

Marco Antoniotti

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Overview

I primarily work on systems and computational biology. Being a computer science by training I therefore work on the boundary of mathematics, computer science and control theory with strong emphasis on statistical analysis, formal and logical methods (practical verification, synthesis and logic) and programming and description languages. In my activities I have always tackled problems both from a theoretical and from a pragmatic and applicative viewpoint, in order to build various systems capable of providing adequate solutions. For the last several years I have applied these methods to systems biology and computational biology, with an emphasis on data analysis for cancer research, especially "cancer progression reconstruction". 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. The TRONCO package and its evolution, LACE are playing a key role in the ongoing Accelerator Award project "Single-cells Cancer Evolution in the Clinic", funded by CRUK and AIRC, where I am co.P.I. for Bioinformatics, in collaboration with Fondazione Ospedale San Raffaele (Milan, Italy), ICR (London, UK), Politecnico (Milan, Italy) and Earlham Institute (Norwich, UK). 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 colleagues of Courant Institute of Mathematical Sciences and Tandon School of Engineering of New York University, USA.

AY 2018-19, present: Adjunct Professor of Bioinformatics, Tandon School of Engineering, New York University, New York, U.S.A.

I worked on the development and delivery of an online graduate course on Translational and Computational Biology also based on many of my group research activities on cancer progression algorithmic reconstructions.

AY 2020-21, present: Research Associate, Istituto Bioimmagini e Fisiologia Molecolare (IBFM), Centro Nazionale per le Ricerche (CNR) Milan, Italy.

Research on the development of computational models of biological systems to study genotype-phenotype relations and drug effects on cancer progressions.

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*

Teaching Experience

- AYs 2018-present: Online 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>
- Spring 2018: Course development 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-present: Lectures in Algorithms and Data Structures, Basic Programming for CS majors, Advanced Programming Languages and Software Engineering Laboratory, Bioinformatics Laboratory, Data and Computational Biology, Department of Informatics, Systems and Communication of the Università degli Studi di 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

- Daniele Ramazzotti, PhD, 2016. Currently Post-doc in the Dept. of Medicine of the Università degli Studi di Milano-Bicocca; previously Post-doc in the Dept. of Pathology, Stanford University, Palo Alto, CA, USA.
- Giulio Spinozzi, PhD, 2017. Currently Post-doc at the Section of Hematology, Department of Medicine Università degli Studi di Perugia, Perugia, Italy.
- Martina Rizza, PhD, 2017. Currently Post-doc at the Università degli Studi di Pavia, Pavia, Italy.

- Lucrezia Patruno, PhD, expected 2022.
- Francesco Craighero, PhD, expected 2022.

- Alessandro Lumaca, MS, 2019.
- Mattia Pennati, MS, 2019.
- Paolo Merola, MS, 2019.
- Lucrezia Patruno, MS, 2019.
- Adam Khayam, MS, 2018.
- Giulio Diurno, MS, 2018.
- Stefano Sarioli, MS, 2017 (Università degli Studi di Milano). Currently Ph.D. student, Università della Svizzera italiana, Lugano, CH.

- Matteo Crespi, MS, 2016.
- Stefano Gandelli, MS, 2016.
- Simone Rubinacci MS, 2015. D.Phil. Oxford University, Oxford, UK 2019.
- Luca De Sano, MS, 2015.
- Andrea Paroni, MS, 2015.

Mentoring

- 2020 Google Summer of Code; National Resource for Network Biology (www.nrn.org). Project: LACEView. Student: Bhavesh Narra (MS student, Centre for Biotechnology, Birla Institute of Technology and Science, Pilani, India)
- 2018 Google Summer of Code; National Resource for Network Biology (www.nrn.org). Project: cyTRON/JS. Student: Lucrezia Patruno (MS student, Università degli Studi di Milano-Bicocca)
- 2017 Google Summer of Code; National Resource for Network Biology (www.nrn.org). Project: cyTRON. Student: Edoardo Galimberti (PhD student, Dipartimento di Informatica, Università degli Studi di Torino)
- 2005 Google Summer of Code; LispNYC. Project: CL-GODB. Student: Samantha Kleinberg (currently Associate Professor of Computer Science, Stevens Institute of Technology, Hoboken, NJ, USA)

Departmental Services

- 2020-present: Department Representative in the Direction Committee of the Biostatistics, Bionformatics, Bioimaging Bicocca Centre, Università degli Studi di Milano-Bicocca
- 2020-present: Commissione Dipartimentale per la Valutazione della Qualità della Ricerca (VQR).
- 2012-2018: 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.
- 2008-2013: Commissione Tesi e Stage
Coordinator; 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

Doctoral Programs

- 2020-present, Collegio di Dottorato “Data Science in Medicine and Nutrition”, Università Humanitas, Milan, Italy.
- 2015-2020: Collegio di Dottorato Dipartimento di Informatica, Sistemistica e Comunicazione.
- 2009-2012: Collegio di Dottorato Dipartimento di Informatica, Sistemistica e Comunicazione.

Como School and Workshop

- Director of the Workshop and School on Cancer Development and Complexity, Como, 2016 – present, <http://cdac2019.lakecomoschool.org>, <http://cdac2021.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.

Program Committees

- 9th 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
- 14th International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics (CIBB2017), Program Committee, Cagliari, Italy, September 2017
- 9th International Conference on Bioinformatics Models, Methods and Algorithms, BIOINFORMATICS 2017, Porto, Portugal, February 2017
- 13th 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, 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.
- 12th 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 – 4th 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, 16th International Conference on Concurrency Theory, San Francisco, U.S.A. August 2005.

Domestic Services

- 2012-2020 Commissione Didattica Gruppo di Informatica (GRIN)

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, BMC Bioinformatics, Nature SREP 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	Horizon 2020, CE, PPPA-AIPC-2020 2020-08-18, European Childhood Cancer Big Data Gateway, (Ex-ChanGe), (role: Co-PI, B4 Centre, Università degli Studi di Milano Bicocca, Coordinator, Pamela Kearns, Institute of Cancer and Genomic Sciences, Paediatric Oncology, University of Birmingham, UK)
2020-2024	Horizon 2020, CE, H2020-SC1-BHC-2018-2020, PCP Action, #874719, <i>Integrated and standardized NGS workflows for Personalised therapy</i> , (Instand-NGS4P) (role: Head of Bioinformatics Unit; Coordinator, Kurt Zatloukal, Institute of Pathology, Medical University of Graz, Austria; Marialuisa Lavitrano, Co-PI, Dipartimento di Medicina e Chirurgia, Università degli Studi di Milano-Bicocca, Milan, Italy).
2018-2023	CRUK/AIRC/FC-AECC Accelerator Award #22790, <i>Single Cell Cancer Evolution in the Clinic</i> (role: Co-PI, Head of Bioinformatics Unit; PI, Giovanni Tonon, Fondazione Ospedale San Raffaele, Milan, Italy).
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 #CA15110. <i>CHARME: Harmonising standardisation strategies to increase efficiency and competitiveness of European life-science research</i> (role: Secondary Proponent and Management Committee Member; Primary Proponent, Dr. Susanne Hollmann, Universität Potsdam, Germany).
2016-2017	Elixir-ITA, <i>TRONCO/CAPRON PDB: Cancer Progression Models Pipeline and Database</i> (role PI)
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).
2006-2008	PRIN 2006. <i>Biologically Inspired Systems and Calculi and their Applications (BISCA)</i> , (role, unit member)
2006-2008	European Commission FP6 Marie Curie IRG grant #MIRG-CT-2005-031140 "BRONTE".

Computer Skills

Programming Languages: C/C++ 30 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 30 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. Newer ecosystems in the more recent past: R, Matlab, Mathematica, Julia.

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: UNIXes, Windows, VxWorks RTOS, VMS, MVS, z/OS.

Other tools: Microsoft Office tools. TeX/LaTeX.

Software Systems, and Software Libraries

cyTRON/js: A web based application providing an interface to the TRONCO suite using the cytoscape.js interface. With Lucrezia Patruno and Daniele Ramazzotti; support provided by Google “Summer of Code” program 2018 and by the National Resource for Network Biology, USA.

cyTRON: A Cytoscape application providing an interface to the TRONCO suite. With Edoardo Galimberti and Daniele Ramazzotti; support provided by Google “Summer of Code” program 2017 and by the National Resource for Network Biology, USA.

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).

Silver Prize for the 10th 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, issued 2010-11-09

Invitations

“Education in AI and Health” Panel Chair, ICAIH 2019 meeting, Milan, November 13-14, 2019.

Grand Challenge Consultation Workshop, CRUK and AIRC meeting, Milan, September 9-10, 2019.

National Resource for Network Biology representative to the Google Summer of Code Mentor Summit (GSoC 2018), Sunnyvale, CA, October 12-14, 2018.

Reconstructing Mutational Graphs of Tumor Evolution from Single Cells Data, BITS 2018 Workshop “Single Cell Revolution”, Molecular Biotechnology Center, Turin, Italy, June 26th, 2018.

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 23rd, 2014.

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

Two Bioinformatics Applications of Common Lisp, International Lisp Conference, Oct. 27-31, 2002, San Francisco, CA, USA, 2002.

Publications

Editorial Contributions

[AMP19] *Network Bioscience* Research Topic, Frontiers in Genetics – Bioinformatics and Computational Biology, Marco Antoniotti, Bud Mishra and Marco Pellegrini eds., www.frontiersin.org/research-topics/7394/network-bioscience, 2019, doi:10.3389/fgene.2019.01160.

International Journals and Book Chapters

[K+20] S. Keating et al, *SBML Level 3: An extensible format for the exchange and reuse of biological models*, *Molecular Systems Biology*, 16 e9110, August 2020, doi:10.15252/msb.20199110.

[PMC+20] L. Patrino, D. Maspero, F. Craighero, F. Angaroni, M. Antoniotti, A. Graudenzi, *A review of computational strategies for denoising and imputation of single-cell transcriptomic data*, *Briefings in Bioinformatics*, accepted, August 2020, doi:10.1093/bib/bbaa222.

[AGR+20] F. Angaroni, A. Graudenzi, M. Rossignolo, D. Maspero, T. Calarco, R. Piazza, S. Montangero, M. Antoniotti, *An optimal control framework for the automated design of personalized cancer treatments*, *Frontiers Bioengineering and Biotechnology – Bioinformatics and Computational Biology*, May 2020, doi: 10.3389/fbioe.2020.00523.

- [DRM+20] C. Damiani, L. Rovida, D. Maspero, I. Sala, L. Rosato, M. Di Filippo, D. Pescini, A. Graudenzi, M. Antoniotti, G. Mauri, *MaREA4Galaxy: metabolic reaction enrichment analysis and visualization of RNA-seq data using Galaxy*, Computational and Structural Biotechnology Journal, 18, 2020, doi: [10.1016/j.csbj.2020.04.008](https://doi.org/10.1016/j.csbj.2020.04.008).
- [MDA+19] Davide Maspero, Chiara Damiani, Marco Antoniotti, Alex Graudenzi, Marzia Di Filippo, Marco Vanoni, Giulio Caravagna, Riccardo Colombo, Daniele Ramazzotti, Dario Pescini, *The Influence of Nutrients Diffusion on a Metabolism-driven Model of a Multi-cellular System*, *Fundamenta Informaticae*, vol. 171, no. 1-4, pp. 279-295, 2020, doi: [10.3233/FI-2020-1883](https://doi.org/10.3233/FI-2020-1883).
- [RGD+19] Daniele Ramazzotti, Alex Graudenzi, Luca De Sano, Marco Antoniotti, Giulio Caravagna, *Learning Mutational Graphs of Individual Tumor Evolution from Single-cell and Multi-region Sequencing Data*, *BMC Bioinformatics*, 20:210, April 26, 2019, doi: [10.1186/s12859-019-2795-4](https://doi.org/10.1186/s12859-019-2795-4).
- [RNG+19] Daniele Ramazzotti, Marco Nobile, Alex Graudenzi, Marco Antoniotti, *Efficient Computational Strategies to Learn the Structure of Probabilistic Graphical Models of Cumulative Phenomena*, *Journal of Computational Science*, vol 30 (January 2019), 2019, doi: [10.1016/j.jocs.2018.10.009](https://doi.org/10.1016/j.jocs.2018.10.009).
- [GMD+18] Alex Graudenzi, Davide Maspero, Marzia Di Filippo, Marco Grugnoli, Claudio Isella, Giancarlo Mauri, Enzo Medico, Marco Antoniotti, Chiara Damiani, *Integration of transcriptomic data and metabolic networks in cancer samples reveals highly significant prognostic power*, *Journal of Biomedical Informatics*, 2018, doi: [10.1016/j.jbi.2018.09.010](https://doi.org/10.1016/j.jbi.2018.09.010).
- [RNA+18] Daniele Ramazzotti, Marco Nobile, Marco Antoniotti, Alex Graudenzi, *Learning the Probabilistic Structure of Cumulative Phenomena with Suppes-Bayes Causal Networks*. *Evolutionary Bioinformatics*, 14:1-10, May 27, 2018, doi: [10.1177/1176934318785167](https://doi.org/10.1177/1176934318785167).
- [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, doi: [10.32614/RJ-2016-032](https://doi.org/10.32614/RJ-2016-032).
- [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](https://doi.org/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: [10.1504/IJDMB.2016.076017](https://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](https://doi.org/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](https://doi.org/10.1093/bioinformatics/btw035).
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- [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](https://doi.org/10.4137/CIN.S19965).
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