Grégory BATT
Senior research scientist (DR1 Inria), PhD, HDR
Head of InBio at Inria de Paris & Institut Pasteur
Director of the Computational Biology Department, Institut Pasteur

Office: Institut Pasteur
28 rue du Dr Roux
75015 Paris, France
Email: `gregory.batt@inria.fr`
Phone: +33 1 40 61 39 99
www: `https://research.pasteur.fr/en/member/gregory-batt/`

Citizenship: French
Born: February 23, 1977

MAIN RESEARCH INTERESTS

Engineering biological systems via predictive modeling. More specifically, I aim at

(i) developing mathematical methods and computational tools for the **analysis and control** of natural biological systems (**systems biology**) and the **design and optimization** of novel, useful biological systems (**synthetic biology**) and

(ii) applying them via **experimental platforms integrating wet and dry 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 (Sorbonne U), H. de Jong (Inria), O. Gandrillon (CNRS), M. Khammash (ETH Zurich), and R. Veitia (Paris Diderot U)
2007	**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. Geiselmann (Grenoble U), N. Halbwachs (Grenoble U), J. Lygeros (ETH Zurich), D. Thieffry (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 07/2023	**Director of the Computational Biology Department** at **Institut Pasteur**
since 10/2017	**Senior research scientist** (DR2 in 2017, DR1 since 2023) at **Inria de Paris** in the InBio research group
since 02/2017	**Group leader of InBio**, a joint research group of **Inria** and **Institut Pasteur**
10/2007 - 09/2017	**Research scientist** at Inria Paris - Rocquencourt and Inria Saclay - Ile-de-France in the Contraintes and Lifeware research groups. Tenured position. Hired CR2 and promoted CR1 in Oct. 2009
01/2007 - 09/2007	**Research associate**: *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	**Research associate**: *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

09/2009 - 08/2022	**Computational biology** (42h) in Master Approches Interdisciplinaires du Vivant of Paris Descartes and Diderot Universities. Coordinator since 2011
09/2016 - 08/2018	**Modélisation et ingénierie pour les systèmes biologiques** (12h) in Institut de Technologie et d'Innovation of Paris Sciences et Lettres (PSL). Co-coordinator with L. Calzone and A. Zinovyev
09/2012 - 08/2017	**Dynamical modeling of cellular regulatory networks** (6h) in Master of Biology of Cellular Systems at Ecole Normale Supérieure of Paris
09/2008 - 08/2017	**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
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, 2015, 2017). Co-organizer and speaker at the International Course on Computational Systems Biology of Cancer at Institut Curie (Paris, 2018). Participant (2014) and Mentor (2015) of *Teaching through Research* leadership program workshops (CRI, Paris).

PRIZES AND AWARDS

- **Prime d'Excellence Scientifique** (2011-2014), **Prime d'Encadremant Doctoral et de Recherche** (2015-2018, 2020-2023), and **Prime Individuelle de Recherche** (2024 - 2026), Inria
- **Gold** (2009) and **Bronze** (2008) **medal**, at international Genetically Eng인nerred Machine competition (iGEM, MIT, Boston), as co-advisor of a student team

PROJECT MANAGEMENT

- **Harnessing biological diversity: a screening and learning approach** (Screen2Learn), IFPEN/Inria lab (2023-2026), with G. Batt (Co-coord, Inria/Pasteur) and Senta Blanquet (Co-coord, IFPEN)
- **Analysis of non-response to antibiotics in vivo: application to *E. coli* urinary tract infections** (Anoruti), PPR Antibiorésistance (2021-2025), with I. El Meouche (Coord., Inserm Paris), G. Batt (Pasteur), and M. Ingersoll (Curie)
- **Whole genome sequencing and artificial intelligence to characterise and diagnose antibiotic resistance and capacity to escape treatment** (Seg2Diag), PPR Antibiorésistance (2021-2026), with P. Glaser (Coord., Pasteur), F. Jay (Paris-Saclay U), G. Batt (Pasteur), T. Naas (Inserm Paris), B. Iorga (CNRS, Gif sur Yvette), Nicolas Gregoire (Inserm Poitiers), and P. Plesiat (Bourgogne U)
- **Control engineering of biological systems for reliable synthetic biology applications** (Cosy-Bio), H2020 FET-Open (2017-2020), with D. di Bernardo (Coord, Tigem), G. Batt (Inria), F. Menolascina (Edinburgh U), M. di Bernardo (Naples U), P. Hersen (Paris Diderot U), M. Khammash (ETHZ), G.-B. Stan (Imperial College), and L. Marucci (Bristol U)
- **Real-time control of synthetic microbial communities** (IPL Cosy), Inria Project Lab (2017-2020), with E. Cinquemani (Coord., Inria), G. Batt (Inria), H. Geiselmann (LIPhy, CNRS/Grenoble Univ.), J.-L. Gouzé (Inria), J.-P. Richard (Inria), F. Bonnans (Inria), B. Laroche (INRA Jouy-en-Josas), and H. Youk (Delft Univ.)
- **Microscopy automation software** (MicroMator), Action de Développement Technologique (2017-2019), coordinated by G. Batt (Inria)
- **Mixed-effect models for cellular processes: methods, tools and applications** (Memip), ANR Générique program (2016-2020) with G. Batt (Coord, Inria), P. Hersen (CNRS/ Paris Diderot), E. Cinquemani (Inria) and M. Lavielle (Inria/Polytechnique)
- **Computer-aided control of gene expression** (Cogex), ANR Générique program (2016-2019), with P. Hersen (Coord., CNRS/Paris Diderot), G. Batt (Inria) and G. Truan (LISBP, CNRS/INSA)
- **Stochastic models: Scalable model checking** (Stoch-MC), ANR Blanc program (2014-2018) with B. Genest (Coord., INRIA), G. Batt (Inria), W. Zielonka (LIAFA), and H. Gimbert (LaBRI).
- **From population models to model populations: single cell observation, modeling, and control of gene expression** (Iceberg), Investissement d'Avenir ANR program (2011-2017), with G. Batt (Coord., Inria), P. Hersen (CNRS/Paris Diderot), O. Gandrillon (CNRS/Lyon1), C. Lhoussaine (CNRS/Lille1), R. Veitia (CNRS/Paris Diderot), and J. Krivine (PPS, CNRS/Paris Diderot)
- **From synthetic networks to artificial tissues** (Syne2Arti), Cosinus ANR program (2010-2014), with G. Batt (Coord., Inria), D. Drasdo (Inria), O. Maler (Verimag), and R. Weiss (MIT)
- **Artificial tissue homeostasis: combining synthetic and computational biology approaches** (TisHom), Inria/MIT Associated team (2012-2015), shared coordination with Prof. Ron Weiss (MIT)
- **Formal probabilistic approaches for robust control of gene expression**, van Gogh grant (2012-2013), shared coordination with Prof. Alessandro Abate (TU Delft, now Oxford

Univ.)

PUBLICATIONS

International peer-reviewed articles

- D. De Marchi, R. Shaposhnikov, S. Gobaa, D. Pastorelli, **G. Batt**, P. Magni, and L. Pasotti (2024), Design and model-driven analysis of synthetic circuits with the Staphylococcus aureus Dead-Cas9 (sadCas9) as a programmable transcriptional regulator in bacteria, *ACS Synthetic Biology*, 13(3):763-780
- Z. Fox, **G. Batt**, J. Ruess (2023), Bayesian filtering for model predictive control of stochastic gene expression in single cells, *Physical Biology*, 20(5):055003
- S. Sosa-Carrillo, H. Galez, S. Napolitano, F. Bertaux* and **G. Batt*** (2023), Maximizing protein production by keeping cells at optimal secretory stress levels using real-time control approaches, *Nature Communications*, 14:3028
- F. Bertaux, S. Sosa-Carrillo, V. Gross, A. Fraisse, C. Aditya, M. Furstenheim, and **G. Batt** (2022), Enhancing bioreactor arrays for automated measurements and reactive control with ReacSight, *Nature Communications*, 13:3363
- C. Aditya, F. Bertaux, **G. Batt**, and J. Ruess (2022), Using single-cell models to predict the functionality of synthetic circuits at the population scale, *Proceedings of the National Academy of Sciences of the U.S.A*, 119(11):e2114438119
- Z.R. Fox, S. Fletcher, A. Fraisse, C. Aditya, S. Sosa-Carrillo, J. Petit, S. Gilles, F. Bertaux, J. Ruess, and **G. Batt** (2022), Enabling reactive microscopy with MicroMator, *Nature Communications*, 13:2199
- C. Aditya, F. Bertaux, **G. Batt***, and J. Ruess* (2021), A light tunable differentiation system for the creation and control of consortia in yeast, *Nature Communications*, 12(1):5829
- A. Davidović, R. Chait, **G. Batt**, J. Ruess (2022), Parameter inference for stochastic biochemical models from perturbation experiments parallelised at the single cell level, *PLoS Computational Biology*, 18(3):e1009950.
- F. Bertaux, J. Ruess, and **G. Batt** (2021), External control of microbial populations for bioproduction: A modeling and optimization viewpoint, *Current Opinion in Systems Biology*, 28:100394
- D. Lunz, **G. Batt**, J. Ruess, and J. F. Bonnans (2021), Beyond the chemical master equation: Stochastic chemical kinetics coupled with auxiliary processes, *PLoS Computational Biology*, 17(7):e1009214
- D. Lunz, **G. Batt**, J. Ruess (2020), To quarantine, or not to quarantine: A theoretical framework for disease control via contact tracing, Epidemics, 34(3):100428
- H.R. Meredith, V. Andreani, H.R. Ma, A.J. Lopatkin, A.J. Lee, D.J. Anderson, **G. Batt**, and L. You (2018), Applying ecological resistance and resilience to dissect bacterial antibiotic responses, *Science Advances*, 4(12):eaau1873.
- J.-B. Lugagne, S. Jain, P. Ivanovitch, Z. Ben Meriem, C. Vulin, C. Fracassi, **G. Batt**, and P. Hersen (2018), Identification of individual cells from z-stacks of bright-field microscopy images, *Scientific reports*, 8(1):11455.
- J.-B. Lugagne, S. Sosa Carrillo, M. Kirch, A. Köhler, **G. Batt***, and P. Hersen* (2017), Balancing a genetic toggle switch by real-time feedback control and periodic forcing, *Nature Communications*, 8:1671.
- S.K. Palaniappan, F. Bertaux, M. Pichene, E. Fabre, **G. Batt***, and B. Genest* (2017), Abstracting the dynamics of biological pathways using information theory: a case study of apoptosis pathway, *Bioinformatics*, 33(13):1980-6.
- C. Versari, S. Stoma, K. Batmanov, A. Llamosi, F. Mroz, A. Kaczmarek, M. Deyell, C. Lhoussaine*, P. Hersen*, and **G. Batt*** (2017), Long-term tracking of budding yeast cells in brightfield microscopy: CellStar and the Evaluation Platform, *Interface*, 14(127):20160705.
- 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: Single-cell parameter estimation of models of gene expression in yeast, *PLoS Computational Biology*, 12(2):e1004706. *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
- 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. *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. *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. *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. *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
- 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. *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
- 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.
- **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 .*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.
- 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.
- **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. . *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.
- **G. Batt***, B. Yordanov, C. Belta and R. Weiss (2007), Robustness analysis and tuning of synthetic gene networks, *Bioinformatics*, 23(**18**):2415-2422. . *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.
- **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.
- 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.
- **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.
- **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 Computer Science 3414, Springer-Verlag, 134-150.
- **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.
- 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.

Book chapters

- F. Bertaux, D. Drasdo and **G. Batt** (2017), System modeling of receptor-induced apoptosis, in O. Micheau ed., *TRAIL, Fas Ligand, TNF and TLR3 in Cancer*, Springer, pp. 291-307.
- 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)

- E. Weill, V. Andréani, C. Aditya, P. Martinon, J. Ruess, **G. Batt*** and J.F. Bonnans* (2019), Optimal control of an artificial microbial differentiation system for protein bioproduction, in *IEEE European Control Conference (ECC'19)*, pp. 2663-8
- M. Kryukov, A. Carcano, **G. Batt** and J. Ruess (2019), Can optimal experimental design serve as a tool to characterize highly non-linear synthetic circuits?, in *IEEE European Control Conference (ECC'19)*, pp.1176-81
- S.K Palaniappan, M. Pichené, **G. Batt**, E. Fabre, and B. Genest (2016), A look-ahead simulation algorithm for DBN models of biochemical pathways, in *International Workshop on Hybrid Systems Biology, HSB 2016*, p. 3-19. Springer
- **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.
- **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. Hofbaur, 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

Tools

- **MicroMator**: Microscopy automation software. Joint work with Steven Fletcher and Sebastien Gilles.

- **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).

STUDENT SUPERVISION

I (co-)supervise or have (co-)supervised more than 10 PhD students.

- **Alicia da Silva** (2023 -), in cosupervision with Senta Blanquet (IFPEN). A screening and learning approach for protein secretion in yeast. Univ Paris Saclay.
- **Henri Galez** (2022 -). Engineering yeast surface display and GPCR signaling for secretion background optimization in bioproduction. Univ Paris Saclay.
- **Viktoriia Gross** (2020 -), in cosupervision with I. El Meouche (Inserm) and E. Denamur (Inserm). An integrative approach to characterize the two sides of enzyme-mediated antibiotic escape: resistance and tolerance. Univ Paris Saclay.
- **Sebastian Sosa-Carrillo** (2018-2021), in cosupervision with François Bertaux (Pasteur). Thesis: Pipeline for the systematic characterization of heterologous protein secretory load to assess bioproduction efficiency. Univ Paris Cité. Dec 15, 2021. Jury: Megan McClean (Univ Wisconsin), Tom Ellis (Imprial College), Nathalie Giglioli-Guivarc'h (Tours Univ), Fayza Daboussi (Toulouse Univ), Cosmin Saveanu (Pasteur).
- **Arthur Carcano** (2018-2021), in cosupervision with J. Ruess (Inria). Thesis: Methods and tools for the optimal design of experiments applied to the efficient characterization of enzyme mediated escape to antimicrobial treatments. Univ Paris Cité. Dec 13, 2021. Jury: Eva Balsa-Canto (CSIC), Béatrice Laroche (INRAE), Eugenio Cinquemani (Inria), Olivier Tenaillon (Inserm).
- **Chetan Aditya** (2018-2021), in cosupervision with Jakob Ruess (Inria). Thesis: Development of a light tunable differentiation system for the creation and control of microbial consortia in *S. cerevisiae*, its single cell characterization for development of predictive models, and application to heterologous expression. Univ Paris Cité. Oct 1, 2021. Jury: Barbara di Ventura (Freiburg U), Sébastien Léon (Inst J. Monod), Leonardo Rios-Solis (Edinburgh U), Delphine Ropers (Inria), G. Yvert (ENS Lyon).
- **Elise Weill-Duflos** (2017), in cosupervision with F. Bonnans (CMAP, Inria). Optimal control of partial differential equation systems: Application to heterogeneous cell populations. Ecole Polytechnique. Resigned within her first year.
- **Virgile Andréani** (2016-2020). Thesis: Modelling and efficient characterization of enzyme-mediated response to antibiotic treatments. Ecole Polytechnique. Dec 17, 2020. Jury: Rosalind Allen (Edinburgh U.), Tobias Bollenbach (Köln U.), Marie Doumic (Inria), Philippe Glaser (Pasteur), Lingchong You (Duke U.).
- **Jean-Baptiste Lugagne** (2012-2016), in cosupervision with P. Hersen (MSC lab, CNRS/Paris 7). Thesis: Real-time control of a genetic toggle switch in *Escherichia coli*, Dec 13, 2016. Jury: Sven Van Teeffelen (Institut Pasteur), Meriem El Karoui (Edinburgh Univ.), Mario Di Bernardo (Naples Univ.), Hidde de Jong (Inria), Jérôme Bonnet (CNRS / Montpellier Univ.).
- **Artémis Llamosi** (2012-2015), in cosupervision with P. Hersen (MSC lab, CNRS/Paris 7). Thesis: Effects of repeated osmotic stress on gene expression and growth: from cell-to-cell variability to cellular individuality in the budding yeast *Saccharomyces cerevisiae*, Dec. 15, 2015. Jury: H. Koeppl (TU Darmstadt), M. Lavielle (Inria/Polytechnique), P. Swain (Edinburgh U), G. Yvert (CNRS, ENS Lyon).
- **François Bertaux** (2011-2016), in cosupervision with D. Drasdo (Mamba research group, Inria). June 15, 2016. Thesis: Cell-based multi-scale modeling for systems and synthetic biology: from stochastic gene expression in single cells to spatially organized cell populations. Jury: E. Barillot (Curie), A. Carbone (Paris6 U), M. Chaplain (St-Andrews U), P. Macklin

(Southern California U), J. Roux (Nice U). Now postdoctoral researcher with S. Marguerat and V. Shahrezaei at Imperial College.

- **Xavier Duportet** (2010-2014), 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 Eligobiotics company.
- **Jannis Uhlendorf** (2009-2013), 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.

I (co-)supervise or have (co-)supervised more than 25 students in masters or engineering schools.

- **Hong Duong Ngo** (Summer 2023) Master student M2 Approches Interdisciplinaires de la Recherche et de l'Enseignement at Univ Paris Cité, in cosupervision with H. Galez and S. Napolitano (Pasteur/Inria)
- **Konstantin Achkasov** (Summer 2023) Master student M1 Molecular Biology at Sorbonne University, in cosupervision with V. Gross (Pasteur/Inria).
- **Henri Galez** (spring 2022) Master student M2 Systems and Synthetic Biology at Paris Saclay Univ, in cosupervision with S. Napolitano (Pasteur/Inria).
- **Hélène Philippe** (spring 2022), Master student M1 Santé Humaine et ingénierie at AgroParisTech, in cosupervision with S. Napolitano (Pasteur/Inria)
- **Thomas Wahl** (Summer 2020) Medical Doctor student and Master 1 at Strasbourg U., in cosupervision with F. Bertaux and O. Borkowski (Pasteur/Inria).
- **Sacha Maire** (Summer 2020) B.Sc. student in Biomedical engineering at Imperial College, in cosupervision with F. Bertaux and O. Borkowski (Pasteur/Inria).
- **Achille Fraisse** (Winter 2019) Master student M2 Biosciences (ENS Lyon), in cosupervision with F. Bertaux (Pasteur/Inria).
- **Mariella Furstenheim** (Spring 2019) Master student M1 Approches Interdisciplinaires du Vivant (Université Paris Descartes), in cosupervision with F. Berteaux (Pasteur/Inria) and S. Sosa Carrillo (Inria/Pasteur).
- **Albin Salazar** (Spring 2019), Master student M2 Approches Interdisciplinaires du Vivant (Université Paris Descartes), in cosupervision with V. Andréani (Inria/Pasteur).
- **Maksim Kriukov** (Summer 2018) AMGEN Scholar Moscow Institute of Physics and Technology, in cosupervision with J. Ruess (Inria/Pasteur).
- **Martin Larralde** (Summer 2018) Master student M2 Computer Science (ENS Paris Saclay), in cosupervision with F. Bertaux (Pasteur/Inria)
- **Elise Weill-Duflos** (Summer 2018) Master student M2 Optimisation, ENSTA ParisTech, in cosupervision with F. Bonnans (Inria/Polytechnique).
- **Shuang Li** (Spring 2018) Master student M2 Approches Interdisciplinaires du Vivant, in cosupervision with V. Andréani (Inria/Pasteur).
- **Arthur Carcano** (Summer 2017) Master student M2 Parisian Master of Research in Computer Science (MPRI, ENS Paris), in cosupervision with J. Ruess (Inria/Pasteur).
- **Elea Greugny** (Summer 2017) 4th year Insa Lyon Engineer, "Bioinformatique et Modélisation" specialization, in cosupervision with J. Ruess (Inria/Pasteur).
- **Sebastian Sosa Carrillo** (Spring 2017) Master student M2 Approches Interdisciplinaires du Vivant.
- **Jean-Baptiste Caron** (Spring 2016) Master student M2 Approches Interdisciplinaires du Vivant, in co-supervision with J.-B. Lugagne and P. Hersen (MSC lab, CNRS/Paris 7).
- **Virgile Andréani** (2015-2016) Master student (ENS Paris / M2).

- **Ewen Corre** (Spring 2016), Master student M2 AIV, 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)
- **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
- **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

- Participation in selection/evaluation committees
  - Member of **recruitment committees** at INRA (CR2, 2017), Inria (CR2, Rennes, 2016) and Evry University (assistant professor, 2009)
  - Member of **project evaluation committees** for EraSynBio1 (2014, Lisbon) and EraSynAPP2 (2015, Gothenburg), for the ITMO Cancer/Inserm call on single-cell approaches to cancer (2018), for the ANR/Investissement d'Avenir call on Nouveaux Systèmes d'Expression (2020 and 2021), for the Bpifrance call on Biomédicament (2020, 2023), and for Pasteur Transverse Research Programs (2021) and Roux Cantarini Grants (2022).
  - **Reviewer** for project evaluation: MIT International Science & Technology Initiatives (MISTI) Global Seed Funds (2018), Leverhulme Trust (2018), 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 and HDR committees** of Eve Tasiudi (2023, ETH Zurich, rapporteur), Romain Aubry (2023, Poitiers University, rapporteur), Esteban Lebrun (2023, Paris-Saclay University), Theo Maire (2022, Delft University, rapporteur), Manish Kushwaha (HDR, INRA and Paris Saclay University, rapporteur), Federica Cella (2021, Genova U., rapporteur), Antoine Barizien (2019, Ecole Potytechnique/Pasteur, Paris, rapporteur), Mathilde Koch (2019, Ecole Polytechnique/INRA, Paris), Arnaud Bonnaffoux (2018, ENS Lyon, president), Benjamin Pfeuty (HDR, 2018, Lille U, rapporteur), Alexandre Deloupy (2018, Sorbonne U, Paris, rapporteur), Giansimone Perrino (2017, Tigem, Naples, rapporteur), Lorena Postiglioni (2017, Tigem, Naples, rapporteur), Stefano Casagranda (Inria Sophia Antipolis, 2017), Adel Mezine (Evry Univ, Evry, 2016, rapporteur), Erwan Bigan (Polytechnique, Paris, 2015, rapporteur), Benjamin Gyori (D Hsu group, NUS, Singapore, Oct 2014, rapporteur), Santiago Videla (A. Siegel/T. Schaub groups, Inria Rennes, June 2014, rapporteur), Alejandro Vignoni (J. Pico group, Universitat Politecnica de Valencia, May 2014), Sucheendra Palaniappan (P.S. Thiagarajan group, NUS, Singapore, June 2013, rapporteur), Andreas Milias-Argeitis (J. Lygeros group, ETHZ, Zurich, March 2013, rapporteur), Filippo Menolascina (D. di Bernardo group, TIGEM, Naples, Jan 2012, rapporteur), Zohra Khalis (G. Bernot group, I3S/ Evry Univ., December 2010), and Jamil Ahmad (O. Roux group, MeForBio team, IRCCyN, Nantes, February 2009).
  - Judge at **iGEM competitions** in 2008 (Boston) and 2013 (Lyon).
- Editorial and reviewing activities:
  - Member of **program committee** for **computational biology conferences**: FOSBE (2016, 2019, 2024), ICSB (2018), 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 **biology** (Nature Communications, Cell Systems, Scientific Reports, ACS Synthetic Biology, Current Opinion in Systems Biology), 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).
- Organization of workshops
  - **Predictive approaches for biological systems engineering**, thematic session (half day) at the JOBIM conference, Nantes, July 2019. 70 participants. Co-organized with Bioss and BioSynSys.
  - **Design, optimization and control for systems and synthetic biology** (2 days), ENS Paris, Paris, Nov 2015. 20 international speakers, 150 participants, 12 nationalities. Co-organized with D. Thieffry (ENS Paris) and P. Hersen (Paris 7 U).
  - **Design, optimization and control for systems and synthetic biology** (2 days), ENS Paris, Paris, June 2012. 15 international speakers, 200 participants, 14 nationalities. Co-organized with D. Thieffry (ENS Paris).
  - **Constructing gene networks: observation, analysis and control** (1 day), Paris 7 U., Paris, January 2009. 10 contributed talks, 50 participants. Co-organized with S. Bottani (Paris 7 U).
  - **Towards systems biology** (3 days), Grenoble U., Grenoble, October 2007. 25 international speakers, 70 participants. Co-organized with O. Maler (Verimag).
- Collective responsibilities
  - **Deputy director** (2017-2023) and **Director** (since 2023) of the **Department of Computational Biology** at Institut Pasteur
  - member of the **Bureau du Comité des Equipes Projet** at Inria Paris (since 2022)
  - member of the **IEEE/CSS Technical Committee on Systems Biology**
  - co-Responsible of the working group on **Symbolic Systems Biology** (GT Bioss) gathering >150 researchers in 25 research teams, member of the scientific board of the French

research network on **Systems and Synthetic Biology** (GdR BioSynSys) gathering 40 labs and 300 researchers, and member of the scientific board of the French research network on **Bioinformatics** (GdR BIM) gathering 56 labs and several hundreds of researchers (2017 - 2021)

- responsible for the Predictive Systems Biology chapter of the 2018-2022 **strategic plan of Inria** (2017)
- member of the scientific committee of **Advanced Lecture Course on Computational Systems Biology** summer school (2015, 2017, 2019)

updated March 2024