

# 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**

Spring and Fall 2018: Lectures on *Translational and Computational Biology*, Tandon School of Engineering, New York University, MS program in Bioinformatics, <http://engineering.nyu.edu/academics/programs/bioinformatics-ms>

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***

Giulio Diurno, MS, 2018.

Matteo Crespi, Stefano Gandelli, MS, 2016.

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.

2013-2015: Gruppo Riesame del Dipartimento.

2010-2013: Commissione dipartimentale per la Valutazione della Qualità della Ricerca (VQR).

2010-2015: 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, 2018, <http://cdac2018.lakecomoschool.org>.
- Director of the Workshop and School on Cancer Development and Complexity, Como, 2017, <http://cdac2017.lakecomoschool.org>.
- 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>.

## Conference Organization

- Program and Organizing Chair, COMBINE 2017, Como, October 9-13, 2017, [http://co.mbine.org/events/COMBINE\\_2017](http://co.mbine.org/events/COMBINE_2017).

## Program Committees

- 9<sup>th</sup> International Conference on Bioinformatics Models, Methods and Algorithms, BIOINFORMATICS 2018, Madeira, Portugal, January 2018
- NETTAB 2017, Methods, tools & platforms for Personalized Medicine in the Big Data Era, Palermo, Italy, October 2017
- 14<sup>th</sup> International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics (CIBB2017), Program Committee, Cagliari, Italy, September 2017
- 9<sup>th</sup> International Conference on Bioinformatics Models, Methods and Algorithms, BIOINFORMATICS 2017, Porto, Portugal, February 2017
- 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

- 2018-2019 FAQC 2018 competitive funding program of the Università degli Studi di Milano-Bicocca.
- 2017-2018 FFABR program of the Ministero dell'Istruzione, dell'Università e della Ricerca.
- 2016-2020 COST Action. *CHARME: Harmonising standardisation strategies to increase efficiency and competitiveness of European life-science research* (role Secondary Proponent and Management Committee Member; Primary Proponent, Dr. Susanne Hollmann, Universität Potsdam, Germany).
- 2016-2017 Elixir-ITA, *TRONCO/CAPRON PDB: Cancer Progression Models Pipeline and Database* (role PI)
- 2010-2012 Regione Lombardia. *RetroNet (Formulazione di ipotesi sul comportamento di reti biochimiche a partire dall'analisi di cicli di retroazione)*. International cooperation with Prof. G. Bader, Donnelly Centre for Cellular + Biomolecular Research, University of Toronto, Toronto, Canada (role PI).
- 2006-2008 PRIN 2006. *Biologically Inspired Systems and Calculi and their Applications (BISCA)*, (role, unit member)
- 2006-2008 European Commission FP6 Marie Curie IRG grant #MIRG-CT-2005-031140 "BRONTE" (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 [bioconductor.org/packages/release/bioc/html/TRONCO.html](http://bioconductor.org/packages/release/bioc/html/TRONCO.html) ).

Silver Prize for the 10<sup>th</sup> OSS World Challenge 2016, Seoul, South Korea (<http://ossaward.org/eng/m0101.do>).

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 # 7,801,841, *Method, Systems, and Software Arrangements for Reconstructing Formal Descriptive Models of Processes from Functional/Modal Data Using Suitable Ontology*, issued 2010-09-21.
4. U.S. Patent #7,831,392 B2, *System and process for validating, aligning and reordering one or more genetic sequence maps using at least one ordered restriction map*, filed 2000-09-28, granted 20101109

## **Invited Talks**

*Reconstructing Cancer Progression Models based on Probabilistic Causation Models*, Models for Oncogenesis, Clonality, and Tumor Progression, MBI, Ohio State University, Columbus, OH, USA, September 26, 2016.

*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

- [ACD+16] Marco Antoniotti, Giulio Caravagna, Luca De Sano, Alex Graudenzi, Giancarlo Mauri, Bud Mishra and Daniele Ramazzotti, *Design of the TRONCO BioConductor Package for TRanslational ONCOlogy*, The R Journal, 8(2), December 2016.
- [CGR+16] G. Caravagna, A. Graudenzi, D. Ramazzotti, R. Sanz-Pamplona, L. De Sano, G. Mauri, V. Moreno, M. Antoniotti, B. Mishra, *Algorithmic Methods to Infer the Evolutionary Trajectories in Cancer Progression*. Proceedings of the National Academy of Sciences (PNAS), June, 27, 2016, doi:10.1073/pnas.1520213113.
- [GCB+16] A. Graudenzi, G. Caravagna, I. M. Bocicor, C. Cava, M. Antoniotti, G. Mauri, *Ordering cancer mutational profiles of cross-sectional copy number alterations*, International Journal of Data Mining and Bioinformatics, 15:1, 2016, doi: <http://dx.doi.org/10.1504/IJDMB.2016.076017>.
- [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, 17:64, February, 2016, doi: 10.1186/s12859-016-0914-z.
- [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, February, 2016, doi: 10.1093/bioinformatics/btw035.
- [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. Antoniotti, *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. Antoniotti, 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. Antoniotti, 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. Antoniotti, *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. Antoniotti, 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. Antoniotti, *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. Antoniotti, 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. Antoniotti, 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. Antoniotti, *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 Antoniotti, 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. Antoniotti, 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. Antoniotti, 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. Antoniotti, *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. Antoniotti, 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.
- [KAT+10] S. Kleinberg, M. Antoniotti, 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.
- [CMN+09] G. Colombo, D. Merico, Z. Nagy, F. De Paoli, M. Antoniotti, 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, doi:10.1017/S0269888909990026.
- [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:10.1371/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, doi:10.1073/pnas.0500554102.
- [APUM05] M. Antoniotti, S. Paxia, N. Ugel, B. Mishra *Simpathica: A Computational System Biology Tool within the VALIS Bioinformatics Environment*, in *Computational Systems Biology*, E. Eils and A. Kriete eds. Elsevier, 2005, doi:10.1016/B978-012088786-6/50024-1.
- [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

[RNG+18] D. Ramazzotti, M. Nobile, A. Graudenzi, M. Antoniotti, Structural Learning of Probabilistic Graphical Models of Cumulative Phenomena, International Conference on Computational Science 2018 (ICCS2018), Wuxi, China, June 2018,  
doi: 10.1007/978-3-319-93698-7\_52.

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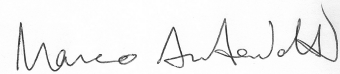


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