CURRICULUM VITAE

VINCENZO MANCA

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Introduzione

Vincenzo Manca si è laureato in Matematica presso l'Università di Pisa nel 1971, dove ha studiato e sotto al guida di Alfonso Caracciolo di Forino (Istituto di Elaborazione dell'Informazione del CNR, dove Caracciolo ha diretto la progettazione logica della CEP, primo calcolatore italiano) e di Ennio De Giorgi (Scuola Normale Superiore, uno dei più grandi matematici italiani del Novecento). È diventato Ricercatore Universitario nel 1980 e professore associato (INF01) nel 1989, insegnando presso le Univerità di Udine e di Pisa. La sua ricerca ha coperto vari temi di matematica discreta e informatica teorica. Dal 2002 è Professore Ordinario presso l'Università di Verona, dove si occupa di modelli matematici di sistemi biologici e di genomica computazionale. Ha scritto diversi libri e articoli scientifici su riviste scientifiche internazionali (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). Il suo libro "Infobiotics" (Springer, 400 pagine, 2013) riassume la sua ricerca dei precedenti 12 anni. È stato visiting/invited professor in molte istituzioni internazionali (EU, USA, Cina, Giappone) e membro del Program/Steering Committee di circa 30 conferenze internazionali. È stato editor/referee di riviste internazionali, e ha diretto progetti di ricerca nazionali (FIRB, PRIN). Nel 2006 ha fondato un Corso di Laurea di primo livello in Bioinformatica e nel 2016 una laurea magistrale in Medical Bioinformatics (entrambi nella classe INF01, esempio unico in Italia), presso l'Università di Verona. È stato fondatore e codirettore del Laboratorio Nazionale CINI Infolife, che riunisce circa 40 nodi italiani di centri accademici di ricerca in Bioinformatica. È stato fondatore ed è attualmente direttore del Centro di BioMedicina Computazionale presso l'Ateneo di Verona.

Date: October 2017.

Ha infine fondato il Museo di Storia dell'Informatica di cui è responsabile presso il Dipartimento di Informatica di Verona. Nel Marzo 2011 la rivista Natural Computing gli ha dedicato un numero speciale per i suoi 60 anni. Attualmente dirige il Gruppo di Ricerca in "Bioinformatica e Calcolo Naturale" (10 ricercatori afferenti) presso il Dipartimento di Informatica dell'Università di Verona.

Manifesto di Ricerca
Negli ultimi 15 anni la mia ricerca si è focalizzata sulle dinamiche cellulari e sulla analisi di genomi con metodi informazionali e computazionali. La convinzione che ha sostenuto queste ricerche si basa sul riconoscere un rapporto strettissimo tra informazione e vita ai vari livelli di organizzazione dei processi metabolici e replicativi cellulari. Il ruolo del calcolo nell'analisi dei processi vitali non è solamente quello, seppur importante, di elaborare i dati che provengono dai laboratori biologici, ma anche quello di scoprire principi intrinseci ai calcoli naturali che la cellula svolge per realizzazione le sue funzionalità primarie e le sue strategie evolutive che determinano le forme viventi. La vita è informazione rappresentata ed elaborata per mezzo di molecole e questa semplice constatazione richiede una profonda prospettiva informazionale da integrare con quelle condotte dai biochimici a dai biologi molecolari. Sono convinto che lungo questa linea di ricerca, che comincia ad emergere in vari centri di ricerca, si possano ottenere chiavi di comprensione del tutto nuove nello studio delle funzioni e delle disfunzioni cellulari.

Campi di Ricerca (indicati in Inglese)

- 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)

Publicazioni: 190. (Lista alla fine, orcid.org/0000-0002-1304-0277, https://iris.univr.it/)
Riviste Internazionali: 61, Libri: 21
Capitoli in libri: 54, Atti di Conferenze: 52, Voci Enciclopediche: 2.

Progetti di Ricerca

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

Comitati di Programma di Conferenze Internazionali

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

Corsi e Conferenze su invito

(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)

Indici e Riconoscimenti

Erdös Number: **3**
(Erdös → Solomon Marcus → Gheorghe Păun → Vincenzo Manca. Arrow means coauthorship. Paul Erdös è uno dei più importanti matematici del '900. L'indice indica la distanza da Erdös come co-autore di articoli matematici).

H-index: $\geq$ **23** (Microsoft Academic Search), $\geq$ **21** (Google scholar), $\geq$ **13** (Scopus). (Scopus manca di più del 50% di pubblicazioni).

Excellence Diploma of Decennale di "Membrane Computing":
"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" (Gheorghe Păun, Presidente della Conferenza WMC10, 2009)

Numero Speciale dedicato a V. Manca
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/
Il lavoro [9] usa le MP grammatiche, introdotte da V.M. nel 2004, nella analisi delle espressioni genetiche permettendo la scoperta di un meccanismo sconosciuto nella regolazione associata ad un tipo di tumore al seno.

Comitati di appartenenza dell'Università di Verona

(1) Presidente del Corso di Laurea in Bioinformatica (2007-2010)
(2) Presidente del Corso di Laurea in Informatica (2008-2010)

(3) Comitato Scientifico “Biblioteca Meneghetti”(2003-2010)
(4) Rappresentante di Facoltà del Progetto“Tandem Università-Scuola” (2003-2006)
(5) Presidente del Centro di BioMedicina Computazionale (dal 2012)

Comitati di valutazione scientifica

(1) 10 “PhD Evaluation Boards”
(2) “Referee” di 4 progetti internazionali (Pisa, Sevilla, Macao, Leiden)
(3) “Referee” per le riviste scientifiche: Theoretical Computer Science, Fundamenta Informaticae, Mathematical Review, Applied and computational mathematics, Discrete Mathematics, Natural Computing, Systems Bioinformatics, BMC Genomics.

Insegnamenti presso l’Università di Verona

(1) Metodi Informazionali - Bioinformatica (2006-2016)
(2) Modelli Biologici Discreti - Bioinformatica (2015-2016)
(3) Calcolo Naturale - Magistrali di Informatica-Ingegneria Informatica e “Medical Bioinformatics” (2002-2014)
(4) Teoria dell’Informazione - Magistrale di Informatica-Ingegneria Informatica (2002-2009)
(5) Calcolo non convenzionale - Magistrale di Informatica (2002-2008)
(6) Infobiotica - Magistrale in Biotecnologie (2007-2009)
(7) Informatica di Base - Magistrale di Informatica (2002-2005)

Relatore di 50 Tesi Magistrali, 8 Tesi di Dottorato (ora ricercatori con posizioni permanenti in Centri di Ricerca).

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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[16] **Manca, V.** Information theory in genome analysis. In M. Gheorghe and I. Petre, editors, *Membrane Computing, CMC16*, pages 1–16. LNCS 9504, Springer, 2015.

[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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