

## *Curriculum Vitae*

EUGENIO CINQUEMANI

Birth in 1976, Italian

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*Languages:* Italian (mother tongue), English (fluent), French (fluent), Spanish (basic)

*Research interests:* Modelling, analysis and identification of biological systems  
Identification, estimation and control for stochastic and switching systems  
Statistical signal processing

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## CURRENT AND PREVIOUS POSITIONS

**since Nov 2009: Research scientist** (“Chargé de Recherche”), Inria Grenoble–Rhône-Alpes, France (Project-Team IBIS)

**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

**Oct 2014: Scientific qualification for associate professorship in automation** (“Abilitazione Scientifica Nazionale”), Italy (sector 09/G1, until Oct 7, 2020)

**Dec 2002: Professional qualification for engineering** (“Esame di Stato”), Italy (score 120/120)

## ACADEMIC FORMATION

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

**Sep 1995 – Jul 2001: Laurea degree** 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

### National and international projects:

- MEMIP: “Mixed-Effects Models of Intracellular Processes : Methods, Tools and Applications” (ANR Société de l'information et de la communication, France), principal investigator (2017-ongoing).

- Maximic: “Optimal control of microbial cells by natural and synthetic strategies’ ” (ANR Société de l’information et de la communication, France), participant (2017-ongoing)
- RESET: “Arrest and restart of the gene expression machinery in bacteria: from mathematical models to biotechnological applications” (Investissements d’Avenir, Bioinformatique, France), participant (2012).
- GemCO: “Model reduction, experimental validation, and control for the gene expression machinery in *E.coli*” (ANR Blanc, France), participant (2010).
- ColAge: “Natural and engineering solutions to the control of bacterial growth and aging” (INRIA-INSERM Large-Scale Initiative Action), participant (2009-2010).
- MetaGenoReg: “Towards an understanding of the interrelations between metabolic and gene regulation: *E.coli* carbon metabolism as a test case” (ANR Biologie Systémique, France), participant (2009-2010).
- YeastX: “Towards an understanding of nutrient signalling and metabolic operation” (SystemsX.ch, Switzerland), participant (2009).
- HYGEIA: “Hybrid systems for biochemical network modelling and analysis” (NEST-4995, European Community), participant (2006-2007).
- RECSYS: “Real-time hybrid estimation and identification algorithms for distributed sensor data processing” (IST-2001-32515, European Community), participant (2003-2005).

#### Other projects:

- CoSy: “Real-time control of synthetic microbial communities” (Inria Project-Lab), project leader (2017-ongoing).
- CoSoft: “Control software for a system of mini-bioreactors” (Inria Action de Développement Technologique), project leader (2017-ongoing).

## STUDENT SUPERVISION

#### Ph.D. theses:

- D.Stefan, “Structural and parametric identification of bacterial regulatory networks” (co-supervision), Inria Grenoble–Rhône-Alpes, Sep 2010-Jun 2014.
- A.M.Gonzalez-Vargas (visiting student), “Design, implementation and testing of identification algorithms for stochastic mixed-effects models of gene expression from single-cell data”, Inria Grenoble–Rhône-Alpes, Jan-Aug 2014.

#### Master theses:

- N.Simeone, “Identification of mixed-effects models of arabinose uptake dynamics in *E.coli*”, Team IBIS, INRIA Grenoble–Rhône-Alpes, October 2011-March 2012.
- A.Shivanandan, “Stochastic modelling and identification of gene expression dynamics in *E.coli*”, Team IBIS, INRIA Grenoble–Rhône-Alpes, October 2010-July 2011.
- E.Balello, “Classificazione e riconoscimento di segnali transienti nel rivelatore Auriga mediante espansioni wavelet” (Classification and recognition of transient signals in the Auriga detector by wavelet expansions, Laurea, with Prof.A.Beghi), Department of Information Engineering, University of Padova, Italy, 2003
- L.Huber and C.Frischknecht, “Modeling and identification of inertial parameters of a SCARA robot” (with Prof.J.Lygeros), Automatic Control Laboratory, ETH Zürich, Switzerland, 2008

## TEACHING ACTIVITIES

### Full courses:

- “Statistics for Systems Biology” (48 hours), in Master on Approches Interdisciplinaires du vivant (AIV) of Universities Paris Diderot and Decartes, Centre Recherches Interdisciplinaires (CRI) Paris, 2013 – 2017.

### Lectures:

- “Modelling and identification of metabolic networks” (4 hours), in Master course “Modelling in Systems Biology” at Phelma, Grenoble INP, 2014 – 2018.
- “Identification of dynamical models of genetic networks” (6 hours), in Master course “Modélisation de réseaux géniques et métaboliques” (Modelling of genetic and metabolic networks) at INSA Lyon, 2010 – 2017.
- “Modeling of stochastic gene expression” (4 hours), in Ph.D. school “Advanced Lecture Course on Computational Systems Biology”, Aussois, France, 2017.
- “Identification of biological systems” (4 hours), in Ph.D. school “Systems Biology”, Bertinoro, Italy, July 2013.
- “New approaches to Bayesian estimation of signals: denoising, regularization networks and wavelets” (12 hours, with Prof. G.Picci), Department of Information Engineering, University of Padova, Italy, 2002.

### Teaching assistance:

- “Linear Systems Theory” (Prof. J.Lygeros), Department of Information Technology and Electrical Engineering, ETH Zürich, Switzerland, 2008 – 2009.
- “Controllo dei processi” (Process control, Prof. G.Picci), Department of Information Engineering, University of Padova, Italy, 2005 – 2006.
- “Fondamenti di Automatica” (Foundations of Automatic Control, Prof. M.Bisiacco), Department of Information Engineering, University of Padova, Italy, 2004.
- “Identificazione dei modelli e analisi dei dati” (Stochastic filtering and system identification, Prof. G.Picci and Prof. S.Pinzoni), Department of Information Engineering, University of Padova, Italy, 2003 – 2004.

## OTHER ACTIVITIES

**Organizer** of the “Fifth International Workshop on Hybrid Systems Biology (HSB)” (with A.Donzé), Grenoble, France, October 20-21, 2016

**Organizer** of the “Workshop on Identification and Control of Biological Interaction Networks” (with D.Ropers), INRIA Grenoble–Rhône-Alpes, February 8, 2011

**Associate editor** for the European Control Conference (ECC, 2013-2016)

**Program committee** member of Static Analysis & Systems Biology (SASB, 2016), Computational Methods in Systems Biology (CMSB, 2018)

## PUBLICATIONS

### Books:

- 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:

- H.de Jong, S.Casagrande, 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* (ISMB 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.Porra, **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*, 27(13)(ISMB 2011):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.Porra, **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.Porra, 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:

**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* (Zurich, 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* (Zurich, 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.Porra, **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.Porra, **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.Porra, 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* (Budapest, Hungary, August 2009), 2827–2832.
- E.C.**, A.Miliadis-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.Miliadis-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.Porra, 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.Porra, 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”. *Proceedings of the 16th International Symposium on Mathematical Theory of Networks and Systems* (July 2004), 254.

#### Theses:

- 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, May 24, 2018

*Eugenio Cinquemani*