



Nonlinear System Identification Using Takagi-Sugeno Multi-model: Optimization via Grey Wolf and Levenberg-Marquardt Algorithm with Application to the Monod System

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ABSTRACT

This paper introduces a novel approach for modeling nonlinear systems using a coupled multi-model framework, specifically based on Takagi-Sugeno models. The proposed method relies on system identification through input-output data, treating the nonlinear system as a black box. Multi-model parameters are derived by minimizing a quadratic criterion that quantifies the difference between the outputs of the nonlinear system and the multimodel. This optimization is carried out using the iterative Levenberg-Marquardt algorithm. To address the convergence and divergence issues common in iterative algorithms due to initial parameter sensitivity, the Grey Wolf Optimizer (GWO) is employed to enhance the optimization process. The GWO-derived parameters are then used as initial values for the Levenberg-Marquardt algorithm, ensuring improved convergence. The proposed method's performance is validated through its application to the Monod system, with results demonstrating its effectiveness and accuracy.

تحديد الأنظمة غير الخطية باستخدام نموذج تاكاجي-سوجينو متعدد النماذج: تحسين باستخدام خوارزمية الذئب الرمادي وخوارزمية ليفنبرغ-ماركوارد مع تطبيق على نظام مونود

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الكلمات المفتاحية:

تحديد الأنظمة
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خوارزمية ليفنبرغ-ماركوارد
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النمذجة بمتعدد النماذج المقترن
متعددة النماذج تاكاجي-سوجينو

الملخص

يقدم هذا البحث طريقة جديدة لنمذجة الأنظمة غير الخطية باستخدام نموذج متعدد النماذج المقترن، يعتمد بشكل خاص على نموذج تاكاجي-سوجينو. تعتمد الطريقة المقترحة على نمذجة النظام الغير خطي من خلال بيانات المدخلات والمخرجات، ومعامله النظام غير الخطي كصندوق أسود. يتم تحديد معالم النموذج المتعددة عن طريق تصغير المعيار التربيعي الذي يحدد الفرق بين مخرجات النظام غير الخطي والنموذج المتعدد. يتم تنفيذ هذا التصغير باستخدام خوارزمية ليفنبرغ-ماركوارد التكرارية. و معالجة مشكلات التقارب والتباعد الشائعة في الخوارزميات التكرارية بسبب حساسية اختيار المعالم الأولية، يتم استخدام خوارزمية الذئب الرمادي لتصغير المعيار التربيعي و المعالم المتحصل عليها تستخدم كمعلمات أولية لخوارزمية ليفنبرغ-ماركوارد، مما يضمن تحسين التقارب. يتم التحقق من حسن أداء الطريقة المقترحة من خلال تطبيقها على نظام مونود، والنتائج تبين فعاليتها ودقتها.

1. Introduction

Modeling nonlinear systems is a crucial research domain in automation, control theory, and computer science due to the complex behavior exhibited by many real-world systems. Nonlinear models are fundamental for accurately simulating, predicting, and controlling the dynamics of various systems across diverse fields such as industrial processes, robotics, aerospace, and environmental management [1]. In these applications, the ability to model nonlinearities allows for enhanced performance and precision, enabling better decision-making and more effective system control.

One promising approach to nonlinear system modeling is the use of

coupled multi-models, specifically Takagi-Sugeno (T-S) multi-models, which offer a robust framework for dealing with the inherent complexities of nonlinear systems. This methodology breaks down a nonlinear system into a set of local linear subsystems, each corresponding to a particular operating region or mode of the system [2]. By utilizing a collection of local linear models, the overall behavior of the nonlinear system can be approximated with high accuracy, and transitions between these local models are governed by smooth weighting functions.

The parameters of the multi-model are typically obtained through the minimization of a quadratic criterion that represents the discrepancy

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between the outputs of the nonlinear system and the multimodel. This optimization process is handled by iterative algorithms, with the Marquardt-Levenberg algorithm being a widely used method due to its efficiency in solving nonlinear least-squares problems [3]. However, the performance of iterative algorithms often depends heavily on the initial parameter values, with poor initialization potentially leading to slow convergence or even divergence.

To address these challenges, the Grey Wolf Optimizer (GWO), a nature-inspired metaheuristic algorithm, is employed to optimize the criterion by providing a robust set of initial parameters for the Marquardt-Levenberg algorithm [4]. The GWO algorithm is known for its simplicity and effectiveness in handling complex optimization problems by mimicking the social hierarchy and hunting strategies of grey wolves in nature. By combining GWO with the Marquardt-Levenberg algorithm, the convergence issues are mitigated, resulting in a more efficient and reliable identification process.

The proposed modeling approach is validated using the Monod system, a well-known nonlinear system that describes microbial growth dynamics. Through simulations, the effectiveness of the proposed method is demonstrated, showing significant improvements in accuracy and convergence. The results indicate that this combined approach offers a powerful tool for modeling and controlling nonlinear systems, especially in applications where conventional methods fall short.

2. The multi-model

The multi-model approach [5] offers a robust and versatile framework for modeling nonlinear systems. It provides an effective alternative to traditional modeling techniques by decomposing the dynamic behavior of a nonlinear system into multiple local operating regions. Each of these regions is characterized by a local linear sub-model, which simplifies the complexity of the system by approximating nonlinear dynamics in smaller, manageable parts.

In this approach, the entire nonlinear system is divided into L operating domains, with each domain corresponding to a specific range of the system's operating conditions. For each of these domains, a local linear model is created to represent the system's dynamics. This division enables a more accurate representation of complex systems that would otherwise be difficult to model using a single global nonlinear model.

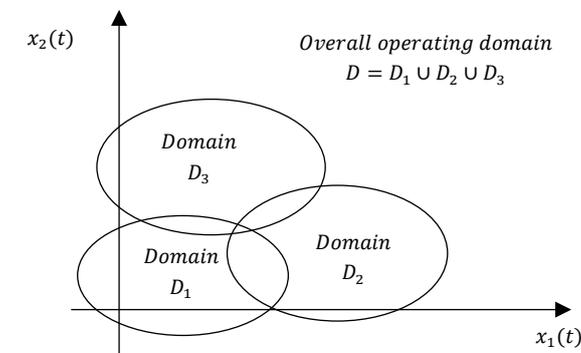


Fig. 1: Principle of the multi-model approach

2.1. Principle of the Multi-Model Approach

The underlying principle of the multi-model approach is illustrated in Figure (1), where a two-dimensional system with operating points defined by coordinates $x(t) = (x_1(t), x_2(t))$, is decomposed into three local operating domains, denoted as D_1, D_2 and D_3 . The overall operating domain D , is the union of these local domains:

$$D = D_1 \cup D_2 \cup D_3$$

Within each of these local domains, a local linear model is constructed. These models individually approximate the behavior of the nonlinear system within their specific domain. The output of each sub-model contributes to the overall system behavior in varying degrees, depending on the current operating conditions. This contribution is regulated by a weighting function that ensures a smooth transition between models as the system moves from one operating region to another.

By employing an interpolation technique, the outputs of the local models are combined to form a global representation of the nonlinear system. This global representation, or multi-model, is valid across the

entire operating domain D , capturing the system's behavior more accurately than a single-model approach.

2.2. Multi-Model Structures

Several structures exist for interconnecting the local sub-models to generate the global output of the multi-model. Two primary structures can be distinguished [6]:

- **Coupled-State (Takagi-Sugeno) Multi-Model:** In this structure, all sub-models share a common state vector, ensuring a unified representation of the system's state across all operating domains. This structure is often used in applications where the system's state must be consistently tracked across different operating regions.
- **Decoupled Multi-Model:** In this alternative structure, each sub-model operates independently with its own state vector, allowing for greater flexibility in representing systems where the states in different operating regions do not need to be directly correlated.

Both of these structures offer powerful tools for capturing the behavior of nonlinear systems, and the choice between them depends on the specific characteristics of the system being modeled and the desired level of complexity in the modeling process.

3. Takagi-Sugeno Multi-model

The Takagi-Sugeno (T-S) multi-model structure, initially introduced in the 1980s by Takagi and Sugeno [7] in the context of fuzzy modeling, has since gained widespread popularity in the multi-modeling domain, thanks to the work of Johansen and Foss [8]. This structure is one of the most widely used frameworks in multi-model approaches due to its versatility and effectiveness. The T-S multi-model is known by various names, such as local model networks with parameter blending, coupled or single-state multi-models with local models, and coupled-state multi-models.

In the state-space representation of the T-S multi-model, the overall system behavior is described by the following equations:

$$\begin{cases} \dot{x}_m(t) = \sum_{i=1}^N \mu_i(\xi(t))(A_i x(t) + B_i u(t) + D_i) \\ y_m(t) = \sum_{i=1}^N \mu_i(\xi(t))(C_i x(t) + E_i u(t) + N_i) \end{cases} \quad (1)$$

Where $x_m(t) \in R^n$ is the state vector common to the sub-models, $u(t) \in R^m$ is the control vector, $y_m(t) \in R^p$ is the output vector.

The activation function $\mu_i(\xi(t)), i \in \{1, \dots, N\}$ determine the contribution of each local model to the overall system output. These functions ensure a smooth transition between the local models and are typically triangular, sigmoidal, or Gaussian in shape. The activation functions must satisfy the following properties:

$$\begin{cases} \sum_{i=1}^N \mu_i(\xi(t)) = 1 \\ 0 \leq \mu_i(\xi(t)) \leq 1 \end{cases} \quad (2)$$

Here, $\xi(t)$ is the decision variable vector, which depends on measurable state variables and possibly on the control input $u(t)$. The number of local models (N) is determined based on the desired modeling accuracy, the system's complexity, and the structure of the activation functions.

4. Multi-model identification methods

Multi-model systems approximate nonlinear systems by interpolating between local linear models. Each local model is considered a valid Linear Time-Invariant (LTI) system near an operating point. There are three primary methods to derive a multi-model system:

A. Identification:

Parameters for each local model are estimated based on input-output data from the system.

B. Linearization:

Local models are derived by linearizing the nonlinear system around different operating points, often resulting in affine models.

C. Convex Polytopic Transformation

Transformation method that assumes a nonlinear mathematical model is available.

In this paper, we focus on the first method—multi-model identification from input-output data.

5. Takagi-Sugeno multi-model identification via input/output data

The process of identifying a Takagi-Sugeno multi-model involves estimating both the parameters of the activation functions and the local models. This is typically done using parametric identification methods, which are based on minimizing a functional that represents the difference between the estimated output of the multi-model $y_m(k)$, and the actual output of the nonlinear system $y(k)$ [9].

The most commonly used functional (or criterion) is the quadratic difference between the two outputs, defined as:

$$J(\theta) = \frac{1}{2} \sum_{k=1}^M \varepsilon(k, \theta)^2 = \frac{1}{2} \sum_{k=1}^M (y_m(k) - y(k))^2 \quad (3)$$

Where M is the observation horizon and θ is the parameter vector of the local models and those of the activation functions. The criterion must be minimized by an iterative procedure because of the nonlinearities of the global model (multi-model) to its parameters. Among the iterative optimization methods of the Quasi-Newton type, the Marquardt method, which is considered one of the most efficient resolution methods, does not require long calculations or large memory space.

6. Marquardt-Levenberg algorithm

If n is iteration index of the Marquardt algorithm and θ^n the value of the solution at iteration n , the update of the estimate is done as follows:

$$\theta^{n+1} = \theta^n - [G(\theta^n)^T G(\theta^n) + \mu_n D^2(\theta^n)]^{-1} G(\theta^n)^T \varepsilon(t, \theta) \quad (4)$$

Where

$G(\theta^n)$: represents the Jacobian matrix

$$\text{So : } G = \begin{bmatrix} \frac{\partial \varepsilon_1(t, \theta)}{\partial \theta_{(1)}} & \frac{\partial \varepsilon_1(t, \theta)}{\partial \theta_{(2)}} & \dots & \frac{\partial \varepsilon_1(t, \theta)}{\partial \theta_{(n)}} \\ \frac{\partial \varepsilon_2(t, \theta)}{\partial \theta_{(1)}} & \frac{\partial \varepsilon_2(t, \theta)}{\partial \theta_{(2)}} & \dots & \frac{\partial \varepsilon_2(t, \theta)}{\partial \theta_{(n)}} \\ \dots & \dots & \dots & \dots \\ \frac{\partial \varepsilon_m(t, \theta)}{\partial \theta_{(1)}} & \frac{\partial \varepsilon_m(t, \theta)}{\partial \theta_{(2)}} & \dots & \frac{\partial \varepsilon_m(t, \theta)}{\partial \theta_{(n)}} \end{bmatrix} \quad (5)$$

$D^2(\theta^n)$: is the diagonal matrix containing the elements of the diagonal of $G^T G$. To remedy the case where the elements of the diagonal are null, we take:

$$D^2(i, i) = G^T G(i, i) + 1 \quad (6)$$

μ_n : is a parameter of Marquardt and which is chosen in such a way that:

$$J(\theta^{n+1}) < J(\theta^n) \quad (7)$$

6.1. The Crucial Choice of Initial Values in Iterative Optimization Algorithms

• Problem:

Iterative optimization algorithms, such as the Marquardt-Levenberg algorithm, are powerful tools for solving complex optimization problems. However, their success depends largely on the choice of initial values. Indeed, a poor initialization can lead to convergence to a local optimum, divergence, or complete failure.

• Judicious Choice of Initial Values

In this work, we propose a method to improve the initialization of the Marquardt-Levenberg algorithm by leveraging the Grey Wolf Optimizer (GWO) algorithm. GWO provides an initial estimate of the parameters by solving the criterion $J(\theta)$, which is then used as the starting point for the Marquardt-Levenberg algorithm. This hybrid approach enhances convergence speed, improves accuracy, and reduces the number of iterations needed for optimization.

7. The grey wolf optimizer (GWO) algorithm

The Grey Wolf Optimizer (GWO) algorithm is a metaheuristic inspired by the social hierarchy and cooperative hunting strategies of grey wolves [10]. In GWO, wolves are categorized into four hierarchical levels: alpha, beta, delta, and omega, based on their dominance and roles within the pack.

- Alpha wolves are the leaders and make key decisions regarding hunting and movements.
- Beta wolves assist the alpha wolves and provide input on decision-making.
- Delta wolves follow the instructions of alpha and beta wolves, ensuring the hunting process is executed.
- Omega wolves are the lowest-ranking members of the pack, responsible for tasks like scouting and tracking prey.

The GWO algorithm simulates three key stages of grey wolf hunting behavior:

A. Searching for Prey

Alpha, beta, and delta wolves explore the search space randomly to locate the prey (i.e., the optimal solution).

B. Encircling Prey

Once the prey is located, the wolves begin to encircle it by gradually moving closer based on a fitness function.

C. Attacking Prey

The wolves then converge on the prey by coordinating their movements and adjusting their positions to secure the prey.

The main steps of the GWO algorithm include:

1) Initialization

Initialize the positions of wolves: X_i for $i = 1, 2, \dots, N$ where N is the number of wolves.

2) Position Update

For each iteration, the positions of the wolves are updated based on the position of the alpha wolf (X_{alpha}), beta wolf (X_{beta}), and delta wolf (X_{delta}) using the following formulas:

$$D = |C \cdot X_{best} - X_i| \quad (8)$$

$$X_i = X_{best} - A \cdot D \quad (9)$$

where A and C are coefficients defined as follows:

$$A = 2a \cdot r_1 - a \quad (10)$$

$$C = 2 \cdot r_2 \quad (11)$$

with a varying from 2 to 0 during iterations and r_1 and r_2 being uniformly random numbers in the interval [0,1].

3) Coefficient Update

The coefficients a , A and C are recalculated at each iteration to refine the search:

$$a = 2 - \frac{2 \cdot \text{iteration}}{\text{max_iterations}} \quad (12)$$

This iterative approach allows the algorithm to converge toward optimal solutions by balancing exploration and exploitation of the search space. GWO has demonstrated its effectiveness in various optimization problems, including those encountered in engineering, planning, and signal processing [11][12].

8. Takagi-Sugeno Representation of the Monod System

8.1. System Description

The Monod model is a key concept in microbiology, representing how microbial growth depends on the concentration of a limiting substrate. It is described by the following set of nonlinear differential equations [13]:

$$\begin{cases} \frac{dC}{dt} = \frac{k_1 SC}{k_2 + S} - k_d C & C(0) = C_0 \\ \frac{dS}{dt} = -\frac{1}{Y} \frac{k_1 SC}{k_2 + S} & S(0) = S_0 \end{cases} \quad (13)$$

Where:

C : The microbial biomass concentration

S : The concentration of the limiting substrate

k_1 : Maximum growth rate

k_2 : Half-saturation constant (the substrate concentration at which the growth rate reaches half its maximum value)

k_d : Microbial death rate

Y : Stoichiometric coefficient (unit varies depending on the reaction).

The Input/output data of system are obtained by simulating equation (13) with the following values:

$$C_0 = 0.5 \text{ g/l} \quad S_0 = 20 \text{ g/l} \quad k_1 = 2.5 \text{ J}^{-1} \\ k_2 = 10 \text{ g/l} \quad k_d = 0.2 \text{ J}^{-1} \quad Y = 0.5$$

The figure (2) shows the growth (C) and substrate consumption (S) obtained through simulation.

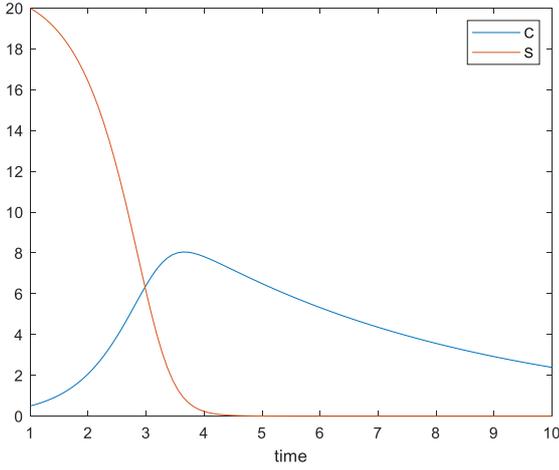


Fig. 2: The evolution of the microbial biomass concentration (C) and substrate concentration (S)

8.2. Takagi-Sugeno Representation of the Monod system Using input-output data

The Monod system serves as a case study for approximating a nonlinear model with multiple local models. A Takagi-Sugeno multi-model is constructed using three coupled local models. The state-space representation is:

$$\dot{x}_m(k+1) = \sum_{i=1}^3 \mu_i(\xi(k))(A_i x_m(k) + D_i) \quad (14)$$

where:

$$\dot{x}_m(k) = \begin{bmatrix} \dot{C}_m(k) \\ \dot{S}_m(k) \end{bmatrix} \quad \text{and} \quad \xi(k) = C(k)$$

$$A_i = \begin{bmatrix} a_{11}^i & a_{12}^i \\ a_{21}^i & a_{22}^i \end{bmatrix}, D_i = \begin{bmatrix} d_1^i \\ d_2^i \end{bmatrix} \quad \text{for } i=1:3$$

The index i corresponds to the i^{th} local model, the activation functions μ_i were constructed as follows:

$$w_i(C(k)) = \exp\left(\frac{-(C(k)-u_i)^2}{2\sigma_i^2}\right) \quad (15)$$

$$\mu_i(C(k)) = \frac{w_i(C(k))}{\sum_{i=1}^3 w_i(C(k))} \quad (16)$$

8.3. Identifying multi-model parameters

The parameters of the multi-model to be identified are the matrices of each local model

$$A_i = \begin{bmatrix} a_{11}^i & a_{12}^i \\ a_{21}^i & a_{22}^i \end{bmatrix} \quad \text{and} \quad D_i = \begin{bmatrix} d_1^i \\ d_2^i \end{bmatrix},$$

as well as the parameters of the activation functions u_i and σ_i ; therefore, the vector of parameters to be identified θ is:

$$\theta = [a_{11}^1 \ a_{12}^1 \ a_{21}^1 \ a_{22}^1 \ a_{11}^2 \ a_{12}^2 \ a_{21}^2 \ a_{22}^2 \ a_{11}^3 \ a_{12}^3 \ a_{21}^3 \ a_{22}^3 \ d_1^1 \ d_1^2 \ d_1^3 \ d_2^1 \ d_2^2 \ d_2^3 \ u_1 \ u_2 \ u_3 \ \sigma_1 \ \sigma_2 \ \sigma_3]$$

The parameters are identified from the minimization of the criterion $J(\theta)$ defined as follows:

$$J(\theta) = \frac{1}{2} \sum_{i=1}^3 [(x_{is}(t) - x_{im}(t))^2] \quad (17)$$

with

$$x_m(k) = \begin{bmatrix} C_m(k) \\ S_m(k) \end{bmatrix}, \quad x_s(k) = \begin{bmatrix} C(k) \\ S(k) \end{bmatrix}$$

represent the output vectors of the multi-model and the nonlinear system, respectively.

9. Optimization and results

a) Optimization using the GWO algorithm

First, we apply the Grey Wolf Optimizer (GWO) algorithm to minimize the criterion $J(\theta)$, yielding:

$$A_1 = \begin{bmatrix} 0.0628 & -0.8809 \\ 0.2499 & 0.1723 \end{bmatrix}, A_2 = \begin{bmatrix} 0.9369 & -0.0512 \\ 0.1007 & 0.2936 \end{bmatrix}$$

$$A_3 = \begin{bmatrix} -0.0942 & 0.9137 \\ -0.5703 & 2.4585 \end{bmatrix}, D_1 = \begin{bmatrix} -0.2377 \\ -1.8642 \end{bmatrix}$$

$$D_2 = \begin{bmatrix} 2.4492 \\ 0.0829 \end{bmatrix}, D_3 = \begin{bmatrix} -0.9142 \\ 1.5096 \end{bmatrix}$$

$$u_1 = 0.6510, \quad u_2 = 1.8905, \quad u_3 = 0.4219$$

$$\sigma_1 = 1.5609, \quad \sigma_2 = 2.2150, \quad \sigma_3 = 2.3202$$

The best optimal value of criterion J found by GWO is:

$$\min(J) = 270.616$$

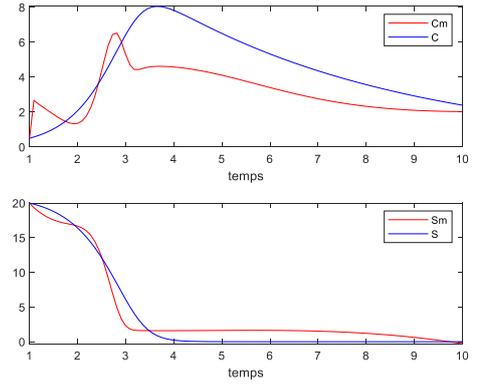


Fig. 3: The microbial biomass concentration (C) and substrate concentration (S) of the nonlinear model, and those of the multi-model (Cm), (Sm).

The estimation of the multi-model parameters using the GWO algorithm shows a relatively high approximation error. As shown in Figure (3), the obtained approximation is clearly unsatisfactory. This suggests that, in this case, the GWO algorithm failed to provide a sufficiently accurate estimation of the multi-model parameters to correctly capture the system's dynamics. This limitation could be related to the nonlinear complexity of the system, as well as the large number of parameters to estimate (24 parameters). Next, we applied the Marquardt algorithm to estimate the multi-model parameters

b) Optimization using Marquardt-Levenberg algorithm

We minimize the criterion (17) by the Marquardt-Levenberg algorithm, The initial values are chosen arbitrarily:

$$\theta_{initial}^i = 0.5 \quad \text{for } i = 1:24$$

after optimization, we obtain:

$$A_1 = \begin{bmatrix} 0.4899 & 0.4872 \\ 0.4879 & 0.4911 \end{bmatrix}, A_2 = \begin{bmatrix} 0.4899 & 0.4872 \\ 0.4879 & 0.4911 \end{bmatrix}$$

$$A_3 = \begin{bmatrix} 0.9756 & 0.0123 \\ -0.4308 & 0.9155 \end{bmatrix}, D_1 = \begin{bmatrix} 0.0922 \\ 0.0070 \end{bmatrix}$$

$$D_2 = \begin{bmatrix} 0.0924 \\ 0.0070 \end{bmatrix}, D_3 = \begin{bmatrix} 0.1101 \\ 2.1111 \end{bmatrix}$$

$$u_1 = -2.2991, \quad u_2 = -2.2983, \quad u_3 = 2.8774$$

$$\sigma_1 = 0.0323, \quad \sigma_2 = 0.0334, \quad \sigma_3 = 0.7355$$

The best optimal value of criterion J found by the Marquardt-Levenberg algorithm is: $\min(J) = 138.8941$

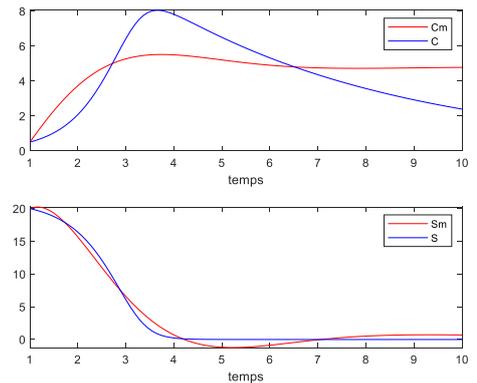


Fig. 4: The microbial biomass concentration (C) and substrate concentration (S) of the nonlinear model, and those of the multi-model (Cm), (Sm).

The Marquardt algorithm produced slightly better results than the GWO algorithm; however, the approximation error remains significant, as shown in figure (4) the fit between the multi-model output and the system output is still imperfect. This is likely due to the choice of initial values, as poor initialization can cause the algorithm to converge to a local optimum, diverge, or fail altogether.

The results obtained with the two optimization algorithms GWO and Marquardt-Levenberg algorithm being unsatisfactory.

c) Optimization by combine the two algorithms GWO algorithm and Marquardt-Levenberg algorithm

We combine the two algorithms by using the parameters obtained from the GWO algorithm as initial values for the Marquardt algorithm. after the optimization, we have found

$$A_1 = \begin{bmatrix} 1.1792 & 0.6794 \\ -1.3353 & -0.3808 \end{bmatrix}, A_2 = \begin{bmatrix} 1.2343 & 1.2752 \\ -2.2783 & -1.5794 \end{bmatrix}$$

$$A_3 = \begin{bmatrix} 0.5657 & -1.9337 \\ 3.0478 & 4.9187 \end{bmatrix}, D_1 = \begin{bmatrix} -0.9535 \\ 15.7277 \end{bmatrix}$$

$$, D_2 = \begin{bmatrix} -2.2609 \\ 29.9834 \end{bmatrix}, D_3 = \begin{bmatrix} 3.1846 \\ -45.2426 \end{bmatrix}$$

$$\sigma_1 = 0.9296, \quad \sigma_2 = 0.8105, \quad \sigma_3 = 0.7859$$

$$u_1 = -2.2017, \quad u_2 = -2.3692, \quad u_3 = -2.2917$$

To evaluate the simulation results, we simulate two models in parallel: the multi-model (14), and the nonlinear model (13). The figure (5) shows the superposition of the nonlinear model output and their approximation by the multi-model.

This combination resulted in a significantly more satisfactory approximation, with a considerably reduced approximation error: **min(J) = 8.7265e-05**

This demonstrates that using parameters obtained from the GWO algorithm as initial values to initialize the Marquardt algorithm significantly enhances its performance, thereby optimizing the estimation of the multi-model parameters

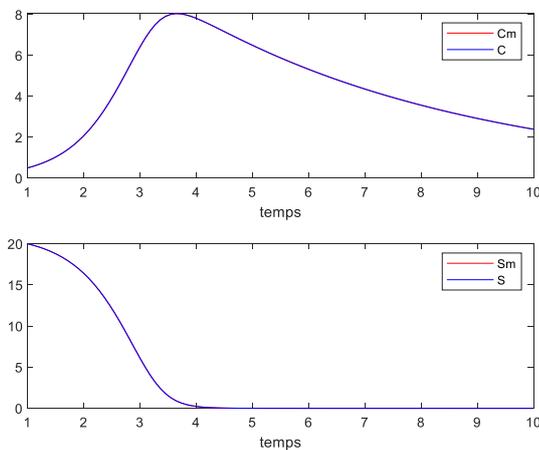


Fig. 5: The microbial biomass concentration (C) and substrate concentration (S) of the nonlinear model, and those of the multi-model (Cm), (Sm).

10. Conclusion

In this paper, we presented a robust approach for modeling nonlinear systems through the use of a Takagi-Sugeno multi-model, combined with the Grey Wolf Optimizer (GWO) and the Marquardt-Levenberg algorithm. The proposed method effectively addresses common challenges in nonlinear system identification, such as the sensitivity to initial parameter values in iterative optimization algorithms. By employing the GWO algorithm for initial parameter estimation and refining them using the Marquardt-Levenberg method, we achieved a significant improvement in convergence and optimization accuracy. The application of this approach to the Monod system -a well-established model in microbiology- demonstrates its capacity to accurately approximate complex nonlinear dynamics.

The results obtained showed that the hybrid method outperformed the individual algorithms in isolation, providing more precise estimates of microbial biomass concentration and substrate consumption. This highlights the potential of the multi-model approach for extending control and diagnostic techniques from linear to nonlinear systems, especially in cases where traditional methods struggle.

While the results are promising, there are several avenues for further exploration. First, future work could investigate the scalability of the proposed method to more complex systems with higher-dimensional state spaces and a larger number of local models. Additionally, integrating alternative metaheuristic algorithms, such as Particle Swarm Optimization (PSO) or Genetic Algorithms (GA), could be explored to compare their effectiveness with GWO in providing robust initial values. These methods could potentially offer even faster

convergence or greater accuracy, particularly for systems with more intricate dynamics.

Another interesting direction for future research would be the real-time implementation of this hybrid approach in practical applications, such as industrial process control or environmental monitoring systems, where nonlinearities often play a crucial role. Testing the algorithm's performance in real-world, noisy environments would be valuable for assessing its robustness and reliability. Furthermore, investigating adaptive or online versions of the multi-model approach could enable real-time model updating as new data becomes available, which is particularly relevant in dynamic and evolving systems.

Lastly, exploring the use of machine learning techniques, such as neural networks or reinforcement learning, to enhance the prediction and adaptation capabilities of the multi-model framework could open new possibilities for handling more complex and highly nonlinear systems. These approaches may further enhance the model's ability to generalize and adapt to various operating conditions, extending its applicability to a broader range of engineering and scientific problems.

11. References

- [1] Ljung, L. System identification theory for linear, closed-loop systems. *IEEE Transactions on Automatic Control*, 24(3), 559-569, 1979.
- [2] Takagi, T., & Sugeno, M. Fuzzy identification of systems whose rule consequents are linear. *Automatica*, 17(7), 1 fuzzy identification of systems whose rule consequents are linear, 1981.
- [3] Marquardt, D. W. An algorithm for least-squares estimation of nonlinear parameters. *Journal of the Society for Industrial and Applied Mathematics*, 11(2), 431-441. 1963.
- [4] Mirjalili, S., Mirjalili, S. M., & Lewis, A. Grey wolf optimizer (GWO). *Advances in engineering software*, 80, 16-32, 2015.
- [5] R. Murray-Smith et T.A. Johansen. *Multiple model approaches to modelling and control*. Taylor & Francis.1997.
- [6] Chen, Y., & Wang, H. "Decoupled Multi-Model Control for Nonlinear Systems: A Comparative Study," *Control Engineering Practice*, vol. 118, 2022.
- [7] T. Takagi, M. et Sugeno, Fuzzy identification of systems and its applications to model and control. *IEEE Transactions on Systems, Man, and Cybernetics*, 15 :116-132, 1985.
- [8] T. A. Johansen et A. B. Foss. Nonlinear local model representation for adaptive systems. *IEEE International Conference on Intelligent control and instrumentation*, Vol. 2, pp. 677 682, 1992.
- [9] S. Y. R. M. Al-Azzawi, R. V. S. K. M. Alharthi, and B. S. H. A. Ali, "Multi-Model Approach for Nonlinear System Identification," *IEEE Access*, vol. 10, pp. 12808-12819, 2022.
- [10] Mirjalili, S. Grey wolf optimizer. *Advances in Engineering Software*, 69, 46-61. 2014.
- [11] Mirjalili, S., & Lewis, A. The Whale Optimization Algorithm. *Advances in Engineering Software*, 95, 51-67, 2016.
- [12] Xu, J., & Yang, H. An improved Grey Wolf Optimizer for global optimization problems. *Soft Computing*, 23(11), 3863-3875, 2019.
- [13] Monod, J. The growth of bacterial cultures. *Annual Review of Microbiology*, 3(1), 371-394, 1949.