International Journal of Innovative
Computing, Information and Control
Volume **8**, Number **2**, February **2012**

 ISSN 1349-4198
pp. 1439–1451

TAKAGI-SUGENO FUZZY MODEL OF NONLINEAR HIV DYNAMICS: CHEBYSHEV-SERIES APPROACH INTEGRATED WITH GENETIC ALGORITHM

Wen-Hsien Ho

Department of Healthcare Administration and Medical Informatics
Kaohsiung Medical University
No. 100, Shi-Chuan 1st Road, Kaohsiung 807, Taiwan
whho@kmu.edu.tw

Received November 2010; revised March 2011

Abstract. *Shifted-Chebyshev-series approach (SCSA) and hybrid Taguchi-genetic algorithm (HTGA) were integrated into a Takagi-Sugeno (TS) fuzzy model nonlinear human immunodeficiency virus (HIV) dynamics. Since only the algebraic computations in SCSA were applied in the TS fuzzy model-based dynamic equations, the proposed model simplified the problem by transforming it into a static optimization problem represented by algebraic equations. In static optimization problems, SCSA and HTGA simultaneously found the optimal antecedent and consequent parameters of the TS fuzzy model by directly minimizing the root-mean-squared-error (RMSE) performance index. An example of the proposed integrated model is given to demonstrate its efficacy.*
Keywords: TS fuzzy model, HIV dynamics, Chebyshev series, Genetic algorithm

1. **Introduction.** Mathematical models of the epidemiological and immunological dynamics of human immunodeficiency virus (HIV) have proven valuable for understanding the HIV pathogenesis (see, e.g., [1-13] and references therein). Therefore, many works have studied the problem of modeling HIV dynamics (see, e.g., [14-22] and references therein). Because the spread of HIV is complex and nonlinear, however, accurate dynamic models are difficult to construct. To improve therapeutic treatment for HIV, a simple and effective computer model of nonlinear HIV dynamics is needed to facilitate analysis of its pathogenesis.

In 1985, Takagi and Sugeno first proposed the use of fuzzy IF-THEN rules in a fuzzy model (TS fuzzy model) [23]. Since then, the TS fuzzy model has proven effective for studying many other nonlinear dynamic systems [24-26]. Unlike the conventional approach of using a single model to describe global behavior in a nonlinear system, the TS fuzzy modeling approach is essentially a multimodel approach in which the simple submodels (typically linear models) are combined to describe the global behavior of the nonlinear system. Each fuzzy rule in a TS fuzzy system has an associated linear dynamic model that expresses its local dynamics and the overall fuzzy model is constructed by combining these rules. Given the demonstrated effectiveness of the TS fuzzy modeling approach in nonlinear systems [24-37], this study developed a TS fuzzy model of nonlinear HIV dynamics.

When designing TS fuzzy models, however, solutions for TS-fuzzy-model-based dynamic equations are usually needed to calculate the approximation error between the nonlinear system and its TS fuzzy model derived by computer simulation. Therefore, Ho and Chou [38,39], Hsieh et al. [40] and Ho et al. [41] proposed the shifted-Chebyshev-series approach (SCSA) as a simple and efficient method of deriving non-iterative, non-differential and

non-integral algorithms suitable for use in constructing computer models to solve TS fuzzy model-based dynamic equations. By converting dynamic problems into a system of algebraic equations, SCSA provides a short and simple solution procedure. Ho and Chou [39] also showed that SCSA outperforms conventional numerical solutions for TS fuzzy model-based dynamic equations.

This study, therefore, used SCSA to transform the TS fuzzy model of nonlinear HIV dynamics into a much simpler static parameter optimization problem represented by algebraic equations. Both the differential and integral computational complexity of the resulting TS fuzzy model of nonlinear HIV dynamics are substantially reduced. When solving static optimization problems, hybrid Taguchi-genetic algorithm (HTGA) simultaneously optimizes the antecedent and consequent parameters of the TS fuzzy model of nonlinear HIV dynamics. The proposed integrative method directly minimizes the root-mean-squared-error (RMSE), a key performance index, in the TS fuzzy model of nonlinear HIV dynamics. The HTGA also incorporates Taguchi method in crossover operations to enhance systematic reasoning ability and optimize the selection of genes needed to generate representative chromosomes for new offspring. The HTGA has global exploration capability, and its robustness is enhanced by two major tools used in the Taguchi experimental design process: (i) signal-to-noise ratio as a quality measure and (ii) orthogonal arrays [42-45]. The proposed integration of SCSA and HTGA is simple, efficient and well-suited for computer modeling. It satisfactorily solves design problems in TS fuzzy models of nonlinear HIV dynamics. An illustrative example demonstrates the efficacy of the proposed integrative method of constructing TS fuzzy models of nonlinear HIV dynamics.

This paper is organized as follows. Section 2 describes the proposed method of integrating SCSA with HTGA in a TS fuzzy model of nonlinear HIV dynamics. Section 3 evaluates the efficiency of the proposed integrative method in an illustrative example of three-dimensional nonlinear HIV dynamics. Finally, Section 4 concludes the study.

2. **Design of the TS Fuzzy Model of Nonlinear Dynamics.**

In the following equation for nonlinear HIV dynamics:

$$\dot{x}(t) = f(x(t)), \tag{1}$$

the initial state vector is $x(0)$, where $x(t) = [x_1(t), x_2(t), \ldots, x_n(t)]^{\mathrm{T}}$ denotes the n-dimensional state vector.

Where N is the number of rules, the nonlinear HIV dynamics in (1) can be represented by the following TS fuzzy model-based dynamic system:

$$\begin{aligned} R^i : \text{IF } \bar{x}_1(t) \text{ is } M_{i1} \text{ and } \ldots \text{ and } \bar{x}_n(t) \text{ is } M_{in}, \\ \text{Then } \dot{\bar{x}}(t) = A_i \bar{x}(t), \end{aligned} \tag{2}$$

and the initial state vector is $\bar{x}(0) = x(0)$, where R^i $(i = 1, 2, \ldots, N)$ denotes the ith implication, $\bar{x}(t) = [\bar{x}_1(t), \bar{x}_2(t), \ldots, \bar{x}_n(t)]^{\mathrm{T}}$ denotes the n-dimensional state vector, $A_i \in R^{n \times n}$ $(i = 1, 2, \ldots, N)$ are the consequent constant matrices, and M_{ij} $(i = 1, 2, \ldots, N)$ and $(j = 1, 2, \ldots, n)$ are the antecedent fuzzy sets.

The resulting TS fuzzy model-based dynamic equation inferred from (2) is

$$\dot{\bar{x}}(t) = \sum_{i=1}^{N} h_i\left(\bar{x}(t)\right) A_i \bar{x}(t), \tag{3}$$

where $h_i(\bar{x}(t)) = w_i(\bar{x}(t)) \Big/ \sum_{i=1}^{N} w_i(\bar{x}(t))$, $w_i(\bar{x}(t)) = \prod_{j=1}^{n} M_{ij}(\bar{x}_j(t))$ and $M_{ij}(\bar{x}_j(t))$ are the Gaussian membership grades of $\bar{x}_j(t)$ in the antecedent fuzzy sets M_{ij} ($i = 1, 2, \ldots, N$ and $j = 1, 2, \ldots, n$) and

$$M_{ij}(\bar{x}_j(t)) = \exp\left(-\frac{[\bar{x}_j(t) - m_{ij}]^2}{2\sigma_{ij}^2}\right), \tag{4}$$

where m_{ij} and σ_{ij} are the center and width, respectively, of the Gaussian membership function of the ith implication of the jth input variable $\bar{x}_j(t)$.

Assuming elements of $\bar{x}(t)$ and $x(t)$ are absolutely integrable within $kt_f \le t \le (k+1)t_f$, where t_f denotes a short time interval selected for independent variable t, let

$$t = kt_f + \eta, \tag{5}$$

$$\bar{x}_k = \bar{x}(kt_f), \tag{6a}$$

$$x_k = x(kt_f), \tag{6b}$$

where $k = 0, 1, 2, \ldots$, and $0 \le \eta \le t_f$.

The state vector $\bar{x}(t)$, within $kt_f \le t \le (k+1)t_f$, can be approximated by the truncated shifted Chebyshev series as

$$\bar{x}(t) = \sum_{s=0}^{m-1} x_s^{(k)} T_s(t) = \tilde{x}^{(k)} T(t), \tag{7}$$

where m is the number of terms required for the shifted Chebyshev series, $T(t) = [T_0(t), T_1(t), \ldots, T_{m-1}(t)]^{\mathrm{T}}$ denotes the $m \times 1$ shifted-Chebyshev-series vector, $x_s^{(k)}$ ($s = 0, 1, \ldots, m-1$) is the $n \times 1$ coefficient vector and $\tilde{x}^{(k)} = \left[x_0^{(k)}, x_1^{(k)}, \ldots, x_{m-1}^{(k)}\right]$ are the $n \times m$ expansion coefficient matrices of $\bar{x}(t)$, in which the shifted Chebyshev series are as follows [39]:

$$\begin{aligned} T_0(t) &= 1, \\ T_1(t) &= (2kt_f + t_f - 2t)/t_f, \\ &\vdots \quad \vdots \quad \vdots \\ T_{r+1}(t) &= ((4kt_f + 2t_f - 4t)/t_f)T_r(t) - T_{r-1}(t), \end{aligned} \tag{8}$$

where $r = 1, 2, 3, \ldots$. Theoretically, the larger the value of m, the more accurate the approximate solutions. In an earlier study [38,39], the author reported that $m \in [4, 8]$ is generally sufficient for solving shifted Chebyshev series problems with satisfactory accuracy.

Before inferring the consequent output, the degree of fulfillment of the antecedent must be computed. Since t_f is a small time interval, the value of $h_i(\bar{x}(t))$, within $kt_f \le t \le (k+1)t_f$, is assumedly a constant and $h_i(\bar{x}(kt_f))$. Therefore, integrating (3) from $t = kt_f$ to $t = t$ into $kt_f \le t \le (k+1)t_f$, obtains

$$\bar{x}(t) - \bar{x}(kt_f) = \sum_{i=1}^{N} h_i(\bar{x}(kt_f)) A_i \int_{kt_f}^{t} \bar{x}(t)dt. \tag{9}$$

Remark 2.1. *Before the consequent output in (3) (i.e., (2)) can be inferred within the small time interval $kt_f \le t \le (k+1)t_f$, the fulfillment of the antecedent in (3) (i.e., (2)) must be computed. Therefore, the value of $h_i(z(t))$ within $kt_f \le t \le (k+1)t_f$, is assumedly constant under the condition that t_f is small. Theoretically, the smaller the value of t_f, the more accurate the approximate solutions. In an earlier study [38,39], the authors showed*

that $t_f \in [0.01, 0.001]$ obtains acceptable accuracy when using shifted Chebyshev series to solve TS fuzzy model-based dynamic differential equations. The author also showed that, compared to conventional numerical methods, the SCSA obtains better solutions for TS fuzzy model-based dynamic differential equations [39]. Therefore, this study proposes a numerical optimization approach that integrates SCSA with HTGA to represent nonlinear HIV dynamics where the value of $h_i(z(t))$ is assumed to be constant within a small time interval $kt_f \le t \le (k+1)t_f$.

According to the following integral property of the shifted Chebyshev series:

$$\int_{kt_f}^{t} T(t)dt = HT(t), \tag{10}$$

(6a) and (7) can recast (9) as

$$\tilde{x}^{(k)} - [\bar{x}_k, 0, 0, \ldots, 0] = \sum_{i=1}^{N} h_i(\bar{x}_k) A_i \tilde{x}^{(k)} H, \tag{11}$$

where H is the following operational integration matrix for the shifted Chebyshev series [38,39]:

$$H = t_f \begin{bmatrix} \frac{1}{2} & -\frac{1}{2} & 0 & \cdots & 0 & 0 & 0 \\ \frac{1}{8} & 0 & -\frac{1}{8} & \cdots & 0 & 0 & 0 \\ -\frac{1}{6} & \frac{1}{4} & 0 & \cdots & 0 & 0 & 0 \\ -\frac{1}{16} & 0 & \frac{1}{8} & \cdots & 0 & 0 & 0 \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ \frac{-1}{2(m-1)(m-3)} & 0 & 0 & \cdots & \frac{1}{4(m-3)} & 0 & \frac{-1}{4(m-1)} \\ \frac{-1}{2m(m-2)} & 0 & 0 & \cdots & 0 & \frac{1}{4(m-2)} & 0 \end{bmatrix}. \tag{12}$$

Equation (11) can be rewritten as

$$\tilde{x}^{(k)} - \sum_{i=1}^{N} h_i(\bar{x}_k) A_i \tilde{x}^{(k)} H = \tilde{Q}^{(k)}, \tag{13}$$

where $\tilde{Q}^{(k)} = [\bar{x}_k, 0, 0, \ldots, 0]$ is an $n \times m$ known matrix.

By applying the Kronecker product, the explicit form for solution $\tilde{x}^{(k)}$ derived from (13) is

$$\hat{x}^{(k)} = \left[I_{mn} - \sum_{i=1}^{N} h_i(\bar{x}_k) H^{\mathrm{T}} \otimes A_i \right]^{-1} \hat{Q}^{(k)}, \tag{14}$$

where I_{mn} denotes the $mn \times mn$ identity matrix, $\hat{x}^{(k)} = \left[x_0^{(k)^{\mathrm{T}}}, x_1^{(k)^{\mathrm{T}}}, \ldots, x_{m-1}^{(k)^{\mathrm{T}}} \right]^{\mathrm{T}}$, $\hat{Q}^{(k)} = \left[\bar{x}_k^{\mathrm{T}}, 0^{\mathrm{T}}, 0^{\mathrm{T}}, \ldots, 0^{\mathrm{T}} \right]^{\mathrm{T}}$ and $\otimes$ denotes the Kronecker product [46].

The above algebraic formula in (14) for calculating $x_s^{(k)}$ $(s = 0, 1, 2, \ldots, m-1)$ is located within any time interval $kt_f \le t \le (k+1)t_f$ $(k = 0, 1, 2, \ldots)$. All these values for $x_s^{(k)}$ provide the information needed to calculate the state vector $\bar{x}(t)$ within the time interval

$kt_f \le t \le (k+1)t_f$. By letting $\eta = t_f$, the following equation can also be obtained from (7):

$$\bar{x}_{k+1} = \tilde{x}^{(k)} T((k+1)t_f), \tag{15}$$

where $k = 0, 1, 2, \ldots$, and $\bar{x}_{k+1} = \bar{x}((k+1)t_f)$. The TS fuzzy model-based dynamic equation in (3) can be solved by the recursive formulae in (4), (14) and (15), which only involve matrix algebra. Therefore, based on the recursive formulae in (4), (14) and (15), the following simplified algorithm is proposed for solving the TS fuzzy model-based dynamic equations in (3) by algebraic computation alone:

Step 1: Given a small time interval t_f, and an initial state vector $x(0)$, set $k = 0$.
Step 2: Calculate $h_i(\bar{x}(kt_f))$ from (4) for $i = 1, 2, \ldots, N$.
Step 3: Calculate $\hat{x}^{(k)}$ from (14).
Step 4: Compute the solution $\bar{x}((k+1)t_f)$ from (15).
Step 5: Set $k = k + 1$ and go to Step 2.

The above algorithm clearly shows that $\tilde{x}^{(k)}$ $(k = 0, 1, 2, \ldots)$ can be determined by specifying one set of the center and width (m_{ij} and σ_{ij}, respectively) of the Gaussian membership function of the antecedent fuzzy sets M_{ij}, and the consequent constant matrices A_i, in which the elements of A_i are denoted as a_{ijl} ($i = 1, 2, \ldots, N$, $j = 1, 2, \ldots, n$ and $l = 1, 2, \ldots, n$), (i.e., by specifying antecedent and consequent parameters $\{m_{ij}, \sigma_{ij}, a_{ijl}\}$). Thus, the state vector $\bar{x}(t)$ in (7) within $kt_f \le t \le (k+1)t_f$ can be calculated. Therefore, the optimal values of antecedent and consequent parameters $\{m_{ij}, \sigma_{ij}, a_{ijl}\}$ for the TS fuzzy model can be obtained by directly minimizing the following RMSE performance index:

$$J = \left[\sum_{k=0}^{q} \frac{(x_{k+1} - \bar{x}_{k+1})^2}{q} \right]^{\frac{1}{2}}, \tag{16}$$

where q denotes the number of sampling data with time interval t_f in the design period T, x_{k+1} is the response of the nonlinear HIV dynamics, and $\bar{x}_{k+1}$ denotes the response of its TS fuzzy model. Here, the approximation error between the nonlinear HIV dynamics and its TS fuzzy model has been minimized.

That is, the value of the performance index in (16) actually depends on the set of antecedent and consequent parameters $\{m_{ij}, \sigma_{ij}, a_{ijl}\}$ ($i = 1, 2, \ldots, N$, $j = 1, 2, \ldots, n$ and $l = 1, 2, \ldots, n$); therefore,

$$J = f(m_{11}, m_{21}, \ldots, m_{Nn}, \sigma_{11}, \sigma_{21}, \ldots, \sigma_{Nn}, a_{111}, a_{112}, \ldots, a_{Nnn}). \tag{17}$$

Hence, the design problem in the TS fuzzy model of nonlinear HIV dynamics is to optimize the set $\{m_{ij}, \sigma_{ij}, a_{ijl}\}$ such that the performance index in (17) is minimized. This design problem is equivalent to the following static optimization problem:

$$\text{minimize } J = f(m_{11}, m_{21}, \ldots, m_{Nn}, \sigma_{11}, \sigma_{21}, \ldots, \sigma_{Nn}, a_{111}, a_{112}, \ldots, a_{Nnn}). \tag{18}$$

subject to $\underline{m}_{ij} \le m_{ij} \le \bar{m}_{ij}$, $\underline{\sigma}_{ij} \le \sigma_{ij} \le \bar{\sigma}_{ij}$ and $\underline{a}_{ijl} \le a_{ijl} \le \bar{a}_{ijl}$, for $i = 1, 2, \ldots, N$, $j = 1, 2, \ldots, n$ and $l = 1, 2, \ldots, n$, where $\underline{m}_{ij}$, $\bar{m}_{ij}$, $\underline{\sigma}_{ij}$, $\bar{\sigma}_{ij}$, $\underline{a}_{ijl}$ and $\bar{a}_{ijl}$ are the values in the actual implementation, respectively. Therefore, the SCSA greatly simplifies the problem of designing TS fuzzy models of nonlinear HIV dynamics by converting the problem into a static optimization problem represented by algebraic equations. The HTGA described below then searches for the optimal solution for the static optimization problem in (18), where (18) is a nonlinear function with continuous variables.

The HTGA combines the traditional genetic algorithm (TGA) [47] with the Taguchi method [48-50]. In the HTGA, the Taguchi method is inserted between the crossover and mutation operations of a TGA. Two major Taguchi tools (signal-to-noise ratio and orthogonal arrays) incorporate the systematic reasoning capability of the Taguchi method

into the crossover operations for systematically selecting optimal genes for crossover operations, which enhances the genetic algorithms. The detailed steps of the HTGA are given below. For a detailed description of the Taguchi method, see Taguchi et al. [48] and Wu [49]. For details regarding the HTGA, see Tsai et al. [42,43], Ho et al. [44] and Ho and Chang [45].

Detailed Steps: HTGA

Step 1: Set parameters.
Input: population size M, crossover rate p_c, mutation rate p_m and number of generations.
Output: the set of $V = \{m_{11}, m_{21}, \ldots, m_{Nn}, \sigma_{11}, \sigma_{21}, \ldots, \sigma_{Nn}, a_{111}, a_{112}, \ldots, a_{Nnn}\}$ and the value of J in (16).

Step 2: Initialize. By using the J in (16), which is the fitness function defined for the HTGA, calculate the fitness values of the initial population, where the randomly generated initial population has chromosomes in the form $V = \{m_{11}, m_{21}, \ldots, m_{Nn}, \sigma_{11}, \sigma_{21}, \ldots, \sigma_{Nn}, a_{111}, a_{112}, \ldots, a_{Nnn}\}$ for the problem in (18).

Step 3: Perform selection operation using roulette wheel approach.

Step 4: Perform crossover operation. The probability of the crossover is determined by the crossover rate p_c.

Step 5: Select a suitable two-level orthogonal array $L_\gamma\,(2^{\gamma-1})$ for the matrix experiments, where γ denotes the number of experimental runs, and $\gamma - 1$ is the number of columns in the orthogonal array. The orthogonal array $L_{128}\,(2^{127})$ is used in the illustrative results given in the next section.

Step 6: Randomly choose two chromosomes at a time to execute the matrix experiments.

Step 7: Calculate the fitness values of the γ experiments in the orthogonal array $L_\gamma\,(2^{\gamma-1})$ by using (16).

Step 8: Calculate the effects of the various factors.

Step 9: Generate one optimal chromosome based on the results from Step 8.

Step 10: Repeat Steps 6 through 9 until the expected number $M \times p_c$ has been met.

Step 11: Generate the population via Taguchi method.

Step 12: Perform mutation operation. The probability of mutation is determined by mutation rate p_m.

Step 13: Generate offspring population.

Step 14: Sort the fitness values in increasing order among the parent and offspring populations.

Step 15: Select the better M chromosomes as the parents of the next generation.

Step 16: Determine whether the stopping criterion has been met. If so, go to Step 17. Otherwise, return to Step 3 and continue through Step 16.

Step 17: Calculate the RMSE performance index in (16) and check if the specified stopping condition has been met. If so, go to Step 18. Otherwise, return to Step 2 and continue through Step 17.

Step 18: Display the optimal chromosome and the optimal fitness value.

3. **Illustrative Example.** Consider the following three-dimensional model of nonlinear HIV dynamics [8,51]:

$$\dot{x}_1(t) = S - dx_1(t) - \beta x_1(t)x_3(t), \tag{19a}$$

$$\dot{x}_2(t) = \beta x_1(t)x_3(t) - \mu_1 x_2(t), \tag{19b}$$

$$\dot{x}_3(t) = kx_2(t) - \mu_2 x_3(t), \tag{19c}$$

where $x_1(t)$ denotes amount (quantity) of healthy CD4+ T cells, $x_2(t)$ denotes the infected CD4+ T cells, $x_3(t)$ denotes the viral load, and the positive constants S, d, β, μ_1, k and μ_2 denote the system parameters for an HIV dynamical model described as the rate of production of the healthy cells, the death rate of the health calls, the infection rate of healthy cells CD4 by virus HIV, the death rate of infected cells, the rate of production of free virus, and the death rate of free virus, respectively. Equation (1a) denotes the population dynamics of the healthy cells. In the presence of HIV, the healthy cells interact with the virus, and its reproduction rate decreases according to the term $-\beta x_1(t)x_3(t)$. Equation (1b) denotes the population dynamics of the infected cells. The growth of infected cells is proportional to the number of healthy cells infected by the virus, and is discounted by the number of cells destroyed $-\mu_1 x_2(t)$. Equation (1c) represents the dynamics of the free virus concentration. The free virus increases in proportion to the infected cells $kx_2(t)$ and the increase is determined by the natural decline rate $-\mu_2 x_3(t)$ [13]. Here, the assumptions are $x_1(t) \in [0.94, 1.0]$, $x_2(t) \in [0.2, 0.27]$ and $x_3(t) \in [0.8, 0.83]$. The system parameters in this example are set as follows: $S = 1$, $d = 0.8$, $\beta = 1$, $\mu_1 = 0.8$, $k = 1$ and $\mu_2 = 0.01078$ [8].

Based on the TS fuzzy model approach (Tanaka and Wang, 2001), the nonlinear HIV dynamics in (19) can be represented by the following TS fuzzy model with eight fuzzy rules:

$$R^1: \text{ IF } \bar{x}_1(t) \text{ is } M_{11} \text{ and } \bar{x}_2(t) \text{ is } M_{12} \text{ and } \bar{x}_3(t) \text{ is } M_{13}, \text{ THEN } \dot{\bar{x}}(t) = A_1\bar{x}(t), \tag{20a}$$

$$R^2: \text{ IF } \bar{x}_1(t) \text{ is } M_{21} \text{ and } \bar{x}_2(t) \text{ is } M_{22} \text{ and } \bar{x}_3(t) \text{ is } M_{23}, \text{ THEN } \dot{\bar{x}}(t) = A_2\bar{x}(t), \tag{20b}$$

$$R^3: \text{ IF } \bar{x}_1(t) \text{ is } M_{31} \text{ and } \bar{x}_2(t) \text{ is } M_{32} \text{ and } \bar{x}_3(t) \text{ is } M_{33}, \text{ THEN } \dot{\bar{x}}(t) = A_3\bar{x}(t), \tag{20c}$$

$$R^4: \text{ IF } \bar{x}_1(t) \text{ is } M_{41} \text{ and } \bar{x}_2(t) \text{ is } M_{42} \text{ and } \bar{x}_3(t) \text{ is } M_{43}, \text{ THEN } \dot{\bar{x}}(t) = A_4\bar{x}(t), \tag{20d}$$

$$R^5: \text{ IF } \bar{x}_1(t) \text{ is } M_{51} \text{ and } \bar{x}_2(t) \text{ is } M_{52} \text{ and } \bar{x}_3(t) \text{ is } M_{53}, \text{ THEN } \dot{\bar{x}}(t) = A_5\bar{x}(t), \tag{20e}$$

$$R^6: \text{ IF } \bar{x}_1(t) \text{ is } M_{61} \text{ and } \bar{x}_2(t) \text{ is } M_{62} \text{ and } \bar{x}_3(t) \text{ is } M_{63}, \text{ THEN } \dot{\bar{x}}(t) = A_6\bar{x}(t), \tag{20f}$$

$$R^7: \text{ IF } \bar{x}_1(t) \text{ is } M_{71} \text{ and } \bar{x}_2(t) \text{ is } M_{72} \text{ and } \bar{x}_3(t) \text{ is } M_{73}, \text{ THEN } \dot{\bar{x}}(t) = A_7\bar{x}(t), \tag{20g}$$

$$R^8: \text{ IF } \bar{x}_1(t) \text{ is } M_{81} \text{ and } \bar{x}_2(t) \text{ is } M_{82} \text{ and } \bar{x}_3(t) \text{ is } M_{83}, \text{ THEN } \dot{\bar{x}}(t) = A_8\bar{x}(t), \tag{20h}$$

with initial condition $[\bar{x}_1(0) \quad \bar{x}_2(0) \quad \bar{x}_3(0)] = [1 \quad 0.2 \quad 0.8]$, where $\bar{x}(t) = [\bar{x}_1(t), \bar{x}_2(t), \bar{x}_3(t)]^{\mathrm{T}}$, $A_i = \begin{bmatrix} a_{i11} & a_{i12} & a_{i13} \\ a_{i21} & a_{i22} & a_{i23} \\ a_{i31} & a_{i32} & a_{i33} \end{bmatrix}$ $(i = 1, 2, \ldots, 8)$, and the M_{ij} $(i = 1, 2, \ldots, 8$ and $j = 1, 2, 3)$ is the antecedent fuzzy set defined as

$$M_{11}(\bar{x}_1(t)) = M_{21}(\bar{x}_1(t)) = M_{31}(\bar{x}_1(t)) = M_{41}(\bar{x}_1(t)) = \exp\left(-\frac{[\bar{x}_1(t) - m_{11}]^2}{2\sigma_{11}^2}\right),$$

$$M_{51}(\bar{x}_1(t)) = M_{61}(\bar{x}_1(t)) = M_{71}(\bar{x}_1(t)) = M_{81}(\bar{x}_1(t)) = \exp\left(-\frac{[\bar{x}_1(t) - m_{21}]^2}{2\sigma_{21}^2}\right),$$

$$M_{12}(\bar{x}_2(t)) = M_{22}(\bar{x}_2(t)) = M_{52}(\bar{x}_2(t)) = M_{62}(\bar{x}_2(t)) = \exp\left(-\frac{[\bar{x}_2(t) - m_{12}]^2}{2\sigma_{12}^2}\right),$$

$$M_{32}(\bar{x}_2(t)) = M_{42}(\bar{x}_2(t)) = M_{72}(\bar{x}_2(t)) = M_{82}(\bar{x}_2(t)) = \exp\left(-\frac{[\bar{x}_2(t) - m_{22}]^2}{2\sigma_{22}^2}\right),$$

$$M_{13}(\bar{x}_3(t)) = M_{33}(\bar{x}_3(t)) = M_{53}(\bar{x}_3(t)) = M_{73}(\bar{x}_3(t)) = \exp\left(-\frac{[\bar{x}_3(t) - m_{13}]^2}{2\sigma_{13}^2}\right),$$

$$M_{23}(\bar{x}_3(t)) = M_{43}(\bar{x}_3(t)) = M_{63}(\bar{x}_3(t)) = M_{83}(\bar{x}_3(t)) = \exp\left(-\frac{[\bar{x}_3(t) - m_{23}]^2}{2\sigma_{23}^2}\right).$$

Thus, the total number of antecedent and consequent parameters $\{m_{11}, m_{21}, m_{12}, m_{22}, m_{13}, m_{23}, \sigma_{11}, \sigma_{21}, \sigma_{12}, \sigma_{22}, \sigma_{13}, \sigma_{23}, a_{111}, a_{112}, \ldots, a_{833}\}$ to be found is 84.

The RMSE performance index is

$$J = \left[\sum_{k=0}^{q} \frac{(x_{k+1} - \bar{x}_{k+1})^2}{q}\right]^{\frac{1}{2}} \tag{21}$$

with time interval $t_f = 0.01$ in the design period $T \in [0, 0.1]$, in which $q = 10$.

Next, the proposed method is used to construct the TS fuzzy model in (20) by integrating SCSA with HTGA such that RMSE performance index in (21) is minimized. In the evolutionary environments of the proposed HTGA: population size is 200, crossover rate is 0.8, mutation rate is 0.1, and generation number is 100.

TABLE 1. Ranges of antecedent and consequent parameters

Parameters		Range
Antecedent parameters	m_{11}	0.94-0.97
	m_{12}	0.97-1
	m_{21}	0.2-0.235
	m_{22}	0.235-0.27
	m_{31}	0.8-0.815
	m_{32}	0.815-0.83
	σ_{uj} $(j = 1, 2, 3 \text{ and } u = 1, 2)$	1-12
Consequent parameters	a_{ijl} $(i = 1, 2, \ldots, 8,\ j = 1, 2, 3 \text{ and } l = 1, 2, 3)$	-12-12

After using the proposed integrative method to execute five independent runs with $m = 4$, $\underline{m}_{uj} \le m_{uj} \le \bar{m}_{uj}$, $\underline{\sigma}_{uj} \le \sigma_{uj} \le \bar{\sigma}_{uj}$ and $\underline{a}_{ijl} \le a_{ijl} \le \bar{a}_{ijl}$ $(i = 1, 2, \ldots, 8,\ j = 1, 2, 3,\ l = 1, 2, 3 \text{ and } u = 1, 2)$, in which the values of $\underline{m}_{uj}$, $\bar{m}_{uj}$, $\underline{\sigma}_{uj}$, $\bar{\sigma}_{uj}$, $\underline{a}_{ijl}$ and $\bar{a}_{ijl}$ are the antecedent and consequent parameter ranges $\{m_{uj}, \sigma_{uj}, a_{ijl}\}$ given in Table 1, the mean RMSE performance index is 0.0009, the standard deviation of RMSE performance indices is 0.0002, the minimal (optimal) RMSE performance index J is 0.0005, and the optimal antecedent and consequent parameters $\{m_{11}, m_{21}, m_{12}, m_{22}, m_{13}, m_{23}, \sigma_{11}, \sigma_{21}, \sigma_{12}, \sigma_{22}, \sigma_{13}, \sigma_{23}, a_{111}, a_{112}, \ldots, a_{833}\}$ are as shown in Table 2. Figure 1 shows the average and optimal convergence results of RMSE performance index J with respect to the number of generations in five independent runs obtained by using HTGA in the TS fuzzy model of HIV

TABLE 2. Optimal antecedent and consequent parameters

Optimal antecedent parameters					
$m_{11} = 0.950$			$\sigma_{11} = 6.097$		
$m_{12} = 0.984$			$\sigma_{12} = 2.221$		
$m_{21} = 0.215$			$\sigma_{21} = 6.327$		
$m_{22} = 0.247$			$\sigma_{22} = 5.468$		
$m_{31} = 0.810$			$\sigma_{31} = 2.071$		
$m_{32} = 0.812$			$\sigma_{32} = 7.004$		
Optimal consequent parameters					
$a_{111} = -2.340$	$a_{112} = 2.895$	$a_{113} = 2.099$	$a_{121} = 2.366$	$a_{122} = -9.352$	$a_{123} = 6.005$
$a_{131} = 7.048$	$a_{132} = 1.778$	$a_{133} = -12.000$	$a_{211} = -2.429$	$a_{212} = -2.979$	$a_{213} = 5.121$
$a_{221} = -2.263$	$a_{222} = -8.359$	$a_{223} = -1.936$	$a_{231} = -10.975$	$a_{232} = -7.230$	$a_{233} = 11.995$
$a_{311} = -4.926$	$a_{312} = 7.925$	$a_{313} = -6.907$	$a_{321} = -2.448$	$a_{322} = 2.581$	$a_{323} = 9.598$
$a_{331} = -3.742$	$a_{332} = -10.243$	$a_{333} = 7.381$	$a_{411} = -8.334$	$a_{412} = -4.823$	$a_{413} = -3.117$
$a_{421} = 3.536$	$a_{422} = -1.098$	$a_{423} = 12.000$	$a_{431} = -2.692$	$a_{432} = 0.043$	$a_{433} = 5.874$
$a_{511} = 2.402$	$a_{512} = 9.521$	$a_{513} = -10.700$	$a_{521} = 10.889$	$a_{522} = -2.900$	$a_{523} = -4.874$
$a_{531} = -12.000$	$a_{532} = -4.428$	$a_{533} = 12.000$	$a_{611} = 9.594$	$a_{612} = 5.758$	$a_{613} = 7.194$
$a_{621} = -8.779$	$a_{622} = -9.451$	$a_{623} = -0.135$	$a_{631} = 6.981$	$a_{632} = -4.799$	$a_{633} = 9.664$
$a_{711} = 8.203$	$a_{712} = -9.764$	$a_{713} = -5.746$	$a_{721} = 3.473$	$a_{722} = 4.801$	$a_{723} = 4.819$
$a_{731} = 11.099$	$a_{732} = -1.811$	$a_{733} = 0.644$	$a_{811} = -4.600$	$a_{812} = 6.515$	$a_{813} = 5.151$
$a_{821} = -12.000$	$a_{822} = -3.697$	$a_{823} = -5.504$	$a_{831} = -9.528$	$a_{832} = 9.108$	$a_{833} = -11.854$

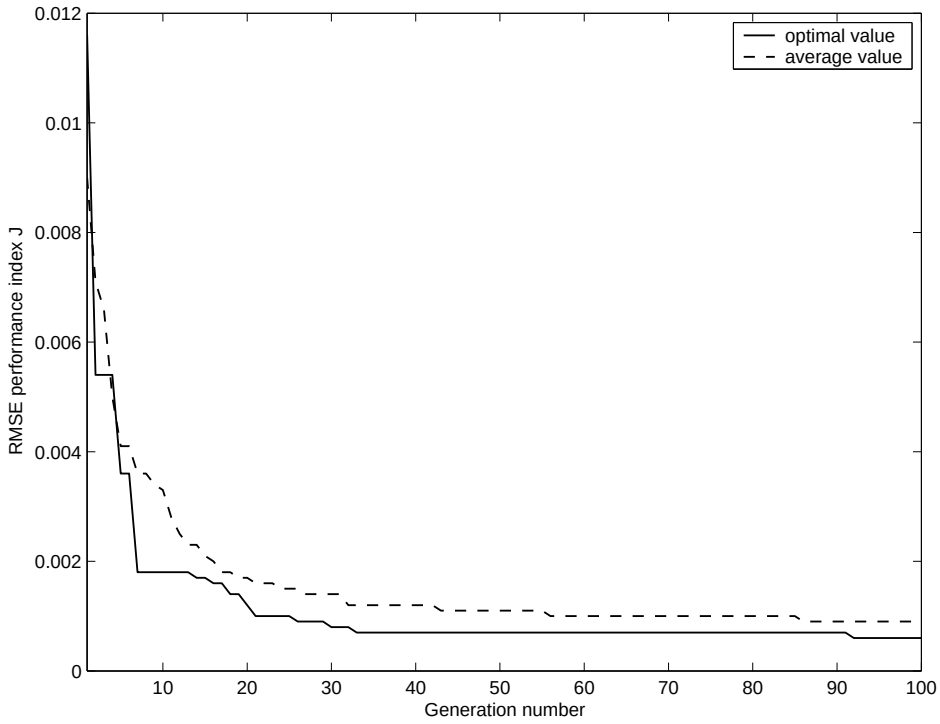

FIGURE 1. Average and optimal convergence results for performance index in five independent runs of HTGA in the TS fuzzy model of HIV dynamics

dynamics in (20). The results show that the integration of HTGA efficiently finds robust and stable solutions.

Figures 2-4, respectively, show the responses for the number of healthy CD4+ T cells $x_1(t)$ and $\bar{x}_1(t)$, for infected CD4+ T cells $x_2(t)$ and $\bar{x}_2(t)$, and for viral load $x_3(t)$ and $\bar{x}_3(t)$ for the nonlinear HIV dynamics in (19) and its TS fuzzy model in (20) when applying the

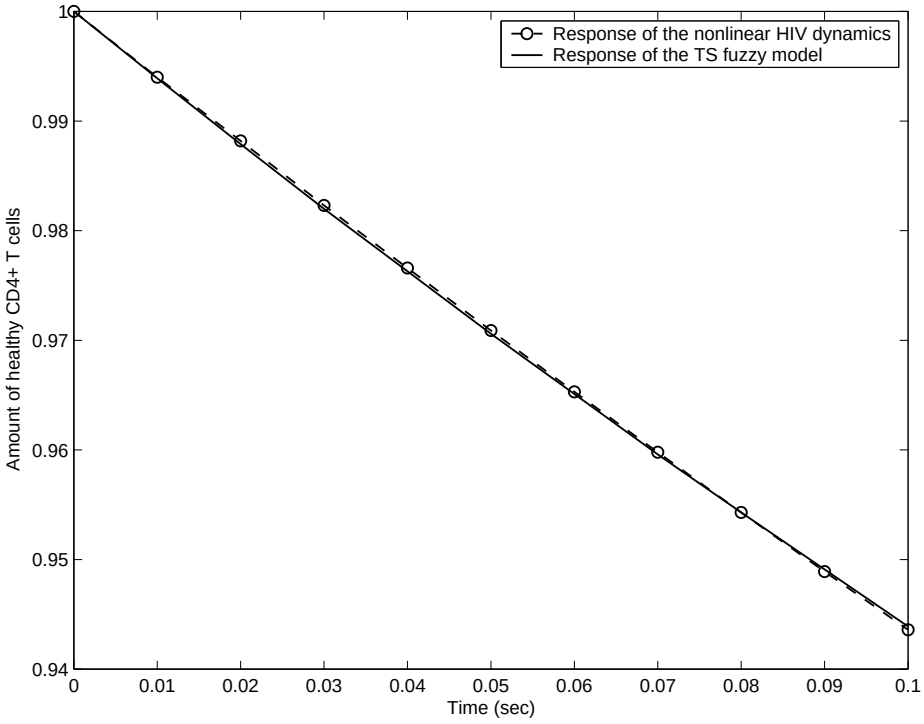

FIGURE 2. Illustrative responses of nonlinear HIV dynamics and its TS fuzzy model for amount of healthy CD4+ T cells $x_1(t)$ and $\bar{x}_1(t)$ when using proposed integrative method

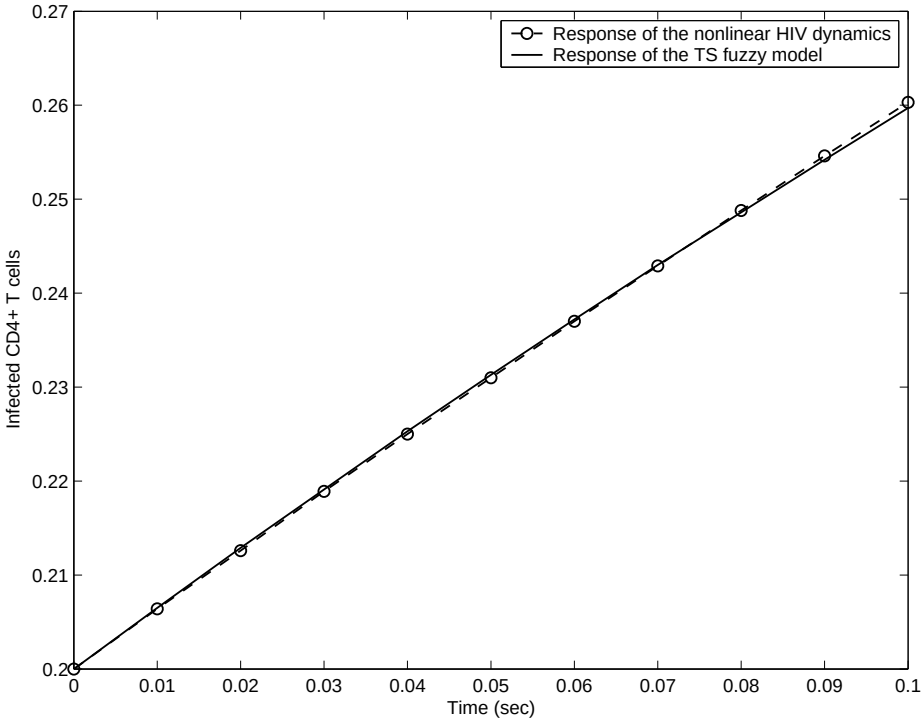

FIGURE 3. Illustrative responses of nonlinear HIV dynamics and its TS fuzzy model for amount of infected CD4+ T cells $x_2(t)$ and $\bar{x}_2(t)$ when using proposed integrative method

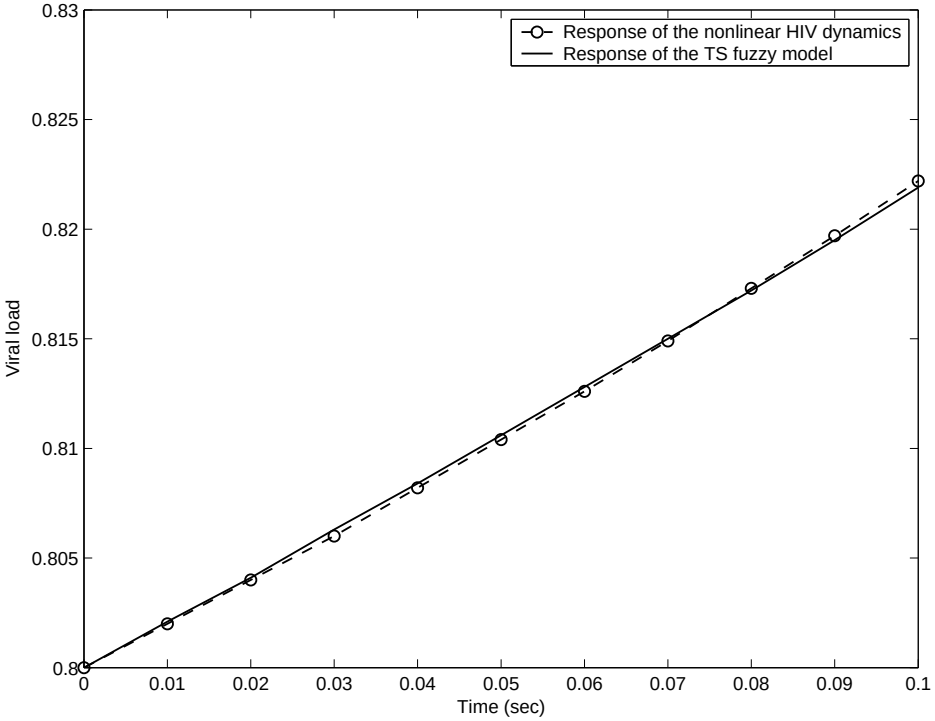

FIGURE 4. Illustrative responses nonlinear HIV dynamics and its TS fuzzy model for viral load $x_3(t)$ and $\bar{x}_3(t)$ when using the proposed integrative method

proposed integrative method. Figures 2-4 and the RMSE performance index J shows that the proposed method of integrating SCSA with HTGA obtains satisfactorily responsive results.

4. **Conclusions.** Based on the SCSA, this study developed an algebraic algorithm for solving TS fuzzy model-based dynamic equations. The proposed algorithm is integrated with HTGA to construct a TS fuzzy model of nonlinear HIV dynamics in which the RMSE performance index is directly minimized. Using SCSA converts the problem of designing a TS fuzzy model of nonlinear HIV dynamics into a static parameter optimization problem represented by algebraic equations. Limiting the algorithm to algebraic computation substantially simplifies the design of TS fuzzy models of nonlinear HIV dynamics. By integrating SCSA with HTGA, the proposed method is non-differential, non-integral, efficient, and suitable for computer implementation. The illustrative example confirmed the effectiveness of the proposed integrated model.

Acknowledgment. This work was supported by the National Science Council, Taiwan, under grant number NSC 99-2320-B-037-026-MY2.

REFERENCES

[1] A. S. Perelson and P. W. Nelson, Mathematical models of HIV dynamics in vivo, *SIAM Review*, vol.41, pp.3-44, 1999.

[2] J. Alvarez-Ramirez, M. Meraz and J. X. Velasco-Hernandez, Feedback control of the chemotherapy of HIV, *Int. J. of Bifurcation and Chaos*, vol.10, pp.2207-2219, 2000.

[3] M. E. Brandt and G. Chen, Feedback control of a biodynamical model of HIV-1, *IEEE Trans. on Biomedical Engineering*, vol.48, pp.754-759, 2001.

[4] H. R. Joshi, Optimal control of an HIV immunology model, *Optimal Control Applications and Methods*, vol.23, pp.199-213, 2002.
[5] A. M. Jeffrey, X. Xia and I. K. Craig, When to initiate HIV therapy: A control theoretic approach, *IEEE Trans. on Biomedical Engineering*, vol.50, pp.1213-1220, 2003.
[6] S. H. Bajaria, G. Webb and D. E. Kirschner, Predicting differential responses to structured treatment interruptions during HAART, *Bulletin of Mathematical Biology*, vol.66, pp.1093-1118, 2004.
[7] D. Verotta, Models and estimation methods for clinical HIV-1 data, *J. of Computational and Applied Mathematics*, vol.184, pp.275-300, 2005.
[8] S. Manseur, N. Messaoudi and Y. Cherruault, Parameter identification of an HIV model by the combined Adomian/Alienor method, *Kybernetes*, vol.35, no.10, pp.1725-1734, 2006.
[9] A. Yates, J. Stark, N. Klein, R. Antia1 and R. Callard, Understanding the slow depletion of memory CD4+ T cells in HIV infection, *PLoS Medicine*, vol.4, no.5, pp.948-955, 2007.
[10] H. Wu, H. Zhu, H. Miao and A. S. Perelson, Parameter identifiability and estimation of HIV/AIDS dynamic models, *Bulletin of Mathematical Biology*, vol.70, pp.785-799, 2008.
[11] L. Cai and X. Li, Stability and Hopf bifurcation in a delayed model for HIV infection of CD4+ T cells, *Chaos, Solitons and Fractals*, vol.42, pp.1-11, 2009.
[12] M. J. Mhawej, C. H. Moog, F. Biafore and C. Brunet-Francois, Control of the HIV infection and drug dosage, *Biomedical Signal Processing and Control*, vol.5, no.1, pp.45-52, 2010.
[13] W. H. Ho and A. L. F. Chan, Hybrid Taguchi-differential evolution algorithm for parameter estimation of differential equation models with application to HIV dynamics, *Mathematical Problems in Engineering*, vol.2011, Article ID 514756, 2011.
[14] D. Wodarz and M. A. Nowak, Mathematical models of HIV pathogenesis and treatment, *BioEssays*, vol.24, pp.1178-1187, 2002.
[15] R. V. Culshaw, S. G. Ruan and G. Webb, A mathematical model of cell-to-cell spread of HIV-1 that includes a time delay, *J. of Mathematical Biology*, vol.46, pp.425-444, 2003.
[16] R. M. Jafelice, L. C. De Barros, R. C. Bassanezi and F. Gomide, Fuzzy modeling in symptomatic HIV virus infected population, *Bulletin of Mathematical Biology*, vol.66, pp.1597-1620, 2004.
[17] B. M. Adams, H. T. Banks, M. Davidian, H. D. Kwon, H. T. Tran, S. N. Wynne and E. S. Rosenberg, HIV dynamics: Modeling, data analysis, and optimal treatment protocols, *J. of Computational and Applied Mathematics*, vol.184, pp.10-49, 2005.
[18] Y. Huang, D. Liu and H. Wu, Hierarchical Bayesian methods for estimation of parameters in a longitudinal HIV dynamic system, *Biometrics*, vol.62, pp.413-423, 2006.
[19] T. Dumrongpokaphan, Y. Lenbury, R. Ouncharoen and Y. S. Xu, An intracellular delay-differential equation model of the HIV infection and immune control, *Mathematical Modelling of Natural Phenomena, Epidemiology*, vol.2, pp.84-112, 2007.
[20] D. Burg, L. Rong, A. U. Neumann and H. Dahari, Mathematical modeling of viral kinetics under immune control during primary HIV-1 infection, *J. of Theoretical Biology*, vol.259, pp.751-759, 2009.
[21] A. S. Rao, K. Thomas, K. Sudhakar and P. K. Maini, HIV/AIDS epidemic in India and predicting the impact of the national response: Mathematical modeling and analysis, *Mathematical Biosciences and Engineering*, vol.6, pp.779-813, 2009.
[22] X. Wang, Y. Tao and X. Song, A delayed HIV-1 infection model with Beddington-DeAngelis functional response, *Nonlinear Dynamics*, vol.62, pp.67-72, 2010.
[23] T. Takagi and M. Sugeno, Fuzzy identification of systems and its applications to modeling and control, *IEEE Trans. on Systems, Man and Cybernetics*, vol.15, pp.116-132, 1985.
[24] R. Babuska, *Fuzzy Modeling for Control*, Kluwer Academic Publishers, Boston, 1998.
[25] S. S. Farinwata, D. Filev and R. Langari, *Fuzzy Control: Synthesis and Analysis*, John Wiley and Sons, Chichester, 2000.
[26] K. Tanaka and H. O. Wang, *Fuzzy Control Systems Design and Analysis: A Linear Matrix Inequality Approach*, John Wiley and Sons, New York, 2001.
[27] S. C. Tong, T. Wang, Y. P. Wang and J. T. Tang, *Design and Stability Analysis of Fuzzy Control Systems*, Science Press, Beijing, 2004.
[28] W.-J. Chang, C.-C. Ku, W. Chang and P.-H. Huang, Passive fuzzy control with relaxed conditions for discrete affine T-S fuzzy systems, *International Journal of Innovative Computing, Information and Control*, vol.3, no.4, pp.853-871, 2007.
[29] W.-H. Ho, J.-T. Tsai, T.-K. Liu and J.-H. Chou, Optimal state-feedback control of time-varying TS-fuzzy-model-based systems by using an integrative computational approach, *International Journal of Innovative Computing, Information and Control*, vol.3, no.4, pp.873-885, 2007.

[30] W. H. Ho and J. H. Chou, Design of optimal controller for Takagi-Sugeno fuzzy model based systems, *IEEE Trans. on Systems, Man and Cybernetics, Part A*, vol.37, pp.329-339, 2007.
[31] H.-Y. Chung and S.-C. Chan, An alternate approach to the analysis of a T-S fuzzy model, *International Journal of Innovative Computing, Information and Control*, vol.4, no.11, pp.3067-3077, 2008.
[32] H. Han, Fuzzy controller design with input saturation, *International Journal of Innovative Computing, Information and Control*, vol.4, no.10, pp.2507-2521, 2008.
[33] L. Luoh, Control design of T-S fuzzy large-scale systems, *International Journal of Innovative Computing, Information and Control*, vol.5, no.9, pp.2869-2880, 2009.
[34] D. Wang, W. Wang and X. Wang, Controller failure analysis for T-S fuzzy systems with time-varying delay via a switched approach, *International Journal of Innovative Computing, Information and Control*, vol.5, no.10(B), pp.3329-3340, 2009.
[35] S. He and F. Liu, Robust finite-time stabilization of uncertain fuzzy jump systems, *International Journal of Innovative Computing, Information and Control*, vol.6, no.9, pp.3853-3862, 2010.
[36] H. Wu and M. Bai, Stochastic stability analysis and synthesis for nonlinear fault tolerant control systems based on the T-S fuzzy model, *International Journal of Innovative Computing, Information and Control*, vol.6, no.9, pp.3989-4000, 2010.
[37] I. Zamani and M. H. Zarif, An approach for stability analysis of T-S fuzzy systems via piecewise quadratic stability, *International Journal of Innovative Computing, Information and Control*, vol.6, no.9, pp.4041-4054, 2010.
[38] W. H. Ho and J. H. Chou, Solutions of Takagi-Sugeno fuzzy-model-based dynamic equations via orthogonal functions, *IEICE Trans. on Fundamentals of Electronics, Communications and Computer Sciences*, vol.E87-A, pp.3439-3442, 2004.
[39] W. H. Ho and J. H. Chou, Solutions of time-varying TS-fuzzy-model-based dynamic equations using shifted Chebyshev series approach, *Int. J. of Systems Science*, vol.36, pp.767-776, 2005.
[40] C.-H. Hsieh, W.-H. Ho and J.-H. Chou, Optimal PID controllers design of PWM feedback time-varying systems using orthogonal-functions approach and genetic algorithm, *International Journal of Innovative Computing, Information and Control*, vol.5, no.2, pp.387-397, 2009.
[41] W.-H. Ho, S.-H. Chen, J.-H. Chou and T.-C. Wang, Design of robust optimal eigenvalue-assignable output feedback PID controllers for linear uncertain multivariable systems via orthogonal function approach and genetic algorithm, *International Journal of Innovative Computing, Information and Control*, vol.6, no.1, pp.409-422, 2010.
[42] J. T. Tsai, T. K. Liu and J. H. Chou, Hybrid Taguchi-genetic algorithm for global numerical optimization, *IEEE Trans. on Evolutionary Computation*, vol.8, pp.365-377, 2004.
[43] J. T. Tsai, J. H. Chou and T. K. Liu, Tuning the structure and parameters of a neural network by using hybrid Taguchi-genetic algorithm, *IEEE Trans. on Neural Networks*, vol.17, pp.69-80, 2006.
[44] W. H. Ho, J. X. Chen, I N. Lee and H. C. Su, An ANFIS-based model for predicting adequacy of vancomycin regimen using improved genetic algorithm, *Expert Systems with Applications*, vol.38, pp.13050-13056, 2011.
[45] W. H. Ho and C. S. Chang, Genetic-algorithm-based artificial neural network modeling for platelet transfusion requirements on acute myeloblastic leukemia patients, *Expert Systems with Applications*, vol.38, pp.6319-6323, 2011.
[46] S. Barnett, *Matrix Methods for Engineers and Scientists*, McGraw-Hill, New York, 1979.
[47] M. Gen and R. Cheng, *Genetic Algorithms and Engineering Design*, John Wiley and Sons, New York, 1997.
[48] G. Taguchi, S. Chowdhury and S. Taguchi, *Robust Engineering*, McGraw-Hill, New York, 2000.
[49] Y. Wu, *Taguchi Methods for Robust Design*, The American Society of Mechanical Engineers, New York, 2000.
[50] W. H. Ho, J. H. Chou and C. Y. Guo, Parameter identification of chaotic systems using improved differential evolution algorithm, *Nonlinear Dynamics*, vol.61, pp.29-41, 2010.
[51] M. A. Nowak and C. R. M. Bangham, Population dynamics of immune responses to persistent viruses, *Sciences New Series*, vol.272, pp.74-79, 1996.