

Grégory BATT

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RESEARCH INTERESTS

Development of mathematical methods and computer tools for the analysis of genetic regulatory networks

keywords: algorithmic analysis and formal verification of hybrid systems, genetic regulatory networks, model validation for systems biology, system design for synthetic biology

CURRENT POSITION

Research associate affiliated with the Center for Information and Systems Engineering and the Center for BioDynamics at Boston University (USA).

EDUCATION

- 2006 **PhD in computer science** at the Université Joseph Fourier (Grenoble, France)
- 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 (France)
- 2000 **Maîtrise of the Magistère de Biologie Moléculaire et Cellulaire** at the Ecole Normale Supérieure de Lyon.
ERASMUS student at Uppsala University (Sweden)
- 1999 *Licence of the Magistère de Biologie Moléculaire et Cellulaire* at the Ecole Normale Supérieure de Lyon
- 1998 General scientific preparation (*BioMathSup* and *BioMathSpé*) for the *Grandes Ecoles* at the Lycée Pierre de Fermat in Toulouse (France). Admitted to the Institut National Agronomique de Paris-Grignon and to the Ecole Normale Supérieure de Lyon

RESEARCH EXPERIENCE

- since 12/2005 **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
- 09/2002 - 11/2005 **PhD student:** *Validation of qualitative models of genetic regulatory networks: a method based on formal verification techniques* in the HELIX research group at INRIA Rhône-Alpes (France), under supervision of Hidde de Jong
- 01/2002 - 08/2002 **Lab training period** (computer science, *DEA*): *Validation of genetic regulatory network models*, in the HELIX research group at INRIA Rhône-Alpes, under supervision of Hidde de Jong
- 06/2001 - 08/2001 **Lab training period** (computer science, *Licence*): *Representation of protein/protein interactions in qualitative models of genetic regulatory networks*, in the HELIX research group at INRIA Rhône-Alpes, under supervision of Hidde de Jong
- 06/1999 - 08/1999 **Lab training period** (biology, *Licence*): *Discovering interactions between cytoskeletal proteins using double hybrid techniques*, in the Pharmacologie et Dynamique du Cytosquelette Microtubulaire research group at the Institut de Pharmacologie et de Biologie Structurale (Toulouse, France), under supervision of Laurent Mazzolini

TEACHING EXPERIENCE

- 09/2002 - 08/2005 **Teaching assistant** in computer science at the Université Joseph Fourier:
- introduction to programming in *Licence Sciences et Technologies* (lecture and lab)
- modeling and simulation of genetic regulatory networks in *Master Sciences, Technologies et Santé* (lab)

SKILLS

Computer science: hybrid systems, model checking, bioinformatics, graph theory, algorithms, programming, operating systems, architecture, software engineering, synchronous languages for reactive systems, operational research, artificial neural networks, data and knowledge bases, distributed systems, human-computer interaction, probability theory.

Biology:

- theoretical: molecular biology, cellular biology and cancer, genetics, immunology, biochemistry, bioinformatics, plant biology, integrated physiology, development and evolution,
- practical: enzymology, chromatography, cloning, fusion proteins, immunolabeling, *in situ* hybridization, genetics in *Drosophila*, yeast, and *E. coli*, sequencing, double hybrid, electronic microscopy.

Languages: English: fluent; German and Swedish: notions.

PUBLICATIONS

Note: Impact Factors (IF) and Acceptance Rates (AR) are given when available.

Journal articles

- **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: 6.019)
- H. de Jong, J. Geiselmann, **G. Batt**, C. Hernandez and M. Page (2003), Qualitative simulation of the initiation of sporulation in *Bacillus subtilis*, *Bulletin of Mathematical Biology*, 66(2):261-300. (IF: 1.48)

Book chapters

- **G. Batt**, C. Belta and R. Weiss (2006), 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, Springer-Verlag. Accepted for publication. (AR: 25%)
- **G. Batt**, C. Belta and R. Weiss (2006), Model checking liveness properties of genetic regulatory networks, in O. Grumberg, M. Huth and B. Cook, eds., *Thirteenth International Conference on Tools and Algorithms for the Construction and Analysis of Systems (TACAS'07)*, Lecture Notes in Computer Science, Springer-Verlag. Accepted for publication. (AR: 26%)
- **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, 206-239.
- **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. (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%)

International peer-reviewed conferences

- **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*, Cold Spring Harbor, NY, USA, 62.
- **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., *Proceedings of the Nineteenth Inter-*

national Joint Conference on Artificial Intelligence (IJCAI'05), Edinburgh, Scotland, 370-375. (AR: 18%)

International workshops and national conferences (peer-reviewed)

- **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. Geurjon, 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 thesis

- **G. Batt** (2006). Validation de modèles qualitatifs de réseaux de régulation génique : une méthode basée sur des techniques de vérification formelle, Université Joseph Fourier.

Research reports

- **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

- **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

- 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 *Escherichia 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 *Escherichia 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 Mathematical Theory of Networks and Systems Conference*, July 2004, Leuven, Belgium.
- Formal validation of models of genetic regulatory networks, in *Modeling and Simulation of Biological Regulatory Processes*, a satellite meeting of the *European Conference on Computational Biology (ECCB'03)*, October 2003, Paris, France.

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