



DANIELA BESOZZI | *Curriculum Vitae*

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Professional Profile

- My research activity is focused on the investigation of the emergent behavior of various complex biological systems, including the computational analysis of networks of interacting, dynamically evolving or self-assembling biomolecules.
- I developed novel modeling, calibration and simulation methodologies, relying on computational intelligence, to define predictive models able to provide new insights and drive specific behaviors by means of controlled stimuli.
- I mainly worked in the fields of Systems Biology, Computational Biology, and Bioinformatics, representing the interface between the wet laboratory and the computational scientists. As a result, I developed the ability of understanding both worlds, facilitating the communication and the mutual comprehension among the researchers in these disciplines. I comprehend and can discuss scientific works in molecular and cellular biology, molecular self-assembly, medicine, systems biology, synthetic biology, bioinformatics, computer science, and mathematics.
- Thanks to my mathematical background, I have an excellent abstraction capability, which is extremely useful for both the formalization and modeling phases. Due to my attitude, I can easily link topics, concepts and tools across different disciplines.
- I am an extremely versatile and curious scientist, as proven by the heterogeneity of my research products and my network of collaborations. I am creative, open minded, keen to computational thinking. I love challenging topics and I am strongly determined in solving open problems in both biological and medical fields.
- I have a long experience in the coordination of interdisciplinary groups of researchers, and in creating a friendly work environment characterized by extreme commitment and productivity.
- In training and education activities, I am totally committed and used to tailor the course syllabus and the teaching material according to the background and interests of the students. I always encourage and welcome the students' active participation, questions and critical discussion in the classroom. I love to disseminate knowledge, curiosity and passion for science.

Research interests

- Systems Biology, Computational Biology, Bioinformatics.
- Mathematical modeling of biological systems (including, but not restricted to, cell proliferation and programmed cell death processes in cancer, dysfunctional processes in leukemia and Parkinson's disease, signal transduction pathways, DNA repair systems).
- Computational Intelligence methods (Swarm Intelligence, Evolutionary Computation, Machine Learning, Fuzzy Logic).
- DNA and peptide self-assembly.
- High performance computing.
- Biomedical image analysis.
- Theoretical computer science (bio-inspired computational paradigms).

Career and education

Academic appointments

- Oct. 2015 - present day: **Associate Professor**
Department of Informatics, Systems and Communication,
University of Milano-Bicocca, Italy.
- Dec. 2002 - Sept. 2015: **Assistant Professor**
Department of Computer Science, University of Milano, Italy.

Education

- Febr. 2004: **Ph.D. in Computer Science**, University of Milano, Italy.
Evaluation: excellent.
- Oct. 2000: **Master's degree in Mathematics**, University of Insubria, Italy.
Grade: 110/110, first class honours.

Academic memberships

- Jan. 2020 - present day: Member of the IEEE CIS Task Force on "Advanced representation in biological and medical search and optimization".
- March 2019 - present day: IEEE member.
IEEE Nanotechnology Council member.
IEEE Life Sciences Community member.
- Aug. 2019 - Aug. 2020: IEEE Computational Intelligence Society member.
IEEE Engineering in Medicine and Biology Society member.
IEEE Brain Community member.

- ❑ June 2018 - present day: Member of Italian Laboratory of Artificial Intelligence and Intelligent Systems (CINI AIIS).
- ❑ March 2015 - Dec. 2017: Member of the Italian Society of Biochemistry and Molecular Biology (SIB), scientific group “Computational and Systems Biology”.
- ❑ Nov. 2015 - March 2019: Member of ICT COST Action IC1406 “High-Performance Modelling and Simulation for Big Data Applications (cHiPSet)”, Working Group “HPC-enabled Modelling for Life Sciences”.
- ❑ Jan. 2013 - Dec. 2016: Research Member at SYSBIO.IT Centre of Systems Biology, Milano, Italy.
- ❑ Jan. 2013 - Dec. 2014: Research Associate at the Institute for Systems Analysis and Computer Science, National Research Council, Rome, Italy.

Awards

- ❑ 2020: **Best Paper Award (nominated)** at the IEEE World Congress on Computational Intelligence (WCCI 2020), IEEE-CEC track.
- ❑ 2019: **Best Paper Award** at the 16th IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology – CIBCB 2019, July 9-11, 2019, Certosa di Pontignano, Italy.
- ❑ 2004: **Best Italian Ph.D. thesis in Theoretical Computer Science**, conferred by the Italian Chapter of the European Association for Theoretical Computer Science (EATCS).
- ❑ 2002: **Best Student Paper Award** at the 8th International Meeting on DNA based computers (DNA8), Hokkaido University, Japan, June 10-13, 2002.

Publications

Journal papers (with peer-review)

- ❑ S. Spolaor, M. Scheve, M. Firat, P. Cazzaniga, D. Besozzi, M.S. Nobile. **Screening for combination cancer therapies with dynamic fuzzy modeling and multi-objective optimization.** *Frontiers in Genetics*, 2021 (to appear).
- ❑ M.S. Nobile, L. Manzoni, F. Fontana, P. Cazzaniga, G. Mauri, G. Saracino, D. Besozzi, F. Gelain. **HyperBeta: characterizing the structural dynamics of proteins and self-assembling peptides.** *Scientific Reports*, 2021 (to appear).
- ❑ R. Tisi, M. Spinelli, A. Palmioli, C. Airoidi, P. Cazzaniga, D. Besozzi, M.S. Nobile, E. Mazzoleni, S. Arnhold, L. De Gioia, R. Grandori, F. Peri, M. Vanoni, E. Sacco. **The Multi-Level Mechanism of**

Action of a Pan-Ras Inhibitor Explains its Antiproliferative Activity on Cetuximab-Resistant Cancer Cells. *Frontiers in Molecular Biosciences* 8:625979, 2021.

- ❑ S. Spolaor, C. Fuchs, P. Cazzaniga, U. Kaymak, D. Besozzi, M.S. Nobile. **Simpful: A User-Friendly Python Library for Fuzzy Logic.** *International Journal of Computational Intelligence Systems*, 13:1, 1687 - 1698, 2020.
- ❑ L. Rundo, A. Tangherloni, D.R. Tyson, R. Betta, C. Militello, S. Spolaor, M.S. Nobile, D. Besozzi, A.L.R. Lubbock, V. Quaranta, G. Mauri, C.F. Lopez, P. Cazzaniga. **ACDC: Automated Cell Detection and Counting for time-lapse fluorescence microscopy.** *Applied Sciences*, 10:18, 6187, 2020.
- ❑ Nobile M.S., Nisoli E., Vlachou T., Spolaor S., Cazzaniga P., Mauri G., P.G. Pelicci, D. Besozzi: **cuProCell: GPU-accelerated analysis of cell proliferation with flow cytometry data**, *IEEE Journal of Biomedical And Health Informatics*, 24(11), 2020.
- ❑ L. Manzoni, D.M. Papetti, P. Cazzaniga, S. Spolaor, G. Mauri, D. Besozzi, M.S. Nobile, **Surfing on fitness landscapes: a boost on optimization by Fourier surrogate modeling**, *Entropy*, 22:3, 2020.
- ❑ M.S. Nobile, G. Votta, R. Palorini, S. Spolaor, H. De Vitto, P. Cazzaniga, F. Ricciardiello, G. Mauri, L. Alberghina, F. Chiaradonna, D. Besozzi. **Fuzzy modeling and global optimization to predict novel therapeutic targets in cancer cells.** *Bioinformatics*, 36(7):2181–2188, 2020.
- ❑ Spolaor S., Nobile M.S., Mauri G., Cazzaniga P., Besozzi D.: **Coupling mechanistic approaches and Fuzzy Logic to model and simulate complex systems**, *IEEE Transactions on Fuzzy Systems*, 28(8), 1748–1759, 2020.
- ❑ L. Rundo, C. Han, Y. Nagano, J. Zhang, R. Hataya, C. Militello, A. Tangherloni, M.S. Nobile, C. Ferretti. P. Cazzaniga, D. Besozzi, S. Vitabile, M.C. Gilardi, G. Mauri, H. Nakayama. **USE-Net: Incorporating squeeze-and-excitation blocks into U-Net for prostate zonal segmentation of multi-institutional MRI datasets.** *Neurocomputing*, 365, 31-43, 2019.
- ❑ D. Besozzi, M. Castelli, P. Cazzaniga, L. Manzoni, M.S. Nobile, S. Ruberto, L. Rundo, S. Spolaor, A. Tangherloni, L. Vanneschi. **Computational Intelligence for Life Sciences**, *Fundamenta Informaticae*, 171:1-4, 57-80, 2019.
- ❑ M.S. Nobile, T. Vlachou, S. Spolaor, D. Bossi, P. Cazzaniga, L. Lanfranccone, G. Mauri, P.G. Pelicci, D. Besozzi. **Modeling cell proliferation in human acute myeloid leukemia xenografts.** *Bioinformatics*, *Bioinformatics*, 35(18):3378–3386, 2019.
- ❑ L. Rundo, A. Tangherloni, M.S. Nobile, C. Militello, D. Besozzi, G. Mauri, P. Cazzaniga. **MedGA: A novel evolutionary method for medical image enhancement.** *Expert Systems with Application*, 119:387-399, 2019.
- ❑ A. Tangherloni, S. Spolaor, L. Rundo, M.S. Nobile, P. Cazzaniga, G. Mauri, P. Liò, I. Merelli, D. Besozzi. **GenHap: A novel computational method based on genetic algorithms for haplotype assembly.** *BMC Bioinformatics* 20(Suppl 4):172, 2019.
- ❑ A. Tangherloni, S. Spolaor, P. Cazzaniga, D. Besozzi, L. Rundo, G. Mauri, M.S. Nobile. **Biochemical parameter estimation vs. benchmark functions: a comparative study of optimization performance and representation design.** *Applied Soft Computing*, 81:105494, 2019.
- ❑ M.S. Nobile, P. Cazzaniga, D. Besozzi, G. Mauri. **ginSODA: massive parallel integration of stiff ODE systems on GPUs.** *Journal of Supercomputing*, 75:12, 7844-7856, 2019.

- ❑ L. Rundo, A. Tangherloni, P. Cazzaniga, M.S. Nobile, G. Russo, M.C. Gilardi, S. Vitabile, G. Mauri, D. Besozzi, C. Militello. **A novel framework for MR image segmentation and quantification based on MedGA**. Computer Methods and Programs in Biomedicine, 176:159-172, 2019.
- ❑ M.S. Nobile, G. Pasi, P. Cazzaniga, D. Besozzi, R. Colombo, G. Mauri. **Fuzzy self-tuning PSO: A settings-free algorithm for global optimization**. Swarm and Evolutionary Computation, 39:70-85, 2018.
- ❑ M.S. Nobile, P. Cazzaniga, A. Tangherloni, D. Besozzi. **Graphics Processing Units in Bioinformatics, Computational Biology and Systems Biology**. Briefings in Bioinformatics, 18(5):870-885, 2017.
- ❑ A. Tangherloni, M.S. Nobile, P. Cazzaniga, D. Besozzi, G. Mauri. **Gillespie's Stochastic Simulation Algorithm on MIC coprocessors**. Journal of Supercomputing, 73:676-68, 2017.
- ❑ A. Tangherloni, M.S. Nobile, D. Besozzi, G. Mauri, P. Cazzaniga. **LASSIE: Simulating large-scale models of biochemical systems on GPUs**. BMC Bioinformatics, 18:246, 2017.
- ❑ L.A. Harris, M.S. Nobile, J.C. Pino, A.L.R. Lubbock, D. Besozzi, G. Mauri, P. Cazzaniga, C.F. Lopez. **GPU-powered model analysis with PySB/cupSODA**. Bioinformatics, 3(21):3492-3494, 2017.
- ❑ M.S. Nobile, A.E. Porreca, S. Spolaor, L. Manzoni, P. Cazzaniga, G. Mauri, D. Besozzi. **Efficient simulation of reaction systems on Graphics Processing Units**. Fundamenta Informaticae, 154(1-4):307-321, 2017.
- ❑ M. Cvijovic, T. Höfer, J. Aćimović, L. Alberghina, E. Almaas, D. Besozzi, A. Blomberg, T. Bretschneider, M. Cascante, O. Collin, P. de Atauri, C. Depner, R. Dickinson, M. Dobrzynski, C. Fleck, J. Garcia-Ojalvo, D. Gonze, J. Hahn, H.M. Hess, S. Hollmann, M. Krantz, U. Kummer, T. Lundh, G. Martial, V. Martins dos Santos, A. Mauer-Oberthür, B. Regierer, B. Skene, E. Stalidzans, J. Stelling, B. Teusink, C.T. Workman, S. Hohmann. **Strategies for structuring interdisciplinary education in Systems Biology**. Nature Journal Systems Biology and Application, 2:16011, 2016.
- ❑ M.S. Nobile, P. Cazzaniga, D. Besozzi, D. Pescini, G. Mauri. **cuTauLeaping: a GPU-powered tau-leaping stochastic simulator for massive parallel analyses of biological systems**. PLOS ONE, 9(3):e91963, 2014.
- ❑ P. Cazzaniga, M.S. Nobile, D. Besozzi, M. Bellini, G. Mauri. **Massive exploration of perturbed conditions of the blood coagulation cascade through GPU parallelization**. BioMed Research International, Special Issue "High-Performance Computing and Big Data in Omics-based Medicine", 2014:863298, 2014.
- ❑ M.S. Nobile, P. Cazzaniga, D. Besozzi, G. Mauri. **GPU-accelerated simulations of mass-action kinetics models with cupSODA**. The Journal of Supercomputing, 69(1):17-24, 2014.
- ❑ P. Cazzaniga, C. Damiani, D. Besozzi, R. Colombo, M.S. Nobile, D. Gaglio, D. Pescini, S. Molinari, G. Mauri, L. Alberghina, M. Vanoni. **Computational strategies for a system-level understanding of metabolism**. Metabolites, 4(4):1034-1087, 2014.
- ❑ F. Amara, R. Colombo, P. Cazzaniga, D. Pescini, A. Csikász-Nagy, M. Muzi Falconi, D. Besozzi, P. Plevani. **In vivo and in silico analysis of PCNA ubiquitylation in the activation of the Post Replication Repair pathway in S. cerevisiae**. BMC Systems Biology, 7:24, 2013.
- ❑ D. Pescini, P. Cazzaniga, D. Besozzi, G. Mauri, L. Amigoni, S. Colombo, E. Martegani. **Simulation of the Ras/cAMP/PKA pathway in budding yeast highlights the establishment of stable oscillatory states**. Biotechnology Advances, 30(1):99-107, 2012.

- ❑ L. Corolli, F. Marini, C. Maj, D. Besozzi, G. Mauri. **An excursion in reaction systems: from computer science to biology**. Theoretical Computer Science, 454:95-108, 2012.
- ❑ D. Besozzi, P. Cazzaniga, D. Pescini, G. Mauri, S. Colombo, E. Martegani. **The role of feedback control mechanisms on the establishment of oscillatory regimes in the Ras/cAMP/PKA pathway in *S. cerevisiae***. EURASIP Journal on Bioinformatics and Systems Biology, 2012:10, 2012.
- ❑ D. Besozzi, P. Cazzaniga, S. Cocolo, G. Mauri, D. Pescini. **Modeling diffusion in a signal transduction pathway: the use of virtual volumes in P systems**. International Journal of Foundations of Computer Science, 22(1):89-96, 2011.
- ❑ A. Leporati, D. Besozzi, P. Cazzaniga, D. Pescini, C. Ferretti. **Computing with energy and chemical reactions**. Natural Computing, 9(2):493-512, 2010.
- ❑ D. Besozzi, N. Busi, P. Cazzaniga, C. Ferretti, A. Leporati, G. Mauri, D. Pescini, C. Zandron. **(Tissue) P systems with cell polarity**. Mathematical Structures in Computer Science, 19(6):1141-1160, 2009.
- ❑ D. Besozzi, P. Cazzaniga, D. Pescini, G. Mauri. **Modelling metapopulations with stochastic membrane systems**. BioSystems, 91(3):499-514, 2008.
- ❑ P. Cazzaniga, D. Pescini, D. Besozzi, G. Mauri, S. Colombo, E. Martegani. **Modeling and stochastic simulation of the Ras/cAMP/PKA pathway in the yeast *Saccharomyces cerevisiae* evidences a key regulatory function for intracellular guanine nucleotides pools**. Journal of Biotechnology, 133(3):377-385, 2008.
- ❑ M. Muskulus, D. Besozzi, R. Brijder, P. Cazzaniga, S. Houweling, D. Pescini, G. Rozenberg. **Cycles and communicating classes in membrane systems and molecular dynamics**. Theoretical Computer Science, 372(2-3):242-266, 2007.
- ❑ D. Besozzi, P. Cazzaniga, D. Pescini, G. Mauri. **Seasonal variance in P system models for metapopulations**. Progress in Natural Science, 17(4):392-400, 2007.
- ❑ D. Pescini, D. Besozzi, G. Mauri, C. Zandron. **Dynamical probabilistic P systems**. International Journal of Foundations of Computer Science, 17(1):183-204, 2006.
- ❑ D. Besozzi, E. Csuhaj-Varjú, G. Mauri, C. Zandron. **On the power and size of extended gemmating P systems**. Soft Computing, 9(9):650-656, 2005.
- ❑ D. Besozzi, G. Mauri, C. Zandron. **Hierarchies of parallel rewriting P systems: A survey**. New Generation Computing, 22(4):331-347, 2004.
- ❑ D. Besozzi, C. Ferretti, G. Mauri, C. Zandron. **P systems with deadlock**. BioSystems, 70(2):95-105, 2003.
- ❑ D. Besozzi, G. Mauri, G. Păun, C. Zandron. **Gemmating P systems: collapsing hierarchies**. Theoretical Computer Science, 296(2):253-267, 2003.

Conference proceedings (with peer-review)

- ❑ M.S. Nobile, P. Cazzaniga, S. Spolaor, D. Besozzi, L. Manzoni. **Fourier Surrogate Models of Dilated Fitness Landscapes in Systems Biology (or how we learned to torture optimization problems until they confess)**. IEEE Conference on Computational Intelligence in Bioinformatics and Computational Biology, 2020.

- ❑ Papetti D.M., Spolaor S., Besozzi D., Cazzaniga P., Antoniotti M., Nobile M.S.: **On the automatic training of fully analogical spiking neuromorphic chips**, IEEE International Joint Conference on Neural Networks (IJCNN 2020), Glasgow, UK, 2020.
- ❑ Nobile M.S., Spolaor S., Cazzaniga P., Papetti D.M., Besozzi D., Ashlock D.A., Manzoni L.: **Which random is the best random? A study on sampling methods in Fourier surrogate modeling**, IEEE Congress on Evolutionary Computation (CEC 2020), Glasgow, UK, 2020.
- ❑ M.S. Nobile, T. Vlachou, S. Spolaor, P. Cazzaniga, G. Mauri, P.G. Pelicci, D. Besozzi. **ProCell: investigating cell proliferation with Swarm Intelligence**, Proceedings of 2019 IEEE Conference on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB 2019), 1-8, 2019.
- ❑ M. Beccuti, P. Cazzaniga, M. Pennisi, D. Besozzi, M.S. Nobile, S. Pernice, G. Russo, A. Tangherloni, F. Pappalardo. **GPU accelerated analysis of Treg-Teff cross regulation in relapsing-remitting multiple sclerosis**. Euro-Par 2018: Parallel Processing Workshops Euro-Par 2018 International Workshops, Turin, Italy, August 27-28, 2018, Revised Selected Papers, 626-637, 2019.
- ❑ A. Tangherloni, L. Rundo, S. Spolaor, M.S. Nobile, I. Merelli, D. Besozzi, G. Mauri, P. Cazzaniga, P. Liò. **High Performance Computing for haplotyping: models and platforms**. Euro-Par 2018: Parallel Processing Workshops Euro-Par 2018 International Workshops, Turin, Italy, August 27-28, 2018, Revised Selected Papers, 650-661, 2019.
- ❑ M.S. Nobile, A. Tangherloni, L. Rundo, S. Spolaor, D. Besozzi, G. Mauri, P. Cazzaniga. **Computational intelligence for parameter estimation of biochemical systems**. Evolutionary Computation (CEC), 2018 IEEE Congress on, IEEE Press, 2018.
- ❑ M.S. Nobile, A. Tangherloni, D. Besozzi, P. Cazzaniga. **GPU-powered and settings-free parameter estimation of biochemical systems**. Evolutionary Computation (CEC), 2016 IEEE Congress on, 32-39, 2016.
- ❑ D. Besozzi. **Reaction-based models of biochemical networks** (*Invited contribution*). Pursuit of the Universal - CiE 2016 (A. Beckmann, L. Biennu, N. Jonoska, eds.), LNCS 9709, 24-34, 2016.
- ❑ P. Cazzaniga, F. Ferrara, M.S. Nobile, D. Besozzi, G. Mauri. **Parallelizing biochemical stochastic simulations: A comparison of GPU and Intel Xeon Phi processors**. Parallel Computing Technologies (Proceedings of 13th International Conference, PaCT 2015) (V. Malyshkin, ed.), LNCS 9251, 363-374, 2015.
- ❑ P. Cazzaniga, M.S. Nobile, D. Besozzi. **The impact of particles initialization in PSO: parameter estimation as a case in point**. Proceedings of 2015 IEEE Conference on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB 2015), 1-8, 2015.
- ❑ M.S. Nobile, G. Pasi, P. Cazzaniga, D. Besozzi, R. Colombo, G. Mauri. **Proactive particles in Swarm Optimization: A self-tuning algorithm based on Fuzzy Logic**. Proceedings of 2015 IEEE International Conference on Fuzzy Systems (FUZZ-IEEE 2015), 1-8, 2015.
- ❑ M. Bellini, D. Besozzi, P. Cazzaniga, G. Mauri, M.S. Nobile. **Simulation and analysis of the blood coagulation cascade accelerated on GPU**. 22nd Euromicro International Conference on Parallel, Distributed and Network-Based Processing (PDP), 2014. IEEE Computer Society Conference Publishing Services (CPS), 590-593, 2014.
- ❑ M.S. Nobile, A.G. Citrolo, P. Cazzaniga, D. Besozzi, G. Mauri. **A memetic hybrid method for the Molecular Distance Geometry Problem with incomplete information**. 2014 IEEE Congress on Evolutionary Computation (CEC 2014), 1014-1021, 2014.

- ❑ D. Besozzi, M.S. Nobile, P. Cazzaniga, D. Cipolla, G. Mauri. **From the inference of molecular structures to the analysis of emergent cellular dynamics: accelerating the computational study of biological systems with GPUs.** Proceedings of the NETTAB 2014 Workshop: from Structural Bioinformatics to Integrative Systems Biology, Torino, 15-17 October 2014, 88-90, 2014.
- ❑ M.S. Nobile, D. Besozzi, P. Cazzaniga, G. Mauri, D. Pescini. **cupSODA: a CUDA-powered simulator of mass-action kinetics.** Proceedings of 12th International Conference on Parallel Computing Technologies (PaCT 2013) (V. Malyshev, ed.), LNCS 7979, 344-357, 2013.
- ❑ M.S. Nobile, D. Besozzi, P. Cazzaniga, D. Pescini, G. Mauri. **Reverse engineering of kinetic reaction networks by means of Cartesian Genetic Programming and Particle Swarm Optimization.** IEEE Congress on Evolutionary Computation (CEC 2013), 1594-1601, 2013.
- ❑ M.S. Nobile, D. Besozzi, P. Cazzaniga, G. Mauri. **The foundation of Evolutionary Petri Nets.** Proceedings of the 4th International Workshop on Biological Processes & Petri Nets (BioPPN 2013), a satellite event of PETRI NETS 2013 (G. Balbo, M. Heiner, eds.), CEUR Workshop Proceedings Vol. 988, 60-74, 2013.
- ❑ D. Besozzi. **Computational methods in Systems Biology: case studies and biological insights (Invited contribution).** Proceedings of the 4th International Workshop on Computational Models for Cell Processes (I. Petre, ed.), EPTCS 116, 3-10, 2013.
- ❑ D. Besozzi, G. Caravagna, P. Cazzaniga, M.S. Nobile, D. Pescini, A. Re. **GPU-powered simulation methodologies for biological systems.** Proceedings of Wivace 2013 - Italian Workshop on Artificial Life and Evolutionary Computation (A. Graudenzi, G. Caravagna, G. Mauri, M. Antonioti, eds.), EPTCS 130, 87-91, 2013.
- ❑ M.S. Nobile, D. Besozzi, P. Cazzaniga, G. Mauri, D. Pescini. **A GPU-based multi-swarm PSO method for parameter estimation in stochastic biological systems exploiting discrete-time target series.** Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics (M. Giacobini, L. Vanneschi, W.S. Bush, eds.), LNCS 7246, 74-85, 2012.
- ❑ M.S. Nobile, D. Besozzi, P. Cazzaniga, G. Mauri, D. Pescini. **Estimating reaction constants in stochastic biological systems with a multi-swarm PSO running on GPUs.** Proceedings of the 14th International Conference on Genetic and Evolutionary Computation Conference Companion. ACM New York, NY, USA, GECCO Companion '12, 1421-1422, 2012.
- ❑ D. Besozzi, P. Cazzaniga, D. Pescini, G. Mauri, S. Colombo, E. Martegani, **Investigating oscillatory regimes in the Ras/cAMP/PKA pathway in *S. cerevisiae*: the role of feedback control mechanisms.** 8th International Workshop on Computational Systems Biology, WCSB 2011 (H. Koeppl, J. Acimovic, J. Kesseli, T. Mäki-Marttunen, A. Larjo, O. Yli-Harja, eds.), TICSP Series #57, 33-36, 2011.
- ❑ D. Besozzi, P. Cazzaniga, D. Pescini, G. Mauri. **An analysis on the influence of network topologies on local and global dynamics of metapopulation systems.** Applications of Membrane Computing, Concurrency and Agent-based Modelling in Population Biology (AMCA-POP 2010) (P. Milazzo, M.J. Pérez-Jiménez, eds.), EPTCS 33, 1-17, 2010.
- ❑ D. Besozzi, P. Cazzaniga, G. Mauri, D. Pescini. **BioSimWare: a software for the modeling, simulation and analysis of biological systems.** Membrane Computing, 11th International Conference (CMC 2010) (M. Gheorghe, T. Hinze, G. Păun, G. Rozenberg, A. Salomaa, eds.), LNCS 6501, 119-143, 2010.

- ❑ D. Besozzi, P. Cazzaniga, G. Mauri, D. Pescini, L. Vanneschi. **A comparison of genetic algorithms and particle swarm optimization for parameter estimation in stochastic biochemical systems.** EvoBIO 2009 (C. Pizzuti, M.D. Ritchie, M. Giacobini, eds.), LNCS 5483, 116-127, 2009.
- ❑ D. Besozzi, P. Cazzaniga, M. Dugo, D. Pescini, G. Mauri. **A study on the combined interplay between stochastic fluctuations and the number of flagella in bacterial chemotaxis.** Proceedings of CompMod2009 - 2nd International Workshop on Computational Models for Cell Processes (R.J. Back, I. Petre, E. de Vink, eds.), EPTCS 6, 47–62, 2009.
- ❑ D. Besozzi, G. Mauri, D. Pescini, C. Zandron. **Membrane systems in Systems Biology.** WODES 2008. 9th International Workshop on Discrete Event Systems (B. Lennartson, M. Fabian, K. Akesson, A. Giua, R. Kumar, eds.), IEEE Press, 275-280, 2008.
- ❑ D. Pescini, D. Besozzi, C. Zandron, G. Mauri. **Analysis and simulation of dynamics in probabilistic P systems.** DNA Computing, 11th International Workshop on DNA Computing (DNA11) (N. Pierce, A. Carbone, eds.), LNCS 3892, 236-247, 2006.
- ❑ P. Cazzaniga, D. Pescini, D. Besozzi, G. Mauri. **Tau leaping stochastic simulation method in P systems.** Membrane Computing, 7th International Workshop (WMC 2006) (H.J. Hoogeboom, G. Păun, G. Rozenberg, A. Salomaa, eds.), LNCS 4361, 298-313, 2006.
- ❑ D. Besozzi, G. Rozenberg. **Formalizing spherical membrane structures and membrane proteins populations.** Membrane Computing, 7th International Workshop (WMC 2006) (H.J. Hoogeboom, G. Păun, G. Rozenberg, A. Salomaa, eds.), LNCS 4361, 18-41, 2006.
- ❑ D. Pescini, D. Besozzi, G. Mauri. **Investigating local evolutions in dynamical probabilistic P systems.** Proceedings of the 7th International Symposium on Symbolic and Numeric Algorithms for Scientific Computing (SYNASC'05), IEEE Computer Press, 440-447, 2005.
- ❑ D. Besozzi, G. Ciobanu. **A P system description of the sodium-potassium pump.** Proceedings of 5th Membrane Computing International Workshop (WMC04) (G. Mauri, G. Păun, M.J. Pérez-Jiménez, G. Rozenberg, A. Salomaa, eds.), LNCS 3365, 210-223, 2005.
- ❑ D. Besozzi, G. Mauri, G. Vaszil, C. Zandron. **Collapsing hierarchies of parallel rewriting P systems without target conflicts.** Proceedings of Membrane Computing International Workshop (WMC03) (C. Martín-Vide, G. Mauri, G. Păun, G. Rozenberg, A. Salomaa, eds.), LNCS 2933, 55-69, 2004.
- ❑ D. Besozzi, G. Mauri, C. Zandron. **Deadlock decidability in partial parallel P systems.** Proceedings of the 9th International Workshop on DNA Based Computers (J. Chen, J. Reif, eds.), LNCS 2943, 55-60, 2004.
- ❑ D. Besozzi, C. Ferretti, G. Mauri, C. Zandron. **Parallel rewriting P systems with deadlock.** Proceedings of the 8th International Workshop on DNA Based Computers (M. Hagiya, A. Ohuchi, eds.), LNCS 2568, 302-314, 2003.
- ❑ D. Besozzi, G. Mauri, C. Zandron. **Parallel rewriting P systems without target conflicts.** Proceedings of Membrane Computing International Workshop (WMC-CdeA2002) (G. Păun, G. Rozenberg, A. Salomaa, C. Zandron, eds.), LNCS 2597, 119-133, 2003.
- ❑ D. Besozzi, C. Zandron, G. Mauri, N. Sabadini. **P systems with gemmation of mobile membranes.** Proceedings of ICTCS01 (A. Restivo, S. Ronchi Della Rocca, L. Roversi, eds.), LNCS 2202, 136-153, 2001.

Book chapters (with peer-review)

- ❑ Vlachou T., Nobile M.S., Ronchini C., Besozzi D., Pelicci P.G.: **An experimental and computational protocol to study cell proliferation in human Acute Myeloid Leukemia xenografts**. In “Leukemia Stem Cells”, Springer Nature Methods in Molecular Biology (C.C. Hernandez and I. Sanchez-Garcia, eds.) 241-258.
- ❑ P. Cazzaniga, M.S. Nobile, A. Tangherloni, D. Besozzi. **Accelerating stochastic simulations using Graphics Processing Units**. In: "Quantitative Biology: Theory, Computational Methods, and Models" (B. Munsky, W. Hlavacek, L. Tsimring, eds.). The MIT Press, 423-440, 2018.
- ❑ M.S. Nobile, D. Cipolla, P. Cazzaniga, D. Besozzi. **GPU-powered evolutionary design of mass-action based models of gene regulation**. In: Evolutionary Computation in Gene Regulatory Network Research (H. Iba, N. Noman, eds.), Wiley, 118-150, 2016.
- ❑ D. Besozzi, P. Cazzaniga, G. Mauri, D. Pescini. **Modeling and analysis of cellular processes with Dynamical Probabilistic P Systems: questions, methods and results**. In: Multidisciplinary Creativity (M. Gheorghe, I. Petre, M.J. Pérez-Jiménez, G. Rozenberg, A. Salomaa, eds.), Spandugino Publ. House, Bucharest, 2015.
- ❑ P. Cazzaniga, D. Besozzi, D. Pescini, G. Mauri. **Molecular diffusion and compartmentalization in signal transduction pathways: an application of membrane systems to the study of bacterial chemotaxis**. In: Applications of Membrane Computing in Systems and Synthetic Biology (M. Gheorghe, P. Frisco, M. Pérez-Jiménez, eds.), Emergence, Complexity and Computation, Springer, Vol. 7, 65-96, 2014.
- ❑ D. Besozzi, I.I. Ardelean. **Cell biology for Membrane Computing**. In: The Oxford Handbook of Membrane Computing (G. Păun, G. Rozenberg, A. Salomaa, eds.), Oxford University Press, 2009.
- ❑ I.I. Ardelean, D. Besozzi, M.H. Garzon, G. Mauri, S. Roy. **P system models for mechanosensitive channels**. In: Applications of Membrane Computing (G. Ciobanu, G. Păun, M.J. Pérez-Jiménez, eds.), Springer-Verlag, Berlin, 2005.
- ❑ D. Besozzi, G. Mauri, C. Zandron. **A survey of latest results on P systems with deadlock**. In: Recent Results in Natural Computing (M.J. Pérez-Jiménez, A. Romero-Jiménez, F. Sancho-Caparrini, eds.), University of Seville, 17-46, 2004.

Miscellaneous

- ❑ C. Gallese, D. Besozzi. **Le sentenze antiscientifiche: un mito creato dai media**. In: *Ius Dicere* in a Globalized World (C.A. d’Alessandro, C. Marchese, eds.), Roma TrE-Press Studies in Law and Social Sciences, 261-294, 2018.
- ❑ D. Besozzi, P. Cazzaniga, D. Pescini, G. Mauri. **A multi-volume approach to stochastic modeling with membrane systems**. In: Algorithmic Bioprocesses (A. Condon, D. Harel, J.N. Kok, A. Salomaa, E. Winfree, eds.), Natural Computing Series, Springer-Verlag, 519-542, 2009.
- ❑ P. Cazzaniga, D. Pescini, F.J. Romero-Campero, D. Besozzi, G. Mauri. **Stochastic approaches in P systems for simulating biological systems**. Proceedings of the 4th Brainstorming Week on Membrane Computing, Volume I (M.A. Gutiérrez-Naranjo, G. Păun, A. Riscos-Núñez, F.J. Romero-Campero, eds.), RGNC REPORT 02/2006, Fenix Editora, Sevilla, 145-165, 2006.

- ❑ D. Besozzi, N. Busi, G. Franco, R. Freund, G. Păun. **Two universality results for (mem)brane systems.** Proceedings of the 4th Brainstorming Week on Membrane Computing, Volume I (M.A. Gutiérrez-Naranjo, G. Păun, A. Riscos-Núñez, F.J. Romero-Campero, eds.), RGNC REPORT 02/2006, Fenix Editora, Sevilla, 49-62, 2006.
- ❑ I.I. Ardelean, D. Besozzi. **Some notes on the interplay between P systems and chemotaxis in Bacteria.** Proceedings of the 4th Brainstorming Week on Membrane Computing, Volume I (M.A. Gutiérrez-Naranjo, G. Păun, A. Riscos-Núñez, F.J. Romero-Campero, eds.), RGNC REPORT 02/2006, Fenix Editora, Sevilla, 41-48, 2006.
- ❑ M. Muskulus, S. Houweling, G. Rozenberg, D. Besozzi, P. Cazzaniga, D. Pescini, R. Brijder. **Reaction cycles in membrane systems and molecular dynamics.** Proceedings of the 4th Brainstorming Week on Membrane Computing, Volume II (C. Graciani Diaz, G. Păun, A. Romero-Jiménez, F. Sancho-Caparrini, eds.), RGNC REPORT 03/2006, Fenix Editora, Sevilla, 185-208, 2006.
- ❑ I.I. Ardelean, D. Besozzi. **On modeling ion fluxes across biological membranes with P systems.** Proceedings of the 3rd Brainstorming Week on Membrane Computing (M.A. Gutiérrez Naranjo, A. Riscos-Núñez, F.J. Romero-Campero, D. Sburlan, eds.), RGNC REPORT 01/2005, 35-42, 2005.
- ❑ S. Aguzzoli, I.I. Ardelean, D. Besozzi, B. Gerla, C. Manara. **P systems under uncertainty: the case of transmembrane proteins.** Proceedings of Brainstorming Workshop on Uncertainty in Membrane Computing, Palma de Mallorca, 8-10 November 2004, Departament de Matemàtiques i Informàtica, Universitat de les Illes Balears, ISBN 84-7632-897-4, 107-117, 2004.
- ❑ S. Aguzzoli, D. Besozzi, B. Gerla, C. Manara. **P systems with vague boundaries: the t-norm approach.** Proceedings of Brainstorming Workshop on Uncertainty in Membrane Computing, Palma de Mallorca, 8-10 November 2004, Departament de Matemàtiques i Informàtica, Universitat de les Illes Balears, ISBN 84-7632-897-4, 97-105, 2004.

Posters and abstracts presented at international conferences (with peer-review)¹

- ❑ * M. Rovetta, D. Besozzi, R. Tisi. **Modeling calcium signaling in *S. cerevisiae* cells in response to hypotonic shock.** 16th International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics (CIBB 2019), Bergamo, Italy, 4-6 September 2019.
- ❑ M.S. Nobile, T. Vlachou, S. Spolaor, D. Bossi, P. Cazzaniga, L. Lanfrancone, G. Mauri, P.G. Pelicci, D. Besozzi. **Modeling cell proliferation in human acute myeloid leukemia xenografts.** ISMB 2018, Chicago, USA, 6-10 July 2018.
- ❑ * N. Toti, A. Tangherloni, M. Beccuti, P. Cazzaniga, M.S. Nobile, D. Besozzi, M. Pennisi, F. Pappalardo. **GPU powered parameter estimation of a large-scale kinetic metabolic network.** 15th International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics (CIBB 2018), Lisbon, Portugal, 6-8 September 2018.
- ❑ * A. Tangherloni, S. Spolaor, L. Rundo, M.S. Nobile, P. Cazzaniga, G. Mauri, P. Liò, D. Besozzi, I. Merelli. **GenHap: evolutionary computation for genotype assembly.** 15th International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics (CIBB 2018), Lisbon, Portugal, 6-8 September 2018.

¹ Items marked with the asterisk indicate works accepted for oral presentations

- ❑ D. Besozzi, M.S. Nobile, P. Cazzaniga, S. Spolaor, G. Mauri. **Dealing with cellular heterogeneity and lack of quantitative parameters in dynamical modeling of biological systems: a fuzzy logic based approach.** CSHL Meeting “Cellular Dynamics & Models”, New York, USA, 11-14 April 2017.
- ❑ * A. Tangherloni, M.S. Nobile, D. Besozzi, G. Mauri, P. Cazzaniga. **LASSIE: a GPU-based large-scale simulator of biological systems.** 14th Annual Meeting of the Bioinformatics Italian Society (BITS), Cagliari, Italy, 5-7 July 2017.
- ❑ P. Cazzaniga, D. Besozzi, M.S. Nobile, S. Spolaor, G. Mauri. **A fuzzy logic based approach to handle cellular heterogeneity and the lack of quantitative parameters in dynamical models of biological systems.** 11th Annual q-bio Conference, New Brunswick, NJ, USA, 25-28 July 2017.
- ❑ * A. Tangherloni, S. Spolaor, L. Rundo, M.S. Nobile, I. Merelli, P. Cazzaniga, D. Besozzi, G. Mauri, P. Liò. **GenHap: A novel computational method based on Genetic Algorithms for haplotype assembly.** NETTAB 2017, Palermo, Italy, 16-18 October 2017.
- ❑ G. Mauri, M.S. Nobile, P. Cazzaniga, D. Besozzi. **High-performance computing in Systems Biology: accelerating the simulation and analysis of large and complex biological systems.** SysMod SIG 2016, Orlando, Florida, USA, 8-12 July 2016.
- ❑ A. Tangherloni, G. Capitoli, P. Cazzaniga, M.S. Nobile, D. Besozzi, G. Mauri. **Deterministic simulations of large-scale models of biochemical reaction networks accelerated on Graphics Processing Units.** International Conference on Systems Biology (ICSB 2016), Barcelona, Spain, 16-20 September 2016.
- ❑ M.S. Nobile, P. Cazzaniga, A. Tangherloni, S. Spolaor, D. Besozzi, G. Mauri. **High-performance computing in Systems Biology: accelerating the simulation and analysis of large and complex biological systems.** International Conference on Systems Biology (ICSB 2016), Barcelona, Spain, 16-20 September 2016.
- ❑ M.S. Nobile, L.A. Harris, E. Shockley, P. Cazzaniga, D. Besozzi, C.F. Lopez, G. Mauri. **GPU-powered sensitivity analysis of a large-scale model of death cell signaling and proliferation in cancer cells.** Third Annual Winter q-bio Meeting, Maui, Hawaii, 17-20 February 2015.
- ❑ M.S. Nobile, P. Cazzaniga, D. Besozzi, D. Cipolla, G. Mauri. **Towards an integrated toolbox for GPU-powered computational analysis of complex biological systems.** Third Annual Winter q-bio Meeting, Maui, Hawaii, 17-20 February 2015.
- ❑ N. Frik, M.S. Nobile, D. Besozzi, T. LaBean. **Useful disorder: Engineering self-assembly and randomized neuromimetic networks for sensing and computation.** 12th Annual Conference on Foundations of Nanoscience: Self-assembled architectures and devices (FNANO15), Snowbird, Utah, 13-16 April 2015.
- ❑ P. Cazzaniga, M.S. Nobile, D. Besozzi, A.G. Citrolo, A. Tangherloni, A. Donizetti, G. Mauri. **Towards a GPU-powered toolbox for the computational analysis of biological systems.** 12th Annual Meeting of the Bioinformatics Italian Society (BITS 2015), Milano, Italy, 3-5 June 2015.
- ❑ M.S. Nobile, L.A. Harris, E. Shockley, J.C. Pino, P. Cazzaniga, D. Besozzi, C.F. Lopez, G. Mauri. **GPU computing for accelerated analyses of a large-scale model of cell fate in cancer cells.** 12th Annual Meeting of the Bioinformatics Italian Society (BITS 2015), Milano, Italy, 3-5 June 2015.
- ❑ * A. Tangherloni, P. Cazzaniga, M.S. Nobile, D. Besozzi, G. Mauri. **Deterministic simulations of large-scale models of cellular processes accelerated on Graphics Processing Units.** CIBB 2015

(Computational Intelligence methods for Bioinformatics and Biostatistics), Napoli, 10-12 September 2015.

- ❑ P. Cazzaniga, R. Colombo, M.S. Nobile, D. Pescini, G. Mauri, D. Besozzi. **GPU-powered sensitivity analysis and parameter estimation of a reaction-based model of the Post Replication Repair pathway in yeast.** WCSB 2013 - 10th International Workshop on Computational Systems Biology, Tampere, Finland, 10-12 June 2013.
- ❑ D. Besozzi, R. Colombo, P. Cazzaniga, M.S. Nobile, D. Pescini, G. Mauri. **A GPU-powered computational analysis of PCNA ubiquitylation processes involved in UV-induced DNA lesions bypass.** ICSB 2013 - 14th International Conference on Systems Biology, Copenhagen, Denmark, 30 August - 3 September 2013.
- ❑ D. Besozzi, P. Cazzaniga, R. Colombo, G. Mauri, M.S. Nobile, D. Pescini. **Accelerating the computational analysis of biological systems by means of Graphics Processing Units.** ICSB 2013 - 14th International Conference on Systems Biology, Copenhagen, Denmark, 30 August- 3 September 2013.
- ❑ P. Cazzaniga, D. Besozzi, D. Pescini, G. Mauri, S. Colombo, E. Martegani. **The role of Ras modulators and feedback control mechanisms on the establishment of oscillations in the Ras/cAMP/PKA pathway in *S. cerevisiae*.** ICSB 2011 - 12th International Conference on Systems Biology, Heidelberg/Mannheim, Germany, 28 August - 1 September 2011.
- ❑ F. Amara, R. Colombo, F. Spadaro, D. Besozzi, M. Muzi-Falconi, P. Plevani. **PCNA ubiquitylation as the wet readout of a Post-Replication Repair computational model.** Ubiquitin and ubiquitin-like modifiers: from functional modules to Systems Biology, Cavtat (Dubrovnik), Croatia, 21-25 September 2011.
- ❑ D. Besozzi, P. Cazzaniga, G. Mauri, D. Pescini. **Effects of stochastic fluctuations on the coordination of flagella in bacterial chemotaxis.** 4th Annual q-bio Conference on Cellular Information Processing, Santa Fe, New Mexico, 11-14 August 2010.
- ❑ F. Amara, D. Besozzi, R. Colombo, I. Mura, M. Muzi-Falconi, P. Plevani. **Post-Replication Repair (PRR) in *Saccharomyces cerevisiae*: a Systems Biology approach.** The interface between the ubiquitin family and the DNA damage response, Red Island, Rovinj, Croatia, 1-5 September 2010.
- ❑ D. Besozzi, P. Cazzaniga, D. Pescini, G. Mauri. **BioSimWare: a simulation environment for stochastic modeling of complex biological systems.** IBS2010 - 14th International Biotechnology Symposium and Exhibition, Biotechnology for the Sustainability of Human Society, Rimini, Italy, 14-18 September 2010 (abstract published in: Journal of Biotechnology, Vol. 150, Suppl.1, 519-520, 2010).
- ❑ * D. Besozzi, P. Cazzaniga, A. Devecchi, P. Landini, D. Pescini. **An *in silico* investigation of different regulation mechanisms of the bacterial second messenger c-di-GMP.** IBS2010 - 14th International Biotechnology Symposium and Exhibition, Biotechnology for the Sustainability of Human Society, Rimini, Italy, 14-18 September 2010 (abstract published in: Journal of Biotechnology, Vol. 150, Suppl.1, 546, 2010).
- ❑ * P. Cazzaniga, D. Pescini, D. Besozzi, G. Mauri, S. Colombo, E. Martegani. **Simulation of the Ras/cAMP/PKA pathway in budding yeast evidences the presence of stable oscillatory states.** IBS2010 - 14th International Biotechnology Symposium and Exhibition, Biotechnology for the

Sustainability of Human Society, Rimini, Italy, 14-18 September 2010 (abstract published in: Journal of Biotechnology, Vol. 150, Suppl.1, 545, 2010).

- ❑ F. Amara, D. Besozzi, A. Csikasz-Nagy, S. Riva, M. Muzi Falconi, P. Plevani. **Analyzing the *Saccharomyces cerevisiae* Post Replication Repair pathway through a Systems Biology approach.** Systems level understanding of DNA damage responses, Egmond aan Zee, The Netherlands, 30 March - 1 April 2009.
- ❑ * D. Besozzi, P. Cazzaniga, M. Dugo, G. Mauri, D. Pescini. **Stochastic modelling and parameter estimation of bacterial chemotaxis.** Information Processing in Cells and Tissues (IPCAT 2009), Ascona, Switzerland, 5-9 April 2009.
- ❑ * P. Cazzaniga, D. Pescini, D. Scotti, D. Besozzi, G. Mauri, S. Colombo, E. Martegani. **Simulation of the Ras/cAMP/PKA pathway in budding yeast evidences the presence of stable oscillatory states.** SysBioHealth 2009, Milano, Italy, 25-27 November 2009.
- ❑ D. Pescini, P. Cazzaniga, D. Besozzi, G. Mauri, S. Colombo, E. Martegani. **Modeling and simulations of the Ras signalling pathway in budding yeast: evidence for oscillatory regimes.** 9th International Conference on Systems Biology (ICSB 2008), Göteborg, Sweden, 22-28 August 2008.
- ❑ * E. Martegani, P. Cazzaniga, D. Besozzi, S. Colombo, G. Mauri. **Stochastic modeling and simulations of the Ras/cAMP/PKA pathway in budding yeast.** SysBioHealth 2007, Milan, Italy, 16-19 October 2007.
- ❑ E. Martegani, R. Tisi, F. Belotti, S. Colombo, C. Paiardi, J. Winderickx, P. Cazzaniga, D. Besozzi, G. Mauri. **Identification of an intracellular signalling complex for Ras/cAMP pathway in yeast: experimental evidences and modelling.** 25th International Specialized Symposium on Yeasts (ISSY 25), Hanasaari, Espoo, Finland, 18-21 June 2006.
- ❑ E. Martegani, P. Cazzaniga, D. Besozzi, S. Colombo, G. Mauri. **Stochastic modeling of the Ras/cAMP signal transduction pathway in yeast.** International Conference on Computational Methods in Systems Biology (CMSB 2006), Trento, Italy, 18-19 October 2006.

Manuscripts under revision

- ❑ A. Tangherloni, F. Ricciuti, D. Besozzi, P. Liò, A. Cvejic. **Analysis of single-cell RNA sequencing data based on autoencoders.** BMC Bioinformatics (pending decision).
- ❑ A. Tangherloni, M.S. Nobile, P. Cazzaniga, G. Capitoli, S. Spolaor, L. Rundo, G. Mauri, D. Besozzi. **FiCoS: a fine- and coarse-grained GPU-powered deterministic simulator for biochemical networks.** Submitted to PLOS Computational Biology.
- ❑ D. Papetti, D.A. Ashlock, P. Cazzaniga, D. Besozzi, M.S. Nobile. **If You Can't Beat It, Squash It: Simplify Global Optimization by Evolving Dilation Functions.** Submitted to CEC 2021.

Manuscripts in preparation²

- ❑ M.S. Nobile, G.V. Ildefonso, P. Cazzaniga, D. Besozzi, C.F. Lopez. **Investigating the role of kinetic parameters in a complex model of TRAIL-induced apoptosis with FST-PSO and Particle Filtering.** To be submitted to Complexity.

² Provisional titles and authors ordering

- ❑ S.G. Riva, A. Tangherloni, M.S. Nobile, P. Cazzaniga, D. Besozzi. **SMGen: A novel generator of synthetic models of biological systems.** To be submitted to Application Notes in Bioinformatics.
- ❑ M. Rovetta, S. Spolaor, M.S. Nobile, P. Cazzaniga, D. Besozzi, R. Tisi. **Modeling the feedback regulations between calcium channels and calcineurin-calmodulin pathway in calcium signaling in *S. cerevisiae* cells in response to hypotonic shock** (journal to be decided).
- ❑ L. Rusinenti, S. Spolaor, P. Cazzaniga, M.S. Nobile, D. Besozzi. **Analysis of complexome dynamics in combinatorial rule-based models of signal transduction pathways** (journal to be decided).
- ❑ D. Besozzi, I. Petre, G. Rozenberg. **Biological aspects of reaction systems** (journal to be decided).

Collaborations (ongoing research projects)³

- ❑ **A multidisciplinary approach for the analysis of pre-leukemic functional features and cell signaling regulation at diagnosis, relapse or in resistant disease for pediatric Acute Lymphoblastic Leukemia (T-ALL and BCP-ALL), to identify new therapeutic targets and design personalized treatment protocols.**
Collaboration with Dr. Giovanni Cazzaniga and Dr. Giuseppe Gaipa, Centro di Ricerca Tettamanti (Fondazione Tettamanti), Centro Maria Letizia Verga, and S. Gerardo Hospital, Monza, Italy.
- ❑ **Multidisciplinary approach for the elucidation of cell proliferation and quiescence in Acute Myeloid Leukemia, by combination of stochastic modeling and simulation with flow cytometry and single-cell RNA-seq data.**
Collaboration with Prof. Pier Giuseppe Pelicci, European Institute of Oncology (IEO), and Department of Oncology and Hemato-Oncology, University of Milano, Italy.
- ❑ **Development of a predictive simulator of DNA-based self-assembling nano-artifacts.**
Collaboration with Prof. Thomas LaBean, Department of Materials Science and Engineering, North Carolina State University, Raleigh, NC, USA, and Prof. Simone Paleari, Department of Mathematics, University of Milano, Italy.
- ❑ **Development of hybrid computational intelligence approaches (based on evolutionary computation and neural networks) for the investigation of topological properties and learning processes of neuro-mimetic networks based on self-assembling DNA molecules.**
Collaboration with Prof. Thomas LaBean, Department of Materials Science and Engineering, North Carolina State University, Raleigh, NC, USA.
- ❑ **Stochastic modeling and compositional drift analysis of liquid-liquid phase separation (LLPS) processes in protein overexpression conditions to identify the mechanisms of LLPS-induced toxicity *in vivo*.**
Collaboration with Prof. Hisao Moriya, Research Core for Interdisciplinary Sciences, Okayama University, Japan.

³ All projects are in collaboration with Dr. Marco S. Nobile, TU/e - Eindhoven University of Technology, The Netherlands, and Prof. Paolo Cazzaniga, University of Bergamo, Italy.

- ❑ **Multidisciplinary approach and definition of a fuzzy logic model to investigate mitochondrial dysfunction in Parkinson's disease.**
 Collaboration with Prof. Mauro Fasano and Dr. Tiziana Alberio, Department of Science and High Technology, University of Insubria, Italy.
- ❑ **Hybrid mechanistic/fuzzy logic modeling of DNA double strand breaks repair by homologous recombination to predict the effects of feedback regulations in mutant yeast strains.**
 Collaboration with Prof. Maria Pia Longhese and Prof. Renata Tisi, Department of Biotechnologies and Biosciences, University of Milano-Bicocca, Italy.
- ❑ **Computational analysis of human samples of renal carcinoma for morphologic classification (using supervised learning methods) and for the identification of patterns in the associated mass-spectrometry data (using unsupervised learning methods).**
 Collaboration with Prof. Fulvio Magni, Prof. Stefania Galimberti and Prof. Fabio Pagni, School of Medicine and Surgery, University of Milano-Bicocca, Italy.
- ❑ **Development of computational intelligence heuristics hybridized with Bayesian approaches, to define novel bio-inspired parameter estimation methods able to converge to nonparametric probability distributions, in the context of lung cancer studies.**
 Collaborations with Prof. Carlos F. Lopez, Department of Biochemistry, Vanderbilt University, Nashville, TN, USA.
- ❑ **Development of machine learning methods for the automatic creation of approximate/ surrogate models in complex multi-dimensional non-convex, non-linear optimization problems.**
 Collaboration with Prof. Leonardo Vanneschi, NOVA IMS, Universidade Nova de Lisboa, Portugal, and Dr. Luca Manzoni, Department of Mathematics and Geosciences, University of Trieste, Italy.
- ❑ **Development of a novel Deep Learning architecture for base-calling using Nanopore's raw electrical signal.**
 Collaboration with Prof. Graziano Pesole, University of Bari, Italy, and Italian National Research Council.

Invited talks

- ❑ Invited speaker at the mini symposium "Computational Biology and Medicine", hosted by the international conference "SciCADE 2017", 11-15 September 2017, Bath, UK.
 Title: "Accelerating numerical integration methods on Graphics Processing Units".
- ❑ Invited speaker at the special session "Computation in biological systems", hosted by the international conference "CiE 2016: Pursuit of the Universal", 27 June - 1 July 2016, Paris, France.
 Title: "Reaction-based models of biochemical networks".
- ❑ Invited speaker at the "4th International Workshop on Computational Models for Cell Processes" (CompMod 2013), 11 June 2013, Turku, Finland.
 Title: "Computational methods in Systems Biology: case studies and biological insights".

- ❑ Invited speaker at the “7th International Workshop on Membrane Computing”, Leiden, The Netherlands, 17-21 July 2006.
Title: “Extended P systems for the analysis of (trans)membrane protein populations”.

Visiting

- ❑ Nov. 20-26, 2016: **Turku Centre for Computer Science (TUCS)**, Åbo Akademy University, Turku, Finland, invited by Prof. Ion Petre.
- ❑ July 2006: **Leiden Institute of Advanced Computer Science (LIACS)**, Leiden, The Netherlands, invited by Prof. Grzegorz Rozenberg.
- ❑ Jan. 2006: **Department of Computer Science**, University of Sevilla, Spain, invited by Prof. Mario de J. Pérez-Jiménez.
- ❑ Sept. 2005 - Oct. 2005: **Leiden Institute of Advanced Computer Science (LIACS)**, Leiden, The Netherlands, invited by Prof. G. Rozenberg.
- ❑ Oct. 2003: **Institute of Biology of the Romanian Academy**, Centre of Microbiology, Bucarest, Romania, invited by Dr. Ioan I. Ardelean.
- ❑ Febr. 2002: **Fraunhofer Gesellschaft, BioMIP** (BioMolecular Information Processing), Sankt Augustin (Bonn), Germany, invited by Prof. John McCaskill.

Program committees

- ❑ “13th International Conference on Health Informatics” (HEALTHINF 2020), 24-26 February, 2020, Valletta, Malta.
- ❑ “Parallel and distributed high-performance computing solutions in Systems Biology”, special session hosted by PDP 2018, 21-23 March 2018, Cambridge, UK.
- ❑ ACM SAC 2018 Track on BIO - Bioinformatics, 9-13 April 2018, Pau, France.
- ❑ “Modeling and Simulation Methods for Systems Biology and Systems Medicine”, special session hosted by CIBB 2018, 15th International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics, 6-8 September 2018, Lisbon, Portugal.
- ❑ “Workshop on Advances in High-Performance Bioinformatics, Systems Biology” (Med-HPC 2018), special session hosted by the 24th International European Conference on Parallel and Distributed Computing (Euro-Par 2018), 27-28 August 2018, Turin, Italy.
- ❑ “Modeling and simulation methods for Systems Biology and Systems Medicine”, special session hosted by CIBB 2017, 7-9 September, 2017, Cagliari, Italy.
- ❑ “HiCOMB 2017, 16th IEEE International Workshop on High Performance Computational Biology”, 29 May 2017, Orlando, FL, USA.

- ❑ ACM SAC 2017 Track on BIO - Computational BIOlogy and BIOinformatics, 27-31 March 2017, Marrakech, Morocco.
- ❑ ACM SAC 2016 Track on “COmputational BIOlogy and BIOinformatics” (CO-BIO2), 3-8 April 2016, Pisa, Italy.
- ❑ “Computational intelligence methods accelerated on parallel and distributed architectures for applications in Bioinformatics, Computational Biology and Systems Biology”, special session hosted by the IEEE World Congress on Computational Intelligence (WCCI) 2016, 25-29 July 2016, Vancouver, Canada.
- ❑ “Parallel and distributed high performance computing solutions for computational intelligence methods”, special session hosted by IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB) 2016, 5-7 October 2016, Chiang Mai, Thailand.
- ❑ “Modeling and simulation methods for Systems Biology and Systems Medicine”, special session hosted by CIBB 2016, 1-3 September 2016, Stirling, Scotland, UK.
- ❑ “XVI Portuguese Conference on Artificial Intelligence” – EPIA 2013, 9-12 September 2013, Angra do Heroísmo, Azores, Portugal.
- ❑ “XV Portuguese Conference on Artificial Intelligence” – EPIA 2011, 10-12 October 2011, Lisbon, Portugal.
- ❑ “Harness Nature for Computing”, Third International Workshop on Natural Computing, 23 September 2008, Yokohama National University, Yokohama, Japan.
- ❑ “International Workshop on Computing with Biomolecules”, 27 August 2008, Wien, Austria.
- ❑ “Second International Workshop on Natural Computing”, 10-13 December 2007, Noyori Conference Hall, Nagoya University, Japan.
- ❑ “Third International Conference on Computational Intelligence, Robotics and Autonomous Systems” - CIRAS2005 (Special Session on Biomolecular Computers and other Bio-inspired Systems), 13-16 December 2005, Singapore.

Organizing committees

International conferences

- ❑ Member of the organizing committee of the symposium “Interdisciplinary Nature of Information Processing”, Milano, Italy, 8 November 2019.
- ❑ Co-chair of the 16th international conference “CIBB 2019 – Computational Intelligence in Bioinformatics and Biostatistics”, Bergamo, Italy, 4-6 September 2019.
- ❑ Co-chair of the special session “Parallel and distributed high-performance computing solutions in Systems Biology”, PDP 2018, Cambridge, UK, 21-23 March 2018.
- ❑ Member of the organizing committee of the “1st International Workshop on Reaction Systems”, Milano, Italy, 11-15 June 2018.

- ❑ Member of the organizing committee of the special session “Parallel and distributed high-performance computing solutions for computational intelligence methods”, IEEE CIBCB 2017, Manchester, UK, 23-25 August 2017.
- ❑ Member of the organizing committee of the special session “Modeling and simulation methods for Systems Biology and Systems Medicine”, CIBB 2016, Stirling, Scotland, UK, 1-3 September 2016.
- ❑ Member of the organizing committee of the special session “Parallel and distributed high performance computing solutions for computational intelligence methods”, CIBCB 2016, Chiang Mai, Thailand, 5-7 October 2016.
- ❑ Member of the organizing committee of “BITS 2015 - Twelfth Annual Meeting of the Bioinformatics Italian Society”, Milano, Italy, 3-5 June 2015.
- ❑ Member of the organizing committee of the “Tenth International Meeting on DNA Computing (DNA10)”, Milano, Italy, 7-10 June 2004.
- ❑ Member of the organizing committee of the “Fifth Workshop on Membrane Computing (WMC5)”, Milano, Italy, 14-16 June 2004.

International schools (doctoral and post-doc level)

- ❑ Member of the organizing committee of the “2nd SYSBIO.IT School on Computational Systems Biology and Bioinformatics”, Milano, Italy, 4-6 October 2017.
- ❑ Scientific coordinator and member of the organizing committee of the “1st SYSBIO.IT School on Computational Systems Biology: An introduction to dynamic modeling, simulation and analysis of biological systems”, Milano, Italy, 7-9 June 2016.

Teaching activity

Academic assignments

- ❑ **“Computational Systems Biology”** (6 ECTS)
Master’s degree program in Industrial Biotechnologies, University of Milano-Bicocca, Italy.
Academic years: 2016-2017, 2017-2018, 2018-2019, 2019-2020, 2020-2021.
- ❑ **“Informatics”** (8 ECTS)
Bachelor’s degree program in Biotechnologies, University of Milano-Bicocca, Italy.
Academic years: 2015-2016, 2016-2017, 2017-2018, 2018-2019, 2019-2020, 2020-2021.
- ❑ **“Mathematics and informatics”** (4 ETCS – Module of Informatics)
Bachelor’s degree program in Biological Sciences, University of Milano-Bicocca, Italy.
Academic years: 2020-2021.
- ❑ **“Bioinformatics Methodologies”** (1 ECTS)
Master’s degree program in Industrial Biotechnologies, University of Milano-Bicocca, Italy.
Academic years: 2017-2018, 2018-2019, 2019-2020, 2020-2021.

- ❑ **“Laboratory of algorithms and data structures”** (6 ECTS)
Bachelor’s degree program in Computer Science, University of Milano-Bicocca, Italy.
Academic year: 2015-2016.
- ❑ **“Systems Biology”** (6 ECTS)
Master’s degree program in Bioinformatics and Molecular Biotechnologies, University of Milano, Italy.
Academic years: 2011-2012, 2012-2013, 2013-2014, 2014-2015.
- ❑ **“Laboratory of Informatics”** (3 ECTS)
Bachelor’s degree program in Biology, University of Milano, Italy.
Academic years: 2013-2014, 2014-2015.
- ❑ **“Introduction to Computational Biology”** (4 ECTS)
Bachelor’s degree program in Industrial and Environmental Biotechnologies, University of Milano, Italy.
Academic years: 2004-2005, 2006-2007, 2007-2008, 2008-2009, 2009-2010.
- ❑ **“Algorithms for Bioinformatics”** (6 ECTS)
Master’s degree program in Functional Genomics and Bioinformatics, University of Milano, Italy.
Academic years: 2003-2004, 2004-2005, 2006-2007, 2007-2008, 2008-2009.
- ❑ **“Fundamentals of Computer Science”** (3 ECTS)
Bachelor’s degree program in Biotechnologies, University of Milano, Italy.
Academic year: 2009-2010.
- ❑ **“Laboratory of Molecular Bioinformatics”** (6 ECTS)
Master’s degree program in Biology, University of Milano, Italy.
Academic year: 2003-2004.
- ❑ **“Laboratory of Informatics”** (4 ECTS)
Bachelor’s degree program in Biotechnologies, University of Milano, Italy.
Academic year: 2002-2003.

Academic assistance

- ❑ **“Introduction to Computational Biology”**
Bachelor’s degree program in Industrial and Environmental Biotechnologies, University of Milano, Italy.
Academic year: 2003-2004.
- ❑ **“Fundamentals of algorithms”**
Bachelor’s degree program in Industrial and Environmental Biotechnologies, University of Milano, Italy.
Academic year: 2002-2003.
- ❑ **“Algorithms and data structures II”**
Master’s degree program in Computer Science, University of Insubria, Como, Italy.
Academic year: 2001-2002.

❑ **“Formal languages and automata theory”**

Master’s degree program in Mathematics, University of Insubria, Como, Italy.
Academic year: 2000-2001.

Ph.D. courses

- ❑ 13-21 July 2020: **Ph.D. course on “Fundamentals of Biostatistics”** (2 ECTS)
Ph.D. Program in Biology and Biotechnology, University of Milano-Bicocca, Italy.
Role: course co-organizer and lecturer, together with Prof. Paolo Cazzaniga, University of Bergamo, Italy, and Dr. Marco S. Nobile, TU/e - Eindhoven University of Technology, The Netherlands.
- ❑ 25-29 July 2019: **Ph.D. course on “Introduction to Machine Learning”** (1 ECTS)
Ph.D. Program in Public Health, University of Milano-Bicocca, Italy.
Role: course co-organizer and lecturer, together with Prof. Paolo Cazzaniga, University of Bergamo, Italy, and Dr. Marco S. Nobile, TU/e - Eindhoven University of Technology, The Netherlands.
- ❑ 25-29 June 2018: **Ph.D. course on “Fundamentals of Biostatistics”** (2 ECTS)
Ph.D. Program in Biology and Biotechnology, University of Milano-Bicocca, Italy.
Role: course co-organizer and lecturer, together with Prof. Paolo Cazzaniga, University of Bergamo, Italy, and Dr. Marco S. Nobile, TU/e - Eindhoven University of Technology, The Netherlands.

International schools (doctoral and post-doc level)

- ❑ 3-5 June 2019: Lecturer at the **“First School on Reaction Systems”**, Toruń, Poland.
- ❑ 21 Nov. 2016: Lecturer at the **“Joint TUCS-BioCity One-day Tutorial on Modern Computational Modelling and GPU-Based Simulation for Life Sciences”** (2 ECTS), Joint TUCS’s Research Program on BioHealth and BioCity’s Research Program on Computational and Molecular Methodologies for Life Sciences, Åbo Akademy University, Turku, Finland.
- ❑ 7-9 June 2016: Lecturer at the **“1st SYSBIO.IT School on Computational Systems Biology: An introduction to dynamic modeling, simulation and analysis of biological systems”**, University of Milano-Bicocca, Italy.

Thesis supervision

- ❑ 2020 - present day: Co-supervisor of a Ph.D. student in Computer Science, University of Milano-Bicocca, Italy.
- ❑ 2016 - 2020: Co-supervisor of a Ph.D. student in Computer Science on the topic: “Fuzzy logic for the modeling and simulation of complex biological systems”, University of Milano-Bicocca, Italy.
- ❑ 2015 - 2018: Co-supervisor of a Ph.D. student in Computer Science on the topic: “High-Performance Computing to tackle complex problems in life sciences”, University of Milano-Bicocca, Italy.

- ❑ 2009 - 2012: Co-supervisor of a Ph.D. student in Biology on the topic: “Bypass of UV-induced DNA lesions in *Saccharomyces cerevisiae*: experimental analysis and *in silico* modeling”, University of Milano, Italy.
- ❑ 2002 - present day: Supervisor of more than 80 thesis for Master’s degree programs (Functional Genomics and Bioinformatics; Biology; Molecular Biotechnologies; Industrial Biotechnologies; Mathematics; Computer Science) and for Bachelor’s degree programs (Biotechnologies; Computer Science) at University of Milano (2002-2015) and University of Milano-Bicocca (2015 - present day), Italy.

Mentoring activity

- ❑ Voluntary mentoring to Master's degree students for the preparation and application to Ph.D. programs. Most of these students are now enrolled in Italian and European Ph.D. programs, or lately got post-doctoral positions in prestigious European universities.
- ❑ Experience in tutoring and assistance to students with specific learning disabilities (dyslexia), autism spectrum disorder, depressive disorder, borderline personality disorder, physical disabilities.

Participation to research projects

- ❑ CINECA LISA (Development Projects), 2017-2018: MOOPT - Multi Objective OPTimization.
- ❑ CINECA ISCRA (Class C Projects), 2017-2018: Fine-grain and spatial simulations of complex biological systems.
- ❑ CINECA LISA 2016 (Development Projects): Large scale simulation of biochemical networks.
- ❑ CINECA ISCRA (Class C Projects), 2015-2016: Fine and coarse-grain simulations of complex biological systems.
- ❑ CINECA ISCRA (Class C Projects), 2013-2014: BioComPLX: a tool for the analysis and reverse engineering of complex biological systems.
- ❑ CINECA LISA 2014 (Production Projects): Massive parallel analysis of complex biological systems.
- ❑ PRIN 2005: Automi e Linguaggi Formali: aspetti matematici e applicativi.
- ❑ PRIN 2004: Systems Biology: modellazione, linguaggi e analisi (Sybilla).
- ❑ PRIN 2003: Linguaggi Formali e Automi: Metodi, Modelli e Applicazioni.
- ❑ European project under the 5th Framework Programme: A Thematic Network on Molecular Computing (MolCoNet, IST-32008-2001).

Applications to funding proposals⁴

❑ **Human Frontier Science Program (HFSP 2020)**

Proposal title: “A Systems Biology approach to investigate liquid-liquid phase separation-induced toxicity”.

Role: Principal applicant.

Co-applicant: Prof. Hisao Moriya, Research Core for Interdisciplinary Sciences, Okayama University, Japan.

❑ **Human Frontier Science Program (HFSP 2018)**

Proposal title: “A wet- and dry-lab methodology to predict cell fate mechanisms at single-cell resolution”.

Role: Co-applicant.

Principal applicant and co-applicant: Prof. Carlos F. Lopez, Department of Biochemistry, Vanderbilt University, Nashville, USA; Prof. Vito Quaranta, Quantitative Systems Biology Center, Vanderbilt University Nashville, USA.

❑ **Michael J. Fox Foundation - 2017 Research Funding Program “Computational Tools for Parkinson’s Disease Therapeutic Development”**

Proposal title: “DynaMoParD - A fuzzy logic dynamic model to identify new Parkinson’s Disease targets”.

Role: Co-PI.

PI: Prof. Mauro Fasano, Department of Science and High Technology, University of Insubria, Italy.

❑ **PRIN 2017 (Program “Progetti di ricerca di Rilevante Interesse Nazionale” - MIUR, Italy)**

Proposal title: “TOPDREAM: Topology driven modelling, a biomarker for INSOMNIA”.

Role: Associated investigator, coordinator of the local research unit.

PI: Prof. Emanuela Merelli, University of Camerino (MC), Italy.

❑ **Human Frontier Science Program (HFSP 2016)**

Proposal title: “Self-assembled biomolecular materials for imitating neuronal circuit functions and behaviors”.

Role: Co-applicant.

Principal applicant and co-applicant: Prof. Thomas LaBean, Materials Science and Engineering, North Carolina State University, Raleigh, USA; Prof. Jennifer Groh, Neurobiology; Psychology and Neuroscience, Duke University, Durham, USA.

❑ **PRIN 2015 (Program “Progetti di ricerca di Rilevante Interesse Nazionale” - MIUR, Italy)**

Proposal title: “GPU-accelerated methods to investigate spatial models of cells: disclosing multi-scale patterns in nuclear gene regulation and molecular signal transduction”.

Role: PI.

⁴ Though not funded, these proposals show the versatility of my expertise and research interests, as well as the variety and strengths of my collaboration network.

FIRB 2012 (Program “Futuro In Ricerca” - MIUR, Italy)

Proposal title: “Handling complexity in biological systems: computational methods and experimental validation”.

Role: PI.

Human Frontier Science Program (HFSP 2011)

Proposal title: “Dissection of Post-Replication Repair by integrated biological and computational approaches”.

Role: Co-applicant.

Principal applicant and co-applicants: Prof. Marco Muzi-Falconi, Department of Biomolecular Sciences and Biotechnologies, University of Milano, Italy; Prof. Philippe Pasero, Genome Dynamics, Institute of Human Genetics, Montpellier, France; Prof. Grant Brown, Department of Biochemistry, University of Toronto, Canada.

FIRB 2010 (Program “Futuro In Ricerca” - MIUR, Italy)

Proposal title: “Handling uncertainty in biological systems: a formal approach and its experimental validation”.

Role: PI.

FIRB 2008⁵ (Program “Futuro In Ricerca” - MIUR, Italy)

Proposal title: “Handling uncertainty in biological systems: a formal approach and its experimental validation”.

Role: PI.

ERC Starting Grant 2007

Proposal title: “BioMoSAyX - Biological systems: Modelling, Simulation, Analysis and eXperimental validation”.

Role: PI.

Referee activity

National and international funding programs

- 2019: 2014-2019 Cancer Plan - Call for Proposals “Single cell approaches for the study of oncogenic processes” organized by ITMO Cancer of the French National Alliance for Life and Health Sciences (AVIESAN) jointly with the French National Cancer Institute (INCa).
- 2016: “Progetti di Ateneo, Scavi e Ricerche archeologiche 2016”, University Ca’ Foscari, Venice, Italy.

⁵ This project proposal received the highest evaluation by national and international reviewers (score equal to 40/40), and a final judgment of project “financeable according to available resources” by a ministerial commission. Although funding were available, none of the projects classified as “financeable according to available resources” for this call was eventually funded because of an arbitrary decision by the Italian Minister of Instruction, University and Research.

- ❑ 2015: TALENT RESEARCH “La ricerca dei talenti – Iniziativa per il supporto dell’indipendenza scientifica dei giovani ricercatori” (Research Talent initiative), Politecnico di Torino, Italy.
- ❑ 2013: PISCOPIA (Marie Curie Fellowship Programme), University of Padova, Italy.
- ❑ 2013: Programme “Futuro in Ricerca 2013” (MIUR), Italy.

Journals

Acta Informatica, Bioinformatics, BioMed Research International, BioSystems, BMC Bioinformatics, Bulletin of Mathematical Biology, Chemical Engineering Communications, Current Genomics, Fundamenta Informaticae, Genome Biology, IEEE Transactions in NanoBioscience, International Journal of Foundations of Computer Science, Journal of Logic and Computation, Journal of Membrane Computing, Mathematics and Computers in Simulation, Natural Computing, PLOS ONE, Soft Computing, Theoretical Computer Science, WIREs Systems Biology and Medicine.

International conferences

Referee for around 50 conferences and workshops on Evolutionary Computation, Bioinformatics, Computational Biology, Systems Biology, Theoretical Computer Science, and bio-inspired computational paradigms:

CEC2004, CEC2005, CEC2006, CEC2007, CEC2008, CEC2016, CEC2017, CIAA2008, CIBB2016, CIBB2017, CIBB2018, CIBB2019, CIBCB2016, CIBCB2017, CiE2007, CiE2009, CiE2010, CiE2012, CiE2013, CiE2014, CIRAS2005, CMC12, DCFS2005, DLT2005, DLT2011, DNA8, DNA10, DNA11, DNA12, EPIA2011, EPIA2013, Euro-Par2018, FASDS-14, HEALTHINF2020, HiCOMB2017, IWCB2008, IWNC2007, IWNC2009, IWNC2012, MecBic2009, PDP2018, SAC2016, SAC2017, SAC2018, SOFSEM2013, STACS2003, STACS2014, UCNC 2014, WMC05, WMSCI2013.

Ph.D. thesis

- ❑ Referee of a Ph.D. thesis in Computer Science (title: “Refinement of biomodels using Petri nets”), Faculty of Science and Engineering, Åbo Akademy University, Turku, Finland, 2016.
- ❑ Referee of a Ph.D. thesis in Computer Science (title: “Computational analysis of biological networks”), University of Verona, Italy, 2010.

Ancillary activities

Administrative assignments in research and training

- ❑ Oct. 2020 - present day: Member of the working group on gender and STEM, University of Milano-Bicocca, Italy.

- ❑ Oct. 2019 - present day: Member of the Scientific Board of “Bicocca Bioinformatics Biostatistics and Bioimaging Centre - B4”
- ❑ Oct. 2019 - present day: Member of the committee for the internationalization (Erasmus program) of the Bachelor’s and Master’s degree courses in Biotechnology, Department of Biotechnology and Biosciences, University of Milano-Bicocca, Italy.
- ❑ Jan. 2019 - present day: Member of the departmental group for the quality assurance in research, Department of Informatics, Systems and Communication, University of Milano-Bicocca, Italy.
- ❑ Jan. 2019 - present day: Member of the departmental study-orientation committee (various orientation activities, open days, etc.) for secondary school students, Department of Informatics, Systems and Communication, University of Milano-Bicocca, Italy.
- ❑ Jan. 2019 - Jan. 2020: Departmental supervisor of the training and research projects in the context of the Italian ministerial program “Alternanza Scuola Lavoro” for secondary school students, Department of Informatics, Systems and Communication, University of Milano-Bicocca, Italy.
- ❑ Mar. 2019: Member of the group of selected professors for oral interview by the Italian ministerial committee (CEV-MIUR) appointed for the assessment of the Bachelor’s degree program in Biotechnologies, Department of Biotechnologies and Biosciences, University of Milano-Bicocca, Italy.
- ❑ Oct. 2017 - present day: Member of the committee for the annual selection of candidates for junior and senior post-doctoral positions available at the Department of Informatics, Systems and Communication, University of Milano-Bicocca, Italy.

Academic assignments in education and training

- ❑ May 2017 - present day: Member of the Board of Training Scientists of the Ph.D. School in Convergent Technologies for Biomolecular Systems (TeCSBi), University of Milano-Bicocca, Italy.
- ❑ Mar. 2016 - present day: Member of the Board of Training Scientists of the Ph.D. School in Biological Sciences and Biotechnology, University of Milano-Bicocca, Italy.
- ❑ Oct. 2013 - Sep. 2015: Member of the Directive Board of the Ph.D. School in Biological and Molecular Sciences, University of Milano, Italy.
- ❑ Apr. 2011 - Sep. 2015: Member of the Board of Training Scientists of the Ph.D. School in Biological and Molecular Sciences, University of Milano, Italy.

Selection boards for Assistant Professor positions

- Nov. - Dec. 2019: Member of the selection board for a position of Assistant Professor in Computer Science at the Department of Informatics, University of Milano, Italy.
- July - Sep. 2018: Member of the selection board for a position of Assistant Professor in Computer Science at the Department of Informatics, University of Verona, Italy.
- July - Sep. 2016: Member of the selection board for a position of Assistant Professor in Computer Science at the Department of Informatics, Systems and Communication, University of Milano-Bicocca, Italy.
- May - June 2007: Member of the selection board for a position of Assistant Professor in Computer Science at the Faculty of Mathematics, Physics and Natural Sciences, University of Verona, Italy.

Doctoral examination boards

- Mar. 2021: Member of the evaluation committee for the doctorate in Computer Science, University of Milano, Italy.
- July 2018: Member of the evaluation committee for the doctorate in Complex Systems for Life Sciences, University of Turin, Italy.
- Sep. 2016: Member of the evaluation committee for the doctorate in Computer Science, University of Insubria, Varese, Italy.
- Feb. 2012: Member of the evaluation committee for the doctorate in Computer Science, University of Milano-Bicocca, Italy.
- Apr. 2011: Member of the evaluation committee for the doctorate in Computer Science, University of Verona, Italy.
- Apr. 2010: Member of the evaluation committee for the doctorate in Computer Science, University of Verona, Italy.

Other selection boards

- Dec. 2015 - present day: Member of the evaluation committee for more than 20 post-doctoral positions and research scholarships at the Department of Informatics, Systems and Communication, University of Milano-Bicocca, and blended-learning tutor positions for the Master's degree program in Computer Science, University of Milano-Bicocca, Italy.

Miscellaneous

- Guest co-editor of “Network-oriented approaches to anticancer drug response”, a Frontiers’ Research Topic in Bioinformatics and Computational Biology.
- Mar. 2015: Participation by invitation to the 2nd workshop on “Training and Education in Systems Biology”, organized by ISBE (Infrastructure for Systems Biology Europe) and ERASysAPP (ERA-Net for Applied Systems Biology), Goteborg, Sweden.
- Nov. 27-28, 2014: Participation by invitation to the 1st workshop on “Training and Education in Systems Biology”, organized by ISBE (Infrastructure for Systems Biology Europe) and ERASysAPP (ERA-Net for Applied Systems Biology), Heidelberg, Germany.
- Mar. 23-24, 2012 - present day: Member of the reviewers board for the evaluation of ministerial funding calls in the research areas ERC LS2_13, LS2_14, PE6_13, and Italian MIUR INF/01.
- Mar. 2011: Participation by invitation to the dissemination event on “Mathematics and Biology: wet computer and virtual cells”, in the context of the scientific and artistic festival “Infinitamente 2011 – Perfezione, errore e differenza”, Verona, Italy.

Languages

- Italian: mother tongue
- English: proficient
- East Greenlandic: basic words

References

- ❑ Prof. Giancarlo Mauri
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