

Grégory BATT

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Born: February 23, 1977

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MAIN RESEARCH INTERESTS

Development and application of computational methods for the understanding of the behavior of biological systems. In particular,

- **analysis and control of natural biological systems (systems biology) and**
- **design and optimization of novel, useful biological systems (synthetic biology)**

EDUCATION

- 2014 **Habilitation à Diriger des Recherches (HDR) in Systems Biology** at the Université Paris Diderot (Paris, France). Design, optimization and control in systems and synthetic biology
Jury: V. Danos (Edinburgh U), F. Devaux (Paris5 U), H. de Jong (Inria), O. Gandrillon (CNRS), M. Khammash (ETH Zurich), and R. Veitia (Paris7 U)
- 2006 **PhD in computer science** at the Université Joseph Fourier (Grenoble, France). Validation of qualitative models of genetic regulatory networks: A method based on formal verification techniques
Jury: G. Bernot (Evry U), H. de Jong (Inria, dir), J. Geiselman (Grenoble U), N. Halbwachs (Grenoble U), J. Lygeros (ETH Zurich), D. Thiéffry (Marseille U)
- 2002 *DEA Informatique: Systèmes et Communication* at the Université Joseph Fourier
- 2001 *Licence of the Magistère d'Informatique et Modélisation* at the Ecole Normale Supérieure de Lyon (ENS Lyon, France)
- 2000 **Maîtrise of the Magistère de Biologie Moléculaire et Cellulaire** at ENS Lyon.
ERASMUS student at Uppsala University (Sweden)
- 1999 *Licence of the Magistère de Biologie Moléculaire et Cellulaire* at ENS Lyon
- 1998 General scientific preparation (*BioMathSup* and *BioMathSpé*) for the *Grandes Ecoles* at the Lycée P. de Fermat in Toulouse (France). Admitted to the Institut National Agronomique de Paris-Grignon and to ENS Lyon

RESEARCH EXPERIENCE

- since 01/2016 **Co-head of Lifeware research group at Inria Saclay - Ile-de-France**
- 10/2007 - 12/2015 **Research scientist at Inria Paris-Rocquencourt** in the Contraintes and Lifeware research groups. Tenured position. Hired CR2 and promoted CR1 in Oct. 2009
- 01/2007 - 09/2007 **Postdoctoral researcher: *Timed abstractions of continuous dynamical systems with applications to gene network analysis***, at Institut National Polytechnique de Grenoble in the Verimag research center (France)
- 12/2005 - 12/2006 **Postdoctoral researcher: *Rational design of synthetic gene networks using formal analysis of hybrid systems***, in Center for Information and Systems Engineering and Center for BioDynamics at Boston University (USA)
- 09/2002 - 11/2005 **PhD student: *Validation of qualitative models of genetic regulatory networks: a method based on formal verification techniques***, at Inria Rhône-Alpes (France), under supervision of H. de Jong
- 01/2002 - 08/2002 **Lab training period (DEA Info): *Validation of genetic regulatory network models***, at Inria Rhône-Alpes, under supervision of H. de Jong
- 06/2001 - 08/2001 **Lab training period (Licence Info): *Representation of protein/protein interactions in qualitative models of genetic regulatory networks***, at Inria Rhône-Alpes, under supervision of H. de Jong
- 06/1999 - 08/1999 **Lab training period (Licence Bio): *Discovering interactions between cytoskeletal proteins using double hybrid techniques***, at the Institut de Pharmacologie et de Biologie Structurale (Toulouse, France), under supervision of L. Mazzolini

TEACHING EXPERIENCE

- since 09/2009 **Computational biology** (48h) in Master Approches Interdisciplinaires du Vivant of Paris Descartes and Diderot Universities. Coordinator since 2011
- since 09/2008 **Computational methods for systems and synthetic biology** (12h) in Master Parisien de Recherche en Informatique of Paris 7 Univ., Ecoles Normales Supérieures of Paris and Cachan, and Ecole Polytechnique
- since 09/2012 **Dynamical Modelling of Cellular Regulatory Networks** (6h) in Master of Biology of Cellular Systems at Ecole Normale Supérieure of Paris
- 09/2002 - 08/2005 Teaching assistant in computer science at the Université Joseph Fourier (3*64h):
- introduction to programming in *Licence Sciences et Technologies*
- modeling and simulation of genetic regulatory networks in *Master Sciences, Technologies et Santé* (lab)

Member of the scientific committee and teacher (6h) at Advanced Lecture Course on Computational Systems Biology (Aussois, summer 2015). Participant (2014) and Mentor (2015) of *Teaching through Research* leadership program workshops (CRI, Paris). Interventions in summer schools *Scientific Trends at the Interfaces: biomathematics-bioinformatics* (8h, Roscoff, France, 2012) and *Informatique Fondamentale* (2h, ENS Lyon, France, 2011).

PROJECT COORDINATION

- **From synthetic networks to artificial tissues** (Syne2Arti), Cosinus ANR Grant (10/2010-03/2014), with **G. Batt** (Coord., Inria), D. Drasdo (Inria), O. Maler (Verimag), and R. Weiss (MIT)
- **From population models to model populations: single cell observation, modeling, and control of gene expression** (Iceberg), Investissement d'Avenir ANR Grant (10/2011-09/2017), with **G. Batt** (Coord., Inria), P. Hersen (MSC, CNRS/Paris7), O. Gandrillon

(BM2A, CNRS/Lyon1), C. Lhoussaine (LIFL, CNRS/Lille1), R. Veitia (IJM, CNRS/Paris7), and J. Krivine (PPS, CNRS/Paris7)

- **Artificial tissue homeostasis: combining synthetic and computational biology approaches** (TisHom), Inria/MIT Associated team (starting 01/2012), shared coordination with Prof. Ron Weiss (MIT)
- **Formal probabilistic approaches for robust control of gene expression**, van Gogh grant (01/2012-12/2013), shared coordination with Prof. Alessandro Abate (TU Delft, now Oxford Univ.)

PUBLICATIONS

Journal impact factors (IF) and conference acceptance rates (AR) are given when available.

International peer-reviewed articles

- A. Llamosi, A.M. Gonzalez-Vargas, C. Versari, E. Cinquemani, G. Ferrari-Trecate*, P. Hersen*, and **G. Batt*** (2016), What population reveals about individual cell identity: parameter variability in yeast gene expression, *PLoS Computational Biology*, 12(2): e1004706. (IF: 4.62) *Co-corresponding authors.
- S. Bogomolov, C. Schilling, E. Bartocci, **G. Batt**, H. Kong, and R. Grosu (2015), Abstraction-based parameter synthesis for multiaffine systems, in 11th International Haifa Verification Conference, HVC 2015, p.19-35. Springer (AR: 50%)
- X. Duportet*, L. Wroblewska, P. Guye, Y. Li, J. Eyquem, J. Rieders, **G. Batt*** and R. Weiss* (2014), A platform for rapid prototyping of synthetic gene networks in mammalian cells, *Nucleic Acids Research*, 42(21):13440-51. (IF: 8.81) *Co-corresponding authors.
- F. Bertaux, S. Stoma, D. Drasdo, and **G. Batt*** (2014), Modeling dynamics of cell-to-cell variability in TRAIL-induced apoptosis explains fractional killing and predicts reversible resistance, *PLoS Computational Biology*, 10(10):e1003893. (IF: 4.83) *Corresponding author.
- L. Maruthi, I. Tkachev, A. Carta, E. Cinquemani, P. Hersen, **G. Batt***, A. Abate* (2014), Towards real-time control of gene expression at the single cell level: a stochastic control approach, *Computational Methods in Systems Biology, CMSB'14*, LNCS/LNBI, Springer, 155-172. (AR: 50%) *Co-corresponding author.
- S. Stoma, A. Donzé, F. Bertaux, O. Maler, **G. Batt*** (2013), STL-based analysis of TRAIL-induced apoptosis challenges the notion of type I/type II cell line classification, *PLoS Computational Biology*, 9(5):e1003056. (IF: 5.22) *Corresponding author.
- A.M. Gonzalez, J. Uhlendorf, J. Schaul, E. Cinquemani, **G. Batt**, G. Ferrari-Trecate (2013), Identification of biological models from single-cell data: a comparison between mixed-effects and moment-based inference, in *12th European Control Conference, ECC'13*
- N.D. Mendes, F. Lang, Y.S. Le Cornec, R. Mateescu, **G. Batt**, and C. Chaouiya (2013), Composition and abstraction of logical regulatory modules: application to multicellular systems, *Bioinformatics*, 29(6):749-757 (IF: 5.47)
- J. Uhlendorf, A. Miermont, T. Delaveau, G. Charvin, F. Fages, S. Bottani, **G. Batt*** and P. Hersen* (2012), Long-term model predictive control of gene expression at the population and single-cell levels, *PNAS*, 109(35):14271-14276. (IF: 9.68) *Co-corresponding author.
- A. Rizk, **G. Batt**, F. Fages and S. Soliman (2011), Continuous valuations of temporal logic specifications with applications to parameter optimization and robustness measures, *Theoretical Computer Science*, 412(26):2827-2839 (IF: 0.84)
- J. Uhlendorf, P. Hersen, and **G. Batt*** (2011), Towards real-time control of gene expression: *in silico* analysis, in *18th IFAC World Congress, IFAC WC'11*. *Corresponding author.
- J. Uhlendorf, S. Bottani, F. Fages, P. Hersen*, and **G. Batt*** (2011), Towards real-time control of gene expression: controlling the HOG signaling cascade, in *16th Pacific Symposium of Biocomputing, PSB'2011*, 16:338-349. *Co-corresponding author.
- R. Grosu, **G. Batt**, F. Fenton, J. Glimm, C. Le Guernic, S.A. Smolka, and E. Bartocci (2011), From cardiac cells to genetic regulatory networks, in *23rd International Conference*

on *Computer Aided Verification, CAV'11*, Lecture Notes in Computer Science 6806, Springer-Verlag, pp. 396-411. (AR: 22%)

- **G. Batt***, M. Page, I. Cantone, G. Goessler, P. Monteiro and H. de Jong (2010), Efficient parameter search for qualitative models of regulatory networks using symbolic model checking, *Bioinformatics*, ECCB10 Special Issue, 26(18):i603-i610 (IF: 4.33; AR: 17%).*Corresponding author.
- A. Rizk, **G. Batt***, F. Fages and S. Soliman (2009), A general computational method for robustness analysis with applications to synthetic gene networks, *Bioinformatics*, ISMB09 Special Issue, 25(12):i169-i178.
- A. Rizk, **G. Batt**, F. Fages and S. Soliman (2008), On a continuous degree of satisfaction of temporal logic formulae with applications to systems biology, in M. Heiner and A.M. Uhrmacher, eds., *Sixth International Conference on Computational Methods in Systems Biology, CMSB'08*, Lecture Notes in Computer Science 5307, Springer-Verlag, 251-268. (AR: 33%)
- O. Maler and **G. Batt** (2008), Approximating continuous systems by timed automata, in J. Fisher, ed., *First International Workshop on Formal Methods in Systems Biology, FMSB'08*, Lecture Notes in Computer Science 5054, Springer-Verlag, pp. 77-89
- **G. Batt**, R. Ben Salah and O. Maler (2008), On timed models of gene networks, in J.-F. Raskin and P.S. Thiagarajan, eds., *Fifth International Conference on Formal Modeling and Analysis of Timed Systems (FORMATS'07)*, Lecture Notes in Computer Science, Springer-Verlag. (AR: 45%)
- **G. Batt***, C. Belta and R. Weiss (2008), Temporal logic analysis of gene networks under parameter uncertainty, joint special issue on Systems Biology of *IEEE Transactions on Circuits and Systems* and *IEEE Transactions on Automatic Control*, 53:215-229. (IF: 2.77/1.139, 2006). *Corresponding author.
- **G. Batt**, H. de Jong, M. Page and J. Geiselmann (2007), Symbolic reachability analysis of genetic regulatory networks using qualitative abstractions, *Automatica*, 44(4):982-989. (IF: 2.27)
- **G. Batt***, B. Yordanov, C. Belta and R. Weiss (2007), Robustness analysis and tuning of synthetic gene networks, *Bioinformatics*, 23(18):2415-2422. (IF: 4.89, 2006). *Corresponding author.
- **G. Batt**, C. Belta and R. Weiss (2007), Model checking genetic regulatory networks with parameter uncertainty, in A. Bemporad, A. Bicchi and G. Buttazzo, eds., *Tenth International Workshop on Hybrid Systems: Computation and Control (HSCC'07)*, Lecture Notes in Computer Science 4416, Springer-Verlag, pp. 61-75. (AR: 25%)
- **G. Batt**, C. Belta and R. Weiss (2007), Model checking liveness properties of genetic regulatory networks, in O. Grumberg and M. Huth, eds., *Thirteenth International Conference on Tools and Algorithms for the Construction and Analysis of Systems (TACAS'07)*, Lecture Notes in Computer Science 4424, Springer-Verlag, pp. 323-338. (AR: 26%)
- B. Yordanov, **G. Batt** and C. Belta (2007), Model checking discrete-time piecewise affine systems: application to gene networks, in M. Athans, ed., *European Control Conference (ECC'07)*, Kos, Greece.
- **G. Batt**, D. Ropers, H. de Jong, J. Geiselmann, R. Mateescu, M. Page and D. Schneider (2005), Validation of qualitative models of genetic regulatory networks by model checking: Analysis of the nutritional stress response in *Escherichia coli*, *Bioinformatics*, 21(Suppl 1):i19-i28. (IF: 6.02)
- **G. Batt**, D. Ropers, H. de Jong, J. Geiselmann, R. Mateescu, M. Page and D. Schneider (2005), Analysis and verification of qualitative models of genetic regulatory networks: A model-checking approach, in L.P. Kaelbling and A. Saffiotti, eds., *Nineteenth International Joint Conference on Artificial Intelligence (IJCAI'05)*, Edinburgh, Scotland, 370-375. (AR: 18%)
- **G. Batt**, D. Ropers, H. de Jong, J. Geiselmann, M. Page and D. Schneider (2004), Qualitative analysis and verification of hybrid models of genetic regulatory networks: Nutritional stress response in *Escherichia coli*, in M. Morari and L. Thiele, eds., *Eighth International Workshop on Hybrid Systems: Computation and Control (HSCC'05)*, Lecture Notes in Com-

puter Science 3414, Springer-Verlag, 134-150. (AR: 44%)

- **G. Batt**, D. Bergamini, H. de Jong, H. Garavel and R. Mateescu (2004), Model checking genetic regulatory networks using GNA and CADP, in S. Graf and L. Mounier, eds., *Eleventh International SPIN Workshop on Model Checking Software (SPIN'04)*, Lecture Notes in Computer Science 2989, Springer-Verlag, 158-163. (AR: 40%)
- H. de Jong, J. Geiselmann, **G. Batt**, C. Hernandez and M. Page (2004), Qualitative simulation of the initiation of sporulation in *Bacillus subtilis*, *Bulletin of Mathematical Biology*, 66(2):261-300. (IF: 1.48)

Book chapters

- J. Uhlendorf, A. Miermont, T. Delaveau, G. Charvin, F. Fages, S. Bottani, P. Hersen and **G. Batt** (2015), In silico control of biomolecular processes, in M. Marchisio, ed, *Computational Methods in Synthetic Biology*, Methods in Molecular Biology Series, Humana (Springer), pp 277-285.
- **G. Batt**, B. Besson, P.-E. Ciron, H. de Jong, E. Dumas, J. Geiselmann, R. Monte, P.T. Monteiro, M. Page, F. Rechenmann, and D. Ropers (2012), Genetic Network Analyzer: A tool for the qualitative modeling and simulation of bacterial regulatory networks, in J. van Helden, A. Toussaint and D. Thieffry, eds, *Bacterial Molecular Networks*. Springer, pp 439-462.
- **G. Batt**, R. Casey, H. de Jong, J. Geiselmann, J.-L. Gouzé, M. Page, D. Ropers, T. Sari and D. Schneider (2005), Qualitative analysis of the dynamics of genetic regulatory networks using piecewise-linear models, in E. Pecou, S. Martinez and A. Maass, eds., *Mathematical and Computational Methods in Biology*. Hermann, pp 206-239.

International workshops and national journals and conferences (peer-reviewed)

- **G. Batt**, H. de Jong, J. Geiselmann, J.-L. Gouzé, M. Page, D. Ropers, T. Sari and D. Schneider (2007), Analyse qualitative de la dynamique de réseaux de régulation génique par des modèles linéaires par morceaux, *Technique et sciences informatiques*, numéro spécial Post-génomique, 26(1-2):11-45.
- **G. Batt**, B. Yordanov, C. Belta and R. Weiss (2007) Robustness analysis and tuning of synthetic gene networks, in C. Brun and G. Didier, eds., *Working Notes of the Journées Ouvertes Biologie, Informatique et Mathématiques (JOBIM'07)*, Marseille, France.
- **G. Batt**, C. Belta and R. Weiss (2006), Robustness analysis and tuning of synthetic gene networks with parameter uncertainties, in *Cold Spring Harbor conference on Engineering Principles in Biological Systems*, 62, Cold Spring Harbor, NY, USA. (AR:< 35%)
- **G. Batt**, D. Ropers, H. de Jong, J. Geiselmann, R. Mateescu, M. Page and D. Schneider (2005), Analysis and verification of qualitative models of genetic regulatory networks: A model-checking approach, in F. Hofbauer, B. Rinner and F. Wotawa, eds., *Working Notes of the Nineteenth International Workshop on Qualitative Reasoning (QR'05)*, Graz, Austria.
- **G. Batt**, D. Ropers, H. de Jong, J. Geiselmann, R. Mateescu, M. Page and D. Schneider (2005), Validation of qualitative models of genetic regulatory networks by model checking: Analysis of the nutritional stress response in *Escherichia coli*, in G. Perrière, A. Guénoche and C. Geourjon, eds., *Working Notes of the Journées Ouvertes Biologie, Informatique et Mathématiques (JOBIM'05)*, 471-482, Lyon, France.
- **G. Batt**, H. de Jong, J. Geiselmann and M. Page (2003), Analysis of genetic regulatory networks: A model-checking approach, in B. Bredeweg and P. Salles, eds., *Working Notes of the Seventeenth International Workshop on Qualitative Reasoning (QR'03)*, 31-38, Brasilia, Brazil.
- **G. Batt**, H. de Jong, J. Geiselmann and M. Page (2003), Analysis of genetic regulatory networks: A model-checking approach, in M. Benerecetti and C. Pecheur, eds., *Working Notes of the Second International Workshop on Model Checking and Artificial Intelligence (MoChArt'03)*, 51-58, Acapulco, Mexico.

PhD and HDR thesis

- **G. Batt** (2014). Design, optimization and control in systems and synthetic biology, Habilitation à Diriger des Recherches in Systems Biology, Paris Diderot University, Paris, France
- **G. Batt** (2006). Validation of qualitative models of genetic regulatory networks: A method based on formal verification techniques, PhD Thesis in Computer Science. Joseph Fourier University, Grenoble, France

Research reports

- F. Bertaux, S. Stoma, D. Drasdo, and **G. Batt** (2014), Dynamics of cell-to-cell variability in TRAIL-induced apoptosis explains fractional killing and predicts reversible resistance, Technical Report Hal-00942885, Inria Paris-Rocquencourt.
- S. Stoma, A. Donzé, F. Bertaux, O. Maler and **G. Batt** (2012), STL-based analysis of TRAIL-induced apoptosis challenges the notion of type I/type II cell line classification, Technical Report RR-8121, Inria Paris-Rocquencourt.
- **G. Batt** and C. Belta (2006), Model checking genetic regulatory networks with applications to synthetic biology, Technical Report 2006-IR-0030, CISE Boston University.
- **G. Batt**, H. de Jong, J. Geiselmann, M. Page, D. Ropers and D. Schneider (2004), Symbolic reachability analysis of genetic regulatory networks using qualitative abstraction, Technical Report RR-5362, Inria Rhône-Alpes.
- **G. Batt** (2002). Représentation des interactions protéine/protéine dans la cadre d'une méthode de modélisation de réseaux géniques, Technical Report RR-4382, Inria Rhône-Alpes.

TOOLS

- **CellStar**: Long-term tracking of single cells from brightfield microscopy images. Joint work with P. Hersen, A. Llamosi, S. Stoma, K. Batmanov, C. Lhoussaine and C. Versari
- **RoVerGeNe**, version **3.0**, for the robust verification of gene networks. Joint work with C. Belta (Boston University).
- **Genetic Network Analyzer**, version **6.0**, for the verification of dynamical properties of genetic regulatory networks. Joint work with H. de Jong and M. Page (Inria Rhône-Alpes).

INVITED TALKS (SELECTED)

- What population reveals about individual cell identity: Single-cell parameter estimation of models of gene expression in yeast, 3rd International Workshop on Synthesis of Complex Parameters, Eindhoven, The Netherlands, Apr 2016
- A multi-scale model for investigating TRAIL resistance in multi-cellular tumor spheroids, Seminar at Department of Biosystems Science and Engineering of ETH Zurich, Basel, Switzerland, March 2016
- A multi-scale model for investigating TRAIL resistance in multi-cellular tumor spheroids, Seminar at Roche Innovation Center, Basel, Switzerland, March 2016
- What population reveals about individual cell identity: estimation of single-cell models of gene expression in yeast, Séminaire du LBMC at Laboratoire de Biologie et de Modélisation de la Cellule, ENS Lyon, Lyon, France, Oct 2015
- A multi-scale model for investigating TRAIL resistance in multi-cellular tumor spheroids, Seminar at Interdisciplinary Computing and Complex BioSystems group, Newcastle University, UK, May 2015
- What population reveals about individual cell identity: estimation of single-cell models of gene expression in yeast, Seminar at Interdisciplinary Computing and Complex BioSystems group, Newcastle University, UK, May 2015

- What population reveals about individual cell identity: estimation of single-cell models of gene expression in yeast, Seminar in Pecreaux Group at Institut de Génétique et Développement de Rennes, Rennes, France, Feb 2015
- What population reveals about individual cell identity: parameter variability in yeast gene expression, short talk in *Integrative cell models: Bridging microbial physiology and systems biology*, Leiden, Netherlands, Jan 2015
- Multi-scale modeling of TRAIL-induced apoptosis: From protein level fluctuations to drug resistance in multicellular spheroids, in *Symbiose seminar at IriSa*, Rennes, Oct 2014
- Cells driven by computers: long-term model predictive control of gene expression in yeast, in seminar of *Laboratoire d'Ingénierie des Systèmes Biologiques et des Procédés*, Toulouse, Sept 2014
- Cells driven by computers: long-term model predictive control of gene expression in yeast, keynote address in *Hybrid Systems: Computation and Control conference (HSCC'14)*, Berlin, Apr 2014
- Cells driven by computers: long-term model predictive control of gene expression in yeast, in *Interdisciplinary seminar of Biologie Computationnelle et Quantitative lab*, Paris, Apr 2014
- Cells driven by computers: long-term model predictive control of gene expression in yeast, in *Sanofi Pharmacometry & Bioinformatics Day*, Chilly-Mazarin, Dec 2013
- Comprendre et contrôler le fonctionnement des cellules: apport de la biologie computationnelle, *Seminar Groupement de recherche interdisciplinaire sur les systèmes biologiques (Grisbi)*, Montpellier, Oct 2013
- Cells driven by computers, *Franco-British Symposium on Synthetic Biology*, French Embassy, London, Oct 2013
- Modeling intrinsic and extrinsic variability: models, model identification methods and noise conversion, *Haredhol seminar*, ENS Paris, Paris, April 2013
- Long-term model predictive control of gene expression, in *Bison seminar*, ETHZ, Zurich, March 2013
- Comprendre et contrôler le fonctionnement des cellules: apport de la biologie computationnelle, in *Colloque Perspectives en biologie de synthèse*, Paris, Dec. 2012
- Long-term model predictive control of gene expression at the population and single-cell levels, in *Model-based analysis and control of cellular processes workshop*, Purdue University, Purdue, Oct. 2012
- Contrôle de l'expression des gènes en temps réel, in *Naturel et artificiel: le vivant et ses représentations*, *Ecole thématique interdisciplinaire de Berder*, Berder, Apr. 2012
- Modeling and analysis in synthetic biology: dealing with parameter uncertainties, in *Vasy team seminar*, Autrans, Nov 2011
- Robustness analysis and tuning of synthetic gene networks, in *Computing department seminar*, NUS school of computing, Singapore, Nov. 2011
- Real-time control of gene expression: in silico analysis, in *Automatique des systèmes hybrides group seminar*, Supelec Rennes, Oct 2011
- Efficient parameter search for qualitative models of regulatory networks, in *Modèles et Analyse des Réseaux: Approches Mathématiques et Informatique* conference, Grenoble, Oct 2011
- Real-time control of gene expression, in *Biomolecular signaling and control group seminar*, ETHZ, Zurich, Oct 2011
- Computer-aided design of complex biological systems, in *Synthetic biology meeting of Société Française de Biologie*, Paris, Sept 2011
- Real-time control of gene expression, in *Computational biology group seminar*, Instituto Gulbenkian de Ciencia, Lisbon, May 2011
- Efficient parameter search for qualitative models of regulatory networks, in *Rule-based modeling and application to biomolecular networks*, Ecole de recherche d'hiver en informatique fondamentale, ENS Lyon, Feb 2011

- Towards real-time control of gene expression: in silico analysis, in *Workshop on identification and control of biological interaction networks*, Grenoble, Feb 2011
- Parameter search for robust dynamical properties with applications to synthetic biology, in *séminaire d'informatique de l'ENS Lyon*, Sept. 2009, Lyon, France
- A general computational method for robustness analysis with applications to synthetic gene networks, in *Modelling and Analysis of Cell Behaviour*, Sept. 2009, Warwick, UK.
- A general computational method for robustness analysis with applications to synthetic gene networks, in *Hybrid Systems Approaches to Computational Biology (HSCB'09)*, Apr. 2009, San Francisco, USA.
- Quantitative robustness estimate of gene network properties, in *Workshop on discrete models of biological networks : from structure to dynamics*, Nov. 2008, Marseille, France.
- Quantitative robustness estimate of gene network properties, in *Workshop on bioinformatical modeling in biology and medicine*, Oct. 2008, Nice, France.
- Robustness analysis and tuning of synthetic gene networks, in *First French Workshop on Synthetic Biology*, March 2008, Paris, France.
- Robustness analysis and tuning of synthetic gene networks, in *Towards Systems Biology Workshop*, October 2007, Grenoble, France.
- Automatic tuning of synthetic gene networks, in *Workshop on Hybrid Systems Biology of Conference on Decision and Control, CDC'06*, December 2006, San Diego, CA, USA. (Presented by C. Belta)
- Validation of genetic regulatory network models, in *Workshop on Hybrid Systems Biology of Conference on Decision and Control, CDC'06*, December 2006, San Diego, CA, USA.
- Combining discrete abstraction and model checking for the analysis of partially-known models of natural and synthetic gene networks, in *MIT Bioinformatics Seminar*, October 2006, Cambridge, MA, USA.
- Formal verification of hybrid models of genetic regulatory networks, in *Dagstuhl Seminar on Verification and Simulation of Dynamic Systems*, May 2006, Schloss Dagstuhl, Germany.
- Validation of qualitative models of genetic regulatory networks by model checking: Analysis of the nutritional stress response in *E. coli*, in *Workshop on Computation of Biochemical Pathways and Genetic Networks*, September 2005, Heidelberg, Germany.
- Validation of qualitative models of genetic regulatory networks by model checking: Analysis of the nutritional stress response in *E. coli*, in *Workshop on Dynamical Modeling and Analysis of Biological Regulatory Networks*, May 2005, Marseille, France.
- Qualitative modeling and simulation of genetic regulatory networks, in *Minisymposium on Cell Biology with Control and System Theory of Conference on Mathematical Theory of Networks and Systems (MTNS'04)*, July 2004, Leuven, Belgium.

STUDENT SUPERVISION

- **François Bertaux** (2011-2015), PhD student, in cosupervision with D. Drasdo (Bang research group, Inria)
- **Artémis Llamosi** (2012-2015), PhD student, in cosupervision with P. Hersen (MSC lab, CNRS/Paris 7)
- **Jean-Baptiste Lugagne** (2012-2016), PhD student, in cosupervision with P. Hersen (MSC lab, CNRS/Paris 7)
- **Virgile Andréani** (2015-2016) Master student (ENS Paris / M2).

ALUMNI

- **Ewen Corre** (Spring 2016), Master student (M2) Approches Interdisciplinaires du Vivant, in cosupervision with P. Hersen and A. Llamosi.
- **Catherine Eisenhauer** (Fall 2015), Master student (M2) Approches Interdisciplinaires du

Vivant, in cosupervision with P. Hersen and J.-B. Lugagne.

- **Melanie Kirch** (Spring 2015), Master student (M2) at University Erlangen-Nuremberg, in cosupervision with P. Hersen and JB Lugagne (MSC lab, CNRS/Paris 7)
- **Agnes Koehler** (summer 2014), Master student (M1) at Technical University of Munich, in cosupervision with P. Hersen and JB Lugagne (MSC lab, CNRS/Paris 7)
- **Valentina Peschetola** (2013-2014), Postdoctoral researcher, with P. Hersen (MSC lab, CNRS/Paris 7).
- **Xavier Duportet** (2010-2014), PhD student, in cosupervision with R. Weiss (MIT). Thesis: Developing new tools and platforms for mammalian synthetic biology: from the assembly and chromosomal integration of large genetic circuits to the engineering of artificial intercellular communication systems, Nov 14, 2014. Jury: D. di Bernardo (Tigem), T. Lu (MIT), D. Mazel (Pasteur), F. Molina (CNRS), R. Veitia (Paris7 U). Now cofounder of PhageX company.
- **Ivy Uszynski** (summer 2014), M.Tech student of Phelma Grenoble, in cosupervision with P. Hersen and V. Peschetola (MSC lab, CNRS/Paris 7). Now Student at EPFL and INP Grenoble
- **Szymon Stoma** (2011-2013), Postdoctoral researcher. Now Data and Image Analysis Scientist at ETH-Zurich, Zurich
- **Jannis Uhlendorf** (2009-2013), PhD student, in cosupervision with P. Hersen (MSC lab, CNRS/Paris 7). Thesis: Real-time feedback control of gene expression, Apr 19, 2013. Jury: C. Dargemont (CNRS, Paris7), D. di Bernardo (Tigem), J. Lygeros (ETH Zurich), G.-B. Stan (Imperial), P. Silberzan (CNRS, Curie I). Now postdoctoral researcher in E. Klipp's group at Humboldt University, Berlin.
- **Zoran Marinkovic** (summer 2013), Master student, M2 AIV. Now PhD student in P. Hersen's group (MSC lab, CNRS/Paris 7).
- **Anne Loechner** (spring 2013), Master student, M1 AIV, cosupervision with P. Hersen and V. Peschetola. Now PhD student at Max-Planck Institute Marburg.
- **Joé Schaul** (summer 2012), Master student, M2 MPRI. Now in startup company in Berlin.
- **Hugues Asofa** (summer 2012), Master student, Ecole Polytechnique, cosupervision with S. Stoma. Now System Integration Engineer at Ansaldo STS, Paris.
- **Julianne Reiders** (spring 2012), Master student, M2 AIV, cosupervision with P. Hersen. Now Graduate Student at University of Pennsylvania.
- **Aishah Prastowo** (spring 2012), Master student, M2 AIV, cosupervision with P. Hersen and J. Uhlendorf. Now graduate student at Oxford University.
- **Gopalakrishnan Kumar** (Summer 2011), M.Tech student, IIT Bombay.
- **Thomas Murarasu** (Summer 2011), Master student, AgroParisTech. Now research engineer at Curie Institute, Paris.
- **Antoine Decrulle** (Winter 2010), Master student, M2 AIV. Now PhD student in A. Lindner's group (CRI, INSERM, Paris).
- **Xavier Duportet** (Fall 2009), Master student, M2 AIV. Now PhD student at Inria/MIT (co-supervision G. Batt/R. Weiss).
- **Shagun Jhaver** (Summer 2009), B.Tech student, IIT Bombay. Now Master Student in Computer Science at the University of Texas (Dallas).
- **Evan Harrell** (Spring 2009), Master student, M2 AIV. Now graduate student at Department of Physiology, Anatomy and Genetics, Oxford University.
- **Thomas Landrain** (Summer 2008), Master student, M2 AIV. Now PhD student in A. Jaramillo's group at Institute of Systems & Synthetic Biology (Evry).

SCIENTIFIC ANIMATION

- Organization of workshops
 - Design, optimization and control for systems and synthetic biology (2 days), ENS Paris,

- Paris, Nov 2015. 20 international speakers, 150 participants, 12 nationalities.
- Design, optimization and control for systems and synthetic biology (2 days), ENS Paris, Paris, June 2012. 15 international speakers, 200 participants, 14 nationalities.
 - Constructing gene networks: observation, analysis and control (1 day), Paris 7 Univ., Paris, January 2009. 10 contributed talks, 50 participants. Co-organized with S. Bottani (Paris 7).
 - Towards systems biology (3 days), Grenoble Univ., Grenoble, October 2007. 25 international speakers, 70 participants. Co-organized with O. Maler (Verimag).
- Participation in scientific committees
 - member of the IEEE/CSS Technical Committee on Systems Biology
 - member of the scientific board of the GDR de Biologie de Synthèse et des Systèmes, in charge of Integrative and predictive biology - Modelling
 - member of the GDR de Bioinformatique Moléculaire, in charge of Biological network modelling, systems biology and synthetic biology
 - member of the scientific committee of Advanced Lecture Course on Computational Systems Biology summer school
 - Participation in selection/evaluation committees
 - Member of recruitment committees at Inria (CR2, Rennes, 2016) and Evry University (assistant professor, 2009)
 - Member of project evaluation committees for EraSynBio1 (2014, Lisbon) and EraSynAPP2 (2015, Gothenburg)
 - Reviewer for project evaluation: EraSynAPP2 (2015), EraSynBio1 & 2 (2014, 2015), CNRS PEPS (2012), ANR JCJC (2008), NUS research grant (Singapore), and NWO (The Netherlands, 2008)
 - Reviewer and/or member of PhD committees of Adel Mezine (Evry Univ, Evry, 2016, rapporteur), Erwan Bigan (Polytechnique, Paris, 2015, rapporteur), Benjamin Gyori (D Hsu group, NUS, Singapore, Oct 2014), Santiago Videla (A. Siegel/T. Schaub groups, Inria Rennes, June 2014), Alejandro Vignoni (J. Pico group, Universitat Politècnica de Valencia, May 2014), Sucheendra Palaniappan (P.S. Thiagarajan group, NUS, Singapore, June 2013), Andreas Miliadis-Argeitis (J. Lygeros group, ETHZ, Zurich, March 2013), Filippo Menolascina (D. di Bernardo group, TIGEM, Naples, Jan 2012), Zohra Khalis (G. Bernot group, I3S/ Evry Univ., December 2010), and Jamil Ahmad (O. Roux group, MeForBio team, IRCCyN, Nantes, February 2009), of MSc committees of Lakshmeesh Maruthi (Abate Group, TU Delft, September 2013) and of Yifan Pan (Abate Group, TU Delft, September 2013), and of PhD advisory committees of Adrien Henry (laboratoire de génétique végétale du Moulon, Orsay, O. Martin) and of Géraldine Célière (Bang group, Inria Paris, D. Drasdo).
 - Judge at iGEM competitions in 2008 (Boston) and 2013 (Lyon).
 - Editorial and reviewing activities:
 - Member of program committee for computational biology conferences: FOSBE (2016), CMSB (2016, 2015), JOBIM (2009, 2012), HMSB/HSB (2011, 2012, 2014)
 - Reviewer for journal and conferences in computational biology (Bioinformatics, PLoS Computational Biology, IEEE/ACM Trans. on Computational Biology and Bioinformatics, Biosystems, CMSB, JOBIM), in control (Automatica, IEEE TCAS, CDC, ACC, ECC), in biology (Integrative Biology, ACS Synthetic Biology, BMC Systems Biology, Journal of Molecular Biology), and in computer science (Theoretical Computer Science, HSCC, CAV)

SCIENCE POPULARIZATION

- Worldviews and Values in Synthetic Biology workshop. *Cells driven by computers - in silico control of gene expression*, June 2014

- Rencontres Inria Industries: Bio-informatique et outils numériques pour les produits de santé. *Cells driven by computers*. Fevr 2014, Lyon
- Press coverage of some of our work: *Ils contrôlent le vivant avec des ordinateurs !* in l'Humanite Dimanche (October 2012), *Focusing the phenotype* in Phys.org (October 2012), *Contrôle d'une cellule assisté par ordinateur* in Journal du CNRS (September 2012), and participation to *Autour de la question* radio program on *Fabriquer le vivant* (RFI, November 2012)
- Fête de la science: posters *(Re)programmer le vivant: Comment concevoir et construire des organismes vivants utiles?* and *Des cellules pilotées par ordinateur* (2 days, October 2012, Rocquencourt)

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