

# Marco Antoniotti

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## Overview

I primarily work on the boundary of mathematics, computer science and biology with strong emphasis on statistical analysis, formal and logical methods (practical verification, synthesis and logic) and simulation approaches. I apply such techniques and tools in the general field of Computational and Systems Biology where, more recently I became interested in “system reconstruction” approaches starting from –omics datasets, especially applied to cancer research. In this context, my laboratory and myself have been working in “network analysis” and “causal/selective relationships reconstruction” of genomic events. Such activities have been complemented with modeling and simulation work where the focus has been in the investigation of clonal populations in certain tissues where it is known cancer originates, e.g., the intestinal crypts for colorectal cancer. In my activities I have always tackled problems both from a theoretical and from a pragmatic and applicative viewpoints, in order to build various systems capable of providing adequate solutions. While for the last ten plus years I have worked on Computational and Systems Biology, before that I worked on problems and examples coming from robotics, automotive and highway systems, and from hardware and software embedded systems.

## Experience, Titles and Activities

**AY 2005-2006, present: Associate Professor with tenure, Università degli Studi of Milan-Bicocca, Department of Systems, Informatics and Communications, Milan, Italy.**

I initially continued my research in the analysis of time-course micro-array experiments in the context of the European Commission Marie Curie IRG BRONTE project. More recently, as a result of the RetroNet project and the forming of the BIMIB group, which I lead, I have started tackling biological tissue simulations using a combination of in-lattice Cellular Potts Model and of Noisy Random Boolean Networks to select the “most appropriate” multi-scale intra-and inter-cellular setup. Always in the same context, my group and myself started working on a “causal/selective relationships reconstruction” of genomic events, such as copy-number variations, which can be measured from Next Generation Sequence (NGS) experiments: the toolset TRONCO can be used as a downstream block of any NGS analysis pipeline. I participated in the EU Project NeuroWEB: design of the architecture of a vertically integrated geographically distributed database aimed at the construction of SNPs-based diagnostic chips for neurological disorders. More recently, I started collaborations with cancer research laboratories (School of Medicine of the Università degli Studi di Milano Bicocca, Milan, Bicocca, Istituto Nazionale dei Tumori, Milan, Italy, Institut Català d’Oncologia, Barcelona, Spain, and the Donnelly Centre for Cellular + Biomolecular Research, University of Toronto, Toronto, Canada) to reconstruct intra and inter cellular interactions in the formation of colon cancer. Meanwhile, I continued my collaboration with the Courant Bioinformatics Group of New York University, USA.

**May 2000-Fall 2005, Summer 2006: Senior Research Scientist, NYU Courant Bioinformatics Group, New York, NY, U.S.A.**

I worked on the development of validation, visualization and database tools for the manipulation of genomic data and simulation of biological processes; most notably I worked on an analysis tool for the “Optical Mapping” technology, which is a precursor of more current sequencing and NGS technologies. I directed the optical mapping sequence validation project, and the Simpathica development group in the context of the DARPA BioSPICE program. In the context of the NSF N2010 Arabidopsis thaliana project I supervised the development of NYUMAD (NYU Microarray Database). I directed the

GOALIE project in the context of the NSF EMT program, where I also did a significant part of the development.

**January 1998 to April 2000: Research Scientist, PARADES E.E.I.G., Rome, Italy.**

I developed embedded systems for automotive applications, and worked on the construction of a software environment, Jester, based on Java, for the synthesis of embedded reactive programs. I also was consulting for Magneti Marelli S.p.A. on hardware/software co-design topics.

**September 1996 to December 1997: Postdoctoral Fellow at California PATH Program, Institute of Transportation Studies, University of California at Berkeley, Berkeley, CA, U.S.A.**

I worked on the SHIFT hybrid system modeling and simulation tool and related software engineering concepts within the National Automated Highway System project sponsored by the U.S. Dept. of Transportation, eventually in the capacity of director of the Software Development Team.

**September 1995 to August 1996: Postdoctoral Fellow at the International Computer Science Institute, Berkeley, CA, U.S.A.**

I worked on hybrid systems simulation and implementation of Priority Encoding Techniques for Internet based video-conferencing.

**Summer 1993: Robotics Laboratory of the Courant Institute of Mathematical Sciences.**

I constructed a Real Time control system for the ED-I manipulator. The system was based on a complex control architecture built on top of the VxWorks RTOS.

**Summer 1992: CISE S.p.A. (ENEL research center), Milan, Italy.**

I wrote the specification for an embedded language to be used as a component of process control applications.

**September 1990: Fulbright Scholarship.**

**August 1988 to August 1990: Quinary S.p.A. Milan, Italy.**

I co-wrote a prototype interface between a CAD and a CAM system (Intergraph tool chain and libraries) for Salvagnini S.p.A., a medium size manufacturing firm.

**August 1987: Award of the Rotary Club of Rome for Laureate Thesis in the field of Artificial Intelligence.**

**Summer 1986: Istituto Mario Negri for Pharmacological Research, Milan, Italy.**

I co-designed and developed a knowledge and data base systems for the management of clinical trials.

## **Education**

September 1995: Ph.D. in Computer Science, Courant Institute of Mathematical Sciences, New York University, New York, USA. Thesis title: *Synthesis and Verification of Controllers for Robotics and Manufacturing Devices with Temporal Logic and the CONTROL-D System*. Advisor: Professor Bud Mishra.

May 1992: Master of Science in Computer Science, Courant Institute, New York University, New York, U.S.A.

July 1986: Laurea in Scienze dell'Informazione "Magna cum Laude", Università degli Studi di Milan, ITALIA. Thesis title: *Analisi di un problema di configurazione e sue possibili soluzioni con tecniche di Intelligenza Artificiale e Ricerca Operativa (Analysis of a Configuration Problem and its Possible Solutions with Artificial Intelligence and Operations Research Techniques)*, Advisor: Dott. Ing. Alberto Stefanini.

## **Teaching Experience**

AYs 2005-15 Lectures in Algorithms and Data Structures, Basic Programming for CS majors, Advanced Programming Languages and Software Engineering Laboratory, Bioinformatics Laboratory, Computational Biology, Department of Informatics, Systems and Communication of the Università Milano-Bicocca, Milan, Italy.

AY 2002-03 Lectures in Bioinformatics, Simulation and Hybrid Systems, within the "System Biology" course held at the Courant Institute of Mathematical Sciences, NYU, U.S.A.

- February 2000 Graduate lectures on Embedded and Reactive Systems and Reactive Programming, Università di Udine, Udine, Italy.
- May 1996 Lectures on Temporal Logic and Verification. Department of Industrial Engineering, Rutgers University, U.S.A.
- AY 1995 CS 101 e CS102 (Introduction to Computer Science) Instructor. Courant Institute of Mathematical Sciences, NYU, U.S.A.
- AYs 1992-1995 Teaching assistant for several courses taught at Courant Institute of Mathematical Sciences, NYU, U.S.A. (Fundamental Algorithms, Distributed Computing, User Interfaces, Programming Languages).

## ***Students***

- Simone Rubinacci MS, 2015. Currently D.Phil. Student at Oxford University, Oxford, UK.
- Daniele Ramazzotti, PhD, 2016. Currently Post-doc in the Dept. of Pathology, Stanford University, Palo Alto, CA, USA.

## ***Departmental Services***

- 2015-present: Collegio di Dottorato Dipartimento di Informatica, Sistemistica e Comunicazione
- 2012-present: Giunta di Dipartimento.
- 2013-present: Gruppo Riesame del Dipartimento.
- 2010-present: Commissione dipartimentale per la Valutazione della Qualità della Ricerca (VQR).
- 2010-present: Commissione Didattica  
Work on the organization of the “Laurea Triennale” (undergraduate) and “Laurea Magistrale” (M.S.) degrees in Computer Science.
- 2009-2012: Collegio di Dottorato Dipartimento di Informatica, Sistemistica e Comunicazione.
- 2008-present: Commissione Tesi e Stage  
Currently presiding; editing of “Tesi” and “Stages” rules for the “Laurea Triennale” (undergraduate) and “Laurea Magistrale” (M.S.) degrees in Computer Science; continuous evaluation of students’ proposals presented as fulfillment of the requirements to be awarded said academic degrees.

## ***International and Domestic Services***

### **Como School and Workshop**

- Director of the Workshop and School on Cancer Development and Complexity, Como, 2016, <http://cdac.lakecomoschool.org>.
- Director of the Workshop and School on Cancer, Evolution and Complexity, Como, 2015, <http://ceac.lakecomoschool.org>.
- Director of the Workshop and School on Cancer, Systems and Complexity, Como, 2014, <http://csac.lakecomoschool.org>.

### **Program Committees**

- 13<sup>th</sup> International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics (CIBB2016), Program Committee, Striling, UK, September 2016.
- Scientific Board member of the Centro di Neuroscienze di Milano, [www.neuromi.it](http://www.neuromi.it), since June 2014.
- Third Workshop on Hybrid Systems and Biology (HSB 2014) Program Committee, Vienna, Austria, July 2014

- Associate Editor (Contributed Papers) for Workshop on Discrete Event Systems (WODES) 2014.
- 12<sup>th</sup> European Conference on Artificial Life (ECAL 2013), program committee.
- Workshop Italiano di Vita Artificiale e Computazione Evolutiva (WIVACE) 2013, Organizing Committee, Milan, Italy, 2013.
- First Workshop on Hybrid Systems and Biology (HSB 2012) Program Committee, Newcastle upon Tyne, UK, September 2012.
- European Lisp Symposium 2012 (ELS 2012) Program Chair, Zadar, Croatia, April 2012
- Institutional contact point for the Virtual Physiological Human European Network of Excellence, 2009-2012.
- European Lisp Symposium 2011 (ELS 2011) Program Committee, Hamburg, Germany, March 2011.
- LATA 2010 – 4<sup>th</sup> International Conference on Language and Automata, Trier, Germany, post-conference special issue reviewer.
- 3rd Workshop "From Biology To Concurrency and back" (FBTC 2010), Program Committee, Paphos, Cyprus, May 2010.
- European Lisp Symposium 2010 (ELS 2010) Program Committee, Lisbon, Portugal, May 2010.
- Symptoms, Signs and Findings: Towards an Ontology of Clinical Phenotypes Evolving in Time (SSF09) Organizing Committee, Milan, Italy, September 2009.
- European Lisp Symposium 2009 (ELS 2009) Chair of the Organizing Committee, Milan, Italy, May 2009.
- Workshop on Discrete Event Systems (WODES) 2008 Program Committee and Invited Session on Systems Biology Chair, Sweden, May 2008.
- European Lisp Symposium 2008 Program Committee, Bordeaux, France, May 2008.
- BioCONCUR Workshop 2005 Program Committee, 16<sup>th</sup> International Conference on Concurrency Theory, San Francisco, U.S.A. August 2005.

## Reviews

Reviewer for IET Systems Biology, IEEE Transactions on Information Technology in Biomedicine, IEEE Engineering in Medicine and Biology Magazine, IEEE Computer, Bioinformatics, Journal of Biomedical Informatics and other publications.

Reviewer for grant applications to the Army Research Office, U.S.A.

Reviewer for grant applications to the Archimedes and Thalys research funding programs, Greece.

Reviewer for grant applications to the Bioinformatique program, Agence Nationale de la Recherche, France.

Reviewer for grant applications to the Science Committee - Multidisciplinary Project Award, Cancer Research, UK.

## Funding

Pending World Cancer Research 2016, *Reconstructing Cancer Progression Models from Cross-Sectional Data: Comparative Ensemble and Individual Tumour Analysis* (role: PI; co-PI: Dr. Rocco Piazza, Università degli Studi di Milano Bicocca).

Pending MIUR, PRIN 2015, *A Comprehensive Study and Validation of Cancer Progression Models and their Use to Provide Personalized Therapies* (role PI, co-PIs: Prof. Alberto Policriti, Università degli Studi di Udine, Dr. Rocco Piazza, Università degli Studi di Milano Bicocca, Dr. Marco Beccuti, Università degli Studi di Torino)

2016-2017	Elixir-ITA, <i>TRONCO/CAPRON PDB: Cancer Progression Models Pipeline and Database</i> (role PI)
2016-2020	COST Action. CHARME: Harmonising standardisation strategies to increase efficiency and competitiveness of European life-science research (role Secondary Proponent; Primary Proponent, Dr. Susanne Hollmann, Universität Potsdam, Germany)
2010-2012	Regione Lombardia. <i>RetroNet (Formulazione di ipotesi sul comportamento di reti biochimiche a partire dall'analisi di cicli di retroazione)</i> . International cooperation with Prof. G. Bader, Donnelly Centre for Cellular + Biomolecular Research, University of Toronto, Toronto, Canada (role PI).
2005-2007	National Science Foundation “ <i>Emerging Models and Technologies for Computation</i> ” grant #0523851 (role Co-PI, PI Prof. Bud Mishra).
2006-2008	European Commission FP6 Marie Curie IRG grant #MIRG-CT-2005-031140 “ <i>BRONTE</i> ” (role PI).

## Computer Skills

**Programming Languages:** C/C++ 25 and more years, construction of run-time systems for higher level languages (SHIFT the first hybrid system simulator) and other libraries; Java 15 years, extension of the language to encompass Esterel synchronous semantics and integration with C-based libraries; Common Lisp 25 and more years; various shells and scripting languages (Perl, Python, Tcl/Tk, Php, Ruby) as needed for the past 25 years. HTML, XML, CSS, RDF, Javascript and other web handling languages and tools as needed.

**Simulation systems:** construction of the SHIFT system and simulation of large sections of California highway system.

**Formal Verification:** extension of model checking algorithms for simulation traces analysis and for construction of discrete controllers.

**Design and Management of Software Projects:** extensive experience in designing and implementing sizable software systems and in managing highly focused developer teams (3-5 people).

**Database experience:** construction of databases to handle genomic data and microarray data; MySQL, PostgreSQL. XML, HTML, RDF and other standard tools used as needed to interface with several publicly available databases.

**Tools:** MSVC, Emacs, Eclipse, Netbeans. Matlab, Octave, R, Maxima. Cadence VCC HW/SW co-design tool.

**Operating Systems:** UNIX, Windows, VxWorks RTOS, and VMS.

**Other tools:** Microsoft Office tools. TeX/LaTeX.

## Software Systems, and Software Libraries

TRONCO: A suite of R programs implementing cancer progression reconstruction algorithms based on a probability-raising notion of causality, which can be reinterpreted as yielding possible progressions from the point of view of selection advantages of a clonal subpopulation.

<http://bimib.disco.unimib.it/index.php/Tronco>, 2014-2015 (available in Bioconductor).

pyTSA: A Python library to easy the analysis of time course *in-silico* experiments.

<http://bimib.disco.unimib.it/index.php/Pytsa>, 2014.

GOALIE: A system for time-course redescription,

(<http://bioinformatics.nyu.edu/~marcoxa/work/GOALIE>) 2005-2006.

CL-GODB: A Common Lisp library to directly access the GO database (<http://www.godatabase.org>).

<http://common-lisp.net/projects/cl-godb>. With S. Kleinberg, support provided by Google “Summer of Code” program. 2005.

Simpathica/XSSYS: Simulation and querying of traces of biological systems; a Natural Language module is included. <http://bioinformatics.nyu.edu/Projects/Simpathica>, 2002-2005.

Jester: A reactive extension for Java in the style of Esterel.

<http://www.parades.rm.cnr.it/projects/jester/jester.html>, PARADES EEIG, Rome, Italy, 1998-2000.

SHIFT: The first Hybrid System simulator with dynamic network capabilities.

<http://path.berkeley.edu/SHIFT>, UC Berkeley Path Project, Berkeley, CA, U.S.A. 1995-1998.

## Patents

1. U.S. Provisional Patent application, Attorney Docket # 242383.US.01-475396-404, *Methods, Computer-accessible Medium, and Systems to Model Disease Progression Using Biomedical Data from Multiple Patients*, filed 2013-10-28.
2. U.S. Patent # 8,572,018 B2, *Method, System and Software Arrangement for Reconstructing Formal Descriptive Models of Processes from Functional/Modal Data Using Suitable Ontology*, issued 2013-10-29.
3. U.S. Patent # 7,831,392, *System and process for validating, aligning and reordering one or more genetic sequence maps using at least one ordered restriction map*, issued 2010-11-09.
4. U.S. Patent # 7,801,841, *Method, Systems, and Software Arrangements for Reconstructing Formal Descriptive Models of Processes from Functional/Modal Data Using Suitable Ontology*, issued 2010-09-21.
5. U.S. Patent application #60/293,254, *Automatic Validation, Alignment, and Reordering of Sequences via Optical Mapping*, filed 2001-05-24
6. U.S. Patent application #60/236,296, *System and Method for a Sequence Validation via Optical Map Matching*, filed 2000-09-28

## Invited Talks

*The Cellular Potts Model*, Tutorial at Hybrid Systems in Biology, 2014, VSL 2014, Vienna, Austria, July 23<sup>rd</sup>, 2014.

*Modelling Colonic Crypts with VCell and SBML/Spatial*, COMBINE 2013, Sept. 16 – 20, Institut Curie, Paris, France, 2013.

## Publications

### International Journals and Book Chapters

[BCG+16] I. M. Bocicor, G. Caravagna, A. Graudenzi, C. Cava, G. Mauri, M. Antoniotti, *Reconstructing Colorectal Cancer Progression through Copy Number Alteration Data*, International Journal of Data Mining and Bioinformatics, to appear, 2016.

[PGC+16] A. Paroni, A. Graudenzi, G. Caravagna, C. Damiani, G. Mauri, M. Antoniotti, *CABeRNET: a Cytoscape app for Augmented Boolean models of gene Regulatory NETWORKs*, BMC Bioinformatics, to appear 2016.

[DCR+16] L. De Sano, G. Caravagna, D. Ramazzotti, A. Graudenzi, G. Mauri, B. Mishra, M. Antoniotti, *TRONCO: an R package for the inference of cancer progression models from heterogeneous genomic data*, Bioinformatics, to appear, 2016.

[CDG+15] G. Castoldi, C. Di Gioia, F. Giollo, R. Carletti, C. Bombardi, M. Antoniotti, F. Roma, G. Zerbini, A. Stella, *Different regulation of miR-29a-3p in glomeruli and tubules in an experimental model of angiotensin II-dependent hypertension: potential role in renal fibrosis*, Clinical and Experimental Pharmacology and Physiology, online December 23<sup>rd</sup>, 2015, doi: 10.1111/1440-1681.12532.

[RGC+15] S. Rubinacci, A. Graudenzi, G. Caravagna, G. Mauri, J. Osborne, J. Pitt-Francis, M. Antoniotti, *CoGNAC: a Chaste plugin for the multiscale simulation of gene regulatory networks driving the spatial dynamics of tissues and cancer*, Cancer Informatics, Suppl. 4, 2015, doi:10.4137/CIN.S19965.

- [CDA15] G. Caravagna, L. De Sano, M. Antonioti, *Automatizing the analysis of stochastic biochemical time-series*, BMC Bioinformatics, 16(Suppl 9):S8, 2015, doi:10.1186/1471-2105-16-S9-S8.
- [RCO+15] D. Ramazzotti, G. Caravagna, L. Olde Loohuis, A. Graudenzi, I. Korsunsky, G. Mauri, M. Antonioti, B. Mishra, *CAPRI: Efficient Inference of Cancer Progression Models from Cross-sectional Data*, Bioinformatics, 31(18), 2015, doi:10.1093/bioinformatics/btv296.
- [OCG+14] L. Olde Loohuis, G. Caravagna, A. Graudenzi, D. Ramazzotti, G. Mauri, M. Antonioti, B. Mishra, *Inferring Tree Causal Models of Cancer Progression with Probability Raising*, PLoS ONE, published: October 9, 2014, doi:10.1371/journal.pone.0108358.
- [GCD+14] A. Graudenzi, G. Caravagna, G. De Matteis, M. Antonioti, *Investigating the relation between stochastic differentiation and homeostasis in intestinal crypts via multiscale modeling*, PLoS ONE, Volume 9, Issue 5, May 28, 2014, doi:10.1371/journal.pone.0097272.
- [CDA+14] G. Caravagna, A. D'Onofrio, M. Antonioti, G. Mauri, *Stochastic Hybrid Automata with non-instantaneous transitions to model biochemical systems with delays*. Information and Computation. Online 2014-01-27, 2014, doi:10.1016/j.ic.2014.01.010.
- [CZG+14] C. Cava, I. Zoppis, M. Gariboldi, I. Castiglioni, G. Mauri, M. Antonioti, *Combined Analysis of Chromosomal Instabilities and Gene Expression for Colon Cancer Progression Inference*, Journal of Clinical Bioinformatics, 2014-01-24, doi:10.1186/2043-9113-4-2.
- [AAL13] A. Alhazov, M. Antonioti, A. Leporati, *Characterizing the Computational Power of Energy-Based P-Systems*, International Journal of Computer Mathematics, Volume 90, Issue 4, April 2013, pages 789-800, 2013, doi:10.1080/00207160.2012.741781.
- [ABC+13] M. Antonioti, G. Bader, G. Caravagna, S. Crippa, A. Graudenzi, G. Mauri, *GESTODIFFERENT: A Cytoscape plugin for the generation and the identification of Gene Regulatory Networks describing a stochastic cell differentiation process*, Bioinformatics, January 2013, doi:10.1093/bioinformatics/bts726.
- [DGA12] G. De Matteis, A. Graudenzi, M. Antonioti, *A review of spatial computational models for multi-cellular systems, with regard to intestinal crypts and colorectal cancer developments*, Journal of Mathematical Biology, May 2012, doi:10.1007/s00285-012-0539-4.
- [ZGB+11] I. Zoppis, E. Gianazza, M. Borsani, C. Chinello, V. Mainini, C. Galbusera, C. Ferrarese, G. Galimberti, S. Sorbi, B. Borroni, F. Magni, Marco Antonioti, G. Mauri, *Mutual Information Optimization for Mass Spectra Data Alignment*, IEEE/ACM Transactions on Computational Biology and Bioinformatics, 99, May 2011, doi:10.1109/TCBB.2011.80.
- [VFM+11] L. Vanneschi, A. Farinaccio, G. Mauri, M. Antonioti, P. Provero, M. Giacobini, *A Comparison of Machine Learning Techniques for Survival Prediction in Breast Cancer*, BioData Mining, 4:11, 2011, doi:10.1186/1756-0381-4-12.
- [RTW+10] N. Ramakrishnan, S. Tadepalli, L. T. Watson, R. F. Helm, M. Antonioti, B. Mishra, *Reverse Engineering Dynamic Temporal Models of Biological Processes and their Relationships*, PNAS, 107(28), 12511-12516, July 22, 2010, doi:10.1073/pnas.1006283107.
- [CMB+10] G. Colombo, D. Merico, G. Boncoraglio, F. De Paoli, J. Ellul, G. Frisoni, Z. Nagy, A. van der Lugt, I. Vassanyi, M. Antonioti, *An Ontological Modelling Approach to Neurovascular Disease Study: the NEUROWEB Case*, Journal of Biomedical Informatics, 43(4), 469-484, August 2010, doi:10.1016/j.jbi.2009.12.005.
- [ACF+10] M. Antonioti, M. Carreras, A. Farinaccio, G. Mauri, D. Merico, I. Zoppis *An Application of Kernel Methods to Gene Cluster Temporal Meta-Analysis*, Computers and Operations Research, 37(8), 2010, doi:10.1016/j.cor.2009.03.011.
- [CMN+09] G. Colombo, D. Merico, Z. Nagy, F. De Paoli, M. Antonioti, G. Mauri, *Ontological modeling at a domain interface: bridging clinical and biomolecular knowledge*, The Knowledge Engineering Review, Special Issue on Ontologies, Conceptualization and Epistemology for Software and System Engineering, 24(3):205-224, 2009.
- [KAT+09] S. Kleinberg, M. Antonioti, S. Tadepalli, N. Ramakrishnan, and B. Mishra, *Systems Biology via Redescription and Ontologies (II): A Tool for Discovery in Complex Systems*, Special Issue on the Proceedings of the Sixth International Conference on Complex Systems, in

*Unifying Themes in Complex Systems*, Vol. VI, A. A. Minai, D. Braha, Y. Bar-Dam eds., Springer, 2009, doi:10.1007/978-3-540-85081-6\_24.

[RLU+08] S. Ryu, S.-C. Lin, N. Ugel, M. Antoniotti, B. Mishra  
*Mathematical Modeling of the formation of Apoptosome in Intrinsic Pathway of Apoptosis*, *Systems and Synthetic Biology*, 2(1-2):49-66, 2008.

[MTB+07] J. P. Mathew, B. S. Taylor, G. D. Bader, S. Pyarajan, M. Antoniotti, A. M. Chinnaiyan, C. Sander, S. J. Burakoff, B. Mishra  
*From Bytes to Bedside: Data Integration and Computational Biology for Translational Cancer Research*, *PLoS Computational Biology*, Volume 3, Issue 2, February 2007, doi:0.1371/journal.pcbi.0030012.

[BAF+05] P. Barbano, M. Antoniotti, J. Feng, M. Spivak, and B. Mishra  
*A Coherent Framework for Multi-resolution Analysis of Biological Networks with Memory: RAS pathway*, *Cell Cycle and Immune System*. *PNAS*, 102(18):6245-6250, 2005.

[APUM05] M. Antoniotti, S. Paxia, N. Ugel, B. Mishra  
*Simpatica: A Computational System Biology Tool within the VALIS Bioinformatics Environment*, in *Computational Systems Biology*, E. Eils and A. Kriete eds. Elsevier, 2005.

[AMP+04] M. Antoniotti, B. Mishra, C. Piazza, A. Policriti, M. Simeoni  
*Taming the Complexity of Biochemical Models through Bisimulation and Collapsing: Theory and Practice*, *Theoretical Computer Science*, 325(1):45-67 2004.

[MA+03] B. Mishra, M. Antoniotti et al., *A Sense of Life: Computational & Experimental Investigations with Models of Biochemical & Evolutionary Processes*, *OMICS – A Journal of Integrative Biology*, (Special Issue on BioCOMP, S. Kumar, ed.), 7(3), 2003.

[APUM03] M. Antoniotti, A. Policriti, N. Ugel, B. Mishra  
*Model Building and Model Checking for Biochemical Processes*, *Cell Biochemistry and Biophysics*, 38:271-286, 2003.

[AFFS01] M. Antoniotti, A. Ferrari, A. Flesca, A. L. Sangiovanni-Vincentelli,  
*JESTER: An Esterel-based Reactive Java Extension for Reactive Embedded Systems Co-Design*, in *System on Chip Methodologies and Design Languages*, Kluwer, 2001

## International Conferences

[CZG+13] C. Cava, I. Zoppis, M. Gariboldi, I. Castiglioni, G. Mauri, M. Antoniotti, *Copy-Number Alterations for tumor progression inference*, 14<sup>th</sup> Conference on Artificial Intelligence in Medicine (AIME13), Murcia, Spain, June 2013, doi:10.1007/978-3-642-38326-7\_16.

[CGA+12] G. Caravagna, A. Graudenzi, M. Antoniotti, G. Mauri and A. D'Onofrio, *Effects of delayed immune-response in tumor immune-system interplay*, First International Workshop on Hybrid Systems and Systems Biology, CONCUR 2012, Newcastle upon Tyne, UK, September 2012.

[GCD+12] A. Graudenzi, G. Caravagna, G. De Matteis, M. Antoniotti, *A multiscale model of intestinal crypts dynamics*, Proc. of the Italian Workshop on Artificial Life and Evolutionary Computation, WIVACE 2012, Parma, Italy, February 2012, ISBN: 978-88-903581-2-8.

[AAF+12] A. Alhazov, M. Antoniotti, R. Freund, A. Leporati, G. Mauri, *Self-Stabilization in Membrane Systems*, Proceedings of the Tenth Brainstorming Week on Membrane Computing, International Conference on Developments in Membrane Computing 2012, Seville, Spain, February 2012.

[AAL12] A. Alhazov, M. Antoniotti, A. Leporati, *Characterizing the Computational Power of Energy-Based P-Systems*, Proceedings of the Tenth Brainstorming Week on Membrane Computing, International Conference on Developments in Membrane Computing 2012, Seville, Spain, February 2012.

[ZBG+12] I. Zoppis, M. Borsani, E. Gianazza, C. Chinello, M. Antoniotti, A. M. Deelder, Y. E. M. van der Burgt, F. Magni, G. Mauri  
*Analysis of Correlation Structures in Renal Cell Carcinoma Patient Data*, International Conference on Bioinformatics Models, Methods and Algorithms (Bioinformatics 2012), Vilamoura, Algarve, Portugal, February 2012.



- [VFG+10] L. Vanneschi, A. Farinaccio, M. Giacobini, M. Antoniotti, G. Mauri, P. Provero  
*Identification of Individualized Feature Combinations for Survival Prediction in Breast Cancer: A Comparison of Machine Learning Techniques*, Proceedings of the EvoBIO 2010 Conference, Evo\* 2010, Istanbul, Turkey, April 2010.
- [Ant08b] M. Antoniotti  
*Modeling Systems Biology from the point of view of Discrete and Hybrid Systems*, Workshop on Discrete Event Systems (WODES 2008), Göteborg, Sweden, May 2008.
- [Ant08] M. Antoniotti  
*CLAZY: Lazy Calling for Common Lisp*, European Lisp Symposium 2008 (ELS08), Bordeaux, France, May 2008.
- [MZA+07] D. Merico, I. Zoppis, M. Antoniotti, G. Mauri  
*Evaluating Graph Kernels for Relation Discovery in GO-annotated Clusters*, KES 2007, WIRN 2007, Vietri sul Mare, Italy, September 2007.
- [CMF+07] G. Colombo, D. Merico, G. Frisoni, M. Antoniotti, F. De Paoli, G. Mauri  
*An ontological modeling approach to neurovascular disease studies: the NEUROWEB case*, NETTAB 2007, Pisa, Italy, June 2007.
- [ZMA+07] I. Zoppis, D. Merico, M. Antoniotti, B. Mishra, G. Mauri,  
*Discovering Relations among GO-annotated Clusters by Graph Kernel Methods*, International Symposium on Bioinformatics Research and Applications (ISBRA) 2007, Atlanta, GA, USA, May 2007.
- [KAT+06] S. Kleinberg, M. Antoniotti, S. Tadepalli, N. Ramakrishnan, and B. Mishra,  
*Remembrance of Experiments Past: A Redescription Based Tool for Discovery in Complex Systems*, International Conference on Complex Systems, Boston, U.S.A. June 2006.
- [MGD+05] V. Mysore, O. Gill, R. Daruwala, M. Antoniotti, V. Saraswat, B. Mishra,  
*Multi-Agent Modeling and Analysis of the Brazilian Food-Poisoning Scenario*, The Agent 2005 Conference on Generative Social Processes, Models, and Mechanisms. Agent 2005, Argonne National Laboratory, & The University of Chicago, 13-15, October 2005.
- [PAM+05] C. Piazza, M. Antoniotti, V. Mysore, A. Policriti, F. Winkler, and B. Mishra  
*Algorithmic Algebraic Model Checking I: Challenges from Systems Biology*, 17<sup>th</sup> International Conference on Computer Aided Verification (CAV05), Edimburgh, Scotland, UK, July 2005.
- [RAM05] N. Ramakrishnan, M. Antoniotti, and B. Mishra,  
*Reconstructing Formal Temporal Models of Cellular Events using the GO Process Ontology*, Bio-Ontologies SIG Meeting, ISMB 2005, Detroit, USA, 2005.
- [ARM05] M. Antoniotti, N. Ramakrishnan, and B. Mishra  
*GOALIE, A Common Lisp Application to Discover Kripke Models: Redescriving Biological Processes from Time-Course Data*, International Lisp Conference 2005, Stanford, CA, U.S.A., June 2005.
- [ALM04] M. Antoniotti, I. T. Lau, B. Mishra  
*Naturally Speaking: A System Biology Tool with Natural Language Based Interfaces*, Biology and Language Modeling Conference (BL2004), Pittsburgh, PA, U.S.A., November 2004.
- [ABC+04] M. Antoniotti, P. Barbano, J. Feng, N. Ugel, B. Mishra  
*Multiple Biological Model Classification: From System Biology to Synthetic Biology*, Proceedings of the BioCONCUR 2004 Workshop, London, U.K., 2004.
- [AMP+03] M. Antoniotti, B. Mishra, C. Piazza, A. Policriti, M. Simeoni  
*Modeling Cellular Behavior with Hybrid Automata: Collapsing and Bisimulation*, Computational Methods in System Biology (CMSB 2003), C. Priami ed., LNCS 2602, Springer 2003
- [APP+03] M. Antoniotti, F. Park, A. Policriti, N. Ugel, B. Mishra  
*Foundations of a Query and Simulation System for the Modeling of Biochemical and Biological Processes*, PSB 2003, Lihu'e, HW, U.S.A., January 2003.
- [APUM02] M. Antoniotti, A. Policriti, N. Ugel, B. Mishra  
*XS-systems: eXtended S-systems and Algebraic Differential Automata for Modeling Cell Behavior*, High Performance Computing (HiPC 2002), S. Sahni, V. K. Prasanna e U. Shukla eds., LNCS 2552, Springer 2002

- [A02] M. Antoniotti  
*Two Bioinformatics Applications of Common Lisp*, ILC 2002, San Francisco, [U.S.A.](#), 2002.
- [AFSS01] M. Antoniotti, A. Ferrari, A. L. Sangiovanni-Vincentelli, E. Sentovich  
*Embedded System Design Specification: Merging Reactive Control and Data Computation*, 40<sup>th</sup> IEEE Conference on Decision and Control (CDC 2001), Orlando, [U.S.A.](#), 2001,  
doi:10.1109/.2001.980331.
- [AFFS00] M. Antoniotti, A. Ferrari, A. Flesca A. L. Sangiovanni-Vincentelli,  
*JESTER: An Esterel-based Reactive Java Extension for Reactive Embedded Systems Co-Design*, Forum on Design Languages 2000, Tübingen, Germany, September 2000
- [ABB+98] M. Antoniotti, A. Balluchi, L. Benvenuti, A. Ferrari, R. Flora, W. Nesci, C. Pinello, C. Rossi, A. L. Sangiovanni-Vincentelli, G. Serra, M. Tabaro,  
*A Top-Down Constraints-Driven Design Methodology for Powertrain Control Systems*, Proceedings of the Global Powertrain Congress, Detroit, MI, U.S.A., October 1998
- [ADG97] M. Antoniotti, A. Deshpande, A. Girault,  
*Microsimulation Analysis of Multiple Merge Junctions under Autonomous AHS Operations*, Proceedings of the IEEE Conference on Intelligent Transportation Systems, Boston, MA, U.S.A. November 1997
- [ADG97b] M. Antoniotti, A. Deshpande, A. Girault,  
*Microsimulation Analysis of a Hybrid System Model of Multiple Merge Junction Highways and Semi-Automated Vehicles*, Proceedings of the IEEE Conference on Systems, Man and Cybernetics, Orlando, FL, U.S.A. October 1997
- [AG97] M. Antoniotti, A. Göllü,  
*SHIFT and SMART-AHS: A Language for Hybrid System Engineering, Modeling and Simulation*, USENIX Conference on Domain Specific Languages, Santa Barbara, CA, U.S.A., October 1997.
- [AM96] M. Antoniotti, B. Mishra,  
*NP-completeness of the Supervisor Synthesis Problem for Unrestricted CTL Specifications*, Workshop on Discrete Event Systems, Edinburgh, Scotland, U.K., 1996.
- [AJM95] M. Antoniotti, M. Jafari, B. Mishra,  
*Applying Temporal Logic Verification and Synthesis to Manufacturing Systems*, Proceedings of the IEEE Conference on Man, Systems and Cybernetics, Vancouver, Canada, 1995.
- [AM95] M. Antoniotti, B. Mishra,  
*Discrete Event Models + Temporal Logic = Supervisory Controller: Automatic Synthesis of Locomotion Controllers*, Proceedings of the IEEE International Conference on Robotics and Automation (ICRA 95), Nagoya, Japan, 1995.
- [AM94] M. Antoniotti, B. Mishra,  
*Automatic Synthesis Algorithms for Supervisory Controllers*, Proceedings of the IEEE Conference on Computer Integrated Manufacturing and Automation Technology (CIMAT 94), Troy, NY, U.S.A., 1994.

## National Conferences

- [CGA+13] Giulio Caravagna, Alex Graudenzi, Marco Antoniotti and Giovanni De Matteis,  
*Analysis of the spatial and dynamical properties of a multiscale model of intestinal crypts*, Italian Workshop on Artificial Life and Evolutionary Computation, Wivace 2013, July 1 – 2, 2013, Milan (MI), Italy.
- [RMA13] Daniele Ramazzotti, Carlo Maj and Marco Antoniotti, *A Model of Colonic Crypts using SBML Spatial*, Italian Workshop on Artificial Life and Evolutionary Computation, Wivace 2013, July 1 – 2, 2013, Milan (MI), Italy.
- [GCD+13] A. Graudenzi, G. Caravagna, G. De Matteis, M. Antoniotti, *Investigating intestinal crypt homeostasis through multiscale modeling*, BITS Annual Meeting 2013, May 21-23, Udine (UD), Italy, <http://bits2013.units.it/>, 2013.

## Submitted and Under Preparation

--- G. Caravagna, A. Graudenzi, D. Ramazzotti, R. Sanz-Pamplona, L. De Sano, V. Moreno, M. Antoniotti, B. Mishra, *Algorithmic Methods to Infer the Evolutionary Trajectories in Cancer Progression*.

## Presentations and Posters at International Conferences

[RCO+15b] D. Ramazzotti, G. Caravagna, L. Olde Loohuis, A. Graudenzi, I. Korsunsky, G. Mauri, M. Antoniotti, B. Mishra, *Efficient Inference of Selective Advantage Relationships in Cancer Progression*, ISMB/ECCB 2015, Dublin, Ireland, July 10 – 14, 2015.

[ALM+13] M. Antoniotti, A. Lakshminarayana, C. Maj, D. Ramazzotti, J. Schaff, *Modelling Colonic Crypts with VCell and SBML/Spatial*, ICSB 2013, Copenhagen, Denmark, Aug. 30 – Sept. 3, 2013.

[BCG+12] Iuliana M. Bocicor, Giulio Caravagna, Alex Graudenzi, Claudia Cava, Giancarlo Mauri, Marco Antoniotti, *Ordering copy number alteration data to analyze colorectal cancer progression*, NETTAB 2012 Workshop on “Integrated Bio-Search”, 14-16 November 2012, Como, Italy, <http://www.nettab.org/2012/>, EMBnet.journal 18 (Supplement B), 2012.

[CZG+12] Claudia Cava, Italo Zoppis, Manuela Gariboldi, James F. Reid, Marco Antoniotti, Giancarlo Mauri, *Chromosome instability for tumor progression inference*, NETTAB 2012 Workshop on “Integrated Bio-Search”, 14-16 November 2012, Como, Italy, <http://www.nettab.org/2012/>, EMBnet.journal 18 (Supplement B), 2012.

[ACC+12] Marco Antoniotti, Giulio Caravagna, Silvia Crippa, Alex Graudenzi, Giancarlo Mauri, *GeneStocDiff: A Cytoscape plugin for the generation and the identification of gene regulatory networks describing the stochastic differentiation process*, Poster at the 13<sup>th</sup> International Conference on Systems Biology (ICSB12), Toronto, Canada, Aug. 19-23, 2012.

[ZBG+12] Zoppis I., Borsani M., Gianazza E., Chinello C., Albo G., Rocco F., Deelder A. M., Yuri E. M. van Der Burgt Y. E. M., Antoniotti M., Magni F., Mauri G., *Characterization of Distinguishing Regions for Renal Cell Carcinoma Discrimination*, Poster at the 2nd IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS), UNLV, Las Vegas, Nevada, Feb. 23-25, 2012.

[AGM+10] M. Antoniotti, E. Gianazza, F. Magni, G. Mauri, I. Zoppis, *A Random Graph Analysis for Time Course Proteomic Data of RCC Patients*, Journal of Biotechnology, 150(supplement), November 2010, doi: 10.1016/j.jbiotec.2010.09.616.

[MCA+08] D. Merico, G. Colombo, M. Antoniotti, G. Mauri *NEUROWEB Project: from clinically-based phenotypes towards genomics integration*, Reading at the “Symptoms, Signs and Findings NCBO Workshop”, Dallas, TX, U.S.A., 2008.

[CMF+07] G. Colombo, D. Merico, G. Frisoni, M. Antoniotti, F. De Paoli, G. Mauri *Ontological Modeling for Neurovascular Disease Studies: Issues in the Adoption of Description Logic*, Poster at Description Logic 2007, Brixen-Bressanone, Italy, 2007.

[APP+02b] M. Antoniotti, F. Park, A. Policriti, N. Ugel, B. Mishra *Simulating Large Biochemical and Biological Processes and Reasoning about their Behavior*, Poster at ICSB 2002, Stockholm, Sweden, December 2002.

[AIM+02] M. Antoniotti, M. Isopi, V. Mittal, N. Ugel, B. Mishra *Mathematically Modeling Stem Cells Populations*, Poster at 2002 Meeting on Genome Sequencing and Biology, CSHL, Cold Spring Harbor, NY, [U.S.A.](http://www.cshl.org), May 2002.

[RAC+01] M. Rejali, M. Antoniotti, V. Cherepinsky, C. Leventhal, S. Paxia, A. Rudra, J. West, B. Mishra *Goals, Design and Implementation of a Versatile MicroArray Data Base*, Poster at CGC 2001, Baltimore, [U.S.A.](http://www.cgc.org), November 2001.

[AAC+01] M. Antoniotti, T. Anantharaman, C.-W. Chang, D. C. Schwartz, B. Mishra *Algorithms for combining Sequences and Maps: Examples from P. falciparum and E. coli*, Poster at GSAC 2001, San Diego, [U.S.A.](http://www.gsa.org), October 2001.

[AAC+01b] M. Antoniotti, T. Anantharaman, C.-W. Chang, J. Colinas, D. C. Schwartz, B. Mishra  
*Algorithms and Analysis for combining Sequences and Maps: Applications to the Malaria Parasite P. falciparum*, Poster at WABI 2001, Aarhus, Denmark, August 2001.

[AFLS99] M. Antoniotti, A. Ferrari, L. Lavagno, A. L. Sangiovanni-Vincentelli,  
*JESTER = Java || Esterel*, Presentation at the 1999 Synchronous Workshop, Hyeres, France, November 1999

[AFLS98] M. Antoniotti, A. Ferrari, L. Lavagno, A. L. Sangiovanni-Vincentelli,  
*Object-Oriented System Level Design for Embedded Reactive Systems*, Presentation at Forum on Design Languages, EPFL, Lousanne, CH, September 1998.

## Presentations and Posters at National Conferences

[RGC+15a] D. Ramazzotti, G. Caravagna, L. Olde Loohuis, A. Graudenzi, I. Korsunsky, G. Mauri, M. Antoniotti, B. Mishra, *An Algorithm for the Efficient Inference of Cancer Progression Models*, BITS Annual Meeting 2015, June 2 – 5, Milan (MI), Italy, 2015

[AMR13] Marco Antoniotti, Carlo Maj, Daniele Ramazzotti, *A SBML/Spatial Model of Colonic Crypts*, BITS Annual Meeting 2013, May 21 – 23, Udine (UD), Italy, <http://bits2013.units.it/>, 2013.

## Technical Reports

[CGR+15] G. Caravagna, A. Graudenzi, D. Ramazzotti, R. Sanz-Pamplona, L. De Sano, V. Moreno, M. Antoniotti, B. Mishra, *Algorithmic Methods to Infer the Evolutionary Trajectories in Cancer Progression*, bioRxiv, 2015 doi: <http://dx.doi.org/10.1101/027359>.

[DCR+15] L. De Sano, G. Caravagna, D. Ramazzotti, A. Graudenzi, G. Mauri, B. Mishra, M. Antoniotti, *TRONCO: an R package for the inference of cancer progression models from heterogeneous genomic data*, bioRxiv doi: <http://dx.doi.org/10.1101/027474>.

[RCO+14] D. Ramazzotti, G. Caravagna, L. Olde Loohuis, A. Graudenzi, I. Korsunsky, G. Mauri, M. Antoniotti, B. Mishra, *Efficient inference of cancer progression models*, 2014, arXiv:1408.4224

[Ant11] M. Antoniotti  
*Generic Equality and Comparison for Common Lisp*, CDR 8, Common Lisp Document Repository, <http://cdr.eurolisp.org/document/8/index.html>, May 2011.

[Ant08b] M. Antoniotti  
*Sub-interval Numerical Types for Common Lisp*, CDR 5, Common Lisp Document Repository, <http://cdr.eurolisp.org/document/5/index.html>, April 2008.

[KAR+07] S. Kleinberg, M. Antoniotti, N. Ramakrishnan, K. P. Unnikrishnan, B. Mishra  
*Modal Logic, Temporal Models and Neural Circuits: What Connects Them*, CIMS TR2007-907, December 2007.

[ARK+05b] M. Antoniotti, N. Ramakrishnan, D. Kumar, M. Spivak, B. Mishra  
*Remembrance of Experiments Past: Analyzing Time Course Datasets to Discover Complex Temporal Invariants*, CIMS TR2005-858, February 2005.

[PAM+05b] C. Piazza, M. Antoniotti, V. Mysore, A. Policriti, F. Winkler, B. Mishra  
*Algorithmic Algebraic Model Checking I: The Case of Biochemical Systems and their Reachability Analysis*, CIMS TR2005-859, February 1005.

[ALM04b] M. Antoniotti, I. T. Lau, B. Mishra, *Naturally Speaking: A System Biology Tool with Natural Language Based Interfaces*, CIMS TR2004-853, June 2004.

[AAPM01] M. Antoniotti, T. Anantharaman, S. Paxia, B. Mishra  
*Genomics via Optical Mapping IV: Sequence Validation via Optical Map Matching*, CIMS TR-811, Courant Institute of Mathematical Sciences, NYU, March 2001.

[AM94b] M. Antoniotti, B. Mishra  
*Automatic Synthesis Algorithms for Supervisory Controllers (Preliminary Report)*, CIMS TR-664, Courant Institute of Mathematical Sciences, NYU, November 1994

[MAHW93] B. Mishra, M. Antoniotti, F. Hansen, R. Wallace,  
*NYU Educational Robotics Project: A Pedagogic Overview*, CIMS TR-653, Courant Institute of  
Mathematical Sciences, NYU, November 1993.

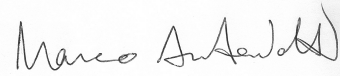
[MA93] B. Mishra, M. Antoniotti,  
*ED I: NYU Educational Robot Design and Evaluation*, CIMS-TR 643, Courant Institute of  
Mathematical Sciences, NYU, Aug. 1993.

[A93] M. Antoniotti,  
Conceptual and Pragmatic Tools for Design and Control of Manufacturing Systems (Petri Nets and  
Ramadge-Wonham Discrete Event Systems), CIMS-TR 664, Courant Institute of Mathematical  
Sciences, NYU, Jul. 1993.

## ***References***

Available upon request.

Milan, May 16, 2016

A handwritten signature in black ink, appearing to read "Marco Antoniotti", is written over a light gray rectangular background.

Marco Antoniotti