

# Enlarging the Domain of Attraction in Nonlinear Polynomial Systems

F. Hamidi, H. Jerbi, W. Aggoune, M. Djemaï, M.N. Abdelkrim

## Façal Hamidi, Mohamed Naceur Abdelkrim

Unité de Recherche Modélisation,  
Analyse et Commande des Systèmes, ENIG, 6029 Gabes, Tunisie.  
Email: faicalhamidi@yahoo.fr, Naceur.Abelkrim@enig.rnu.tn

## Houcem Jerbi

University of Hail, College of Engineering  
P.O.Box 2440, Hail, Kingdom of Saudi Arabia.  
Email: h.jerbi@uoh.edu.sa

## Wahiba Aggoune

ECS-Lab, Equipe Commande des Systèmes,  
ENSEA, 6 avenue du Ponceau, 95014 Cergy, France.  
Email: aggoune@ensea.fr

## Mohamed Djemaï

Univ. Lille Nord de France, F-59000 Lille,  
France. UVHC, LAMIH, CNRS, UMR 8201,  
Campus du Mont Houy F-59313, Valenciennes, France.  
Email: mohamed.djemaï@univ-valenciennes.fr

**Abstract:** This paper addresses the problem of enlarging the Domain of Attraction (**DA**) based on a Generalized Eigenvalue Problem (**GEVP**) approach. The main contribution is the maximization of the (**DA**) while characterizing the asymptotic stability region by a Lyapunov Function. Such result is obtained using a Genetic Algorithm (**GA**). A theoretical proof of the validity of the obtained domain is developed. An illustrative example ends the paper.

**Keywords:** Nonlinear Polynomial Systems, LMI, Genetic Algorithm, Stability.

## 1 Introduction

The problem of enlarging the Domain of Attractions (**DA**) has been the topic of an important number of research works (see for example [2] [4], [5], [6] [11], [13] and the references cited therein). The **DA** is defined as the set of initial conditions from which the states converge to the asymptotically stable equilibrium point [7]. As a result, it is essential to identify the shape of this region whenever one has to study the stability of a system. For this purpose, we exploit the fundamental theory of Lyapunov stability (see [3], [12]). Indeed, for a particular Lyapunov function, the largest estimated region of asymptotic stability can be defined as the largest level set of the Lyapunov function included in the region where its derivative is negative. In a recent work [3], the author proposes a static nonlinear feedback input, which allows enlarging the **DA**. The proposed controller is polynomial in the measurable output; it exploits relaxations based on the sum of squares of polynomials in order to prove that the lower bound of the maximum achievable largest estimated domain of attraction and a corresponding controller can be computed via a generalized eigenvalue problem. The main advantage of the methodology is that the problem is formulated as a quasi-convex Linear Matrix Inequalities (**LMI**) ([1], [3], [10]).

The main purpose of this work is to develop an exact method allowing the maximization of the **DA**. The objective of this work is to improve the approach adopted in [3] by combining the

Genetic Algorithm (**GA**) as an advanced optimization strategy to the LMI technique in order to maximize the **DA**. The parameter optimizing approach will simultaneously deal with the Lyapunov Function and the control input parameters. Based on the Reverse Trajectory Method (**RTM**) one can accurately determine a preliminary maximal region of asymptotic stability and thereafter define the parameter of the maximal Lyapunov Function ([8], [9], [12]). This allows to define precisely the initial values and the constraints related to the required parameters of the investigated Lyapunov function.

## 2 Problem Statement and Notations

Consider the continuous-time polynomial system

$$\dot{x} = f(x) + g(x)u; \quad y = h(\tilde{x}) \tag{1}$$

where  $f(\cdot), g(\cdot)$  and  $h(\cdot)$  are polynomial functions such that  $f(0) = 0, g(0) = 0$  and  $h(0) = 0$ . (The equilibrium point is the origin). In what follows, we assume that  $x \in R^n$  is the state vector,  $u \in R^p$  is the input vector and  $y \in R^q$  is the measurable output. The control input is supposed to be a polynomial function of the form

$$u = U\phi(h(\tilde{x})) \tag{2}$$

where  $\phi(\cdot)$  is a given polynomial function of the output and  $h(\tilde{x})$  and  $u$  are defined by :

$$h(\tilde{x}) = [\tilde{x}^{[1]}, \tilde{x}^{[2]}, \dots, \tilde{x}^{[q]}]; \quad u = \sum_{i=1}^q u_i \tilde{x}^{[i]} \tag{3}$$

with  $\tilde{x}^{[i]}$  is the non-redundant Kronecker power of the state vector  $x$  to the  $i^{th}$  order,  $q$  is a truncation order and  $U \in R^{p \times r}$  is a matrix belonging to the interval matrix:

$$U = \{ U = [U_1, \dots, U_q] : U_i \in (U_i^-, U_i^+), i = 1, \dots, q \}$$

For the seek of simplicity and for explaining our approach, we consider the case of  $q = 2$ . We obtain  $U_1 = [u_1, u_2], U_2 = [u_3, u_4, u_5]$  and consequently

$$u = u_1x_1 + u_2x_2 + u_3x_1^2 + u_4x_1x_2 + u_5x_2^2$$

The domain of attraction of the controller is the set of states which can be steered towards the terminal region. This paper is devoted to enlarge this domain. The size of the **DA** depends on the control parameters, and the chosen Lyapunov function. A wise and optimal choice of both of these may yield a bigger domain of attraction. The size of the region depends on the computed controller, the constraints on the system and the procedure used to compute it. Thus, the most used procedure to enlarge the domain of attraction are based on a polynomial control. This leads to a greater number of parameters and therefore, to a greater computational effort. In this paper, a formulation of the problem, focused on enlarging the domain of attraction without increasing the computational effort is presented. The optimization problem formulation, and hence the computational effort is similar to the original one but with a larger domain by using the Genetic Algorithm approach.

For this purpose, we proceed in three steps :  
 -First, we exploit the method described in [3] to derive an initial **DA**.

-Second, we implement a **GA** combined with a Linear Matrix Inequalities **LMI** approach to determine explicitly a maximal parameterized Lyapunov Function.

-Third, the implementation of the **RTM** leads to a maximized asymptotic stability region, while giving an accurate idea on numerical values of the Lyapunov function parameters. The second step is finally reapplied in order to define the maximal Lyapunov function and its corresponding **DA**. A parameter optimization will cover in this step both the Lyapunov function parameters and those of the polynomial control input.

### 3 Preliminaries results

Before proceeding further, we will give some preliminary results.

Let  $V(x) \in R$  be a positive definite, radially unbounded and continuously differentiable function. The bounded set

$$\Omega(c) = \{x \in R^n / V(x) \leq c\} \quad (4)$$

is an estimate of the region of attraction if  $\Omega \subset \mathcal{D}$  where  $\mathcal{D} = \{x \in R^n / \dot{V}(x, U) < 0\} \cup \{0\}$ . The time derivative of  $V(x, U)$  along trajectory of system (1) is given by

$$\begin{aligned} \dot{V}(x, U) &= \frac{\partial V(x)}{\partial x} f(x) + \frac{\partial V(x)}{\partial x} g(x) U \phi(h(\tilde{x})) \\ &= L_f V(x) + L_g V(x) U \phi(h(\tilde{x})) \end{aligned} \quad (5)$$

where  $L_f V(x)$  (resp.  $L_g V(x)$ ) is the Lie derivative of  $V(x)$  along the polynomial function vector  $f(x)$  (resp.  $g(x)$ ). In what follows, we shall denote  $L_g V(x) U \phi(h(\tilde{x}))$  by  $L_{(g,U)} V(x)$  for simplicity; i.e.  $L_{(g,U)} V(x) = L_g V(x) U \phi(h(\tilde{x}))$ .

The largest estimate of the **DA** is given by  $\Omega(c^*(U))$  where :

$$c^*(U) = \inf_{x \in R^n} V(x) \quad \text{such as} \quad \dot{V}(x, U) = 0 \quad \text{for each matrix} \quad U \in \mathcal{U}. \quad (6)$$

The optimal value of  $c^*(U)$  is obtained by

$$c^* = \sup_{U \in \mathcal{U}} c^*(U). \quad (7)$$

In [3], it has been proven that for any given  $c \in R$ ,  $c \leq c^*$  if there exists  $U \in \mathcal{U}$  and  $s(x)$  a positive definite polynomial such that

$$\dot{V}(x, U) + (c - V(x)) s(x) < 0 \quad (8)$$

then the polynomial degrees of  $V(x)$  and  $\dot{V}(x, U)$  are  $2\delta_V$  and  $\delta_L$  respectively. If we choose  $s(x)$  degree to be  $2\delta_s$  such that

$$\delta_s \geq \frac{\delta_L}{2} - \delta_V \quad (9)$$

it follows that the degree of the polynomial

$$t(x, U, c, s(x)) = \dot{V}(x, U) + (c - V(x)) s(x) \quad (10)$$

is equal to  $2\delta_m$  where  $\delta_m = \delta_V + \delta_s$ .

An approach based on both Square Matricial Representation (**SMR**) and Complete Square Matrix Representation (**CSMR**) of polynomials is used in order to determine an appropriate

optimization problem [3]. The CSMR provides all the possible representations of a polynomial in terms of a quadratic form.

The CSMR matrix of  $t(x, U, c, s(x))$  is given by

$$T(\alpha, U, c, S) = D_f(\alpha) + D_g(U) + cW_1(S) - W_2(S) \tag{11}$$

where  $D_f(\alpha)$  is the CSMR of  $L_f V(x)$ ,  $\alpha \in R^{\tau(n, \delta_m)}$ ,  $D_g(U)$  is the SMR of  $L_{(g,U)} V(x)$ ,  $W_1(S)$  and  $W_2(S)$  are the SMR of  $s(x)$  and  $V(x)s(x)$ .

The condition (8) with (11) implies that if

$$\hat{c}^* = \sup_{U \in \mathcal{U}, \alpha, S > 0} c \text{ such that } T(\alpha, U, c, S) < 0; \quad \text{then} \quad \hat{c}^* \leq c^* \tag{12}$$

*Theorem 1.* ([3]) *The lower bound  $\hat{c}^*$  is given by*

$$\hat{c}^* = \frac{-\lambda^*(U)}{1 + \mu\lambda^*(U)} \tag{13}$$

where  $\lambda^*(U)$  is the solution of the following GEVP

$$\lambda^*(U) = \inf_{U \in \mathcal{U}, \alpha, S > 0, \lambda} \lambda \tag{14}$$

such that  $\begin{cases} 1 + \mu\lambda > 0; & U \in \mathcal{U}; & S > 0 \\ \lambda W(S) > D_f(\alpha) + D_g(U) - W_2(S) \end{cases}$

with  $\mu$  being any positive scalar and

$$W(S) = K^T \left( \begin{pmatrix} 1 & 0 \\ 0 & \mu V \end{pmatrix} \otimes S \right) K. \tag{15}$$

The symbol  $\otimes$  is the Kronecker's product and the matrix  $K$  satisfies

$$\begin{pmatrix} 1 \\ x^{\{\delta_v\}} \end{pmatrix} \otimes x^{\{\delta_s\}} = K x^{\{\delta_m\}} \tag{16}$$

where  $x^{\{\delta_m\}} \in R^{\varsigma(n, \delta_m)}$ ,  $\alpha \in R^{\tau(n, \delta_m)}$ ,  $x^{\{\delta_v\}} \in R^{\varsigma(n, \delta_v)}$ ,  $x^{\{\delta_s\}} \in R^{\varsigma(n, \delta_s)}$ ,  $K \in R^{\varsigma(n, \delta_s)(\varsigma(n, \delta_v)+1) \times \varsigma(n, \delta_m)}$  and the quantities  $\varsigma(n, \delta_m)$  and  $\tau(n, \delta_m)$  are given by

$$\begin{aligned} \varsigma(n, \delta_m) &= \frac{(n + \delta_m)!}{n! \delta_m!} - 1 \\ \tau(n, \delta_m) &= \frac{1}{2} \varsigma(n, \delta_m) (\varsigma(n, \delta_m) + 1) - \varsigma(n, 2\delta_m) + n. \end{aligned}$$

### 4 Main Results

In this section, we present the main results of the paper. For this, we go back to the **RTM** introduced in [12], for estimating the Region of Asymptotic Stability (RAS) through reversing the system trajectory flow. Our main aim is to enlarge the RAS resulting from the method described in [3]. The idea consists in determining the maximal RAS of the system obtained via the implementation of the **RTM**. This allows determining an analytical expression of the maximal **DA** included in the RAS. Such a result is not given by the **RTM**, which finally gives an interesting graphical representation of the RAS. We want to compute an analytical expression of

the RAS in terms of a Lyapunov function. We consider, for this purpose, a quadratic Lyapunov function of the form:

$$V(x) = x^T P x, \quad \text{where } P = P^T > 0 \quad (17)$$

For the sake of simplicity, we assume that  $P \in R^2$ , with  $P = \begin{bmatrix} p_1 & p_2 \\ p_2 & p_3 \end{bmatrix}$ , so that :

$V(x) = p_1 x_1^2 + 2p_2 x_1 x_2 + p_3 x_2^2$ . The results are generalizable for matrices of larger sizes.

By using such a Lyapunov function we can express the RAS in terms of an ellipsoid in  $(x_1, x_2)$  plane which will be contained in the RAS obtained by the trajectory reversing method. The idea consists in estimating the parameters  $p_i, (i = 1, 2, 3)$  and  $u_i, (i = 1, 2, 3, 4, 5)$  via a genetic algorithm. By combining this algorithm with an LMI optimization we can obtain the largest ellipsoid contained in the RAS. The candidate solutions  $p_i, (i = 1, 2, 3)$  and  $u_i, (i = 1, 2, 3, 4, 5)$  are chosen arbitrarily and can be regarded as individuals. Each variable can be considered as a gene and the different steps of the Genetic Algorithm can be expressed as follows :

1. *Initial population* : Each individual in the population is represented by a chromosome that is coded in binary form.
2. *Selection* : In the selection process, strings must be of suitable fitness to be selected as a factual member in creating a new population.
3. *Replication* : In this process, the best strings which have a greater probability than others will be member of the next generation.
4. *Crossover* : Two random chromosomes are selected in recreation process. They will be exposed to the crossover rate and they will swap from the crossover points. The experienced boundary for crossover rate is from 0.6 to 0.9.
5. *Mutation* : We underline mutation relevance in just one way : for each bit we generate a random number and if it is less than the specified mutation probability, we flip the bit. If it is "one" we change it to "zero" and vice versa. The values, which are the boundaries for mutation rate, are between 0.1 and 0.3. In order to estimate, the parameter, by means of a genetic algorithm, we must encode the vector into binary code in order to let the parameters with genetic algorithm easier.

*Theorem 2.* In this work, a **GA** is used to estimate the parameters  $p_i, (i = 1, 2, 3)$  and  $u_i, (i = 1, \dots, 5)$  where the next constraint is satisfied by :

$$p_1 > 0, p_3 > 0 \quad \text{and} \quad p_1 \cdot p_3 > (p_2)^2. \quad (18)$$

*Theorem 3.* Each iteration of the **GA** optimization routine, results in new parameters values  $p_i, (i = 1, 2, 3)$ ,  $u_i, (i = 1, \dots, 5)$  and  $\hat{c}^*$  which is a solution of the LMI corresponding to this set of parameters. The genetic algorithm leads to the best set of parameters  $p_i, (i = 1, 2, 3)$  and  $u_i, (i = 1, \dots, 5)$  which are used in the computation of the best solution  $\hat{c}^*$  (defined by (13)) which is the solution of the LMI (14).

- The set of variables  $\{p_i, i = 1, 2, 3\}$  and  $\{u_i, i = 1, \dots, 5\}$  are encoded into the gene candidate.
- The fitness value is given by the maximum  $c^*$  for which there exists a feasible solution of the LMI optimization.

- The global optimization of the variables  $p_i, (i = 1, 2, 3)$  and  $u_i, (i = 1, \dots, 5)$  is performed by the genetic operators (selection, recombination and mutation).

The fitness function is evaluated in two steps as follows :

First Step	Second Step:
<i>Set <math>p_i, (i = 1, \dots, 3)</math> as gene candidates</i> <i>while</i> $p_1 > 0, p_3 > 0$ and $p_1.p_3 > (p_2)^2$ <i>Apply the LMI Optimization</i> <i>If <math>c_j &gt; c_i, j &gt; i; i, j = 1, \dots, N</math></i> <i>Write <math>p_{j1}, p_{j2}, p_{j3}</math></i> <i>end</i> <i>end</i> <i>return <math>\hat{c}^* = c_j</math> as fitness value.</i>	<i>Set <math>p_i, (i = 1, \dots, 3)</math> as gene candidates</i> <i>Set <math>u_i, (i = 1, \dots, 5)</math> as gene candidates</i> <i>while : <math>p_1 &gt; 0, p_3 &gt; 0</math> and <math>p_1.p_3 &gt; (p_2)^2</math></i> <i>Apply the LMI Optimization</i> <i>If <math>c_j &gt; c_i, j &gt; i; i, j = 1, \dots, N</math></i> <i>Write <math>p_{j1}, p_{j2}, p_{j3}, u_{j1}, u_{j2}, u_{j3}, u_{j4}, u_{j5}</math></i> <i>end</i> <i>end</i> <i>return <math>\hat{c}^* = c_j</math> as fitness value.</i>

The following flowchart, in figure 1, presents the main steps needed to implement the synthesized algorithm, according to which, we can maximize the region of asymptotic stability. The obtained solution is specified by the definition of a maximal quadratic Lyapunov function.

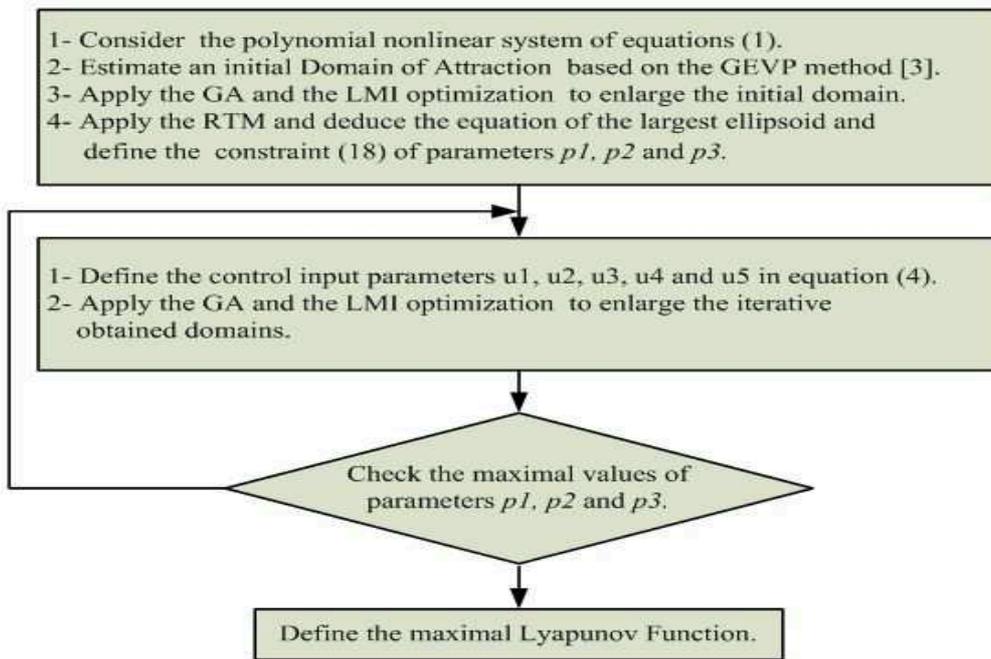


Figure 1: Flowchart of Advanced LMI Optimization Algorithm for Maximizing the DA

## 5 Illustrative Example

Consider the following polynomial nonlinear system [3]:

$$\begin{cases} \dot{x}_1 = x_2 \\ \dot{x}_2 = -x_1 - x_2 + x_2^2 + x_1^2 x_2 + u \end{cases} \quad (19)$$

Consider a controller that is linear in  $y_1 = x_1$ ; that is,  $u = u_1x_1$ , with :  $\mathcal{U} = \{U = u_1 : -2 \leq u_1 \leq 2\}$ . In order to find the shape of the **DA**, we employ a Lyapunov function of the form :

$$V(x) = p_1x_1^2 + 2p_2x_1x_2 + p_3x_2^2 \tag{20}$$

Since the degree  $\delta_L$  of  $\dot{V}(x, U)$  is 4, we can select  $\delta_s = 1$  which implies  $\delta_m = 2$ . Vectors  $x^{\{\delta_v\}}$ ,  $x^{\{\delta_s\}}$  and  $x^{\{\delta_m\}}$  are selected as:  $x^{\{\delta_v\}} = x^{\{\delta_s\}} = (x_1, x_2)^T$  and  $x^{\{\delta_m\}} = (x_1, x_2, x_1^2, x_1x_2, x_2^2)^T$  which implies that:

$$D_f(\alpha, p_{1,2,3}) = \begin{pmatrix} -2p_2 & (p_1 - p_2 - p_3) & 0 & \alpha_1 & \alpha_2 + p_2 \\ (p_1 - p_2 - p_3) & (2p_2 - 2p_3) & -\alpha_1 & -\alpha_2 & p_3 \\ 0 & -\alpha_1 & 0 & p_2 & \alpha_3 \\ \alpha_1 & -\alpha_2 & p_2 & -2(\alpha_3 - p_3) & 0 \\ \alpha_2 + p_2 & p_3 & \alpha_3 & 0 & 0 \end{pmatrix}$$

$$D_g(p_{1,2,3}) = \begin{pmatrix} 2p_2u_1 & p_3u_1 & 0 & 0 & 0 \\ p_3u_1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix}; S = \begin{pmatrix} s_1 & s_2 \\ s_2 & s_3 \end{pmatrix}$$

$$W(S, p_{1,2,3}) = \begin{pmatrix} s_1 & s_2 & 0 & 0 & 0 \\ s_2 & s_3 & 0 & 0 & 0 \\ 0 & 0 & \mu p_1 s_1 & \mu \alpha & 0 \\ 0 & 0 & \mu \alpha & \mu \alpha & \mu \gamma \\ 0 & 0 & 0 & \mu \gamma & \mu p_3 s_3 \end{pmatrix}; W_2(S, p_{1,2,3}) = \begin{pmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & p_1 s_1 & \alpha & 0 \\ 0 & 0 & \alpha & \beta & \gamma \\ 0 & 0 & 0 & \gamma & p_3 s_3 \end{pmatrix}$$

with  $\alpha = p_1s_2 + p_2s_1, \beta = p_1s_3 + 4p_2s_2 + p_3s_1$  and  $\gamma = p_2s_3 + p_3s_2$ .

We propose to encode the parameters  $p_i$  into 7 bits code :  $p_i = (p_{0i}, p_{1i}, p_{2i}, p_{3i}, p_{4i}, p_{5i}, p_{6i})$ , and put them into a chromosome as follows :

$$\begin{cases} Pop\_size = 50; & Crossover\_rate = 0.65; \\ Mutation = 0.1; & Max\_generations = 100. \end{cases} \tag{21}$$

Note that we consider the LMI representation as a fitness function for the genetic program. Then, we obtain:  $p_1 = 3.5; p_2 = 1.5; p_3 = 5.5$ .

This result justifies a domain of attraction that is larger than that obtained through the direct method [3]. The result of this study is shown in Fig. 2 where  $\mu = \frac{1}{100}$ . In this figure, solid line  $\dot{V}(x, U) = 0$ , and  $V(x) = 2.5244$  obtained by the GA method. Dashed line the  $\dot{V}(x, U) = 0$  and  $V(x) = 1.2324$  obtained by the method developed in [3].

When we apply the RTM described in ([12]), the result given in Fig. 3 represents the region of asymptotic stability of the system under consideration. Hence, the equation of the largest **DA** is given by

$$V(x) = 9x_1^2 + 4.4x_1x_2 + 15.5x_2^2 = 9.5.$$

When implementing our proposed method based on the LMI and the GA, we obtain the following result, with input  $u = 0.4864x_1$ :

$$V(x) = 9.5x_1^2 + 4x_1x_2 + 15.5x_2^2 = 8.5066$$

The result of this study is depicted in Fig. 4 which shows that the resulting domain of attraction is larger than the initial one given by [3]. In this figure, solid line indicates the  $\dot{V}(x, U) = 0$  and  $V(x) = 8.5066$  obtained via the proposed method with GA, the dashed line indicates the  $\dot{V}(x, U) = 0$  and  $V(x) = 1.2324$  result in [3].

Now, we investigate the maximization of the **DA** by estimating parameters  $p_1, p_2$  and  $p_3$  of the Lyapunov function and  $u_1, u_2, u_3, u_4$  and  $u_5$  of the control input. Consequently, we have

$$u = u_1x_1 + u_2x_2 + u_3x_1^2 + u_4x_1x_2 + u_5x_2^2 \tag{22}$$

with  $\mathcal{U} = \{U = [u_1, u_2, \dots, u_5] : -2 \leq u_i \leq 2, i = 1, \dots, 5\}$

We propose to encode the parameters  $p_i$  and  $u_i$  into 7 bits code

$$p_i = (p_{0i}, p_{1i}, p_{2i}, p_{3i}, p_{4i}, p_{5i}, p_{6i})$$

$$\text{and } u_i = (u_{0i}, u_{1i}, u_{2i}, u_{3i}, u_{4i}, u_{5i}, u_{6i})$$

and put them into a chromosome as described in equation (21). This implies that  $D_f(\alpha, p_{1,2,3}), S, W(S, p_{1,2,3})$  and  $W_2(S, p_{1,2,3})$  remains unchanged, while  $D_g(u_{1,2,3,4,5}, p_{1,2,3})$  is defined as :

$$D_g(u_{1,2,3,4,5}, p_{1,2,3}) = \begin{pmatrix} 2p_2u_1 & (p_3u_1 + p_2u_2) & p_2u_3 & (p_3u_3 + p_2u_4) & 0 \\ (p_3u_1 + p_2u_2) & 2p_3u_2 & 0 & (p_2u_5 + p_3u_4) & p_3u_5 \\ p_2u_3 & 0 & 0 & 0 & 0 \\ (p_3u_3 + p_2u_4) & (p_2u_5 + p_3u_4) & 0 & 0 & 0 \\ 0 & p_3u_5 & 0 & 0 & 0 \end{pmatrix}$$

The result of this study yields

$$V(x) = 9.5x_1^2 + 3.9x_1x_2 + 15.5x_2^2 = 38.6183$$

which means that the input is written as

$$u = 0.6348x_1 - 1.9996x_2 + 0.0006x_1^2 - 0.0015x_1x_2 - 1.0044x_2^2$$

In Figure 5, we represent the different **DA**(s) by continuous lines (which allow elliptic forms). The dash-dotted curves represent the constraints. Clearly, the largest (**DA**) is obtained when we optimize both parameters of the LF and those of the control input. In this figure, the DA (blue line) illustrates the results obtained through the optimization of parameters  $p_1, p_2, p_3, u_1, u_2, u_3, u_4$  and  $u_5$  by combining GA and LMI. DA with red line : obtained results while optimizing parameters  $p_1, p_2, p_3, u_1$  by combining the GA and LMI [2]. DA with the black line : obtained results by optimizing parameters  $p_1, p_2, p_3, u_1$ , with LMI [3]. This result demonstrates the consistency of the proposed method.

## 6 Conclusion

In this paper, the problem of enlarging the attraction domain for nonlinear controlled systems is investigated. We were particularly interested in the class of nonlinear polynomial systems which represents a large class of physical nonlinear dynamics that can be approximated by polynomials using Taylor series expansions. We rely on an optimization approach based on Linear Matrix Inequality (LMI) to compute an initial region of attraction. The main contribution consists in the determination of an explicit **DA** by using a parameterized Lyapunov function. The parameters of both the Lyapunov function and nonlinear control input are computed by combining the Genetic Algorithm and an LMI approach. The implementation of the reverse trajectory method leads to represent the largest elliptic shape of the RA. An illustrative example has demonstrated the efficiency of the established results.

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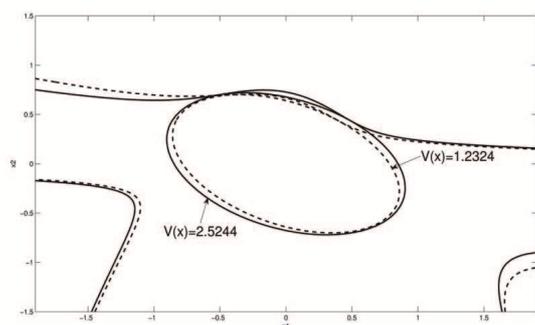


Figure 2:  $\dot{V}(x, U) = 0$ , and  $V(x)$ .

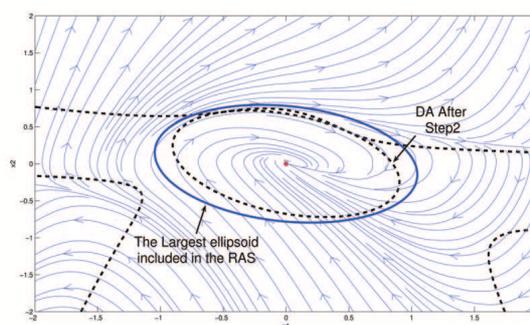


Figure 3: Largest Ellipsoid Included in RAS

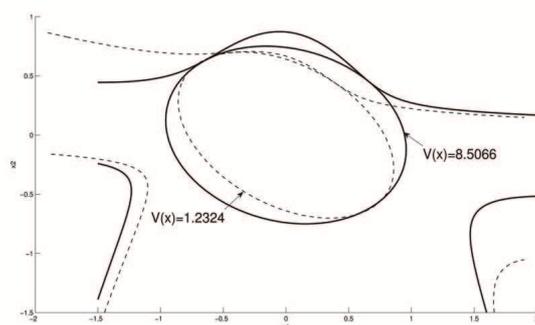


Figure 4:  $\dot{V}(x, U) = 0$  and  $V(x)$ .

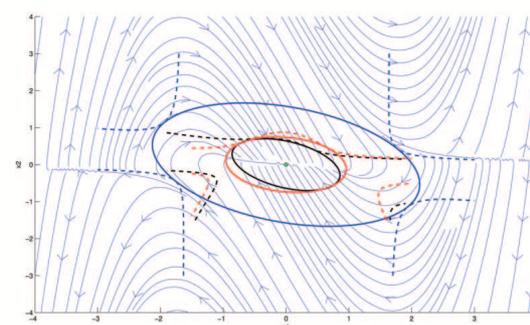


Figure 5: DA by combining GA and LMI.

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