Curriculum Vitae Eugenio CINQUEMANI

Birth:	1976, Italian
Work address:	Centre Inria de l'Université Grenoble Alpes 655 avenue de l'Europe, Montbonnot – 38334 Saint Ismier cedex, France
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E-mail:	`eugenio.cinquemani@inria.fr`
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Languages:	Italian (mother tongue), English (fluent), French (fluent), Spanish (basic)
Research interests:	Modelling, analysis, identification and control of biological systems Identification, estimation and control for stochastic and switching systems Statistical signal processing

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CURRENT AND PREVIOUS POSITIONS

since Oct 2023: Senior research scientist ("Directeur de Recherche"), Inria center of the Université Grenoble Alpes, France (Project-Team MICROCOSME)

Nov 2009 – Sep 2023: Research scientist ("Chargé de Recherche"), Inria Grenoble – Rhône-Alpes, France (Project-Team IBIS, then MICROCOSME)

Oct 2006 – Oct 2009: Post-Doc, Automatic Control Laboratory, Swiss Federal Institute of Technology (ETH) Zürich, Switzerland

May 2005 – Apr 2006: Research assistant ("Assegno di Ricerca"), Department of Information Engineering, University of Padova, Italy

PROFESSIONAL QUALIFICATIONS

Habilitation à Diriger des Recherches, Informatique et mathematiques appliquées (accreditation to supervise research, informatics and applied mathematics), obtained Nov 2019, France

Abilitazione Scientifica Nazionale (accreditation for associate professorship), Settore 09/G1 (Automation, until May 31, 2030) and 09/G2 (Bioengineering, until May 5, 2030), obtained May 2021, Italy

Esame di Stato, Ingegneria (Professional qualification for engineering), obtained Dec 2002, Italy (score 120/120)

ACADEMIC FORMATION

Jan 2002 – Feb 2005: Ph.D. in Automation and Operations Research, Department of Information Engineering, University of Padova, Italy

Sep 1995 – Jul 2001: Laurea in Computer Engineering, specialization in Automatic Control, University of Padova, Italy (grade 110/110 *summa cum laude*)

Aug 1999 – Jun 2000: Exchange student at the University of California – Berkeley

RESEARCH PROJECTS

Responsibilities:

- Ctrl-AB: "Optimization and control of the productivity of an algal-bacterial consortium" (ANR Mathématiques et sciences du numérique pour la biologie et la santé, France), **coordinator and partner leader** for Inria Grenoble – Rhône-Alpes, 2021 – ongoing.
- MEMIP: "Mixed-Effects Models of Intracellular Processes : Methods, Tools and Applications" (ANR Société de l'information et de la communication, France), **partner leader** for Inria Grenoble – Rhône-Alpes, 2016 – 2021.
- CoSy: "Real-time control of synthetic microbial communities" (Inria Project-Lab), **project leader**, 2017 – 2021.
- CoSoft: "Control software for a system of mini-bioreactors" (Action de Développement Technologique, Inria Grenoble – Rhône-Alpes), **project leader**, 2017 – 2019.
- OptiCo: "OPTImal COntrol software for microbial communities in a system of mini-bioreactors" (Action de Développement Technologique, Inria), **project leader**, 2019 – 2021
- Plug-N-Bio: "A plug-and-play platform for reproducible microbial culture control experiments" (Action de Développement Technologique, Inria), **project leader**, 2022 – ongoing

Participation:

- ARBOREAL: Branching resource allocation processes for the analysis and inference of phenotypic growth variability (ANR JCJC – Aline Marguet), 2023 – ongoing.
- IMOCEP: Innovations for modeling of growth – from a cellular level to pediatric development (PEPR Maths-Vives), 2024 – ongoing.
- RECOM: Competition of RNAs for RNase E, a mechanism regulating their degradation and the energy and carbon metabolism in the cell (ANR Biochimie et chimie du vivant), 2023 – ongoing.
- AnaComBa: Analysis of bacterial communities: stochastic modelling (Équipe-Action PERSYVAL-lab), 2021 – 2024
- RIB-ECO (RIBonucleotide ECOnomy): "Engineering RNA life cycle to optimize economy of microbial energy: Application to the bioconversion of biomass-derived carbon sources" (ANR Bioéconomie : technologies spécifiques et approches systèmes), 2018 – 2022.
- Maximic: "Optimal control of microbial cells by natural and synthetic strategies" (ANR Société de l'information et de la communication, France), 2017 – 2023.
- RESET: "Arrest and restart of the gene expression machinery in bacteria: from mathematical models to biotechnological applications" (Investissements d'Avenir, Bioinformatique, France), 2012.
- GemCO: "Model reduction, experimental validation, and control for the gene expression machinery in *E.coli*" (ANR Blanc, France), 2010.

- ColAge: "Natural and engineering solutions to the control of bacterial growth and aging" (INRIA-INSERM Large-Scale Initiative Action), 2009 – 10.
- MetaGenoReg: "Towards an understanding of the interrelations between metabolic and gene regulation: *E.coli* carbon metabolism as a test case" (ANR Biologie Systémique, France), 2009 – 10.
- YeastX: "Towards an understanding of nutrient signalling and metabolic operation" (SystemsX.ch, Switzerland), 2009.
- HYGEIA: "Hybrid systems for biochemical network modelling and analysis" (NEST-4995, European Community), 2006 – 07.
- RECSYS: "Real-time hybrid estimation and identification algorithms for distributed sensor data processing" (IST-2001-32515, European Community), 2003 – 05.

STUDENT SUPERVISION

Ph.D. students:

- R.Asswad ("Development of control strategies for synthetic microbial consortia", Inria / Univ. Grenoble Alpes), co-supervision, Oct 2022 – ongoing.
- E.Reginato ("Development, analysis, and inference of stochastic models of gene expression in growing cell populations", Inria / Univ. Grenoble Alpes), co-supervision, Oct 2020 – ongoing.
- M.Sangster ("Development, characterization and control of *E.coli* communities on an automated experimental platform", Inria / Univ. Grenoble Alpes), co-supervision, Oct 2019 – May 2023.
- D.Stefan ("Structural and parametric identification of bacterial regulatory networks", Inria / Univ. Joseph Fourier Grenoble), co-supervision, Sep 2010 – Jun 2014.
- A.M.Gonzalez-Vargas ("Design, implementation and testing of identification algorithms for stochastic mixed-effects models of gene expression from single-cell data", Univ. of Pavia), visiting student, Jan – Aug 2014.
- S.Berthoumieux ("Methods for identification of biochemical network models", Inria / Univ. Lyon 1), external supervision 2009 – 12.

Master students:

- Supervision of the M2 internship of Geoffrey Roudaut (M.Sc. at Phelma – Grenoble INP, 2021), A.Flatrès (M.Sc. at Université Claude Bernard – Lyon 1, 2020), U.A.Anyaegbunam (M.Sc. at Université Paris Diderot and Descartes, 2016), Ç.Ak (M.Sc. at École Politechnique, 2014), E.Köksal (M.Sc. at Bogazici University, Istanbul, 2012 – 2013), A.Shivanandan (M.Sc. at Université Joseph Fourier, Grenoble, 2010 – 11)
- Co-supervision of the M2 thesis of E.Sideris (M.Sc. at University of Patras, 2019), N.Simeone (Laurea at University of Pavia, 2011 – 12), E.Balello (Laurea at University of Padova, 2003), L.Huber and C.Frischknecht (M.Sc. at ETH Zürich, 2008)
- Supervision of M1 internships (K.Kurma, 2015; D.Samuylov, 2013; ; M.J.Frontini, 2010)

TEACHING ACTIVITIES

Courses in M.Sc. programs:

- Heading and teaching of “Statistics” (M1, 20+ hours/year of teaching, supervision of 10+ hours/year of practical sessions) at the Centre Recherches Interdisciplinaires (CRI, Master AIV: “Approches Interdisciplinaires du vivant”, Université Paris Diderot et Decartes), then Learning Planet Institute (LPI, Master AIRE: “Interdisciplinary Approaches to Research and Teaching”, Université Paris Cité), 2013 – 24.
- Teaching of “Modelling and identification of metabolic networks” (4 hours/year), in the course “Modelling in Systems Biology”, for the Master program “Biomedical Engineering”, Phelma, Grenoble INP, 2014 – 25
- Teaching of “Identification of dynamical models of genetic networks” (6 hours/year), in the course “Modélisation de réseaux géniques et métaboliques”, for the Master program “Bioinformatique et Modélisation”, INSA Lyon, 2010 – 19

Courses in Ph.D. schools:

- “Modeling of stochastic gene expression” (4 hours), in “Advanced Lecture Course on Computational Systems Biology”, Aussois, France, 2017
- “Identification of biological systems” (4 hours), in Ph.D. school “Systems Biology”, Bertinoro, Italy, 2013
- “New approaches to Bayesian estimation of signals: denoising, regularization networks and wavelets” (12 hours), Department of Information Engineering, University of Padova, Italy, 2002

Teaching assistance:

- “Linear Systems Theory”, Department of Information Technology and Electrical Engineering, ETH Zürich, 2008 – 09.
- “Controllo dei processi” (Process control), Department of Information Engineering, University of Padova, 2005 – 06.
- “Fondamenti di Automatica” (Foundations of Automatic Control), Department of Information Engineering, University of Padova, 2004.
- “Identificazione dei modelli e analisi dei dati” (Stochastic filtering and system identification), Department of Information Engineering, University of Padova, 2003 – 04.

OTHER ACTIVITIES

Co-organizer of the “19th conference on Computational Methods in Systems Biology (CMSB)”, Bordeaux, France and online, September 22 – 24, 2021

Organizer of the workshop on “Modelling Heterogeneous Populations with applications in Biology”, INRIA Grenoble – Rhône-Alpes, France (online), May 17 – 18, 2021

Co-organizer of the “Fifth International Workshop on Hybrid Systems Biology (HSB)”, Grenoble, France, October 20 – 21, 2016

Co-organizer of the “Workshop on Identification and Control of Biological Interaction Networks”, INRIA Grenoble – Rhône-Alpes, February 8, 2011

Associate editor for the European Control Conference (ECC, 2013 – 25)

Program committee member of Static Analysis & Systems Biology (SASB, 2016 – 19), Computational Methods in Systems Biology (CMSB, 2018 – 25), Hybrid Systems Biolgy (HSB, 2019), IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB, 2019–2021)

Committee member of CES (since 2015), CDT (since 2018), CUMI (since 2009), and CRCN jury (2021,2022) at Inria Grenoble – Rhône-Alpes; at disposal for Inria CAP (since 2016)

PUBLICATIONS

Books:

E.C., L.Paulevé (Eds.), "Special Issue of the 19th International Conference on Computational Methods in Systems Biology", *BMC Bioinformatics Supplements*, 24(1), 2023 (online)

E.C., L.Paulevé (Eds.), "Computational Methods in Systems Biology" (Proceedings of the 19th international conference, CMSB 2021), *Lecture Notes in Bioinformatics* (LNBI) 12881, Springer, 2021.

E.C., A.Donzé (Eds.), "Hybrid Systems Biology" (Proceedings of the 5th international workshop, HSB 2016), *Lecture Notes in Bioinformatics* (LNBI) 9957, Springer, 2016.

Journal papers:

A.Pavlou, **E.C.**, C.Pinel, N.Giordano, M.van Melle-Gateau, I.Mihalcescu, J.Geiselmann, H.de Jong, "Single-cell data reveal heterogeneity of investment in ribosomes across a bacterial population", *Nature Communications*, 16:285, 2025

C.Martinez, **E.C.**, H.de Jong, J.-L.Gouzé, "Optimal protein production by a synthetic microbial consortium: Coexistence, distribution of labor, and syntrophy", *Journal of Mathematical Biology*, 87(23), 2023

A.Pavlou, **E.C.**, J.Geiselmann, H.de Jong, "Maturation models of fluorescent proteins are necessary for unbiased estimates of promoter activity", *Biophysical Journal*, 121(21):4179–4188, 2022

A.dos Reis de Souza, D.Efimov, A.Polyakov, J.-L.Gouzé, **E.C.**, "State observation in microbial consortia: a case study on a synthetic producer-cleaner consortium", *International Journal of Robust and Nonlinear Control* (Special Issue on Control-Theoretic Approaches for Systems in the Life Sciences), 33(9): 5011–5022, 2023 (online publication 2021)

M.Mauri, J.-L.Gouzé, H.de Jong, **E.C.**, "Enhanced production of heterologous proteins by a synthetic microbial community: Conditions and trade-offs", *PLoS Computational Biology*, 16(4):e1007795, 2020.

A.Marguet, M.Lavielle, **E.C.**, "Inheritance and variability of kinetic gene expression parameters in microbial cells: Modelling and inference from lineage tree data", *Bioinformatics* (Proc. of ISMB/ECCB 2019), 35(14):i586–i595, 2019.

E.C., "Stochastic reaction networks with input processes: Analysis and application to gene expression inference", *Automatica*, 101:150–156, 2019.

E.C., "Identifiability and Reconstruction of Biochemical Reaction Networks from Population Snapshot Data", *Processes* (Special Issue on Computational Synthetic Biology), 6(9):136, 2018.

H.de Jong, S.Casagranda, N.Giordano, **E.C.**, D.Ropers, J.Geiselmann, J.-L.Gouzé, "Mathematical modelling of microbes: Metabolism, gene expression and growth", *Journal of the Royal Society Interface*, 14:20170502, 2017.

M.Morin, D.Ropers, **E.C.**, J.C.Portais, B.Enjalbert, M.Cocaign-Bousquet, "The Csr system regulates *Escherichia coli* fitness by controlling glycogen accumulation and energy levels", *mBio*, 8(5):e01628–17, 2017.

E.C., V.Laroute, M.Cocaign-Bousquet, H.de Jong, D. Ropers, “Estimation of time-varying growth, uptake and excretion rates from dynamic metabolomics data”, *Bioinformatics* (Proc. of ISMB/ECCB 2017), 33(14):i301–i310, 2017.

A.Llamosi, A.M.Gonzalez-Vargas, C.Versari, **E.C.**, G.Ferrari-Trecate, P.Hersen, G.Batt, “What population reveals about individual cell identity: Single-cell parameter estimation of models of gene expression in yeast”, *PLoS Computational Biology*, 12(2):e1004706, 2016.

D.Stefan, C.Pinel, S.Pinhal, **E.C.**, J.Geiselmann, H.de Jong, “Inference of quantitative models of bacterial promoters from time-series reporter gene data”, *PLoS Computational Biology*, 11(1):e1004028, 2015.

M.A.Rapsomaniki, **E.C.**, N.N.Giakoumakis, P.Kotsantis, J.Lygeros, Z.Lygerou, “Inference of protein kinetics by stochastic modeling and simulation of Fluorescence Recovery After Photobleaching experiments”. *Bioinformatics*, 31(3):355–362, 2015.

S.Berthoumieux, M.Brilli, D.Kahn, H.de Jong, **E.C.**, “On the identifiability of metabolic network models”, *Journal of Mathematical Biology*, 67(6-7):1795–1832, 2013.

R.Porreca, **E.C.**, J.Lygeros, G.Ferrari-Trecate, “Invalidation of the structure of genetic network dynamics : A geometric approach”, *International Journal of Robust and Nonlinear Control*, Special Issue on System Identification for Biological Systems, 22(10):1140–1156, 2012.

P.Hokayem, **E.C.**, D.Chatterjee, F.Ramponi, J.Lygeros, “Stochastic receding horizon control with output feedback and bounded controls”, *Automatica*, 48(1):77–88, 2012.

E.C., M.Agarwal, D.Chatterjee, J.Lygeros, “Convexity and convex approximations of discrete-time stochastic control problems with constraints”. *Automatica*, 47(9):2082–2087, 2011.

S.Berthoumieux, M.Brilli, H.de Jong, D.Kahn, **E.C.**, “Identification of metabolic network models from incomplete high-throughput datasets”. *Bioinformatics* (Proc. of ISMB/ECCB 2011), 27(13):i186–i195, 2011. *Selected as Outstanding Student Paper (Ian Lawson Van Toch Memorial Award) at ISMB/ECCB 2011.*

D.Chatterjee, **E.C.**, J.Lygeros, “Maximizing the probability of attaining a target prior to extinction”. *Nonlinear Analysis: Hybrid Systems*, 5:367–381, 2011.

R.Porreca, **E.C.**, J.Lygeros, G.Ferrari-Trecate, “Identification of genetic network dynamics with unate structure”. *Bioinformatics*, 26(9):1239–1245, 2010.

E.C., A.Milias-Argeitis, S.Summers, J.Lygeros, “Stochastic dynamics of genetic networks: modelling and parameter identification”. *Bioinformatics*, 24(23):2748-2754, 2008.

E.C., G.Pillonetto, “Wavelet estimation by Bayesian thresholding and model selection”. *Automatica*, 44(9):2288–2297, 2008.

K.Koutroumpas, **E.C.**, P.Kouretas, J.Lygeros, “Parameter identification for stochastic hybrid systems using randomized optimization: A case study on subtilin production by *Bacillus subtilis*”. *Nonlinear Analysis: Hybrid Systems*, 2(3):786–802, 2008.

E.C., R.Porreca, G.Ferrari-Trecate, J.Lygeros, “Subtilin production by *Bacillus subtilis*: Stochastic hybrid models and parameter identification”. *IEEE Transactions on Circuits and Systems-I* and *IEEE Transactions on Automatic Control*, Joint Special Issue on Systems Biology, 53:38–50, 2008.

E.C., M.Micheli, “State estimation in stochastic hybrid systems with sparse observations”. *IEEE Transactions on Automatic Control*, 51(8):1337–1342, 2006.

E.C., “A superposition principle for the Kalman filter”. *Systems and Control Letters*, 55(1):38–44, 2006.

Conference papers:

R.Asswad, J.-L.Gouzé, **E.C.**, “Single- and multi-objective performance optimization of an algal-bacterial synthetic process”. In *Proceedings of the 64rd IEEE Conference on Decision and Control*, (Rio de Janeiro, Brazil, December 9-12, 2025). To appear.

R.Asswad, W.Djema, O.Bernard, J.-L.Gouzé, **E.C.**, "Optimization of microalgae biosynthesis via controlled algal-bacterial symbiosis". In *Proceedings of the 63rd IEEE Conference on Decision and Control*, (Milan, Italy, December 16-19, 2024).

R.Asswad, **E.C.**, J.-L.Gouzé, "Kalman-based approaches for online estimation of bioreactor dynamics from fluorescent reporter measurements". In *Proceedings of the 22nd European Control Conference*, (ECC, Stockholm, Sweden, June 25-28, 2024).

E.Reginato, A.Marguet, **E.C.**, "Inference of tree-structured auto-regressive models of gene expression parameters from generation-snapshot data". In *Proceedings of the 22nd European Control Conference*, (ECC, Stockholm, Sweden, June 25-28, 2024).

A.Marguet, **E.C.**, "Identification of stochastic gene expression models over lineage trees". In *Proceedings of the 19th IFAC sympusium on System Identification* (SysId, Padova, Italy/online, July 13-16, 2021), IFAC-PapersOnLine 54(7):150–155, 2021

E.C., "Inference of the statistics of a modulated promoter process from population snapshot gene expression data". In *Proceedings of the 21th IFAC World Congress* (Berlin, Germany, July 12 – 17, 2020), IFAC-PapersOnLine 53(2): 16767–16772, 2020

E.C., F.Mairet, I.Yegorov, H.de Jong, J.-L. Gouzé, "Optimal control of bacterial growth for metabolite production: The role of timing and costs of control". In *Proceedings of the 17th European Control Conference* (ECC, Napoli, Italy, June 25-28, 2019).

E.C., "Structural identification of biochemical reaction networks from population snapshot data". In *Proceedings of the 20th IFAC World Congress* (Toulouse, July 9-14, 2017), IFAC-PapersOnLine 50(1):12629–12634.

E.C., "On observability and reconstruction of promoter activity statistics from reporter protein mean and variance profiles". In *Proceedings of the 5th International Workshop on Hybrid Systems Biology* (Grenoble, October 20-21, 2016), Lecture Notes in Bioinformatics (LNBI) 9957:147–163, Springer.

A.M. Gonzalez-Vargas, **E.C.**, G. Ferrari-Trecate, "Validation methods for population models of gene expression dynamics". In *Proceedings of the 6th IFAC Conference on Foundations of Systems Biology in Engineering* (Magdeburg, October 9-12, 2016), IFAC-PapersOnLine 49(26):114-119, 2016.

E.C., "Reconstruction of promoter activity statistics from reporter protein population snapshot data". In *Proceedings of the 54th IEEE Conference on Decision and Control* (Osaka, December 15-18, 2015).

E.C., "Reconstructing statistics of promoter switching from reporter protein population snapshot data". In *Proceedings of the 4th International Workshop on Hybrid Systems Biology* (Madrid, September 4-5, 2015), Lecture Notes in Bioinformatics (LNBI) 9271:3–19, Springer.

L.R.M. Maruthi, I.Tkachev, A.Carta, **E.C.**, P.Hersen, G.Batt, A.Abate, "Towards real-time control of gene expression at the single cell level: A stochastic control approach". In *Proceedings of the 12th International Conference on Computational Methods in Systems Biology* (Manchester, November 17-19, 2014), Lecture Notes in Computer Science (LNCS) 8859:155–172, Springer.

A.Gonzalez, J.Uhlendorf, J.Schaul, **E.C.**, G.Batt, G.Ferrari-Trecate, "Identification of biological models from single-cell data: A comparison between mixed-effects and moment-based inference". In *Proceedings of the 12th European Control Conference* (ECC, Zurich, Switzerland, July 17-19, 2013).

A.Carta, **E.C.**, "State estimation for gene networks with intrinsic and extrinsic noise : A case study on *E.coli* arabinose uptake dynamics". In *Proceedings of the 12th European Control Conference* (ECC, Zurich, Switzerland, July 17-19, 2013).

S.Berthoumieux, D.Kahn, H.de Jong, **E.C.**, "Structural and practical identifiability of approximate metabolic network models". In *Proceedings of the 16th IFAC symposium on System Identification* (Brussels, July 11-13, 2012), IFAC Proceedings Volumes 45(16):1719–1724, 2012.

R.Porreca, **E.C.**, J.Lygeros, G.Ferrari-Trecate, “Learning the structure of genetic network dynamics: A geometric approach”. In *Proceedings of the 18th IFAC World Congress*, (Milano, Italy, August 28 – September 2, 2011), IFAC Proceedings Volumes 18(1):11654–11659.

R.Porreca, **E.C.**, J.Lygeros, G.Ferrari-Trecate, “Structural identification of unate-like genetic network models from time-lapse protein concentration measurements”. In *Proceedings of the 49th IEEE Conference on Decision and Control* (Atlanta, GA, USA, December 15-17 2010), 2529–2534.

P.Hokayem, **E.C.**, D.Chatterjee, F.Ramponi, J.Lygeros, “Stochastic receding horizon control with output feedback and bounded control inputs”. In *Proceedings of the 49th IEEE Conference on Decision and Control* (Atlanta, GA, USA, December 15-17, 2010), 6095–6100.

P.Hokayem, **E.C.**, D.Chatterjee, J.Lygeros, “Stochastic MPC with imperfect state information and bounded controls”. In *Proceedings of the UKACC International Conference on Control* (Coventry, UK, September 2010).

E.C., R.Porreca, J.Lygeros, G.Ferrari-Trecate, “Canalizing structure of genetic network dynamics: Modelling and identification via mixed-integer programming”. In *Proceedings of the 48th IEEE Conference on Decision and Control* (Shanghai, China, December 2009), 5618–5623.

D.Chatterjee, **E.C.**, G.Chaloulos, J.Lygeros, “On stochastic control up to a hitting time”. In *Proceedings of the 48th IEEE Conference on Decision and Control* (Shanghai, China, December 2009), 531–536.

D.Chatterjee, **E.C.**, J.Lygeros, “Probabilistic regulation in stochastic hybrid systems subject to safety constraints”. In *Proceeding of the IFAC Conference on Analysis and Design of Hybrid Systems* (Zaragoza, Spain, September 2009), IFAC Proceedings Volumes 42(17):286–291, 2009.

M.Agarwal, **E.C.**, D.Chatterjee and J.Lygeros, “On convexity of stochastic optimization problems with constraints”. In *Proceedings of the 10th European Control Conference* (ECC, Budapest, Hungary, August 2009), 2827–2832.

E.C., A.Milias-Argeitis, S.Summers, J.Lygeros, “Local identification of piecewise deterministic models of genetic networks”. In *Proceedings of the 12th Hybrid Systems: Computation and Control conference* (2009), R.Mujumdar and P.Tabuada Eds., Lecture Notes in Computer Science, 5469:105–119, Springer.

E.C., V.Roukos, Z.Lygerou, J.Lygeros, “Numerical analysis of FRAP experiments for DNA replication and repair”. In *Proceedings of the 47th IEEE Conference on Decision and Control* (Cancun, Mexico, December 2008), 155–160.

E.C., A.Milias-Argeitis, J.Lygeros, “Identification of Genetic Regulatory Networks: A Stochastic Hybrid Approach”. In *Proceedings of the 17th IFAC World Congress* (Seoul, Korea, July 2008), IFAC Proceedings Volumes 41(2):301–306, 2008.

E.C., R.Porreca, G.Ferrari-Trecate, J.Lygeros, “A general framework for the identification of jump Markov linear systems”. In *Proceedings of the 46th IEEE Conference on Decision and Control* (New Orleans, USA, December 2007), 5737–5742.

E.C., R.Porreca, G.Ferrari-Trecate, J.Lygeros, “Parameter identification for stochastic hybrid models of biological interaction networks”. In *Proceedings of the 46th IEEE Conference on Decision and Control* (New Orleans, USA, December 2007), 5180–5185.

K.Koutroumpas, **E.C.**, J.Lygeros, “Randomized optimization methods in parameter identification for biochemical network models”. In *Proceedings of the 2nd Foundations of Systems Biology in Engineering conference* (September 2007).

E.C., G.Picci, “Identification of wood rings from sparse tomographic data”. In *Proceedings of the 45th IEEE Conference on Decision and Control* (San Diego, USA, December 2006), 3706–3711.

E.C., M.Micheli, G.Picci, “Fault detection in a class of stochastic hybrid systems”. In *Proceedings of the 43rd IEEE Conference on Decision and Control* (Paradise Island, Bahamas, December 2004), 3197–3203.

E.C., M.Micheli, G.Picci, "State estimation and prediction in a class of stochastic hybrid systems". In *Proceedings of the 16th International Symposium on Mathematical Theory of Networks and Systems* (July 2004), 254.

Theses:

E.C., *Identification, estimation and control of gene expression and metabolic network dynamics.* Habilitation à Diriger des Recherches, École Doctorale MSTII, Université Grenoble-Alpes, France, November 2019.

E.C., *Estimation problems in jump Markov systems.* Ph.D. Thesis (Supervisor: Prof. G.Picci), Department of Information Engineering, University of Padova, Italy, February 2005.

E.C., *Approccio Bayesiano alla deconvoluzione mediante wavelets* (Bayesian approach to deconvolution using wavelets). Laurea Thesis (Supervisor: Prof. G.Picci), University of Padova, Italy, July 2001.

Montbonnot, August 7, 2025

Eugenio Cinquemani