Brief Curriculum vitae
2021

Gouzé Jean-Luc

Senior researcher
Directeur de Recherches DR1 INRIA (the French National Institute for Research in Computer Science and Control) http://www.inria.fr

Head of the BIOCORE (Biological control of artificial ecosystems) team

Organization: INRIA, France
Unit: Sophia Antipolis
Team: EPI BIOCORE
Address: BIOCORE, INRIA Sophia Antipolis, 2004, route des Lucioles, B.P. 93 06902 Sophia-Antipolis Cedex, France
E-mail: gouze@sophia.inria.fr
Telephone: 33 4 92 38 78 75
Fax: 33 4 92 38 78 58
Web page (my team): http://www.inria.fr/equipes/biocore
Web page (personal): http://www-sop.inria.fr/members/Jean-Luc.Gouze/JLGouze-eng.html

Main Research interests

biomathematics, mathematical modelling of biological phenomena, population dynamics, ordinary differential equations, theory of non-linear systems and control, optimal management of renewable resources, bioreactors models, biochemical networks models.

Academic experience

2010 Head of BIOCORE research team

1997 Research Director (Directeur de Recherche) INRIA, COMORE research group

1996 Head of COMORE research group (Modelling and Control of Renewable Resources), INRIA

1996 Tenure (Habilitation à diriger les recherches) (University of Nice)
title: Qualitative mathematical analysis of biological models
Board : J. Demongeot, R. Arditi, C. Lobry, E. Walter, P. Bernhard, P. Nival, A. Sciandra.

1983-1995 Researcher (Chargé de recherches) at INRIA, (Institut National de Recherches en Informatique et en Automatique) Sophia-Antipolis
MIAOU research group (Control theory)

1980-1983 Doctoral Thesis from the Paris XI University
Advisors: J.P. Changeux (neurobiologist, Institut Pasteur) and J.M. Lasry (mathematician, Paris IX)
"Sur la structuration de la jonction neuromusculaire; régression de la multi-innervation pendant le développement; modèle mathématique et simulation" (mathematical model of synaptic network)

1977-1980 Graduated from the engineering school Ecole Centrale de Paris (Applied Mathematics Department).
Master thesis : mathematical models of skin diving

Born 5/21/58 in Tours, France.

Research programs, grants, industrial collaborations (2000 - 2020)

ARC GDyn (2002-2004)
Coordination of the action GDyn with H. de Jong (HELIX INRIA). The aim is the analysis of dynamical piecewise linear models of genetic regulatory networks (see http://www-sop.inria.fr/comore/arcgdyn/arcgdyn-eng.html). The ARC involves mathematicians, computer scientists, and biologists from the E.N.S. Ulm Paris, the INRIA Rhone-Alpes, Rocquencourt and Sophia-Antipolis, the Haute Alsace University (Mulhouse) and the Joseph Fourier University (Grenoble).

Action ACI IMPBIO BacAttract (2004-2006)
Action funded by the Ministère de la Recherche. The aim is the mathematical modelling and analysis of some well known gene networks.

Action ACI IMPBIO MathResoGen (2004-2006)
Mathematical modelling of genetic and metabolic networks

AS Asinbio (2002-2004)
Participant in the Action Spécifique "Observers for systems with unknown inputs" of the RTP50 "STIC et Environnement" funded by the CNRS.

TELEMAC: 2001-2005
Participation in the European project (with industrial partners) TELEMAC (Tele-monitoring and Advanced Tele-control of High-Yield Wastewater Treatment Plants); coordinated by O. Bernard (Comore) from the scientific point of view and B. Le Dantec (Ercim) for administration (see http://www.ercim.org/telemac). Partners are ERCIM, INRIA COMORE, INRA (Laboratoire des Biotechnologies de l'environnement, Narbonne), APPLITEK (captors, Belgium), Department of Applied Mathematics, Biometrics and Process Control, Gent University, Belgique), Council for the Central Laboratory of the Research Councils (CCLRC), Information Technology Department, (England), SPES (Information technologies, Italy), University of Santiago de Compostella (USC)(Spain), ENEA Waste water Treatment and Water Cycle Unit (Italy), AGRALCO (Spain), PSPc (Belgium), Tequila SAUZA S.A. (Mexico), The University of Guadalajara (UDG) (Mexico), ALLIED DOMECQ SPIRITS and WINE LTD. (DOMECQ UK), Allied Domecq Brasil Industria e Comercio Limitada (Brazil). The total budget was around 4.5 Meuros.

European project HYGEIA (2005-2007)
HYGEIA (Hybrid Systems for Biochemical Network Modeling and Analysis) is a NEST ADVENTURE STREP European project. The objective of HYGEIA is to exploit recent developments in the area of hybrid systems to address open problems in modeling and analysis of biochemical networks. Participants: Sosso, Helix, Comore (INRIA) Patras Univ. (Greece), European Molecular Biology Laboratory (Heidelberg) , Rockefeller University (New-York).

European Network of Excellence HYCON(2005-2007)
The objective of the NoE HYCON (Hybrid Control: Taming Heterogeneity and Complexity of Networked Embedded Systems) is establishing a durable community of leading researchers and practitioners who develop and apply the hybrid systems approach to the design of networked embedded control systems as found, e.g., in industrial production, transportation systems, generation and distribution of energy, communication systems, genetic systems (see http://www.ist-hycon.org/.)

Shamash 2007 2010
Shamash is a project funded by the ANR in the national program for research in bioenergy. Its objective is to produce biodiesel from microalgae. Shamash, coordinated by O. Bernard, includes 9 partners, for a total budget of 2.8 Millions Euros. The role of Comore is to design a model of the process in order to better understand the dynamical mechanisms that lead to the transient storage of lipids. The second step will then consist in defining optimal conditions to maximize the oil production. See http://www-sop.inria.fr/comore/shamash/

MetaGenoReg 2006-2009 The objective of this project, funded by ANR (Systems Biology), is to model and analyze the interaction between metabolic and genetic regulations, with the example of the carbon metabolism of E. coli. Partners are Helix, Comore (INRIA), Univ. Joseph Fourier (Grenoble), and INSA Toulouse. The project is directed by D. Kahn (Helix, INRIA).

GeMCo 2010 2014

The objective of this project is to do model reduction, experimental validation, and control for the gene expression machinery in E. coli. The project is funded by ANR (2010-BLAN-0201-01) and coordinated by M. Chaves (Comore, INRIA)

ColAge 2008 2014
The goal of this joint INRIA-INSERM consortium is to study bacterial growth and aging by using mathematical modelling and computational predictions to design and implement a *de novo* biological system. This Large-Scale Initiative Action is partly funded by INRIA and supervised by H. Berry (Alchemy, INRIA).

ANR-RESET 2012-2017 The objective of this project is to control the growth of E. coli cells in a precise way, by arresting and restarting the gene expression machinery of the bacteria in an efficient manner directed at improving product yield and productivity. RESET is an Investissements d'Avenir project in Bioinformatics (managed by ANR) and it is coordinated by H. de Jong (Ibis, Inria)

ANR-ICycle 2016-2020: This project aims at understanding the communication pathways between the cell division cycle and the circadian clock, using mathematical modeling and control theory to construct and implement two coupled synthetic biological oscillators. Project coordinated by M. Chaves.

SysBioDRez: Marie Curie International Incoming Fellowship FP7 (EC-PEOPLE) is a multidisciplinary CNRS-INRIA project for the collaboration of Jeremie Roux (researcher) with both Paul Hofman (scientist in charge) and Jean-Luc Gouzé (partner lab), with the objective of linking in vitro quantitative dynamics to primary tumor samples profiling in order to determine the resistance probability of a specific combination of anti-cancer drugs in lung cancer, using computational methods.

SIGNALIFE: 2010-2019 Biocore is part of this Labex (scientific cluster of excellence) whose objective is to build a network for innovation on Signal Transduction Pathways in life Sciences, and is hosted by the University of Nice Sophia Antipolis.

ANR - Maximic: 2017-2021 The goal of the project (2017-2021) is to design and implement control strategies in a bacterium from producing at maximal rate a high value product. It is coordinated by H. de Jong (IBIS Grenoble), and involves members of Biocore and McTao.

Inria Project Lab, Cosy: (2017-...) This proposal aims at exploiting the potential of state-of-art biological modeling, control techniques, synthetic biology and experimental equipment to achieve a paradigm shift in control of microbial communities. We will investigate, design, build and apply an automated computer-driven feedback system for control of synthetic microbial communities, not just accounting for but rather leveraging population heterogeneity in the optimal accomplishment of a population-level task. The development of methodologies of general applicability will be driven by and applied to two different applications closely connected with real-world problems in the biomedical and biotechnological industry. The consortium is composed of the four Inria

project-teams IBIS, BIOCORE, COMMANDS, NON-A, the Inria Action Exploratoire INBIO, as well as the external partners BIOP (Université Grenoble Alpes, including members of IBIS), MaIAge (INRA), and YoukLAB (TU Delft).

ANR Ctrl-AB, project coordinator : https://anr.fr/Project-ANR-20-CE45-0014

The objectives of the Ctrl-AB project (2021-2024) are (i) to develop new control methods for the optimization of the productivity of a microbial community, and (ii) to demonstrate the effectiveness of these methods on a synthetic algal-bacterial consortium. Interestingly, co- culturing of E. coli with Chlorella leads to higher biomass and lipid productivity. Improved growth of Chlorella occurs despite competition of E. coli for the same substrates. On top of its ability to produce molecules like vitamins, which are necessary for algal growth, the bacteria also produce carbon dioxide (CO2), which is the substrate of the photosynthesis of the algae. The algae can pro- duce oxygen (O2) fuelling bacterial growth, thus giving rise to a mutualistic pattern of interactions giving rise to several challenge for modelling anc controlling this artificial ecosystem.

PhD students (2000 - 2021)

PhD in progress: A. Yabo, "Control and optimal control of bacterial growth", since October 2018, Université Côte d'Azur. Supervisors J.-L. Gouzé and J.-B. Caillau (McTao).
PhD in progress: A. Dos Reis de Souza, "Estimation and Control Methods for Microbial Communities", since October 2018, Université de Lille. Supervisors: J.-L. Gouzé and D. Efimov (Valse, Inria Lille).
L. Chambon (2020) "Control of models of genetic regulatory networks", Univ. Nice Sophia Antipolis. Supervisor J.-L. Gouzé.
C. Lopez-Zazueta (2018) "Use of Perturbation Theory to optimize metabolic production of biofuels by microalgae.", Univ. Nice Sophia Antipolis, supervisors O. Bernard and J.-L. Gouzé.
S. Casagranda (2017) "Reduction of biological networks models", since Nov. 2013, UNSA. Supervisor: J.-L. Gouzé and D. Ropers (Ibis INRIA Grenoble)
I. Belgacem (2015) "Controle de systèmes de régulation génétique", UNSA. Supervisor: J.-L. Gouzé.
A. Carta, (2014) "Analysis and Control of models of biological regulatory systems. Application to growth control in E. coli", UNSA. Supervisors: J.-L. Gouzé and M. Chaves.
J. Rault, (2012) "Modélisation mathématique structurée en taille du zooplancton, UNSA. Supervisors: J.-L. Gouzé and E. Benoit.
I. Ndiaye, (2010) "Méthodes d'analyse de modèles de régulation cellulaire", UNSA, Supervisor: J.-L. Gouzé ; Co-Advisor: M. Chaves
G. Robledo, (2006) Quelques résultats sur la commande du chemostat (mathematical control of bioreactors), UNSA
V. Lemesle, *Modélisation mathématique structurée de la croissance cellulaire en chemostat : analyse et estimation* (Structured mathematical models for cellular growth in the chemostat) thèse de doctorat, UNSA, 2004
L. Mailleret, *Stabilisation globale de systèmes dynamiques positifs mal connus ; applications en biologie.* (Global stabilization of positive uncertain dynamical

systems in biology) thèse de doctorat, UNSA, 2004
M. Verdoit, *Caractérisation et modélisation de la dynamique spatiale et saisonnière de populations benthiques et démersales exploitées de la mer Celtique* (Models for spatial dynamics of fishes) thèse de doctorat, university P.M. Curie, 2003
J. Arino, *Modélisation structurée de la croissance du phytoplancton en chemostat* (Structured models for phytoplankton growth in the chemostat) thèse de doctorat, university Joseph Fourier, 2001.

Teaching activities

Present:
"Modeling biological networks", 4th year students, Génie Biologique, Polytech'Nice, University of Nice - Sophia Antipolis
"Discrete and continuous approaches to model gene regulatory networks", Master of Science in Computational Biology (M2), University of Nice - Sophia Antipolis.

Mathematical models in biology at the Master of biological oceanography from the University Pierre et Marie Curie, Paris VI, and EPU UNSA, until 2010

Past activities:
Modeling and control of bioprocesses at ISIA (Institut Supérieur en Informatique et Automatique, École des Mines de Paris).
CIMPA school in Tlemcen (Algéria, 2003) and Nouakchott (Mauritania, 2005); models of bioprocesses and fisheries.
School/workshop on mathematics and renewable resources at the Centro de Modelamiento Matematico of the Universidad de Chile (in Santiago, Chile, two weeks in April 2004).
Regular formations of mathematics and mathematical modelling to biologists (researchers) at INRA Lusignan.

Other activities

Memeber of the editoriel board of the journal Frontiers in Applied Mathematics and Statistics (Mathematical Biology).
see https://www.frontiersin.org/journals/applied-mathematics-and-statistics/sections/mathematical-biology#editorial-board

Member of the scientific committee of Académie 4 of Idex UCA-Jedi.
Member of the INRIA committee supervising the doctoral theses.
Member of the steering committee of Labex SIGNALIFE of the University of Nice-Sophia-Antipolis, and of COREBIO PACA.
Member of the board of the SFBT (French Speaking Society for Theoretical Biology).
http://sfbt.math.cnrs.fr/fr/sfbt/org/index.html.

Member of the Commission Scientifique Spécialisée MBIA (evaluation committee for Mathematics, Biometry and AI) of INRA, that evaluates the scientific

career of INRA researchers (until 2010).

Member of the Commission d'Evaluation (scientific committee for the evaluation of researchers) of INRIA (until 2005).
Organization of the evaluation of the BIO theme at INRIA (2005), see http://www-sop.inria.fr/comore/evaluation/

Reviewer for many journals SIAM Appl. Maths, Mathematical Biosciences, J. Process Control, J. Math. Biology, Systems and Control Letter, ... and conferences.

Participation in committees for PhD theses (regularly).

Program committee for (recently) POSTA (Multidisciplinary International Symposium on Positive systems, theory and applications,), CIFA , "Stic et Environnement", BIOMATH ...
Expert committee for Aquae INRA/Cemagref projects, for RTP50 CNRS "STIC et Environnement".

Publications

Journals (1997 - 2021)

[1] Agustín Gabriel Yabo, Jean-Baptiste Caillau, Jean-Luc Gouzé, Hidde De Jong, and Francis Mairet. Dynamical analysis and optimization of a generalized resource allocation model of microbial growth. To appear in SIADS (SIAM Journal on Applied Dynamical Systems) , 2021.

[2] Carlos Martínez and Jean-Luc Gouzé. Global dynamics of the chemostat with overflow metabolism. *Journal of Mathematical Biology*, 82(3), February 2021.

[3] Francis Mairet, Jean-Luc Gouzé, and Hidde De Jong. Optimal proteome allocation and the temperature dependence of microbial growth laws. *npj Systems Biology and Applications*, 7(14), 2021.

[4] Hussein Kanso, Bénédicte Quilot-Turion, Mohamed-Mahmoud Memah, Olivier Bernard, Jean-Luc Gouzé, and Valentina Baldazzi. Reducing a model of sugar metabolism in peach to catch different patterns among genotypes. *Mathematical Biosciences*, 321:108321, March 2020.

[5] Lucie Chambon, Ismail Belgacem, and Jean-Luc Gouzé. Qualitative control of undesired oscillations in a genetic negative feedback loop with uncertain measurements. *Automatica*, 112:108642, February 2020.

[6] Agustín Gabriel Yabo, Jean-Baptiste Caillau, and Jean-Luc Gouzé. Optimal bacterial resource allocation: metabolite production in continuous bioreactors. *Mathematical Biosciences and Engineering*, 17(6):7074–7100, 2020.

[7] Alex Dos Reis De Souza, Jean-Luc Gouzé, Denis Efimov, and Andrey Polyakov. Robust Adaptive Estimation in the Competitive Chemostat. *Computers & Chemical Engineering*, 142:107030, November 2020.

[8] Marco Mauri, Jean-Luc Gouzé, Hidde De Jong, and Eugenio Cinquemani. Enhanced production of heterologous proteins by a synthetic microbial community: Conditions and trade-offs. *PLoS Computational Biology*, 16(4):e1007795, 2020.

[9] Alex Dos Reis De Souza, Denis Efimov, Andrey Polyakov, and Jean-Luc Gouzé. Robust Stabilization of Competing Species in the Chemostat. *Journal of Process Control*, 87:138–146, 2020.

[10] Claudia López Zazueta, Olivier Bernard, and Jean-Luc Gouzé. Dynamical reduction of linearized metabolic networks through quasi steady state approximation. *AIChE Journal*, 65(1):18–31, 2019.

[11] Ivan Yegorov, Francis Mairet, Hidde De Jong, and Jean-Luc Gouzé. Optimal control of bacterial growth for the maximization of metabolite production. *Journal of Mathematical Biology*, 78(4):985–1032, 2019.

[12] J.-A. Sepulchre, S. Reverchon, J.-L. L. Gouzé, and W. Nasser. Modeling the bioconversion of polysaccharides in a continuous reactor: A case study of the production of oligo-galacturonates by Dickeya dadantii. *Journal of Biological Chemistry*, 294(5):1753–1762, Feb. 2019.

[13] M. Chaves, D. A. Oyarzun, and J.-L. Gouzé. Analysis of a genetic-metabolic oscillator with piecewise linear models. *Journal of Theoretical Biology*, 462:259 – 269, Feb. 2019.

[14] I. Belgacem, S. Casagranda, E. Grac, D. Ropers, and J.-L. Gouzé. Reduction and stability analysis of a transcription-translation model of RNA polymerase. *Bulletin of Mathematical Biology*, 80(2):294–318, 2018.

[15] C. López Zazueta, O. Bernard, and J.-L. Gouzé. Analytical Reduction of Nonlinear Metabolic Networks Accounting for Dynamics in Enzymatic Reactions. *Complexity*, 2018:1 – 22, Aug. 2018.

[16] I. Yegorov, F. Mairet, and J.-L. Gouzé. Optimal feedback strategies for bacterial growth with degradation, recycling and effect of temperature. *Optim. Control Appl. Meth.*, 39, 2018.

[17] C. Poignard, M. Chaves, and J.-L. Gouzé. A Stability Result for Periodic Solutions of Nonmonotonic Smooth Negative Feedback Systems. *SIAM Journal on Applied Dynamical Systems*, 17(2):1091 – 1116, Apr. 2018.

[18] S. Casagranda, S. Touzeau, D. Ropers, and J.-L. Gouzé. Principal process analysis of biological models. *BMC Systems Biology*, 12:68, 2018.

[19] J.-A. Sepulchre, F. Mairet, and J.-L. Gouzé. Optimization and control of bio-conversion of polymeric substrate in the chemostat. *AIChE Journal*, 63(11):4738–4747, 2017.

[20] H. De Jong, S. Casagranda, N. Giordano, E. Cinquemani, D. Ropers, J. Geiselmann, and J.-L. Gouzé. Mathematical modelling of microbes: metabolism, gene expression and growth. *Journal of the Royal Society Interface*, 14(136):1–14, Nov. 2017.

[21] F. Mairet and J.-L. Gouzé. Hybrid Control of a Bioreactor with Quantized Measurements. *IEEE Transactions on Automatic Control*, 61(5):1385 – 1390, 2016.

[22] N. Giordano, F. Mairet, J.-L. Gouzé, J. Geiselmann, and H. De Jong. Dynamical allocation of cellular resources as an optimal control problem: Novel insights into microbial growth strategies. *PLoS Computational Biology*, 12(3):e1004802, Mar. 2016.

[23] C. Poignard, M. Chaves, and J.-L. Gouzé. Periodic Oscillations for Non Monotonic Smooth Negative Feedback Circuits. *SIAM Journal on Applied Dynamical Systems*, 15(1):257–286, 2016.

[24] J. Roux, J.-L. Gouzé, and P. Hofman. Intraclonal heterogeneity in tumors and its impact on precision medicine. *médecine/sciences*, 31(1):28–31, Jan. 2015.

[25] A. Carta, M. Chaves, and J.-L. Gouzé. Continuous-switch piecewise quadratic models of biological networks: Application to bacterial growth. *Automatica*, 61:164–172, 2015.

[26] W. Abou-Jaoudé, M. Chaves, and J.-L. Gouzé. Links between topology of the transition graph and limit cycles in a two-dimensional piecewise affine biological model. *Journal of Mathematical Biology*, 69(6-7):1461–1495, Dec. 2014.

[27] I. Belgacem and J.-L. Gouzé. Global stability of enzymatic chain of full reversible Michaelis-Menten reactions. *Acta Biotheoretica*, 61(3):425–436, 2013.

[28] M. Chaves, E. Farcot, and J.-L. Gouzé. Probabilistic approach for predicting periodic orbits in piecewise affine differential models. *Bulletin of Mathematical Biology*, 75(6):967–987, 2013.

[29] J. Rault, E. Benoît, and J.-L. Gouzé. Stabilizing effect of cannibalism in a two stages population model. *Acta Biotheoretica*, 61:119–139, 2013.

[30] G. Robledo, F. Grognard, and J.-L. Gouzé. Global stability for a model of competition in the chemostat with microbial inputs. *Nonlinear Analysis: Real World Applications*, 13(2):582–598, 2012.

[31] I. Ndiaye and J.-L. Gouzé. Global stability of reversible enzymatic metabolic chains. *Acta Biotheoretica*, 61(1):41–57, 2012.

[32] Abou-Jaoudé, W., Chaves, M., and Gouzé, J. L. (2011). A theoretical exploration of birhythmicity in the p53-mdm2 network. *PLoS ONE*, 6(2):e17075.

[33] Chaves, M. and Gouzé, J. (2011). Exact control of genetic networks in a qualitative framework: the bistable switch example. *Automatica*, 47:1105–1112.

[34] Chaves, M., Tournier, L., and Gouzé, J. L. (2010b). Comparing Boolean and piecewise affine differential models for genetic networks. *Acta Biotheoretica*, 58(2):217–232.

[35] Farcot, E. and Gouzé, J.-L. (2010a). Limit cycles in piecewise-affine gene network models with multiple interaction loops. *International Journal of Systems Science*, 41(1):119–130.

[36] Ndiaye, I., Chaves, M., and Gouzé, J. L. (2010). Oscillations induced by different timescales in signal modules regulated by slowly evolving protein-protein interactions. *IET Systems Biology*, 4(4):263–276.

[37] Serhani, M., Gouzé, J.-L., and Raissi, N. (2010). Dynamical study and robustness for a nonlinear wastewater treatment model. *Nonlinear Analysis: Real World Applications*, 12:487–500.

[38] E. Farcot and J.-L. Gouzé. Periodic solutions of piecewise affine gene network models with non uniform decay rates: The case of a negative feedback loop. *Acta Biotheoretica*, 57(4):429–455, 2009.

[39] J.-L. Gouzé and V. Lemesle. Two simple growth models in the chemostat. *ARIMA*, 2008.

[40] M. Moisan, O. Bernard, and J.-L. Gouzé. Near optimal interval observers bundle for uncertain bioreactors. *Automatica*, 45:291–295, 2009.

[41] V. Lemesle and J.-L. Gouzé. A simple unforced oscillatory growth model in the chemostat. *Bulletin of Mathematical Biology*, 70:344–357, 2008.

[42] L. Mailleret, J.-L. Gouzé, and O. Bernard. Global stabilization of a class of partially known positive systems. *Automatica*, 44:2128–2134, 2008.

[43] G. Batt, H. de Jong, J. Geiselmann, J.-L. Gouzé, M. Page, D. Ropers, T. Sari, and D. Schneider. Analyse qualitative de la dynamique de réseaux de régulation génique par des modèles linéaires par morceaux. *TSI Technique et Science Informatiques*, 26:11–46, 2007.

[44] Casey, R., de Jong, H., and Gouzé, J.-L. (2006). Piecewise-linear models of genetic regulatory networks: Equilibria and their stability. *Journal of Mathematical Biology*, 52:27-56.

[45] Gouzé, J.-L. and Robledo, G. (2005a). Feedback control for nonmonotone competition models in the chemostat. *Nonlinear Analysis: Real World Applications*, 6:671–690.

[46] J.-L. Gouzé and G. Robledo. Robust control for an uncertain chemostat model. *Internat. J. Robust Nonlinear Control*, 16(3):133–155, 2006.

[47] Lemesle, V. and Gouzé, J. L. (2005a). A biochemically based structured model of phytoplankton growth in the chemostat. *Ecological Complexity*, 2:21–33.

[48] Lemesle, V. and Gouzé, J. L. (2005b). An hybrid bounded error observer for uncertain bioreactor models. *Bioprocess and Biosystems Engineering*, 27:311–318.

[49] Mailleret, L., Gouzé, J.-L., and Bernard, O. (2005). Nonlinear control for algae growth models in the chemostat. *Bioprocess and Biosystem Engineering*, 27:319–327.

[50] H. de Jong, J.-L. Gouzé, C. Hernandez, M. Page, T. Sari, and H. Geiselmann (2004). Qualitative simulation of genetic regulatory networks using piecewise-linear models. *Bull. Math. Biol*, 66:301–340.

[51] O. Bernard and J.-L. Gouzé (2004). Closed loop observers bundle for uncertain biotechnological models. *J. Process. Contr.*, 14:7:765–774.

[52] J.-L. Gouzé and T. Sari (2003). A class of piecewise linear differential equations arising in biological models. *Dynamical systems*, 17:299–316.

[53] Rapaport, A. and Gouzé, J.-L. (2003). Parallelotopic and practical observers for nonlinear uncertain systems. *Int. Journal. Control*, 76:237–251.

[54] Arino, J., Gouzé, J.-L., and Sciandra, A. (2002). A discrete, size-structured model of phytoplankton growth in the chemostat. Introduction of non constant cell division. *J. Math. Biol.*, 45:313–33.

[55] Arino, J. and Gouzé, J.-L. (2002). A size-structured, non conservative ODE model of the chemostat. *Mathematical Biosciences*, 177-178:127–145.

[56] Bernard, O. and Gouzé, J.-L. (2002). Global qualitative behavior of a class of nonlinear biological systems: application to the qualitative validation of phytoplankton growth models. *Artif. Intel.*, 136:29–59.

[57] Hadj-Sadok, M. Z. and Gouzé, J. L. (2001). Estimation of uncertain models of activated sludge process with interval observers. *Journal of Process Control*, 11(3):299–310.

[58] Karama, A., Bernard, O., Gouzé, J., Benhammou, A., and Dochain, D. (2001). Hybrid neural modelling of an anaerobic digester with respect to biological constraints. *Wat. Sci. Technol.*, 43(7):1–8.

[59] Touzeau, S. and Gouzé, J.-L. (2001). Regulation of a fishery: from a local optimal control problem to an "invariant domain" approach. *Natural Resource Modeling*, 14(2):311–333.

[60] Gouzé, J. L., Rapaport, A., and Hadj-Sadok, Z. (2000). Interval observers for uncertain biological systems. *Ecological modelling*, 133:45–56.

[61] Bernard, O. and Gouzé, J.-L. (1999). Nonlinear qualitative signal processing for biological systems: application to the algal growth in bioreactors. *Mathematical Biosciences*, 157:357–372.

[62] Touzeau, S. and Gouzé, J.-L. (1998). On the stock-recruitment relationships in fish population models. *Environmental modelling and assessment*, 3:87–93.

[63] Gouzé, J.-L. (1998). Positive and negative circuits in dynamical systems. *Journal Biol. Syst.*, 6(1):11–15.

Book chapters

[1] F. Mairet and J.-L. Gouzé. Control of a Bioreactor with Quantized Measurements. In F. Fages and C. Piazza, editors, *Formal Methods in Macro-Biology*, volume 8738 of *Lecture Notes in Computer Science*, pages 47–62. Springer International Publishing, 2014.

[2] G. Bernot, J.-P. Comet, A. Richard, M. Chaves, J.-L. Gouzé, and F. Dayan. Modeling and analysis of gene regulatory networks. In F. Cazals and P. Kornprobst, editors, *Modeling in Computational Biology and Biomedicine*, pages 47–80. Springer, 2013.

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Some French acronyms

ADEME Agence de l'Environnement et de la maitrise de l'Energie
CIMPA Centre International de Mathématiques Pures et Appliquées
CNRS Centre National de la Recherche Scientifique
ENS Ecole Normale Supérieure

ERCIM European Research Consortium for Informatics and Mathematics
I3S Laboratoire Informatique, Signaux et Systèmes de Sophia-Antipolis
INRA Institut National de la Recherche Agronomique
IST Information Society Technologies
LOV Laboratoire d'Océanographie de Villefranche-sur-Mer
STIC Sciences et Technologies de l'Information et de la Communication
UMR Unité Mixte de Recherche
UNSA Université de Nice Sophia Antipolis