

Machine learning algorithm for the numerical solution of the epidemiological disease model

Sima naraghi¹

Department of Mathematics, Faculty of Mathematical Sciences, Shahid Beheshti University, Email:
s_naraghi@sbu.ac.ir

Hassan Dana Mazraeh

Department of Computer and Data Sciences, Faculty of Mathematical Sciences, Shahid Beheshti University, Email:
h.danamazraeh@sbu.ac.ir

Kourosh Parand

Department of Computer and Data Sciences, Faculty of Mathematical Sciences, Shahid Beheshti University, Email:
k_parand@sbu.ac.ir

Abstract

In this paper, we introduce a novel hybrid approach that combines support vector regression with the spectral method to solve infectious disease models. Our results demonstrate that this innovative method effectively addresses the challenges of solving dynamical systems, providing accurate and efficient solutions.

Keywords: Supervised learning algorithm, Least squares support vector regression machines, collocation method, Biology dynamical system.

Mathematics Subject Classification [2010]: 13D45, 39B42

1 Introduction

Many natural phenomena have been modeled using mathematical models such as differential equations or statistics [4, 5]. In this way, some problems in biology and medicine have been modeled, and the importance of these models appears in personalized treatment and disease control diseases [6].

In this way, infectious diseases have been modeled using differential equations and solved by various methods [1, 8]. One of the important models in epidemiology is the Susceptible-Infected-Removed (SIR) model, which was introduced by Ronald Ross and Kermack [7]. Subsequently, the researchers have been solved the model by using various methods[9, 10]. The model comprises a system of three interconnected non-linear ordinary differential equations for which no explicit analytical solution exists. The model has been developed by many researchers in form of stochastic, fractional or modified by vaccinate effect [11, 12, 13]. The main SIR model has been introduced as following:

$$\begin{cases} \frac{\partial S}{\partial t} = -\beta SI, \\ \frac{\partial I}{\partial t} = \beta SI - vI, \\ \frac{\partial R}{\partial t} = vI, \end{cases} \quad (1)$$

¹Speaker

Which $R(t) = N - S(t) - I(t)$ and N shows the total population.

On the other hand, some of machine learning algorithms presented for prediction and classification on the real data such as image, text [2, 3] and recently, machine learning methods and artificial intelligence algorithms have emerged as effective solutions for solving these equations, demonstrating impressive accuracy [14]. One standout method is least squares support vector regression (LS-SVR) [15], which has been successfully applied to a diverse range of equations since its introduction by Suykens et al [16, 17].

The method presented by Suykens and Mehrkanon employs radial basis functions as the kernel, has gained significant attention from scientists due to its high accuracy and efficiency in solving equations and other researchers developed the method [18, 19].

This paper introduces a hybrid method that combines the strengths of LS-SVR and collocation method. Section 2 provides a brief overview of LS-SVR and legendre polynomials, followed by a detailed explanation of the combined method. Section 3 presents the results obtained, and the final section discusses and concludes the findings.

2 Legendre LS-SVR methd

In [16] the authors have presented the LS-SVR for regression problem as follows:

$$\begin{aligned} & \underset{\mathbf{w}, b, \mathbf{e}}{\text{minimize}} && \frac{1}{2} \mathbf{w}^T \mathbf{w} + \frac{\gamma}{2} \mathbf{e}^T \mathbf{e} \\ & \text{subject to} && y_i = \mathbf{w}^T \boldsymbol{\varphi}(x_i) + b + e_i, \quad i = 1, \dots, N, \end{aligned} \quad (2)$$

Here $\gamma \in \mathbb{R}^+, b \in \mathbb{R}, \mathbf{w} \in \mathbb{R}^h, \varphi(\cdot) : \mathbb{R} \rightarrow \mathbb{R}^h$ is the feature map and h is the dimension of the feature space. The dual solution is formed as follows:

$$\left[\begin{array}{c|c} \Omega + I_N/\gamma & \mathbf{1}_N \\ \hline \mathbf{1}_N^T & 0 \end{array} \right] \left[\begin{array}{c} \boldsymbol{\alpha} \\ b \end{array} \right] = \left[\begin{array}{c} \mathbf{y} \\ 0 \end{array} \right] \quad (3)$$

where $\Omega_{ij} = K(x_i, x_j) = \varphi(x_i)^T \varphi(x_j)$ is the ij -th entry of the positive definite kernel matrix. $\mathbf{1}_N = [1, \dots, 1]^T \in \mathbb{R}^N, \boldsymbol{\alpha} = [\alpha_1, \dots, \alpha_N]^T, \mathbf{y} = [y_1, \dots, y_N]^T$ and I_N is the identity matrix.

For solving the systems of ODEs by machine learning algorithm, at first, we describe the system of differential equation as following:

$$\begin{cases} u_1(t) = F_1(t, u_1, u_2, \dots, u_n), \\ u_2(t) = F_2(t, u_1, u_2, \dots, u_n), \\ u_3(t) = F_3(t, u_1, u_2, \dots, u_n), \end{cases} \quad (4)$$

subject to

$$u_i^{(m)}(x_0) = u_{im}, \quad (5)$$

which $m = 0, 1, \dots, n_i - 1, i = 1, 2, \dots, n$. We can rewrite the method as following:

$$\begin{aligned} L_1(w_1, \lambda_1, e_1) &= \frac{1}{2} w_1^T w_1 + \frac{\gamma}{2} e_1^T e_1 - \lambda_1 (u_1(t) - F_1), \\ L_2(w_2, \lambda_2, e_2) &= \frac{1}{2} w_2^T w_2 + \frac{\gamma}{2} e_2^T e_2 - \lambda_2 (u_2(t) - F_2), \\ L_3(w_3, \lambda_3, e_3) &= \frac{1}{2} w_3^T w_3 + \frac{\gamma}{2} e_3^T e_3 - \lambda_3 (u_3(t) - F_3). \end{aligned} \quad (6)$$

Now, by using K.K.T condition, we can reduced the optimization problem to an algebraic system of equations.

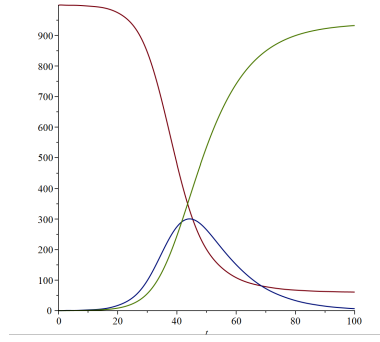


Figure 1: Legendre Least Square support Vector Regression method for numerical solution SIR model

3 Experimental Results

In this section, we demonstrate the results obtained using our proposed method for solving Eq. (1) with $S(0) = 999$, $I(0) = 1$, $R(0) = 0$ and $\beta = 0.0003$, $v = 0.1$. Tables 1, 2, and 3 illustrate the approximate solutions of the presented approach and we show the solution of the model by Legendre Lssvr method in figure 1.

Table 1: Table of numerical result for Suspected cases in SIR model

t	LS-SVR method
0	998.9993
20	974.5587
40	480.2506
60	108.1149
80	67.311
100	60.9674

Table 2: Table of numerical result for Infected cases in SIR model

t	LS-SVR method
0	1.0007
20	17.03959
40	274.6853
60	150.7034
80	33.1469
100	6.5646

Table 3: Table of numerical result for Removed cases in SIR model

t	LS-SVR method
0	-0.003
20	8.4050
40	245.0639
60	741.1814
80	899.5418
100	932.4678

4 Conclusion

In this paper, we presented an innovative hybrid method based on LS-SVR and Legendre collocation method for solving an epidemiological disease model described in Eq. (1). The results showed that the presented method is capable of solving this model accurately.

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Email: s_naraghi@sbu.ac.ir

Email: h_danamazraeh@sbu.ac.ir

Email: k_parand@sbu.ac.ir