CURRICULUM VITAE

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)

Emanuela Merelli

PROFESSIONAL ADDRESS:

Università di Camerino, Computer Science

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POSITION

Full Professor of Computer Science at Università di Camerino (Unicam)

APPOINTMENTS

· Member of Academic Senate of the University of Camerino
· Vi-President of Italian Chapter of EATCS
· Member of the Board of the CINI Laboratory of Big Data and Data Science
· Coordinator of PhD in Computer Science and Mathematics, ISAS-University of Camerino (2010 – 2022)
· Member of the Council of the European Association for Theoretical Computer Science (2017 – 2021)
· Fellow member of the COST Action CA19122, EU Net for Gender Balance in Informatics (2020-2024)
· Delegate to the European Mobility of the University of Camerino (2011 – 2012)
· Head of Computer Science Div., School of Science and Tech., University of Camerino (2006 – 2012)
· 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)
· Delegate to ISO/WG6 for Italy, Editor of OSI/WG6-Presentation 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)

PROFESSIONAL CONTRIBUTIONS

· Scientific Coordinator "Biomolecules computing cell behaviour" project funded by Diatech Pharmaco-genetics srl, (2022-2024)
· Project Coordinator of the EC FP7, FET Proactive, "TOPDRIM: Topology Driven Methods for Modelling Complex Systems", GA N. 318121, (2012-2015)
· Principal Investigator of the ERASMU+ KA2 HEI Cooperation for Innovation, "Data Science Pathways to Re-image Education", Grant n.2016-1-IT02-KA203-024645, (2014-2020)
· 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 FESR 2007-2013, "AALISABETH: "Ambient-Aware LIfeStyle tutoring, Aiming at a BETter Health" project, (2013-2015)

· Principal Investigator of 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 IT-MIUR-Strategic Research Project, "O2I: Oncology over Internet –
  Methodologies, Models, Techniques and Tools, per Information Extraction and Retrieval", (2002-2005)
· Principal Investigator of CIPE MARCHE "SICOM: SIstemi COoperativi e Multiagente", (2003-2004)

EXPERT and EVALUATOR

· European Commission: FP7, H2020, Horizon-EIC
· Italian Ministry for Research and Education, MIUR
· Fulbright US-Italy Program
· Quatar National Research Fund, QNRF
· Region Marche, Regione Lombardia, Provincia di Trento - R&D&I and Technology Transfer
· Galileo Program for the Italo-French Cooperation

TEACHING ACTIVITIES

· Distributed Calculus and Coordination[1] · Multiagent Systems Lab.[1] · Algorithms and Data Structures[1]
· Machine Learning[1] · Computability Theory[1] · Data Science & TDA · Information Systems and DB · Algorithms and Complexity · Operational Research · Non-linear Optimisation · Methods and Programming Languages. (1 current academic year)

MEMBERSHIPS

· Member of EATCS (European Association for Theoretical Computer Science)
· Member of ACM (Association for Computing Machinery)
· Member of Bioinformatics Italian Society (BITS)
· Member of Gruppo GNCS (Gruppo Nazionale per il Calcolo Scientifico)

FOUNDING MEMBER OF SPIN-OFF

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

SCIENTIFIC ACTIVITIES

REFEREE

ACM Transaction on Computational Biology and Bioinformatics · Acta Informatics, Springer · American Mathematical Society · 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 · Scientific Report, Nature · 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. Special issues on:
 · 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)
 · 4th CS2Bio Workshop Interaction between Computer Science and Biology, vol. 299, (2013)
 · 2nd FBTC Workshop From Biology To Concurrency and Back, vol. 229, issue 1, (2009)
 · 1st FBTC Workshop From Biology To Concurrency and Back, vol. 194, issue 3, (2008)

ICALP Proceedings:
 · ICALP 2022, LIPIcs Vol. 229 (2022)
 · ICALP 2021, LIPIcs Vol. 198 (2021)
 · ICALP 2020, LIPIcs Vol. 168 (2020)
Springer Proceedings in Complexity. Proceedings of :
 · ECCS 2014, ISBN 978-3-319-29228-1 (2016)
Transaction on Computational Systems Biology, Springer. Special issue on:
 · 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

DISSEMINATION ACTIVITIES

· Member of ICALP Steering Committee
· Chair and co-chair of several events with an interdisciplinary character, among which the International
  School on Concurrency and Complexity through Topology for Young Researchers. Jointly organised in
  2015 by the European Association for Theoretical Computer Science and the TOPDRIM EU-project.
· Member of many program committees of workshops and conferences
· Advisor and Mentor of several brilliant PhD Candidates among which Leonardo Mariani, Ezio Bartocci,
and Nicola Paoletti

RESEARCH ACTIVITIES

Author or co-author of about a hundred peer-reviewed articles in 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): $\sim$ 329 Scholar (172 Scopus) citations. h-Index 28 Scholar (18 Scopus), total citation 2244 Scholar (1110 Scopus)

MAIN FIELD OF RESEARCH

Topological Field Theory of Data and S[B] models of computation, agent-oriented modelling & multi-level complex systems, bio-inspired formal methods. Computational biology of RNA Folding. n-body interaction for the Immune System metaphor of memory evolution. The

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**; [19-20]

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; [27]

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; [23]

iv) An algebraic language for RNA structure comparison [10], so as new bio-inspired formal methods such as BioAgent, **SHAPE Calculus**, BIOSHAPE, and Biological Oscillators synchronization language (BOSL), for modelling, simulating and analysing autonomous agents represented as geometric shapes whose internal behavior allows them to interact, bind and move in a Euclidian space; [42,43]

v) the construction of Hermes, an agent-based middleware for mobile computing [59] at the basis of **Orion** an agent-based spatial simulator for MAS.

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; [29]

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; [25]

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; [33-35]

x) a model of cell cycle viewed as a 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; [38]

xi) a new data model, Resourceome, that allows the managing of declarative and procedural knowledge with a unique model whose actions connect the use of a resource to its domain; [61]

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 Northern Adriatic Sea; [30]

xiii) a new heuristic method combines Tabu Search and Shifting Bottleneck and solves the optimization problem of job shop scheduling in a better time [64].

INVITED TALKS

2022 May, Tampa, USA. "The topology of RNA folding"
     Workshop on Discrete and Topological Models in Molecular Biology

2019 August, Stony Brook, USA. "A topological Interpretation of Interactive Computation"
     Symposium in honor of Scott Smolka on the occasion of 65th birthday

2019 February, Lugano, "Topology Driven Methods for Complex Systems an alternative approach to Machine Learning. Theory and some Applications" IDSIA-Dalle Molle Institute for Artificial Intelligence

2019 November, Milan, "Interdisciplinary: an obstacles course rising" Symposium in honour of G Mauri

2019 September, Como, "Present and future of Theoretical Computer Science (not only) in Italy"
     Panel-ICTCS

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 "Tutorial on Topological data analysis: 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. "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 Tesei)

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

LIST OF SELECTED PUBLICATIONS

1. D. Marchei, E. Merelli: RNA secondary structure factorization in prime tangles BMC Bioinformatics, 23, 345 (2022)

2. M. Quadrini, L. Tesei, E. Merelli: Automatic generation of pseudoknotted RNAs taxonomy. BMC Bioinformatics, 23, 575 (2022)

3. S. Maestri, E. Merelli, M. Pettini: Agent-based models for detecting the driving forces of biomolecular interactions. Scientific Reports, 12(1), 1878 (2022)

4. M. Belenchia, G. Rocchetti, S. Maestri, A. Cimadamore, R. Montironi, M. Santoni, E. Merelli: Agent-Based Learning Model for the Obesity Paradox in RCC. Frontiers in Bioengineering and Biotechnology, 9, 642760 (2021)

5. A. Mancini, L. Vito, E. Marcelli, S. Pucciarelli, E. Merelli: Machine learning models predicting multidrug-resistant urinary tract infections using dsaaS. BMC Bioinformatics, 21, 347 (2020)

6. M. Piangerelli, S. Maestri, E. Merelli: Visualising 2-simplex formation in metabolic reactions. Journal of Molecular Graphics and Modelling, vol. 97 (2020)

7. M. Quadrini, L. Tesei, E. Merelli: ASPRAlign: A tool for the alignment of RNA secondary structures with arbitrary pseudoknots. Bioinformatics, 36(11), pp. 3578–3579 (2020)

8. M. Quadrini, E. Merelli, R. Piergallini: Label core for understanding RNA structure. LNCS-LNBI, vol. 12313 (2020)

9. S. Maestri, E. Merelli: Algebraic characterisation of non-coding RNA. LNCS-LNBI, vol 12313 (2020)

10. S. Maestri, E. Merelli: Process calculi may reveal the equivalence lying at the heart of RNA and proteins. Scientific Reports, vol. 9 n. 1 (2019)

11. E. Merelli, A. Wasilewska: Topological interpretation of interactive computation. LNCS, vol. 11500 (2019)

12. M. Quadrini, L. Tesei, E. Merelli: An algebraic languages fo RNA structure comparison. BMC Bioinformatics, vol. 20, n. 161 (2019)

13. M. Piangerelli, L. Tesei, E. Merelli: A Persistent Entropy Automaton for the Dow Jones Stock Market. LNCS vol. 11761 (2019)

14. M. Quadrini, E. Merelli, R. Piergallini: Loop grammars to identify RNA structural patterns. Proc. of BIOINFORMATICS (2019)

15. L. Bettini, E. Merelli, F. Tiezzi: X-Klaim is back. LNCS vol. 11665 (2019)

16. M. Piangerelli, M. Rucco, L. Tesei, E. Merelli: Topological classifier for detecting the emergence of epileptic seizures. BMC Research Notes, vol. 11(1) (2018)

17. M. Quadrini, E. Merelli: Loop-loop interaction metrics on RNA secondary structures with pseudoknots. BIOINFORMATICS (2018)

18. J. H. Johnson, L. Tesei, M. Piangerelli, E. Merelli, R. Paci, N. Stojanovic, P. Leitão, J. Barbosa, M. Amador: Big Data: Business, Technology, Education, and Science. Ubiquity vol. 2 n. 1 (2018)

19. 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)

20. M. Rucco, R. González-Díaz, M. J. Jiménez, 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)

21. 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)

22. 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)

23. 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)

24. 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)

25. E. Merelli, N. Paoletti, L. Tesei: Adaptability checking in complex systems. Science of Computing Programming, vol.115-116, (2016)

26. Rucco Matteo, Castiglione Filippo, Merelli Emanuela, Pettini Marco. Characterisation of the Idiotypic Immune Network Through Persistent Entropy. In: Proceedings of ECCS 2014. p. 117-128, Springer (2016)

27. E. Merelli, M. Rucco, P. Sloot and L. Tesei: Topological Characterization of Complex Systems: Using Persistent Entropy. Entropy, 17(10), (2015)

28. E. Merelli, I. Petre: From Computer Science to Biology and Back. Theor. Comput. Sci. vol.608, (2015)

29. E. Merelli, M. Pettini, M. Rasetti: Topology driven modeling: the IS metaphor, *Natural Computing Journal, NACO*, 14(3), Springer, (2015)

30. P. Giannini, E. Merelli, A. Troina: Interactions between Computer Science and Biology. Theor. Comput. Sci. vol.587, (2015)

31. 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)

32. 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

33. E. Merelli, M. Rasetti: *Non locality, topology, formal languages: new global tools to handle large data sets, Procedia Computer Science*, vol.18, (2013)

34. 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)

35. P. Liò, N. Paoletti, M. A. Moni, K. Atwell, E. Merelli, M. Viceconti: Modelling osteomyelitis. BMC Bioinformatics 13(S-14): S12 (2012)

36. 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)

37. P. Liò, E. Merelli, N. Paoletti: Disease processes as hybrid dynamical systems. *Int. Workshop on Hybrid Systems.* Newcastle, (2012)

38. 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)

39. 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)

40. R. Alfieri, E. Bartocci, E. Merelli, L. Milanesi: Modeling the cell cycle: From deterministic models to hybrid systems. *Journal of Biosystems* 105(1), 2011

41. 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)

42. P. Liò, E. Merelli, N. Paoletti, M. Viceconti: A Combined Process Algebraic and Stochastic Approach to Bone Remodeling. Electr. Notes Theor. Comput. Sci. vol.277, (2011)

43. E. Bartocci, F. Corradini, E. Merelli, L. Tesei: Detecting Synchronisation of Biological Oscillators by by Model Checking. *Theoretical Computer Science* 411(20), (2010)

44. 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)

45. 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)

46. 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)*, Cancum, Messico, (2010)

47. 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)

48. 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)

49. 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)

50. 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)

51. 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)

52. E. Bartocci, F. Corradini, E. Merelli, L. Tesei. Model Checking Biological Oscillators. *Electronic Notes in Theoretical Computer Science* 229(1), (2009)

53. N. Cannata, F. Corradini, E. Merelli, F. Piersigilli, L. Vito Towards Bioinformatics Resourceomes. *Biomedical Data and Applications* 13-36, (2009)

54. N. Cannata, F. Corradini, E. Merelli. Multiagent modelling and simulation of carbohydrate oxidation *International Journal of Modelling, Identification and Control* (IJMIC), 1(3), (2008)

55. 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)

56. E. Merelli et al. Agents in Bioinformatics, Computational and Systems Biology. *Briefing in Bioinformatics*, 8(1), (2007)

57. E. Merelli, M. Young. Validating MAS with mutation. *International Journal of Multiagent and Grid Systems* 3(2), (2007)

58. 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)

59. 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)

60. Bartocci, E., Cacciagrano, D., Cannata, N., (...), Milanesi, L., Romano, P.. An agent-based multi-layer architecture for bioinformatics grids *EEE Transactions on Nanobioscience* 6(2), (2007)

61. F. Corradini, E. Merelli: Hermes: Agent-Based Middleware for Mobile Computing. *SFM 2005* LNCS Vol. 3465. 234-270, (2005)

62. 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)

63. N. Cannata, E. Merelli, R.B. Altman. Time to organize the Bioinformatics Resourceome. *PloS Computational Biology*, Vol. 1, Num. 7, (2005)

64. M. Luck and E. Merelli. Agents in Bioinformatics. *The Knowledge Engineering Review*, vol. 20, Num. 2 117-125, Cambridge University Press, (2005)

65. 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)

66. 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)

67. 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)

68. F. Caneschi, E. Merelli. An architecture for an asn.1 encoder/decoder. *Computer Networks, North Holland*, vol.14, (1987)

Camerino, October 2023   Prof. Emanuela Merelli