Chiara Damiani

CURRICULUM VITAE

PERSONAL INFORMATION

SURNAME	Damiani
NAME	Chiara
E-MAIL	chiara.damiani@unimib.it
NATIONALITY	Italian
DATE AND PLACE OF BIRTH	Bergamo, 18-07-1982

CURRENT POSITION

From 1-11-2019	**Research assistant (tenure track)** in Computer Science	Department of Biotechnologies and Biosciences - University of Milan-Bicocca

BIOSKETCH

- 9 years of post-doc research experience in bioinformatics and computational systems biology
- PhD in Multiscale Modeling, Computational Simulations and Characterization in Material and Life Sciences
- Key responsibilities: regulatory gene network analysis, metabolic network inference, metabolomics and transcriptomics data analysis, clinical –*omics* data integration, multi-scale simulation of multicellular systems, such as heterogeneous tumor cell populations, single-cell RNA-seq data analysis, inference and simulation of molecular interaction mechanisms
- Main methodologies: Information Theory, Boolean networks, Flux Balance Analysis, stochastic and deterministic modeling, Machine Learning
- International experience: visiting scientist at Institute for Biocomplexity and Informatics, University of Calgary (Canada) and Vrije University Amsterdam (Netherlands)
- Speaker at 10 international conferences and several seminars, 6 national conference - of which 1 as invited speaker - and at 3 invited seminars
- Co-author of 42 publications indexed in Scopus and/or WoS, of which;
    - 16 as first author
    - 17 as corresponding author
    - 5 as last author
- H-index 11; Citations: 327 (source: Scopus - February 12th, 2021)
- More than 400 hours of teaching activity in Computer Science, Bioinformatics and Systems Biology, including a Lecturer contract, a PhD course, a lecture series abroad and invited lectures at international schools
- Supervision of students: 1 PhD, 5 Master's, 5 Bachelor's
- Scientific responsibility 1 post-doc
- Chair of 3 conference tracks, member of the program committee of 19 conferences and of the organizing committee of 9 conferences
- Participation to European and national funded projects (ITFOC, Sysbio, Mitica, NEDD)

EDUCATION

TITLE	COURSE OF STUDY	UNIVERSITY	YEAR	FINAL GRADE AND PROJECT
DOCTOR OF PHILOSOPHY	Doctoral School in Multiscale Modeling, Computational Simulations and Characterization in Material and Life Sciences	University of Modena and Reggio Emilia	2011	Thesis: Dynamics of interacting genetic networks Supervisors: Prof. Roberto Serra and Prof. Claudio Giberti
MASTER'S DEGREE	Specialization degree in Economics, Networks and Innovation Management (2 years)	University of Modena and Reggio Emilia	2007	Grade: *110/110 with honors* Thesis: Interacting Random Boolean Networks Supervisors: Prof. Marco Villani and Roberto Serra
BACHELOR'S DEGREE	Degree in Economics, Networks and Information (3 years)	University of Modena and Reggio Emilia	2004	Grade: 110/110 with honors Thesis: Integration between a Learning Management System and a Content Management System Supervisor: Tommaso Minerva

PREVIOUS POSITIONS

PERIOD	POSITION	INSTITUTION
From 1-01-2017 to 30-06-2019	Senior post-doc fellow (S.S.D. INF/01) within the candidate proposed project "Tackling cancer heterogeneity with multi-scale modeling", under the scientific direction of Prof. Giancarlo Mauri	Department of Informatics, Systems and Communication - University of Milan Bicocca
From 1-03-2017 to 30-04-2017	Contract-work for the project "Deep Learning for Life Sciences" under the scientific direction of Prof. Giancarlo Mauri	Department of Informatics, Systems and Communication - University of Milan Bicocca
From 11-2012 to 11-2016	Post-doc fellow (S.S.D. INF/01) within the research project "Modeling and simulation of biological systems", within the grant SysBionet, under the scientific direction of Prof. Giancarlo Mauri	Department of Informatics, Systems and Communication - University of Milan Bicocca
From 01-2011 to 11-2012	Junior Researcher within the projects "Computational Tools for Systems Biology" and "Molecular models for genetic regulation, transcription and translation"	The Microsoft Research - University of Trento Centre for Computational and Systems Biology
From 11-2007 to 01-2008	Research Fellow (S.S.D ING-INF-05) within the project "Interaction models among genetic networks of communicating cells" under the scientific supervision of Prof. Roberto Serra	Department of Social, Cognitive and Quantitative Sciences - University of Modena e Reggio Emilia
From 04-2008	Contract-work for organization and research	Department of Social, Cognitive and Quantitative

to 09-2008	activities within the MITICA project	Sciences - University of Modena e Reggio Emilia
From 06-2007 to 10-2007	Research project: simulation of the behavior of interacting Random Boolean Networks	Department of Social, Cognitive and Quantitative Sciences - University of Modena e Reggio Emilia
From 01-2004 to 06-2004	Internship: Development of the open-source LMS "Moodle"	University of Modena e Reggio Emilia – Faculty of Communication and Economics
From 12-2003 to 06-2004	Collaboration to the European Project "E3 – e-contexts, e-technologies, e-learning"	Reggio Emilia Municipality

PERIOD OF LEAVE

From 02-11-2018 to 13-04-2018 and from 16-05-2019 to 16-06-2019	Maternity leave (6 months)

RESEARCH VISITING

From 23-08-2017 to 04-09-2017	Visiting scientist at Prof Hans Westerhoff's lab	Department of Molecular Cell Physiology, Vrije University Amsterdam
From 08-2009 to 02-2010	Visiting PhD research student under the supervision of Prof. Stuart Kauffman	Institute for Biocomplexity and Informatics, University of Calgary

HONOURS AND AWARDS

Second Prize 'University of Milano Bicocca Young Talents' patronized by Lincei National Academy - macro-area: informatics and mathematical sciences; information and industrial engineering - year 2016

Best Oral Presentation Award for the presentation 'Linking alterations in metabolic fluxes with shifts in metabolite levels by means of kinetic modeling' at the conference WIVACE 2016, Workshop on Artificial Life and Evolutionary Computation, 4-6 October 2016, Salerno

PhD scholarship from 01-2008 to 01-2011 by Italian Ministry of University and Research

Master's degree and bachelor's degree with honors

PROJECTS

From 03-2017 to date	Formal participant in the European project "ITFOC, Information Technology: The Future of Cancer Treatment" the FLAG-ERA Joint Transnational Call (JTC) 2016 proposal and **task leader** of task "T6.3 Development of constraint-based models of tissue-specific or patient-specific metabolic networks" within WP6 (modeling and prediction algorithms)
From 01-11-2012 to date	**WP leader** of WP 'Computational modeling of metabolism' within SYSBIO/ISBE.IT Centre of Systems Biology - Italian candidate node for ISBE - an ESFRI Research Infrastructure project:
From 01-11-2012 to 31-12-2016	Research fellow within the project SysBioNet, a MIUR initiative for the Italian Roadmap of European Strategy Forum on Research Infrastructures (ESFRI)
From 2014 to 2015	Participant in RetroNet through the ASTIL project [12-4-5148000-40], U.A 053, Regione Lombardia 2010
From 2014 to 2015	Participant in NEDD - Network Enabled Drug Design [ID14546A Rif SAL-7], Fondo Accordi Istituzionali 2009

From 2010 to 2011	Participant in DICE - Designing Informative Combinatorial Experiments for Living Technology (Funded by Fondazione di Venezia)
From 2007 to 2010	Participant in MITICA (MIUR-FISR nr. 2982/Ric)

SCIENTIFIC RESPONSIBILITY

From 01-2021 to date	Scientific responsible of post-doc research fellow Bruno Giovanni Galuzzi on the topic "Data Integration and Artificial intelligence in Life Sciences"

PUBLICATIONS

*corresponding author
#equal contributor of first author
Q quartile

INTERNATIONAL JOURNALS

M. S. Nobile; V Coelho; D. Pescini; C Damiani*. *Accelerated global sensitivity analysis of genome-wide constraint-based metabolic models.* **Bmc Bioinformatics** (in press)
- ❖ 5 year impact factor: **3.213**
- ❖ **Q1** (2019) Computer Science Applications, Biochemistry (SJR)

C. Damiani, D. Gaglio, E., Sacco, L. Alberghina & M. Vanoni. *Systems metabolomics: from metabolomic snapshots to design principles.* **Current Opinion in Biotechnology**, 63, 190-199, **2020**. DOI: https://doi.org/10.1016/j.copbio.2020.02.013
- ❖ 5-year Impact Factor: **8.940**
- ❖ **Q1** (2019) Bioengineering, Biotechnology, Biomedical engineering (SJR)

C. Damiani*, L. Rovida, D. Maspero, I. Sala, L. Rosato, M. Di Filippo & G. Mauri G. *MaREA4Galaxy: Metabolic reaction enrichment analysis and visualization of RNA-seq data within Galaxy.* **Computational and Structural Biotechnology Journal**, 18, 993, **2020**. DOI: 10.1016/j.csbj.2020.04.008
- ❖ 2019 Impact Factor: **6.018**
- ❖ **Q1** (2019) Computer Science Applications, Biotechnology, Biophysics, Genetics (SJR)

D. Maspero, M. Di Filippo, C. Damiani, G. Caravagna, R. Colombo, D. Ramazzotti, M. Antoniotti, A. Graudenzi, M. Vanoni and D. Pescini. *The influence of nutrients diffusion on a metabolism-driven model of a multi-cellular system*. **Fundamenta Informaticae,** 171. 1-4. 279-295, **2020.** DOI: 10.3233/FI-2020-1883
- ❖ 5-year Impact Factor: **0.667**
- ❖ **Q3** (2017) Theoretical Computer Science (SJR)

A. Graudenzi, Davide Maspero, Chiara Damiani*, *FBCA, A Multiscale Modeling Framework Combining Cellular Automata and Flux Balance Analysis.* **Journal of Cellular Automata**, *Vol. 0, pp. 1–21,* **2019**.
- ❖ 5-year Impact Factor: **0.789**
- ❖ **Q3** (2017) Computer Science (SJR)

C. Damiani*, D. Maspero, M. Di Filippo, R. Colombo, D. Pescini, A. Graudenzi, H. V. Westerhoff, L. Alberghina, M. Vanoni and G. Mauri. *Integration of single-cell RNA-seq data into population models to characterize cancer metabolism*, **PLoS Computational Biology**, 15(2), e1006733, **2019**. DOI: 10.1371/journal.pcbi.1006733
- ❖ 5-year Impact Factor: **4.834**
- ❖ **Q1** (2017) Computational Theory and Mathematics (SJR)
- ❖ **Q1** (2017) Mathematical and Computational Biology (JCR)

A. Graudenzi, D. Maspero, M. Di Filippo, M. Gnugnoli, C. Isella, G. Mauri, E. Medico, M Antoniotti and C. Damiani*. *Integration of transcriptomic data and metabolic networks in cancer samples reveals highly significant prognostic power*. **Journal of Biomedical Informatics**, 87: 37-49, **2018**. DOI: 10.1016/j.jbi.2018.09.010
- ❖ 5-year Impact Factor: **3.12**
- ❖ **Q1** (2017) Computer Science Applications (SJR), Health Informatics (SJR)

R. Colombo, C. Damiani, D. Gilbert, M. Heiner, G. Mauri and D. Pescini. *Emerging ensembles of kinetic parameters to characterize observed metabolic phenotypes*. **BMC Bioinformatics**, 19(7):251, **2018**. DOI: 10.1186/s12859-018-2181-7

- ❖ 5-year Impact Factor 2017: **3.114**
- ❖ **Q1** (2017) Computer Science Applications (SJR)
- ❖ **Q1** (2017) Mathematical and Computational Biology (JCR)

C. Damiani, R. Colombo, D. Gaglio, F. Mastroianni, D. Pescini, H.V. Westerhoff, G. Mauri, M. Vanoni and L. Alberghina. *A metabolic core model elucidates how enhanced utilization of glucose and glutamine, with enhanced glutamine-dependent lactate production, promotes cancer cell growth: The WarburQ effect*. **PLoS Computational Biology**, 13(9): e1005758, **2017**. DOI: 10.1371/journal.pcbi.1005758
- ❖ 2017 Impact Factor: **3.955**
- ❖ **Q1** Computational Theory and Mathematics (SJR)
- ❖ **Q1** Computational Theory and Mathematics (SJR)

C. Damiani*, M. Di Filippo, D. Pescini, D. Maspero, R. Colombo and G. Mauri. *popFBA: tackling intratumour heterogeneity with Flux Balance Analysis*. **Bioinformatics,** 33: i311–i318, **2017**. doi: 10.1093/bioinformatics/btx251
- ❖ 2017 Impact Factor: **5.481**
- ❖ **Q1** Computer Science Applications (SJR)

D. Gaglio, S. Valtorta, M. Ripamonti, M. Bonanomi, C. Damiani, S. Todde, A. S. Negri, F. Sanvito, F. Mastroianni, A. Di Campli, G. Turacchio, G. Di Grigoli, S. Belloli, A. Luini, M. C. Gilardi, L. Alberghina and R. M. Moresco. *Divergent in vitro/in vivo responses to drug treatments of highly aggressive NIH-Ras cancer cells: A PET imaging and metabolomics-mass-spectrometry study*. **Oncotarget**, 7(32): 52017–52031, **2016**. DOI: 10.18632/oncotarget.10470

- ❖ 2016 Impact Factor: **5.168**
- ❖ **Q1** Oncology (SJR)

M. Villani, D. Campioli, C. Damiani, A. Roli, A. Filisetti and R. Serra. *Dynamical regimes in non-ergodic random Boolean networks.*
Natural Computing, 16(2): 353-363, **2017.** DOI: 10.1007/s11047-016-9552-7
- ❖ 2016 Impact Factor: **0.778**
- ❖ **Q3** Computer Science Applications (SJR)
- ❖ **Q4** Computer Science, Artificial Intelligence (JCR)
- ❖ **Q4** Computer science, Theory & Methods (JCR)

M. Di Filippo, R. Colombo, C. Damiani, D. Pescini, D. Gaglio, M. Vanoni, L. Alberghina and G. Mauri. *Zooming in cancer metabolic rewiring with tissue specific constraint-based models*. **Computational Biology and Chemistry,** 62: 60-69, **2016**. DOI: 10.1016/j.compbiolchem.2016.03.002
- ❖ 2016 Impact Factor: 1.331
- ❖ **Q2** Computational Mathematics (JCR)
- ❖ **Q3** Computer science, Interdisciplinary Applications (JCR)

A. Paroni, A. Graudenzi, G. Caravagna, C. Damiani, G. Mauri and M. Antoniotti. *CABeRNET: a Cytoscape app for Augmented Boolean models of gene Regulatory NETworks*. **BMC Bioinformatics,** 17(1): 64, **2016**. DOI: 10.1186/s12859-016-0914-z
- ❖ 2016 Impact Factor 2017: **2.448**
- ❖ **Q1** Computer Science Applications (SJR)

M. Villani, A. Filisetti, A. Graudenzi, C. Damiani, T. Carletti and R. Serra. *Growth and Division in a Dynamic Protocell Model*. **Life**, 4(4): 837-864, **2014**. DOI: 10.3390/life4040x\837

P. Cazzaniga, C. Damiani#, D. Besozzi, R. Colombo, M.S. Nobile, D. Gaglio, D. Pescini, S. Molinari, G. Mauri, L. Alberghina and M. Vanoni. *Computational Strategies for a System-Level Understanding of Metabolism*. **Metabolites**, 4(4): 1034-1087, **2014**. DOI: 10.3390/metabo4041034
- ❖ Q2 Endocrinology, Diabetes and Metabolism (SJR)

R. Serra, A. Filisetti, M, Villani, A. Graudenzi, C. Damiani and T. Panini. *A stochastic model of catalytic reaction networks in protocells*. **Natural Computing**, *13*(3): 367-377, **2014**. DOI: 10.1007/s11047-014-9445-6
- ❖ 2014 Impact Factor: **0.757**
- ❖ **Q2** Computer Science Applications (SJR)
- ❖ **Q3** Computer science, Theory & Methods (JCR)

C. Damiani*, D. Pescini, R. Colombo, S. Molinari, L. Alberghina, M. Vanoni, and G. Mauri. *An ensemble evolutionary constraint-based approach to understand the emergence of metabolic phenotypes*. **Natural Computing,** *13*(3): 321-331, **2014**. DOI: 10.1007/s11047-014-9439-4
- ❖ 2014 Impact Factor: **0.757**
- ❖ **Q2** Computer Science Applications (SJR)
- ❖ **Q3** Computer science, Theory & Methods (JCR)

C. Damiani*, A. Filisetti, A. Graudenzi, and P. Lecca. *Parameter sensitivity analysis of stochastic models: Application to catalytic reaction networks.* **Computational Biology and Chemistry**, 42:5–17, **2013**. ISSN 1476-9271. DOI: 10.1016/j.compbiolchem.2012.10.007

- ❖ 2013 Impact Factor: **1.595**
- ❖ **Q2** Computational Mathematics (SJR)
- ❖ **Q2** Computer science, Interdisciplinary Applications (JCR)

C. Damiani*, R. Serra, M. Villani, S.A. Kauffman, and A. Colacci. *Cell-cell interaction and diversity of emergent behaviours*. **IET Systems Biology**, 5(2):137–144, **2011**. ISSN 1751-8849. DOI: 10.1049/iet-syb.2010.0039.
- ❖ 2011 Impact Factor: **1.349**
- ❖ **Q2** Modeling and Simulation (SJR)
- ❖ **Q3** Mathematical and Computational Biology (JCR)

Graudenzi, R. Serra, M. Villani, C. Damiani e A. Colacci, and S. A. Kauffman. *Dynamical properties of a Boolean model of gene regulatory network with memory*. **Journal of Computational Biology**, 18(10):1291–303, **2011**. DOI: 10.1089/cmb.2010.0069
2011 Impact Factor **1.564**
- ❖ **Q1** Computational Theory and Mathematics (SJR)
- ❖ **Q1** Computational Mathematics (SJR)
- ❖ **Q1** Modeling and simulation (SJR)
- ❖ **Q2** Computer Science, Interdisciplinary Applications (JCR)

ITALIAN JOURNALS

R. Serra, M. Villani, C. Damiani, A. Graudenzi, and A. Colacci. *Comunicazione cellulare, livelli e strutture ordinate*. **Sistemi Intelligenti**, 2:209-220, **2008**. ISSN 1120-9550. DOI: 10.1422/27403.

CONFERENCE PROCEEDINGS: LECTURE NOTES IN COMPUTER SCIENCE

D. Maspero, M. Di Filippo, F. Angaroni, D. Pescini, G. Mauri, G., M. Vanoni, A. Graudenzi, C. Damiani* (2019, September). *Integration of Single-Cell RNA-Sequencing Data into Flux Balance Cellular Automata*. In International Meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics **Lecture Notes in Computer Science** 207-215. Springer, Cham. DOI

C. Damiani, D. Pescini & M. S. Nobile. *Global Sensitivity Analysis of Constraint-Based Metabolic Models*. In International Meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics, **Lecture Notes in Computer Science** 11925:179-186, 2018. Springer, Cham. DOI: https://doi.org/10.1007/978-3-030-34585-3_16

A. Graudenzi, D. Maspero e C. Damiani*. *Modeling Spatio-Temporal Dynamics of Metabolic Networks with Cellular Automata and Constraint-Based Methods.* In: G. Mauri, S. El Yacoubi, A. Dennunzio, K. Nishinari, L. Manzoni (eds) Cellular Automata. ACRI 2018. **Lecture Notes in Computer Science,** 11115:16-29, **2018**. Springer, Cham. DOI:10.1007/978-3-319-99813-8_2

R. Colombo, C. Damiani, G. Mauri, Dario Pescini. *Constraining mechanism based simulations to identify ensembles of parametrizations to characterize metabolic features.* In: Bracciali A., Caravagna G., Gilbert D., Tagliaferri R. (eds) Computational Intelligence Methods for Bioinformatics and Biostatistics. CIBB 2016. **Lecture Notes in Computer Science** (Lecture Notes in Bioinformatics)**,** 10477:107-117, Springer, Cham, **2017**. DOI: 10.1007/978-3-319-67834-4_9

F. Cumbo, M. Nobile, C. Damiani, R. Colombo, G. Mauri e P. Cazzaniga. *COSYS: A Computational Infrastructure for Systems Biology*. In: Bracciali A., Caravagna G., Gilbert D., Tagliaferri R. (eds) Computational Intelligence Methods for Bioinformatics and Biostatistics. CIBB 2016. **Lecture Notes in Computer Science** (Lecture Notes in Bioinformatics)**,** 10477:82-92, Springer, Cham, **2017**. DOI: 978-3-319-67834-4_7

C. Damiani*, S. A. Kauffman, R. Serra, M. Villani, e A. Colacci. *Information transfer among coupled random Boolean networks*. In S. Bandini, H.Umeo, S.Manzoni, e G.Vizzari, editors, Cellular Automata, 9th International Conference on Cellular Automata for Research e Industry, (ACRI 2010, Ascoli Piceno, 21-24 September). **Lecture Notes in Computer Science**, 6350:1–11. Springer-Verlag Berlin Heidelberg, **2010**. DOI: 10.1007/978-3-642-15979-4_1

R. Serra, M. Villani, C. Damiani, A. Graudenzi, e A. Colacci. *The diffusion of perturbations in a model of coupled random Boolean networks*. In H. Umeo, S. Morishiga, K. Nishinari, T. Komatsuzaki, e S. Bandini, editors, Cellular Automata (proceedings of 8th International Conference on Cellular Auotomata ACRI 2008, Yokohama, September 2008). **Lecture Notes in Computer Science,** volume 5191/2008: 315– 322, Springer-Verlag Berlin Heidelberg, **2008**. DOI: 10.1007/978-3-540-79992-4_40xw

CONFERENCE PROCEEDINGS: COMMUNICATIONS IN COMPUTER AND INFORMATION SCIENCE

D. Maspero, A. Graudenzi, S. Singh, D. Pescini, G. Mauri, M. Antoniotti e <u>C. Damiani</u>*#. *Synchronization Effects in a Metabolism-Driven Model of Multi-cellular System* in Artificial Life and Evolutionary Computation **Communications in Computer and Information Science,** 900: 115-126, Springer, Cham, **2019.** DOI**:** https://doi.org/10.1007/978-3-030-21733-4_9

<u>C. Damiani</u>*, R. Colombo, M. Di Filippo, D. Pescini, G. Mauri. Linking alterations in metabolic fluxes with shifts in metabolite levels by means of kinetic modeling. In: Rossi F., Piotto S., Concilio S. (eds) Advances in Artificial Life, Evolutionary Computation, and Systems Chemistry. WIVACE 2016. **Communications in Computer and Information Science**, 708: 138-148, Springer, Cham, **2017**. DOI: 10.1007/978-3-319-57711-1

M. Di Filippo, <u>C. Damiani</u>*, R. Colombo, D. Pescini, D., and G. Mauri (2017). *Constraint-based modeling and simulation of cell populations*. In: Rossi F., Piotto S., Concilio S. (eds) Advances in Artificial Life, Evolutionary Computation, and Systems Chemistry. WIVACE 2016. **Communications in Computer and Information Science**, 708:126-137. Springer, Cham, **2017**. DOI: 978-3-319-57711-1_11

A. Graudenzi, <u>C. Damiani</u>*, A. Paroni, A. Filisetti, M. Villani, R. Serra e M. Antoniotti. *Investigating the role of network topology and dynamical regimes on the dynamics of a cell differentiation model*. Proceedings of Wivace 2014, Italian Workshop on Artificial Life and Evolutionary Computation, 14-15 May 2014, Vietri sul Mare, Salerno, Italy. In Advances in Artificial Life and Evolutionary Computation, **Communications in Computer and Information Science** 445:151-168, Springer International Publishing, **2014**. DOI: 10.1007/978-3-319-12745-3_13

A. Filisetti, M. Villani, C. Damiani, A. Graudenzi, A. Roli, W. Hordijk, e R: Serra. *On RAF sets and autocatalytic cycles in random reaction networks.* Proceedings of Wivace 2014, Italian Workshop on Artificial Life and Evolutionary Computation, 14-15 maggio 2014, Vietri sul Mare, Salerno, Italy. In Advances in Artificial Life and Evolutionary Computation, **Communications in Computer an Information Science** 445:113-126, Springer International Publishing, **2014,** DOI: 10.1007/978-3-319-12745-3_10

CONFERENCE PROCEEDINGS: IEEE (INDEXED IN SCOPUS AND WoS)

<u>C. Damiani</u>* e P. Lecca. *Model identification using correlation-based inference and transfer entropy estimation*. Proceedings of the UKSIM 5th European Symposium on Computer Modeling and Simulation, EMS 2011, Madrid, 16-18 November, 2011, 0:129–134. **IEEE 2011**. ISBN 978-1-4673-0060-5. DOI: 10.1109/EMS.2011.58

CONFERENCE PROCEEDINGS: EPCTS (INDEXED IN SCOPUS)

C. <u>Damiani</u>, R. Colombo, S. Molinari, D. Pescini, D. Gaglio, M. Vanoni, L. Alberghina e G. Mauri. *An ensemble approach to the study of the emergence of metabolic and proliferative disorders via Flux Balance Analysis*. In: Alex Graudenzi, Giulio Caravagna, Giancarlo Mauri, e Marco Antoniotti, editors, EPTCS 130 Proceedings of Wivace 2013 - Italian Workshop on Artificial Life and Evolutionary Computation. Milan, Italy, 1-2 luglio 2013. **Electronic Proceedings in Theoretical Computer Science EPCTS, 2013**. DOI: 10.4204/EPTCS.130.

<u>C. Damiani</u>, A. Filisetti, A. Graudenzi, M. Villani, e R. Serra. *Recent developments in research on catalytic reaction networks*. In Alex Graudenzi, Giulio Caravagna, Giancarlo Mauri, e Marco Antoniotti, editors, EPTCS 130 Proceedings of Wivace 2013 - Italian Workshop on Artificial Life and Evolutionary Computation. Milan, Italy, 1-2 luglio 2013. **Electronic Proceedings in Theoretical Computer Science EPCTS, 2013**. DOI: 10.4204/EPTCS.130.

R. Serra, A. Filisetti, A. Graudenzi, C. Damiani, e M. Villani. A model of protocell based on the introduction of a semi-permeable membrane in a stochastic model of catalytic reaction networks. In Alex Graudenzi, Giulio Caravagna, Giancarlo Mauri, e Marco Antoniotti, editors, Proceedings of Wivace 2013 - Italian Workshop on Artificial Life and Evolutionary Computation. Milano, 1-2 luglio, 2013, 2013. **Electronic Proceedings in Theoretical Computer Science EPCTS, 2013** DOI: 10.4204/EPTCS.130.

CONFERENCE PROCEEDINGS: WORLD SCIENTIFIC (INDEXED IN WoS)

<u>C. Damiani</u>, M. Villani, Ch. Darabos, e M. Tomassini. *Dynamics of interconnected Boolean networks with scale-free topology*. In M. Villani R. Serra e I. Poli, editors, Artificial Life and evolutionary computation, proceeding of WIVACE 2008, Venezia, 8-10 September 2008, pg. 271–283. **World Scientific, 2008**. ISBN 978-981-4287-44- 9.

R. Serra, M. Villani, <u>C. Damiani</u>, A. Graudenzi, P. Ingrami, e A. Colacci. *Investigating cell criticality*. In G. Minati e A. Pessa, editors, Towards a general theory of emergence, pages 271–283. **World Scientific, 2007**.

<u>C. Damiani</u>, A. Graudenzi, e M. Villani. *How critical random Boolean networks may be affected by the interaction with others*. In M. Villani R. Serra e I. Poli, editors, Artificial Life and evolutionary computation, proceeding of WIVACE 2008, pg.

271–283**. World Scientific, 2008**. ISBN 978-981-4287-44- 9.

BOOK CHAPTERS (INDEXED IN SCOPUS AND/OR WOS)

M. Di Filippo, <u>C. Damiani</u>, M. Vanoni, D. Maspero, G., Mauri, L. Alberghina and D. Pescini, *Single-cell digital twins for cancer preclinical investigation*. In **Metabolic Flux Analysis in Eukaryotic Cells**, 331-343, **2020**. DOI: 10.1007/978-1-0716-0159-4_15

G. De Sanctis, R. Colombo, <u>C. Damiani</u>, E. Sacco, M. Vanoni. *Omics and clinical data integration.* In: Integration of Omics Approaches and Systems Biology for Clinical Applications. Antonia Vlahou (Editor), Fulvio Magni (Editor), Harald Mischak (Editor), Jerome Zoidakis (Editor). 248-273, **Wiley, 2018.**
ISBN: 978-1-119-18395-2. DOI:10.1002/9781119183952

<u>C. Damiani</u>*. *Modelling the influence of cell signaling on the dynamics of gene regulatory networks*. In Paola Lecca, editor, Biomechanics of Cells and Tissues, volume 9 of **Lecture Notes in Computational Vision and Biomechanics**, 9:103–130, Springer Netherlands, **2013**. ISBN 978-94-007-5889- 6. DOI: 10.1007/978-94-007-5890-2_5

OTHER CONFERENCE PROCEEDINGS

A. Filisetti, A. Graudenzi, <u>C. Damiani</u>, M. Villani, e R. Serra. *The role of backward reactions in a stochastic model of catalytic reaction network.* In Liò Pietro, Miglino Orazio, Nicosia Giuseppe, Nolfi Stefano, e Pavone Mario (editors), Advances in Artificial Life ECAL 2013 2-6 settembre 2013, Taormina, Italy Proceedings of the twelfth European Conference on the Synthesis e Simulation of Living Systems, page number 793. **MIT press, 2013**. DOI: 10.7551/978-0-262-31709-2-ch114. **RANK B in Computer Science (CORE2018)**

A. Graudenzi, R. Serra, M. Villani, <u>C. Damiani</u>, A. Colacci, e S. A. Kauffman. *Timing of molecular processes in a synchronous Boolean model of genetic regulatory network*. In **Proceedings** of the European Conference on Complex Systems, ECCS 09, Warwick 21-25 settembre, **2009**.

<u>C. Damiani</u>, A. Graudenzi, R. Serra, A. Colacci M. Villani, e S. A. Kauffman. *On the fate of perturbations in critical random Boolean networks.* In **Proceedings** of the European Conference on Complex Systems, ECCS 09, Warwick 21-25 September, **2009**.

R. Serra, M. Villani, <u>C. Damiani</u>, A. Graudenzi, A. Colacci, e S. A. Kauffman. *Interacting random Boolean networks.* In J. Jost e D. Helbing, editors, **Proceedings** of ECCS07: European Conference on Complex Systems, paper 35, **2007**.

PHD THESIS

<u>C. Damiani.</u> *Dynamics of Interacting Genetic Networks*. PhD thesis within the PhD school Multiscale Modelling, Computational Simulations and Characterization in Material and Life Sciences, Modena and Reggio Emilia University. Supervisor: Claudio Giberti. Co-supervisor: Roberto Serra. **2011**.

ABSTRACTS IN CONFERENCE PROCEEDINGS

D. Maspero, M. Di Filippo, R. Colombo, D. Pescini, A. Graudenzi, H. V. Westerhoff, L. Alberghina, M. Vanoni, G. Mauri and <u>C. Damiani</u>*. *Constraint-based modeling of human single cells to investigate metabolic heterogeneity in cancer subpopulations*. ISMB/ECCB **2019**, 27th International conference on Intelligent Systems for Molecular Biology (ISMB) and 18th European Conference on Computational Biology.

<u>C. Damiani</u>, R. Colombo, D. Paone, G. Mauri and D. Pescini *Relevant fluxes in metabolic steady-states* WIVACE 2017 book of abstracts, **2017.**

<u>C. Damiani</u>*, R. Colombo, M. Di Filippo, D. Pescini and G. Mauri, *Linking alterations in metabolic fluxes with shifts in metabolite levels by means of kinetic modeling*, WIVACE/BIONAM 2016 book of abstracts, **2016**.

M. Di Filippo, <u>Chiara Damiani</u>, Riccardo Colombo, Dario Pescini and G. Mauri, *Constraint-based Modeling and Simulation of Cell Populations*, WIVACE/BIONAM 2016 book of abstracts, **2016**.

<u>C. Damiani</u>, R. Colombo, M. Di Filippo, D. Gaglio, F. Mastroianni, D. Pescini, H. V. Westerhoff, G. Mauri, M. Vanoni e L. Alberghina *Unraveling the design principles of cancer metabolism with constraint-based modeling.* Proceedings of FISV 2016 XIV Congress of the Italian Federation of Life Sciences, Roma, 20-23 September, **2016**.

R. Colombo, <u>C. Damiani</u>, M. Di Filippo, D. Pescini, D. Gaglio, L. Alberghina, M. Vanoni e G. Mauri. *Constraint-based approaches to investigate heterogeneity of metabolic phenotypes.* Proceedings of BITS 2015, Twelfth Annual Meeting of the Bioinformatics Italian Society- University of Milan "Bicocca", 3-5 June, **2015.**

M. Fedeli, T. A. Renzi, D. Morpurgo, T-P. Nguyen, <u>C. Damiani</u>, G. Rossetti, M. Pagani, S. Abrignani, P. Dellabona, e G. Casorati. *mirna control of the gene expression program controlling inkt cell development* (abstract). In Proceedings del 6th International Symposium on CD1 and NKT Cells, Gleacher Center, Chicago, IL USA, 23 -27 September **2011**.

POSTERS IN CONFERENCE PROCEEDINGS

M. Di Filippo, R. Colombo, <u>C. Damiani</u>, D. Pescini, D. Gaglio, M. Vanoni, L. Alberghina, G. Mauri *Zooming-in on cancer metabolic rewiring with tissue specific constraint-based models,* 17th International Conference on Systems Biology (ICSB 2016), Barcelona, 16-20 September **2016**.

<u>C. Damiani</u>, R. Colombo, D. Pescini, M. Di Filippo, Marco Vanoni, G. Mauri, L. Alberghina, *A computational strategy to investigate alternative metabolic responses to the same stimulus*, 58th National Meeting of the Italian Society of Biochemistry and Molecular Biology, Urbino, 14-16 September **2015.**

R. Colombo, <u>C. Damiani</u>, D. Pescini, M. Di Filippo, L. Alberghina, M. Vanoni, G. Mauri, *Constraint-based approaches to investigate heterogeneity of metabolic phenotypes*, BITS 2015, Twelfth Annual Meeting of the Bioinformatics Italian Society, Milano, 3-5 June, **2015**.

R. Serra, A. Filisetti, M. Villani, A. Graudenzi e <u>C. Damiani</u>, *Stochastic dynamics of chemical reaction networks in a stylized protocell model,* ECCS'14, European Conference on Complex systems, Lucca, 22-26 September **2014**.

<u>C. Damiani</u>, D. Pescini, R. Colombo, S. Molinari, M. Vanoni, L. Alberghina, G. Mauri, *Ensemble evolutionary flux balance analysis for metabolic network modeling,* BITS2014, Eleventh Annual Meeting of the Bioinformatics Italian Society, Roma, February 26-28, **2014**.

R. Colombo, <u>C. Damiani</u>, D. Gaglio, D. Pescini, G. Mauri, E. Sacco, S. Molinari, L. Alberghina, e M. Vanoni. *Flux balance analysis approaches towards the definition of cancer-specific metabolic rewiring*, ICSB2013 - 14th International Conference on Systems Biology, Copenhagen, 29 August – 4 September **2013**.

<u>C. Damiani</u> *An ensemble approach to the study of the emergence of the Warburg effect via flux balance analysis*, Technology and Human Health: Advances in Systems Medicine, Palmstedtsalen, Chalmers, 29 August **2013**.

M. Fedeli, V. Milli, T. A. Renzi, D. Morpurgo, T-P. Nguyen, <u>C. Damiani</u>, G. Rossetti, M. Pagani, S. Abrignani, P. Dellabona, e G. Casorati. *miRNA regulation of INKT cell development*, Milan meets immunology 2, IFOM-IEO campus, Milano 23 April, **2012**.

M. Fedeli, T. A. Renzi, D. Morpurgo, T-P. Nguyen, <u>C. Damiani</u>, G. Rossetti, M. Pagani, S. Abrignani, P. Dellabona, G. Casorati. *miRNA regulation of the gene expression program controlling INKT cell development*, Milan meets immunology 1, San Raffaele Scientific Institute, Milano, 20 September **2011**.

SUPERVISION OF STUDENTS

ACADEMIC YEAR	CLASS/COURSE OF STUDY	THESIS
2020/2021	Master's degree in Industrial Biotechnologies, University of Milano-Bicocca	Ilaria Vergani, Quantitative Analysis and omics data integration for the description of *Zygosaccharomyces bailii* yeast metabolism
2019/2020	Master's degree in Industrial Biotechnologies, University of Milano-Bicocca	Giovanni Schiesaro, Integration of Transcriptomics and Metabolomics Data to Investigate Metabolic Heterogeneity in Breast Cancer Cells
2018/2019	Bachelor's degree in Computer Science, University of Milano-Bicocca	Lorenzo Rovida, Implementazione MaREA e tool di clustering su Galaxy
2015/2018	PhD in Biology and Biotechnologies (curriculum	Marzia Di Filippo, *New constraint-based approaches to tackle the multiple sides of cell metabolic plasticity and heterogeneity*

	Systems Biology), University of iMilano-Bicocca	
2017/2018	Bachelor's degree in Computer Science, University of Milano-Bicocca	Vasco Coelho, *Accelerated genome-wide sensitivity analysis of constraint-based metabolic models*
2016/2017	Master's degree in Industrial Biotechnologies, University of Milano-Bicocca	Davide Maspero, *Investigating Cancer Heterogeneity and Progression with multi-scale Modeling*
2017/2018	Bachelor's degree in Computer Science, University of Milano-Bicocca	Vasco Coelho, *Accelerated genome-wide sensitivity analysis of constraint-based metabolic models*
2017/2018	Bachelor's degree in Computer Science, University of Milano-Bicocca	Irene Sala, *Front-end integration of the MaREA Pipeline in Galaxy*
2017/2018	Bachelor's degree in Computer Science, University of Milano-Bicocca	Luca Rosato, *Back-end integration of the MaREA Pipeline in Galaxy*
2013/2014	Master's degree in Industrial Biotechnologies	Roberto Mancuso, *Analysis of the relationship between "noise" and cellular differentiation, by means of computational biology techniques*
2012/2013	Master's degree in Industrial Biotechnologies	Sara Molinari, *An ensemble approach for computational Studies of Metabolic Rewiring in Cancer Cells*

TEACHING EXPERIENCE

ACADEMIC YEAR	CLASS/ COURSE OF STUDY	POSITION	INSTITUTION	
2019/2021 – 2020/2021	Databases - Bachelor's degree in Computer Science	Teacher Assistant	Department of Informatics Systems and Communication - University of Milan Bicocca	
2019/2020	Informatics for Earth Sciences (SSD: INF/01) - Bachelor's degree in Earth and environmental Sciences	Teacher Assistant	Department of Earth and Environmental Sciences - University of Milan Bicocca	
2018/2019	"Bayesian Learning and Bayesian classifiers" – module of the	Responsible for a series of lectures from 6th to 9th May 2019	**NOVA Information Management School, Universidad NOVA de Lisboa (Portugal)**	

	course of Machine Learning of the master's degree in Data Science and Advanced Analytics			
2018/2019	Computer Science – Master's degree in Marketing, Business communication and Global markets	Tutoring (paid for 57 hrs)	School of economics and statistics – University of Milano-Bicocca	
2017/2018 (Cycle XXXI)	A Swiss army knife for Bioinformatics (S.S.D INF/01) – PhD in Biology and Biotechnologies	Teacher of the PhD course (8 ore – 1 CFU)	University of Milano-Bicocca	
2017/2018	Computer Science - Bachelor's degree in economics and business	Tutoring (paid for 60 hrs)	University of Milano-Bicocca	
2017/2018	Computational Systems Biology – Master's degree in Industrial Biotechnologies	Invited lecture (3h)	University of Milano-Bicocca	
2016/2017	2st SYSBIO.IT School on Systems Biology and Bioinformatics	Member of the scientific committee and chair of a session	University of Milano-Bicocca	
2016/2017	Informatics for Earth Sciences (SSD: INF/01) - Bachelor's degree in Earth and environmental Sciences	Temporary Lecturer (paid for 28 hours, 6 ECTS) – fully in charge for the course	Department of Earth and Environmental Sciences - University of Milan Bicocca	
2016/2017	Computer Science – Bachelor's degree in economics and business	Tutoring (paid for 17 hours)	School of Economics and Statistics – University of Milano-Bicocca	
2016/2017	Computer Science – Master's degree in Marketing, Business communication and Global markets	Tutoring (paid for 16 hours)	School of Economics and Statistics – University of Milano-Bicocca	
2016/2017	Programming – Bachelor's degree in economics and	Tutoring (paid for 14 hours)	School of Economics and Statistics – University of Milano-Bicocca	

	enterprise administration			
2016/2017	Computer Science -Bachelor's degree in economics and business	Tutoring (paid for 10 hours)	School of Economics and Statistics – University of Milano-Bicocca	
2016/2017	Bioinformatics technologies (SSD: INF/01) – Master's degree in Industrial Biotechnologies	Teacher assistant (pair for 8 hours)	University of Milano-Bicocca	
2016/2017	2nd SyBSyM Como School – Systems Biology and Systems Medicine: Towards a Precision Medicine. September 26-30, 2016	Invited lecturer (2 hours)	Lake Como School of Advanced Studies	
2016/2017	1st SYSBIO.IT School on Computational Systems Biology An introduction to dynamic modeling, simulation and analysis of biological systems	Member of the scientific committee and responsible for one lecture and tutor for one hands-on session	University of Milan Bicocca	
2015/2016	Data base and information systems programming – Bachelor's degree in economics and enterprise administration	Tutoring (paid for 14 hrs)	University of Milano-Bicocca	
2015/2016	General informatics – Bachelor's degree in economics and business	Tutoring (paid for 14 hrs)	University of Milano-Bicocca	
2015/2016	Systems Biochemistry – Master's degree in Industrial Biotechnologies	Responsible for two lectures (paid for 4 hrs)	University of Milano-Bicocca	
2014/2015	Informatics - Master's degree in Marketing, Business communication and Global markets	Tutoring (paid for 47 hrs)	University of Milano-Bicocca	
2014/2015	Systems	Responsible for a lecture (2 hrs)	University of Milano-Bicocca	

	Biochemistry – Master's degree in Industrial Biotechnologies			
2014/2015	Systems Biology – Master's degree in Molecular Biotechnologies and Bioinformatics	Responsible for two lectures and one lab (paid for 4+2 hrs)	University of Milano-Bicocca	
2014/2015	Systems Biology and Systems Medicine: Precision Biotechnology and Therapies" Como Lake School of Advanced Studies – September 21-27, 2014	Invited lecturer (3hrs)	University of Milano-Bicocca and University of Amsterdam	
2013/2014	Informatics for earth sciences – Bachelor degree in Earth sciences	Teacher assistant (paid for 24 hrs)	University of Milano-Bicocca	
2013/2014	Systems Biochemistry – Master's degree in Industrial Biotechnologies	Responsible for a lecture (2 hrs)	University of Milano-Bicocca	
2013/2014	Systems Biology – Master's degree in Molecular Biotechnologies and Bioinformatics	Responsible for two lectures and two labs (paid for 4+4 hrs)	University of Milano	
2010/2011	Algorithmic Modelling - Master's degree in Informatics	Responsible for a lecture (2 hours)	University of Trento	
2009/2010	History of Complexity - Master's degree in Economics, Networks and Information	Responsible for a lecture (4 hours)	University of Modena and Reggio Emilia	
2004/2005	Bachelor's degree in marketing and Communication (distance learning)	Review and publication of materials on the on-line degree web-site	University of Modena and Reggio Emilia	
2002/2003	Informatics – bachelor's degree in communication science	Teacher assistant (paid for 30 hours)	University of Modena and Reggio Emilia	

CONFERENCES AND SEMINARS

DATE	TITLE	PLACE	ORAL COMMUNICATION/PARTICIPATION
From 04-09-2019 to 06-09-2019	CIBB 2019: Computational Intelligence methods for Bioinformatics and Biostatistics	University of Bergamo	Speaker
From 17-09-2018 to 21-09-2018	13th International Conference on Cellular Automata for Research and Industry, ACRI 2018	Como School of Advanced Studies	Speaker
Da 02-07-2018 a da 06-07-2018	Congress of the Italian Society of Applied and Industrial Mathematics (SIMAI) (mini symposium 'Mathematical Modeling in Systems Biology')	Faculty of civil and industrial engineering, Sapienza University	**Invited speaker**
Da 25-06-2018 a 26-06-2018	Metabolism and Nutrition: from molecules to systems, annual meeting of the groups 'Membranes', 'Nutrition' and 'Computational and Systems Biology' of the Italian Society of Biochemistry (SIB)	Academy of Science of the Bologna Institute	Speaker
23-05-2018	3rd MetaboMI Meeting, Lipidomics in Metabolism and Diseases. Challenges in Technologies and Applications.	IRCCS Istituto di Ricerce Farmacologiche, Mario Negri, Milano.	Attendee
From 19-09-2017 to 21-09-2017	WIVACE 2017, Workshop on Artificial Life and Evolutionary Computation	European Centre for Living Technology, Università Ca' Foscari	Attendee and chair of one session
From 07-09-2017 to 09-09-2017	CIBB 2017: Computational Intelligence methods for Bioinformatics and Biostatistics	Cagliari University	Speaker and track chair

From 21-7-2017 to 25-7-2017	ISMB/ECCB 2017, 25th Conference on Intelligent Systems for Molecular Biology and 16th European Conference on Computational Biology **RANK A** in computer science (CORE)	Prague Congress Centre	Speaker and poster presentation
From 6-10-2016 to 7-10-2016	BIONAM 2016, workshop on bio-nanomaterials.	Salerno University, Italia	Attendee
From 4-10-2016 to 6-10-2016	WIVACE 2016, Workshop on Artificial Life and Evolutionary Computation	Salerno University, Italia	Speaker
From 20-09-2016 to 23-09-2016	FISV, XIV Congress of the Italian Federation of Life Sciences	Sapienza, Roma University, Italia	Speaker
16-09-2016	Unraveling the design principles of cancer metabolic rewiring with constraint-based modeling	Explora Biotech Srl, Venezia Mestre	Invited Seminar
Da 8-07-2016 a 12-07-2016	SysMod *(SIG)* at ISMB 2016, Intelligent Systems for Molecular Biology **RANK A (CORE)**	Orlando, Florida	Speaker
11-03-2016	SYSBIO-EPIGEN joint workshop - EPIGENETICS AND SYSTEMS BIOLOGY The most relevant topics of Epigenetics in the frame of a Systems Biology Approach	University of Milano-Bicocca	Invited Speaker
16-04-2016	Modeling cancer metabolic rewiring	Department of Biotechnologies and Biosciences, University of Milan-Bicocca	Seminar
From 14-09-2015 to 16-09-2015	58th National Meeting of the Italian Society of Biochemistry and Molecular Biology	Urbino, Italy	Poster presentation
From 28-01-2015 to 30-01-2015	O2 for personalized medicine: from inspiration to aspiration	Amsterdam, Netherlands	Attendee
From 12-09-2013 to 14-09-2013	Synthetic Modeling of Life and Cognition: Open Questions	University of Bergamo	Attendee

29-08-2013	Technology and Human Health: Advances in Systems Medicine	Palmstedtsalen, Chalmers	Poster presentation
From 30-08-2013 to 03-09-2013	ICSB 2013 - 14th International Conference on Systems Biology	Copenhagen, Denmark	Poster presentation
From 1-07-2013 to 2-07-2013	WIVACE 2013, Italian Workshop on Artificial Life and Evolutionary Computation	Milan, Italy	Speaker
From 26-03-2012 to 30-03-2012	SAC 2012, the 27th Symposium On Applied Computing	Riva del Garda (Trento), Italy	Attendee
From 16-11-2011 to 18-11-2011	EMS 2011, UKSim 5th European Modeling Symposium on Mathematical Modeling and Computer Simulation	Madrid, Spain	Speaker
From 30-11-2010 to 3-12-2010	From Programming Languages to Personalized Healthcare	Trento, Italy	Attendee
From 21-09-2010 to 24-09-2010	ACRI 2010 (IX International Conference on Cellular Automata for Research and Industry)	Ascoli Piceno, Italy	Speaker
From 22-01-2010 to 24-01-2010	The First Kananaskis Computational Biology Symposium	Kananaskis AB, Canada	Attendee
From 22-08-2009 to 24-08-2009	The IBI Symposium on Biocomplexity, in celebration of Stuart Kauffman's 70th Birthday	Banff AB, Canada	Attendee
From 08-09-2008 to 10-09-2008	WIVACE 2008, Italian Workshop on Artificial Life and Evolutionary Computation	Venice, Italy	Speaker
From 10-03-2008 to 12-03-2008	Protocell Modeling (workshop)	Ca' Minich, Venice, Italy	Attendee
From 01-10-2007 to 5-10-2007	European Conference on Complex Systems 2007	Dresden, Germany	Speaker
From 05-09-2007 to 07-09-2007	WIVACE 2007, Italian Workshop on Artificial Life and Evolutionary Computation	Sampieri (Ragusa), Italy	Speaker
From 12-09-2006 to 15-09-2006	Third Italian workshop on Artificial Life	Siena, Italy	Attendee
From 18-10-2004 to 29-10-2004	Seminars on Social Networks Analysis	Institute of Mathematical Behavioural Sciences, University of California, Irvine	Attendee
From 02-07-2004 to 09-07-	41st Course of the International School of	Erice, Sicily, Italy	Attendee

| 2004 | Mathematics "G. Stampacchia" on "Evolution and Computation" | | |

PROGRAM COMMITTEES MEMBERSHIP

LOD 2020, The Sixth International Conference on Machine Learning, Optimization, and Data Science – July 19-22, 2020 – Certosa di Pontignano, Siena – Tuscany, Italy

SAC 2020, The 35th ACM/SIGAPP Symposium On Applied Computing, Brno, Czech Republic, March 30 – April 3, 2020

CIBB 2019, Computational Intelligence methods for Bioinformatics and Biostatistics, Bergamo, September 4-6, 2019

LOD 2019, 5th International Conference on machine Learning, Optimization & Data science – Certosa di Pontignano (Siena), September 10-13, 2019

CIBB 2018, 15th International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics, Caparica, Portugal, September 6-8, 2018

SAC 2019, The 34th ACM/SIGAPP Symposium on Applied Computing, Limassol, Cyprus, April 8-12 2019

LOD 2018, 4th International Conference on machine Learning, Optimization and Data science (LOD 2018), Volterra (Pisa), September 13-16, 2018.

CIBB 2017, 14th International Meeting on Computational Intelligence methods for Bioinformatics and Biostatistics, Cagliari, September 7-9 2017

SAC 2018, The 33rd ACM/SIGAPP Symposium on Applied Computing, Pau (Francia), April 9 – 13, 2018

DataMod 2017, 6th International Symposium "From Data to Models and Back (DataMod)" Trento (Itala), September 4-5, 2017

WIVACE 2017, Workshop on Artificial Life and Evolutionary Computation, Venezia, September 21-23, 2017

MOD 2017, The Third International Conference on Machine Learning, Optimization and Big Data, Volterra (Toscana, Italia), September 14-17, 2017

SAC 2017, The 32nd ACM/SIGAPP Symposium on Applied Computing, Marrakech, Morocco, March 27 – 31, 2017

WIVACE 2016, Workshop on Artificial Life and Evolutionary Computation, Salerno, October 4-7, 2016

SAC 2016, The 31st ACM/SIGAPP Symposium on Applied Computing, Pisa (Italia), April 4-8 2016

WIVACE 2015, Workshop on Artificial Life and Evolutionary Computation, Bari, September 23-24, 2015

SAC 2015, The 30th ACM/SIGAPP Symposium on Applied Computing, Salamanca (Spagna), April 13 – 17, 2015

SAC ACM 2014, 29th Symposium On Applied Computing, Gyeongju (Korea), March 24 – 28, 2014

ECAL 2013,12th European Conference on Artificial Life, Taormina (Sicilia), September 2-6, 2013

ORGANIZING AND SCIENTIFIC COMMITTEES

Chair of the special session 'Intelligence methods for molecular characterization and dynamics in translational medicine' at **CIBB 2019**: Computational Intelligence methods for Bioinformatics and Biostatistics, Bergamo, September 4-6, 2019

Member of the scientific committee and chair of a session at **2nd SYSBIO.IT School** on Systems Biology and Bioinformatics, University of Milano-Bicocca, October 4-6, 2017

Chair of the special session "Modeling and simulation methods for systems biology and systems medicine" at **CIBB 2018**, 15th International Conference on Computational Intelligence methods for Bioinformatics and Biostatistics, Caparica, Portugal, September 6-8, 2018

Member of the local organizing commitee of **COMBINE 2017**, Meeting of The "Computational Modeling in Biology" Network, Milano, October 9-13, 2017

Chair of the special session "Modeling and simulation methods for systems biology and systems medicine" at **CIBB 2017**, 14th International Meeting on Computational Intelligence methods for Bioinformatics and Biostatistics, Cagliari, September 7-9, 2017

Member of the scientific committee of **1st SYSBIO.IT** School on Computational Systems Biology An introduction to dynamic modeling, simulation and analysis of biological systems, University of di Milano-Bicocca, June 7-9, 2016

Member of the organizing committee of the special session "Modeling and simulation methods for systems biology and systems medicine" at **CIBB 2016**, 13th International Meeting on Computational Intelligence methods for Bioinformatics and Biostatistics, Stirling, Scozia (UK), September 1-3, 2016

Member of the local organizing committee of **WIVACE 2013**, Italian Workshop of Artificial life and Evolutionary Computation, Milano, July, 1-2, 2013

Member of the local organizing committee of **AIxIA 09**, XI Conference of the Italian Association for Artificial Intelligence, Reggio Emilia, December 9-12, 2009

Member of the local organizing committee of **Wivace 08**, Workshop on Artificial Life and Evolutionary Computation, Venice, September 9-12, 2008

Member of the local organizing committee of The Management of Complexity, The Complexity of Management, Reggio Emilia, July 12 2007

PAPER REVIEWING AND EDITORIAL ACTIVITY

Associate Editor of **BMC Bioinformatics.**

❖ **Q1** Computer Science Applications (SJR)

Member of the Editorial Board of the international journal **The Open Bioinformatics Journal**

Member of the Editorial Board of the international **Journal of Autonomous Intelligence**

PAPER REVIEWING AND EDITORIAL ACTIVITY

Reviewer of **PhD thesis** in Information Technology XXXII cycle, University of Parma (year 2016/2019). PhD candidate: Laura Sani. Title: ''Detection of relevant structures in complex systems: an information-theoretic approach with applications to machine learning and pattern recognition"

Reviewer for the international journal of Annals in Translational Medicine

Reviewer for the international journal of Computers in Biology And Medicine

Reviewer for the international journal of Biomedical Informatics

Reviewer for the international journal BMC Systems Biology

Reviewer for the international journal Computational and Mathematical Methods in Medicine

Reviewer for the international journal Computational Biology Journal

Reviewer for the conference SAC 2019, The 34th ACM/SIGAPP Symposium On Applied Computing, Limassol, Cyprus, 8-12 april 2019

Reviewer for the conference SAC 2018, The 33rd ACM/SIGAPP Symposium On Applied Computing, April 9 - 13, 2018, Pau, France

Reviewer for the conference WIVACE 2017, Workshop on Artificial Life and Evolutionary Computation, Venice, 21-23 September 2017

Reviewer for the conference MOD 2017, The Third International Conference on Machine Learning, Optimization and Big Data, September 14-17, 2017, Volterra - Tuscany, Italy

Reviewer for the international Journal of Computational Biology and Chemistry

Reviewer for the conference CIBB 2016, 13th International Meeting on Computational Intelligence methods for Bioinformatics and Biostatistics, Stirling, Scotland UK, September 1-3, 2016

Reviewer for the conference SAC 2017 The 32nd ACM/SIGAPP Symposium on Applied Computing, Marrakech, Morocco, 27 – 31 March, 2017

Reviewer for the conference WIVACE 2016, Workshop on Artificial Life and Evolutionary Computation, Salerno, 4-7 October 2016

Reviewer for the conference SAC 2016 The 31st ACM/SIGAPP Symposium on Applied Computing, 4-8 April 2016, Pisa, Italy

Reviewer for the conference WIVACE 2015, Workshop on Artificial Life and Evolutionary Computation, 23-24 September 2015, Bari

Reviewer for the conference SAC 2015 The 30th ACM/SIGAPP Symposium on Applied Computing, April 13 – 17, Salamanca, Spain

Reviewer for the conference SAC ACM 2014, 29th Symposium on Applied Computing, March 24 - 28, Gyeongju, Korea

Subreviewer for the conference ECAL 2013,12th European Conference on Artificial Life, 2-6 September, Taormina Sicily

Reviewer for the conference WIVACE 2013, Italian Workshop on Artificial Life and Evolutionary Computation, 1-2 July 2013, Milano

Reviewer for a book chapter in Models of the Ecological Hierarchy, From Molecules to the Ecosphere (Developments in Environmental Modelling), Ferenc Jordan and Sven Erik Jorgensen (editors), 2012

Reviewer for the international journal Transactions on Computational Systems Biology

Reviewer for ECCS 2011 European Conference on Complex Systems

OTHER EDUCATIONAL ACTIVITIES

PERIOD	ACTIVITY	INSTITUTION
From 2-02-2015 to 06-02-2015	Training Course: Data Integration in the Life Sciences	Lorentz Center
From 25-08-2013 to 29-08-2013	Advanced Course on Metabolic Engineering and Systems Biology	Chalmers University of Technology
From 05-08-2008 to 21-08-2008	International summer school "Introduction to Bioinformatics", 4 ECTS, Grade: 4 (very good)	University of Helsinki
From 09-2005 to 07-2006	Exchange European Program "Erasmus"	Faculty of "Ciencès Economòmiques i Empresarials", Barcelona University

SCIENTIFIC ASSOCIATIONS

- ❖ Italian Society of Bioinformatics BITS (from November 2018)
- ❖ Italian Society of Biochemistry and Molecular Biology SIB - Computational and Systems Biology group (from January 2015)
- ❖ International Society for Computational Biology ISCB (from April 2016 to April 2018)
- ❖ Scientific Director of Biochronicles – association for the dissemination of scientific knowledge

MAIN COLLABORATIONS

Odemir M. Bruno, University of Sao Paulo, Head of the Scientific Computing Group

Giulio Caravagna, School of Informatics, University of Edinburgh - Department of Computer Science and Engineering (DISI)

Timoteo Carletti, Department of Mathematics and Namur Center for Complex Systems - naXys, University of Namur

Paolo Cazzaniga, Department of human and social sciences, Università degli Studi di Bergamo

Annamaria Colacci, Agenzia Regionale Prevenzione Ambiente (ARPA) Emilia Romagna

Fabio Cumbo, Institute for Systems Analysis and Computer Science, Italian National Research Council

David Gilbert, College of Engineering, Design and Physical Sciences, Brunel University

Monika Heiner, Computer Science Department, Brandenburg University of Technology Cottbus-Senftenberg

Stuart Kauffman, Institute for Biocomplexity and Informatics, University of Calgary

Davide Rambaldi, Istituto Europeo dei tumori

Maya Fedeli, IRCCS San Raffaele Scientific Institute, Milan, Italy

Daniela Gaglio, Institute of Molecular Bioimaging and Physiology, National Research Council (IBFM-CNR), Segrate, Italy

Enzo Medico e Claudio Isella, Istituto di Candiolo – IRCCS

Dario Pescini, Department of statistics and quantitative methods, University if Milano-Bicocca

Irene Poli, European Centre for Living Technology (ECLT)

Andrea Roli, Department of Computer Science and Engineering, Università di Bologna

Marco Tomassini, Information Systems Institute ISI – HEC, University of Lausanne

Hans Westerhoff, Manchester Centre for Integrative Systems Biology, School of Chemical Engineering and Analytical Science, University of Manchester, Manchester, United Kingdom

Wim Wordick, SmartAnalytiX.com, Lausanne, Switzerland

LANGUAGES

LANGUAGE	LEVEL
Italian	Mother tongue
English	Fluent
Spanish	Fluent
French	Basic

TECHNICAL SKILLS

PROGRAMMING LANGUAGES AND SOFTWARE	Python, MATLAB, C++, R, Html, PHP, mySQL, Java, BlenX, LaTeX
OTHER SKILLS	Data analysis and manipulation, data mining, stochastic modeling, network and parameter inference, sensitivity analysis, Flux Balance Analysis, network analysis, Information theory

REFERENCES

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