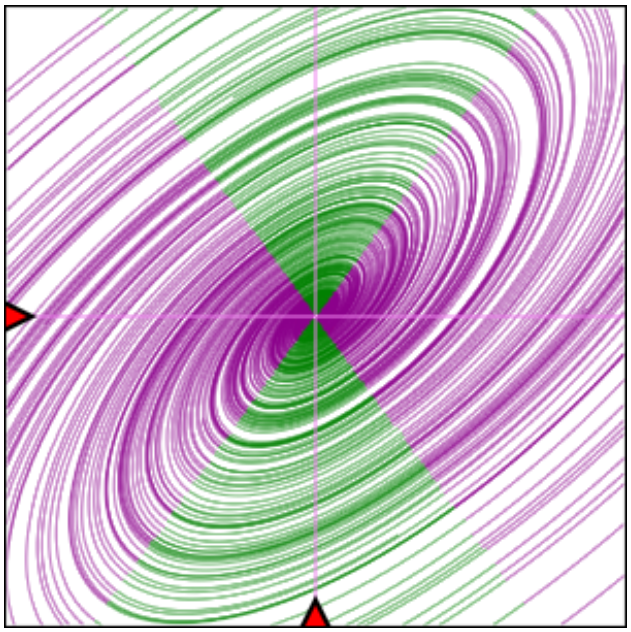

Figure 9: Stable focus on the plane (R, I) with $S = const$ and $A < C$

Figure 9 shows a sample phase portrait on the plane (R, I) with $\dot{S} = 0$ in the neighborhood of the equilibrium point.

2. If $\lambda_1 < 0, \lambda_{2,3} = x \pm iy, x < 0$, where $\lambda_1, x, y \in \mathbb{R}$, then the equilibrium point is an unstable node-focus.

3. If $\lambda_1 < 0, \lambda_{2,3} = \pm iy$, where $\lambda_1, y \in \mathbb{R}$, then the equilibrium point is an unstable node-center.

4. If $\lambda_1 < 0, \lambda_{2,3} > 0$, then the equilibrium point is an unstable saddle-node.

We have no other options because of constraints on A and C.

4 Conclusion

In this paper we have deduced the condition for a stable solution in two models of the epidemic. We found the line of change in stability for instability $\beta N = \gamma_1$ in the model $SIRS$ and $A = C$ in the model $SEIRS$. This shows that in diseases there are parameters that we can influence, so that the epidemic does not turn into a cycle. The general case of these models were described in [1]. However, we were able to add a visual representation of the trajectories in the neighborhood of the equilibrium points of the system.

The models considered are fairly simple, they do not take into account neither mortality nor fertility. In subsequent works, we plan to consider the effect of vaccination, extend the model to an non-closed population and look at the simultaneous course of two different diseases in one group.

References:

[1] H.W. Hethcote and P. van den Driessche, *Some epidemiological models with nonlinear incidence*, Journal of Mathematical Biology, 1991.

[2] *PhaPl: Phase Plane Helper*, URL: https://phapl.github.io/phapl.en.html , (2018).

[3] Cherepanov A., *PhaPl: software to plot and research phase portraits automatically,* Otkrytoe obrazovanie, Vol.21, No.3, 2017, pp. 66–72. (Russian)

[4] Meurer, Aaron and Smith, Christopher P. and Paprocki, Mateusz and Čertík, Ondřej and Kirpichev, Sergey B. and Rocklin, Matthew and Kumar, et al., *SymPy: symbolic computing in Python,* PeerJ Computer Science, Vol.3, 2017, e103, https://doi.org/10.7717/peerj-cs.103

[5] Diekmann O. and Heesterbeek J.A.P. *Mathematical Epidemiology of Infectious Diseases: Model Building, Analysis and Interpretation,* John Wiley and Sons, 2000.

[6] A.Bratus, A.Novozhilov, A.Platonov, *Dynamic systems and models in biology*, Draft, published in Russian, 2011.