Decoupling Control of Penicillin Fermentation Processes Based on MLS-SVM Inversion

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Abstract

Specific to typical multi-variable, strong-coupling and nonlinear penicillin fermentation process, by combination of an inverse system method and a support vector machine theory, a nonlinear robust decoupling control method based on MLS-SVM inversion is proposed. Firstly, a dynamic system model is developed based on material balance relation of fed-batch fermentation process, and existence of inverse system is analyzed. Secondly, an inverse model has been developed offline by use of fitting capacity of MLS-SVM; online correction was made by use of differential evolution (DE) algorithm on the basis of deviation information. Finally, to connect the inverse model and original system in serial into a compound pseudo-linear system, and based on characteristics of pseudo-linear system, introduce internal model controller for closed-loop control of the system. Simulation result shows that such control method can realize dynamic decoupling control of penicillin fermentation process; the system boasts very strong parameter robustness and good resistance against interference

Keywords: Fed-batch fermentation, support vector machine, inverse system method, decoupling control, internal model controller

1. Introduction

As the first kind of antibiotic purified and clinically used on a large scale, penicillin has initiated a new era in antibiotic therapy and now is the antibiotic in the largest global demand [1-2]. However, as the fermentation process of penicillin involves growth, reproduction and metabolism of microorganism. During such fermentation, multiple parameters feature a multi-variable, strong coupling and uncertain nonlinear dynamic interactions. In order to further improve the fermentation production efficiency and product yield, it is necessary to research this multi-variable nonlinear system and design a feasible and effective decoupling control method. Existing control methods to this point can only realize static decoupling similar to fermentation process rather than realizing fully dynamic decoupling of the system, which does not meet the demand for decoupling control of penicillin fermentation process is of great theoretical significance and application value [3-4].

In recent years, the linear method of nonlinear system, inverse system has been provided an effective approach for decoupling control of nonlinear systems because of its clear concept and simple method. However, the application of the inverse system method requires the associated object's mathematical model and specific system parameters to be established. Moreover, the analytic expression of the inverse system should be accurately determined. All these considerations greatly limit the application of the inverse system method in decoupling control of complicated non-linear systems. Specific to the foregoing "bottlenecks", some scholars have introduced the idea of intelligent control into the inverse system method, using a neural network to distinguish between inverse model of non-linear systems, and applied that to decoupling control of fermentation [5-6]. However, in this method, the process system model for inverse system analysis is based on simplified model of Monod equation, which ignored many non-linear components, making it inconsistent with the practice of fermentation site and not practical to the original non-linear coupling system. Furthermore, the traditional neural network method is based on the asymptotic theory of sample approximates to infinite, while in such a complicated non-linear system as biological fermentation process, it is difficult to obtain accurate sample data. Additional problems exist such as model structure selection, algorithm convergence, uniqueness of solution, *etc.*

On the basis of this, in this project, using a mechanism model approach, a dynamic system model is developed based on the material balance relation in penicillin fed-batch fermentation processes. With respect to the multi-variable nonlinear coupling model, the inverse system method is combined with a support vector machine theory, and a decoupling method for penicillin fermentation process based on multiple output least squares support vector machine (MLS-SVM) inversion is proposed. As a further step, to ensure the system's control precision and stability, and in the light of the characteristics of pseudo-linear system, the feedback controller is designed based on internal model control principles. The simulation result shows that this method can achieve feedback linearization of nonlinear coupling system while presenting very strong parameter robustness and strong resistance against interference.

2. Main Title Process Modelling and Reversibility Analysis

2.1. Mathematical Model

The concentrations of mycelia and metabolite in various fed-batch liquids were assumed to be 0 [2]. According to the material balance relation Eq. (1) of various substances (mycelia, substrate, and metabolite, H+ *etc.*) in the fed-batch fermentation process, a system dynamic model was developed, as in (1).

$$\frac{\mathrm{d}x}{\mathrm{d}t} = \mu(X, S, P, \mathrm{pH})X - \frac{x}{V}\frac{\mathrm{d}V}{\mathrm{d}t} \tag{1}$$

Where $x \in \{X, S, P, pH\}$, X, S, P, pH, V are biomass concentration, substrate concentration, product concentration, pH value and the volume of the fermentation liquor respectively; μ is the specific rate of various substances.

In the fed-match fermentation process of penicillin, various substrates were fed continuously as per specific concentrations to provide the necessary carbon source, nitrogen source, inorganic salt and precursor substances, as well as to adjust and control the pH value of the fermentation liquor to be maintained in an optimal range. The fermentation volume V and pH varied as the addition of various substrates. Their balance equations were expressed respectively as

$$\frac{\mathrm{d}V}{\mathrm{d}t} = f_c + f_{nh} + f_s + f_{paa} \tag{2}$$

$$\frac{\mathrm{dpH}}{\mathrm{d}t} = \gamma(X, S, P, \mathrm{pH})X - \frac{\mathrm{pH}}{V}\frac{\mathrm{d}V}{\mathrm{d}t} + \frac{S_{nh}f_{nh} - S_cf_c - S_{paa}f_{paa}}{V}$$
(3)

Where f_c , f_{nh} , f_s and f_{paa} are feeding rates of glucose, aqueous ammonia, monopotassium phosphate (KDP) and phenylacetic acid (PAA) respectively; S_c , S_{nh} , S_{paa} are the flow liquid concentrations of glucose, aqueous ammonia, and PAA respectively; and γ is the specific consumption rate of H+.

As the only restrictive substrate of penicillin fermentation, carbon source was required in a large quantity and would be consumed at a comparatively quickly.

Considering the influence of the source of carbon (glucose) in the fermentation process, the balance equation of substrates was expressed as

$$\frac{\mathrm{d}S}{\mathrm{d}t} = -\nu(X, S, P, \mathrm{pH})X + \frac{S_c}{V}f_c - \frac{S}{V}\frac{\mathrm{d}V}{\mathrm{d}t} \tag{4}$$

Where v is the specific consumption rate of various substrates.

In the stage of penicillin synthesis, the hydrolysis reactions of the precursor substance (PAA) and penicillin would significantly affect the penicillin yield. The influence of the PAA addition and hydrolysis rate K on the fermentation process has been considered in the following balance equation of product concentration

$$\frac{\mathrm{d}P}{\mathrm{d}t} = \rho(X, S, P, \mathrm{pH})X - KP + \frac{K_{paa}}{V}f_{paa} - \frac{P}{V}\frac{\mathrm{d}V}{\mathrm{d}t}$$
(5)

Where K_{paa} is inhibition constant and ρ is specific production rate of the product.

Select status variables $\mathbf{x} = (x_1, x_2, x_3, x_4, x_5)^T = (X, S, P, pH, V)^T$ and input variable $\mathbf{u} = (u_1, u_2, u_3, u_4)^T = (f_c, f_{nh}, f_s, f_{paa})^T$. Its system status equation (6) can be expressed as:

$$\begin{aligned}
\dot{x}_{1} &= \mu(x_{1}, x_{2}, x_{3}, x_{4})x_{1} - \frac{x_{1}}{x_{5}} \sum_{i=1}^{4} u_{i} \\
\dot{x}_{2} &= -\nu(x_{1}, x_{2}, x_{3}, x_{4})x_{1} + \frac{s_{1}u_{1}}{x_{5}} - \frac{x_{2}}{x_{5}} \sum_{i=1}^{4} u_{i} \\
\dot{x}_{3} &= \rho(x_{1}, x_{2}, x_{3}, x_{4})x_{1} - s_{2}x_{3} + \frac{s_{3}u_{4}}{x_{5}} - \frac{x_{3}}{x_{5}} \sum_{i=1}^{4} u_{i} \\
\dot{x}_{4} &= \gamma(x_{1}, x_{2}, x_{3}, x_{4})x_{1} + \frac{s_{4}u_{2} - s_{1}u_{1} - s_{5}u_{4}}{x_{5}} - \frac{x_{4}}{x_{5}} \sum_{i=1}^{4} u_{i} \\
\dot{x}_{5} &= \sum_{i=1}^{4} u_{i} = u_{1} + u_{2} + u_{3} + u_{4}
\end{aligned}$$
(6)

Where $\mu, \nu, \rho, \eta, \gamma$ are all the analytical functions of status variable; $s_i (i = 1, 2, \dots, 5)$ are all constants other than zero.

Take 4 feeding $u_1 \sim u_4$ as input control variable, the preceding $4 X(x_1), S(x_2), P(x_3)$ and pH(x_4) of the 5 status variables as control variables, and $V(x_5)$ as middle parameter, and build the following system mathematic model of penicillin fermentation process:

$$\begin{cases} \dot{\boldsymbol{x}} = f(\boldsymbol{x}, \boldsymbol{u}) \\ \boldsymbol{y} = (y_1, y_2, y_3, y_4)^{\mathrm{T}} = (x_1, x_2, x_3, x_4)^{\mathrm{T}} \end{cases}$$
(7)

2.2. Model Reversibility Analysis

Specific to the nonlinear strong coupling system mathematical model (7), decoupling processing of multi-variable nonlinear system is based on the inverse system theory.

The inverse system method requires that status (output) feedback can be used for realizing the original system's " α th-order integral inverse system" only if the original system is reversible, so as to finish the transformation from nonlinear decoupling system to pseudo-linear decoupling system. Below is the analysis of the

reversibility of penicillin fermentation process, with its inverse system model being established.

Lemma 1 the necessary and sufficient condition for reversibility of System Σ within certain realm of points (x_0, u_0) : The system has relative order $\{a_1, a_2, \dots, a_q\}$,

and
$$\sum_{i=1}^{i=q} a_i \leq n$$
.

The interactor algorithm was used to analyze the reversibility of the penicillin fermentation process, with the analysis process as follows [6]:

Initially, calculate the derivative of output $\mathbf{y} = (y_1, y_2, y_3, y_4)^T$ to time, until the implicit input $\mathbf{u} = (u_1, u_2, u_3, u_4)^T$. It can be known from Equation (6) that output of first-order derivative \mathbf{y} already meets requirements:

$$\dot{\mathbf{y}} = \begin{pmatrix} \dot{y}_{1} \\ \dot{y}_{2} \\ \dot{y}_{3} \\ \dot{y}_{4} \end{pmatrix} = \begin{cases} \mu y_{1} - \frac{y_{1}}{x_{5}} \left(\sum_{i=1}^{4} u_{i} \right) \\ -\nu y_{1} + \frac{s_{1}u_{1}}{x_{5}} - \frac{y_{2}}{x_{5}} \left(\sum_{i=1}^{4} u_{i} \right) \\ \rho y_{1} - s_{2}y_{3} + \frac{s_{3}u_{4}}{x_{5}} - \frac{y_{3}}{x_{5}} \left(\sum_{i=1}^{4} u_{i} \right) \\ \gamma y_{1} + \frac{s_{4}u_{2} - s_{1}u_{1} - s_{5}u_{4}}{x_{5}} - \frac{y_{4}}{x_{5}} \left(\sum_{i=1}^{4} u_{i} \right) \end{cases}$$
(8)

As x_1, x_2, x_3, x_4, x_5 are all greater than zero and $s_i (i = 1, 2, \dots, 5)$ are all not 0, let Jacobian matrix $\mathbf{J} = \frac{\partial \dot{\mathbf{y}}}{\partial u^T} = \partial(y_1, y_2, y_3, y_4) / \partial(u_1, u_2, u_3, u_4)$, so

$$\operatorname{rank}[\mathbf{J}] = \operatorname{rank} \begin{bmatrix} -\frac{y_1}{x_5} & -\frac{y_1}{x_5} & -\frac{y_1}{x_5} & -\frac{y_1}{x_5} \\ \frac{s_1 - y_2}{x_5} & -\frac{y_2}{x_5} & -\frac{y_2}{x_5} & -\frac{y_2}{x_5} \\ -\frac{y_3}{x_5} & -\frac{y_3}{x_5} & -\frac{y_3}{x_5} & \frac{s_3 - y_3}{x_5} \\ -\frac{s_1 + y_4}{x_5} & \frac{s_4 - y_4}{x_5} & -\frac{y_4}{x_5} & -\frac{s_5 + y_4}{x_5} \end{bmatrix} = \operatorname{rank} \begin{bmatrix} 1 & 1 & 1 & 1 \\ s_1 & 0 & 0 & 0 \\ 0 & 0 & 0 & s_3 \\ -s_1 & s_4 & 0 & -s_5 \end{bmatrix} = 4 \quad (9)$$

Thereby

$$\det[\mathbf{J}] = \det\begin{bmatrix} -\frac{y_1}{x_5} & -\frac{y_1}{x_5} & -\frac{y_1}{x_5} & -\frac{y_1}{x_5} \\ \frac{s_1}{x_5} & 0 & 0 & 0 \\ 0 & 0 & 0 & \frac{s_3}{x_5} \\ -\frac{s_1}{x_5} & \frac{s_4}{x_5} & 0 & -\frac{s_5}{x_5} \end{bmatrix} = \frac{s_1}{x_5} \frac{s_3}{x_5} \begin{bmatrix} -\frac{y_1}{x_5} & -\frac{y_1}{x_5} \\ \frac{s_4}{x_5} & 0 \end{bmatrix} = -\frac{s_1 s_3 s_4 y_1}{x_5^4} \neq 0 \quad (10)$$

The system' vector relative order is $\boldsymbol{\alpha} = (\alpha_1, \alpha_2, \alpha_3, \alpha_4)^{\mathrm{T}} = (1, 1, 1, 1)^{\mathrm{T}}$; from Lemma 1, it is known that $\sum_{i=1}^{4} a_i \le 4$, the penicillin fermentation process is reversible. From

implicit function existence theorem and Equations (6)~(8), its inverse system can be expressed as:

$$\boldsymbol{u} = \begin{pmatrix} u_1 \\ u_2 \\ u_3 \\ u_4 \end{pmatrix} = \begin{pmatrix} \varphi_1(y_1, \dot{y}_1, y_2, \dot{y}_2, y_3, \dot{y}_3, y_4, \dot{y}_4, x_5) \\ \varphi_2(y_1, \dot{y}_1, y_2, \dot{y}_2, y_3, \dot{y}_3, y_4, \dot{y}_4, x_5) \\ \varphi_3(y_1, \dot{y}_1, y_2, \dot{y}_2, y_3, \dot{y}_3, y_4, \dot{y}_4, x_5) \\ \varphi_4(y_1, \dot{y}_1, y_2, \dot{y}_2, y_3, \dot{y}_3, y_4, \dot{y}_4, x_5) \end{pmatrix}$$
(11)

However, it is difficult to get the analytical expression of the inverse model expression (11). But in recent years, the support vector machine algorithm has become research subject of interest, breaking the thinking limitation of empirical risk minimization inductive principle, providing a new perspective for machine learning based on empirical risk minimization inductive principle, while at the same time solving such problems as learning and local minimum arising out of neural network algorithm, featuring good generalization ability and system identification ability [7-9]. Therefore, it is suitable for solving the non-linear identification problem of complicated non-linear system. Based on this, this project uses support vector machine's strong approximation ability towards non-linear function to identify the four non-linear functions $\varphi_1, \varphi_2, \varphi_3, \varphi_4$ in Expression (11).

3. Inverse System Identification and Decoupling Control

3.1. MLS-SVM Algorithm

Traditional LS-SVM is built upon a multi-input/single-output, so it is hard to realize the multi-input/multi-output system [10-11]. To meet the requirements for identification of penicillin fed-batch fermentation (multi-input/multi-output) inverse model, the algorithm has been improved as follows.

Traditional LS-SVM defines the following optimization problems, given L pairs of sample set $\{(x_i, y_i)\}_{i=1}^l$:

$$\min J(\boldsymbol{w}, b, \boldsymbol{\xi}) = \frac{1}{2} \boldsymbol{w}^{\mathrm{T}} \boldsymbol{w} + \gamma \frac{1}{2} \sum_{i=1}^{l} \boldsymbol{\xi}_{i}^{2}$$
s.t. $y_{i} = \boldsymbol{w}^{\mathrm{T}} \varphi(\boldsymbol{x}_{i}) + b + \boldsymbol{\xi}_{i} \quad i = 1, 2, \cdots, l$
(12)

Where ξ is relaxing factor, and γ is penalty parameter.

In this work, relaxing factor in Optimization Problem (12) is replaced by quadratic loss function of error, and based on the original LS-SVM problem, present the original problem of MLS-SVM:

$$\min J(\boldsymbol{w}, b, \boldsymbol{\xi}) = \frac{1}{2} \sum_{i=1}^{n} \boldsymbol{w}_{i}^{\mathrm{T}} \boldsymbol{w}_{i} + \frac{1}{2} \gamma_{i} \sum_{i=1}^{n} \boldsymbol{\xi}_{i} \boldsymbol{\xi}_{i}^{\mathrm{T}}$$

$$s.t. \quad y_{i} = \boldsymbol{w}_{i}^{\mathrm{T}} \varphi_{i}(\boldsymbol{x}) + \boldsymbol{\gamma}^{\mathrm{T}} b_{i} + \boldsymbol{\xi}_{i} \quad i = 1, 2, \cdots, l$$
(13)

Where $\xi \in \mathbf{R}^{l \times n}$, *n* is the number of output variables; $\varphi_i(\mathbf{x}) = [\varphi_i(\mathbf{x}_1), \cdots, \varphi_i(\mathbf{x}_l)]$.

With introduction of Lagrange multiplier a, $a \in \mathbb{R}^{m \times l}$, m being input vector number, and Problem (14) becomes:

$$\max L = \frac{1}{2} \sum_{i=1}^{l} \boldsymbol{w}_{i}^{\mathrm{T}} \boldsymbol{w}_{i} + \frac{1}{2} \sum_{i=1}^{l} \boldsymbol{\xi}_{i} \boldsymbol{\xi}_{i}^{\mathrm{T}} - \sum_{i=1}^{l} \boldsymbol{a}_{i}^{\mathrm{T}} (\boldsymbol{w}_{l}^{\mathrm{T}} \boldsymbol{\varphi}_{i}(\boldsymbol{x}) + \boldsymbol{\gamma}^{\mathrm{T}} \boldsymbol{b}_{i} + \boldsymbol{\xi}_{i} - \boldsymbol{y}_{i})$$
(14)

According to KKT [12-13]optimization conditions

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$$\begin{cases} \frac{\partial L}{\partial \boldsymbol{w}_{i}} = 0 \Rightarrow \boldsymbol{w}_{i} = \varphi(\boldsymbol{x}_{i})\boldsymbol{a}_{i}^{\mathrm{T}} \\ \frac{\partial L}{\partial \boldsymbol{b}_{i}} = 0 \Rightarrow \boldsymbol{\gamma}^{\mathrm{T}}\boldsymbol{a}_{i}^{\mathrm{T}} = 0 \\ \frac{\partial L}{\partial \boldsymbol{\xi}_{i}} = 0 \Rightarrow \boldsymbol{a}_{i} = \boldsymbol{\xi}_{i}, i = 1, 2, \cdots, l \\ \frac{\partial L}{\partial \boldsymbol{\xi}_{i}} = 0 \Rightarrow \boldsymbol{w}_{i}^{\mathrm{T}}\varphi_{i}(\boldsymbol{x}) + \boldsymbol{\gamma}^{\mathrm{T}}\boldsymbol{b} + \boldsymbol{\xi}_{i} - \boldsymbol{y}_{i} = 0, i = 1, 2, \cdots, l \end{cases}$$
(15)

After organizing of Equation (15), ξ_i and w are removed, and the optimization problem is transformed into solving of the following equation set

$$\begin{bmatrix} b_i & \boldsymbol{a}_i \end{bmatrix} \begin{bmatrix} 0 & \boldsymbol{\gamma}^{\mathrm{T}} \\ \boldsymbol{\gamma} & K_i(\boldsymbol{x}_i, \boldsymbol{x}) + I \end{bmatrix} = \begin{bmatrix} 0 & \boldsymbol{y}_i \end{bmatrix}$$
(16)

Where $K(\mathbf{x}_n, \mathbf{x})$ meets the kennel function of Mercer conditions; in this work, RBF kennel function $K(\mathbf{x}_i, \mathbf{x}_j) = \exp[-|\mathbf{x}_i - \mathbf{x}_j|^2/(2\sigma^2)]$ is used, with σ being kennel width.

As matrix
$$\begin{bmatrix} 0 & \boldsymbol{\gamma}^{\mathrm{T}} \\ \boldsymbol{\gamma} & K_{i}(\boldsymbol{x}_{i}, \boldsymbol{x}) + I \end{bmatrix}$$
 is non-singular, so
$$\begin{bmatrix} b_{i} & \boldsymbol{a}_{i} \end{bmatrix} = \begin{bmatrix} 0 & \boldsymbol{y}_{i} \end{bmatrix} \begin{bmatrix} 0 & \boldsymbol{\gamma}^{\mathrm{T}} \\ \boldsymbol{\gamma} & K_{i}(\boldsymbol{x}_{i}, \boldsymbol{x}) + I \end{bmatrix}^{-1}$$
(17)

So *i*th output of MLS-SVM is:

$$f_i(\boldsymbol{x}) = \boldsymbol{a}_i K(\boldsymbol{x}_i, \boldsymbol{x}_j) + b_i \tag{18}$$

Regarding the MLS-SVM system identification, selection of kennel function parameter σ and penalty parameter γ exerts a strong influence over building of the inverse model. Traditional parameter selection methods are mostly based on experience and trial-error methods, making it difficult to ensure precision and computing speed. In order to obtain a soft-sensing model with relatively high prediction effect, this project applies differential evolution algorithm to make online optimization and adjustment of MLS-SVM.

3.2. Differential Evolution Algorithm

Differential Evolution (DE) algorithm is a simple but very effective real parameter random optimization algorithm [14-15]. DE uses computing steps similar to a standard evolution algorithm, including three operations: variation, crossover and selection. But other than a traditional evolution algorithm, DE uses proportional difference vectors generated by varied individuals randomly selected to interfere with the population individuals of the current generation, hence there is no need for using singular probability distribution to generate the offspring. In DE algorithm, D-dimension real parameter vectors $X_i^t = \{x_{i1}^t, \dots, x_{iD}^t\} \in S(i = 1, \dots, NP)$ in the number of NP constitute a generation of population $P^t = \{X_i^t, \dots, X_{NP}^t\}$ and make parallel direct search in the search space; here $t = 0, 1, \dots, T_{max}$ represents the evolved generation.

In variation operation, variation vector $V_i^t = (v_{i1}^t, \dots, v_{iD}^t)$ is generated by way of carrying out variation operation on every target individual X_i^t [16], *i.e.* based on Equation (19).

$$V_i^t = X_{r1}^t + F \cdot (X_{r2}^t - X_{r3}^t)$$
(19)

Where r_1, r_2, r_3 is the integer randomly selected from the set $\{i = 1, 2, \dots, NP\}$ and different from each other; *F* is the scale factor with value range being [0.4,1], which is used for controlling scaling of differential vector.

To enhance the potential diversity of the population, target vector X_i^t and its variation vector V_i^t make cross-operation [17], *i.e.* generating a test vector $U_i^t = (u_{i1}^t, \dots, u_{iD}^t)$ according to Equation (20).

$$u_{ij}^{t} = \begin{cases} v_{ij}^{t}, & \text{rand}_{ij} \leq \text{CR or } j = j_{\text{rand}} \\ x_{ij}^{t}, & \text{otherwise} \end{cases}$$
(20)

Where rand_{*ij*} is an evenly distributed random number of [0-1], which decides whether element *j* of test *i* is contributed by variation vector or target vector; $j_{rand} \in [1, 2, \dots, D]$ is the randomly selected dimension number index, which ensures at least one element of the test vector U_i^t is contributed by variation vector; V_i^t is a probability constant.

Greedy strategy is used for selection operation. Equation (21) is used to compare the objective function value (fitness) of test vector with objective function of the target individual. If the former is smaller or equal to the latter, the test vector will take the place of the corresponding target individual and enter the next generation, otherwise the target vector remains unchanged.

$$X_{i}^{t+1} = \begin{cases} U_{i}^{t}, & f(U_{i}^{t}) \leq f(X_{i}^{t}) \\ X_{i}^{t}, & \text{otherwise} \end{cases}$$
(21)

Where f is objective function. The objective function selected in this project for DE operation is the square of the deviation between MLS-SVM output value and the off-line analysis value.

DE algorithm is based on a simple theory. A small number of controlled parameters and fast convergence speed results in an effective global optimal search algorithm. It is comparatively suitable for solving complicated optimization problems, so use of DE's global search capability to make on-line optimization and adjustment on performance parameters σ and γ of MLS-SVM will result in a relatively accurate inverse system model.

3.3. Inverse System Identification

The MLS-SVM is used to identify the inversely extended model (11) of the penicillin fermentation process, with specific steps of the identification process as follows:

Firstly, Data Acquisition. In the working area of the penicillin fermentation process, an adequate excitation signal is applied to the system. On the precondition of meeting the sampling theorem, the timing sampling on excitation input signal is set as $u = \{u_1, u_2, u_3, u_4\}$. The output response is $y = \{y_1, y_2, y_3, y_4\}$ and the internal status x_5 , thus obtaining the original data sample set $\{u, y, x_5\}$.

Secondly, Data Processing. Regarding the structure of the inverse model established according to Equation (11), a higher order numerical differentiation method is used (five points derivation method is used herein) to calculate the first-order derivative $\dot{y} = {\dot{y}_1, \dot{y}_2, \dot{y}_3, \dot{y}_4}$ of $y = {y_1, y_2, y_3, y_4}$, thus obtaining training data sample set ${y, \dot{y}, x_5}$ and u, with the former being the inverse model input and the latter being the inverse model output (*i.e.* expected output).

Finally, off-line fitting and on-line correction. Based on the input/output data set, the MLS-SVM undergoes off-line training and learning, and uses a crossover verification method to determine the corresponding initial parameters (σ and γ), thus building the initial inverse model. According to the analysis value of the actual fed-batch fermentation

process and deviation information output by inverse model, proceed to further use DE algorithm to optimize MLS-SVM performance parameters.

Figure1 is the online correction diagram of the inverse model of the penicillin fermentation process. In Figure, 4 differentiators are added to obtain the first-order derivative.



Figure 1. Online Correction Figure of MLS-SVM Inverse Model

3.4. Internal Model Decoupling Control

The corrected MLS-SVM inverse model is taken as the feed-forward controller and is connected in serial with the penicillin fermentation process, thus forming a pseudo-linear compound system. In this way, a multi-variable and strong coupling complicated nonlinear system is, by way of feedback linearization, decoupled into 4 pseudo-linear compound systems independent other (first-order of each integral procedure $1/(a_{i1}s + a_{i0})$ i = 1,2,3,4). However, the compounded pseudo-linear system is not an ideal linear system. Simply taking MLS-SVM inverse model as the controller to make an open loop control on penicillin fermentation process often fails to achieve good control results. Additionally, due to inevitable errors in identification, the inverse system method itself is not satisfactory in identifying errors, which is also a problem in the application of inverse system method in engineering.

In recent years, internal model control method, arising from chemical industrial process control, has found extensive applications in industrial control. Both theoretical analysis and simulation results show this method can effectively refrain the interference and be strong over model mismatch. Therefore, in this project, the internal model controller is introduced based on MLS-SVM inverse decoupling control so as to compensate for the weakness of inverse system method in interference resistance and control strength.

The system's vector relative order is $\alpha = (\alpha_1, \alpha_2, \alpha_3, \alpha_4)^T = (1, 1, 1, 1)^T$, based on the inverse system principle and same-order principle of internal model control, so

$$\begin{cases}
G_{mi}(s) = \frac{1}{a_{i1}s + a_{i0}} \\
F_i(s) = \frac{1}{(\lambda_i + s)^{n_i}} & i = 1, 2, 3, 4 \\
G_c(s) = F(s)G_{m-}(s)
\end{cases}$$
(22)

Where $G_{m.}(s)$ is the reversible part of $G_{mi}(s)$; $F_i(s)$ is the low-pass filter, and λ_i, n_i respectively are constant and order number of filter.

The structure of decoupling control of MLS-SVM inversion internal model of penicillin fermentation process is as shown in Figure 2.



Figure 2. Structure of Internal Model Decoupling Control Based on MLS-SVM Inversion

4. Simulation Result and Analysis

The penicillin fed-batch fermentation process is the object for experimental research. To bring the experiment close to the actual penicillin fermentation process, the initial conditions of various batches are set at various settings, the feeding strategies of various substrates varying correspondingly to enlarge batch differences. The tank pressure is controlled between 0~0.07 Mpa and the temperature in the early and medium periods is controlled at about 26°C and then in late period, about 24°C. The stirring speed is controlled between 150~250rpm, and concentration of the precursor PAA <1kg/m3.

As in actual penicillin fed-batch fermentation process, fermentation liquor pH (x_4) is often separately controlled by a PID circuit. This project only makes experimental analysis and simulation over biomass concentration X (x_1) , substrate concentration S (x_2) and product concentration P (x_3) . To verify the advantage of decoupling control method of MLS-SVM inversion internal model, the inverse system for comparison uses the traditional PID method for closed-loop control. Both systems make simulation on decoupling performance and strength of the performance.

The initial performance parameter of MLS-SVM uses empirical values as follows: $\sigma^2 = [1.0, 1.0, 1.0]$ and $\gamma = [10, 10, 10]$. Following DE correction, performance parameters of MLS-SVM are: $\sigma^2 = [0.46, 0.96, 0.72]$ and $\gamma = [9.8, 7.7, 8.5]$. Parameters of internal model controller: $\lambda_1 = 1.2$, $\lambda_2 = 1.4$, $\lambda_3 = 1.6$, $n_i = 1$, $a_{i0} = a_{i1} = 1$, i = 1, 2, 3.

4.1. Decoupling Result Analysis

To survey the decoupling results of the system, supposing the substrate concentration is constantly $8 \text{g} \cdot \text{L}^{-1}$, product concentration is constantly $1.0 \text{g} \cdot \text{L}^{-1}$, and biomass concentration makes a move from $6 \sim 8 \text{g} \cdot \text{L}^{-1}$. Comparison of decoupling result is shown in Figure 3. As Figure 3 shows, with the control of PID, when biomass concentration receives a sudden increase, both substrate concentration and product concentration experience remarkable fluctuation, with relatively strong coupling. But with the control of MLS-SVM inversion internal model, the static error is almost eliminated and the decoupling result is relatively good.

International Journal of Multimedia and Ubiquitous Engineering Vol.11, No.4 (2016)



Figure 3. Comparison of Decoupling Result: Biomass Concentration (a); Substrate Concentration (b); Product Concentration (c)

4.2. Analysis of Strength

To survey the strength of the system, assuming that biomass concentration is $6 g \cdot L^{-1}$, substrate concentration is constantly $8 g \cdot L^{-1}$ and product concentration is constantly $1.0 g \cdot L^{-1}$; an additional 30% strong external interference signal is suddenly applied at 120h. The robustness result comparison is shown in Figure 4. The comparison of response arising from the two control methods, as shown in Figure 4 indicates that with the control of MLS-SVM inversion internal model, robustness control result is good, with less fluctuation triggered by external interference, and the closed-loop system can achieve a very good tracing effect.



Figure 4. Comparison of Robustness Result: Biomass Concentration (a); Substrate Concentration (b); Product Concentration (c)

The simulation result shows that the internal model control method of MLS-SVM inversion can realize dynamic decoupling among various parameters during penicillin fermentation process. Moreover, in the case of external interference, parameter disturbance or nonlinear modelling error, the system features very good performance. So the robustness and interference resistance of internal model decoupling control method of MLS-SVM inversion are proven.

5. Conclusion

To further enhance penicillin fermentation production efficiency and product yield, based on development of penicillin fed-batch fermentation multi-variable nonlinear dynamic model, feedback linearization decoupling control is made on a nonlinear model on the basis of inverse system method and support vector machine theory. To compensate for the dynamic status with no model of the pseudo-linear system following the decoupling and to refrain interference and to refrain interference, interval model control method is used for designing a feedback controller with interference resistance and strong robustness, thus realizing decoupling robustness control of multi-variable nonlinear system during penicillin fermentation process. Simulation research shows the nonlinear dynamic model is practical and that the MLS-SVM inversion robustness decoupling control method is effective for penicillin fermentation process.

References

- G. A. Montaque, A. J. Morris and J. R. Bush, "Consideration in control scheme development for Fermentation process control", Control Process System IEEE, vol. 8, no. 3, (2002), pp. 44-48.
- [2] J. Chen, L. Q. Liu and G. C. Du, "Fermentation Process Optimization Theory and Techniques", Chemical Industry Press, Beijing, (2009).
- J. S. Alford, "Bioprocess control: advances and challenges. Compute. Chem. Engineering, vol. 30, no. [3] 10, (2006), pp.1464-1475.
- F. Du, M. Lei and Q. Liu, "Advanced control in fermentation process", Information and Control, vol. [4] 33, no. 3, (2004), pp. 314-317.
- [5] X. Z. Dai, W. C. Wang and Y. H. Ding, "Assumed "inherent sensor" inversion based ANN dynamic soft-sensing method and its application in erythromycin fermentation process", Computers and Chemical Engineering, vol. 30, no. 8, (2006), pp.1203 -1225.
- [6] X. Z. Dai, "Neural Network Inverse Control Method of Multivariable Nonlinear systems", Science Press, Beijing, (2005).
- [7] G. Tai, J. C. Wang, Y. Ge, H. J. Liu and L. W. Yang, "Gravitational search algorithm-least squares support vector machine model forecasting on hourly urban water demand", Control Theory & Application, vol. 31, no. 10, (2014), pp.1377-1382.
- L. Liu, T. Y. Wang, Y. X. Jiang, M. Hu and Q. Ning, "Tool wear state recognition based on hyper-[8] sphere support vector machine", Transactions of the Chinese Society for Agricultural Machinery, vol. 42, no. 1, (2011), pp. 218-222.
- [9] W. H. Xu, Y. J. Xu, L. L. Dong and Y. Li, "Level-set and SVM based target recognition of image sonar", Chinese Journal of Scientific Instrument, vol. 33, no 1, (2012), pp. 49-55.
- [10] W. Liu, J. P. Wang and C. H. Liu, "Lycopene content prediction based on support vector machine with particle swarm optimization", Transactions of the Chinese Society for Agricultural Machinery, vol. 43, no. 4, (2012), pp.143-147,155.
- [11] H. Q. Wang, C. Y. Ji and B. X. Gu, "In-greenhouse cucumber recognition based on machine vision and least squares support vector machine", Transactions of the Chinese Society for Agricultural Machinery, vol. 43, no. 3, (2012), pp.163-167.
- [12] K. Y. Zergat and B. Amrouche, "New scheme based on GMM-PCA-SVM modelling for automatic speaker recognition", International Journal of Speech Technology, vol. 17, no. 4, (2014), pp. 373-381.
- [13] Y. Erfanifard, N. Behnia and V. Moosavi, "Tree crown delineation on VHR aerial imagery with SVM classification technique optimized by Taguchi method: A case study in Zagros woodlands", International Archives of the Photogrammetry, vol. 40, no. 1, (**2013**), pp.153-158. [14] Y. T. Huang, L. Wang and Q. D. Wu, "A hybrid PSO-DE algorithm for smart home energy
- management", Lecture Notes in Computer Science, vol. 8795, (2014), pp.292-300.
- [15] L. H. Wu, Y. N. Wang, S. W. Zhou and X. F. Yuan, "Research and application of pseudo parallel differential evolution algorithm with dual subpopulations", Control Theory & Applications, vol. 24, no. 3, no 3, (2007), pp.453-458.

International Journal of Multimedia and Ubiquitous Engineering Vol.11, No.4 (2016)

- [16] X. Q. Wang, N. Luo and Z. C. Ye, "Differential evolution algorithm based on Kriging and its application in styrene plant optimization", CIESC Journal, vol. 64, no. 12, (**2013**), pp. 4563-4570.
- [17] P. Wang, L. Liu, Z. Chen, Y. J. Zhai and J. L. Zhou, "PID Parameter tuning based on improved DE algorithm and the application", Journal of Chinese Society of Power Engineering, vol. 35, no. 3, (2015), pp. 191-196.

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