

CURRICULUM VITAE



Emanuela Merelli

GENERAL INFORMATION

Citizen: Italian

Born: San Ginesio, Italy, 9 August 1960

Two children: Costanza and Giovanni

Education: Laurea in Scienze dell'Informazione (University of Pisa)

PhD in Artificial Intelligent Systems (University of Ancona)

PROFESSIONAL ADDRESS:

Università di Camerino, Computer Science

via Madonna delle Carceri, 9, I-62032 Camerino

office: +39 0737 402567, mobile: +39 338 3990412

fax: +39 0737 402561, e-mail: emanuela.merelli@unicam.it

home-page: <http://www.emanuela.merelli.eu>

POSITION

Full Professor of Computer Science at Università di Camerino

APPOINTMENTS

- Member of Academic Senate, representing the School of Science and Technology, (2017 –)
- Full professor of Computer Science at Università di Camerino, chiamata diretta Art.24, comma 6, DL 240/2010, (2015 –)
- Qualification as Full professor of Computer Science (Abilitazione scientifica nazionale, prima fascia, 01/B1-Informatica, Bando MIUR 2012) (2014)
- Delegate of the Rector to the International (European) Mobility activities, (2011 – 2012)
- Coordinator of PhD in Computer Science, International School of Advanced Studies, (2010 –)
- Head of Computer Science Division, School of Science and Technology, (2006 – 2012)
- Associate professor of Computer Science at Università di Camerino (2006 – 2015)
- Vice-chair of the Scientific Advisory Board, Master in BioMedical Image Processing, (2001 - 2006)
- Assistant professor of Computer Science at Università di Camerino (2001 – 2006)

EXTERNAL APPOINTMENTS

- Member of the EATCS Council (European Association Theoretical Computer Science) (2017 –)
- Fulbright Scholar at University of Oregon, Computer Science Dep., Eugene, US, (2005 – 2006)
- Visiting Researcher at University of East Anglia, School of Information System, Norwich, UK, (1998)
- Research Fellow at National Research Institute (CNR), Pisa, Italy, (1987)
- Italian Delegate to ISO/WG6, Editor of OSI/WG6-Presentaion Layer, (1986 – 1987)
- Scientist Fellow at European Networking Center, IBM, Heidelberg, Germany, (1985 – 1986)
- Honorary Scholar at Ing. C. Olivetti S.p.A., Ivrea, Italy, (1984 – 1985)

TEACHING ACTIVITIES

- Data Science and TDA¹ · Distributed Calculus and Coordination¹ · Algorithms and Data Structures¹
- Information Systems and Database · Methods and Programming Languages
- Algorithms and Complexity · Operational Research · Non-linear Optimization

¹ current academic year

MEMBERSHIPS

- Member of Bioinformatics Italian Society (BITS), (2006)
- Member of Gruppo GNCS (Gruppo Nazionale per il Calcolo Scientifico), (2009)
- Member of the Consorzio Interuniversitario Nazionale per la Fisica della Atmosfere e Idrosfere, (2011)
- Vice-President “Centro Studi Gentiliani”, Italian Society for the International Law, (2015)

PROFESSIONAL CONTRIBUTIONS

- Principal Investigator of the ERASMU+ 2014-2020 KA2 HEI Cooperation for Innovation, “Data Science Pathways to Re-image Education”, Grant n.2016-1-IT02-KA203-024645
- Coordinator of the EC FP7, FET Proactive, “TOPDRIM: Topology Driven Methods for Modelling Complex Systems” project, GA N. 318121, (2012-2015)
- Principal Investigator of the COST Action on “Reversible Computation: extending horizon of computing” IC1405, (2015-2017)
- Principal Investigator of the IT Flagship, RITMARE, “Agent-oriented modelling for spacial and temporal multiscale analysis, simulation and prediction of a dynamics population in the marine ecosystem” project SP2-WP2-AZ2-UO05, (2012-2016)
- Principal Investigator of the POR MARCHE FESR 2007-2013, “AALISABETH: “Ambient-Aware LifeStyle tutoring, Aiming at a BETter Health” project, (2013-2015)
- Principal Investigator of the IT MIUR, FIRB, “LITBIO: Interdisciplinary Laboratory of Bioinformatics Technologies”, project, (2005-2009)
- Scientific delegate at FP6, NoE, Virtual Physiological Human- Network of Excellence, (2009-2011)
- Principal Investigator of the IT Strategic Research Project, “O2I: Oncology over Internet – Methodologies, Models, Techniques and Tools, per Information Extraction and Retrieval”, (2002-2005)
- Principal Investigator of the CIPE MARCHE “SICOM: SIstemi COoperativi e Multiagente”, (2003-2004)

EXPERT and EVALUATOR

- European Commission DG CONNECT (ex-INFISO), Future and Emerging Technologies, (since 2011)
- Italian Ministry for Research and Education, MIUR, (since 2012)
- Fulbright US-Italy Program, (since 2007)
- Qatar National Research Fund, QNRF, (since 2006)
- Region Marche - Research, Development, Innovation and Technology Transfer, (since 2011)

REFEREE

- ACM Transaction on Computational Biology and Bioinformatics
- Acta Informatics, Springer
- Applied Mathematics and Computation, Elsevier
- Bioinformatics, Oxford Journal
- BioSystems, Elsevier Journal
- BMC Bioinformatics
- Briefings in Bioinformatics, Oxford Journal
- Bulletin of Mathematical Biology
- Computer and Industrial Engineering, Elsevier
- Data and Knowledge Engineering, Elsevier
- IEEE Transaction on Parallel and Distributed Computing
- International Journal of Computer Mathematics
- International Journal for Production Research

- International Journal of Modelling, Identification and Control
- International Journal on Software Tools for Technology Transfer, Springer
- Journal of Theoretical Biology, Elsevier
- Neural Computing and Applications, Springer Journal
- PLOS, Computational Biology
- PLOS ONE
- Robotics and Computer-Integrated Manufacturing, Elsevier
- Simulation, Modelling Practice and Theory, Elsevier
- Theoretical Computer Science, Elsevier
- Transactions on Computational Systems Biology, Springer

GUEST EDITOR

Journal of Theoretical Computer Science - Theory of Natural Computing, Elsevier.

- From Computer Science to Biology and Back, vol. 608, (2015)
- Interaction between Computer Science, Complex Systems and Biology, vol. 587, (2015)
- Hybrid Automata and Oscillatory Behaviour in Biological Systems, vol. 411, issue 20, (2010)
- Concurrent Systems Biology: to Nadia Busi (1968-2007), vol. 410, issue 33-34: P.3037-3038, (2009)

Journal of Electronic Proceedings of Theoretical Computer Science

- Proceedings of 5th CS2Bio Workshop Interaction between Computer Science and Biology, vol. 306, (2014)
- Proceedings of 4th CS2Bio Workshop Interaction between Computer Science and Biology, vol. 299, (2013)
- Proceedings of 2nd FBTC Workshop From Biology To Concurrency and Back, vol. 229, issue 1, (2009)
- Proceedings of 1st FBTC Workshop From Biology To Concurrency and Back, vol. 194, issue 3, (2008)

Springer Proceedings in Complexity Springer

- Proceedings of ECCS 2014, ISBN 978-3-319-29228-1 (2016)

Transaction on Computational Systems Biology, Springer

- Model and Metaphors from Biology to Bioinformatics and Back, vol. 3737 (2005)

AWARDS

FET11: The European Future Technologies Conference and Exhibition. The 3rd Price for the Best Poster: Methodological Bridges for Complex Systems. co-authors: Pietro Lio and Nicola Paoletti. <http://www.fet11.eu/awards>

FOUNDING MEMBER FO SPIN-OFF

- NGB: New Generation Bioinformatics dell'Universit di Camerino (2010) <http://www.engeebee.com>
- eLios: eLinking on line services S.r.l., Universit di Camerino (2007) <http://www.e-lios.eu>

OTHER ACTIVITIES

- Chair and co-chair of several events with an interdisciplinary character, last of which an International School on Concurrency and Complexity through Topology for Young Researchers, Jointly organized by the European Association for Theoretical Computer Science and the TOPDRIM project, (2015)
- Member of many program committees of workshops and conferences
- Advisor and Tutor of several brilliant PhD Candidates

MAIN FIELD OF RESEARCH

Topological Field Theory of Data and new models of computation, concurrency theory, agent-oriented modelling & multi-level complex systems, bio-inspired formal methods. Computational biology of RNA Folding and Immune System Memory Evolution.

PROFESSIONAL ACTIVITIES

Author or co-author of about a hundred peer reviewed articles on international journals and volumes. Most cited paper: “A tabu search method guided by shifting bottleneck for the job shop scheduling problem”, E. Merelli, F. Pezzella, European Journal of Operational Research 120 (2), 297-310, (2000) ~ 282 citations (2017).

MOST RELEVANT CONTRIBUTIONS

The most relevant contributions in the various areas are:

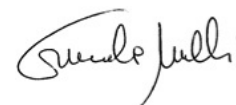
- i) a research program towards a new strategy for mining data through data language that turns out to be the shape language: **Topological Field Theory of Data**; [3]
- ii) an extension to n-body interactions of Parisi’s idiotypic network model to study the memory evolution of human **Immune System** as a topological application of the S[B] paradigm; [11]
- iii) **the S[B] machine** a new model of computation supporting data-driven evolution of the model. It’s characterized by two entangled levels of description, global and local: *the environment*, properly the semantic context where *the computation* takes place through a pool of interacting agents each of which behaves as a deterministic machine; [7]
- iv) new bio-inspired formal languages such as BioAgent, SHAPE Calculus, BIOSHAPE and BOSL, for modelling, simulating and analysing autonomous agents represented as geometric shapes whose internal behavior allows them to interact, bind and move in an Euclidian space; [26,27]
- v) the construction of Hermes, an agent-based middleware for mobile computing; [42]
- vi) the design and implementation of jHoles algorithm based on Holes, persistent homology and clique weight rank homology, to study the connectivity features of complex networks. Applications on epidermal tumour diagnosis; [13]
- vii) **Persistent Entropy**, a new measure of complexity defined as a function of Betti barcodes strongly related to the topological structure of the data space and a methodology to construct a persistent entropy automaton from topological data analysis; [9]
- ix) a wide study on bone remodelling as a multiscale, multilevel system - based on Spatial P Systems, complex automata and BioShape, by combining process algebraic and stochastic approach and by modelling some pathologies such as osteomyelitis and osteoporosis; [17-19]
- x) a model of cell cycle viewed as model reduction of an hybrid system that captures the crucial features of a dynamical system. The use of hybrid automata technology allows us to describe the cellular system by combining continuous behavior with discrete events; [21]
- xi) a new data model, Resourceome, that allows to manage declarative and procedural knowledge with a unique model whose actions connect the use of a resource to its domain; [44]
- xii) the design and development of DISPAS, Demersal fish Stock Probabilistic Agent-based Simulator, to investigate and understand sustainability in the exploitation of fishery resources, by focusing on common sole (*Solea solea*) stock in the North-ern Adriatic Sea; [14]
- xiii) a new heuristic method combines Tabu Search and Shifting Bottleneck and solves the optimization problem of job shop scheduling in a better time [47].

MAIN INVITED TALKS

- 2017 June, Wien, “A topological view of Compositionality of Process Algebra”, Open Problems in Concurrency Theory, IFIP Group
- 2016 December, Berkeley, USA. “Topological Approach to Compositionality in Complex Systems”, Simon Institute
- 2016 September, Amsterdam, “On topological characterization of complex systems”, DyM-CS- CCS
- 2016 September, Cagliari, IT “Tutorial on Topological data analysis with jHoles and persistent entropy” KBWeb
- 2016 July, Wien, “Topological Field Theory of Data: A program towards a novel strategy for mining data through data language”, DataMOD
- 2015 December, New York, USA. “Topological Field Theory of Data”, BICT
- 2015 June, London, “TOPDRIM a global vision of data: non-locality, topology, formal languages: new tools to handle large data set”, NGS
- 2015 March, Brussels, “Topological Field Theory of Data, the new science for computer science”, EU FET seminar
- 2012 August, Taormina, IT. “The Immune System as a Metaphor for Topology Driven Patterns Formation in Complex Systems” at the Int. Conference on Artificial Immune Systems”
- 2011 September, Palermo, IT. “Self-adaptive systems for Ageing and Quality of Life” at the AI*IA workshop on Technological Challenges and Scenarios of the Ageing Society”
- 2009 April 16, San Francisco, USA. “Model Checking Biological Oscillators” at HSCB’09 on “Hybrid Systems Approaches to Computational Biology”
- 2007 September 18, Reykjavik, IS. “Agent-based Modelling and Simulation in Systems Biology” at School of Computer Science, Reykjavik University
- 2007 October 25, Pisa. “Agent-based Modelling and Simulation in Systems Biology” at MiniWorkshop on “Computational Approach to Biology” Scuola di dottorato Galileo Galilei. (Joint with Nicola Cannata and Luca Tesi)
- 2007 November 8, Stony Brook, USA. “Agent-based Modelling and Simulation in Systems Biology” at Dept. of Computer Science State University of New York
- 2007 December 10, Milano. “Orion Framework for systems Biology applications” at BioinfoGRID (Bioinformatics Grid Application for Life Science) Symposium 2007.
- 2005 February 1, Stanford University. “Agent in Bioinformatics” at Center for Biomedical Computation

Camerino, 13th June 2017

Prof. Emanuela Merelli



LIST OF SELECTED PUBLICATIONS

1. D. Cacciagrano, F. Corradini, E. Merelli, L. Tesei: Uniformity in Multiscale Models: From Complex Automata to BioShape. *J. Cellular Automata* vol. 12 n.5 (2017)
2. M. Rucco, R. Gonzalez-Daz, M. J. Jimnez, N. Atienza, C. Cristalli, E. Concettoni, A. Ferrante, E. Merelli: A new topological entropy-based approach for measuring similarities among piecewise linear functions. *Signal Processing* vol. 134 (2017)
3. M. Rasetti, E. Merelli: The Topological Field Theory of Data: mining data beyond complex networks. In *Advances in Disordered Systems, Random Processes and Some Applications*, eds P. Contucci, C. Giardina', Cambridge University Press (2016)
4. M. Rasetti, E. Merelli: The Topological Field Theory of Data: a program towards a novel strategy for mining data through data language. *J. Physics: Conf. Series*, vol.626, (2015)
5. A.L. Mamuye, E. Merelli, L. Tesei: Graph Grammar for Modeling RNA Folding Evolution as a Self-Adaptive System. *Proceedings of Graphs as Models, Electronic Proceedings in Theoretical Computer Science*, Vol. 231, (2016)
6. E. Merelli, M. Piangerelli, M. Rucco, D. Toller: A topological approach for multivariate time series characterization: the epileptic brain. *EAI Endorsed Trans. Self-Adaptive Systems* 2(7): e5 (2016)
7. E. Merelli, N. Paoletti, L. Tesei: Adaptability checking in complex systems. *Science of Computing Programming*, vol.115-116, (2016)
8. Rucco Matteo, Castiglione Filippo, Merelli Emanuela, Pettini Marco. Characterisation of the Idiopathic Immune Network Through Persistent Entropy. In: *Proceedings of ECCS 2014*. p. 117-128, Springer (2016)
9. E. Merelli, M. Rucco, P. Sloot and L. Tesei: Topological Characterization of Complex Systems: Using Persistent Entropy. *Entropy*, 17(10), (2015)
10. E. Merelli, I. Petre: From Computer Science to Biology and Back. *Theor. Comput. Sci.* vol.608, (2015)
11. E. Merelli, M. Pettini, M. Rasetti: Topology driven modeling: the IS metaphor, *Natural Computing Journal, NACO*, 14(3), Springer, (2015)
12. P. Giannini, E. Merelli, A. Troina: Interactions between Computer Science and Biology. *Theor. Comput. Sci.* vol.587, (2015)
13. J. Binchi, E. Merelli, M. Rucco, G. Petri, F. Vaccarino: jHoles: A Tool for Understanding Biological Complex Networks via Clique Weight Rank Persistent Homology. *Electr. Notes Theor. Comput. Sci.* vol.306, (2014)
14. Pierluigi Penna, Nicola Paoletti, Giuseppe Scarcella, Luca Tesei, Mauro Marini, Emanuela Merelli: DISPAS: An Agent-Based Tool for the Management of Fishing Effort. *SEFM Workshops 2013*: 362-367
15. E. Merelli, M. Rasetti: *Non locality, topology, formal languages: new global tools to handle large data sets*, *Procedia Computer Science*, vol.18, (2013)

16. E. Merelli, M. Rasetti: The Immune System as a Metaphor for Topology Driven Patterns Formation in Complex Systems. *Int. Conference on Artificial Immune Systems*. Taormina, (2012)
17. P. Liò, N. Paoletti, M. A. Moni, K. Atwell, E. Merelli, M. Viceconti: Modelling osteomyelitis. *BMC Bioinformatics* 13(S-14): S12 (2012)
18. N. Paoletti, P. Lio', E. Merelli, M. Viceconti: Multilevel Computational Modeling and Quantitative Analysis of Bone Remodeling. *IEEE/ACM Trans. Comput. Biology Bioinformatics*, 9(5), (2012)
19. P. Liò, E. Merelli, N. Paoletti: Disease processes as hybrid dynamical systems. *Int. Workshop on Hybrid Systems*. Newcastle, (2012)
20. F. Buti, F. Corradini, E. Merelli, L. Tesei: A Geometrical Refinement of Shape Calculus Enabling Direct Simulation. *Conference on Simulation, Meth. And Techn. And Appl.* Rome, (2012)
21. E. Bartocci, P. Liò, E. Merelli, N. Paoletti: Multiple Verification in Complex Biological Systems: The Bone Remodelling Case Study. *Trans. Computational Systems Biology* vol.14, (2012)
22. R. Alfieri, E. Bartocci, E. Merelli, L. Milanese: Modeling the cell cycle: From deterministic models to hybrid systems. *Journal of Biosystems* 105(1), 2011
23. F. Buti, D. Cacciagrano, F. Corradini, E. Merelli, L. Tesei: A Uniform Multiscale Meta-model of BioShape. *Electr. Notes Theor. Comput. Sci.* vol.277, (2011)
24. P. Li, E. Merelli, N. Paoletti, M. Viceconti: A Combined Process Algebraic and Stochastic Approach to Bone Remodeling. *Electr. Notes Theor. Comput. Sci.* vol.277, (2011)
25. E. Bartocci, F. Corradini, E. Merelli, L. Tesei: Detecting Synchronisation of Biological Oscillators by Model Checking. *Theoretical Computer Science* 411(20), (2010)
26. E. Bartocci, M.R. Di Berardini, D. Cacciagrano, E. Merelli, L. Tesei: Timed Operational Semantics and Well-Formedness of Shape Calculus. *Scientific Annals of Computer Science*, vol.20, (2010)
27. E. Bartocci, M.R. Di Berardini, F. Corradini, E. Merelli, L. Tesei: Shape Calculus. A Spatial Mobile Calculus for 3D Shapes. *Scientific Annals of Computer Science* vol. 20, (2010)
28. E. Bartocci, D. Cacciagrano, F. Corradini, E. Merelli, and L. Vito. A Resourceome for the automation of in-silico biological experiments. Appearing in proceedings of *International Conference on Computational and Systems Biology and Microbiology (BioSysCom)*, Cancun, Messico, (2010)
29. F. Buti, D. Cacciagrano, F. Corradini, E. Merelli, L. Tesei. BioShape: a spatial shape-based scale-independent simulation environment for biological systems. Appearing in proceedings of *International Conference on Computational Science (ICCS)*, Amsterdam, (2010)
30. F. Buti, D. Cacciagrano, F. Corradini, E. Merelli, M. Pani, L. Tesei: Bone remodelling in BioShape. In *CS2BIO 2010: Interactions between Computer Science and Biology*, 1st International Workshop, (2010)
31. D. Cacciagrano, F. Corradini, E. Merelli. Bone Remodelling: a Complex Automata-based model running in Bioshape *ACRI 2010: The Ninth International Conference on Cellular Automata for Research and Industry*, Ascoli Piceno (Italy), (2010)
32. E. Bartocci, F. Corradini, E. Merelli, L. Tesei: Detecting synchronisation of biological oscillators by model checking. *Theor. Comput. Sci.* 411(20): 1999-2018 (2010). *Theor. Comput. Science* 411(20), (2010)

33. F. Buti, F. Corradini, E. Merelli, E. Paschini, P. Penna, L. Tesei: An Individual-based Probabilistic Model for Fish Stock Simulation. *AMCA-POP* 37-55, (2010)
34. E. Bartocci, F. Corradini, E. Merelli, L. Tesei. Model Checking Biological Oscillators. *Electronic Notes in Theoretical Computer Science* 229(1), (2009)
35. N. Cannata, F. Corradini, E. Merelli, F. Piersigilli, L. Vito Towards Bioinformatics Resourceomes. *Biomedical Data and Applications* 13-36, (2009)
36. N. Cannata, F. Corradini, E. Merelli. Multiagent modelling and simulation of carbohydrate oxidation *International Journal of Modelling, Identification and Control (IJMIC)*, 1(3), (2008)
37. E. Bartocci, F. Corradini, R. Grosu, E. Merelli, O. Riganelli, S. A. Smolka. StonyCam: A Formal Framework for Modeling, Analyzing and Regulating Cardiac Myocytes. *Concurrency, Graphs and Models*, LNCS vol.5065, (2008)
38. E. Merelli et al. Agents in Bioinformatics, Computational and Systems Biology. *Briefing in Bioinformatics*, 8(1), (2007)
39. E. Merelli, M. Young. Validating MAS with mutation. *International Journal of Multiagent and Grid Systems* 3(2), (2007)
40. N. Cannata, F. Corradini, E. Merelli. A Resourceomic Grid for Bioinformatics. *International Journal of Grid Computing: Theory, Methods and Applications: Future Generation Computer Systems Journal*, 23(3), (2007)
41. E. Bartocci, F. Corradini, E. Merelli, L. Scortichini. BioWMS: a web-based Workflow Management System for Bioinformatics. *BMC Bioinformatics Int. Journal*, vol.8 suppl.1, (2007)
42. F. Corradini, E. Merelli: Hermes: Agent-Based Middleware for Mobile Computing. *SFM 2005* LNCS Vol. 3465. 234-270, (2005)
43. N. Cannata, F. Corradini, E. Merelli, A. Omicini, A. Ricci. An agent-oriented conceptual framework for Systems Biology. *Transaction on Computational Systems Biology*, LNBI Vol. 3737, 105-122, Springer, (2005)
44. N. Cannata, E. Merelli, R.B. Altman. Time to organize the Bioinformatics Resourceome. *PLoS Computational Biology*, Vol. 1, Num. 7, (2005)
45. M. Luck and E. Merelli. Agents in Bioinformatics. *The Knowledge Engineering Review*, vol. 20, Num. 2 117-125, Cambridge University Press, (2005)
46. F. Corradini, L. Mariani, and E. Merelli. An agent-based approach to tool integration. *Software Tools for Technology Transfer*, Vol. 6 Num. 3, 231-244, Springer Journal, (2004)
47. E. Merelli, F. Pezzella. A tabu search method guided by a shifting bottleneck for a job shop scheduling. *European Journal of Operational Research*, vol. 120, (2000)
48. R. De Leone, R. Capparuccia, E. Merelli. A successive overrelaxation back propagation algorithm for neural network training. *IEEE Transactions on Neural-Networks*, 9(3), (1998)
49. F. Caneschi, E. Merelli. An architecture for an asn.1 encoder/decoder. *Computer Networks, North Holland*, vol.14, (1987)