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Research Article

Analysis with Variable Step Size Strategy of Some SIR Epidemic Models

Bazı SIR Salgın Hastalık Modellerinin Değişken Adım Genişliği Stratejisi ile Analizi

Gülnur Çelik Kızılkan[1*], Ahmet Duman[1], Kemal Aydın[2]

[1]Necmettin Erbakan University, Faculty of Science, Department of Mathematics and Computer Science, Konya, Turkey
[2]Selçuk University, Faculty of Science, Department of Mathematics, Konya, Turkey

Abstract

In this paper, we have aimed to investigate the effectiveness of the variable step size strategy for some SIR epidemic models. We have applied the variable step size strategy to the SIR model and its modifications using real data.

Keywords: Epidemic model, SIR model, Step size strategy, System of non-linear differential equations, Variable step size

Öz

Bu çalışmada, bazı SIR salgın hastalık modelleri için değişken adım genişliği stratejisinin etkinliğini incelemeyi amaçladık. SIR modeli ve onun modifikasyonlarına gerçek veriler kullanarak değişken adım genişliği stratejisini uyguladık.

Anahtar Kelimeler: Salgın hastalık modeli, SIR modeli, Adım genişliği stratejisi, Lineer olmayan diferensiyel denklem sistemi, Değişken adım genişliği

1. Introduction

Selection of step size is one of the most important concepts in numerical integration of differential equation systems. For the use constant step size, it must be investigated how should be selected the step size in the first step of numerical integration. If the selected step size is large in numerical integration, computed solution can diverge from the exact solution. And if the chosen step size is small; calculation time, number of arithmetic operations, the calculation errors start to increase. So, in the region where the solution changes rapidly, step size should be chosen small. Inversely, we should choose bigger step size in the region where the solution changes slowly. So, it is not practical to use constant step size in numerical integration. In literature, step size strategies have been given for the numerical integration. One of these strategies is given for the Cauchy problem

$$X'(t) = AX(t) + \varphi(t,X), X(t_0) = X_{0'} \qquad (1.1)$$

where $A = (a_{ij}) \in R^{N\times N}$, $X \in R^N$ and $\varphi \in C^1([t_0 - T, t_0 + T] \times R^N)$ in (Çelik Kızılkan 2009, Çelik Kızılkan and Aydın 2012). The step size has been obtained as $h_i \le N^{-1/4}\left(\frac{2\delta_L}{N^2\alpha^2\beta_{i-1} + N\alpha\gamma_{i-1} + \zeta_{i-1}}\right)^{1/2}$, such as local error is smaller than δ_L - error level for the Cauchy problem (1.1). Here $\alpha = \max_{1\le i,j\le N}|a_{ij}|$, $\max_{1\le j\le N}\left(\sup_{t_{i-1}\le\tau_i<t_i}|z_j(\tau_i)|\right) \le \beta_{i-1}$, $\max_{1\le j\le N}\left(\sup_{t_{i-1}\le\tau_i<t_i}|\varphi_j(\tau_i, z(\tau_i))|\right) \le \gamma_{i-1}$, $\max_{1\le j\le N}\left(\sup_{t_{i-1}\le\tau_i<t_i}\left|\frac{d\varphi_j}{dt}(\tau_i, z(\tau_i))\right|\right) \le \zeta_{i-1}$.

Many dynamical system models are represented by non-linear differential equation systems as in (1.1). The epidemic models is one of these systems also attracted attention in recent years (for example see, Chauhan et all 2014, Chinviriyasit and Chinviriyasit 2010, Harko et all 2014, Keeling and Rohani 2008, Murray 2002). The classical epidemic model is SIR model. The SIR model was introduced in (Kermack and McKendrick 1927) and has played a major role in mathematical epidemiology. The SIR model is used in epidemiology to compute the amount of susceptible, infected, recovered people in a population.

In this study, we have aimed to obtain the numerical solutions of some SIR epidemic models applying our variable step size strategy (SSS) for non-linear differential equations in (Çelik Kızılkan 2009, Çelik Kızılkan and Aydın 2012). In

*Corresponding Author: gckizilkan@konya.edu.tr

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section 2, the step size strategy for the non-linear systems has been remained. In section 3, SIR epidemic model has been given with its variants. SIR model has been applied to some diseases as influenza and hepatitis C and obtained numerical solutions with variable step size strategy.

2. The Variable Step Size Strategy for Non-linear Differential Equation System

2.1. Step Size Strategy (SSS)

Let us consider the Cauchy problem

$$X'(t) = AX(t) + \varphi(t,X), X(t_0) = X_0 \tag{2.1}$$

and assume that the solution of (2.1) is unique and exists on the region $D = \{(t,X): t \in [t_0,T], |x_j - x_{j0}| \le b_j\}$, where $A = (a_{ij}) \in R^{N\times N}$, $X \in R^N$ and $\varphi \in C^1([t_0 - T, t_0 + T]\times R^N)$. The vector of local error of the Cauchy problem (2.1) is

$$LE_i = -\frac{1}{2}h_i^2\{A^2 Z(\tau_{ij}) + A\varphi(\tau_{ij}, Z(\tau_{ij})) + \varphi'(\tau_{ij}, Z(\tau_{ij}))\},$$
$$\tau_{ij} \in [t_{i-1}, t_i). \tag{2.2}$$

Euler method has been used when obtaining local error (2.2). The upper bound of local error for the Cauchy problem (2.1)

$$\|LE_i\| \le \frac{1}{2}\sqrt{N}\,h_i^2\{N^2\alpha^2\beta_{i-1} + N\alpha\gamma_{i-1} + \zeta_{i-1}\}, \tag{2.3}$$

where

$$\alpha = \max_{1\le i,j\le N}|a_{ij}|, \max_{1\le j\le N}\Big(\sup_{t_{i-1}\le\tau_i<t_i}|z_j(\tau_i)|\Big) \le \beta_{i-1},$$
$$\max_{1\le j\le N}\Big(\sup_{t_{i-1}\le\tau_i<t_i}|\varphi_j(\tau_i, z(\tau_i))|\Big) \le \gamma_{i-1},$$
$$\max_{1\le j\le N}\Big(\sup_{t_{i-1}\le\tau_i<t_i}\Big|\frac{d\varphi_j}{dt}(\tau_i, z(\tau_i))\Big|\Big) \le \zeta_{i-1}. \tag{2.4}$$

According to the upper bound of local error given by inequality (2.3); the step size is calculated with

$$h_i \le N^{-1/4}\left(\frac{2\delta_L}{N^2\alpha^2\beta_{i-1} + N\alpha\gamma_{i-1} + \zeta_{i-1}}\right)^{1/2}, \tag{2.5}$$

where $\alpha, \beta_{i-1}, \gamma_{i-1}$ and ζ_{i-1} as in (2.4); in the i-th step of the numerical integration of the Cauchy problem (2.1) such as the local error is smaller than δ_L- error level (Çelik Kızılkan 2009, Çelik Kızılkan and Aydın 2012).

2.2. Step Size Algorithm (SSA)

Algorithm SSA calculates the step sizes given by equation (2.5) and the numerical solution of the Cauchy problem (2.1) using these step sizes (Çelik Kızılkan and Aydın 2012).

Step 0 (Input): t_0, T, b, h^*, δ_L, X_0, $\varphi(t,X)$, A

Step 1: Calculate α as in (2.4) and $\frac{d\varphi(t,X)}{dt}$.

Step 2: Calculate $\beta_{i-1}, \gamma_{i-1}$ and ζ_{i-1} as in (2.4).

Step 3: Calculate step size $\hat{h}_i$ as in (2.5).

Step 4: Control step size with K-algorithm (see, (Çelik Kızılkan 2004) for K-algorithm).

Step 5: Calculate $t_i = t_{i-1} + h_i$ and $Y_i = (I + h_i A)\,Y_{i-1} + h_i\varphi(t_{i-1}, Y_{i-1})$.

3. Numerical Analysis of SIR Epidemic Models

The well-known SIR model was introduced in (Kermack and McKendrick 1927) to study the propagation of epidemics. In this model, the population is classified into three groups : (i) the group of individuals who are uninfected and S- susceptible of catching the disease, (ii) the group of individuals who are I- infected by the concerned pathogen, (iii) the group of R- recovered individuals who have acquired a permanent immunity to the disease (Bastin 2012). Let's now introduce SIR model and its variants and get its numerical solutions with the variable step size strategy SSS.

3.1. The SIR Model without Demography

To introduce the model, let us consider, (i) a closed population (no births, no deaths, no migration), (ii) spatial homogeneity, (iii) disease transmission by contact between susceptible and infected individuals.

Figure 1 represents SIR model without vital dynamics (births and deaths). We get the following the basic SIR model

$$\begin{pmatrix} ds/dt \\ di/dt \\ dr/dt \end{pmatrix} = \begin{pmatrix} 0 & 0 & 0 \\ 0 & -\gamma & 0 \\ 0 & \gamma & 0 \end{pmatrix}\begin{pmatrix} s \\ i \\ r \end{pmatrix} + \begin{pmatrix} -\beta si \\ \beta si \\ 0 \end{pmatrix}, \tag{3.1}$$

where $s(t) = S(t)/N$, $i(t) = I(t)/N$ and $r(t) = R(t)/N$ are the susceptible, infected and recovered fractions, respectively and total population $N = S + I + R$. This model you can see for example (Bastin 2012, Harko et all 2014, Hethcode 2000, Keeling and Rohani 2008).

Example 1. For a particular virus name as Hong Kong flu in New York City in the late 1960's assume that there was a trace level of infection in the population, say, 10 people.

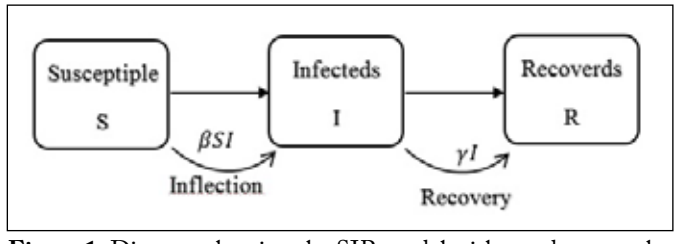


Figure 1. Diagram showing the SIR model without demography.

Table 1. The values of h_n, s_n, i_n, r_n which has been calculated with the algorithm SSA.

n	h_n	s_n	i_n	r_n
1	0.3398087231	0.9999997842	0.000001341926180	$1.438523594\text{x}10^{-7}$
2	0.3398087526	0.9999995562	0.000001417925841	$2.958517798\text{x}10^{-7}$
3	0.3398087840	0.9999993153	0.000001498229677	$4.564596651\text{x}10^{-7}$
⋮	⋮	⋮	⋮	⋮
245	0.4784428768	0.4895001886	0.03660913531	0.4738919453
246	0.4808422134	0.4851917994	0.03504978528	0.4797596845
247	0.4831710661	0.4810834276	0.03351314302	0.4854046985
⋮	⋮	⋮	⋮	⋮
384	0.4434840051	0.4128860620	0.00001468078848	0.5871005273
385	0.2310648	0.4128853617	0.00001425034949	0.5871016580

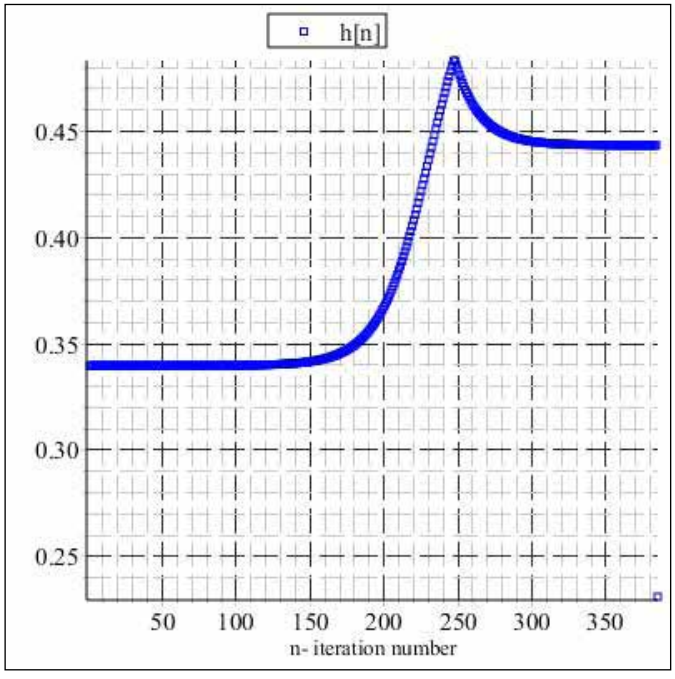


Figure 2. The step sizes obtained from SSA for Example 1.

The population is approximately 7,900,000 in the case of New York City in those days. Thus, the initial values for the population variables are $s(0) = 1$, $i(0) = 1.27\text{x}10^{-6}$ and $r(0) = 0$. Suppose that the average period of infectiousness at three days, so that would suggest $\gamma = 1/3$. If we guess that each infected would make a possibly infecting contact every two days, then β would be 1/2. We have been taken this data in (Mathematical Association of America 2016). Let us calculate the numerical solution of this problem using SSA with the values of $h^* = 10^{-12}$, $\delta_L = 10^{-1}$. The step sizes and the values of *s, i, r* obtained at each step have been summarized in Table 1. Figure 2 shows the obtained step sizes from SSA at each step of the numerical integration.

The numerical solutions are given in Figure 3A and the plots of $i(t)$ versus $s(t)$ is given in Figure 3B for $\gamma = 1/3, \beta = 1/2$.

3.2. The SIR Model with Demography

This SIR model is almost the same as the SIR epidemic model (3.1) above, except that it has an inflow of newborns into the susceptible class at rate ϑN and deaths in the classes at rates μS, μI, and μR. The SIR model with vital dynamics (births and deaths) given by

$$\begin{pmatrix} ds/dt \\ di/dt \\ dr/dt \end{pmatrix} = \begin{pmatrix} -\mu & 0 & 0 \\ 0 & -(\gamma+\mu) & 0 \\ 0 & \gamma & -\mu \end{pmatrix} \begin{pmatrix} s \\ i \\ r \end{pmatrix} + \begin{pmatrix} -\beta si + \vartheta \\ \beta si \\ 0 \end{pmatrix}. \qquad (3.2)$$

Here, $s(t) = S(t)/N$, $i(t) = I(t)/N$ and $r(t) = R(t)/N$. Figure 4 represents SIR model with demography. For this model you can see for example (Bastin 2012, Chinviriyasit 2010, Harko et all 2014, Hethcode 2000, Keeling and Rohani 2008).

If the birth rate is not equal to the death rate, population will not constant. Namely, if $\vartheta > \mu$ the population increases and if $\vartheta < \mu$ population decreases. Although it is unreal situation, death rate and the birth rate are be taken equal to get constant polpulation in applications, generally.

Example 2. Let consider datas related infection of the Hepatitis C in Portugal from 1996 until 2007 for SIR models with demography. Suppose the population of Portugal in those years is 10.3 million and let be 1.8 percent of the population have received infections. So, the initial values are $s(0) = 0.9$, $i(0) = 0.018$ and $r(0) = 0.082$. In (Correia et al 2011) the parameter β, γ, μ and ϑ are given montly as $\beta = 0.001$, $\gamma = 0.039$, $\mu = 0.001$ and $\vartheta = 0.006$. Now calculate the numerical solution of this problem using SSA with the values of $h^* = 10^{-12}$, $\delta_L = 10^{-1}$. The step sizes and the values of *s, i, r* obtained at each step have been summarized in Table 2.

Table 2. The values of h_n, s_n, i_n, r_n which has been calculated with the algorithm SSA.

n	h_n	s_n	i_n	r_n
1	2.905040421	0.9147686445	0.01595543255	0.08380112506
2	2.882748950	0.9293860146	0.01415768754	0.08535337220
3	2.861181228	0.9438563128	0.01257502645	0.08668896142
⋮	⋮	⋮	⋮	⋮
29	2.467387917	1.278804031	0.0007557341208	0.09222683011
30	2.456525458	1.290399395	0.0006838489908	0.09207267528
⋮	⋮	⋮	⋮	⋮
55	2.240151467	1.557881177	0.00006446746847	0.08744470839
56	1.9715541	1.566638857	0.00005958143281	0.08727726336

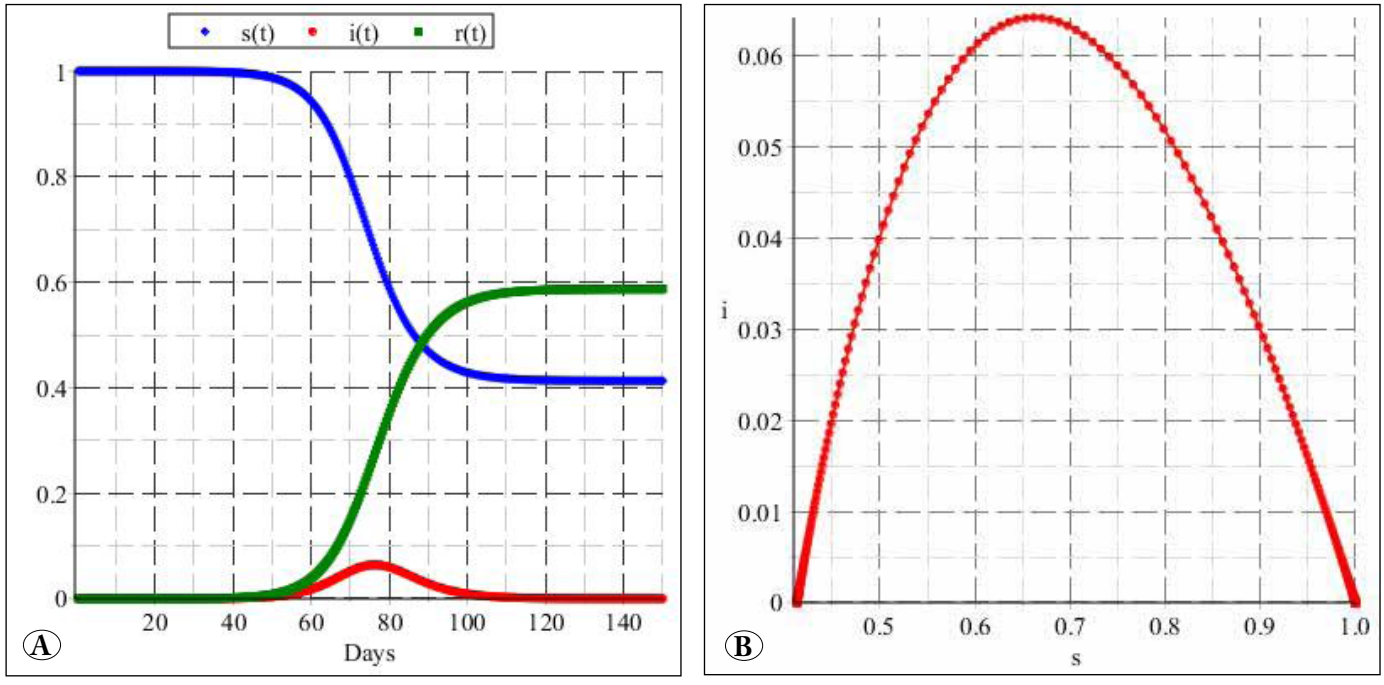


Figure 3. A) The numerical solutions obtained from SSA for Example 1. **B)** The plots of $i(t)$ versus $s(t)$ for Example 1.

In Figure 5, the obtained step sizes at the each step of the numerical integration are demonstrated.

The numerical solutions of Example 2 are summaried in Figure 6A. Because of $\vartheta > \mu$, population increase naturally. Figure 6B shows the plots of $i(t)$ versus $s(t)$ for Example 2.

As we have mentioned above, the birth rate is assumed to be the same as the death rate in some applications. For example let us take $s(0) = 0.5$, $i(0) = 0.4$ and $r(0) = 0.1$, $\beta = 0.8$, $\gamma = 0.2$, $\mu = 0.3 = \vartheta$ (Dadlani 2013).

The graphics for the numerical solutions of s, i, r and $i(t)$ due to $s(t)$ are given below in Figure 7A and Figure 7B, respectively. The data obtained is consistent with in (Dadlani 2013).

3.3. The SIR Model with Vaccination

In addition to SIR model as (3.1) and (3.2) if we assume that the susceptibles are vaccinated against the disease, the spread of the epidemic decreases. With the vaccination rate σ, the model is now written as follows

$$\begin{pmatrix} ds/dt \\ di/dt \\ dr/dt \end{pmatrix} = \begin{pmatrix} -\mu & 0 & 0 \\ 0 & -(\gamma+\mu) & 0 \\ 0 & \gamma & -\mu \end{pmatrix} \begin{pmatrix} s \\ i \\ r \end{pmatrix} + \begin{pmatrix} -\beta si + \vartheta + \mu\sigma \\ \beta si \\ 0 \end{pmatrix}, \quad (3.3)$$

where $s(t) = S(t)/N$, $i(t) = I(t)/N$ and $r(t) = R(t)/N$. This model is the variant of SIR model with demography. Figure 8 represents SIR model with vaccination. For this model you can see for example (Bastin 2012, Chauhan et all 2014, Cui et all 2014, Keeling and Rohani 2008).

Example 3. For this model consider data given in (Chauhan et all 2014). Take the initial values of the system are $s(0) = 0.65$, $i(0) = 0.1$ and $r(0) = 0.25$. The parameters are considered as $\beta = 3.5, \mu = 0.5 = \vartheta$ and $\sigma = 0.6$ in (Chauhan et all 2014). Table 3 summaries the obtained step sizes and the values of s, i, r at the each step of the numerical integration.

Figure 9 shows the obtained step sizes at the each step of the numerical integration.

The numerical solutions are given in Figure 10A and the plots of $i(t)$ versus $s(t)$ is given in Figure 10B for Example 3.

Remark. The calculation process takes too long. when the constant step size used for the numerical solution of the SIR model. Generally, SSS generates larger step sizes than the constant step sizes. For instance, one can see an example using the constant step sizes for numerical integration of the SIR model in (Freihat and Handam 2014). The calculation was made in $n = 1000$ iteration taking step size $h = 0.05$ for $t \in [0.50]$ in (Freihat and Handam 2014). For the

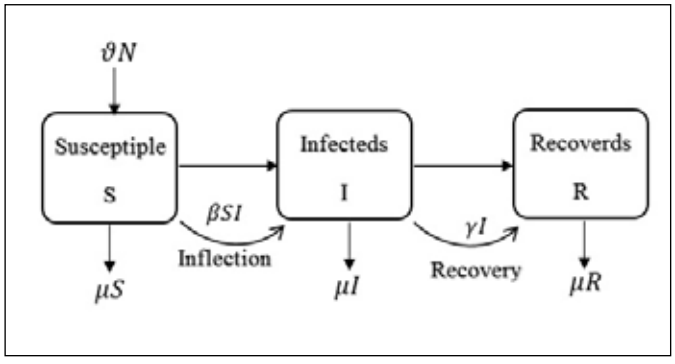


Figure 4. Diagram showing the SIR model with demography.

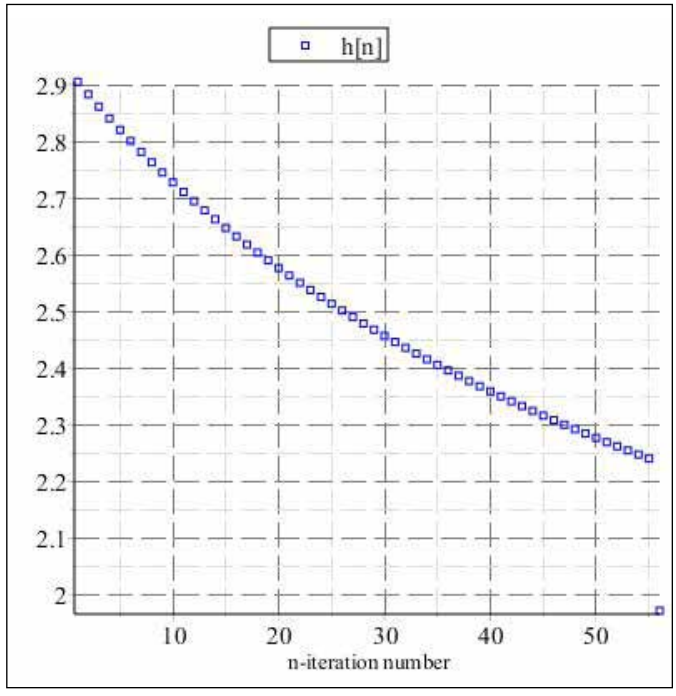
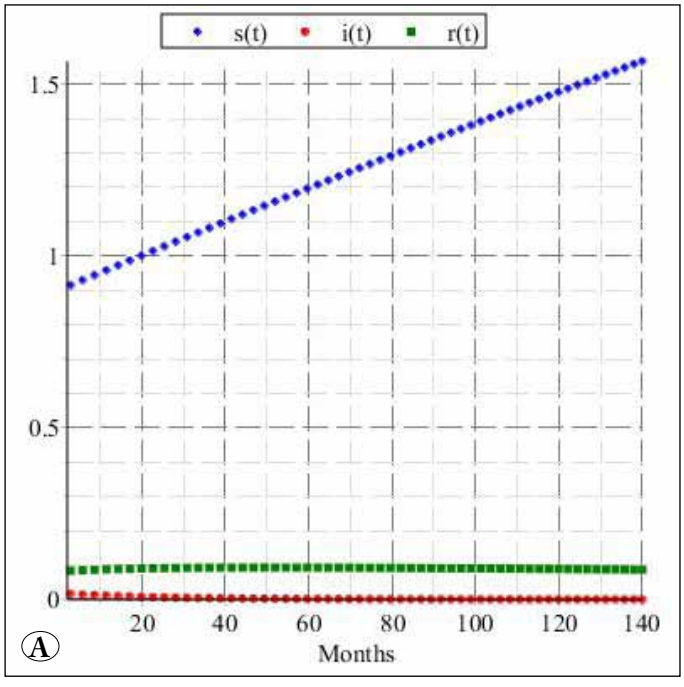


Figure 5. The step sizes obtained from SSA for Example 2.



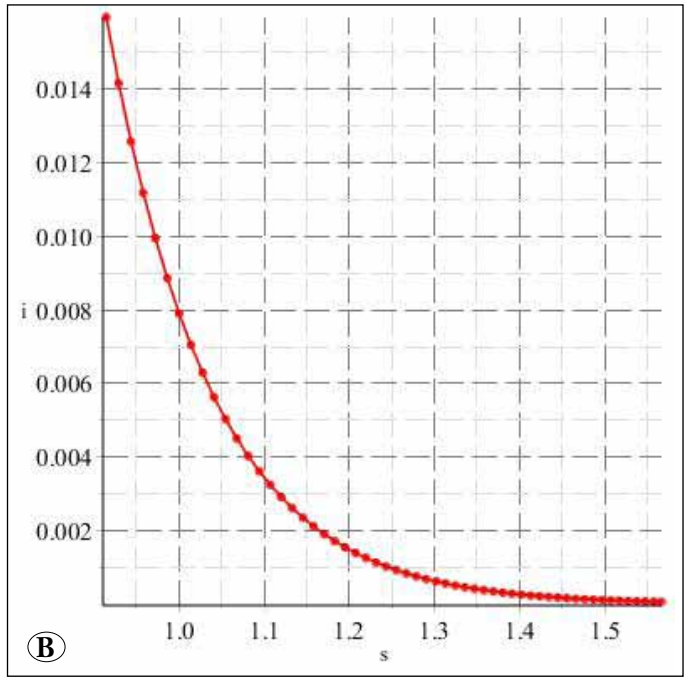


Figure 6. A) The numerical solutions obtained from SSA for Example 2 (Hepatitis C in Portugal). **B)** The plots of $i(t)$ versus $s(t)$ for Example 2 (Hepatitis C in Portugal).

Table 3. The values of h_n, s_n, i_n, r_n which has been calculated with the algorithm SSA.

n	h_n	s_n	i_n	r_n
1	0.1330360639	0.6074284596	0.1126384261	0.2400222952
2	0.1370574845	0.5650813170	0.1253328179	0.2312928389
3	0.1415878096	0.5233114463	0.1376703384	0.2237915153
⋮	⋮	⋮	⋮	⋮
17	0.2183228375	0.2281775162	0.1219671833	0.1732911819
18	0.2180512468	0.2287053605	0.1135772960	0.1676955510
19	0.2172557528	0.2303825989	0.1058321096	0.1618167999
⋮	⋮	⋮	⋮	⋮
63	0.1833116132	0.3269311155	0.03449952633	0.03967922288
64	0.02912975	0.3270096941	0.03448022436	0.03960378125

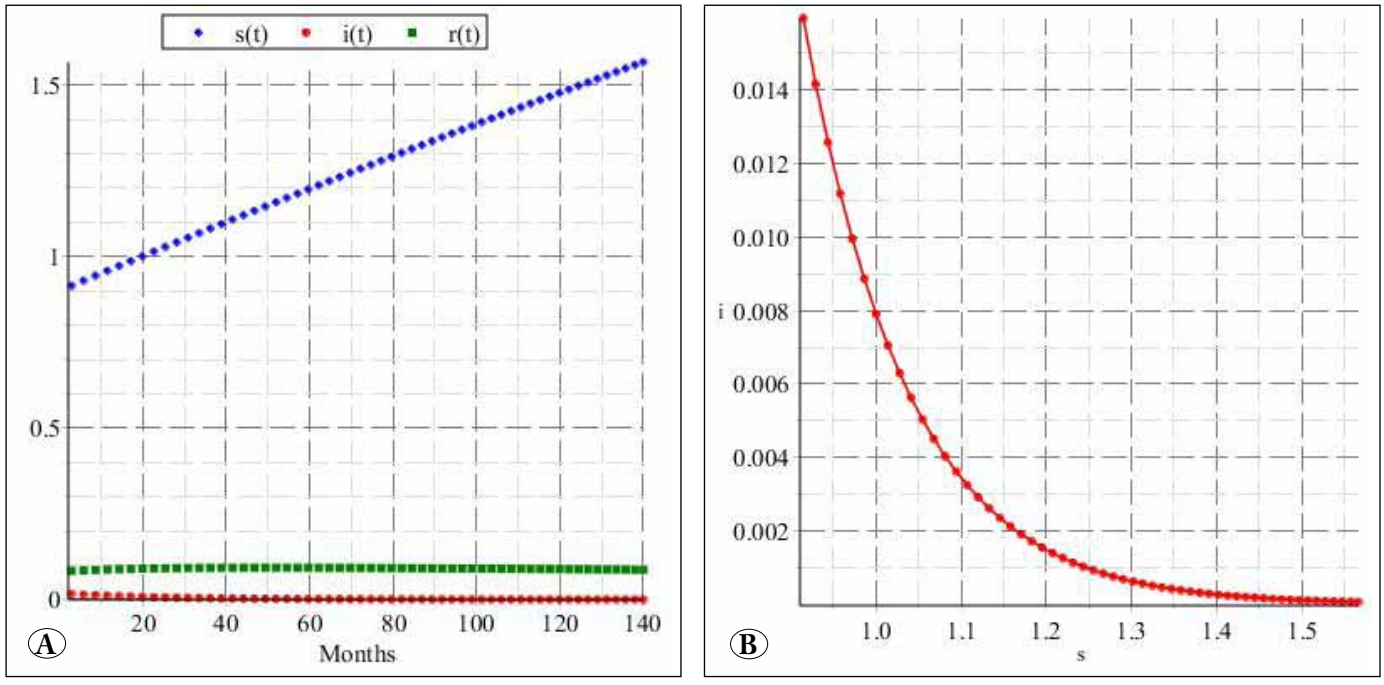


Figure 7. A) The numerical solutions obtained from SSA for $s(0) = 0.5$, $i(0) = 0.4$ and $r(0) = 0.1$, $\beta = 0.8$, $\gamma = 0.2$, $\mu = 0.3 = \vartheta$. **B)** The plots of $i(t)$ versus $s(t)$ for $s(0) = 0.5$, $i(0) = 0.4$ and $r(0) = 0.1$, $\beta = 0.8$, $\gamma = 0.2$, $\mu = 0.3 = \vartheta$.

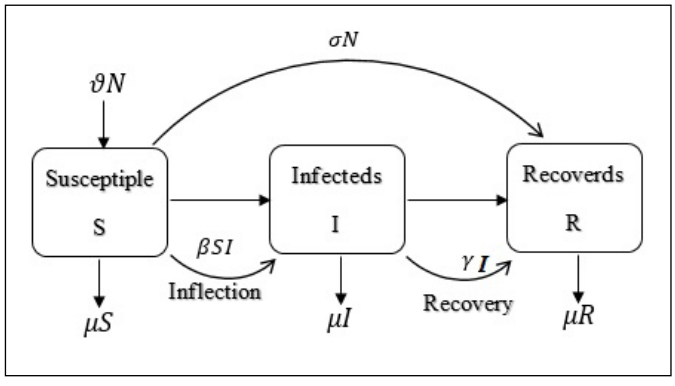


Figure 8. Diagram showing the SIR model with vaccination.

same example, if the step sizes from SSS are used, then the calculation process has been completed in only $n = 30$ steps. Consequently, it can be said that SSS is an effective variable step size strategy. Figure 11 shows that SSS generates the bigger step sizes.

4. Conclusion

In this study, the numerical solutions of the basic SIR model and its variants, which are the epidemiological model widely used in recent years, have been considered. The numerical solutions of these models have been obtained applying our variable step size strategy SSS. If someone had wanted to

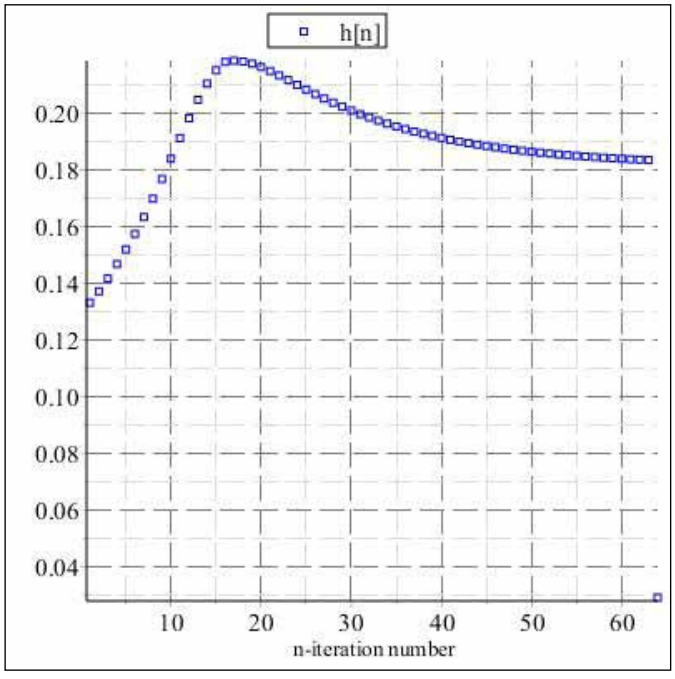
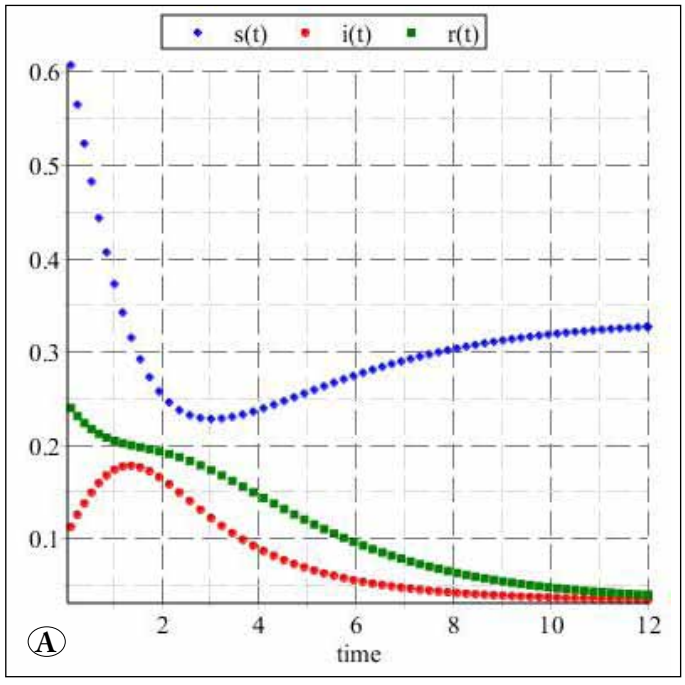


Figure 9. The step sizes obtained from SSA for Example 3.

use constant step size, he must choose the smallest step size obtained with SSS to get closer numerical solution to the exact solution. This situation shows us that it is not practical to use constant step size. In this study, SSS has been applied to some SIR models for epidemics as influenza and hepatitis C. The effectivesess of SSS and SSA are seen by these examples. The obtained results are supported by tables and figures. The figures of solutions obtained from SSA are compatible with the existing ones in the literature. It has been observed that the numerical methods with SSS are appropriate for numerical solutions of SIR models.



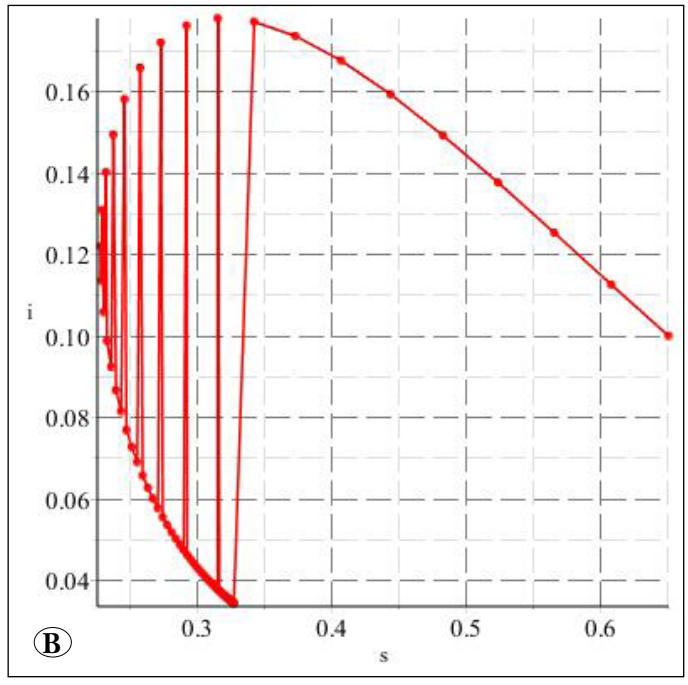


Figure 10. A) The numerical solutions obtained from SSA for $s(0) = 0.65$, $i(0) = 0.1$ and $r(0) = 0.25$, $\gamma = 0.5$, $\beta = 3.5$, $\mu = 0.5 = \vartheta$ and $\sigma = 0.6$. **B)** The plots of $i(t)$ versus $s(0) = 0.65$, $i(0) = 0.1$ and $r(0) = 0.25$, $\gamma = 0.5$, $\beta = 3.5$, $\mu = 0.5 = \vartheta$ and $\sigma = 0.6$.

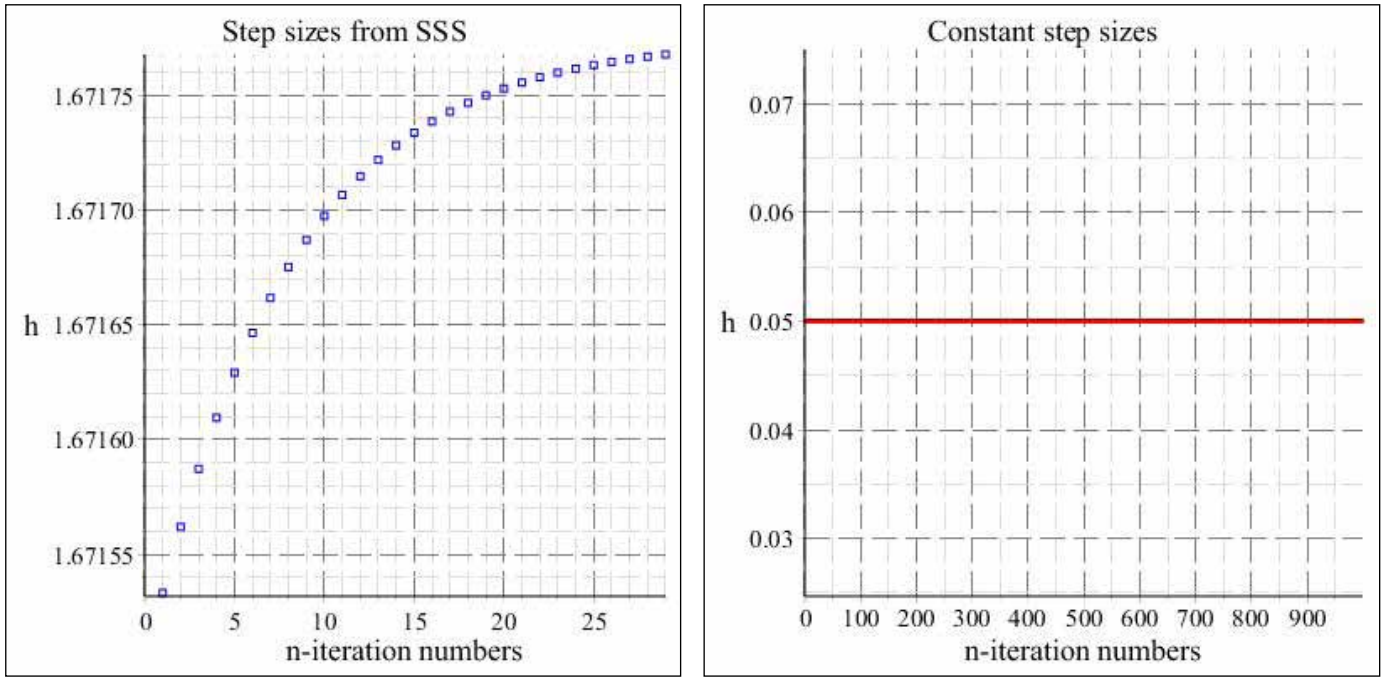


Figure 11. The step sizes for SIR model without demography for the parameters γ = 0.001, β = 0.072.

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