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A Brief Tutorial on Quadratic Stability of Linear Parameter-Varying Model for Biomathematical Systems

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A Brief Tutorial on Quadratic Stability of Linear Parameter-Varying Model for Biomathematical Systems

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- Mathematical modeling of biological problems is a vast area of study in applied mathematics, which is useful for understanding the dynamic relationship between different types of populations or biological systems. For example, species interaction [1], delivery of drugs [2], infectious disease spread [3, 4], development and pattern formation in biological systems [5], genetics and molecular models [6, 7] are some of several other possibilities of investigation.
- Linear parameter-varying (LPV) systems are able to represent linear dynamics affected by time-varying parameters, time-varying systems constructed by means of identification techniques, or even to approximate nonlinear systems by a set of local linear models.



- We want to use the LPV system theory to analyze the local stability of a well-known compartimental model: the SIRS.
- Also, the tutorial presented in this paper is particularly interested in explaining in details how to use the MATLAB^(R) software with the aid of parsers ROLMIP [8], YALMIP [9], and the semidefinite programming solver SeDuMi [10].
- Our main motivation in this study-tutorial resides in the particular nonlinear structure of some biomathematical systems. In many cases they are given in terms of polynomials that can be conveniently explored in an LPV modeling.



- The proposed investigation provides a theoretical stability certificate based on the Lyapnunov stability theory [11] for LPV systems and also allows a deep understanding of the dynamic behavior of linearized models of nonlinear systems.
- The LPV model favors future research in the design context (synthesis of filters or controllers for biological systems), working as a prior study in this field.



- The stability of linear time-invariant (LTI) systems can be assured through an eigenvalue analysis of the dynamic matrix.
- This strategy is not a necessary neither sufficient condition to guarantee the stability in LPV context.
- LPV system can be characterized by the existence of a continuously differentiable Lyapunov function

$$v(x(t),\theta(t)) = x(t)' P(\theta(t)) x(t)$$
(1)

where $P(\theta(t))$ is a parameterized symmetric and positive definite matrix such that

$$A(\theta(t))'P(\theta(t)) + P(\theta(t))A(\theta(t)) + \frac{d}{dt}P(\theta(t)) < 0,$$
 (2)



• Another result, more conservative but simpler to be programmed, is based on the notion of quadratic stability which is derived when the matrix *P* is constant. In this case,(2) becomes

$$A(\theta(t))'P + PA(\theta(t)) < 0, \tag{3}$$

where P is a symmetric and positive definite constant matrix referred to as the Lyapunov matrix [12].



Consider an autonomous LPV system [13, 14] with standard continuous-time space-state formulation given by

$$\frac{dx(t)}{dt} = A(\theta(t))x(t)$$
(4)

where $x(t) \in \mathbb{R}^{n_x}$ represents the state vector. There are two main distinct structures to describe the time-varying dynamic matrix $A(\theta(t))$: polytopic and affine. In the polytopic case, the representation of matrix $A(\theta(t))$ is given by a convex combination of *m* known vertices, that is

$$A(\theta(t)) = \sum_{j=1}^{m} \theta_j(t) A_j, \quad \theta(t) \in \Lambda_m,$$
(5)

where A_1, \ldots, A_m are the vertices of the polytope and $\theta(k) = (\theta_1(t), \ldots, \theta_m(t))$ is a vector of time-varying parameters belonging to a compact set called unit simplex and given by the equation

$$\Lambda_m = \left\{ \sum_{i=1}^m \theta_i(t) = 1, \ \theta_i(t) \ge 0, \ i = 1, \dots, m \right\}.$$
(6)



On the other hand, the dynamic matrix $A(\theta(t))$ with *m* interval time-varying parameters in the *affine* form is represented as

$$A(\theta(t)) = A_0 + \sum_{i=1}^{m} \theta_i(t) A_i, \ \theta_i(t) \in [\underline{\theta_i}, \overline{\theta_i}],$$
(7)

where A_0, A_1, \ldots, A_m are known matrices and $\theta_i(t), i = 1, \ldots, m$, are time-varying parameters with known lower and upper bounds, respectively given by $\underline{\theta_i}$ and $\overline{\theta_i}$. Note that, differently from the polytopic representation where the parameters must sum up one for all t, in the affine dependency model the parameters $\theta_i(t), i = 1, \ldots, m$, are all independent. However, it is possible to convert the affine model (7) into a polytopic model (5) by evaluating the LPV system at the extremes points of all combinations of the interval parameters.



- The model investigated in this paper is the famous Susceptible-Infected-Removed-Susceptible (SIRS) [15], also known as Kermack and McKendrick model, which predicts the distribution and number of cases of an infectious disease.
- This model has three compartments: the susceptible (S(t)), the infected (I(t)), and the removed (R(t)) populations.

Parameters

Tabela: Description of the variables of SIRS model.

	Description
S(t)	Susceptible individual
I(t)	Infected individual
R(t)	Removed individual
μ	Natural mortality rate for every population
β	Transmission probability by contact between $S(t)$ and $I(t)$
γ	Conversion rate of infected to removed people
V	Rate of removed to susceptible people

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Matlab Implementation

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System of differential equations

The model is given by the following system of differential equations:

$$\frac{dS(t)}{dt} = -\beta S(t)I(t) + \gamma R(t),$$

$$\frac{dI(t)}{dt} = \beta S(t)I(t) - \nu I(t),$$

$$\frac{dR(t)}{dt} = \nu I(t) - \gamma R(t).$$
(8)

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Equilibrium points and Jacobian Matrix

From the biological point of view, it is interesting to determine a coexistence equilibrium such that the population is a positive number. This equilibrium point is given by:

$$(\tilde{S},\tilde{I}) = \left(\frac{v}{\beta}, \frac{N - \frac{v}{\beta}}{v + \gamma}\right) \quad \text{with} \quad \frac{N - \frac{v}{\beta}}{v + \gamma} > 0.$$
 (9)

It is necessary that $N > \frac{v}{\beta}$ to obtain a positive equilibrium point. Additionally, system (8) is associated with the following Jacobian matrix:

$$J(S,I) = \begin{bmatrix} -(\beta I + \gamma) & -(\beta S + \gamma) \\ \beta I & \beta S - \nu \end{bmatrix}.$$
 (10)

At the coexistence equilibrium point, we have $tr J(\tilde{S}, \tilde{I}) = -(\beta \tilde{I} + \gamma) < 0$ and $det J(\tilde{S}, \tilde{I}) = \beta \tilde{I}(\nu + \gamma) > 0$.

For the MATLAB implementation, firstly, define a valid parametric region for system (8).

Parameters	Bounded values
N	1
β	0.5
$v(t)\in [\underline{v},\overline{v}]$	[0.25,0.4]
γ	0.3
$\tilde{I}(t)\in\left[\underline{I},\overline{I} ight]$	[-0.22,0.9091]

Tabela: Bounds of the time-varying parameters of System (8).



Secondly, determine the linearized version of system (8) around the coexistence equilibrium point, that is, rewrite (9) in the standard LPV structure given in (4).

$$\begin{bmatrix} \frac{dS(t)}{dt} \\ \frac{dI(t)}{dt} \end{bmatrix} = \begin{bmatrix} -\beta(\tilde{I}(t) + \gamma) & -(v(t) + \gamma) \\ \beta\tilde{I}(t) & 0 \end{bmatrix} \begin{bmatrix} S(t) \\ I(t) \end{bmatrix}.$$
 (11)

Structures: Polytopic or Affine

• The polytopic structure for the LPV system (12) is given by

Methodology

$$\begin{aligned} \mathcal{A}(\theta(t)) &= \theta_1(t) \begin{bmatrix} -\beta(\underline{l}+\gamma) & -(\underline{\nu}+\gamma) \\ \beta \underline{l}(t) & 0 \end{bmatrix} + \theta_2(t) \begin{bmatrix} -\beta(\overline{l}+\gamma) & -(\underline{\nu}+\gamma) \\ \beta \overline{l} & 0 \end{bmatrix} \cdots \\ \cdots &+ \theta_3(t) \begin{bmatrix} -\beta(\underline{l}+\gamma) & -(\overline{\nu}+\gamma) \\ \beta \underline{l} & 0 \end{bmatrix} + \theta_4(t) \begin{bmatrix} -\beta(\overline{l}+\gamma) & -(\overline{\nu}+\gamma) \\ \beta \overline{l} & 0 \end{bmatrix} \end{aligned}$$

$$(12)$$

where $\theta(t) = (\theta_1(t), \ldots, \theta_4(t)) \in \Lambda_4$.

- Note that, the Jacobian matrix is time-varying, since it depends on time-varying parameters v(t) and *l*(t), meaning that it can be written using *polytopic* or *affine* structure.
- Despite *l*(t) depends only on the variation of v(t), the relationship between these two parameters is not linear. Then, v(t) and *l*(t) can be handled as independent interval parameters in the affine structure (two parameters) and all the possible combinations of their bounds must be used to obtain the polytopic structure (four vertices).

On the other hand, the affine structure (7) yields the dynamic matrix

$$A(\theta(t)) = \begin{bmatrix} -\beta\gamma & -\gamma \\ 0 & 0 \end{bmatrix} + \theta_1(t) \begin{bmatrix} 0 & -1 \\ 0 & 0 \end{bmatrix} + \theta_2(t) \begin{bmatrix} -\beta & 0 \\ \beta & 0 \end{bmatrix},$$
(13)

where $\theta_1(t) = v(t) \in [0.25, \ 0.4]$ and $\theta_2(t) = \tilde{l}(t) \in [-0.22, \ 0.9091]$.



- Initialize the parameters according to the Table 2, as shown below: $\beta = 0.5; \quad \gamma = 0.3; \quad \underline{v} = 0.25; \quad \overline{v} = 0.6; \quad \underline{I} = -0.22; \quad \overline{I} = 0.9091;$
- Define matrix coefficients A_i in the affine case:
 % % Matrix coefficients of the LPV system in the affine form A0 = [-βγ -γ; 0 0];
 A1 = [0 -1; 0 0];
 A2 = [-β 0; β 0];
 Indicate the degree of dependence on time-varying parameters using the corresponding value of λⁱ vector

Af{1} = {[0 0],A0}; Af{2} = {[1 0],A1}; Af{3} = {[0 1],A2};

 Analogously to what was done in the affine case, define in MATLAB the matrix vertices for the politopic case:



 Create a ROLMIP object (function rolmipvar [8]) for the affine structure of the dynamic matrix containing both the system information and the degrees of time-varying parameters:

```
% bounds of time-varying parameters
Bounds = [\bar{v} \ \underline{v}; \overline{l} \ \underline{l}];
% ROLMIP object for affine structure
Arolm = rolmipvar(Af,'A',Bounds)
```

 Create a ROLMIP object (function rolmipvar [8]) for the *polytopic* structure of the dynamic matrix containing both the system information and the degrees associated to the time-varying parameters:

```
N = size(Ap,2); % Number of vertices
g = 1; % degree of dependence on the parameters
% ROLMIP object for polytopic structure
Arolm = rolmipvar(Ap,'A',N,g)
```



• Define a ROLMIP object for the symmetric ('sym') and constant (degree 0) Lyapunov matrix *W* using *affine* structure:

 n_x = size(A0,1); % system order p = size(Bounds,1); % number of time-varying parameters N_{af} = 2*ones(1,p); % dimension of W g_{af} = 0*ones(1,p); % degree of W (quadratic stability) % ROLMIP object for W with affine structure W = rolmipvar(n_x , n_x , ' W_{af} ', 'sym', N_{af} , g_{af});

 Define a ROLMIP object for the symmetric ('sym') and constant (degree 0) Lyapunov matrix W using polytopic structure: n_x = size(Ap1,1); % system order g_p = 0; % degree of W (quadratic stability) W = rolmipvar(n_x, n_x, 'W_p', 'sym', N, g_p)



From this step forward, polytopic and affine structures uses the same code in MATLAB to solve the LMIs.

In this step, the LMI conditions to guarantee that P is positive definite and the feasibility of (3) are created.
 % % Quadratic Stability Conditions

```
LMI_pos = W>0;
% LMI (3)
LMI_stb = Arolm'*W + W*Arolm < 0;
LMI = [LMI_stb,LMI_pos];
```



 Finally, to verify the validity of the results provided by optimization solver (that is, positivity or negativity of the LMIs), we can evaluate the signal of the constraints residue using the MATLAB function checkset from YALMIP as follows:

```
% % validation of solution
pmin = min(checkset(LMIs));
if (pmin>0)
fprintf('Stability assured');
W_n=double(W);
else
fprintf('Stability not verified');
W_n=[];
end
```



 In the numerical example using the presented code for solving the quadratic stability problem, we obtained the matrix

$$W = \begin{bmatrix} 1.1289 & 0.6754 \\ 0.6754 & 3.0556 \end{bmatrix},$$
 (14)

for both affine and polytopic structures. Furthermore, we have pmin = 0.0032 > 0 which ensures that W is a Lyapunov matrix, that is, P = W is a symmetric and positive definite matrix which satisfies (2). In other words, the stability for all parametric uncertain domain is ensured.

• As a counterexample, let us consider $\beta = 0.6$ and repeat the experiment. In this case, the minimum residue is pmin $= -1.8 \times 10^{-12}$ which implies that the LPV model (with $\beta = 0.6$) is not quadratically stable.



- Usually, to validate (LTI) models, the global stability is studied using Lyapunov's theory.
- To neglect the parameter variations may be reasonable and acceptable in some cases, but it is very helpful to consider these variations to obtain a more accurate representation of some important phenomenon.
- Then, using the LPV theory, one can study the asymptotic stability of the linearized version of non-linear biological problems taking into account the time-variations of the model.
- This paper showed a systematic way to program the quadratic stability test using the parsers ROLMIP and YALMIP from MATLAB considering both affine and polytopic representations for the dynamic matrix.
- ROLMIP parser allows to avoid manual programming and calculation of a high number of inequalities, that is greater as the number of time-varying parameters increases, making this task unfeasible in practice.



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W. F. Fagan, R. S. Cantrell, and C. Cosner, "How habitat edges change species interactions." *The American Naturalist*, vol. 153, no. 2, pp. 165–182, 1999, pMID: 29578760. [Online]. Available: https://doi.org/10.1086/303162



J. Siepmann and N. A. Peppas, "Hydrophilic matrices for controlled drug delivery: An improved mathematical model to predict the resulting drug release kinetics (the "sequential layer" model)," *Pharmaceutical Research*, vol. 17, no. 10, pp. 1290–1298, Oct 2000. [Online]. Available: https://doi.org/10.1023/A:1026455822595



J. Giesecke, Modern infectious disease epidemiology. CRC Press, 2017.



C. C. E. Morillo, R. A. L. Carrasco, and J. a. F. da Costa Meyer, "Dinâmica de hiv e posterior aids." Proceeding Series of the Brazilian Society of Computational and Applied Mathematics, vol. 6, no. 2, 2018.

S. Kondo and T. Miura, "Reaction-diffusion model as a framework for understanding biological pattern formation," *science*, vol. 329, no. 5999, pp. 1616–1620, 2010.



N. Takahata and T. Maruyama, "A mathematical model of extranuclear genes and the genetic variability maintained in a finite population," *Genetical Research*, vol. 37, no. 3, p. 291–302, 1981.



K. Faust and J. Raes, "Microbial interactions: from networks to models," *Nature Reviews Microbiology*, vol. 10, pp. 538 EP –, Jul 2012, review Article. [Online]. Available: https://doi.org/10.1038/nrmicro2832



C. M. Agulhari, C. Oliveira, and P. L. Peres, "Robust Imi parser: A toolbox to construct Imi conditions for uncertain systems," in Congresso Brasileiro de Automática (CBA 2012), Campina Grande, PB, Brasil, 2011.



J. Löfberg, "YALMIP: A toolbox for modeling and optimization in MATLAB," Taipei, Taiwan, September 2004, pp. 284–289, http://yalmip.github.io.



J. F. Sturm, "Using SeDuMi 1.02, a MATLAB toolbox for optimization over symmetric cones," vol. 11, no. 1–4, pp. 625–653, 1999, http://sedumi.ie.lehigh.edu/.

- Q. Kong, "Lyapunov stability theory," in A Short Course in Ordinary Differential Equations. Springer, 2014, pp. 61–100.
- H. K. Khalil, "Nonlinear systems," Upper Saddle River, 2002.



C. Hoffmann and H. Werner, "A survey of linear parameter-varying control applications validated by experiments or high-fidelity simulations," *IEEE Transactions on Control Systems Technology*, vol. 23, no. 2, pp. 416–433, 2014.



J. Mohammadpour and C. W. Scherer, *Control of linear parameter varying systems with applications*. Springer Science & Business Media, 2012.



- L. Edelstein-Keshet, Mathematical models in biology. SIAM, 2005.
- W. F. Fagan, R. S. Cantrell, and C. Cosner, "How habitat edges change species interactions." *The American Naturalist*, vol. 153, no. 2, pp. 165–182, 1999, pMID: 29578760. [Online]. Available: https://doi.org/10.1086/303162



J. Siepmann and N. A. Peppas, "Hydrophilic matrices for controlled drug delivery: An improved mathematical model to predict the resulting drug release kinetics (the "sequential layer" model)," *Pharmaceutical Research*, vol. 17, no. 10, pp. 1290–1298, Oct 2000. [Online]. Available: https://doi.org/10.1023/A:1026455822595



J. Giesecke, Modern infectious disease epidemiology. CRC Press, 2017.



C. C. E. Morillo, R. A. L. Carrasco, and J. a. F. da Costa Meyer, "Dinâmica de hiv e posterior aids." Proceeding Series of the Brazilian Society of Computational and Applied Mathematics, vol. 6, no. 2, 2018.



S. Kondo and T. Miura, "Reaction-diffusion model as a framework for understanding biological pattern formation," *science*, vol. 329, no. 5999, pp. 1616–1620, 2010.



N. Takahata and T. Maruyama, "A mathematical model of extranuclear genes and the genetic variability maintained in a finite population," *Genetical Research*, vol. 37, no. 3, p. 291–302, 1981.



K. Faust and J. Raes, "Microbial interactions: from networks to models," *Nature Reviews Microbiology*, vol. 10, pp. 538 EP –, Jul 2012, review Article. [Online]. Available: https://doi.org/10.1038/nrmicro2832



C. M. Agulhari, C. Oliveira, and P. L. Peres, "Robust Imi parser: A toolbox to construct Imi conditions for uncertain systems," in *Congresso Brasileiro de Automática (CBA 2012), Campina Grande, PB, Brasil,* 2011.



J. Löfberg, "YALMIP: A toolbox for modeling and optimization in MATLAB," Taipei, Taiwan, September 2004, pp. 284–289, http://yalmip.github.io.



J. F. Sturm, "Using SeDuMi 1.02, a MATLAB toolbox for optimization over symmetric cones," vol. 11, no. 1–4, pp. 625–653, 1999, http://sedumi.ie.lehigh.edu/.



Q. Kong, "Lyapunov stability theory," in A Short Course in Ordinary Differential Equations. Springer, 2014, pp. 61–100.



H. K. Khalil, "Nonlinear systems," Upper Saddle River, 2002.



C. Hoffmann and H. Werner, "A survey of linear parameter-varying control applications validated by experiments or high-fidelity simulations," *IEEE Transactions on Control Systems Technology*, vol. 23, no. 2, pp. 416–433, 2014.



J. Mohammadpour and C. W. Scherer, *Control of linear parameter varying systems with applications*. Springer Science & Business Media, 2012.



L. Edelstein-Keshet, Mathematical models in biology. SIAM, 2005.