CURRICULUM VITAE

VINCENZO MANCA

- Affiliation: Dipartimento di Informatica, Università di Verona
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Introduction

Vincenzo Manca graduated in Mathematics in 1971 at the University di Pisa, where he studied having as mentors Alfonso Caracciolo di Forino (Institute of Information Processing, CNR Pisa, who projected the first Italian electronic computer) and Ennio De Giorgi (*Scuola Normale Superiore - Pisa*, the most famous Italian mathematician of '900). He became research associate in 1980 and was associate professor at the universities of Udine (1989-1992) and Pisa (1992-2002). Since 2002 he is Full Professor in Computer Science at the University of Verona. His research covers a wide class of topics from discrete mathematics to the algorithmic models of biological systems. Currently his research is focused on Bioinformatics and Computational Genomics. He is author of 190 scientific publications on international journals and series (Bioinformatics, BMC Genomics, BioSystems, Molecular BioSystems, Bioinformatics, American J.of Bioinformatics and Computational Biology, Journal of Bioinformatics and Proteomics Review, Mathematical BioSciences, Natural Computing, Theoretical Computer Science, J. of Logic and Algebraic Programming, Int. J. of Found. of Comp. Sci., Fundamenta Informaticae, J. of Symbolic logic, Oxford Handbooks, Springer Series). His book *Infobiotics: information in biotic systems* (400 pp. Springer 2013) [18] summarizes his research of previous 12 years. He was editor/referee of many international journals, and member of the Program/Steering Committee for 30 international conferences. He was visiting/invited professor in many universities and international conferences, and was PI of several research projects (FIRB, PRIN), cooperating with many international research groups (EU, USA, Japan). He advised 8 Ph.D students and tutored about 50 graduate students. He was president of the Bachelor Courses in Informatics and Bioinformatics at the University of Verona, founder of the second one in 2006, and in 2016 of the Master Course in *Medical Bioinformatics* (LM18, the University of Verona). He is the president of CBMC (Center for BioMedical Computing) of the same university. He was promoter, and member of the Scientific Committee, of the National

Date: October 2017.

Laboratory of Bioinformatics, *Infolife* of CINI (Informatics National Consortium Italian Universities), which coordinates 40 nodes of academic groups spread in Italy. In March 2011 the Journal *Natural Computing* (Springer) dedicated to him a special issue in honor to his 60 birthday.

Research Statement
In the last 15 years, my research was mainly devoted to cell dynamics and genomes. The main inspiration was the idea that algorithms, computations, and information theory could be precious instruments supporting the experimental biological research, in order to reveal deep logics underlying life phenomena. Computer is not only important in processing biological data (of course, this is essential). In fact, Computer Science and Discrete Mathematics are conceptual framework where develop new interpretation keys of life. The most evident example of this claim is given by genome sequencing. Abstractly, it is essentially a problem of string reconstruction, starting from some string fragments. Specific cases of this problem was studied, with motivations coming from mathematical theories, by the great mathematicians Arthur Cayley (in 1949) and Nicolaas Govert de Bruijn (in 1946). Life is based on molecules supporting information, and this is the reason of the intrinsic connection between calculus and life. I tried to support this statement in my recent book *Infobiotics* [22], and I am deeply convinced that, along this direction, new comprehension will be gained in the next future.

Research Fields

- Computational Genomics (2009-2015)
- Computational Systems Biology (2002-2015)
- Bioinformatics (2002-2015)
- Natural Computing (2002-2014)
- Formal Languages (1990-2008)
- Discrete Mathematics (1990 -2008)
- Algorithms and Computability (1980-1998)
- Mathematical Logic (1972-2000)

Publications: 190. (List at end of CV, orcid.org/0000-0002-1304-0277, https://iris.univr.it/)
International Journals: 61, Books: 21
Chapters in books: 54, Proceedings of Conferences: 52, Encyclopedia Items: 2.

Research Projects

- PRIN 2004 Principal Investigator: Symbolic Models of cellular dynamics (24 months)
- FIRB 2003 Principal Investigator: Biomolecular Algorithms for NP complete problems (36 months)

Journal Editorial Boards and International Program Committees

(1) J. of Bioinformatics and Proteomics Review (since 2014)

(2) Triangle: Languages Mathematical Approaches (since 2012)
(3) FBTC 2008 (Iceland) PC member
(4) COMPMOD 2009 (the Netherlands) PC member
(5) MeCBIC 2009 (Italia) PC member
(6) AFLAS 2008 (China) PC member
(7) UC 2007 (Canada) PC member
(8) UC 2009 (Portugal) PC member
(9) NICSO 2008 (Spain) PC member
(10) NICSO 2010 (Spain) PC member
(11) WIVACE 2009 (Italy) PC member
(12) FBTC 2007 (Portugal) PC member
(13) ForLing (Spain) PC member
(14) IWNC 2007 (Japan) PC member
(15) IWNAC 2009 (Spain) PC member
(16) WMC06 2005 (Austria) PC member
(17) WMC07 2006 (The Netherlands) PC member
(18) WMC08 2007(Greece) PC member
(19) HPCC-08 (China): PC member (China)
(20) Steering Committee of Membrane Computing Conference (2010-2015)
(21) MC11 2010 (Germany) PC member
(22) MC12 2011(France) PC member
(23) MC13 2012 (Hungary) PC member
(24) MC14 2013: (Moldova) PC member
(25) ACM 2012 (China) PC member
(26) IWINAC 2007 (Spain) PC member
(27) IWINAC 2009 (Spain) PC member
(28) IWINAC 2010 (Spain) PC member
(29) IWINAC 2011 (Spain) PC member
(30) TPNC 2012 (Spain) PC member
(31) IWNC 2012 (Japan) PC member
(32) IWNC 2013 (Japan) PC member
(33) CIBB & PRIBB 2013 (France) PC member
(34) CMC16 2015 (Spain) PC member
(35) CINI (National Consortium of Italian Universities for Informatics, Scientific Committee of National Laboratory *Infolife*, since 2013)
(36) UCNC 2017 (Unconventional Computation and Natural Computation 2017, June 5-9, 2017), University of Arkansas

Invited Lectures and Courses

(1) MFCS (Mathematical Foundation of C.S.)1998, Brno (DNA Computing)
(2) Computing with Biomolecules, Mangalia (Black Sea) 1997
(3) Membrane Computing Conferences (2002, 2004, 2006, 2009, 2013, 2015)

(4) Universities of Beijng and Whuan (2006)
(5) Università di Catania (2007)
(6) Univertitat Rovira i Virgili, Tarragona (2007)
(7) Universities of Kyoto, Nagoya (2007)
(8) Univertidad de Sevilla (2008)
(9) Centro Internazionale di Bertinoro (2008)
(10) Università di Pisa (2008, 2009)
(11) Università Federico II di Napoli (2009)
(12) Univesidad Complutense de Madrid (2010)
(13) Scuola Internazionale di Lipari (2010)
(14) University Eötvös Loránd of Budapest (2013)
(15) Università di Roma III (2013)
(16) CNR - AICA Didamatica 2013, Pisa (2013)
(17) IIT (Italian Institute of Technology) Genova (2013)
(18) CMC16 (Membrane Computing Conference), Valencia (2015)

Indexes and Honors

Erdös Number: **3**
(Erdös → Solomon Marcus → Gheorghe Păun → Vincenzo Manca. Arrow means coauthorship. Paul Erdös is the most famous mathematician of last century. This index is used by mathematicians as a measure of closeness to research excellence).

H-index: ≥ **23** (Microsoft Academic Search), ≥ **21** (Google scholar), ≥ **13** (Scopus). They are not updated (Scopus lacks more than 50% of publications).

Excellence Diploma of Decennial Membrane Computing workshop:
"awarded to V.M., a forerunner of Membrane Computing, the creator of MP systems area, the most original and systematic framework for biological applications in terms of membrane computing" (The PC Chairman Gheorghe Păun, WMC10, August 2009)

Dedicated Special Issue
Natural Computing, Volume 10, Number 1, March 2011. Part I: Special Issue "Modelling Bioprocesses" "Dedicated to Prof. V. Manca on the Occasion of his 60th Birthday (Foreword by Roberto Barbuti, Giuditta Franco and Gheorghe Păun)". Guest Editors: Roberto Barbuti, G. Franco, Gheorghe Paun, Jon Timmis, Paul S. Andrews, Susan Stepney and Russell Deaton.

Global Medical Discovery
Key Scientific Article Contributing to excellence in biomedical research, January 11, 2015.
https://globalmedicaldiscovery.com/category/key-scientific-articles/page/2/
The paper is [9], where the theory of MP grammars, introduced by V.M. in 2004 and developed by his research group in 10 years, was applied to the analysis of gene expression in breast cancer cells, by revealing an unknown regulatory mechanism.

Academic Committees at the University of Verona

(1) President of the Bachelor Degree in Bioinformatics (2007-2010)

(2) President of the Bachelor Degree in Informatics (2008-2010)
(3) Scientific Committee of "Biblioteca Meneghetti"(2003-2010)
(4) Faculty Representative in the Project "Tandem Università-Scuola" (2003-2006)
(5) Scientific Committee of the Center of BioMedical Computing (2006-2012)
(6) President of the Sci. Comm. of the Center of BioMedical Computing (since 2012)

Scientific Evaluation

(1) 10 PhD Evaluation Boards (national and international)
(2) Referee of 4 national and international projects (Pisa, Sevilla, Macao, Leiden)
(3) Referee for international journals, among them: Theoretical Computer Science, Fundamenta Informaticae, Mathematical Review, Applied and computational mathematics, Discrete Mathematics, Natural Computing, Systems Bioinformatics, BMC Genomics.

Teaching at the University of Verona

(1) Informational Methods - Bachelor in Bioinformatics (2006-2016)
(2) Discrete Biological Models - Bachelor in Bioinformatics (2015-2016)
(3) Natural Computing - Master Bioinformatics and Medical Biotech. (2002-2014)
(4) Information Theory - Master in Computer Sci. and Eng. (2002-2009)
(5) Unconventional Computing - Master in Computer Sci. and Eng. (2002-2008)
(6) Infobiotics - Master in Biotechnology (2007-2009)
(7) Essentials of Informatics - Master in Computer Science (2002-2005)

Mentor of 50 Master Theses, 8 Phd Theses, now researchers with permanent positions in Research Centers.

Publications

[1] **Manca, V.** A Note on Archimedes' The Sand Reckoner. *Cornell University Library ArXiv.org*, 2018.
[2] **Manca, V.** *Topics in Discrete Mathematics*. To appear, 2018.
[3] **Manca, V.** *Principi Informazionali*. To appear, 2018.
[4] **Manca, V.** A Brief Philosophical Note on Information. In *Towards Integrative Machine Learning and Knowledge Extraction*. LNCS 10344, Springer, 2017.
[5] **Manca, V.** Multiset generalization of balanced chemical reactions. *Bulletin of the International Membrane Computing Society, I M C S*, II:157–158, 2016.
[6] **Manca, V.** The Infinite Egg. In *Liber Amicorum For G. Rozenberg*, pages 90–93. Turku Center for Computer Science, 2017.
[7] Franco G. and **Manca, V.** Case study: Decoding genomic information. In S. Stepney and M. Amos, editors, *Computational Matter*. Springer, 2017.
[8] **Manca, V.** The principles of informational genomics. *Theoretical Computer Science C*, 2017.
[9] **Manca, V.** An informational proof of H-theorem. *OALib Journal (Modern Physics)*, 2017.
[10] **Manca, V.** Mathematical laws of genomes. *Journal of Bioinformatics and Proteomics Review*, 3(1), 1-2, 2016.
[11] **Manca, V.** Grammars for Discrete Dynamics. In Andreas Holzinger, editor, *Machine Learning for Health Informatics - LNAI 9605*, pages 37–58. Springer, 2016.
[12] V. Bonnici and **Manca, V.** Informational laws of genome structures. *Scientific Reports*, 6, 28840, 2016.

[13] **Manca, V.** Research lines in infogenomics. *Journal of Bioinformatics and Proteomics Review*, 1(1), 1-4, 2015.

[14] V. Bonnici and **Manca, V.** Recurrence distance distributions in computational genomics. *Amer. J. Bioinformatics & Computational Biology*, Vol. 3, N. 1:5 – 23, 2015.

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[17] R. H. Guiraldelli-Gracini and **Manca, V.** Automatic translation of mp+v systems to register machines. In M. Gheorghe and I. Petre, editors, *Membrane Computing CMC16*. LNCS 9504, Springer, 2015.

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[19] A. Castellini, D. Paltrinieri, and **Manca, V.** Mp-geneticsynth: Inferring biological network regulations from time series. *Bioinformatics*, 31:785–787, 2015.

[20] L. Marchetti and **Manca, V.** Mptheory java library: a multi–platform java library for systems biology based on the metabolic p theory. *Bioinformatics*, 31:1328–1330, 2015.

[21] V. Bonnici and **Manca, V.** Infogenomics tools: a computational suite for informational analysis of genomes. *Journal of Bioinformatics and Proteomics Review*, 1:7–14, 2015.

[22] **Manca, V.** On the lexicographic representation of numbers. *Cornell University Library ArXiv.org*, pages 1–15, 2015.

[23] A. Bollig-Fischer, L. Marchetti, C. Mitrea, J. Wu, A. Kruger, **Manca, V.**, and S. Draghici. Modeling time-dependent transcription effects of her2 oncogene and discovery of a role for e2f2 in breast cancer cell-matrix adhesion. *BIOINFORMATICS*, 30:3036–3043, 2014.

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[36] **Manca, V.** and L. Marchetti. Solving dynamical inverse problems by means of metabolic p systems. *BioSystems*, 109:78–86, 2012.
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[38] R. Lombardo and **Manca, V.** Milieu-m: Visual manipulation and programming for multi-membranes. *International Journal of Information Theories and Applications*, 19:319–327, 2012.
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[52] **Manca, V.** and L. Marchetti. Metabolic approximation of real periodical functions. *J. of Logic and Algebraic Programming*, 79:363–373, 2010.
[53] **Manca, V.**, J. Suzuki, and Y. Suzuki. *Language as a Complex System:*, chapter An XML Representation of Basic Japanese Grammar, pages 215–244. Cambridge Scholars Publishing, 2010.
[54] **Manca, V.** and L. Marchetti. *Membrane Computing CMC11*, volume 6501, chapter Golbeter's mitotic oscillator entirely modeled by MP systems, pages 273–284. Springer Verlag, 2010.
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[57] A. Castellini, **Manca, V.**, and Y. Suzuki. *Membrane Computing, WMC 2009*, volume LNCS 5957, chapter Metabolic P system flux regulation by artificial neural networks, pages 196–209. Springer, 2010.
[58] G. Franco, S. Lampis, G. Vallini, and **Manca, V.** Toward an experimental evidence of genetic drift. In *Proceedings of the 16th Int. Conf. on DNA Computing and Molecular Programming - DNA16*, pages 204–205, 14–17 June 2010.

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[67] **Manca, V.** *Algorithmic Bioprocesses*, chapter Log-Gain Principles for Metabolic P Systems, pages 585–605. Springer Verlag, 2009.

[68] A. Castellini and **Manca, V.** *WMC9 2008*, volume LNCS 5391, chapter MetaPlab: A Computational Framework for Metabolic P Systems, pages 157–168. Springer Verlag, 2009.

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[81] **Manca, V.**, G. Franco, S. Lampis, and G. Vallini. The phenomenon of sampling and growing in biopopulations. In *DNA 14: Proceedings of the 14th International Meeting on DNA Computing*, pages 187–188, Opava – CZE, June 2-6, 2008. Silesian University.

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[87] L. Bianco, **Manca, V.**, L. Marchetti, and M. Petterlini. Psim: a simulator for biomolecular dynamics based on p systems. In *Evolutionary Computation*, volume 2007 IEEE (CEC 2007), pages 883–887. IEEE, September 25-28 2007.

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[93] P. Bottoni, A. Labella, **Manca, V.**, and V. Mitrana. Superposition based on watson-crick-like complementarity. *Theory of Computing Systems*, 39:503–524, 2006.

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[96] **Manca, V.** *Membrane Computing*, volume LNCS 4361, chapter MP Systems Approaches to Biochemical Dynamics: Biological Rhythms and Oscillations, pages 86–99. Springer, Berlin, 2006.

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