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ANALYSIS OF SIR MODEL FOR PREDICTING THE SPREAD OF MEASLES

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Introduction. The main task of the health care system in any country is to control the spread of infectious diseases. The social consequences, as well as the material losses, strongly demonstrate the need to predict the occurrence of epidemics. Measles is one of the most contagious diseases. In Ukraine, according to the Public Health Center of the Ministry of Health of Ukraine, more than 115,000 people have contracted measles since summer 2017, 41 of whom have died [1]. Simulation of the measles spreading allows to predict new outbreaks of measles and evaluate the strategy to prevent them.

The aim of this paper is to analyze the SIR epidemic model for simulation of the spread of infectious diseases and to select the appropriate model extension for modeling the spread of measles.

Epidemiology of measles. Measles is a viral infectious disease that starts in the respiratory system. Symptoms of measles generally first appear within 10 to 12 days of exposure to the virus. They include cough, fever, runny nose, red eyes, sore throat white spots inside the mouth. A widespread skin rash is a classic sign of measles. This rash lasts up to 7 days.

Measles can be spread through the air. An infected person release the virus into the air through coughing or sneezing. A susceptible person that is exposed to the measles virus has a 90 percent chance of becoming infected. An infected person is contagious for 4 days before the characteristic rash appears and for another four days after the rash.

Getting vaccinated is the best way to prevent measles. Two doses of the vaccine are approximately 97% effective at preventing measles, while one dose is about 93% effective. When rates of vaccination within a population are greater than 92% outbreaks of measles typically no longer occur. During 2000 – 2017, measles vaccination prevented an estimated 21.1 million deaths throughout the world [2].

The classical SIR model. A significant contribution to the mathematical modeling of epidemics has been made by W. O. Kermack and A. G. McKendrick in their scientific work "A Contribution to the Mathematical Theory of Epidemics" [3], published in 1927. The SIR model, which was described in their scientific work, is now one the most popular models for modeling the spread of infectious diseases. The authors divided the whole population into three groups:

– S (t) – susceptible individuals who are not yet infected;
– I (t) - infected individuals capable of transmitting infection to susceptible people;
– R (t) - individuals who have been cured and immune to the disease therefore unable to contract the disease or transmit the infection.

This model is named SIR (Susceptible – Infected – Recovered), where the first letters of every group name had been used.

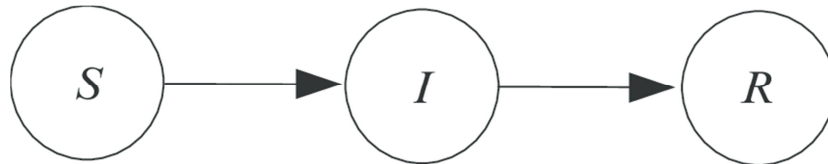The transition of individuals from one group to another in this model is shown in Figure 1:

Fig. 1. The transition of individuals from one group to another in the SIR model

Assuming that population number is constant and equal to N = S (t) + I (t) + R (t), Kermak and McKendrick obtained the following equations to describe the epidemic:

$$\frac{dS}{dt} = -\beta I \frac{S}{N}, \tag{1}$$

$$\frac{dI}{dt} = \beta I \frac{S}{N} - \gamma I, \tag{2}$$

$$\frac{dR}{dt} = \gamma I, \tag{3}$$

where β - transmission probability;
1/γ - the average duration of the infectious period.

The SIR model assumes that all individuals in the population may equally be infected with the rate β. The first equation describes the dynamics of the number of individuals who are susceptible to the disease: an infected individual at a certain rate infects the susceptible individual. The second equation describes the dynamics of the number of infected individuals: the difference between the number of infected and the number of recovered individuals. The third equation describes the dynamics of recovery of the infected individual: at some speed the infected individual recovers.

Many modifications to the SIR model have been developed: SI model, which is successfully used to for modelling life-threatening epidemics of diseases (for example, herpes), SEIR model with an additional, "incubation" stage of the disease (for example, tuberculosis, measles), SIS model that is suitable for diseases without incubation period and without lifelong immunity (for example, rhinoviruses or venereal diseases such as gonorrhea or chlamydia).

SEIR model. The SEIR model divides the whole population into four groups: Susceptible (S), Exposed (E), Infected (I), Recovered (R). Exposed group is a number of individuals who are already infected with the disease but not able to transmit it.

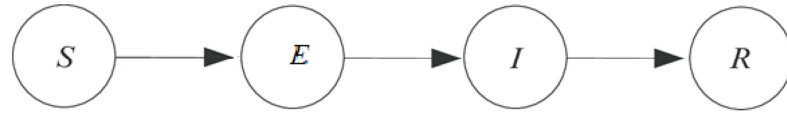The transition of individuals from one group to another in this model is shown in Figure 1:

Fig. 1. The transition of individuals from one group to another in the SEIR model

The SEIR model system is made of four differential equations:

$$\frac{dS}{dt} = -\beta I \frac{S}{N}, \tag{4}$$

$$\frac{dE}{dt} = \beta I \frac{S}{N} - \alpha E, \tag{5}$$

$$\frac{dI}{dt} = \alpha E - \gamma I, \tag{6}$$

$$\frac{dR}{dt} = \gamma I, \tag{7}$$

where β - transmission probability;

α - the average duration of the infectious period ;

$1/\gamma$ - the average duration of the infectious period.

This model has a disadvantage as it does not consider the possibility of being vaccinated. Our modification of the SEIR model contains both vaccination rate and vaccine efficacy as a way to decrease the number of susceptible and infected individuals:

$$\frac{dS}{dt} = -\beta I \frac{S}{N} - evS, \tag{8}$$

$$\frac{dE}{dt} = \beta I \frac{S}{N} - \alpha E, \tag{9}$$

$$\frac{dI}{dt} = \alpha E - \gamma I, \tag{10}$$

$$\frac{dR}{dt} = \gamma I + evS, \tag{11}$$

where e - vaccine efficacy;

v - vaccination rate.

A certain amount of susceptible will be vaccinated and move into the recovered class without becoming infected.

Conclusions. An analysis of SIR mathematical model of the spread of infectious diseases and its modifications is made in this article. In particular, SEIR model is considered and its features are described. An epidemiological characteristics of measles are studied. An appropriate model for modeling the spread of measles is selected and improved by adding two parameters: vaccination and vaccine efficacy.

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УДК 004.9

ВИКОРИСТАННЯ ІНТЕЛЕКТУАЛЬНОГО АНАЛІЗУ ДАНИХ ДЛЯ ДОСЛІДЖЕННЯ МОДЕЛІ ВИБОРЧОЇ КОМПАНІЇ

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Постановка проблеми. Дослідження аналітичних методів Microsoft SQL в галузі інтелектуального аналізу даних для створення моделі виборчої компанії. Для цього необхідно виділити підмножини вирішуваних завдань, провести порівняльний аналіз методів інтелектуального аналізу даних для вибраних типів завдань і на практичному прикладі визначити випадки, для яких більш привабливим є той чи інший метод.

Різноманіття методів для вирішення цього завдання ставить перед аналітиком питання вибору алгоритму, який найкращим чином придатний підходить під поставлені вимоги задачі [1, 2]. Так, у разі кластеризації, рекомендується використовувати ієрархічні методи, якщо заздалегідь невідомо число кластерів і потрібно отримати детальне уявлення про структуру даних. У свою чергу, ітеративні методи характеризуються більш високою стійкістю по відношенню до шумів і викидів, некоректного вибору метрики, включенню в аналіз незначущих атрибутів, але вимагають апріорної вказівки числа кластерів. У разі вибору методу класифікації необхідно брати до уваги такі параметри, як