Curriculum Vitae

Name	Marie Nikolski
Date of birth	22 november 1972, St Petersbourg, Russia
Current employment	research scientist at the CNRS, France since 01/09/2002
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Employment

2002 -	**Research Scientist (CR1)** at the CNRS, France
2001 - 2002	**Research Engineer** at Synopsis, Boston, USA
1999 - 2001	**ATER** at the l'University of Bordeaux, France

Diplomas and Education

1996 - 2000	**PhD** in Computer Science from the University of Bordeaux under the supervision of Antoine Rauzy **Title :** *Binary Decision Diagrams and Applications to Reliability Analysis* Defened on the January, 20 2000
1994 - 1996	**Masters in Computer Engineering** ENSEIRB (Ecole Nationale Suprieure d'Electronique, Informatique et Radiocommunications de Bordeaux)
1995 - 1996	**Masters in Computer Science** University of Bordeaux
1994	**Summer session in Computer Science** at the University of California at Berkeley

Macha Nikolski received her doctoral degree in Computer Science in 2000 from the University Bordeaux 1 under the direction of Antoine Rauzy, on the subject of binary decision diagrams and their application to the reliability analysis of complex industrial systems. She subsequently worked for two years in the United States as a research engineer for Synopsys, before returning to France in 2002 to a position as Research Scientist (Chargée de Recherches) in the CNRS. As a founding member of the Mabiovis team in the LaBRI and the Magnome team in the INRIA, she works with biologists in comparative genomics and systems biology. In comparative genomics she has developed algorithms for data-mining analysis of genomic data through consensus clustering, and for large-scale combinatorial analysis of genome formation through chromosomal rearrangements. The goal of this work is to construct comprehensive views of the history and function of genomes, through the development of multi-scale representations of the mathematical relations between genes, and of algorithmic descriptions of the mechanisms of genome evolution.

In systems biology her recent research is on multi-scale hybrid and stochastic modeling of cell behaviour, through the development of a mixed-formalism modeling platform called BioRica. The focus of this work is to develop network descriptions of cell behaviour (interaction, metabolic, and regulation networks), and link them together into hierarchical models of complete systems that admit high-performance simulation. This approach has been successfully used in e.g. generalizing a single-cell model of transmission of oxidatively damaged proteins from mother to daughter cells, to a structured population model in which one can identify specific lineages with effective strategies that increase survival of the population.

She is active in the French Génolevures Consortium (GDR CNRS) and the European Yeast Systems Biology Network (FP6), in which she is a contracting partner. Since starting with the CNRS in 2002, Macha Nikolski has 14 papers in refereed international journals (605 total citations, h-index 9 according to Scopus).

Advised PhD Thesis

- Hayssam Soueidan, defence to be held Nov. 2009 (co-directed with D. Sherman)
- Géraldine Jean, defended Dec. 2008 (co-directed with S. Dulucq)
  Title: In silico method for genome rearrangement analysis: from identification of common markers to ancestral reconstruction
- Florian Iragne, defended Dec. 2007 (co-directed with D. Sherman)
  Title: Méthodes informatiques de prédiction et de comparaison de réseaux d'interactions protéine-protine partir de données de la gnomique compare

Currently I'm co-directing the following PhD students: Nicolas Loira (with Dr. D. Sherman, Université de Bordeaux), Anasua Sarkar (with Prof. Ujjwal Maulik, Jadavpur University, India), Nikolay Viahhi (with Prof. B. Novikov, St.-Petersbourg University, Russia)

Advised Masters Thesis and Post-docs

- Adrien Goeffon (postdoc, 2007-2009)
- Hélène Ferry-Demazet (postdoc, 2005-2006)
- Advisor for Master's Thesis of Damien Girons, 2008
  Title: Identification de bloques synténiques chez les espèces distantes
- Co-advisor with G. Sutre for Master's Thesis of Hayssam Soueidan, 2004
  Title: Abstraction de modèles AltaRica stochastiques
- Co-advisor with D. Sherman for Master's Thesis of Jean-Paul Soularue, 2004
  Title: Inférence de réseaux d'interactions biomolécumalires à partir de sources d'information hétérogènes
- Marc Chiavarenni (pre-doc, 2003)
  Title: Modèlisation par automates de modes pour les systèmes biologiques

Software tools

- Modeling and simulation plateform for biological systems *BioRica*
- Genomic database *Génolevures* and associated analysis tools
- Analysis of ancestral architectures package *Faucils*
- Vizualisation tool for protein-protein interaction networks *ProViz*
- Formal verification suite *Formality* (Synopsys)

Involvement in scientific community

- Member of the International Society for Computational Biology (ISCB) since 2005
- Member of the Scientific Program Committee of MCCB 2009, WABI 2009, AlBio 2008, JOBIM 2007
- Reviewer for Scientific Journals and Conferences TSI, TCS, Plos. Comp. Bio
- Reviewer for Grant Calls by ANR (AMPBio, Masses de Donnes)
- Member of Hiring Committees (Université d'Evry 2005-2007, INRIA Saclay 2008-2009, Université de Bordeaux 2009)
- Organizer of seminars (Bioinformatics seminar in Bordeaux 2003-2004, Journées Thmatiques de Bioinformatique 2003)

Grants

I have been in charge of or participated in the coordination of the following grants.

- PI for Bordeaux in the *Yeast Systems Biology Network* (CA under the FP6)
- GDR *Génolevures* 2, 3 and 4 (CNRS GDR 2354)
- ACI "Jeunes Chercheurs" *Saccaromyces siliceus*

I have participated in the following grants.

- ANR Blanc *Genarise* (ANR-05-BLAN-0331)
- ACI IMPBio *Génolevures En Ligne* (IMPB114)

Invited talks

- 6th GTGC meeting (Groupe de Travail en Gnomique Comparative), 2009, title "Reconstructing ancestral architectures from highly divergent eukaryote genome sequences"
- 3rd International Workshop on Algorithms in Bioinformatics, Moscow, Russia, 2008, title "Mining the semantics of genome super-blocks to infer ancestral architectures"
- International Conference on Systems Biology and Signal Transduction, Bordeaux, 2005, title "Discrete Modeling: methodology and application to Yeast"
- Yeast 2003 International Conference, Gotheborg, Sweden, 2003, title "Rule-based homolgy prediction as an aid to manual curation of Yeast genomes

- Workshop MGED 2003, Aix-en-Provence, France, 2003, titre de prsentation ”Malako, a system for type-safe comparison of microarray data from multiple sources”
- International Workshop on Systems Biology of Yeast, 2003, title ”Saccharomyces siliceus”

Publications [1]

International Journals: [1, 2, 3, 6, 7, 11, 12, 13, 14, 15, 17, 18, 19, 20]

International Conferences: [4, 5, 7, 8, 10, 21, 29, 22, 23, 24, 26, 27, 28]

National Conferences, Posters, Short Publications: [9, 16, 15, 30, 31, 32, 33, 34, 25]

References

[1] The Genolevures Consortium. Comparative genomics of protoploid genomes of saccharomycetaceae defines the orthologous gene set and basic yeast proteome repertoire. *accepted for publication in Genome Research*, 2009.

[2] D. Sherman, T. Martin, M. Nikolski, C. Cayla, J.L. Souciet, and P. Durrens. Genolevures: protein families and synteny among complete hemiascomycetous yeast proteomes and genomes. *Nucleic Acids Research*, 37(database issue):D550–D554, 2009.

[3] G. Jean, D. Sherman, and M. Nikolski. Mining the semantics of genome super-blocks to infer ancestral architectures. *accepted for publication in the Journal of Computational Biology*, 2009.

[4] H. Soueidan, G. Sutre, and M. Nikoski. Qualitative transition systems for the abstraction and comparison of transient behavior in parametrized dynamic models. In *accepted for publication in Lecture Notes in Bioinformatics (CMSB)*, 2009.

[5] N. Vyahhi, A. Goeffon, M. Nikolski, and D. Sherman. Swarming along the evolutionary branches sheds light on genome rearrangement scenarios. In *accepted for publication in GECCO*, 2009.

[6] P. Durrens, M. Nikolski, and D. Sherman. Fusion and fission of genes define a metric between fungal genomes. *Plos Computational Biology*, 4(10), 2008.

[7] M. Cvijovic, H. Soueidan, D. Sherman, E. Klipp, and M. Nikolski. Exploratory simulation of cell ageing using hierarchical models. In *Genome Informatics Series, ISSN: 0919-9454*, volume 21, pages 114–125, 2008.

[8] A. Goeffon, M. Nikolski, and D. Sherman. An efficient probabilistic population-based descent for the median genome problem. In *Proceedings of GECCO 2008 (ISBN:978-1-60558-130-9)*, pages 315–322, 2008.

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[1] If a publication appears both in the “International Journals” and “International Conferences” section, this means that selected papers from the conference were published in a special issue of a journal (e.g. reference [7]).

[9] G. Jean, D. Sherman, and M. Nikolski. Reconstruction and visualization of genome rearrangements within the kuyveromyces. Proceedings of the ESF-EMBO Symposium on Comparative Genomics of Eukariotic Microorganisms, Poster, 2008.

[10] D.J. Sherman H. Soueidan and M. Nikolski. Biorica: A multi model description and simulation system. In *Proceedings of the 2nd Foundations of Systems Biology in Engineering (FOSBE)*, pages 279–287, Sttugart, 2007. Fraunhofer IRB Verlag. ISBN 978-3-8167-7436-5.

[11] G. Jean and M. Nikolski. Genome rearrangements: a correct algorithm for optimal capping. *Information Processing Letters,*, 104(1):14–20, 2007.

[12] F. Iragne, M. Nikolski, and D. Sherman. Extrapolation of metabolic pathways as an aid to modelling completely sequenced non-saccharomyces yeasts. *FEMS Yeast Res.*, 8: 132–139, 2007.

[13] M. Nikolski and D. Sherman. Family relationships: should consensus reign? - consensus clustering for protein families. *Bioinformatics*, 23(2):e71–e76, 2007.

[14] D. Sherman, P. Durrens, E. Beyne, M. Nikolski, and J.-L. Souciet. Genolevures complete genomes provide data and tools for comparative genomics of hemiascomycetous yeasts. *Nucleic Acids Research*, 34(Database Issue):D432–D435, 2006.

[15] A. Barre, V. Jouffe, C. Lartigue, M. Nikolski, A. Blanchard, and P. Sirand-Pugnet. Annotation transfert based on orthology relationships: reannotation of mycoplasma genomes from the pneumoniae group. JOBIM'06 poster, 2006.

[16] H. Soueidan, G. Sutre, and M. Nikolski. Model checking AllTL properties over set automata. In *Proceedingds of MOdelling and VErifying parallel Processes (MOVEP)*, pages 377–383, 2006.

[17] F. Iragne, M. Nikolski, B. Mathieu, D. Auber, and D. Sherman. ProViz: protein interaction visualization and exploration. *Bioinformatics*, 21(2):272–274, 2005.

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International Meeting of the Microarray Gene Expression Data Society, pages 127–129, 2003.

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[34] M. Nikolski, D. Sherman, and P. Williams. Unifying two formula rewriting techniques for circuit verification and risk assessment. Tech. Report TR-1293-03, LaBRI, University of Bordeaux-1, 2001.