



Paolo Cazzaniga

Department of Human and Social Sciences, University of Bergamo, Italy

☎ (+39) 0352052933 | ✉ paolo.cazzaniga@unibg.it

Work experience

June 2021 - Present Day: Associate Professor at the University of Bergamo, Department of Human and Social Sciences

February 2011 - May 2021: Assistant Professor at the University of Bergamo, Department of Human and Social Sciences

January 2013 - December 2014: Research Associate at the Institute for Systems Analysis and Computer Science (IASI) - CNR, Roma

May 2010 - January 2011: Post-doc at the University of Milano – Bicocca. Research project: “Stochastic and hybrid simulation and analysis of mathematical models of biological systems”

December 2009 - February 2010: Research collaboration at the University of Milano – Bicocca. Research project: “Development of a stochastic simulator for the GPU”

Education and training

2010: PhD in Computer Science at the University of Milano – Bicocca. Dissertation title: “Stochastic algorithms for biochemical processes”. Supervisor Prof. Giancarlo Mauri

September 2005 - September 2006: Pre-doctoral scholarship at the University of Milano – Bicocca. Project title: “Biomolecular algorithms for computationally complex problems”

2005: Master degree in Informatics at the University of Milano – Bicocca. Dissertation title: “Storage device in membrane systems”. Supervisor Prof. Giancarlo Mauri

Awards

2019: Best paper award at the IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB 2019), Certosa di Pontignano, Siena, Italy. Paper entitled “ProCell: Investigating cell proliferation with Swarm Intelligence”

2018: Awarded by the Italian Ministry of Education, Universities and Research (MIUR) with the “Fondo per il finanziamento delle attività base di ricerca” (FFABR) project

2016: NVIDIA Academic GPU grant. Awarded with a NVIDIA GPU Titan X donated by the NVIDIA Corporation

Scientific activity

My research is located in the multidisciplinary field of Systems Biology. My activities range from the definition of mathematical models of complex (biological) systems to the simulation of their temporal dynamics by means of deterministic, stochastic or hybrid algorithms. I also define and apply different methodologies for the analysis of the emergent behavior of the systems under investigation (e.g., parameter sweep analysis, parameter identifiability, sensitivity analysis).

My research effort also concerns the definition, implementation (for CPUs and GPUs) and application of Artificial Intelligence methods to problems in the fields of Bioinformatics, Systems Biology and Biomedicine, like, for instance, inferring the full haplotype of a cell starting from read sequencing data, estimating the unknown information of a complex system (e.g., molecular concentrations and kinetic constants in the case of biological systems), enhancing the appearance and visual quality of biomedical images.

I have already successfully applied different methods, such as Particle Swarm Optimization, Genetic Algorithms and Deep Neural Networks, to these problems.

Currently, I am actively collaborating with:

- Prof. Pietro Liò, University of Cambridge, concerning the development of evolutionary computation methods for genotype assembly;
- Prof. Daniela Besozzi and Giancarlo Mauri, University of Milano-Bicocca, concerning the definition of computational methods for Systems Biology;
- Prof. Daniel Ashlock, University of Guelph, concerning the definition and enhancement of optimization strategies for complex problems;
- Dr. Carlos F. Lopez, Vanderbilt University, School of Medicine, concerning the GPU-based analyses of large scale biological models;
- Prof. Pier Giuseppe Pelicci, European Institute of Oncology, concerning the modeling of cell proliferation in human acute myeloid leukemia;
- Prof. Ferdinando Chiaradonna and Maria Pia Longhese, University of Milano-Bicocca, concerning the application of hybrid fuzzy logic based modeling and simulation approaches to study complex biological systems;
- Dr. Renata Tisi, University of Milano-Bicocca, concerning the analysis of calcium homeostasis;
- Prof. Hitoshi Iba, University of Tokyo, concerning the automatic inference and parameterization of synthetic biochemical networks;
- Prof. Enzo Martegani, University of Milano-Bicocca, concerning the computational investigation of signaling pathways in yeast *S. cerevisiae*.

Research interests

- Artificial Intelligence, Machine Learning, Computational Intelligence
- Systems Biology, Computational Biology, Bioinformatics
- Mathematical modeling and simulation of complex biological systems
- High Performance Computing
- Biomedical image analysis

Publications

Journals

1. M.S. Nobile, F. Fontana, L. Manzoni, P. Cazzaniga, G. Mauri, G.A.A. Saracino, D. Besozzi, F. Gelain. **HyperBeta: characterizing the structural dynamics of proteins and self-assembling peptides**, Scientific reports, vol. 11, 7783, 2021
2. 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
3. L. Rundo, A. Tangherloni, P. Cazzaniga, M. Mistri, S. Galimberti, R. Woitek, E. Sala, G. Mauri, M.S. Nobile. **A CUDA-powered method for the feature extraction and unsupervised analysis of medical images**, The Journal of Supercomputing, 2021
4. 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, 12:617935, 2021

5. 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, vol. 13:1, pp. 1687-1698, 2020
6. M.S. Nobile, E. Nisoli, T. Vlachou, S. Spolaor, P. Cazzaniga, G. Mauri, P.G. Pelicci, D. Besozzi. **cuProCell: GPU-accelerated analysis of cell proliferation with flow cytometry data**, IEEE Journal of Biomedical and Health Informatics, vol. 24:11, pp. 3173-3181, 2020
7. 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, vol. 10:18, pp. 6187, 2020
8. 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**, vol. 22:3, pp. 285, 2020
9. D. Besozzi, L. Manzoni, M.S. Nobile, S. Spolaor, M. Castelli, L. Vanneschi, P. Cazzaniga, S. Ruberto, L. Rundo, A. Tangherloni. **Computational Intelligence for Life Sciences**, Fundamenta Informaticae, vol. 171, no. 1-4, pp. 57-80, 2020
10. S. Spolaor, M.S. Nobile, G. Mauri, P. Cazzaniga, D. Besozzi. **Coupling Mechanistic Approaches and Fuzzy Logic to Model and Simulate Complex Systems**, IEEE Transactions on Fuzzy Systems, 28(8), pp. 1748-1759, 2020
11. 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), pp. 2181-2188, 2020
12. L. Rundo, C. Han, Y. Nagano, J. Zhang, R. Hataya, C. Militello, A. Tangherloni, M.S. Nobile, C. Ferretti, D. Besozzi, M.C. Gilardi, S. Vitabile, G. Mauri, H. Nakayama, P. Cazzaniga. **USE-Net: incorporating Squeeze-and-Excitation blocks into U-Net for prostate zonal segmentation of multi-institutional MRI datasets**, Neurocomputing, vol. 365, pp. 31-43, 2019
13. 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, p. 105494, 2019
14. 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 by using MedGA**, Computer Methods and Programs in Biomedicine, 176, pp. 159-172, 2019
15. 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(4), p. 172, 2019
16. 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, 35(18), pp. 3378-3386, 2019
17. L. Rundo, A. Tangherloni, M.S. Nobile, C. Militello, D. Besozzi, G. Mauri, P. Cazzaniga. **MedGA: a novel evolutionary method for image enhancement in medical imaging systems**. Expert Systems with Applications, 119, pp. 387-399, 2019
18. M.S. Nobile, P. Cazzaniga, D. Besozzi, G. Mauri. **ginSODA: massive parallel integration of stiff ODE systems on GPUs**. Journal of Supercomputing, 75 (12), pp. 7844-7856, 2019
19. M.S. Nobile, P. Cazzaniga, D. Besozzi, R. Colombo, G. Mauri, G. Pasi. **Fuzzy Self-Tuning PSO: A settings-free algorithm for global optimization**. Swarm and Evolutionary Computation, 30, pp. 70-85, 2018
20. 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, 33(21), pp. 3492-3494, 2017
21. A. Tangherloni, M.S. Nobile, D. Besozzi, G. Mauri, P. Cazzaniga. **LASSIE: simulating large-scale models of biochemical systems on GPUs**. BMC Bioinformatics, 18(1), pp. 1-18 2017
22. 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, pp. 1-4, 2017

23. M.S. Nobile, P. Cazzaniga[†], A. Tangherloni, D. Besozzi. **Graphics Processing Units in Bioinformatics, Computational Biology and Systems Biology**. Briefings in Bioinformatics, 18(5), pp. 870–885, 2017
24. A. Tangherloni, M.S. Nobile, P. Cazzaniga, D. Besozzi, G. Mauri. **Gillespie's Stochastic Simulation Algorithm on MIC coprocessors**. Journal of Supercomputing, pp. 1-11, 2016
25. 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), 2014
26. 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 - High-Performance Computing and Big Data in Omics-based Medicine, Article ID 863298, 2014
27. 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), pp. 17-24, 2014
28. 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
29. 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
30. 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
31. 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), pp. 99-107, 2012
32. 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), pp. 89-96, 2011
33. A. Leporati, D. Besozzi, P. Cazzaniga, D. Pescini, C. Ferretti. **Computing with energy and chemical reactions**. Natural Computing, 9(2), pp. 493-512, 2010
34. 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), pp. 1141-1160, 2009
35. 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), pp. 377-385, 2008
36. D. Besozzi, P. Cazzaniga, D. Pescini, G. Mauri. **Modelling metapopulations with stochastic membrane Systems**. BioSystems, 91(3), pp. 499-514, 2008
37. 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), pp. 242-266, 2007
38. D. Besozzi, P. Cazzaniga, D. Pescini, G. Mauri. **Seasonal variance in P system models for metapopulations**. Progress in Natural Science, 17(4), pp. 392-400, 2007

[†]co-first author, *co-corresponding author

Book chapters and contributed volumes

1. P. Cazzaniga, M.S. Nobile, A. Tangherloni, D. Besozzi. **Accelerating stochastic simulations of mechanistic models of biological systems: Advantages and issues in the parallelization on Graphics Processing Units**. In Quantitative Biology: Computational Methods and Examples (B. Munsky, W. Hlavacek, L. Tsimring eds.), MIT Press, 2018.

2. M.S. Nobile, D. Cipolla, P. Cazzaniga, D. Besozzi. **GPU-powered evolutionary design of mass-action based models of gene regulation.** In: Evolutionary Algorithms in Gene Regulatory Network Research (H. Iba, N. Noman eds.), Wiley, 2016
3. 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.), 40-51, Spandugino, 2015
4. 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
5. P. Cazzaniga, M. Gheorghe, N. Krasnogor, G. Mauri, D. Pescini, F.J. Romero-Campero. **Probabilistic/stochastic models.** In: The Oxford Handbook of Membrane Computing, (G. Păun, G. Rozenberg, A. Salomaa, eds.), Oxford University Press, 2009
6. D. Besozzi, P. Cazzaniga, D. Pescini, G. Mauri. **A multivolume approach to stochastic modelling 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

Conference Proceedings

1. 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.** 2020 IEEE Conference on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB), Via del Mar, Chile, pp. 1-8, 2020
2. D.M. Papetti, S. Spolaor, D. Besozzi, P. Cazzaniga, M. Antoniotti, M.S. Nobile. **On the automatic calibration of fully analogical spiking neuromorphic chips.** 2020 IEEE International Joint Conference on Neural Networks (IJCNN), Glasgow, United Kingdom, pp. 1-8, 2020
3. M.S. Nobile, S. Spolaor, P. Cazzaniga, D.M. Papetti, D. Besozzi, D.A. Ashlock, L. Manzoni. **Which random is the best random? A study on sampling methods in Fourier surrogate modeling.** 2020 IEEE Congress on Evolutionary Computation (CEC), Glasgow, United Kingdom, pp. 1-8, 2020
4. L. Rundo, A. Tangherloni, S. Galimberti, P. Cazzaniga, R. Woitek, E. Sala, M.S. Nobile, G. Mauri, **HaraliCU: GPU-Powered Haralick Feature Extraction on Medical Images Exploiting the Full Dynamics of Gray-Scale Levels.** 15th International Conference on Parallel Computing Technologies (PaCT 2019), Almaty, Kazakhstan, 2019
5. M.S. Nobile, T. Vlachou, S. Spolaor, P. Cazzaniga, G. Mauri, P.G. Pelicci, D. Besozzi, **ProCell: Investigating cell proliferation with Swarm Intelligence.** IEEE Conference on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB 2019), Certosa di Pontignano, Siena, Italy, 2019
6. M.S. Nobile, P. Cazzaniga, D.A. Ashlock, **Dilation Functions in Global Optimization.** IEEE Congress on Evolutionary Computation (CEC 2019), Wellington, New Zealand, 2019
7. 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.** European Conference on Parallel Processing, LNCS, 11339, 650-661, 2019
8. 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.** European Conference on Parallel Processing, LNCS, 11339, 626-637, 2019
9. M.S. Nobile, A. Tangherloni, L. Rundo, S. Spolaor, D. Besozzi, G. Mauri, P. Cazzaniga. **Computational intelligence for parameter estimation of biochemical systems.** IEEE Congress on Evolutionary Computation (CEC 2018), 1-8, 2018
10. A. Tangherloni, L. Rundo, S. Spolaor, P. Cazzaniga, M.S. Nobile. **GPU-Powered Multi-Swarm Parameter Estimation of Biological Systems: A Master-Slave Approach.** 26th Euromicro International Conference on Parallel, Distributed and Network-based Processing (PDP), 2018

11. S. Spolaor, A. Tangherloni, L. Rundo, M.S. Nobile, P. Cazzaniga. **Reboot strategies in particle swarm optimization and their impact on parameter estimation of biochemical systems.** Proceedings of IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB2017), Manchester (UK), 2017
12. D. Ramazzotti, M.S. Nobile, P. Cazzaniga, G. Mauri, M. Antoniotti. **Parallel implementation of efficient search schemes for the inference of cancer progression models,** Proceedings of IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB2016), Chiang Mai (Thailand), 2016
13. A. Tangherloni, M.S. Nobile, P. Cazzaniga. **GPU-powered Bat Algorithm for the parameter estimation of biochemical kinetic values,** Proceedings of IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB2016), Chiang Mai (Thailand), 7 2016
14. F. Cumbo, M.S. Nobile, C. Damiani, R. Colombo, G. Mauri, P. Cazzaniga. **COSYS: Computational Systems Biology infrastructure,** 13th International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics (CIBB2016), Stirling (UK), 2016
15. A. Re, G. Caravagna, D. Pescini, M.S. Nobile, P. Cazzaniga. **Approximate simulation of chemical reaction systems with micro, meso and macro-scales,** 13th International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics (CIBB2016), Stirling (UK), 2016
16. M.S. Nobile, A. Tangherloni, D. Besozzi, P. Cazzaniga. **GPU-powered and settings-free parameter estimation of biochemical systems,** IEEE World Congress on Computational Intelligence 2016, Vancouver (Canada), 2016
17. 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,** 12th International Meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics (CIBB2015), Naples (Italy), 2015
18. P. Cazzaniga, M.S. Nobile, D. Besozzi. **The impact of particles initialization in PSO: parameter estimation as a case in point,** 2015 IEEE Conference on Computational Intelligence in Bioinformatics and Computational Biology, August 12-15, Niagara Falls, (Canada), 2015
19. 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 the 2015 IEEE International Conference on Fuzzy Systems (FUZZ-IEEE 2015), Istanbul (Turkey), pp. 1–8, 2015
20. P. Cazzaniga, F. Ferrara, M.S. Nobile, D. Besozzi, G. Mauri. **Parallelizing biochemical stochastic simulations: a comparison of GPUs and Intel Xeon Phi coprocessors,** Proceedings of the 13th International Conference on Parallel Computing Technologies (PaCT 2015), Petrozavodsk (Russia). V. Malyshkin (Ed.). Lecture Notes in Computer Science. Vol. 9251, pp. 363–374, 2015
21. 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
22. M. Bellini, D. Besozzi, P. Cazzaniga, G. Mauri, M.S. Nobile. **Simulation and analysis of the blood coagulation cascade accelerated on GPU.** PDP2014 - Special Session “Advances in High-Performance Bioinformatics, Systems and Synthetic Biology”, 12-14 February 2014, Torino, Italy
23. 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 and M. Antoniotti, eds.), EPTCS 130, 87–91, 2013
24. 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 and M. Heiner, eds.), CEUR Workshop Proceedings Vol. 988, 60-74, 2013
25. 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

26. 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
27. 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 fourteenth International Conference on Genetic and Evolutionary Computation Conference Companion. ACM New York, NY, USA, GECCO Companion '12, 1421-1422, 2012
28. 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
29. 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**. Eighth International Workshop on Computational Systems Biology, WCSB 2011, June 6-8, 2011, Zürich, Switzerland, (H. Koepl, J. Acimovic, J. Kesseli, T. Mäki-Marttunen, A. Larjo, O. Yli-Harja, eds.), TICSP Series #57, 33-36, 2011
30. 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, Jena, Germany, August 24-27, 2010. Revised Selected Papers, (M. Gheorghe, T. Hinze, G. Păun, G. Rozenberg, A. Salomaa, eds.), LNCS 6501, 119-143, 2010
31. 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
32. E. Mosca, P. Cazzaniga, D. Pescini, I. Merelli, G. Mauri, L. Milanesi. **Stochastic simulations on a grid framework for parallel sweep applications in biological models**. HiBi09 - High Performance Computational Systems Biology Workshop, 14-16 October 2009 - Trento, Italy
33. P. Cazzaniga, G. Mauri, L. Milanesi, E. Mosca, D. Pescini. **A novel variant of tissue P systems for the modelling of biochemical systems**. Proceedings of the 10th International Workshop on Membrane Computing, WMC 2009 (G. Paun, M.J. Perez-Jimenez, A. Riscos-Nunez, G. Rozenberg, A. Salomaa, eds.), LNCS 5957, 210-226, 2010
34. 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
35. P. Cazzaniga, D. Pescini, L. Vanneschi, D. Besozzi, G. Mauri. **A Comparison of Genetic Algorithms and Particle Swarm Optimization for Parameter Estimation in Stochastic Biochemical Systems**, Proceedings of EvoBio 2009, LNCS 5483, 116-127, 2009
36. D. Pescini, P. Cazzaniga, C. Ferretti, G. Mauri. **First steps towards a wet implementation for tau-DPP**. 9th International Workshop, WMC 2008 (D. Corne et al. eds.), LNCS 5391, 355-373, 2009
37. P. Cazzaniga, D. Pescini, D. Besozzi, G. Mauri. **Tau leaping stochastic simulation method in P systems**. 7th International Workshop, WMC 2006 (H.J. Hoogeboom, G. Paun, G. Rozenberg, A. Salomaa, eds.), LNCS 4361, 298-313, 2006
38. P. Cazzaniga, A. Leporati, G. Mauri, C. Zandron, **P Systems with Memory**, 6th International Workshop, WMC 2005, Vienna, Austria, July 18-21, 2005, Revised Selected and Invited Papers, (R. Freund, Gh. Paun, G. Rozenberg, A. Salomaa, eds.), LNCS 3850, 165-180, 2006

Other

1. 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, August 30 - September 3, 2013

2. 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, August 30 - September 3, 2013
3. 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, June 10-12, 2013
4. 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*.** ICSB2011 - 12th International Conference on Systems Biology, Heidelberg/Mannheim, August 28 - September 1, 2011
5. 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, September 14-18, 2010. (Abstract in: Journal of Biotechnology, Vol. 150, Suppl.1, 545, 2010.
6. 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, September 14-18, 2010. (Abstract in: Journal of Biotechnology, Vol. 150, Suppl.1, 546, 2010.
7. 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, September 14-18, 2010. (Abstract in: Journal of Biotechnology, Vol. 150, Suppl.1, 519-520, 2010.
8. D. Besozzi, P. Cazzaniga, G. Mauri, D. Pescini. **Effects of stochastic fluctuations on the coordination of flagella in bacterial chemotaxis.** Fourth Annual q-bio Conference on Cellular Information Processing, Santa Fe, New Mexico, August 11-14, 2010
9. 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.** Poster at Sysbiohealth Symposium 2009, Milano, Italy, November 2009
10. E. Mosca, P. Cazzaniga, D. Pescini, G. Mauri, L. Milanese. **A stochastic, discrete model for the simulation of the action potential.** Poster at Sysbiohealth Symposium 2008, Bologna, Italy, November 2008
11. 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.** Poster at ICSB 2008 - International Conference on Systems Biology, Goteborg, Sweden, August 2008
12. P. Cazzaniga, D. Pescini, D. Besozzi, G. Mauri, S. Colombo, E. Martegani. **Stochastic Modeling and Simulations of the Ras/-cAMP/PKA Pathway in budding Yeast.** Poster at Sysbiohealth Symposium 2007, Milano, Italy, October 2007
13. E. Martegani, P. Cazzaniga, D. Pescini, D. Besozzi, S. Colombo, G. Mauri. **Stochastic modeling of the Ras/cAMP/PKA signal transduction pathway in yeast.** Poster at Computational Methods in Systems Biology (CMSB), Trento, Italy, October 2006
14. 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.** Poster at ISSY 25 - 25th International Specialized Symposium on Yeasts, Hanasaari, Espoo, Finland, June 2006

Research periods abroad

January 2008 - July 2008: Visiting period at the Laboratory for Foundations of Computer Science (LFCS) - Supervisor: Prof. Stephen Gilmore, University of Edinburgh, Scotland

January 2006: Visiting period at the "Department of Computer Science" - Supervisor: Prof. Mario de Jesús Pérez Jiménez, University of Seville, Spain

Teaching activity

Doctoral courses

January 2021 - February 2021: “Statistics and computational tools for the analysis of quantitative data”

Ph.D. Program in Human capital formation and labour market relations, University of Bergamo

Role: course co-organizer and lecturer, together with Prof. Andrea Greco, University of Bergamo

2018 - present day: 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. Prof. Daniela Besozzi, University of Milano-Bicocca, 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. Daniela Besozzi, University of Milano-Bicocca, Italy, and Dr. Marco S. Nobile, TU/e - Eindhoven University of Technology, The Netherlands

Academic assignments

2015 - present day: Information and Communication Technologies (ICT)

Special needs teacher courses, University of Bergamo, Italy

2011 - present day: Fundamentals of Informatics (6 ECTS)

Bachelor of Educational Studies, University of Bergamo, Italy

2015 - present day: Statistical methods for the Human Sciences (6 ECTS)

Bachelor of Educational Studies, University of Bergamo, Italy

2017 - present day: IT for the Communication (6 ECTS)

Bachelor of Communication Sciences, University of Bergamo, Italy

2019 - present day: Fundamentals of Informatics and Statistics (6 ECTS)

Bachelor of Psychological Studies, University of Bergamo, Italy

Academic assistance

2009: Algorithms for Bioinformatics

Master degree in Biotechnology, University of Milano, Italy

2008 - 2009: Perl and Java programming

Bachelor in Computer Science, University of Milano-Bicocca, Italy

International schools (doctoral and post-doc level)

4-6 October 2017: Member of the organizing committee of the “2nd SYSBIO.IT School on Computational Systems Biology and Bioinformatics”, University of Milano-Bicocca, Milano, Italy

7-9 June 2016: Lecturer 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”, University of Milano-Bicocca, Milano, Italy

Supervision

- **Scientific advisor** of a post-doctoral position funded under the STaRs Programme of the University of Bergamo
- **co-advisor of 1 PhD Students** in Informatics, University of Milano-Bicocca

Supervision of master students

- 4 Master thesis of Molecular Biotechnologies and Bio-Information Technology, University of Milano
- 3 Master thesis of Informatics, University of Milano-Bicocca
- 2 Master thesis of Informatics, University of Milano

Supervision of bachelor students

- 4 Bachelors of Informatics, University of Milano-Bicocca
- 5 Bachelors of Informatics, University of Milano
- 30 Bachelors of Educational Studies, University of Bergamo
- 10 Bachelors of Psychological Studies, University of Bergamo
- 3 Bachelors of Industrial and Environmental Biotechnology, University of Milano
- 1 Bachelors of Communication Sciences, University of Bergamo
- 1 Master thesis of Pedagogical Studies, University of Bergamo

Ancillary activities

Administrative assignments

2013 - present day: Contact person for the definition of the study plans for the students of the bachelor of Educational Studies, Department of Human and Social Sciences, University of Bergamo

2015 - present day: Chair of the committee for the evaluation of the scientific production of the Department of Human and Social Sciences, University of Bergamo

2016 - present day: Member of the council of the Centre of educational technologies and communications of the University of Bergamo

2018 - present day: Member of the Joint Committee Teachers-Students of the Department of Human and Social Sciences, University of Bergamo

May 2017 - October 2018: Member of the council of the Department of Human and Social Sciences, University of Bergamo

Selection boards

Member of the evaluation committee of several post-doctoral positions and research scholarships at the Department of Human and Social Sciences of the University of Bergamo

Conferences/Talks

- Speaker at the 7th International Workshop on Membrane Computing, Leiden, The Netherlands, 2006. Title of the talk: "Tau leaping stochastic simulation method in P systems"
- Speaker at IEEE Congress on Evolutionary Computation, Beijing, China, 2014. Title of the talk: "A memetic hybrid method for the Molecular Distance Geometry Problem with incomplete information"
- Speaker at IEEE World Congress on Computational Intelligence, Vancouver, Canada, 2016. Title of the talk: "GPU-powered and settings free parameter estimation of biochemical systems"
- Speaker at the 13th International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics, Stirling, UK, 2016. Title of the talk: "COSYS: Computational Systems Biology infrastructure"
- Speaker at IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology, Chiang Mai, Thailand, 2016. Title of the talk: "GPU-powered Bat Algorithm for the parameter estimation of biochemical kinetic values"

- Speaker at BITS 2017 - 14th Annual Meeting of the Bioinformatics Italian Society, Cagliari, Italy, 2017. Title of the talk: “LASSIE: a GPU-based large-scale simulator of biological systems”
- Speaker at the 26th Euromicro International Conference on Parallel, distributed and network-based Processing, Cambridge, UK, 2018. Title of the talk: “GPU-powered Multi-Swarm Parameter Estimation of Biological Systems: A Master-Slave Approach”

Principal investigator of research projects

April 2021 - Today: Project “MaLeCoB2: Machine learning for the investigation of complex biological systems 2.0” - CINECA Italian SuperComputing Resource Allocation (ISCRA)

June 2020 - March 2021: Project “MaLeComB: Machine learning for the investigation of complex biological systems” - CINECA Italian SuperComputing Resource Allocation (ISCRA)

December 2017 - September 2018: Project “FISCo 2.0: Fine-grain and spatial simulations of complex biological systems” - CINECA Italian SuperComputing Resource Allocation (ISCRA)

April 2017 - October 2017: Project “SPASMO: Spatial Analysis and Simulation of large-scale Models” - CINECA Interdisciplinary Laboratory for Advanced Simulation (LISA)

February 2017 - November 2017: Project “FISCo: Fine-grain and spatial simulations of complex biological systems” - CINECA Italian SuperComputing Resource Allocation (ISCRA)

Research projects

January 2020 - Today: Member of the IEEE CIS Task Force on advanced representation in biological and medical search and optimization

January 2013 - Today: Member of the ISBE/SYSBIO.IT Centre of Systems Biology (www.sysbio.it)

2015 - 2016: Project “FiCoS: Fine and coarse-grain simulations of complex biological systems” - Italian SuperComputing Resource Allocation (ISCRA)

2014 - 2015: Project “PACoS: Massive parallel analysis of complex biological systems” - CINECA LISA 2014 (Production Projects)

April 2013 - March 2014: Project “BioComPLX: a tool for the analysis and reverse engineering of complex biological systems” - IsC10_BioPLX, CINECA ISCRA (Class C Projects)

February 2007 - February 2009: Member of the Italian PRIN (Programma di Ricerca Scientifica di Rilevante Interesse Nazionale) project: “Sistemi e calcoli per la descrizione e l’analisi di processi biologici: estensioni quantitative, studio dell’espressività e simulazione (Bisca)”. Coordinator: Prof. Pierpaolo Degano, University of Pisa

May 2006 - May 2007: Integrated Action Italy-Spain - Italian Ministry of Education, Universities and Research

November 2004 - November 2006: Member of the Italian PRIN (Programma di Ricerca Scientifica di Rilevante Interesse Nazionale) project: “Systems Biology: modellazione, linguaggi e analisi (SYBILLA)”. Coordinator: Prof. Corrado Priami, University of Trento

Public engagement projects

December 2019 - Today: Member of the project “Restiamo Umani” funded by the University of Bergamo. Coordinator: Prof. Cristiana Ottaviano

May 2018 - December 2018: Member of the project “Le radici culturali della violenza: per una comunità di adulti responsabili” funded by the University of Bergamo. Coordinator: Prof. Cristiana Ottaviano

Organising Committee

1. **General Chair** of the **16th International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics (CIBB 2019)**, September 4-6, 2019, Bergamo, Italy
2. **Chair** of the Organising Committee of the **2nd SYSBIO.IT School on Computational Systems Biology**, October 4-6, 2017, Milan, Italy
3. **Chair** of the Organising Committee of the special session: **Parallel and distributed high-performance computing solutions in Systems Biology**, hosted by the 26th Euromicro International Conference on Parallel, distributed and network-based Processing, March 21-23, 2018, Cambridge, UK
4. Member of the Organising Committee of the special session: **Modeling and simulation methods for Systems Biology and Systems Medicine**, hosted by CIBB 2017 - 14th International Conference on Computational Intelligence Methods for Bioinformatics and Biostatistics, September 7-9, 2017, Cagliari, Italy
5. **Chair** of the Organising Committee of the special session: **Parallel and Distributed High Performance Computing Solutions for Computational Intelligence Methods**, hosted by the IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB 2016), October 5-7, 2016, Chiang Mai, Thailand
6. **Chair** of the Organising Committee of the special session: **Modeling and simulation methods for Systems Biology and Systems Medicine**, hosted by CIBB 2016 - 13th International Conference on Computational Intelligence Methods for Bioinformatics and Biostatistics, September 1-3, 2016, Stirling, UK
7. Member of the Organising Committee of **AAIM 2016 - 11th International Conference on Algorithmic Aspects in Information and Management**, July 18-20, 2016, Bergamo, Italy
8. Member of the Organising Committee of the **1st SYSBIO.IT School on Computational Systems Biology**, June 8-10, 2016, Milan, Italy
9. Member of the Organising Committee of **BITS 2015 - Twelfth Annual Meeting of the Bioinformatics Italian Society**, June 3-5, 2015, Milan, Italy
10. Member of the Organising Committee of **DLT 2011 - Developments in Language Theory** - University of Milano-Bicocca

Program Committee

1. Member of the Program Committee of **ECTA 2019 - 11th International Conference on Evolutionary Computation Theory and Applications**, September 17-19, 2019, Vienna, Austria
2. **Chair** of the Program Committee of the special session: **Parallel and distributed high-performance computing solutions in Systems Biology**, hosted by the 26th Euromicro International Conference on Parallel, distributed and network-based Processing, March 21-23, 2018, Cambridge, UK
3. Member of the Program Committee of the special session: **Modeling and simulation methods for Systems Biology and Systems Medicine**, hosted by CIBB 2017 - 14th International Conference on Computational Intelligence Methods for Bioinformatics and Biostatistics, September 7-9, 2017, Cagliari, Italy
4. **Chair** of the Program Committee of the special session: **Parallel and Distributed High Performance Computing Solutions for Computational Intelligence Methods**, hosted by the IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB 2016), October 5-7, 2016, Chiang Mai, Thailand
5. **Chair** of the Program Committee of the special session: **Modeling and simulation methods for Systems Biology and Systems Medicine**, hosted by CIBB 2016 - 13th International Conference on Computational Intelligence Methods for Bioinformatics and Biostatistics, September 1-3, 2016, Stirling, UK
6. Member of the Program Committee of **ACM-SAC 2017 Conference Track on Bioinformatics**, Marrakech, Morocco, March 27-31, 2017

7. Member of the Program Committee of **ACM-SAC 2016 Conference Track on Computational Biology and Bioinformatics**, Pisa, Italy, April 3-8, 2016
8. Member of the Program Committee of **ICANNGA 2013 - 11th International Conference on Adaptive and Natural Computing Algorithms**, Lausanne, Switzerland

Editorial board

April 2021 - Today: Topic Editor of **Symmetry** journal by MDPI

December 2016 - January 2019: Member of the editorial board of **Neurocomputing** journal, Elsevier

Editors in chief: Prof. Zidong Wang and Prof. Steven Hoi

Guest Editor

- **Computational Intelligence Methods for Bioinformatics and Biostatistics.** 16th International Meeting, CIBB 2019, Bergamo, Italy, September 4-6, 2019 Revised Selected Papers, Editors: P. Cazzaniga, D. Besozzi, I. Merelli, L. Manzoni, **Lecture Notes in Bioinformatics, Springer**
- **Computational Intelligence Methods for Bioinformatics and Biostatistics.** Editors: P. Cazzaniga, M. Raposo, D. Besozzi, I. Merelli, A. Staiano, A. Ciaramella, R. Rizzo, L. Manzoni, **BMC Bioinformatics Supplement**

Referee activity

- Reviewer for different international conferences and scientific journals in the field of Artificial Intelligence, Systems Biology, Soft Computing and Natural Computing
- Reviewer for national and international research project proposals
- Member of the reviewer board for the Italian Ministry of Education, Universities and Research for ERC sectors LS2_14 (Biological systems analysis, modelling and simulation), PE6_12 (Scientific computing, simulation and modelling tools), LS2_13 (Systems biology)

Languages

- Italian: mother tongue
- English: proficient
- Spanish: elementary