



Carito Guziolowski
Born January 27, 1982
carito.guziolowski@irisa.fr
www.irisa.fr/symbiose/carito_guziolowski

INRIA Bretagne Atlantique
Université de Rennes 1
35042 Rennes, France
+33 (0)2 99 84 71 16

Ph. D. Candidate

Engineer in Computer Science

Professional Experience

Keywords

- Qualitative modelling, transcriptional regulation, boolean constraint resolution, discrete systems, systems biology.

Academic Experience

- Jan. 2009 • Academic visitor at Centre of Mathematical Modelling - Universidad de Chile, Santiago, Chile. Applying qualitative modelling over *Acidithiobacillus ferrooxidans* regulatory interactions.
- 2006 • Master Internship at Symbiose Project - INRIA Bretagne Atlantique, Rennes, France. Testing a new approach of qualitative modelling in *Escherichia coli* transcriptional regulatory network.
- 2005 • Research Engineer at Functional Genomics for the Nectarine Fruit - Universidad Andres Bello, Santiago, Chile. Developing a data management system for large EST projects.
- Research Engineer at Centre of Mathematical Modelling - Universidad de Chile, Santiago, Chile. Installation of GenDB, a genome annotation system for prokaryotic genomes.

Development

- BioQuali • Co-author of BioQuali plugin for Cytoscape (A framework for analysing and visualizing regulatory data). This plugin allows the user to visualize the qualitative analysis of large scale regulatory networks.
- Co-author of BioQuali on-line web form. An on-line tool dedicated to the analysis of compatibilities between an interaction graph and microarray data.
- Contributor of the PyQuali/BioQuali Python library. This library allows the user to build Python programs, which interrogate large scale networks and datasets. Its results are computed efficiently and in short time.
- N-map • Co-author of the N-map software. This program was built for the comparison of biological sequences without taking into account their sequential order.
- Juice • Contributor in the development of Juice, a data management system for large EST projects.
- GenDB • Installation of the GenDB framework, intended to the annotation of prokaryotic genomes in the Bioinformatics Laboratory of the Centre of Mathematical Modelling - Universidad de Chile, Santiago, Chile.

Teaching

- 2007-2009 • Exercise and practical sessions on UML and Java programming, Ecole Nationale de la Statistique et de l'Analyse de l'Information, Bruz, France (90 hours)
- 2002 • Exercise and practical sessions on Introduction to Algorithmic and Programming Languages, Universidad de Chile, Santiago, Chile (annual course).

Education and Awards

Education

- 2006 - 2009 • Ph.D. Candidate in Computer Science, (expected graduation date: November 2009) at Université de Rennes 1, Rennes, France. Dissertation Topic: “Qualitative Modelling of large scale regulatory networks”. Advisor: Anne Siegel.
- 2005 - 2006 • Master in Bioinformatics (*mention bien*) at Université de Rennes 1, Rennes, France.
- 2002 - 2005 • Engineer in Computer Science (graduated with high distinction) at Universidad de Chile, Santiago, Chile.
- 1999 - 2002 • Licentiate in Engineering Sciences mention Computer Science (graduated with distinction) at Universidad de Chile, Santiago, Chile.

Awards

- 2005-2006 • Franco-Chilean Scholarship for an internship experience granted by CONICYT¹ and INRIA².
- 2006-2009 • Franco-Chilean Scholarship for doctoral studies granted by CONICYT and the French Embassy.

List of Publications

Peer reviewed journal articles

- 2009 • Guziolowski, C., Blachon, S., Radulescu, O., Baumuratova, T., Stoll, G., Siegel, A., “Designing logical rules to model the response of biomolecular networks with complex interactions: an application to cancer modelling”, *IEEE/ACM Trans Comput Biol Bioinform.*, in preparation.
- Guziolowski, C., Bourdé, A., Moreews, F., Siegel, A., “BioQuali Cytoscape Plugin: Analysing the global consistency of regulatory networks”, *BMC Genomics*, *BMC Genomics*, vol. 10, pp. 244, 2009.
- 2008 • Veber, P., Guziolowski, C., Le Borgne, M., Radulescu, O., Siegel, A., “Inferring the role of transcription factors in regulatory networks”, *BMC Bioinformatics*, vol. 9, pp. 228, 2008.
- 2007 • Guziolowski, C., Veber, P., Le Borgne, M., Radulescu, O., Siegel, A., “Checking Consistency Between Expression Data and Large Scale Regulatory Networks: A Case Study”, *Journal of Biological Physics and Chemistry*, vol. 7, pp. 37-43, 2007.
- Didier, G. and Guziolowski, C., “Mapping Sequences by Parts”, *Algorithms for Molecular Biology*, vol. 2, pp. 11, 2007.
- 2006 • Latorre, M., Silva, H., Saba, J., Guziolowski, C., Vizoso, P., Martinez, V., Maldonado, J., Morales, A., Caroca, R., Cambiazo, V., Campos-Vargas, R., Gonzalez, M., Orellana, A., Retamales, J., Meisel, L.A., “JUICE: a data management system that facilitates the analysis of large volumes of information in an EST project workflow”, *BMC Bioinformatics*, vol. 7, pp. 513, 2006.

Conference proceedings

- 2009 • Gebser, M., Guziolowski, C., Schaub, T., Siegel, A., Thiele, T., Veber, P., “Prediction and Repair in Large Biological Networks with Answer Set Programming”, *PADL'10: 12th International Symposium on Practical Aspects of Declarative Languages*. Madrid, Spain, January, 2010, submitted.
- Blachon, S., Stoll, G., Guziolowski, C., Zinovyev, A., Barillot, E., Siegel, A., Radulescu, O., “Method for relating inter-patient gene copy numbers variations with gene expression via gene influence network” *BMIINT: Biomedical Informatics and Intelligent Methods in the Support of Genomic Medicine*. Thessaloniki, Greece, April 2009, AIAI, pp 72-87.
- 2008 • Guziolowski, C., Gruel, J., Radulescu, O., Siegel, A. “Curating a large-scale regulatory network by evaluating its consistency with expression datasets”, *CIBB'08: 5th International Conference on Bioinformatics and Biostatistics*, Salerno, Italy 2008, Lecture Notes in Computer Science, vol. 5488, pp. 144-155, Springer (selected paper).

¹Chilean National Commission for Scientific and Technological Research

²French National Institute for Research in Computer Science and Automatic

List of Publications (continued)

- 2007 • Siegel, A., Guziolowski, C., Veber, P., Radulescu, O., Le Borgne, M., “Qualitative response of interaction networks: application to the validation of biological models”, Contribution to minisymposium New Research in Bioinformatics. ICIAM’07: 6th International Congress on Industrial and Applied Mathematics, Zurich 2007, PAMM, vol. 7, no. 1, pp. 1121803-1121804.

Non peer reviewed publications

- 2008 • Guziolowski, C., Veber, P., Le Borgne, M., Radulescu, O., Siegel, A. “Analysing regulatory networks using a qualitative approach”, *Genomes to Systems*, Manchester, UK, 2008 (poster session).
- 2006 • Siegel, A., Guziolowski, C., Veber, P., Radulescu, O., Le Borgne, M., “Optimiser un plan d’expérience partir de modles qualitatifs?”, *BioFutur* vol. 275, pp. 27, 2006

Oral communications

- 2009 • Workshop in Gen2Bio: Les rencontres Biotech organisés par OUEST-genopole: “Plugin BioQuali pour Cytoscape: un nouvel outil mis en place sur la plate-forme” (La Boule, France).
- 2008 • JOBIM 2008 satellite meeting: Dynamical modelling and simulation of biological networks: “Adding missing post-transcriptional regulations to a regulatory network” (Lille, France).
- Séminaire Bioinformatique at Symbiose Team, INRIA - Centre Bretagne Atlantique: “Mapping sequences by parts” (Rennes, France).
- 2007 • Cinquièmes Rencontres autour de la plate-forme Bio-informatique Genouest: “BioQuali: tool for analysing regulatory networks” (Rennes, France).
- 2nd International Course in Yeast Systems Biology, ICYSB: “Inferring the role of transcription factors in regulatory networks”, (Göteborg, Sweden).
- 2006 • RIAMS’06: Réseaux d’interaction, analyse, modélisation et simulation “Checking Consistency Between Expression Data and Large Scale Regulatory Networks: A Case Study” (Lyon, France).

Research in-team

- “Qualitative functions to better model the EWS/FLI-1 signalling network”, SITCON project meeting, Institut Curie, Paris, December, 2008.
- “Adding missing post-transcriptional regulations to a regulatory network”, SITCON project meeting, Institut Curie, Paris, May, 2008.

Divers

Languages

- Spanish - native
- English - fluent
- French - fluent
- Polish - basic

Research Interests

- My research area is the modelling of regulatory networks. I have started in this area just before starting with my Ph. D. studies, all our models have been analysed using qualitative modelling. In this approach, we discretize the regulations in the network and the changes in expression of the network components, and we study the consistency of these changes with the network topology using a causal rule. One of the main issues of my research has been to confront large scale regulatory data with experimental outputs using qualitative modelling. The confrontation between these data outputs inconsistencies, regions in the network or data in the experiments that did not satisfy the rule, that contribute to the curation of the regulatory model. We may also obtain new observations over some network components that are necessary to explain the experimental data. The qualitative modelling framework existed before the start of my Ph. D.; since then, I have contributed to improve the functionalities on the Python library Pyquali/Bioquali in order to adapt it to the needs we were encountering, and to create friendly applications that broaden the use of this type of analysis by prospective users.

Using this approach we have analysed data issued from prokaryotic networks models, as *Escherichia coli*, *Corynebacterium*, *Acidithiobacillus ferrooxidans*; and of higher (and more complex) eukaryotic network models, as *Saccharomyces cerevisiae*, and the signalling network of the Ewing tumour oncogene EWS/FLI-1. In these latter ones we have corrected our modelling rules by incorporating boolean functions of regulations; and also we have divided the components of the networks to differentiate the type of regulation (transcriptional or post-transcriptional) they receive. In order to validate or to question our results, the literature information of each of these organisms and the constant contact with biologists was very important. Our experience using this approach tell us that the casual rule applies better to prokaryotic systems, as post-transcriptional events are few; when working with eukaryotic systems the casual rule is too general and new detailed functions of regulation need to be added.

My current work as a Ph. D. student has lead to some results concerning: (1) the validation of the casual consistency rule in real biological large scale data, (2) prediction of the role of transcription factor regulations using several datasets of experimental observations, (3) deciding a measure to compute a distance between a model an expression data. Currently, I am working on better formulating this distance criteria. Also, on how to explain, and in the future revert, phenotypes in a cancer signalling network. Another project I have is to apply our qualitative modelling approach to guide the construction of a regulatory network model for *Acidithiobacillus ferrooxidans*.