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A MATHEMATICAL *SIR* MODEL FOR EPIDEMIC EMERGENCY

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Abstract: Outbreaks of infectious diseases are one of the worst scourges in the history of mankind that have affected its flow. First they were tied to the supernatural beings, then they were used as a cause for wars and state internal showdowns, only then as a matter of medicine. For a long time, epidemics of infectious diseases have been considered only as a medical phenomenon, but by expanding the fields of security procedures, this phenomenon is classified in a group of emergency. It was found that in these situations there is certain mathematical regularity that can predict possible consequences. In order to be mathematically modeled performance of the epidemic in a large population need to be grouped into departments. Agreed standard labels for these units as *S* (for susceptible – exposed), *I* (infected) and *R* (recovered), so this model is called the *SIR* model. This is a simple model for many infectious diseases including measles, mumps and rubella. Number of persons in each department may vary in time, and it follows that the precise numbers must be calculated as a function of time *t: S (t), I (t)* and *R (t).*
Key words: outbreak, an emergency, *SIR* model, an infectious disease.

1. Introduction

Some threats to human race were known centuries ago, but they were not perceived as a security problem. Thus for centuries, also millennia, people feared infectious diseases. In ancient times, during the Peloponnesian War, Athens lost its primacy in the war with Lacedaemons precisely because its population was decimated by the plague. During this outbreak, Athens lost almost a quarter of its population, including their leader Pericles.

The first recorded plague pandemic occurred in Egypt in 541, expanded beyond the borders of the state and killed almost half of the population of North Africa, Europe and South and Central Asia. The second began in 1346 and killed a

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third of Europe's population by 130 years of its duration[1], while the third came in the sixties of the nineteenth century and caused the deaths of 12 million people (Jović, Savić, 2004: 145). During the twentieth century the pandemic infectious diseases occurred on several occasions. In the twilight of World War I, in 1918, there appeared influenza (Spanish fever – H1N1) in the American Midwest that spread with incredible speed, and soon engulfed Russia, China and the entire United States, where it was transmitted to pigs, and made its new mutations. This flu infected about one third of the world's population (500 million), according to some estimation about 40 million people died. Other flu pandemics occurred in the 1957, the so-called Asian flu (H2N2), where, according to the World Health Organization, about 24% of world population was affected. The next pandemic Hong Kong flu (H3N2) occurred in 1968 and according to some estimations between 1 and 4 million inhabitants died from its effects (Vučić-Janković, Knežević, Kanazir 2006: 19–26).

While many vaccines for infectious diseases are available, diseases continue to cause suffering and death worldwide, especially in developing countries. In the developed countries, chronic diseases such as cancer and cardiovascular disease are devoted more attention than infectious diseases, but infectious diseases are still common cause of death. For instance, HIV (AIDS) has become an important infectious disease in the industrialized and developing countries. So far, this disease killed around 30 million people, while, by comparison, during World War II approximately 28 million people were killed. The National Security Council of the U.S.A. in a special report from 2000 provided a review of the possible sequence of events in the world in terms of outbreaks of infectious diseases. According to the experts of the Council, infectious diseases represent one of the most common causes of death of people. The report noted that infectious diseases exceedingly slow socioeconomic development of developing countries and previous communist countries and regions. This will adversely affect the development of democracy in them and transition, and the humanitarian disaster and conflicts among the population. In this regard the following table lists the effects of globalization and technical and technological development of the movement and development of infectious diseases. Based on their study the factors that contribute to the return and consolidation of infectious diseases, as well as new forms of infectious diseases are (The National Intelligence Council, 2000: 33–65):

- demographic change and human behavior (Dengue/hemorrhagic fever, sexually transmitted diseases, giardiasis, for example),
- technology and industry (toxic shock syndrome, atypical infections, inflammation of the intestine followed by bleeding, hemolytic uremic syndrome),

[1] According to some research, its appeasement began in 1353, but with longer breaks and to a less extent continued until the end of the fifteenth century. It caused the death of 25 million Europeans. For the epidemic as the main culprits, the Christians proclaimed that Jews had ostensibly decided to poison all Christians. Thus many Jews were tried and they were often punished for their "misdeeds" by burning at the stake bonfires, they were forbidden for many years to appear in cities, etc. The starting point of a pandemic was in northern China and Mongolia, where the trade routes spread to Europe. (Djarmati, S., Aleksic, Dj. *Destructive forces*, Belgrade, 2004, 140–142.)

– economic development and impoverishment of arable land (Lyme disease, malaria, plague, rabies, yellow fever, Rift-Valley fever, schistosomiasis),
– world travel and international trade (malaria, cholera, Pneumococcal pneumonia),
– the ability of adaptation and mutation of microbes (influenza, HIV, malaria, infections caused by Staphylococcus Aureus),
– reducing the quality of public health measures (rabies, tuberculosis, “trench” fever, diphtheria, whooping cough, cholera), and
– climate change (malaria, dengue, cholera, yellow fever).

2. Epidemic Emergencies

Epidemics of infectious diseases is the appearance of disease in a place with more people, whose number is increasing day by day and has some specific features related to infectious diseases. ”An epidemic of infectious disease is an increase in the number of patients suffering from infectious diseases that is higher than usual in a particular population and in a given time“ (*Službeni glasnik RS*, 125/04). Patient is (or can be) a source of infection, indicating the anti-epidemic fighting strategy. The source of infection may not even be clinically ill. Finally, the level of collective immunity determines the occurrence and course of the epidemics, which leads to the conclusion that the inhabitants of certain areas may be resistant to the agents of the relevant infectious diseases, but such resistance cannot develop such resistance towards e.g. radiation (Radovanović 2000: 7).

In the framework of the World Health Organization the epidemic of infectious disease means ”occurrence and transmission of disease from one person to another or from animals to humans in the community and simultaneously in a particular territory, and the occurrence of the disease spreading“ (Infections and infectious diseases, 2001: 3). The World Health Organization has a special department that deals with outbreaks of infectious diseases. Special attention within that department focuses on the so-called Highly Infectious Diseases under what are considered ”diseases that are transmissible from person to person, causing a high-risk disease on people’s life and a great danger in places (quarantines) for health care in the communities, demanding special measures of control (Brouqui, Ippolitto: 2).“

In the document of the Prime Minister office of the United Kingdom ”Dealing with accidents“ epidemic of infectious disease may in some cases reach the level of so-called major emergencies. Such an emergency situation causes death and injury to people, breaking the normal functioning of society and so on. Upon the opinion of the creators of this act, epidemic disease may cause full societal disintegration of society and political community, since modern diseases are highly infectious and cause a high percentage of mortality. Upon the draft Law on Civil Protection in March 2008, compiled by the Ministry of Defense of the Republic of Serbia, outbreaks of infectious diseases are treated as a natural disaster. As an emergency situation, in terms of the draft, the epidemic disease becomes at the moment when ”the risks and threats or the consequences of the epidemic on population, environment and material goods, such a scale and intensity to their occurrence or consequences cannot be prevented or remedied by regular action by agencies and services, and mitigation and removal of special measures must be used". In the laws and legal acts of many countries and international organizations and professional associations, an outbreak of infectious disease is classified in a group of emergency situations, as for its suppression and recovery of the population from its effects the necessary emergency measures and the use of extraordinary means and forces are required. Epidemics of infectious diseases are an emergency situation and in all known forms have the most unpredictable onset, course and completion. It is because of the impossibility of observation with the naked eye and unknown to the people; it is one of the most insidious and has a deterrent effect. Several times during the history of outbreaks of infectious diseases revealed that it is deadlier than war, technical and technological disasters, earthquakes, floods, etc. It is a common "companion" of other emergencies, crises and disasters, natural or any other character. Because of this, it is necessary that the security experts show more interest in this problem.

3. Mathematical Modeling of Epidemic

Based on previous studies of outbreaks of infectious diseases, diseases result from the state of health and disease state, which is a product of constantly interacting forces and their mutual reactions in the frame of the ecological systems that are people as hosts with all elements of the animate and inanimate nature. As a basic principle, ecological approach to explaining the disease or pathological condition becomes necessary. Thus, the result is a construction of several epidemiological models.

First, mathematical models clarify the interaction between the factors responsible for the current incidence, and to assessment of possible epidemiological situation. These models are used for the prediction of the effects of some interventions, such as the effectiveness of alternative measures to prevent and repress the disease. This is a theoretical concept developed with remarkable practical benefits, but it is recommended that the epidemiologist with strong knowledge of mathematics with the assistance of mathematicians or biostatisticians use these model approaches (Christie, Gordon, Heller, 1997).

The structure of incidence and mortality in the developed world is gradually bifurcating to non-infectious diseases. This trend is reflected in the development of epidemiology. Hence, among epidemiologists there is a need for an acceptable way of making disease models. Such a model is an ecological (epidemiological) triad. This model requires excellent knowledge of all factors causing disease, characteristics of the host and the environment. Agents that cause disease, the body that suffers the consequences of their actions and the environment in which the agent and host face are in a constant strive for mutual respect and balancing, which is to be understood as a kind of dynamic reconciliation. This model has shown good results when the epidemiological studies included exceedingly victims of plague and when the causes, as agents, are separated from other host factors and the environment. Wheel model with its core part represents the man, a host with genetic determinants in the center. It is surrounded by areas, schematically divided into biological, physical and socio-economic, which are tightly bound. Vogriklov chain is a model that relies on the knowledge of epidemiology of certain infectious diseases by directing practical measures against those factors by whose exclusion they achieve the easiest and most effective series breaking and prevention of further expansion of the disease. Wheel model and the network of causality are focused on steadily expanding the application of epidemiological methods in studying chronic non-infectious diseases, exceedingly unrelated to specific agents or they are considered as an integral part of the environment. Network model of causality is one of the modern approaches to elucidation of disease etiology. Basically this model is that disease does not depend only on one factor, but from a low of causal components linked into a chain in which each of them is preceded by a low, and so together they form a network of causality. The limits of the network are difficult to determine because the sequence of cause and effects is almost infinite, and their overall knowledge is impossible because it goes beyond human capabilities.

In many sciences experiments can be performed in order to gather information and establish appropriate hypotheses. However, experiments with the spread of infectious diseases among humans cannot be made. The data obtained from outbreaks that occur naturally are usually incomplete with regard to the need to obtain a complete picture about the epidemic. This absence of reliable data prevents the estimation of parameters of the epidemic so that it is only possible to estimate the range of values for some parameters. As repeatable experiments and true information are not available in epidemiology, mathematical models and computer simulation must be used to realize the necessary theoretical experiments. The necessary calculations can be easily carried out for different values of the parameters and data.

Replacement of the studied object by its image – mathematical model and its study is the essence of mathematical modeling. Research work that is not done on the very object (occurrence, process) but on its model provides the ability to painlessly and relatively quickly, without high expenses and, as a rule, in all imaginable situations, investigate the behavior of the very object. The dissemination of ideas and methods from one area to another activity is useful and contributes to the development of both activities. Analogies that are thereby established are undoubtedly useful and can accelerate development activities, but, of course, with one restriction – one must accurately determine the boundaries of the usage of analogy. Any excess of these limits could lead to large errors. Mathematical models have limitations and shortcomings which we need to be aware of, e.g. for the modeling of epidemics of infectious diseases we must know that the interaction of transmission in the population is very complex, and it is extremely difficult to cover the enormous scale of the dynamics of disease spreading. Spreading of infectious diseases involves not only factors based on disease like cause of disease and ways of transmission, but also social, cultural, demographic and economic factors. It is known that the probability of getting the disease is not constant in time. The common experience is that some disorders are more frequent in winter, the other in summer that is, depending on weather conditions. Moreover, with the children's illnesses, there is a huge influence of school calendar, so during school vacations, the probability of getting these diseases are declining. So, for many groups of diseases one should consider the strength of infection depending on the periodic (seasonal) varying of the number of contacts. For these reasons we are forced to do modeling of many such simplifications, e.g. when we use an epidemiological model for the microscopic description (role of a single infection) and then we use it to predict macroscopic behavior of the spread of disease in the population.

4. Assumptions of the Model and Marking

The study of disease occurrence is called epidemiology. The epidemic is unusually large, short-term disease occurrence. Analysis of epidemic models can be deterministic and stochastic. They differ in that as the relationship

Figure 1: Schematic division into groups with SIR model

between the values that appear in the analysis of epidemics, at the deterministic model, they are expressed by differential equations, while the stochastic models are expressed by difference equation. In this paper we use the so-called deterministic *SIR* model. *SIR* model was first created by Kermack and McKendrick ("The contribution to the mathematical theory of epidemics.") and played a major role in mathematical epidemiology. In the model, the observed population is divided into three groups: the susceptible S, the infected with I, the recovered R and these groups are changing over time, i.e. functions from *t – S (t), I (t)* and *R (t).*

The sensitive are those who are not infected or immune, the infected are those who are infected and can transmit the disease, and the recovered are those who are infected, recovered and permanently immune. In this epidemiological model the following assumptions have been made:

The considered population has constant size that we mark with N large enough so that the size of each group can be considered as a continuous variable. It is assumed that the infection lasts a short time, so that all who belong to the group are born sensitive. We assume also that the number of deaths in the period is equal for members of all three groups; the number of births and deaths from natural causes is equal and negligibly small for a given period of time so that the entire population is stationary.

The population is homogeneously mixed. The daily number of contacts α is the average number of adequate contacts per infected during the day. Adequate contact of infected is the interaction that results in a second infected individual if he is from the group of the susceptible. The average number of the susceptible infected from one infected per day is αS and the average number of the susceptible infected by one group per day is αSI . The daily number of contacts α does not vary during the season. The type of direct and indirect contacts adequate for transmission depends on the disease.

The number of individuals who have recovered and left the group of the infected is proportional to the number of the infected with a constant β ratio, and is called the daily number of shifts to recovery. The latent period is zero (the latent period is defined as the period between the time of exposure to infection and time of infection). Based on given assumptions, we can write the following relations (Murray, 2001; Brauer et al, 2008):

$$\frac{dS}{dt} = -\alpha SI; \frac{dI}{dt} = \alpha SI - \beta I; \frac{dR}{dt} = \beta I; S(0) > 0; I(0) > 0; R(0) \geq 0 \qquad (4.1)$$

This system is nonlinear and does not allow general analytical solution. However, significant results can be derived analytically [11–13]. First, it is noted that:

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0; S(t) + I(t) + R(t) = const = N \qquad (4.2)$$

Then, you can find links between the parameters that characterize α and β size groups in the population. Designation ∞ refers to the moment when the epidemic ends. t_{dur} refers to the time spread of the epidemic. R_0 is called the basic reproductive number. If $R_0 < 1$, there is an epidemic. If $R_0 > 1$, there are no conditions for the occurrence of epidemics. [13]

$$\beta = \frac{1}{t_{dur}}; \frac{\alpha}{\beta} = \frac{\ln S(0) - \ln S(\infty)}{K - S(\infty)}; K \approx S(0) + I(0); R_0 = \frac{\alpha N}{\beta} \qquad (4.3)$$

If we eliminate the dependence on time from the system of equations (4.1), we can show the dependence of *I* from *S* in the so-called phase plane and find a connection between the corresponding parameters.

As the system of equations (4.1) is nonlinear, the question of stability of the system that this equation describes is raised. The answer to the question of the stability of the system can be obtained by linearization of system of equations (4.1) (Edelstein-Keshet, 2005). However, stability is not really the primary issue of this model. Some typical questions are of interest (Hetcote, 2000: 599–653): (1) How many of the sensitive are infected? (2) What is the number of peaks in the infected? (3) When does the epidemic experience peak? (4) How does the maximum number of the infected depend on the initial number of the infected?

One of the interesting predictions of S-I-R model is that epidemic stops when the infected disappear and not the sensitive. To demonstrate the possibilities of this model, we analyzed an epidemic of enterocolitis that appeared in Topola, near Kragujevac in 2002 (Obaveštenje Ministarstva zdravlja RS). The data on the epidemic are given in Table 1.

Days	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
The number of the infected	7	48	102	90	67	38	35	18	15	7	14	26	17	8	16	7	2

Table 1

Since Topola, according to the statistics (*Podaci Republičkog zavoda za statistiku RS*), has 25,292 inhabitants and 31 settlements, the population to which the model applies has 816 inhabitants. Epidemic lasts for 17 days and 522 inhabitants were infected. Using Mathematica 7.0 appropriate numerical solutions of the system were found (4.1) in case of epidemics in Topola and given in the graphs.

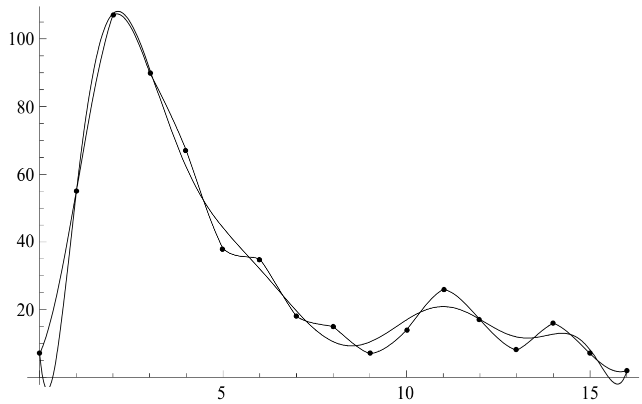

Figure 2: The number of the infected according to the data – blue colour. In red colour the fitted curve is presented which gives the number of the infected over time.

From Equation (4.3), we find parameters - $\alpha = 3.62 \cdot 10^{-3}$ and $\beta = 1.875$.

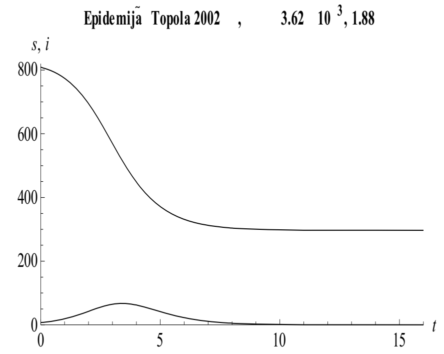

Figure 3: The dependence of the number of the infected I and number of the sensitive S on time

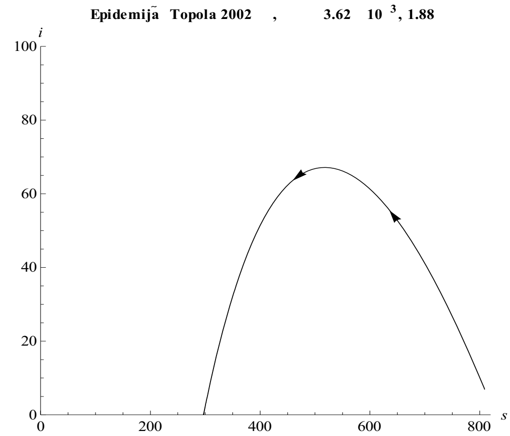

Figure 4: Dependence of I from S given in the phase plane

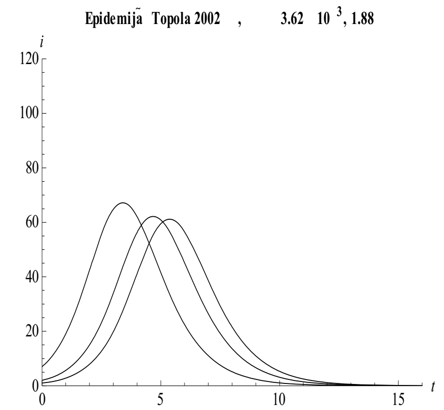

Figure 5: The dependence of the maximum of the epidemic from the initial number of the infected I (0) during time

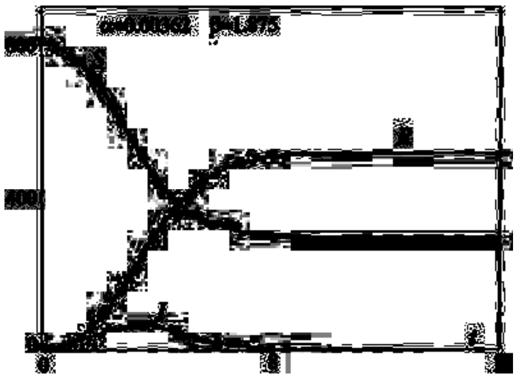

Figure 6: The dependence of S (t), I (t) and R (t)

From Figure 2, it can be found that the maximum of the epidemic is achieved on the second day and the maximum number of the infected is 108, which pretty well fits the actual facts. From Figure 3, one sees how a number of the sensitive S decreases with time up to certain values when it comes to saturation, i.e. no more affected. It also corresponds to annulling the number of the infected. On Figure 4, in the phase plane it can be observed as the number of the infected increases (arrows indicate the direction of development of the epidemic) and then decreases to zero when saturation is achieved with the Figure 3.

On Figure 5, the dependence of the maximum size from the initial number of the infected $I(0)$ is shown. It is obvious that the maximum $I(t)$ will be higher if $I(0)$ is higher. The Figure 6 shows, for comparison, change of all three groups considered in a function of time. The basic reproductive number is $R_0 = 1.5754 > 1$, and this indicates the existence of conditions for the occurrence of epidemic. To avoid further spread of the epidemic it is necessary that [4–5] $1-1/R_0 = 36.52\%$ of the total population *N* should be vaccinated. The essence of modeling is to find the relationships between the parameters of infectious diseases and that they are used for calculations of the effective mass vaccination program aimed at preventing the spread of epidemics.

5. Conclusion

Many challenges, risks and security threats in the modern history are multiplied and thus their number is steadily increasing. One such security issue is an epidemic of infectious disease for which the seventies of last century were considered that it is as a public health problem overcome and the triumph of primarily the World Health Organization confirmed that vaccination has managed to overcome this scourge forever. Then we have problems just because pathogens eventually managed to become resistant to the existing medical treatments. It became important to approach the problem in a new way.

One of the ways that may largely participate in fighting infectious diseases is a mathematical modeling of epidemic. Based on the epidemic that occurred, we can manufacture models of possible outbreaks at any territory, and therefore we can mitigate their effects. The replacement of the studied object by its image and its investigation is the essence of mathematical modeling. However, we must maintain awareness that these models have a lot of deficiencies, as in the case of outbreaks of infectious diseases when they have to take into account the relations in the society, but it is impossible to cover a wide scale dynamics of the infection spreading.

SIR mathematical model was first made by Kermack and McKendrick and played a core role in mathematical epidemiology. In the model, the observed population is divided into three groups: the susceptible S, the infected I and the recovered R and these groups are changing over time, i.e. functions of t – S (t), I (t) and R (t). The susceptible are those who are not infected or immune, the infected are those who are infected and can transmit the disease, and the recovered those who are infected, recovered and constantly immune. Based on the study of the epidemic of enterocolitis that appeared in Topola near Kragujevac in 2002, it was concluded that the epidemic modeling core of infectious diseases is to find relations between parameters of infection and that they are used for calculations of the effective mass vaccination program to prevent the expansion of the epidemic.

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7. References

Brauer, F. et al.,(2008). *Mathematical Epidemiology*. Springer.

Brouqui P., Ippolitto G. *Clinical Managementof Highly Infectious Diseases*, *ce. M.*

Christie, D., Gordon, I, Heller, F. R. (1997). *Epidemiology*, University of New South Wales, Second Edition, Sydney.

Dealing with disaster (2004). (Revised Third Edition). Cabinet Office.

Vučić-Janković, M., Knežević, T., Kanazir, M. (2006). Efikasnost mera javnog zdravlja u toku pandemije gripa, SARS-a i ptičjeg gripa. *Javno zdravlje i vanredne situacije*. Beograd: Glasnik Instituta za javno zdravlje.

Edelstein-Keshet, L. (2005). *Mathematical Models in Biology*. SIAM.

Hetcote, H. W. (2000). *SIAM review*, Vol.42, No. 4.

Zakon o zaštiti stanovništva od zaraznih bolesti. *Službeni glasnik RS*. 125/04.

Infections and infectious diseases. (2001). World Health Organization, International Federation of Red Cross and Red Crescent Societies.

Jović, R., Savić, A. (2004) *Bioterorizam – Biološki rat – Biološko oružje*. Beograd: Institut za političke studije, Centar za istraživanje bezbednosti i terorizma.

Murray, J. D. (2001). *Mathematical Biology 1*, Springer.

Nacrt Zakona o civilnoj zaštiti. (2008). Ministarstvo odbrane Republike Srbije. Beograd.
National Intelligence Council (2000). National Intelligence Estimate: The Global Infectious Disease Threat and Its Implications for the United States, *Enviromental Change & Security Project Report*, Issue 6.
Obaveštenje Ministarstva zdravlja RS. 01–1951, 8. 9. 2002.
Radovanović, Z. (2000). *Terenska epidemiologija*. Beograd: Medicinski fakultet.
Wikipedia. *Infectious Diseasses.*
Wikipedia. (2003). *Podaci Republičkog zavoda za statistiku RS.*

MATEMATIČKI *SIR* MODEL EPIDEMIJSKIH VANREDNIH SITUACIJA

Rezime

Mnogi izazovi, rizici i pretnje bezbednosti se u savremenoj istoriji multiplikuju i time se njihov broj neumitno povećava. Jedno od takvih bezbednosnih pitanja je epidemija infektivnih bolesti, za koje se sedamdesetih godina prošlog veka smatralo da su kao javnozdravstveni problem prevaziđene, te je od strane prevashodno Svetske zdravstvene organizacije trijumfalno potvrđeno da je imunizacija uspela da nadiđe tu pošast zauvek. Problemi su tek predstojali, jer su patogeni vremenom uspeli da postanu rezistentni na postojeće medicinske tretmane. Postalo je značajno kako pristupiti problemu na nov način.

Jedan od načina koji u velikoj meri mogu učestvovati u suzbijanju zaraznih bolesti jeste matematičko modelovanje epidemije. Na osnovu epidemija koje su se dogodile, mogu se izraditi modeli mogućih epidemija na bilo kojoj teritoriji, te se, stoga, mogu ublažiti njihove posledice. Zamena proučavanog objekta njegovim likom – matematičkim modelom i njegovim izučavanjem – jeste bit matematičkog modelovanja. Doduše, moramo se voditi svešću da ti modeli imaju mnogo nedostataka, kao u slučaju epidemije zaraznih bolesti, kada se moraju uzeti u obzir odnosi u društvu, što nije moguće obuhvatiti širokom skalom dinamike širenja infekcije.

Matematički *SIR* model je prvi sačinjen od strane Kermaka i Mekendrika i odigrao je ključnu ulogu u matematičkoj epidemiologiji. U modelu je posmatrana populacija podeljena na tri grupe: osetljive *S*, inficirane *I*, i oporavljene *R* i te grupe se menjaju tokom vremena tj. funkcije su od t – $S(t)$, $I(t)$ i $R(t)$. Osetljivi su oni koji nisu inficirani ni imuni, inficirani su oni koji su inficirani i mogu preneti bolest, a oporavljeni su oni koji su inficirani, oporavili su se i konstantno su imuni. Ispitivanjem epidemije enterokolitisa koja se pojavila u Topoli kod Kragujevca 2002. godine, došlo se do zaključka da je srž modelovanja epidemija zaraznih bolesti pronalaženje odnosa između parametara infekcije i da oni služe za proračune o delotvornom programu masovne vakcinacije u cilju sprečavanja ekspanzije epidemija.