

**SINTESI CURRICULUM VITAE AI FINI DELLA PUBBLICAZIONE NELLA SEZIONE
AMMINISTRAZIONE TRASPARENTE**

**FORMATO
EUROPEO PER IL
CURRICULUM
VITAE**



INFORMAZIONI PERSONALI

Nome e Cognome	MARIANNA MILANO
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**ISTRUZIONE
E FORMAZIONE**

Titoli di Studio Universitari	<i>DOTTORATO DI RICERCA</i>
• Date (da – a)	<i>28/03/2019</i>
• Nome e tipo di istituto di istruzione o formazione	<i>Università "Magna Graecia" di Catanzaro</i>
• Qualifica conseguita	<i>DOTTORATO DI RICERCA in "Biomarcatori delle malattie croniche e complesse", curriculum "Nuove Tecniche di Risonanza Magnetica e Bioinformatica applicate alle Neuroscienze", ciclo XXXI, A.A. 2015/2016</i>
Votazione	
Titoli di Studio e attività di aggiornamento post-universitari	<i>DOTTORE MAGISTRALE IN INGEGNERIA BIOMEDICA</i>
• Date (da – a)	<i>20/07/2011</i>
• Nome e tipo di istituto di istruzione o formazione	<i>Università "Magna Graecia" di Catanzaro</i>
• Qualifica conseguita	<i>Laurea Specialistica in Ingegneria Biomedica Conseguita</i>
Votazione	<i>110/110 e Lode</i>

TITOLI SCIENTIFICI E	
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PUBBLICAZIONI	2025 Abilitazione Scientifica Nazionale -ASN- alle funzioni di Professore di Prima Fascia nel settore concorsuale 09/H1 – Sistemi di Elaborazione delle Informazioni nel V quadrimestre, validità dal 13/11/2025 al 13/11/2037. 2025 Professore Associato, G.S.D. 09/IINF-05 Sistemi di elaborazione delle informazioni - S.S.D. IINF-05/A Sistemi di elaborazione delle informazioni, afferente al Dipartimento di Scienze Mediche e Chirurgiche presso Università “Magna Graecia” di Catanzaro. 2025-2023 Ricercatore Universitario a tempo determinato di tipo B, SC 09/H1 SSD ING-INF/05, afferente al Dipartimento di Scienze Mediche e Chirurgiche presso Università “Magna Graecia” di Catanzaro. 2023 Abilitazione Scientifica Nazionale -ASN- alle funzioni di Professore di Seconda Fascia nel settore concorsuale 09/H1 – Sistemi di Elaborazione delle Informazioni nel VI quadrimestre, validità dal 17/12/2023 al 17/12/2034. 2023-2022 Ricercatore Universitario a tempo determinato di tipo A, SC 09/H1 SSD ING-INF/05, afferente al Dipartimento di Scienze Mediche e Chirurgiche presso Università “Magna Graecia” di Catanzaro. 2021 Titolare Assegno di Ricerca dal titolo “Algoritmi efficienti per l’ allineamento e l’ analisi di reti biologiche”, SSD ING-INF/05, afferente Dipartimento di Scienze Mediche e Chirurgiche presso Università “Magna Graecia” di Catanzaro (Secondo Rinnovo). 2021-2020 Titolare Assegno di Ricerca dal titolo “Algoritmi efficienti per l’ allineamento e l’ analisi di reti biologiche”, SSD ING-INF/05, afferente Dipartimento di Scienze Mediche e Chirurgiche presso Università “Magna Graecia” di Catanzaro (Primo Rinnovo). 2020-2019 Titolare Assegno di Ricerca dal titolo “Algoritmi efficienti per l’ allineamento e l’ analisi di reti biologiche”, SSD ING-INF/05, afferente Dipartimento di Scienze Mediche e Chirurgiche presso Università “Magna Graecia” di Catanzaro. 2018-2015 Dottorato di Ricerca in “Biomarcatori delle malattie croniche e complesse”, curriculum “Nuove Tecniche di Risonanza Magnetica e Bioinformatica applicate alle Neuroscienze”, ciclo XXXI, A.A. 2015/2016, Università “Magna Graecia” di Catanzaro. 2015 Titolare Assegno di Ricerca dal titolo “Metodi e algoritmi per la gestione efficiente, l’integrazione e l’analisi bioinformatica, statistica e data mining di grossi volumi di dati omici e clinici”, NELL’AMBITO DEL PROGETTO PRIN 2010NFEBL 003, SSD ING-INF/05, afferente Dipartimento di Scienze della salute presso Università “Magna Graecia” di Catanzaro. 2015-2013 Titolare Assegno di Ricerca dal titolo “Annotazione ed interrogazione di dati semi-strutturati e applicazioni nel turismo”, NELL’AMBITO DEL PROGETTO DICET INMOTO - COD. ID: DIM09, SSD ING-INF/05, afferente Dipartimento di Scienze Mediche e Chirurgiche presso Università “Magna Graecia” di Catanzaro.
	2025 1. Agapito, G., Cannataro, M., Cinaglia, P., & Milano, M. (2025). Ten practical tips and tricks to improve the effectiveness of biological network alignment. PLOS Computational Biology, 21(9), e1013386. 2. Milano, M., Cinaglia, P., Guzzi, P. H., & Cannataro, M. (2025). A computational approach to study age-related modifications of the genes involved in Parkinson's disease. Computers in Biology and Medicine, 196, 110765. 3. Arbitrio, M., Milano, M., Lucibello, M., Altomare, E., Staropoli, N., Tassone, P., ... & Agapito, G. (2025). Bioinformatic challenges for pharmacogenomic study: tools for genomic data analysis. Frontiers in Pharmacology, 16, 1548991. 2024 1. Guzzi, P.H., Roy, A., Milano, M. et al. Non parametric differential network analysis: a tool for unveiling specific molecular signatures. BMC Bioinformatics 25, 359

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	2023 - Cinaglia, P., Milano, M., & Cannataro, M. (2023). Multilayer network alignment based on topological assessment via embeddings. <i>BMC bioinformatics</i>, 24(1), 416. - Milano, M., Agapito, G., & Cannataro, M. (2023). An exploratory application of multilayer networks and pathway analysis in pharmacogenomics. <i>Genes</i>, 14(10), 1915. - Dondi, R., Guzzi, P. H., Hosseinzadeh, M. M., & Milano, M. (2023). Dense subgraphs in temporal social networks. <i>Social Network Analysis and Mining</i>, 13(1), 128. - Milano, M., Cinaglia, P., Guzzi, P. H., & Cannataro, M. (2023). Aligning cross-species interactomes for studying complex and chronic diseases. <i>Life</i>, 13(7), 1520. - Milano, M., & Cannataro, M. (2023). Network models in bioinformatics: Modeling and analysis for complex diseases. <i>Briefings in Bioinformatics</i>, 24(2), bbad016. - Dagliati, A., Strasser, Z., Shakeri Hossein Abad, Z., Klann, J. G., Waghlikar, K., Mesa, R., ... & Estiri, H. (2023). Characterization of Long Covid Temporal Sub-Phenotypes by Distributed Learning from Electronic Health Record Data. - Sperotto, F., Gutiérrez-Sacristán, A., Makwana, S., Li, X., Rofeberg, V. N., Cai, T., ... & Liu, M. (2023). Clinical phenotypes and outcomes in children with multisystem inflammatory syndrome across SARS-CoV-2 variant eras: a multinational study from the 4CE consortium. <i>EClinicalMedicine</i>, 64. - Moal, B., Orioux, A., Ferté, T., Neuraz, A., Brat, G. A., Avillach, P., ... & Jouhet, V. (2023). Acute respiratory distress syndrome after SARS-CoV-2 infection on young adult population: International observational federated study based on electronic health records through the 4CE consortium. <i>Plos one</i>, 18(1),

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	2022 Milano, M., 2022. Using Gene Ontology to Annotate and Prioritize Microarray Data. In Microarray Data Analysis (pp. 273-287). Humana, New York, NY.
	2019 - Milano, M. (2019). Gene Prioritization Tools. S., Gribskov, M., Nakai, K. and Schon- bach, C. (eds.), Encyclopedia of Bioinformatics and Computational Biology, vol. 1, pp. 907-914. Oxford: Elsevier. - Milano, M. (2019). Tools for Semantic Analysis Based on Semantic Similarity. S., Gribskov, M., Nakai, K. and Schonbach, C. (eds.), Encyclopedia of Bioinformatics and Computational Biology, vol. 1, pp. 889-895. Oxford: Elsevier. - Milano, M. (2019). Computing Languages for Bioinformatics: R. S., Gribskov, M., Nakai, K. and Schonbach, C. (eds.), Encyclopedia of Bioinformatics and Computational Biology, vol. 1, pp. 199-205. Oxford: Elsevier
	2015 Agapito, G., Milano, M. Ontology-Based Analysis of Microarray Data. Methods in Molecular Biology DOI 10.1007/7651 2015 249. Editore Springer.
	• Comunicazioni a congressi nazionali e internazionali, atti di conferenza
	2025 - Milano, M., Cinaglia, P., Cannataro, M., & Guzzi, P. H. (2025, July). Biological Community Detection with Graph Neural Network and Network Curvature Analysis on Gene Co-expression Networks. In International Conference on Computational Science (pp. 285-296). Cham: Springer Nature Switzerland. - Cinaglia, P., Pingitore, G., Milano, M., & Cannataro, M. (2025, July). A Machine Learning-Based Framework for Predicting Candidate Drug Side Effects from Biological Networks. In International Conference on Computational Science (pp. 82-93). Cham: Springer Nature Switzerland.

	2024 1. Milano, M., Lazzaro, I., & Cannataro, M. (2024, July). Multilayer Networks: A Survey on Models, Analysis of Algorithms and Database. In International Work-Conference on Bioinformatics and Biomedical Engineering (pp. 202-216). Cham: Springer Nature Switzerland. 2. Lazzaro, I., Milano, M., & Cannataro, M. (2024, June). A Pipeline for the Analysis of Multilayer Brain Networks. In International Conference on Computational Science (pp. 86-98). Cham: Springer Nature Switzerland. 3. Barillaro, L., Milano, M., Caligiuri, M. E., Dalenberg, J. R., Agapito, G., Biehl, M., & Cannataro, M. (2024, June). A Graph-Theory Based fMRI Analysis. In International Conference on Computational Science (pp. 72-85). Cham: Springer Nature Switzerland. 4. Cinaglia, P., & Milano, M. (2024, June). A Method for Inferring Candidate Disease-Disease Associations. In International Conference on Computational Science (pp. 97-104). Cham: Springer Nature Switzerland. 2023 1. Agapito, G., Cannataro, M., Cinaglia, P., Guardasole, G., & Milano, M. (2023, December). Use Predictive Learning Model to Tackle Data Breaches in Healthcare Domain. In 2023 IEEE International Conference on Bioinformatics and Biomedicine (BIBM) (pp. 3273-3279). IEEE. 2022 a. Milano, M., Cannataro, M.,(2021). CCTV: a new network- based methodology for the analysis and visualization of COVID-19 data BITS 2022, 18th Annual Meeting of the Bioinformatics Italian Society. 27-29 Giugno 2022, Verona. 2021 1. Milano, M., Cannataro, M.,(2021). CCTV: a new network-based methodology for the analysis and visualization of COVID-19 data. In 2nd Workshop on High Performance Computing Methods and Interdisciplinary Applications for Fighting the COVID-19 Pan- demic IEEE International Conference on Bioinformatics Biomedicine, December 9-12, 2021, Huston, TX, USA. 2. Agapito, G., Milano, M., Cannataro, M. (2021). Parallel Network Analysis and Communities Detection (PANC) Pipeline for the Analysis and Visualization of COVID-19 Data. In 17th Computational Intelligence Methods for Bioinformatics and Biostatistics CIBB 2021, 15-17 November 2021; 3. Milano, M., Cannataro, M.,(2021). A novel network-based methodology for analysis of COVID-19 data. SEBD (Sistemi Evoluti per Basi di Dati)- Italian
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	Symposium on Advanced Database Systems, 5-9 September 2021, Pizzo, Italy. - Agapito G., Milano, M., Cannataro, M.,(2020). A New Parallel Methodology for the Network Analysis of COVID-19 data. In 26th International European Conference on Parallel and Distributed Computing for Life Sciences (PDCLifeS) Workshops, of Euro- Par 2020, August, 24-28, 2020, Virtual Conference; 2019 - Agapito G., Cannataro, M., Guzzi, P. H., Milano, M.(2019). Mining Association Rules From Disease Ontology. In 2019 IEEE International Conference on Bioinformatics and Biomedicine (BIBM) (pp. 2239-2243). IEEE. - Agapito G., Cannataro, M., Guzzi, P. H., Milano, M.(2019). The impact of gene ontology evolution on gene ontology GO-term information content. In NETTAB / BBCC 2019 Meeting, November 11-13, 2019 Salerno; - Milano, M., Guzzi, P. H., Cannataro, M. (2019). Towards Local Alignment of Multiple Networks: Multi-GLAlign. In Parallel and Cloud-based Bioinformatics and Biomedicine (ParBio) Workshop, held in ACM Conference on Bioinformatics, Computational Biology and Health Informatics, September 7-10, 2019 Niagara Falls, NY, USA; - Agapito G., Cannataro, M., Guzzi, P. H., Milano, M. (2019). Learning Weighted Association Rules in Human Phenotype Ontology. Computational Intelligence methods for Bioinformatics and Biostatistics CIBB 2019, September 4-9 2019, Bergamo. - Agapito G., Cannataro, M., Guzzi, P. H., Milano, M. (2019). Parallel Learning of Weighted Association Rules in Human Phenotype Ontology. In 25th International European Conference on Parallel and Distributed Computing for Life Sciences (PDCLifeS) Workshops, of Euro-Par 2019, August, 26-30, 2019, Gottingen, GE; - Milano, M. , Guzzi, P. H., Cannataro, M. (2019). A New Local Alignment Algorithm for Heterogeneous Networks. In 16th Annual Meeting of the Bioinformatics Italian Society, BITS 2019, June 26-28 2019, Palermo. 2018 - Milano, M., Guzzi, P. H., Cannataro, M. (2018). HetNetAligner: A Novel Algorithm for Local Alignment of Heterogeneous Biological Networks. In Proceedings of the 2018 ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics (pp. 598-599). - Milano, M., Hayes, W., Veltri, P., Cannataro, M., Guzzi, P. H. (2018). SL- GLAlign: Improving the Local Alignment of Biological Networks through Simulated Annealing. In Proceedings of the 2018 ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics (pp. 577-578). ACM. - Milano, M.; Veltri, P., Cannataro, M., Guzzi, P. H.; Towards Heterogeneous Network Alignment: Design and Implementation of a large-scale data processing framework. In 24th International European Conference on Parallel and Distributed Computing , Euro- Par 2018 Workshops, LNCS 11339 proceedings. 2017 - Milano, M., Guzzi, P. H., Cannataro, M. (2017). Using Multi Network Alignment for Analysis of Connectomes. Procedia Computer Science, 108, 1155-1164.
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	2016 1. Milano, M.; Cannataro, M.; Guzzi, P. H., GLAlign: Using Global Graph Alignment to Improve Local Graph Alignment. In International Workshop on Biological Network Driven Analysis (BNDA) 2016 held in IEEE International Conference on Bioinformatics and Biomedicine (BIBM) December 15-18, 2016 Shenzhen, China 2. Milano, M.; Tymofiyeva, O.; Xu, D; Hess, C; Cannataro, M.; Guzzi, P. H., Using Network Alignment for Analysis of Connectomes: Experiences from a Clinical Dataset. In Workshop on Data Mining and Visualization for Brain Science-BrainKDD 2016, held in ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (BCB'16) October 2-5, 2016 Seattle, WA, USA 3. Milano, M.; Guzzi, P. H.; Cannataro, M., Using Ontologies and Semantic Similarity Measures for Prioritization of Gene Regulatory Networks. In Annual Meeting of Bioinformatics Italian Society June 15-17, 2016, Salerno, Italy 2015 1. Agapito G.; Milano, M.; Guzzi, P. H.; Cannataro, M., Efficient Learning of Association Rules from Human Phenotype Ontology . In Parallel and Cloud-based Bioinformatics and Biomedicine (ParBio) Workshop, held in ACM Conference on Bioinformatics, Computational Biology and Health Informatics September 29-12, 2015 Atlanta, GA, USA 2. Guzzi, P.; Milano, M.; Swarup R., Towards the Assessment of GRN Algorithms based on (Disease) Ontology. In Parallel and Cloud-based Bioinformatics and Biomedicine (Par- Bio) , held in ACM Conference on Bioinformatics, Computational Biology and Health Informatics September 29-12, 2015 Atlanta, GA, USA 2014 1. Milano, M.; Agapito G.; Guzzi, P. H.; Cannataro, M., Biases in Information Content Measurement of Gene Ontology Terms . In IEEE International Conference on Bioinformatics and Biomedicine (BIBM),(Belfast, 2-5 November 2014) 2. Agapito G.; Milano, M.; Guzzi, P. H.; Cannataro, M., Improving Annotation Quality in Gene Ontology by Mining Cross-Ontology Weighted Association Rules . In IEEE International Conference on Bioinformatics and Biomedicine (BIBM), (Belfast, 2-5 November 2014) 3. Agapito G.; Milano, M.; Cannataro, M.; Guzzi, P. H., A novel weighted association rule mining algorithm to improve annotation quality in Gene Ontology. In Bringing Maths to Life Workshop (BMTL),(Napoli, 27-29 October 2014) 4. Milano, M.; Guzzi, P. H.; Veltri, P.; Cannataro, M., A web-based tool to Analyze Semantic Similarity Networks . In ACM Conference on Bioinformatics, Computational Biology and Biomedical Informatics (ACM BCB) (Newport Beach CA, 20-23 September) 5. AGAPITO GIUSEPPE, CALABRESE Barbara, CANNATARO Mario, CARE Iliara, FALCONE Daniela, GUZZI Pietro Hiram, IELPO Nicola, LAMPRINOUDI Theodora, MILANO Marianna, SIMEONI Mariadelina, Pofiling basic health information of tourists: towards a recommendation system for the adaptive delivery of medical certified nutrition contents. In International Conference on High Performance Computing and Simulation (HPCS), July 2014. Pages 616-620. IEEE.
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MADRELINGUA	ITALIANO
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ALTRE LINGUE

	INGLESE
• Capacità di lettura	eccellente
• Capacità di scrittura	eccellente
• Capacità di espressione orale	eccellente

EVENTUALI ULTERIORI ALTRI TITOLI O ESPERIENZE VALUTABILI	2024 Referente Erasmus CdS Ingegneria Informatica e Biomedica 2023 Membro Collegio dei Docenti - Dottorato in Intelligenza artificiale, ingegneria biomedica e informatica
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