

Curriculum Vitae

Barbara Di Camillo

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Citation metrics (last update: January 2023):

Number of journal papers (international peer reviewed): 110

Number of congress papers (international peer reviewed): 14

Total number of citations: 4053 (Scopus) - 6211 (Google Scholar)

h-index: 28 (Scopus) - 35 (Google Scholar)

Scopus IDs: 12771391500

Google Scholar ID: Barbara Di Camillo

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A. Position

September 1st, 2020 – present: Full Professor (INF 01) at Information Engineering Department, University of Padova.

March 1st, 2017 – August 31th, 2020: Associate Professor (INF 01) at Information Engineering Department, University of Padova.

April 1st 2006 – February 28th 2017: Assistant Professor (ING/INF 06) at Information Engineering Department, University of Padova.

B. Education and training

- 2000 Master Degree in Electronic Engineering, July, 11th, 2000, University of Padova.
- 1999-2000 Erasmus student at University of Aberdeen (Computer Science and Engineering Department), Scotland, UK.
- 2002 Visiting scientist at Mayo Clinic (Rochester, MN, USA), “endocrinology research group” led by Dr. S. Nair.

- 2003 Visiting scientist at “Bioinformatics Center of University of Technology of Graz” (Graz, Austria), leaded by Prof. Trajanoski.
- 2004 PhD in Bioengineering, January 15th, 2004, University of Padova with the thesis: ““Modelling dynamic gene expression profiles: insulin regulation in skeletal muscle.
- 2004-2006 Post-Doc at Information Engineering Department, University of Padova.

C. Research activity

Barbara Di Camillo research activity is centered in the development and application of advanced modeling, data mining and machine learning methods for high-throughput biological and clinical data analysis in the field of Bioinformatics and Health Informatics. She has developed and applied machine learning methods for predictive modeling in medicine, integrating molecular, clinical and environmental variables.

In particular, she has developed and applied different advanced data mining and machine learning methods for robust biomarker discovery, predictive modeling and clustering of gene expression data, 16S and bulk RNA sequencing data and single cell data.

Barbara Di Camillo has also a great expertise in biological network inference using differential equation-based models, Boolean and Bayesian Networks for deterministic and stochastic modeling of disease progression, transcriptional networks and signaling pathways.

D. Awards

- 2019-2020 "Best performing teams (3rd place)" at "Metagenomics Diagnosis for Inflammatory Bowel Disease Challenge (MEDIC)", sbv IMPROVER Computational Challenge series
- 2019 Second place at Start Cup Veneto 2019 as member of the team "EuBiome s.r.l." limited liability company (spin off of the University of Padova), for microbiota transplantation.
- 2017 “Best reviewer award” at Artificial Intelligence in Medicine (AIME 2017), June 21-24, 2017, Vienna, Austria.

- 2014 "Reverse engineering the human microbiota" best poster award at NETTAB 2014, from structural bioinformatics to integrative systems biology, Turin, Italy, October 2014
- 2012 "Bridging the gap between molecular –omics studies and multiscale modeling". Lecture Horizon 2020 at the third National Congress of Bioengineering, Rome, June 2012.
- 2011 "Best performing team" at the "first large-scale community-based critical assessment of protein function annotation (CAFA) experiment", for the high-throughput automatic annotation of protein function, ECCB, Wien, June 2011.
- 2010 Honorable Mention for Best Performers (fourth place) in the Systems Genetics Challenge: "Predict disease phenotypes and infer Gene Networks from Systems Genetics data" at DREAM 5 (Dialogue for Reverse Engineering Assessments and Methods), Joint RECOMB Satellite Conference on Regulatory Genomics, Systems Biology and DREAM5 November 16-20, 2010. Columbia University New York, USA.
- 2010 Award at the VI International Workshop on Waldenstrom's Macroglobulinemia for the abstract "Distinct gene expression signature of malignant and microenvironmental cells from Waldenström's Macroglobulinemia patients: comparison with expression profiling of the same cell counterparts from normal and chronic lymphocytic leukemia subjects". October 9, 2010, Venice, Italy.
- 2009 Best performing team at DREAM 4 (Dialogue for Reverse Engineering Assessments and Methods), Challenge 3: "Predict phosphoprotein measurements using an interpretable, predictive network", Joint RECOMB Satellite Conference on Regulatory Genomics, Systems Biology and DREAM4. December 2-6, 2009. Broad/MIT, Cambridge, MA, USA.
- 2004 "Best PhD Thesis" of "National Group of Bioengineering", Brixen, Italy, September 2004.
- 2004 Finalist at Start Cup as leader of the group "Gensys", for the advanced analysis in proteomics and transcriptomics.

E. Scientific and program committee membership and meeting organization

- **Program committee** member at "Congress of the National group of Bioengineering", June 21-23 2023, Padova, Italy.

- **Program committee** member at Artificial Intelligence in Medicine (AIME) since 2017
- **Program committee** member at RECOMB since 2019
- **Conference Chair** at Bioinformatics Italian Society Meeting BITS June 27-29 2022, Verona, Italy.
- **Organizing and program committee** member at RECOMB 2020, 24th International Conference on Research in Computational Molecular Biology. May 10-13, 2020 – Padova, Italy
- **Program committee** member at the 6th International Conference on Machine Learning, Optimization, and Data Science (LOD 2020), Certosa di Pontignano, Siena - Tuscany, Italy, July 19-22, 2020.
- **Program chair** of the 16th IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology. July 9-11, 2019 – Certosa di Pontignano, Siena - Tuscany, Italy
- **Program committee** member at the 5th International Conference on machine Learning, Optimization and big Data (LOD 2019), Certosa di Pontignano, Siena - Tuscany, Italy, September 10-13, 2019.
- **Program committee** member at the 4th International Conference on machine Learning, Optimization and big Data (LOD 2018), Volterra (Pisa), Tuscany, Italy, September 13-16, 2018.
- **Program committee** member at “NETTAB 2017 “Methods, tools & platforms for Personalized Medicine in the Big Data Era” October 16-18, 2017, Palermo, Italy.
- **Program committee** member at the 3rd International Conference on Machine learning, Optimization and big Data (MOD 2017), Volterra (Pisa), Tuscany, Italy, September 17-21, 2017.
- **Organization** of the DREAM 10 - ALS Stratification Prize4Life Challenge (<http://dreamchallenges.org/challenges/>). RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges, November 16-18, 2015, Philadelphia, Pennsylvania, USA.
- **Program committee** member at “IEEE International Conference on Healthcare Informatics 2015 (ICHI 2015)”, October 21-23, 2015, Dallas, Texas USA.
- **Program committee** member at “IEEE International Conference on Healthcare Informatics 2014 (ICHI 2014)”, 15-17 September 2014, Verona, Italy.

- **Program committee** member at “Congress of the National group of Bioengineering”, June 25-27 2014, Pavia, Italy.
- **Program committee** member at “International Synthetic and Systems Biology Summer School: Biology Meets Engineering and Computer Science”, June, 15-19 2014, Taormina, Italy.
- **Program committee** member at “12th European Conference on Artificial Life (ECAL 2013)”, September 2-6, 2013, Taormina, Italy.
- **Organizing committee** at the workshop “IDAMAP 2012: Intelligent Data Analysis in Biomedicine and Pharmacology”, November 22 2012, Pavia, Italy.
- **Program committee** member at “NETTAB 2011 workshop on Clinical Bioinformatics”, October 12-14, 2011, Pavia, Italy.

F. Invited talks

- “The Long Path to Usable AI” at the Korean Society of Medical and Biological Engineering meeting (KOSOMBE) as a special guest lecturer of the AI-machine learning session. Seoul, Korea, 3-5 November 2022.
- “From Single-Cell to Multi-Cells Information Systems Analysis” at the workshop “Complex Systems: from Physics to Biomedicine” " in honor of Giorgio Parisi, Nobel Laureate for Physics. May 10th 2022, Rome, Italy
- “I big data nelle neuroscienze transazionali” at Accademia di Medicina di Torino, February 18th 2022, Torino, Italy
- “Exploiting artificial intelligence to predict diseases onset and progression” at International conference on laboratory medicine: the ethics of quality and artificial intelligence in laboratory medicine. September 23rd, 2021 Padova, Italy
- “Reverse engineering single cell data: challenges and perspectives” at EMBO Workshop: Network inference in biology and disease, 10 – 13 September 2019, Naples, Italy.
- “MAST: a multi-agent based spatio-temporal model of the interaction between immune system and tumor growth feeded with single-cell data” at the "5th International Synthetic & Systems Biology Summer School - Biology meets Engineering & Computer Science" 25-29 July 2018, Certosa di Pontignano, Siena – Tuscany, Italy.
- “Getting stable lists of biomarkers from high-throughput data: integrating prior knowledge in the learning process” ScalPer’16: Scalable Approaches to High

Performance and High Productivity Computing, October 7-12, 2016, Bertinoro, Italy.

- “Systems Biology: a Multifaceted Approach to Reveal Disease Mechanisms” Mini-symposium in Bioinformatics at the 37th annual international conference of the IEEE Engineering in Medicine and Biology Society, August 25-29, 2015, Milan, Italy.
- "Measuring differential gene expression with RNA-seq: challenges and strategies for data analysis", NGS 2015 Milan: towards single cell analysis, March 10-11, 2015, Milan, Italy.
- “From genetic variants to RNAs differential network wiring: toward a system level understanding of chronic lymphocytic leukemia” 8th summer school on Biology, Information, and Computation, Cancer Bioinformatics workshop, September 9-13, 2013, Trieste, Italy.
- “From genetic variants to RNAs and protein signaling networks towards a system level understanding of biology” STATSEQ meeting on Gene Network Inference with Systems genetic data and beyond. March 28-29, 2013, AgroParisTech, Paris, France.
- “Understanding genotype-phenotype interaction through pathway analysis” Calcolo Scientifico e Bioinformatica oggi, January 13, 2013, CRIBI, Padova, Italy.
- “A gene network simulator” BioINF 2008: Teoria dell'informazione in genomica e proteomica. June 16-17 2008, Pisa, Italy.
- “Comparison of three feature selection methods in time series expression studies”. Third Bioinformatics Meeting on Machine Learning for Microarray Studies of Disease. September 15-16, 2006, Genova, Italy.
- “Importance of integration in modeling dynamic data of gene expression” Biobanks for functional genomics: integrating data, integrating models. March 7-8, 2006 , ITC-irst Trento, Italy.
- “From dynamic microarray expression data to gene network by reverse engineering”. May 26, 2003, Wallenberg Laboratory, University Hospital MAS, Lund University of Malmö, Sweden.
- “Reverse Engineering Methods”. January 27, 2003, Bioinformatics Center of University of Technology of Graz, Graz, Austria.

- “Data Mining in Genomics and Geosciences”. at Coimbra Group Symposium, July 2002, Jena, Germany.
- “Clustering applied to expression data”. ESMTB School of Biology and Mathematics of Cells: Physiology, Kinetics and Evolution, June 2001, Sigüenza, Spain.

G. Membership

Barbara Di Camillo is a member of the Italian society of Bioinformatics (BITS) of the National Group of Bioengineering (GNB), of the International Society for Computational Biology (ICCB) and of the IEEE Engineering in Medicine and Biology Society (EMBS), of the Italian Society of Biomedical Informatics (SIBIM), of CINI-AIIS (“Artificial Intelligence and Intelligent Systems”) and CINI-InfoLife.

Since November 2022, Barbara Di camillo is member (socio corrispondente) of the "Accademia Galileiana di Scienze Lettere e Arti" in Padua.

H. Referee/Editor activity

Journals’ editorial and referee activity

Associate Editor of the **IEEE Journal of Biomedical and Health Informatics, J-BHI** since 2020.

Review Editor of **Frontiers in Genetics - Bioinformatics and Computational Biology** since 2019.

Guest Editor of the Special Issue: “From translational bioinformatics computational methodologies to personalized medicine” **Journal of Biomedical informatics**. Barbara Di Camillo and Rosalba Giugno, 2022-2023

Guest Editor of the Special Issue: “Deep Learning for Genomics” **IEEE/ACM Transactions on Computational Biology and Bioinformatics**. Barbara Di Camillo; Giuseppe Nicosia 2021

Guest Editor of the Special Issue: “Data Science in Smart Healthcare: challenges and opportunities” to be published in **IEEE Journal of Biomedical and Health Informatics**, 2020. Barbara Di Camillo; Giuseppe Nicosia; Francesca Buffa; Benny Lo. 2020. <https://ieeexplore.ieee.org/xpl/tocresult.jsp?isnumber=9248684>

Guest Editor of the Special Issue: “Single-Cell Data Analysis: Resources, Challenges and Perspectives” **Frontiers in Genetics**, 2020

Barbara Di Camillo is serving as referee for the following international journals: Bioinformatics, PLoS ONE, BMC Bioinformatics, BMC Genomics, Journal of Biomedical Informatics, Computer Methods and Programs in Biomedicine, Computers in Biology and Medicine, Statistical Applications in Genetics and Molecular Biology.

Projects' referee activity

Barbara Di Camillo is serving as referee for Cineca (ERC: LS2_11 Computational biology; PE6_13 Bioinformatics, biocomputing, and DNA and molecular computation; LS2_14 Biological systems analysis, modeling and simulation) and since 2018 she is registered to Reprise.

In 2014 she has served as referee for the “Competitive Research Grants King Abdullah University of Science and Technology”, Thuwal, Saudi Arabia and for the “NILS Science and Sustainability program”, Universidad Complutense de Madrid, Spain.

In 2019 she has served as referee for the Swiss National Science Foundation.

I. Funding

Granted funding and Principal Investigator (PI) or work package (WP) leader responsibility

- 2021-2024 European Project H2020: “BRAINTEASER: BRinging Artificial INTelligence home for a better cAre of amyotrophic lateral sclerosis and multiple SclERosis”. ROLE: UniPD PI, WP leader and technical-scientific manager of the project. 585,800 € granted.
- SID_UNIPD 2021-2022 Project Grants: “tRajectoriEs of baCtErial NeTwoRks from hEalthy to disease state and back (RECENTRE)”. ROLE: PI. 49.000 € granted.
- 2018-2021 PRIN (Call 2017): “Deconstruct and rebuild phenotypes: a multimodal approach toward personalized medicine in ALS (DECIPHER-ALS)”. ROLE: Unit PI. 214.000 € granted.
- 2018-2021 (call 2016) Ministry of health grant: Progetti ordinari di Ricerca Finalizzata: “Identification of geNetic and envlronmental deTerminants of onset and progression of ALS (INITIALS)”. ROLE: Unit PI. 85.000 € granted.

- 2017 Ateneo Strategic Research Infrastructure Grant: “CAPRI: Calcolo ad Alte Prestazioni per la Ricerca e l’Innovazione” ROLE: PI. 327.500 € granted.
- 2017-2020 Information Engineering Department, University of Padova “Proactive Project Grant”: “From Single-Cell to Multi-Cells Information Systems Analysis ROLE: PI. 220.000 € granted.
- BIRD_UNIPD 2017 Project Grants: “Monitoring and Modeling Environmental Antimicrobial Resistance Loading into the Environment”. ROLE: PI. 25.000 € granted.
- 2016-2019 European Project H2020: “PULSE: Participatory Urban Living for Sustainable Environments”. ROLE: UniPD PI and WP leader. 414,500 € granted.
- 2016-2018 Agreement on Industrial, Scientific and Technological Research and Development Cooperation between Italy and Israel - Israeli Ministry of Science, Technology and Space and the Directorate General for Political and Security Affairs of the Ministry of Foreign Affairs and International Cooperation: “CompALS: Computational analysis of the clinical manifestations and predictive modelling of ALS”. ROLE: PI. 100.000 € granted.
- 2016-2018 Ateneo Junior Project Grants: “Systems biology approach to single cell RNA sequencing”. ROLE: PI. 23.620 € granted.
- 2015-2017 Ateneo Junior Project Grants: “Dynamic Modeling of TOR signaling pathway through systems biology approaches”. ROLE: PI. 24.998 € granted.
- 2014-2016 Ateneo Junior Project Grants: “Integrative epigenomic and genomic computational methods for high-throughput sequencing data”. ROLE: PI. 23.092 € granted.
- 2011-2013 PhD Program Grant CARIPARO: “RNA sequencing for quantitative transcriptomics”. ROLE: PI. 60.000 € granted.
- 2011-2012 Ateneo Project Grants: “Models of RNA sequencing data variability for quantitative transcriptomics”. ROLE: PI. 53.373 € granted.
- 2009-2010 Ateneo Project Grants: “Methods for the integration of background knowledge in kernel-based learning algorithms for the robust identification of biomarkers in genomics”. ROLE: Unit PI. 42.000 € granted.

Contracts

- 2021-2023 Contract with Associazione ONLUS Malattie del Sangue: “Analisi di dati di trascrittomica e stratificazione di pazienti affetti da IgM Monoclonal

Gammopathy of Undetermined Significance and Waldenström's Macroglobulinemia". ROLE: PI. 12.000 €.

- 2020 Contract with FIND (Foundation for Innovative New Diagnostics, Geneva, Switzerland): "Identification of hematological and protein biomarkers for bacterial vs. non-bacterial infections" ROLE: PI. 15.000 €.
- 2019-2021 Contract with Ospedale Niguarda Ca' Granda, Milano: "Analisi di dati di espressione genica di pazienti affetti da Leucemia Mieloide Cronica nell'ambito del protocollo REL – Philosophy 34." ROLE: PI. 40.000 €.
- 2018-2019 Contract with Associazione ONLUS Malattie del Sangue: "Analisi di dati di trascrittomico e stratificazione di pazienti affetti da IgM Monoclonal Gammopathy of Undetermined Significance and Waldenström's Macroglobulinemia". ROLE: PI. 14.030 €.
- 2017-2020 Contract with Arsenal (Veneto's Research Centre for eHealth Innovation): "Sviluppo di modelli Big Data e loro applicazione in Sistemi di Supporto alla Decisione Clinica nell'ambito del Progetto Fascicolo Sanitario Elettronico regionale del Veneto" supporting a 3 years PhD student. Role: co-investigator
- 2017-2019 Contract with CORIS Veneto (Consorzio per la ricerca sanitaria nel Veneto) : "Machine learning in ambito sanitario per passare da una medicina tradizionale a una medicina predittiva, di iniziativa (mirata a prevenzione e benessere) e personalizzata in un ottica Value-Based Healthcare," supporting a 2 years Postdoc position. ROLE: PI. 58.000 €.
- 2016-2017 Contract with Associazione ONLUS Malattie del Sangue: "Analisi di dati di microarray di pazienti affetti da Macroglobulinemia di Waldenstrom". ROLE: PI. 14.030 €.
- 2014-2016 Contract with Ospedale Niguarda Ca' Granda, Milano: "Analisi di dati di espressione genica di pazienti affetti da Leucemia Mieloide Cronica nell'ambito del protocollo REL – Philosophy 34." ROLE: PI. 36.600 €.
- 2013-2014 Contract with Associazione ONLUS Malattie del Sangue: "Analisi di dati di espressione genica di pazienti affetti da leucemia linfatica cronica e da Macroglobulinemia di Waldenstrom". ROLE: PI. 14.030 €.
- 2011-2012 Contract with Associazione ONLUS Malattie del Sangue: "Analisi di dati di microarray di pazienti affetti da leucemia linfatica cronica e da macroglobulinemia di Waldenstrom". ROLE: PI. 13.915 €

Participation to national/international projects

- 2020-2025 AIRC Grants 2019: IMMUNOlogical microenvironment in Rectal Adenocarcinoma Treatment (IMMUNOREACT)". ROLE: Co-investigator.
- 2017-2019 Ateneo Project Grants: "Algorithms for Networks Analysis and Bioinformatics Applications". ROLE: Co-investigator.
- 2017-2019 Agreement on Industrial, Scientific and Technological Research and Development Cooperation between Italy and Israel - Israeli Ministry of Science, Technology and Space and the Directorate General for Political and Security Affairs of the Ministry of Foreign Affairs and International Cooperation: "EBA_PRISM - Evolutionary-based approach for predicting protein interaction sites and residue mutation impact". ROLE: Co-PI
- 2014-2015 Progetti di Ricerca di Ateneo: "Neuroimaging Genetics: Models and Methods to Integrate Brain Phenotype and Genotype". ROLE: Co-investigator.
- 2013-2015 European Project FP7: "MOSAIC: MOdels and Simulation techniques for discovering diAbetes Influence faCtors". ROLE: Collaborator.
- 2013 Attrezzature Scientifiche finalizzate alla Ricerca: "Piattaforma Cloud per l'erogazione di risorse e servizi configurabili di calcolo scientifico". ROLE: Collaborator and management committee member.
- 2009-2013 IMI Call topic FP7: The Innovative Medicines Initiative (IMI) Call_2008_1_08: "SUMMIT : SUrrogate markers for Micro- and Macro-vascular hard endpoints for Innovative diabetes Tools". ROLE: Collaborator – Work package activities coordination – steering committee meetings.
- 2010-2012 Progetti di Strategici di Ateneo: "Algorithms and Architectures for Computational Science and Engineering". ROLE: Collaborator.
- 2008-2012 European Project FP7: "DIADVISOR: Personal Glucose Predictive Diabetes Advisor". ROLE: Collaborator.
- 2007- 2008 Fondazione CARIPARO-Progetti di Eccellenza: "Inference of transcriptional regulatory pathways from integrative analysis of gene and protein data". ROLE Collaborator.
- 2006-2007 Ministero della Università e della Ricerca Scientifica – PRIN: "Dynamic models of gene and protein expression in endothelial progenitor cells in evolution of diabetes". ROLE: Collaborator.
- 2004-2005 Ministero della Università e della Ricerca Scientifica – PRIN: "Dynamic modeling of microarray gene expression profiles". ROLE: Collaborator.

J. Language Skills (CEFR level)

Italian: native speaker (C2)

English: advanced (C1)

K. Teaching

Courses

- Lecturer at “**Computational Genomics**” (held in English, 6 CFUs), second cycle degree course in Bioengineering and second cycle degree course in ICT for Internet and Multimedia, Information Engineering Department, University of Padova (A.A. 2018-2019 - present).
- Lecturer at “**Elementi di Informatica e Programmazione**” (9 CFUs), first cycle degree course in Biomedical Engineering, Information Engineering Department, University of Padova (A.A. 2018-2019 - present).
- Lecturer at the second level Master “**Machine learning and big data in precision medicine and biomedical research**”, University of Padova (A.A. 2018-2019 - present). **Director** of the master since 2019.
- Lecturer at “**Fondamenti di Informatica**” (9 CFU), first cycle degree course in Cognitive Psychology and Psychobiology, Department of General Psychology, University of Padova (A.A. 2017-2018).
- Lecturer at “**Bioingegneria per la Genomica**” (6 CFUs), second cycle degree course in Bioengineering, Information Engineering Department, University of Padova (A.A. 2008-2009 - 2017-2018).
- Teaching assistant at “**Sistemi e Modelli**” first cycle degree course in Information engineering, Information Engineering Department, University of Padova (A.A. 2010-2011 - 2014-2015).
- Teaching assistant at “**Informatica Sanitaria**” (10 hours teaching activity on SQL), second cycle degree course in Bioengineering, Information Engineering Department, University of Padova (A.A. 2006-2007 - 2010-2011).
- Lecturer at **Introduzione alla Programmazione**, first cycle degree in Computer Science, Department of Mathematics, Università di Padova (A.A. 2008-2009).
- Lecturer at “**Metodi Computazionali**” (3 CFU) and “**Elaborazione Dati**” (3 CFU) at **Bioingegneria per la Genomica**, second cycle degree course in

Bioengineering, Information Engineering Department, University of Padova (A.A. 2006-2007; 2007-2008).

PhD students supervision

- Supervisor of PhD students in **Bioengineering or Information Engineering**: Sara Nasso (cycle XXIII), Tiziana Sanavia (cycle XXIV), Francesca Finotello (cycle XXVI), Emanuele Trifoglio (cycle XXVI), Giacomo Baruzzo (cycle XXIX), Ilaria Patuzzi (cycle XXXI), Erica Tavazzi (cycle XXXIII), Marco Cappellato (cycle XXXV), Chiara Roversi (cycle XXXV), Giulia Cesaro (cycle XXXVII), Isotta Trescato (cycle XXXVII), Mikele Milia (cycle XXXVIII)
- Referee of The PhD thesis of Danila Vella, PhD in **Computer Science**, Università di Milano Bicocca, 2018 (Tutor: Prof. Giancarlo Mauri); Elisabetta Satua, PhD in **Bioinformatics**, Università di Pavia, 2018 (Tutor: Prof. Riccardo Bellazzi); Federica Torricelli, PhD in **Bioengineering and Bioinformatics**, 2017, Università di Pavia (Tutor: Prof. Riccardo Bellazzi); Rosario Di Stefano, PhD in **Computer science**, 2017, Università di Verona (Tutor: Prof. Franco Fummi); Salvatore Masecchia, PhD in **Computer science**, 2013, Università di Genova (Tutor: Prof. Alessandro Verri); Alessia Visconti, PhD in **Science and High Technology (Computer Science Area)**, 2012, Università di Torino (Tutor Prof. Marco Botta).
- Member of the Doctoral External Committee at University of Pavia, PhD in **Bioengineering and Bioinformatics** in 2011.
- 2013-present: Member of the board of lecturers of the PhD school in Information Engineering

L. Institutional responsibilities at the University of Padova

- 2019 –present: Director of the management committee of CAPRI, a shared memory high performance computer infrastructure for research and innovation owned by 14 Departments at University of Padova and INFN_Padova.
- 2019 –present: Director of the Master (second level) in “Machine learning and big data in precision medicine and biomedical research”, University of Padova.
- 2019–present: Member of the Management Board of the PhD School in Information Engineering (Consiglio Direttivo della Scuola di Dottorato in Ingegneria dell’Informazione), as representative of SSD ING-INF/05 and INF/01

- 2018 – present: Governing board member of the interdepartmental center for bioinformatics and innovative biotechnologies
- 2014-present: Management committee member of the cloud-computing infrastructure at the University of Padova.
- 2013-present: Member of the board of lecturers of the PhD school in Information Engineering
- 2017: Member of the commission for the assessment of Senior Post Doc fellowships.
- 2014-2017: Member of the Department Board.
- 2012: Member of the commission for the assessment of Ateneo Projects and Junior Post Doc fellowships.
- 2007-2012: Member of the board of lecturers of the PhD school in Bioengineering

M. Technology Transfer

- 2019: Founding member of the start up EuBiome s.r.l. limited liability company (spin off of the University of Padova) for microbiota transplantation.
- 2020: “Method for determining the prognosis of disease progression and survival for patients affected by amyotrophic lateral sclerosis”. Currently under patenting (International Patent Application No. PCT/IT2020/000057)