

**Procedura valutativa per la copertura di n. 1 posto di Professore Universitario di prima fascia per il Settore concorsuale 09/G2– Settore scientifico disciplinare ING-INF/06 presso il Dipartimento di Ingegneria informatica, automatica e gestionale “Antonio Ruberti” – Facoltà di Ingegneria dell’informazione, informatica e statistica – codice concorso 2021POR071**

Decreto Rettrice Sapienza, Università di Roma n. 3298/2021 del 10.12.2021, codice concorso 2021POR071

**LORENZO FARINA**  
Curriculum Vitae per la pubblicazione

Place: Rome  
Date: 24-12-2021

**Part I – General Information**

Full Name	Lorenzo Farina
Spoken Languages	Italian, English

**Part II – Education**

Type	Year	Institution	Notes
University graduation	1992	Sapienza, University of Rome	Master degree (5 years) in Electronic Engineering, bio-engineering curriculum, with the score of 110/110 <i>cum laude</i>
PhD	1998	Sapienza, University of Rome	PhD in Systems Engineering

**Part III – Appointments**

IIIA – Academic Appointments

Start	End	Institution	Position
2013	present	Sapienza, University of Rome	Associate Professor, ING-INF/06
2012	2023	Ministry of Education, University and Research (Italy)	Italian National scientific habilitation as full Professor in ING-INF/04
2000	2013	Sapienza, University of Rome	Associate Professor, ING-INF/04
1996	2000	Sapienza, University of Rome	Assistant Professor (ricercatore), ING-INF/04

### IIIB – Other Appointments

Start	End	Institution	Position
2-1997	3-1997	Research School of Information Sciences and Engineering, Australian National University, Canberra, Australia	Departmental visitor
2-1995	8-1995	Tecnobiomedica S.p.A.	Technical manager for a project of remote monitoring of high risk cardiological patients
9-1994	12-1994	UNICEF, East and Southern Africa Regional Office	Consultant for emergency programs
9-1993	8-1994	National Research Council (CNR)	Fellowship
12-1992	3-1993	Centro Interdipartimentale di Ricerca in Informatica Territoriale e Ambientale, Politecnico di Milano	Scientific consultant for mathematical modelling in ecology

### Part IV – Teaching Experience

#### IVA – Teaching duties

Year	Institution	SSD	Lecture/Course
2019-present	Sapienza University of Rome	ING-INF/06	Course on “Bioinformatics and Computational Medicine”, MSc in Statistical Sciences (9 CFU)
2021-present	Sapienza University of Rome	ING-INF/06	Course on “Computational System Biology”, BSc in Bioinformatics (6 CFU)
2018-2020	Sapienza University of Rome	ING-INF/06	Course on “Modelling and Simulation of Biomolecular Dynamical Systems”, BSc in Bioinformatics (6 CFU)
2018-2019	Sapienza University of Rome	ING-INF/06	Course on “Bioengineering for Genomics”, MSc in Biomedical Engineering (9 CFU)
2015-2019	Sapienza University of Rome	ING-INF/06	Course on “Models of Biological Systems”, MSc in Biomedical Engineering (6 CFU)
2015-2017	Sapienza University of Rome	ING-INF/06	Course on “Bioinformatics”, MSc in Biomedical Engineering (3 CFU)
2015-2017	Sapienza University of Rome	ING-INF/06	Course on “Computational Methods for Molecular Biology”, MSc in Biomedical Engineering (6 CFU)
2003 - 2014	Sapienza University of Rome	ING-INF/04	Course on “Foundations of Automatic Control”, MSc in Management Engineering (6 CFU)
2002-2014	Sapienza University of Rome	ING-INF/04	Course on “Dynamic Modelling for Management Engineering”, MSc in Management Engineering (6 CFU)
2002	Sapienza University of Rome	ING-INF/04	Course on “Systems Theory”, MSc in Management Engineering

1999-2001	Sapienza University of Rome	ING-INF/04	Course on “Modelling and Simulation”, MSc in Computer Science Engineering
1999-2001	Sapienza University of Rome	ING-INF/04	Course on “Modelling of Environmental Systems” BSc in Environmental Engineering
1995	Sapienza, University of Rome at Latina	ING-INF/04	Course on “Automatic Control”
1994	Sapienza, University of Rome at Latina	ING-INF/04	Course on “Automatic Control”
1994	Centro Teoria dei Sistemi (CNR), Milano	ING-INF/04	Course on “Positive linear systems”

#### IVB – Invited presentations (seminars, lectures and courses)

Year	Institution / Workshop / Conference	Lecture/Course/Seminar
2021	Master in Immuno Oncology, Sapienza University / Roche Foundation for personalized medicine, October 21 <sup>st</sup>	The network language for precision medicine
2021	Master in Immuno Oncology, Sapienza University / Roche Foundation for personalized medicine, February 18 <sup>th</sup>	Network medicine and immune oncology: a new frontier
2020	Precision Medicine: from tumour biology to clinical trials, December 3 <sup>rd</sup> , Fondazione Policlinico Gemelli	Network-based approaches: a paradigm shift in medicine
2020	STITCH Sapienza Information Based Technology Innovation Center for Health, October 20 <sup>th</sup>	Precision medicine: what barriers remain for multidisciplinary
2020	STITCH Sapienza Information Based Technology Innovation Center for Health, March 4 <sup>th</sup>	Network medicine adventures: a computational survival kit for physicians
2019	Top Seminar di oncologia “Breathing Ideas” del 28-29 Giugno 2019, Boehringer Ingelheim, Italia	Seminar on “Artificial intelligence in oncology”
2019	Worshop on “From a modern to a trasformative medicine: a tribute to William Osler”, Sapienza University of Rome, May 16 <sup>th</sup> , 2019, Rome	Lecture on “The SWIM methodology - a network medicine approach to the identification of key genes: applications in oncology”
2019	Sapienza Information-Based Technology InnovaTion Center for Health	Seminar on “Introduction to network medicine”
2018	Sapienza/Harvard First International Conference on Network Medicine and Big Data: The Transformation of Medicine September 24-26, 2018, Rome, Italy	Lecture on “Key node roles’ in co-expression networks: from grapevine to cancer”
2018	“Santa Lucia” Foundation, Rome	Seminar on “Network medicine in a nutshell”

2018	3 <sup>rd</sup> SysBio School on Computational Biology, May 10 <sup>th</sup> , 2018	Plenary lecture on “The emerging paradigm of network medicine”
2017	Accademia Nazionale dei Lincei, Palazzina dell’auditorio. Roma, 31 Maggio 2017	Seminar on “Heuristics and metaphors in bioinformatics”
2014	EPIGEN workshop - Progetto Bandiera Epigenomica (CNR), Mondello 9-12 Settembre 2014	Lecture on “ <i>In-vivo</i> genome wide identification of messengers stability from time-series expression data”
2014	Sapienza School for Advanced Studies	Seminar on “Complex biological networks”
2013	Sapienza School for Advanced Studies	Seminar on “Modelling issues in the post-genomic era”
2013	Ing Seminar, Scienza e tecnologia del XXI secolo, Campus Biomedico – Centro Convegni Casalmentano, Roma, 10-13 Ottobre 2013	Lecture on “Biological models and mathematical models”
2012	Workshop on Embodied Intelligence: an epistemological outline, IEEE International Conference on Biomedical Robotics and Mechatronics, June 24-27, Rome, 2012	Lecture on “What we talk about when we talk about feedback”
2010	Yeast Model Convention, September 22-25 2010, Rome	Lecture on “Dynamics of gene expression in post-transcriptional regulation”
2009	Workshop on “Network pharmacology”, Fondazione Sigma-tau and Istituto Superiore di Sanità	Lecture on “Links, flows and perturbations: systemic responses of biological networks”
2009	Center for Biological Systems Analysis, February 4, 2009, Freiburg (Germany)	Seminar on “Behavioral dynamic modeling of fast responses: the E. coli SOS system as a case study”
2008	BiCi Workshop on Biological Networks: modeling, analysis and integration, 16-20 September, Bertinoro, 2008	Lecture on “Leads and lags: gene relationships beyond co-expression”
2007	Rome Oncogenomic Center, Regina Elena Cancer Institute	Seminar on “Knowledge engineering for systems biology”
2006	International School for Advanced Studies (SISSA), Trieste	Seminar on “Inferring gene networks from gene expression time series”
2006	University of L’Aquila	Seminar on “The systems biology approach to molecular biology”
2005	University of Padua	Seminar on “Computational challenges in the post-genomic era”
2005	Workshop on “Systems biology: the state of art”, PhD program in Pasteurian Sciences, October 24 <sup>th</sup> , 2005	Lecture on “Gene regulation, a dynamic perspective”

2004	BCB 2004, Second Bertinoro Computational Biological Meeting, 12-19 June, 2004	Lecture on “Regulation of biochemical networks as interconnections: the behavioural approach.”
2004	Advanced course in Molecular Biotechnologies, Department of Genetics and Molecular Biology, Sapienza University of Rome	Lecture on “Structure and dynamics of the regulation systems in the post-genomic research”
2004	PhD program in Biophysics, Sapienza University of Roma, May 19 <sup>th</sup> , 2004	Lecture on “Dynamic models of gene-to-gene interactions”
2004	Workshop on “Complexity and Modeling of Biological Networks”, German Research Center for Biotechnology, Braunschweig, Germany, October 4-6-8, 2004	Lecture on “Tolerance and failure propagation analysis of metabolic networks”
2004	Hamilton Institute Workshop on Nonnegative Matrices: Theory and Applications, July 11th-14th 2004, Dublin	Lecture on “The positive side of filters”
2004	Graduate School in Systems and Control 2004 – 2005, Katholieke Universiteit Leuven, Belgium	Course on “Positive linear systems”
2002	AT&T Labs–Research, Middletown, NJ, USA	Lecture on “The design of fiber optic filters”
2002	Yale University, USA	Lecture on “Positive systems and the multi-disciplinary flavor of systems theory”

## Part V – Organization of Institutional Activities and Scientific Events

Year	Title
2019	Proposer and drafter (with Professors Antonella Polimeni, Stefania Basili, Franco Marinozzi and Zaccaria del Prete) appointed by the Dean of the Faculty of Information engineering, Computer Science and Statistics, of the MSc in Medicine and Surgery “HT), Sapienza, University of Rome.
2017	Proposer and drafter (with Giuseppe Macino – Faculty of Medicine and Rodolfo Negri – Faculty of Biological Sciences) of the BSc in Bioinformatics at Sapienza, University of Rome.
2003-2018	Co-chairman of the International Symposium on Positive Systems: Theory and Applications (POSTA), editions 2003 (first), 2016 and 2018 and Co-editor of the Conference proceedings published as Lecture Notes in Control and Information Sciences, Springer-Verlag, London
2002-2005	Scientific coordinator of “Incontri al Chiostro”, a series of public meetings on scientific issues, held at the “Chiostro” of the Faculty of Engineering, Sapienza University of Rome. Invited speakers: Domenico Parisi, Lucio Russo, Giorgio Israel, Piergiorgio Odifreddi, Ernesto Di Mauro, Marcello Cini, Maurizio Ferraris, Antonio Lepschy, Oliviero Stock.

**Part VI – Memberships of editorial board of journals, society, PhD Board of Teachers and awards**

Year	Title
2019-present	Member of the Board of Teachers, PhD in Network Oncology and Precision Medicine, Sapienza University of Rome. The relevance to the bioengineering field is presented in the official web page describing the aims of the PhD course: <a href="https://phd.uniroma1.it/web/NETWORK-ONCOLOGY-AND-PRECISION-MEDICINE_nD3663_IT.aspx">https://phd.uniroma1.it/web/NETWORK-ONCOLOGY-AND-PRECISION-MEDICINE_nD3663_IT.aspx</a> where it is explicitly reported the ssd ING-INF/06 and its role in the PhD program:  <i>“The Ph.D. board of teachers skill are in the field of oncology in cell and molecular biology, clinical diagnostics and therapy as well as in the field of medical statistics and bioengineering informatics.”</i>  <i>“il dottorato propone un collegio di docenti in cui sono rappresentate competenze oncologiche di biologia cellulare e molecolare, diagnostica clinica e terapia ed anche competenze relative alla statistica medica e alla bioingegneria informatica.”</i>
2021-present	Member of the Editorial Board of “Bioengineering”: <a href="https://www.mdpi.com/journal/bioengineering">https://www.mdpi.com/journal/bioengineering</a> , a journal indexed by Scopus, with Citescore: 6.1, Impact Score: 4.49 (expected IF: 4.486), and with a Scimago (SJR) ranking of Q2 for the category “Bioengineering”: <a href="https://www.scimagojr.com/journalsearch.php?q=21100886380&amp;tip=sid&amp;clean=0">https://www.scimagojr.com/journalsearch.php?q=21100886380&amp;tip=sid&amp;clean=0</a>
2021-present	Member of the Editorial Board of “Biology” – Bioinformatics section: <a href="https://www.mdpi.com/journal/biology">https://www.mdpi.com/journal/biology</a> a journal indexed by Scopus with an IF: 5.79, and with a JCR ranking of Q1 for the category “Agricultural and biological science”: <a href="https://www.scimagojr.com/journalsearch.php?q=21100316035&amp;tip=sid&amp;clean=0">https://www.scimagojr.com/journalsearch.php?q=21100316035&amp;tip=sid&amp;clean=0</a>
2018	Member of the Board awarding the doctorate <i>honoris causae</i> in “Innovative Biomedical Technologies in Clinical Medicine”, Sapienza University of Rome, to Prof. Joseph Loscalzo, Chair of the Department of Medicine, Brigham and Women Hospital, Harvard University
2019-present	Vice-president of the Board of Teachers, BSc in Bioinformatics, Sapienza University of Rome
2018	Member of the Board of Teachers, PhD in Innovative Biomedical Technologies in Clinical Medicine, Sapienza University of Rome
2018-present	Member of the Sapienza/Harvard “Network Medicine Consortium” <a href="https://www.network-medicine.org/">https://www.network-medicine.org/</a>
2018-2021	Research Associate, Institute for Systems Analysis and Computer Science (IASI - CNR)
2014	SysBio award 2014 for the best paper of the year, Plant Cell (2014), 26(12), pp. 4617-4635
2013-present	Member of the GNB (Gruppo Nazionale Bioingegneria)
2006-2009	Member of the Board of Teachers, PhD in Biophysics, Sapienza University of Rome
2005-2008	Jury member of the “Ruberti Prize”, IEEE Control Systems Society

2003 and 2016	Member of the scientific committee of the International Symposium on Positive Systems, Theory and Applications (POSTA).
2003-2004	Member of the Board of Teachers, PhD in Systems Engineering, Sapienza University of Rome
2001	“Guillemin-Cauer Best Paper Award” of the IEEE Transactions on Circuits and Systems II, with L. Benvenuti and B.D.O. Anderson

## Part VII - Books

Year	Title
2017	F. Cacace, L. Farina, R. Setola and A. Germani (Eds.), Positive Systems. Proceedings of the Fifth International Symposium on Positive Systems (POSTA 2016). Lecture Notes on Control and Information Sciences, v. 471, Springer-Verlag, Heidelberg (2017)
2008	L. Benvenuti, A. De Santis, L. Farina. <i>Sistemi dinamici per l'ingegneria dell'informazione ed economico-gestionale: modellistica, analisi e controllo</i> . McGraw Hill, 2008.
2003	L. Benvenuti, A. De Santis and L. Farina (Eds.), Positive Systems. Proceedings of the First Multidisciplinary Symposium on Positive Systems (POSTA 2003). Lecture Notes on Control and Information Sciences, v. 294, Springer-Verlag, Heidelberg
2000	L. Farina, S. Rinaldi, <i>Positive Linear Systems: Theory and Applications</i> , Pure and Applied Mathematics: A Wiley-Interscience Series of Text, Monographs, and Tracts, John Wiley & Sons, New York, 2000. <b>The book has received to date 2444 citations according to Google Scholar Citations</b> , i.e. more than 116 citations per year on average. The citations trend is constantly increasing from year 2000. For year 2021, a number of 217 citations are reported. See: <a href="https://scholar.google.com/citations?view_op=view_citation&amp;hl=it&amp;user=8gWEa78AAAJ&amp;alert_preview_top_rm=2&amp;citation_for_view=8gWEa78AAAJ:35N4OoGY0k4C">https://scholar.google.com/citations?view_op=view_citation&amp;hl=it&amp;user=8gWEa78AAAJ&amp;alert_preview_top_rm=2&amp;citation_for_view=8gWEa78AAAJ:35N4OoGY0k4C</a>

## Part VIII – Research Activities

VIIIA – From 1994 to 2004 (positive systems theory and applications)

Keywords	Brief Description
Positive systems	<i>Italian</i>
Compartmental systems	La mia attività di ricerca nel periodo 1994-2005, si è svolta in larghissima parte sulla parte di modellistica con sistemi di equazioni differenziali ordinarie (teoria dei sistemi) e solo in modo marginale sulla parte di teoria del controllo. Infatti, sia la mia tesi di laurea che di dottorato hanno trattato temi di teoria dei sistemi, e più precisamente l'impatto della positività delle variabili di stato, ingresso e uscita su problemi tipici della teoria dei sistemi, e cioè raggiungibilità, osservabilità, identificazione e realizzazione. Oggetto di studio sono quindi stati i cosiddetti “sistemi positivi” e cioè sistemi (ODE) le cui variabili di stato posso solo assumere valori positivi (o non-negativi) per dei vincoli dovuti alla natura fisica delle variabili stesse, come concentrazioni di specie chimiche o molecolari. Su questo tema ho pubblicato nel 2000 un libro con il Prof. Sergio Rinaldi (Politecnico di Milano) edito da Wiley dal titolo “Positive linear systems: theory and applications”:
Modelling and identification of biological systems	

<https://www.wiley.com/en-us/Positive+Linear+Systems%3A+Theory+and+Applications-p-9780471384564>

dove è presente un capitolo intero dedicato ai sistemi compartimentali. Infatti, la classe dei sistemi positivi stabili coincide con i sistemi compartimentali, a meno di fattori di scala nella quantificazione delle variabili di stato (si veda l'articolo n. 36). Come è noto, lo studio delle proprietà dei sistemi compartimentali è uno dei temi "storici" della bioingegneria che si occupa di modelli di sistemi fisiologici (dai componenti cellulari, agli apparati ed agli organi). In particolare, la mia attività di ricerca nel settore dei sistemi compartimentali (si vedano ad esempio gli articoli n. 34, 36, 74, 75 e 89) è evidenziata dal fatto che il problema su cui si è concentrata principalmente la mia attività di ricerca in questo periodo, è quello del problema della "realizzazione positiva" che nasce proprio come problema relativo alla determinazione del numero di compartimenti (e cioè di organi) coinvolti nella dinamica di un farmaco (o tracciante) iniettato per via endovenosa sulla base della sola misura della sua concentrazione nel circolo sanguigno. Il problema è ben descritto per esempio nel volume: F. Kajiyama, S. Kodama, H. Abe, Eds., *Compartmental Analysis. Medical Applications and Theoretical Background*, S. Karger, 1984, nel capitolo 4 intitolato: "Realization problems in linear compartmental systems". Pertanto, il problema della realizzazione dei sistemi compartimentali coincide con lo stesso problema per i sistemi positivi. Analogamente, anche le proprietà di raggiungibilità, osservabilità ed identificabilità dei sistemi compartimentali coincide con gli stessi problemi nei sistemi positivi. Naturalmente, il vincolo di positività sulle variabili di stato è presente anche in altri sistemi, come per esempio nei filtri ad accoppiamento di carica o in fibra ottica, che mi ha permesso di applicare la teoria della realizzazione positiva anche in questi ambiti (ottenendo "Guillemin-Cauer award" della IEEE Circuits and Systems Society per il 2001, insieme a B.D.O. Anderson e L. Benvenuti).

#### *English*

My research activity in the period 1994-2005, has been carried out largely on the part of modeling with systems of ordinary differential equations (systems theory) and only marginally on the part of control theory. In fact, both my undergraduate and doctoral theses dealt with system theory topics, and more precisely with the impact of positivity of state, input and output variables on typical system theory problems, namely reachability, observability, identification and realization. The object of study were therefore the so-called "positive systems", i.e. systems (ODE) whose state variables can only take positive values (or non-negative) for the constraints due to the physical nature of the variables themselves, such as concentrations of chemical or molecular species. On this topic I have published in 2000 a book with Prof. Sergio Rinaldi (Politecnico di Milano) published by Wiley entitled "Positive linear systems: theory and applications"

<https://www.wiley.com/en-us/Positive+Linear+Systems%3A+Theory+and+Applications-p-9780471384564>

where there is an entire chapter devoted to compartmental systems. In fact,



the class of stable positive systems coincides with compartmental systems, barring scaling factors in the quantification of state variables (see article n. 36). As is well known, the study of the properties of compartmental systems is one of the "historical" topics of bioengineering dealing with models of physiological systems (from cellular components to apparatuses and organs). In particular, my research activity in the field of compartmental systems (see, for example, articles n. 34, 36, 74, 75 and 89) is highlighted by the fact that the problem on which my research activity has mainly focused in this period, is that of the problem of "positive realization" which arises precisely as a problem related to the determination of the number of compartments (i.e., organs) involved in the dynamics of a drug (or tracer) injected into the bloodstream on the basis of the measurement of its concentration in the bloodstream alone. The problem is well described for example in the volume: F. Kajiya, S. Kodama, H. Abe, Eds., *Compartmental Analysis. Medical Applications and Theoretical Background*, S. Karger, 1984, in chapter 4 entitled: "Realization problems in linear compartmental systems". Therefore, the realization problem for compartmental systems coincides with the same problem for positive systems. Similarly, the reachability, observability, and identifiability properties of compartmental systems also coincide with the same problems for positive systems. It goes without saying, that the positivity constraint on the state variables is also present in other systems, such as in charge-coupled or fiber-optic filters, which allowed me to apply the theory of positive realization also in these areas (obtaining "Guillemin-Cauer award" of the IEEE Circuits and Systems Society for 2001, together with B.D.O. Anderson and L. Benvenuti).

#### VIIIB – From 2005 to 2021 (bioinformatics and network medicine)

Keywords	Brief description
Bioinformatics	<i>Italian</i>
Computational biology and medicine	Ho preso servizio il 1 Novembre 2000 come professore associato nel settore disciplinare ING-INF/04 (Automatica) ed ho conseguito l'abilitazione nazionale a professore ordinario nello stesso settore disciplinare nella tornata 2012. Nel 2013, il CUN ha positivamente valutato la mia richiesta di cambio di settore disciplinare da ING-INF/04 a ING-INF/06, in considerazione della congruità della mia attività di ricerca e curriculum con il settore disciplinare ING-INF/06. Tale mia richiesta si era resa necessaria in seguito al pensionamento di due strutturati Sapienza del settore disciplinare ING-INF/06, che avrebbe avuto come conseguenza lo spegnimento del corso di laurea magistrale in Ingegneria Biomedica, a causa dei requisiti di legge che impongono un numero minimo di docenti incardinati nei settori caratterizzanti. A seguito del cambio di settore nel 2013, la mia attività didattica e di ricerca - già orientata verso l'ambito biologico - si è quindi definitivamente rivolta verso l'area bio-medica, come testimoniato dagli articoli prodotti elencati nella sezione X e dai corsi da me svolti descritti nella sezione IV.
Network biology	
Network medicine	La mia attività di ricerca nel periodo 2005-2021, si è dedicata alla bioinformatica e all'analisi modellistica/computazionale di dati e segnali biomedici molecolari (trascrittomica, proteomica, epigenomica,

microbiomica, metabolomica, ecc.). Inizialmente sono state sviluppate tematiche di maggiore rilevanza biologica e, in seguito al mio cambio di settore disciplinare, l'attività di ricerca si è rivolta allo sviluppo di metodologie biomediche a fini diagnostici, prognostici, predittivi e terapeutici. La metodologia bioinformatica di analisi di dati molecolari da me maggiormente utilizzata in ambito medico è definita in letteratura come "network medicine" e consiste nell'applicazione della scienza delle reti complesse alla medicina molecolare. I principali risultati della ricerca biomedica svolta riguardano l'individuazione di meccanismi molecolari alla base dello sviluppo e progressione di malattie complesse, come per esempio le patologie tumorali (tumore al seno, glioblastoma, tumore alla tiroide) o respiratorie croniche (COPD). Altri risultati della ricerca riguardano il cosiddetto "riposizionamento dei farmaci" e cioè metodologie basate su reti per l'individuazione di farmaci approvati dagli enti regolatori (FDA, AIFA), che possano essere proposti per la sperimentazione clinica in relazione a patologie differenti, risparmiando così sui tempi ed i costi associati alla prima fase del trial clinico di valutazione del dosaggio e della tossicità. Questo approccio è stato usato, per esempio, nel caso del CoViD-19. L'attività di ricerca si svolge anche in collaborazione con oncologi, patologi, clinici e radiologi, ordinari Sapienza, come il Proff. Sebastiano Filetti, Carlo Catalano, Paolo Marchetti, Marianna Nuti, Elisabetta Ferretti e con i Proff. Edwin Silverman (Direttore della Channing Division of Network Medicine) e Joseph Loscalzo (Direttore del Dipartimento di Medicina) della Harvard Medical School, BWH, Boston, USA..

#### *English*

I took office on November 1, 2000 as associate professor in the ssd ING-INF/04 (Automatica) and I obtained the national habilitation as full professor in the same ssd in the 2012 round. In 2013, the CUN has positively evaluated my request for change of ssd from ING-INF/04 to ING-INF/06, in view of the congruity of my research activity and curriculum with the disciplinary sector ING-INF/06. This request was made necessary by the retirement of two Sapienza staff members in the disciplinary field ING-INF/06, which would have resulted in the shutdown of the Master's degree program in Biomedical Engineering, due to legal requirements that impose a minimum number of faculty members in the characterizing areas. Following the change of field in 2013, my teaching and research activity - already oriented towards the biological area - has therefore definitively turned towards the bio-medical area, as evidenced by the articles produced listed in section X and the courses I conducted described in section IV.

My research activity in the period 2005-2021, has been devoted to bioinformatics and modeling/computational analysis of molecular biomedical data and signals (transcriptomics, proteomics, epigenomics, microbiomics, metabolomics, etc.). Initially, topics of major biological relevance were developed and, following my change of disciplinary field, my research activity turned to the development of biomedical methodologies for diagnostic, prognostic, predictive and therapeutic purposes. The bioinformatic methodology of molecular data analysis that I use most in the medical field is defined in the literature as "network medicine" and consists in the application of the science of complex

networks to molecular medicine. The main results of the biomedical research carried out concern the identification of molecular mechanisms underlying the development and progression of complex diseases, such as cancer (breast cancer, glioblastoma, thyroid cancer) or chronic respiratory disease (COPD). Other research results concern the so-called "drugs repositioning", i.e. network-based methodologies for the identification of drugs approved by regulatory agencies (FDA, AIFA), which can be proposed for clinical trials in relation to different diseases, thus saving time and costs associated with the first phase of the clinical trial regarding dose and toxicity assessment. This approach has been used, for example, in the case of CoViD-19. The research activity is also carried out in collaboration with oncologists, pathologists, clinicians and radiologists, full Professors of Sapienza University, such as Professors Sebastiano Filetti, Carlo Catalano, Paolo Marchetti, Marianna Nuti, Elisabetta Ferretti and with Professors Edwin Silverman (Head of the Channing Division of Network Medicine) and Joseph Loscalzo (Head of the Department of Medicine) from Harvard Medical School, BWH, Boston, USA.

## Part IX – Summary of Scientific Achievements

Indexing and citations: SCOPUS

Impact Factor at the time of publication: Web of Science

Product type	Number	Data Base	Start	End
Articles, Letters, Reviews, Short surveys	72	Scopus	1994	2021
Conference proceedings	12	Scopus	1996	2019
Book Chapter	3	Scopus	2009	2019
Editorial	1	Scopus	2017	2017
Erratum	3	Scopus	2006	2017

Total Impact factor	199.05
Average Impact Factor per Product	2.76
Total Citations (all products)	2409
Average Citations (all products)	26.47
Total Citations (Journal papers)	2346
Average Citations (Journal papers)	32.58
Hirsch (H) index	26 <sup>1</sup>
Normalized H index*	0.96

\*H index divided by the academic seniority (27 years).

<sup>1</sup> Article n. 85 has a currently missing citations in the SCOPUS database. See section XIX below.

- Number of articles/reviews/letter/short surveys published over the last 10 years (2012-2021): **34<sup>2</sup>** (ASN threshold: 34)
- Number of citations in the last 15 years: (2007-2021): **1365** (ASN threshold: 876)
- h-index over the last 15 years (2007-2021): **19<sup>3</sup>** (ASN threshold: 17)

## Part X – List of the publications selected for the evaluation procedure

Indexing and citations. Source: SCOPUS

Impact Factor at the time of publication. Source: Web of Science

1. Palumbo, M.C., Colosimo, A., Giuliani, A., **Farina, L.**, Functional essentiality from topology features in metabolic networks: A case study in yeast, *FEBS Letters* 579:21, pp. 4642-4646, 2005, Cit: 56, IF: 3.415
2. **Farina, L.**, De Santis, A., Salvucci, S., Morelli, G., Ruberti, I., Embedding mRNA stability in correlation analysis of time-series gene expression data, *PLoS Computational Biology* 4:8(e1000141), 2008, Cit: 10, IF: 5.895.
3. **Farina, L.**, Germani, A., Mavelli, G., Palumbo, P., Identification of regulatory network motifs from gene expression data, *Journal of Mathematical Modelling and Algorithms* 9:3, pp. 233-245, 2010, Cit: 5, IF: 1.280.
4. Cacace, F., Paci, P., Cusimano, V., Germani, A., **Farina, L.**, Stochastic Modeling of Expression Kinetics Identifies Messenger Half-Lives and Reveals Sequential Waves of Coordinated Transcription and Decay, *PLoS Computational Biology* 8:11(e1002772), 2012, Cit: 10, IF: 4.867.
5. De Santis, M., Rinaldi, F., Falcone, E., Lucidi, S., Piaggio, G., Gurtner, A., **Farina, L.**, Combining optimization and machine learning techniques for genome-wide prediction of human cell cycle-regulated genes, *Bioinformatics* 30:2, pp. 228-233, 2014, Cit: 4, IF: 4.981.
6. Paci, P., Colombo, T., **Farina, L.**, Computational analysis identifies a sponge interaction network between long non-coding RNAs and messenger RNAs in human breast cancer, *BMC Systems Biology* 8:1(83), 2014, Cit: 172, IF: 2.435.
7. Palumbo, M.C., Zenoni, S., Fasoli, M., Massonnet, M., **Farina, L.**, Castiglione, F., Pezzotti, M., Paci, P., Integrated network analysis identifies fight-club nodes as a class of hubs encompassing key putative switch genes that induce major transcriptome reprogramming during grapevine development, *Plant Cell* 26:12, pp. 4617-4635, 2014, Cit: 74, IF: 9.338.
8. Palumbo, M.C., **Farina, L.**, Paci, P., Kinetics effects and modeling of mRNA turnover, *Wiley Interdisciplinary Reviews: RNA* 6:3, pp. 327-336, 2015, Cit: 14, IF: 4.519.
9. Paci, P., Colombo, T., Fiscon, G., Gurtner, A., Pavesi, G., **Farina, L.**, SWIM: A computational tool to unveiling crucial nodes in complex biological networks, *Scientific Reports* 7:(44797), 2017, Cit.: 34, IF: 4.122.
10. Conte F, Fiscon G, Licursi V, Bizzarri D, D'Antò T, **Farina L**, Paci P. A paradigm shift in medicine: A comprehensive review of network-based approaches. *Biochim Biophys Acta Gene Regul Mech.* 2020 Jun;1863(6):194416. doi: 10.1016/j.bbagr.2019.194416. Epub 2019 Aug 2. PMID: 31382052, Cit: 41, IF: 4.49
11. Petti M, Verrienti A, Paci P, **Farina L**. SEaCorAl: Identifying and contrasting the regulation-correlation bias in RNA-Seq paired expression data of patient groups. *Computer in Biology and Medicine* 2021 Jun 15;135:104567, Cit: 0, IF: 4.589

<sup>2</sup> Article n. 16 has been published on December 2021, and therefore it is not currently present in the SCOPUS database yet. See section XIX below.

<sup>3</sup> Articles n. 14 and n. 62 have 4 (2 each) currently missing citations in the SCOPUS database. See section XIX below.

12. Petti, M., Bizzarri, D., Verrienti, A., Falcone, R., **Farina, L.**, Connectivity Significance for Disease Gene Prioritization in an Expanding Universe, *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2020, 17(6), pp. 2155–2161, 8821247, Cit: 3, IF: 3.71
13. Paci, P., Fiscon, G., Conte, F., Silverman, E.K., **Farina, L.**, Integrated transcriptomic correlation network analysis identifies COPD molecular determinants, *Scientific Reports*, 2020, 10(1), 3361, Cit: 11, IF: 4.379
14. Fiscon, G., Conte, F., **Farina, L.**, Paci, P., SAveRUNNER: A network-based algorithm for drug repurposing and its application to COVID-19, *PLoS Computational Biology*, 2021, 17(2), e1008686, Cit: 19, IF: 4.71
15. Paci P, Fiscon G, Conte F, Wang RS, **Farina L**, Loscalzo J. Gene co-expression in the interactome: moving from correlation toward causation via an integrated approach to disease module discovery. *NPJ Systems Biology & Applications* 2021 Jan 21;7(1):3, Cit: 15, IF: 4.33
16. **L. Farina**, Network as a language for precision medicine, *Ann. Ist. Super. Sanità*, 2021, 57(4):331-344, Cit: 0, IF: 1.663

## Part XI – Other publications

XIA – Articles, letters and review indexed by SCOPUS

17. **Farina, L.**, A note on discrete-time positive realizations, *Systems and Control Letters* 22:6, pp. 467-469, 1994, Cit: 4, IF: 0.517.
18. **Farina, L.**, Benvenuti, L., Positive realizations of linear systems, *Systems and Control Letters* 26:1, pp. 1-9, 1995, Cit: 32, IF: 0.517.
19. **Farina, L.**, Necessary conditions for positive realizability of continuous-time linear systems, *Systems and Control Letters* 25:2, pp. 121-124, 1995, Cit: 13, IF: 0.517.
20. Anderson, B.D.O., Deistler, M., **Farina, L.**, Benvenuti, L., Nonnegative realization of a linear system with nonnegative impulse response, *IEEE Transactions on Circuits and Systems I: Fundamental Theory and Applications* 43:2, pp. 134-142, 1996, Cit: 134, IF: 0.565.
21. Benvenuti, L., **Farina, L.**, On the class of linear filters attainable with charge routing networks, *IEEE Transactions on Circuits and Systems II: Analog and Digital Signal Processing* 43:8, pp. 618-622, 1996, Cit: 16, IF: 0.374.
22. **Farina, L.**, Minimal order realizations for a class of positive linear systems, *Journal of the Franklin Institute* 333:6, pp. 893-900, 1996, Cit: 5, IF: 0.026.
23. Benvenuti, L., **Farina, L.**, Discrete-time filtering via charge routing networks, *Signal Processing* 49:3, pp. 207-215, 1996, Cit: 25, IF: 0.432.
24. **Farina, L.**, On the existence of a positive realization, *Systems and Control Letters* 28:4, pp. 219-226, 1996, Cit: 100, IF: 0.517.
25. **Farina, L.**, Benvenuti, L., Polyhedral reachable set with positive controls, *Mathematics of Control, Signals, and Systems* 10:4, pp. 364-380, 1997, Cit: 16, IF: 0.294.
26. Benvenuti, L., **Farina, L.**, A note on minimality of positive realizations, *IEEE Transactions on Circuits and Systems I: Fundamental Theory and Applications* 45:6, pp. 676-677, 1998, Cit: 20, IF: 0.739.
27. **Farina, L.**, Benvenuti, L., Invariant polytopes of linear systems, *IMA Journal of Mathematical Control and Information* 15:3, pp. 233-240, 1998, Cit: 21; IF: 0.586.
28. Benvenuti, L., **Farina, L.**, Constrained control for uncertain discrete-time linear systems, *International Journal of Robust and Nonlinear Control* 8:7, pp. 555-565, 1998, Cit: 11, IF: 0.256.

29. Benvenuti, L., **Farina, L.**, Anderson, B.D.O., Filtering through combination of positive filters, *IEEE Transactions on Circuits and Systems I: Fundamental Theory and Applications* 46:12, pp. 1431-1440, 1999, Cit: 38, IF: 0.877.
30. Benvenuti, L., **Farina, L.**, An example of how positivity may force realizations of 'large' dimension, *Systems and Control Letters* 36:4, pp. 261-266, 1999, Cit: 32, IF: 0.846.
31. Benvenuti, L., **Farina, L.**, Anderson, B.D.O., De Bruyne, F., Minimal positive realizations of transfer functions with positive real poles, *IEEE Transactions on Circuits and Systems I: Fundamental Theory and Applications* 47:9, pp. 1370-1377, 2000, Cit: 43, IF: 0.595.
32. Benvenuti, L., **Farina, L.**, The design of fiber-optic filters, *Journal of Lightwave Technology* 19:9, pp. 1366-1375, 2001, Cit: 40, IF: 2.014,
33. Valcher, M.E., **Farina, L.**, An algebraic approach to the construction of polyhedral invariant cones, *SIAM Journal on Matrix Analysis and Applications* 22:2, pp. 453-471, 2001, Cit: 16, IF: 0.756.
34. Benvenuti, L., De Santis, A., **Farina, L.**, On model consistency in compartmental systems identification, *Automatica* 38:11, pp. 1969-1976, 2002, Cit: 12, IF: 1.630.
35. De Santis, A., **Farina, L.**, Identification of positive linear systems with Poisson output transformation, *Automatica* 38:5, pp. 861-868, 2002, Cit: 7, IF: 1.630.
36. Benvenuti, L., **Farina, L.**, Positive and compartmental systems, *IEEE Transactions on Automatic Control* 47:2, pp. 370-373, 2002, Cit: 62, IF: 1.553.
37. Benvenuti, L., **Farina, L.**, Linear programming approach to constrained feedback control, *International Journal of Systems Science* 33:1, pp. 45-53, 2002, Cit: 7, IF: 0.305.
38. Benvenuti, L., **Farina, L.**, Minimal positive realizations: A survey of recent results and open problems, *Kybernetika* 39:2, p. 217-228, 2003, Cit: 2, IF: 0.319.
39. Benvenuti, L., **Farina, L.**, A tutorial on the positive realization problem, *IEEE Transactions on Automatic Control* 49:5, pp. 651-664, 2004, Cit: 261, IF: 1.545.
40. Benvenuti, L., **Farina, L.**, Eigenvalue regions for positive systems, *Systems and Control Letters* 51:3, pp. 325-330, 2004, Cit: 41, IF: 0.782.
41. Benvenuti, L., **Farina, L.**, The geometry of the reachability set for linear discrete-time systems with positive controls, *SIAM Journal on Matrix Analysis and Applications* 28:2, pp. 306-325, 2006, Cit: 7, IF: 1.798.
42. Benvenuti, L., **Farina, L.**, Nonnegative matrices in digital signal processing, *Signal Processing* 86:9, pp. 2388-2392, 2006, Cit: 0, IF: 0.669.
43. Tsuchiya, M., Wong, S.T., Yeo, Z.X., Colosimo, A., Palumbo, M.C., **Farina, L.**, Crescenzi, M., Mazzola, A., Negri, R., Bianchi, M.M., Selvarajoo, K., Tomita, M., Giuliani, A., Gene expression waves: Cell cycle independent collective dynamics in cultured cells, *FEBS Journal* 274:11, pp. 2878-2886, 2007, Cit: 32, IF: 3.396.
44. Palumbo, M.C., Colosimo, A., Giuliani, A., **Farina, L.**, Essentiality is an emergent property of metabolic network wiring, *FEBS Letters* 581:13, pp. 2485-2489, 2007, Cit: 28, IF: 3.263.
45. **Farina, L.**, De Santis, A., Morelli, G., Ruberti, I., Dynamic measure of gene co-regulation, *IET Systems Biology* 1:1, pp. 10-17, 2007, Cit: 8, IF: 2.143.
46. Modonesi, C., **Farina, L.**, Licata, I., Germano, R., Zbilut, J.P., Giuliani, A., A contemporary pathology of science, *Annali dell'Istituto Superiore di Sanità* 44:3, pp. 211-213, 2008, Cit: 1, IF: 0.343.
47. Palumbo, M.C., **Farina, L.**, De Santis, A., Giuliani, A., Colosimo, A., Morelli, G., Ruberti, I., Collective behavior in gene regulation: Post-transcriptional regulation and the temporal compartmentalization of cellular cycles, *FEBS Journal* 275:10, pp. 2364-2371, 2008, Cit: 20, IF: 3.139.
48. Soranzo, N., Zampieri, M., **Farina, L.**, Altafini, C., mRNA stability and the unfolding of gene expression in the long-period yeast metabolic cycle, *BMC Systems Biology* 3:(18), 2009, Cit: 5, IF: 4.064.

49. Palumbo, P., Mavelli, G., **Farina, L.**, Alberghina, L., Networks and circuits in cell regulation, *Biochemical and Biophysical Research Communications* 396:4, pp. 881-886, 2010, Cit: 6, IF: 2.595.
50. Romagnoli, G., Cundari, E., Negri, R., Crescenzi, M., **Farina, L.**, Giuliani, A., Bianchi, M.M., Synchronous protein cycling in batch cultures of the yeast *Saccharomyces cerevisiae* at log growth phase, *Experimental Cell Research* 317:20, pp. 2958-2968, 2011, Cit: 2, IF: 3.580.
51. Camiolo, S., **Farina, L.**, Porceddu, A., The relation of codon bias to tissue-specific gene expression in *Arabidopsis thaliana*, *Genetics* 192:2, pp. 641-649, 2012, Cit: 29, IF: 4.389.
52. Fasoli, M., Dal Santo, S., Zenoni, S., Tornielli, G.B., **Farina, L.**, Zamboni, A., Porceddu, A., Venturini, L., Bicego, M., Murino, V., Ferrarini, A., Delledonne, M., Pezzotti, M., The grapevine expression atlas reveals a deep transcriptome shift driving the entire plant into a maturation program, *Plant Cell* 24:9, pp. 3489-3505, 2012, Cit: 231, IF: 9.251.
53. Cacace, F., **Farina, L.**, Germani, A., Manes, C., Internally positive representation of a class of continuous time systems, *IEEE Transactions on Automatic Control* 57:12, pp. 3158-3163, 2012, Cit: 19, IF: 2.718.
54. Dal Santo, S., Tornielli, G.B., Zenoni, S., Fasoli, M., **Farina, L.**, Anesi, A., Guzzo, F., Delledonne, M., Pezzotti, M., The plasticity of the grapevine berry transcriptome, *Genome Biology* 14:6(r54), 2013, Cit: 117, IF: 10.465.
55. Belli Kullán, J., Lopes Paim Pinto, D., Bertolini, E., Fasoli, M., Zenoni, S., Tornielli, G.B., Pezzotti, M., Meyers, B.C., **Farina, L.**, Pè, M.E., Mica, E., miRVine: A microRNA expression atlas of grapevine based on small RNA sequencing, *BMC Genomics* 16:1(393), 2015, Cit: 41, IF: 3.867.
56. Colombo, T., **Farina, L.**, Macino, G., Paci, P., PVT1: A rising star among oncogenic long noncoding RNAs, *BioMed Research International* 2015(304208), 2015, Cit: 162, IF: 2.134.
57. Benvenuti, L., **Farina, L.**, Revisiting the linear recursions with nonnegative coefficients problem, *Linear Algebra and Its Applications* 535, pp. 191-194, 2017, Cit: 1, IF: 0.972.
58. Guarascio, F., **Farina, L.**, Topological analysis of migration flows (the case of political refugees), *International Journal of Computational Economics and Econometrics* 7:4, pp. 359-380, 2017. Cit: 7, IF: 0.861
59. Conte, F., Fison, G., Chiara, M., Colombo, T., **Farina, L.**, Paci, P., Role of the long non-coding RNA PVT1 in the dysregulation of the ceRNA-ceRNA network in human breast cancer, *PLoS ONE* 12:2(e0171661), 2017, Cit: 82, IF: 2.766.
60. Fison, G., Conte, F., **Farina, L.**, Paci, P., Network-based approaches to explore complex biological systems towards network medicine, *Genes* 9:9(437), 2018, Cit: 35, IF: 3.331.
61. **Farina, L.**, Paci, P., A feature-based integrated scoring scheme for cell cycle-regulated genes prioritization, *Journal of Theoretical Biology* 459, pp. 130-141, 2018, Cit: 0, IF: 2.19.
62. Falcone, R., Conte, F., Fison, G., Pecce, V., Sponziello, M., Durante, C., **Farina, L.**, Filetti, S., Paci, P., Verrienti, A., BRAF V600E -mutant cancers display a variety of networks by SWIM analysis: prediction of vemurafenib clinical response, *Endocrine* 64:2, pp. 406-413, 2019, Cit: 19, IF: 3.633.
63. Falcone, R., Strigari, L., **Farina, L.**, Marchetti, P., Response to: Comment on "Impact of tumor site on the prognosis of small bowel adenocarcinoma", *Tumori*, 2019, 105(6), pp. 532, Cit: 1, IF: 2.098.
64. Silverman, E.K., [...], **Farina L.**, [...], Baumbach, J., Molecular networks in Network Medicine: Development and applications, *Wiley Interdisciplinary Reviews: Systems Biology and Medicine*, 2020, 12(6), e1489. Cit: 56, IF: 3.542.
65. Panebianco V, Pecoraro M, Fison G, Paci P, **Farina L**, Catalano C. Prostate cancer screening research can benefit from network medicine: an emerging awareness. *NPJ Syst Biol Appl.* 2020 May 7;6(1):13. doi: 10.1038/s41540-020-0133-0, Cit: 10, IF: 4.33

66. Pecce V, Verrienti A, Fiscon G, Sponziello M, Conte F, Abballe L, Durante C, **Farina L**, Filetti S, Paci P. The role of FOSL1 in stem-like cell reprogramming processes. *Sci Rep*. 2021 Jul 19;11(1):14677, Cit: 2, IF: 4.379
67. P. Sibilio, S. Bini, G. Fiscon, M. Sponziello, F. Conte, V. Pecce, C. Durante, P. Paci, R. Falcone, G. D. Norata, **L. Farina**, Antonella Verrienti, In silico drug repurposing in COVID-19: a network-based analysis, *Biomedicine & Pharmacotherapy*, 2021, 111954, ISSN 0753-3322, Cit: 2, IF: 6.529
68. Cipollari S, Guarrasi V, Pecoraro M, Bicchetti M, Messina E, **Farina L**, Paci P, Catalano C, Panebianco V. Convolutional Neural Networks for Automated Classification of Prostate Multiparametric Magnetic Resonance Imaging Based on Image Quality. *J Magn Reson Imaging*. 2021 Aug 9. Cit: 1, IF: 4.261
69. S. Colonnese, M. Petti, **L. Farina**, F. Cuomo, Learning Protein-to-Protein Interaction via Graph Signal Processing, *IEEE Access* (2021) 9, pp. 142681-142692, Cit:0, IF:3.367
70. V. Panebianco, M. Pecoraro, F. Conte. G. Carnicelli, G. Catanzaro, E. Splendiani, **L. Farina**, C. Catalano, Network analysis integrating microRNA expression profiling with MRI biomarkers and clinical data for prostate cancer early detection: a proof-of-concept study, *Biomedicine* (2021) 9 (10), art. no. 1470, Cit: 0, IF: 6.081
71. M. Petti, **L. Farina**, S. Lucidi, L. Palagi, M. De Santis, MOSES: A new approach to integrate interactome topology and functional features for disease gene prediction, *Genes*, 2021, 12 (11), art. no. 1713, Cit: 0, IF: 4.096

#### XIB – Other publications type indexed by SCOPUS

72. Farina, L., Finite-time reachability for a class of input constrained linear systems, Proceedings of the IEEE Conference on Decision and Control 3, pp. 2355-3592, 1996.
73. Benvenuti, L., Di Giamberardino, P., Farina, L., Trajectory tracking for a PVTOL aircraft: A comparative analysis, Proceedings of the IEEE Conference on Decision and Control 2, pp. 1563-1567, 1996.
74. Farina, L., Is a system representable as a compartmental system? ECC 1997 - European Control Conference n. 7081900, pp. 18-20, 1997
75. Benvenuti, L., Farina, L., How many compartments do we really need? Proceedings of the American Control Conference 6, pp. 4614-4619, 2002.
76. Farina, L., Ruisi, P., Positivity of multi-exponential models, IFAC Proceedings Volumes (IFAC-PapersOnline) 15:1, pp. 53-57, 2002.
77. Benvenuti, L., De Santis, A., Farina, L., Embedding a-priori positivity in systems modelling, Proceedings of the American Control Conference 6, pp. 4626-4631, 2002.
78. Benvenuti, L., Farina, L., Erratum: "A note on minimality of positive realizations" (IEEE Transactions on Circuits and Systems), IEEE Transactions on Circuits and Systems I: Regular Papers 53:1, pp. 215, 2006.
79. Tsuchiya, M., Wong, S.T., Yeo, Z.X., Colosimo, A., Palumbo, M.C., Farina, L., Crescenzi, M., Mazzola, A., Negri, R., Bianchi, M.M., Selvarajoo, K., Tomita, M., Giuliani, A., Erratum: Gene expression waves. Cell cycle independent collective dynamics in cultured cells (FEBS Journal (2007) 274 (2878-2886)), FEBS Journal 274:12, pp. 3198, 2007.
80. Benvenuti, L., Farina, L., The importance of being positive: Admissible dynamics for positive systems, Lecture Notes in Control and Information Sciences 389, pp. 55-62, 2009.
81. Cacace, F., Farina, L., Germani, A., Palumbo, P., Discrete-time models for gene transcriptional regulation networks, Proceedings of the IEEE Conference on Decision and Control n. 5717984, pp. 7618-7623, 2010.



82. Cacace, F., Farina, L., Germani, A., Manes, C., A method for internally positive realization of continuous time systems, Proceedings of the IEEE Conference on Decision and Control n. 5717901, pp. 4978-4983, 2010.
83. Farina, L., Discussion on: "Representation of a class of MIMO systems via internally positive realization", European Journal of Control 16:3, pp. 305-306, 2010.
84. Cacace, F., Farina, L., Setola, R., Germani, A., Preface, Lecture Notes in Control and Information Sciences, 471, pp. V-VI, 2017.
85. Tieri, P., Farina, L., Petti, M., Astolfi, L., Paci, P., Castiglione, F. Network inference and reconstruction in bioinformatics, Encyclopedia of Bioinformatics and Computational Biology: ABC of Bioinformatics, 2018, pp.805-813
86. Fiscon, G., Conte, F., Farina, L., Pellegrini, M., Russo, F., Paci, P., Identification of Disease-miRNA Networks Across Different Cancer Types Using SWIM, Methods in Molecular Biology, 1970, pp. 169-181, 2019.
87. Angelini, M., Blasilli, G., Farina, L., Lenti, S., Santucci, G., NEMESIS (NETwork MEDicine analySIS): Towards visual exploration of network medicine data, VISIGRAPP 2019 - Proceedings of the 14th International Joint Conference on Computer Vision, Imaging and Computer Graphics Theory and Applications, 3, pp. 322-329, 2019.

#### XIC – Other publications not indexed by SCOPUS

88. L. Farina, On the existence of a positive realization, International Symposium MTNS 96, Washington University, St. Louis, MO, 1996
89. L. Farina, Is a system representable as a compartmental system?, European Control Conference ECC97, Bruxelles, 1997
90. L. Benvenuti, L. Farina, B.D.O. Anderson and F. De Bruyne, Minimal discrete-time positive realizations of transfer functions with positive real poles, International Symposium MTNS 98, Padova, I, 1998
91. L. Farina and M.E. Valcher, An algebraic approach to the construction of polyhedral invariant cones, International Symposium MTNS 98, Padova, I, 1998
92. L. Benvenuti and L. Farina, Invariance and feedback control with state and input constraints, 6-th IEEE Mediterranean Conference on Control and Systems, Alghero, I, 1998
93. Benvenuti, L., Farina, L., Anderson, B.D.O., The positive side of filters, *IEEE Circuits and Systems Magazine* 1:3, pp. 32-35, 2001, Cit: 5, IF: 1.148.
94. L. Benvenuti and L. Farina, The design of fiber-optic filters, 8th International Conference on Advances in Communications and Control, Crete, Greece, 2001
95. L. Benvenuti, A. De Santis and L. Farina, Identification of positive linear systems, 8th International Conference on Advances in Communications and Control, Crete, Greece, 2001.
96. M.E. Valcher and L. Farina, On the construction of matrix invariants with applications, 1st IFAC Symposium on System Structure and Control: workshop on max-plus algebra, Prague, Czech Republic, 2001
97. L. Benvenuti and L. Farina, Minimality of positive systems, recent results and open problems, 1st IFAC Symposium on System Structure and Control: workshop on max-plus algebra, Prague, Czech Republic, 2001
98. L. Farina, Positive systems in the state space approach: main issues and recent results, International Symposium on Mathematical Theory of Networks and Systems, MTNS 2002, Notre Dame IN, USA, 2002
99. L. Benvenuti and L. Farina, The geometry of the reachability cone for discrete-time systems. International Symposium on Mathematical Theory of Networks and Systems. Katholieke Universiteit Leuven, Belgium, 2004

100. L. Benvenuti, A. De Santis and L. Farina, Positive Filters with Charge Routing Networks for Image Processing. International Symposium on Mathematical Theory of Networks and Systems. Katholieke Universiteit Leuven, Belgium, 2004
101. C. De Persis and L. Farina, Long--run tolerance of metabolic networks to transient random faults, International Symposium on Mathematical Theory of Networks and Systems. Katholieke Universiteit Leuven, Belgium, 2004
102. I. Mogno, L. Farina, A fast reconstruction algorithm for gene networks, Intelligent Systems for Molecular Biology (ISMB) / European Conference on Computational Biology (ECCB), Glasgow, July 31 - August 4, 2004
103. L. Farina, Biochemical networks regulation as interconnection, BCB 2004, Second Bertinoro Computational Biology Meeting, June 12 - 19, 2004
104. L. Farina, Tolerance and failure propagation analysis of metabolic networks, Workshop on "Complexity and Modeling of Biological Networks", German Research Center for Biotechnology, Braunschweig, Germany, October 15-16, 2004
105. M.C. Palumbo, A. Colosimo, A. Giuliani and L. Farina, Inferring the essentiality of different mutations of *Saccharomyces Cerevisiae* from the position of the corresponding enzymes in the metabolic network, Workshop on Complexity in the Living, CISB - University of Rome "La Sapienza", September 28 - 30, 2004
106. M.C. Palumbo, A. Colosimo, A. Giuliani and L. Farina, Spotting topological and functional criticalities in metabolic networks, International Workshop on Systems Biology, Milano, May 12-13, 2005
107. M.C. Palumbo, L. Farina, A. Giuliani and A. Colosimo, Coupled functional criticalities in metabolic networks, First Maga Circe Conference on Metabolic Systems Analysis, Sabaudia, Italy, March 26-29, 2006
108. M.C. Palumbo, L. Farina, A. Giuliani and A. Colosimo, 'Linking' network topology to gene lethality: enzyme inhibition and mutants, StatPhys23: Complex Networks: from Biology to Information Technology, Pula, Italy, July 2-6, 2007
109. L. Farina, L. Grippo, S. Lucidi and G. Paziienza, Radial basis functions for the identification of cell cycle regulated genes in human cancer cells, Mini EURO Conference on Computational Biology, Bioinformatics and Medicine, Rome, Italy, September 15-17 2008
110. Lorenzo Farina, Alfredo Germani, Gabriella Mavelli and Pasquale Palumbo, Prediction of gene regulatory network motifs using the expression time course of targets genes, Mini EURO Conference on Computational Biology, Bioinformatics and Medicine, Rome, Italy, September 15-17, 2008
111. P. Palumbo, G. Mavelli, L. Farina and L. Alberghina, The "circuit" metaphor in molecular systems biology, SysBioHealth Symposium, Milan, Italy, November 25-27, 2009
112. A. Verrienti, P. Paci, R. Falcone, F. Conte, M. Sponziello, G. Fiscon, V. Pecce, F. Rosignolo, G. Grani, L. Lamartina, V. Ramundo, C. Durante, L. Farina, S. Filetti. Network analysis of expression profiling data in papillary thyroid cancer, American Thyroid Association Conference, Washington DC, October 3-7, 2018
113. R. Falcone, P. Paci, A. Verrienti, G. Fiscon, M. Sponziello, F. Conte, V. Pecce, F. Rosignolo, G. Grani, L. Lamartina, V. Ramundo, C. Durante, L. Farina, S. Filetti, Prediction of response to vemurafenib in BRAF V600E mutant cancers based on a network approach, European Society for Medical Oncology Congress, Munich (Germany), October 19-23, 2018
114. Maria Concetta Palumbo, Lorenzo Farina, Alfredo Colosimo, Kyaw Tun, Pawan K. Dhar and Alessandro Giuliani, Networks everywhere? Some general implications of an emergent metaphor, *Current Bioinformatics* (2006) 1 219-234

115. M.C. Palumbo, L. Farina, A. Colosimo and A. Giuliani, Metabolic Networks. In: Handbook on Biological Networks, World Scientific Publishing Company, ISBN/ISSN: 9812838791 (2009)
116. [...], Farina, L. [...] Gut Microbiota Meta-omics Charts Supporting Cystic Fibrosis Patients' Laboratory and Clinical Management, Journal of clinical gastroenterology (2016), 50 p. S222

#### XID – Current missing citations in SCOPUS database

- Article n. 85 is cited by the following article, indexed by SCOPUS, but not currently present in the database:
  1. Ye X, Zhang W, Futamura Y, Sakurai T. Detecting Interactive Gene Groups for Single-Cell RNA-Seq Data Based on Co-Expression Network Analysis and Subgraph Learning. *Cells*. 2020 Aug 21;9(9):1938.
- Article n. 14 is cited by the following articles, indexed by SCOPUS, but not currently present in the database:
  1. Zhou Y, Zhang Y, Lian X, Li F, Wang C, Zhu F, Qiu Y, Chen Y. Therapeutic target database update 2022: facilitating drug discovery with enriched comparative data of targeted agents. *Nucleic Acids Res*. 2021 Oct 28:gkab953. doi: 10.1093/nar/gkab953.
  2. L. Farina, Network as a language for precision medicine, *Ann. Ist. Super. Sanità*, 2021, 57(4):331-344
- Article n. 62 is cited by the following articles, indexed by SCOPUS, but not currently present in the database:
  1. Marchetti P. Agnostics of immunological therapies in monotherapy and in association: impacts on clinical governance and on the patient's journey. *Recenti Prog Med*. 2021 Dec;112(12):811-815.
  2. L. Farina, Network as a language for precision medicine, *Ann. Ist. Super. Sanità*, 2021, 57(4):331-344

Rome, December 24<sup>th</sup>, 2021

Signature ...