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Research Article

ALGEBRIC METHOD AND LSCR TECHNIQUE FOR ESTIMATING THE PARAMETERS OF A BIOREACTOR

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ABSTRACT

In this paper, we are interested in identifying the parameters of a bioreactor in the case of a nitrification process. To represent the uncertainties that affect these parameters, we focus on the set approach based on interval arithmetic, in particular set inversion, to obtain guaranteed results. First, a method of studying observability and identifiability by an algebraic method is carried out. The LSCR (Leave out Sign-dominant Correlation Regions) method used in this article for the identification of parameters is based on the construction of non-asymptotic confidence regions for the parameters of the dynamic system. This method, using the calculation of the correlation functions, makes it possible to construct regions containing the real value of the parameters to be identified with a guaranteed probability and with a minimum knowledge of noise. For guaranteed results, set inversion has been associated with this approach.

Keywords: Estimation, Bioreactor, LSCR method, Set inversion, Interval arithmetic.

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1. INTRODUCTION

Whatever the domains, it is sometimes essential to call on a modeling of the system that one seeks to study. This procedure uses knowledge in many fields and generally leads to complex models. The identification or the experimental modeling makes it possible to describe physical systems by combining information a priori related to the knowledge to experimental results directly obtained on the system to be identified. These experimental measurements are often affected by noise errors that are added to modeling errors as well as errors introduced by calculator rounding errors [1]. The identification of the parameters uses techniques whose effectiveness depends on the modeling as well as the chosen estimation algorithms. The most used are the least squares or their variants which are easy to use and have a low cost of calculation. However, they present problems of convergence and an often biased estimate. This is one of the reasons why scientists have been looking for new, more robust identification methods. This study applies to the field of biotechnology as part of a wastewater treatment process. The aim is to identify the parameters of a bioreactor in the context of a nitrification process of ammoniacal nitrogen.The first models to describe such processes are those reported by the International Association on Water Pollution (IAW) [2]; one of these is the activated sludge model [3] which uses the Monod kinetics. It is a complex model with lots of parameters whose identification by statistical methods proves to be difficult or even impossible. These models are not appropriate for online control.

Some models can be considered for online control of an activated sludge process, using models like ARMAX [4], fuzzy logic [5] and neural networks [6].The last two methods allow easier handling of nonlinearities. Other author [7] suggested identifying the parameters of a chemostat using genetic algorithms.The set technique that will be applied is an approach that has been known for many years. It was first established by R. Moore [8], then Neumaier [9] and Hansen [10]. In this context, a variable is represented by one set $\mathbb{X}$ called the set of likelihood or domain, assumed to contain the real value x. the set methods can actually be used in many areas. They can find applications for estimating the uncertain parameters, robotics for the identification of the dynamic parameters [11,12] as The use of interval arithmetic is not new in the field of biotechnology [13,14]. Set methods are well suited for

biotechnology applications due to the large error interval introduced during measurement acquisition. First, a differential algebraic approach [2,24,25] is used to study the observability and identifiability of the system. Indeed, models of biotechnological processes are often described in terms of differential algebraic equations which therefore lend themselves well to this approach.

The LSCR method described in this article enables us to obtain a confidence region which must satisfy two conditions: have a guaranteed probability and be focused around the desired parameter. this method is interesting because it requires not many assumptions about the noise for the construction of confidence regions and remains effective even in the presence of non-modeled dynamics. The theory of this approach is developed in [15,16]. The disadvantage of this approach is that it provides us results by gridding and did not give us a guaranteed numerical result. For more, it is applied only in a small area. To remedy this, M.Kieffer [17] combines set inversion at this approach to improve the result. In this work, we apply this method to identify the parameters of a nitrification model.

The paper is organized as follows, in section 1.1 describes the essential of LSCR approach, it will be followed in section 1.2 by the basic definitions of interval arithmetic as well as the principle of set inversion. In section 1.3 a summary of the algebraic method is given, then one present the model of bioreactor, whose one want to identify the dynamic parameters, in section 2. Simulation results and discussion are given in the section 3 followed by a conclusion.

1.1 The LSCR approch

The method that we use in this article to identify the parameters of a bioreactor, is the approach LSCR (Leave out Sign-dominant Correlation Regions). The principle is based on the construction of a confidence area Φ, from the calculation of empirical correlation functions. One of the interesting aspect of the method is obtaining confidence regions where the searched parameters are known with a guaranteed probability, whatever the size of the data set .

The assumptions on noise are reduced, we can just assume that it is a signal symmetrically distributed around zero, and its variance can take any value. However, the intensity of the noise will influence the width of the confidence region. The procedure for calculating that

confidence regions by the LSCR method is as follows:

1. Suppose we try to identify parameters p of a system S, we define the prediction error ε(p) , representing the difference between the noisy sampled data on the output of the system y(t), and the output of model y_m (t).

$$\varepsilon(p) = y_t - \hat{y}_m(p) \text{ for } t = 1, 2, \ldots, k \quad (1)$$

2. Select one integer $e \geq 0$ .Then, for $t=1+r,\ldots,N+e = K$,compute :

$$f^{\varepsilon}_{t-e,e} = \varepsilon_{t-e}(p)\ \varepsilon_t(p) \quad (2)$$

3. Consider a set I={1,…,N} for a number of data N, and a collection G of subset $I_i \subseteq I$,I = 1,…M which is a group with respect to the symmetric difference, ie : $(I_i \cup I_j) - (I_i \cap I_j) \in G$,if $I_i, I_j \in G$, and then compute the estimates of the correlation

$[\varepsilon_{t-e}(p)\ \varepsilon_t\ (p)]$, given by: $g^{\varepsilon}_{i,e}\ (p) = \sum_{k \in I_i} f^{\varepsilon}_{k,e}(p)$ i=1,…,M (3)

For $p=p_0$, we have: $E\ [\varepsilon_{t-e}(p_0)\ \varepsilon_t\ (p_0)] = 0$ (4)

One concludes than, the empirical estimates are a random variables sequence with zero mean for $p = p_0$. Thereafter, we compute a number of correlation estimates using different subsets of data, then the principle is to remove the regions of the parameter space where the empirical estimates are positive (or negative) too often .

4. let an integer $q \geq 0$ in an interval

$[1, \frac{M+1}{2}]$ and find the region $\Phi^{\varepsilon}_{e,q}$, so that at least q of the $g^{\varepsilon}_{i,e}$ (p) are larger than zero and at least q are smaller than zero. The probability that p belong to $g^{\varepsilon}_{i,e}$ (p) is

1- $\frac{2q}{M}$. The region $\Phi^{\varepsilon}_{e,q}$ depends on the values r and q , as well as the set of intervals that form the group G, the generation method of this group is described by Gordon [18] One can defined $\Phi^{\varepsilon}_{e,q}$ formelly by:

$\Phi^{\varepsilon}_{e,q} = \Phi^{\varepsilon,+}_{e,q} \cap \Phi^{\varepsilon,-}_{e,q}$ such as

$\Phi_{\varepsilon,q}^{\varepsilon,+}$ = {$p \in \mathbb{P}$ such that $\sum_{i=1}^{m} \xi_i^{\varepsilon,+} \geq q$ } (5)

$\Phi_{\varepsilon,q}^{\varepsilon,-}$ = {$p \in \mathbb{P}$ such that $\sum_{i=1}^{m} \xi_i^{\varepsilon,-} \geq q$ }

$\mathbb{P}$ represente the prior domain for the parameter p and:

$$\xi_i^{\varepsilon,-}(p) = \begin{cases} 1 \ if \ -g_{i,\varepsilon}^{\varepsilon} \geq 0 \\ 0 \ else \end{cases}$$

and (6)

$$\xi_i^{\varepsilon,+}(p) = \begin{cases} 1 \ if \ g_{i,\varepsilon}^{\varepsilon} \geq 0 \\ 0 \ else \end{cases}$$

Then, the set $\Phi_{\varepsilon,q}^{\varepsilon,+}$ contains all the values p ∈ P such that at least q of the funtions $g_{i,\varepsilon}^{\varepsilon}$ (p) a smaller than zero while that $\Phi_{\varepsilon,q}^{\varepsilon,-}$ contains all the values p ∈ P such that at least q of the funtions $g_{i,\varepsilon}^{\varepsilon}$ (p) a larger than zero .

1.2 Set inversion

An interval, denoted by [x], is a bounded and connected set of $\mathbb{R}$ which is defined by:

$$[x]=(\underline{x}, \overline{x})= \{ x \in R \mid \underline{x} \leq x \leq \overline{x} \} \quad (7)$$

The real numbers $\underline{x}$ and $\overline{x}$ are the lower and upper bounds of [x], respectively all intervals within $\mathbb{R}$ are denoted by $\mathbb{IR}$, basic mathematical operations are extended to intervals.

Let [x] ∈ $\mathbb{IR}$, then, we define.

Its lower bound: inf ([x]) = $\underline{x}$

Its upper bound: sup ([x]) = $\overline{x}$

Its width: w ([x]) = $\overline{x} - \underline{x} \geq 0$ (8)

Its Middle: mid ([x]) = $\frac{\overline{x}+\underline{x}}{2}$

Its radius**:** rad ([x]= $\frac{\bar{x}-\underline{x}}{2} \geq 0$

A box (or interval vector) [**x**] is a compact of $\mathbb{R}$, defined by the cartesian product of n intervals.Therefore:

$$[\mathbf{x}] = [\underline{x}_1,\bar{x}_1] \times [\underline{x}_2,\bar{x}_2]\times,\ldots, [\underline{x}_n,\bar{x}_n]$$
$$= [x_1]\times [x_2]\times,\ldots,[x_n] \quad (9)$$

Let f be a funct ion of $\mathbb{R}^n \longrightarrow \mathbb{R}^m$,The interval function [f] of $\mathbb{IR}^n \longrightarrow \mathbb{IR}^m$ is an inclusion function for f if:

$$\forall [x] \in ,f[x] \subseteq [f][x]$$
$$\text{Or } [f]([x]) \supset \{ f(x) \mid x \in [x]\} \quad (10)$$

Consider a set $\mathbb{X}$ in $\mathbb{R}^n$ and a function f : f: $\mathbb{R}^n \longrightarrow \mathbb{R}^m$

let $\mathbb{Y}$ a subset of $\mathbb{R}^m$ defined as follows:

$$\mathbb{Y} = f(\mathbb{X}) \quad (11)$$

The set inversion is the characterization of a set $\mathbb{S}$, as the inverse image of set the by the function f:

$$\mathbb{S} = \{x\in \mathbb{X} \mid f(x) \in \mathbb{Y} \} = f^{-1}(\mathbb{Y}) \quad (12)$$

1.3 Algorithm SIVIA

The algorithm SIVIA (Set Inversion Via Interval Analysis) [19] can be used to solve any problem of set inversion. SIVIA is a recursive algorithm which enables to , from a sufficiently wide initial box, two subsets framing the solution set $\mathbb{S}$, such as:

$$\underline{\mathbb{S}} \subseteq \mathbb{S} \subseteq \bar{\mathbb{S}} \quad (13)$$

The inner approximation (or framing) $\underline{\mathbb{S}}$ represents all paved called acceptable or feasible boxes. This set contains all the solutions to be sought. However, there may be acceptable solutions that are not within $\bar{\mathbb{S}}$ If the expression $[x]\cap \bar{\mathbb{S}} = \emptyset$ can be demonstrated, then the box [x] is unacceptable and will be deleted. If the box is neither acceptable nor unacceptable, then [x] is said to be undetermined. The algorithm will then cut the box along the longest side

into two sub-boxes which will be tested in turn, in order to decide whether they will be retained or discarded. The process is reiterated until a box with a width reaching a certain thres hold value ε is obtained ($\varepsilon < 0$); this value is set by the experimenter. In all other cases, the box will be said to be indeterminate.

The Algorithm

SIVIA (Input: [*t*], [**x**], η, Output: $\underline{\mathbb{X}}$, $\overline{\mathbb{X}}$)

1. If [*t*] ([**x**]) = [0], rejected [**x**]

2. If [*t*] ([**x**]) = [1], $\underline{\mathbb{X}}$: = $\underline{\mathbb{X}}$ ∪ [**x**] , $\overline{\mathbb{X}}$:= $\overline{\mathbb{X}}$ ∪[**x**]

3. If *w* ([**x**]) ≤η, $\overline{\mathbb{X}} := \overline{\mathbb{X}} \cup [\mathbf{x}]$

4. Bisected [**x**] en ([x_1] [x_2])

SIVIA (I:[t] , x_1 ,η; O : $\underline{\mathbb{X}}$, $\overline{\mathbb{X}}$)

SIVIA (I : [t] , x_2 ,η; O : $\underline{\mathbb{X}}$, $\overline{\mathbb{X}}$)

1.4 Guaranteed characterization

The disadvantage of the LSCR approach is the difficulty to characterize numerically these confidence regions. M.Kieffer [18] brought an improvement to this approach by combining with them set-methods, especially, the set inversion, which permits to guarantee the results. The addition of a contractor will allow for implementation for high dimensions. In LSCR, one characterize a set:

$$\Phi_q = \{\, p \in P \text{ such as } \sum_{i=1}^{m} \xi_i(p) \geq q \,\} \qquad (14)$$

where: $\xi_i(p) = \begin{cases} 1 \; if \; g_{i,e}^{\varepsilon} \geq 0 \\ 0 \; else \end{cases}$

This set can be reformulated as a problem of set-inversion:

$$\Phi_q = \mathbb{P} \cap \xi^{-1} \; ([q,m]) \qquad (15)$$

With: $\xi_p = \sum_{i=1}^{m} \xi_i(p)$

Set theory owns two weak points: the first is the exponential increase of the simulation time with the number of parameters to estimate. The second is the pessimism, having two origins:

the dependency phenomenon where a variable appears more than once in an expression and the wrapping effect, when one characterizes a set by a box, which is not always minimal.To remedy this problem,We introduce the centred inclusion function wich is performed as follow.

Let f be a differentiable function of $D \subset \mathbb{R}^n \longrightarrow \mathbb{R}$

For some m ∈ ([p])

$$[f_{i,c}\ ]([p]) = f_i(m) + ([p] - m)^T [J_i\ ])([p]) \qquad (16)$$

$$= f_i(m) + \sum_{j=1}^{n_p} ([p_j] - m_j)[\ J_{i,j}](p])$$

$[\ J_{i,j}\ ]$ represent the natural inclusion function for the Jacobien of f To solve the identification problem using the set inversion, it consists of replacing the test for inclusion on the pavement [p] by a contracting phase to eliminate inconsistent values of [p].

1.5 The algebraic method

The study of observability and identifiability problems using differential algebraic methods dates back to the early 1990s [20] [21] [22]. The principle of the method used in this article [23] consists in verifying the observability of a latent variable x compared, for example, to two variables v and w, if each component of x is solution of an algebraic equation not differential with coefficients dependent on v and w and a finite number of their time derivatives. In fact, to verify the observability of a variable x with respect to, v and w of a system:

$$P_i\left(v, \frac{\partial v}{\partial t}, \frac{\partial^2 v}{\partial t^2}, \ldots, w, \frac{\partial w}{\partial t}, \frac{\partial^2 w}{\partial t^2}, \ldots, x, \frac{\partial x}{\partial t}, \frac{\partial^2 x}{\partial t^2}, \ldots, \xi, \frac{\partial \xi}{\partial t}, \frac{\partial^2 \xi}{\partial t^2}\right) = 0 \qquad (17)$$

Then, for i = 1, 2,…, we compute a characteristic set of all differential polynomials with respect to a classification whose order {{v, w}, {x}, {ξ}} must be respected. This classification means that all the derivatives of v and w are less than x and all the derivatives of x are less than ξ. This characteristic set will be represented by a set E of differential polynomials, each directed by one and only one of the variables. We conclude that x is observable with respect to v and w if and only if, each component of it leads to a differential polynomial in E. To do this, a REDUCE package called astb [23] is used.

2. APPLICATION TO THE BIOREACTOR

In practice, the modeling of this kind of process is difficult due to the living character of bacteria which are represented by complex functions involving poorly known parameters. In order to represent the uncertainties that affect these parameters, we focus on the interval approach. For this application, a mathematical model is used to describe a biological wastewater treatment with activated-sludge process. Ammonia nitrogen is treated by nitrification-denitrification reaction, involving two populations of autotrophic bacteria. Nitrification is the biological oxidation of ammoniacal nitrogen; it occurs through two steps: first, nitratation by ammonium-oxidizing bacteria (AOB) and second, nitritation by nitride-oxidizing bacteria (NOB).

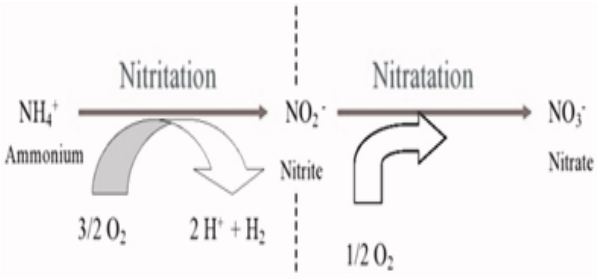


Fig.1. Nitrification Reaction

Thus, to represent the state of this bioreactor, six variables are required:the bacterial concentrations, called biomasses and denoted by X_1 and X_2,as well as the substrate concentrations S_1, S_2 and S_3 ,S_{in} is the concentration of the incoming substrate. The above model represents the dynamic evolution of these state variables.

$$\dot{S}_1 = D\,(S_{in} - S_1) - k_1\,\mu_1(s_1)\,X_1$$

$$\dot{X}_1 = (\mu_1\,(s_1) - D)\,X_1$$

$$\dot{S}_2 = k_1\,\mu_1\,(s_1)\,X_1 - k_2\,\mu_2\,(s_2)\,X_2 - S_2\,D$$

$$\dot{X}_2 = (\mu_2\,(s_2) - D)\,X_2 \qquad (18)$$

$$\dot{S}_3 = k_2\,\mu_2\,(s_2)\,X_2 - S_3\,D$$

with $\mu_1\,(s_1) = \mu_{max1}\,\frac{S_1}{S_1 + ks_1}$ and, $\mu_2\,(s_2) = \mu_{max2}\,\frac{S_2}{S_2 + ks_2}$

$\mu_1(s_1)$ and $\mu_2(s_2)$ are the biomass growth rates. They are modeled by Monod kinetics [26]. μ_{max1} and μ_{max2} are the maximum specific growth rates, k_1 and k_2 are the stoichiometric coefficients which represent the respective yields of biomasses X_1 and X_2 ks_1 and ks_2 are the half-saturation constants for the growth corresponding to the cell affinity for the substrate of each bacterial population. D is the dilution rate, such that, $D=\frac{Q_{in}}{V}$ where Q_{in} is the input flow of the bioreactor and V its volume . The observability of the yields k_1 and k_2 of the system described by equations **(18)** is tested by calculating the characteristic set of the following set of differential polynomials.

$$\begin{cases} \dot{S}_1 = D\,(Sin - S1) - k1\,\mu1(s1)\,X1 \\ \dot{X}_1 = (\mu1\,(s1) - D)\,X1 \\ S_2 = k1\,\mu1(s1)\,X1 - k2\,\mu2(s2)\,X2 - S2\,D \\ \dot{X}_2 = (\mu2(s2) - D)\,X2 \\ \dot{S}_3 = k2\,\mu2\,(s2)\,X2 - S3\,D \\ \mu_1(S_1 + k_{s1}) = \mu_{1max} S_1 \\ \mu_2(S_1 + k_{s2}) = \mu_{2max} S_2 \\ y_1 = X_1 \\ y_2 = X_2 \\ y_3 = S_1 \\ y_4 = S_2 \\ y_5 = S_3 \end{cases} \quad (19)$$

with respect to the ranking :

$$\{\{y_1, y_2, y_3, y_4, y_5, D, Sin\},\{k_1,k_2\},\{X_1, X_2, S_1, S_2, S_3,\mu_1,\mu_2\}\} \quad (20)$$

Lemme

The yields k1 and k_2 are observable with respect to y_1, y_2, y_3, y_4, y_5, D, S_{in} since the differential polynomial which introduces k_1 and k_2 (lines 24 and 25 in the appendix are of order 0 in k_1 and k_2). In addition, k_1 and k_2 are identifiable with respect to y_1, y_2, y_3, y_4, y_5, D, S_{in}.

3. RESULTS AND DISCUSSION

First, we simulated the model with parameters and measurements taken from the literature [27] over a period of 220 days.

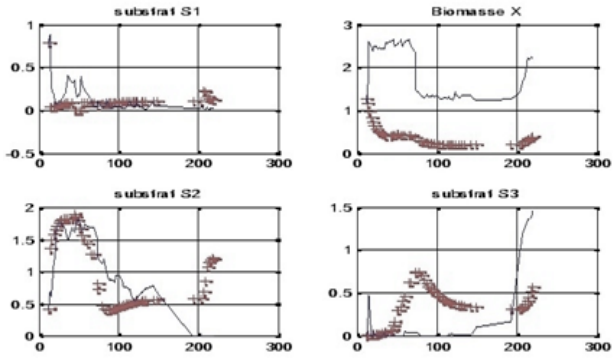


Fig.2. Simulations of recorded measurements (+), Nitrification model grey

Subsequently, the identification of model parameters was conducted through the least squares criterion, using the lsqnonlin Matlab function. The selected parameters to identify are the maximal growth rates μ_{max1} and μ_{max2} for the two bacterial populations X_1 and X_2, respectively, as well as their efficiencies ks_1 and ks_2. The yields k_1 and k_2 are obtained by the algebraic method (equation 24 and 25).

k_1=0.7390, k_2= 1.1940

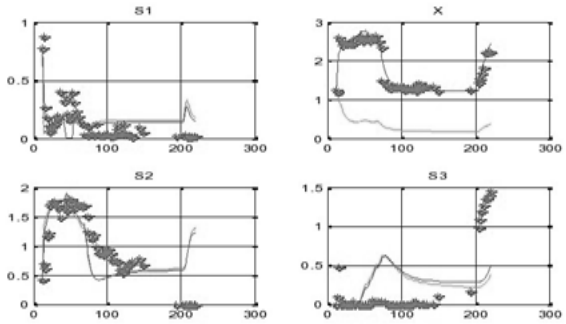
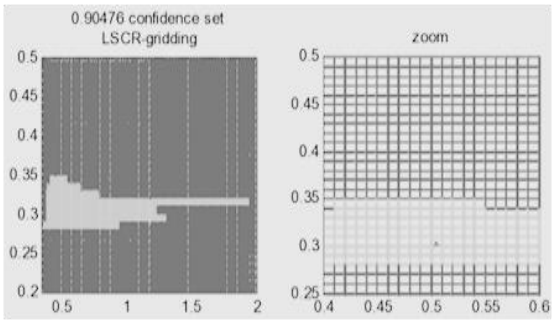
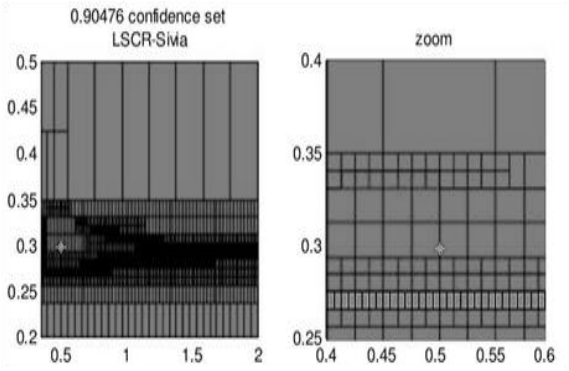


Fig.3. Least squares parameter identification, Recorded measurements: asterisked curve Simulated model: grey curve, Model by the least squares method: black curve

To test the LSCR method, we start by determining a confidence area corresponding to the maximum growth rate,μ_{max1} and μ_{max2}, other parameters are kept constant.The initial research set in parameter space is P=[0.35,1.5]×[0.2,1]. For measures, n = 48 and parameter r =1, q = 3 corresponds to a 90,47% confidence area. All these simulations were made with a precision ε=0.01 on core I3. The Figure (4-a), represents the confidence region $\Phi^{\varepsilon}_{\varepsilon,q}$ obtained with a grid step-size ε =0.01, in T=8s.



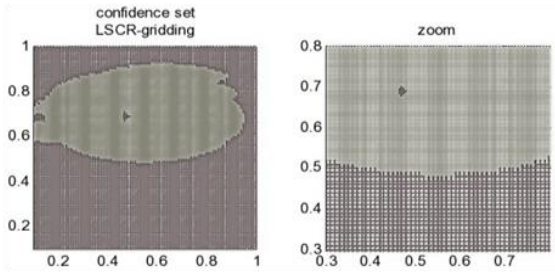
(a) [Griding-LSCR]



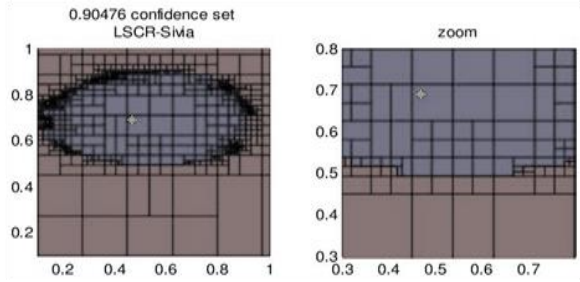
(b) [Sivia :Natural inclusion function]

Fig.4. (a) Gridding of seach space obtened by LSCR ,(b) Paving of domain with Sivia and their zooming around the apriori parameter(*) concerning the maximum growth rate, μ_{max1} and μ_{max2}

On the Figure (4-b) are represented, the solutions pavers obtained by the Sivia algorithm, using the natural inclusion function, they are obtained in t=67,18s. On Figure (5), are represented, solutions pavers corresponding to half saturation constant Ks1 and Ks2, obtained by Sivia, and improved by using the centered form of the inclusion function, simulation time has been reduced to t=49,93s.The centered form avoids an overestimation of the sought domain, and introducing a contractor reduces the computational complexity due to the number of bisections used by Sivia.



(a)[Griding-LSCR]



(b)[Sivia : centered inclusion function]

Fig.5. (a) Gridding of seach space obtened by LSCR ,(b) Paving of domain with Sivia and their zooming around the apriori parameter (*) concerning half saturation constant Ks1 and Ks2

Table 1. recapitulatif results

Parameter	A priori parameter	Estimate Parameter (Least Square)	LSCR + Sivia
μ_{max1}	[0.45 ,0.5]	0.5049	[0.3951,1 .0655]
μ_{max2}	0 ,27	0.2994	[0.2749, 0.3032]
Ks1	[0.3, 0.48]	0.43	[0.2828, 0.8946]
Ks2	[0.65, 0.7]	0.67	[0.5359, 0.7891]

4. CONCLUSION

One of the great difficulties in microbial ecology is to study the ecological function of the dominant microbial populations in their environment. The measures identified are associated with relatively large uncertainties. The ensemblist methods may be interesting to use. The strong points of the LSCR method are the minimum assumptions about the additive noise and obtaining a result with a guaranteed probability. This improved method developed by M.Kieffer provides guaranteed results. Indeed, sivia algorithm associated with a contractor evaluates the interior and exterior approximations of non asymptotic confidence regions determined by LSCR. Note also that the use of centered form of the inclusion function, contributes to a reduction of simulation time as well as to the reduction of confidence Region.

5. ACKNOWLEDGEMENTS

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8. Appendix

$$- S_{in} D+Dy_5 + Dy_4 + Dy_3+ \quad 5+ \ {}_4+ \ 3 \qquad \textbf{(21)}$$

$$- \dot{S}_{in}D^2y_1 - \dot{S}_{in}D\dot{y}_1 - S_{in}\dot{D}y_1 +S_{in}D^2\dot{y}_1+ S_{in}D\ddot{y}_1 - \dot{D}\dot{y}_3y_1 + \dot{D}y_3\dot{y}_1 + D^2y_3\dot{y}_1-D^2y_3\dot{y}_1 + D\ddot{y}_3y_1 - Dy_3\ddot{y}_1 + \ddot{y}_3\ddot{y}_1 - \dot{y}_3 \ddot{y}_1 \qquad \textbf{(22)}$$

$$S_{in}\dot{D}D\dot{y}_2y_1 + S_{in}\dot{D}Dy_2\dot{y}_1+S_{in}D^3\dot{y}_2y_1 - S_{in}D^3y_2\dot{y}_1+S_{in}D^2\ddot{y}_2y_1 - S_{in} D^2y_2\ddot{y}_1+S_{in} D\ddot{y}_2\dot{y}_1 - S_{in} D\dot{y}_2\ddot{y}_1 +\dot{D}D\dot{y}_4y_2y_1+\dot{D}Dy_4\dot{y}_2y_1.+ \dot{D}Dy_3\dot{y}_2y_1-\dot{D}Dy_3\dot{y}_1y_2- \dot{D}\dot{y}_4y_2\dot{y}_1+ \dot{D}\dot{y}_2y_4\dot{y}_1 + \dot{D}\dot{y}_2y_1\dot{y}_3 - \dot{D}\dot{y}_3y_2\dot{y}_1+ D^3\dot{y}_4y_2y_1 - D^3y_4\dot{y}_2y_1-D^3y_3\dot{y}_2y_1 + y_3y_2\dot{y}_1+D^2\ddot{y}_4y_2y_1+ D^2\dot{y}_4y_2\dot{y}_1 - D^2\ddot{y}_2+y_4y_1 - D^2\dot{y}_2y_4\dot{y}_1- D^2\dot{y}_3y_1\dot{y}_2 ...+D^2\dot{y}_3y_2\dot{y}_1 -D^2y_3\ddot{y}_2y_1+D^2y_3y_2\ddot{y}_1+ D\ddot{y}_4\dot{y}_2y_1 +D\ddot{y}_4y_2\dot{y}_1 - D\dot{y}_4\ddot{y}_2y_1 – Dy_4\ddot{y}_2\dot{y}_1 -\dot{y}_3\ddot{y}_2y_1 +D\dot{y}_3y_2\ddot{y}_1 - Dy_3\ddot{y}_2\dot{y}_1+ Dy_3\dot{y}_2\ddot{y}_1+ \ddot{y}_4\dot{y}_2\dot{y}_1 - \dot{y}_4\dot{y}_1-\ddot{y}_2\dot{y}_3\dot{y}_1+\ddot{y}_1\dot{y}_3\dot{y}_2 \qquad \textbf{(23)}$$

$$-S_{in} D+Dy_3+Dy_1k_1+\dot{y}_3+\dot{y}_1k_1 \qquad \textbf{(24)}$$

$$-S_{in} D+k_2 Dy_2+k_2 \dot{y}_2+Dy_4+Dy_3+\dot{y}_4+\dot{y}_3 \qquad \textbf{(25)}$$

$-X_1+y_1$ **(26)**

$-X_2+y_2$ **(27)**

$-S_1+y_3$ **(28)**

$y_4 - S_2$ **(29)**

y_5-S_3 **(30)**

$-Dy_1-\dot{y}_1+y_1\mu_1$ **(31)**

$-Dy_2-\dot{y}_2+y_2\mu_2$ **(32)**

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