TO MAGNIFICO RETTORE OF UNIVERSITA' DEGLI STUDI DI MILANO **ID CODE 6705**

I the undersigned asks to participate in the public selection, for qualifications and examinations, for the awarding of a type B fellowship at **Dipartimento di Informatica**

Scientist- in – charge: **Prof. Giorgio Valentini**

Jessica Gliozzo

CURRICULUM VITAE

PERSONAL INFORMATION

Surname	Gliozzo
Name	Jessica

PRESENT OCCUPATION

Appointment	Structure
Research fellow (type B fellowship)	Department of Computer Science "Giovanni Degli Antoni", Università degli Studi di Milano, Milan, Italy

EDUCATION AND TRAINING

Degree	Course of studies	University	year of achievement of the degree
Degree	Master's degree in Molecular Biotechnology and Bioinformatics (Biotecnologie Molecolari e Bioinformatica)	Università degli Studi di Milano	2016
Specialization			
PhD	Computer Science (Informatica)	Università degli Studi di Milano	2024
Master			
Degree of medical specialization			
Degree of European specialization			
Other	Bachelor's degree in Medical Biotechnology	Università degli Studi di Milano	2014

	(Biotecnologie Mediche)		

REGISTRATION IN PROFESSIONAL ASSOCIATIONS

Date of registration	Association	City
None	-	-

FOREIGN LANGUAGES

Languages	level of knowledge
Italian	Native Language
English	C1

AWARDS, ACKNOWLEDGEMENTS, SCHOLARSHIPS

Year	Description of award
2015	Scholarship "BANDO PER BORSE DI STUDIO ALL'ESTERO AI FINI DELLA PREDISPOSIZIONE DELLA TESI DI LAUREA MAGISTRALE ANNO ACCADEMICO 2015/2016 I EDIZIONE" funded by Università degli Studi di Milano.
2017	Scholarship (1 year) on the project "Analisi genomica alla definizione di una terapia molecolare personalizzata dei linfomi T aggressivi refrattari alla chemioterapia" (1383/2014 – All.Convenzione LUMC/EB – Tema n.1) funded by U.O.C. Dermatologia - Fondazione IRCCS Ca' Granda – Ospedale Maggiore Policlinico (Milan, Italy).
2018	Scholarship (1 year) on the project "Analisi genomica finalizzata alla definizione di una terapia molecolare personalizzata dei linfomi T aggressivi refrattari alla chemioterapia" (Atti 1653/2017 – All.Finanziamento privato/EB – Tema n.1) funded by U.O.C. Dermatologia - Fondazione IRCCS Ca' Granda – Ospedale Maggiore Policlinico (Milan, Italy).
2019	Scholarship (1 year) on the project "Studio genomico mediante Next Generation Sequencing (NGS) delle patologie proliferative emopoietiche primitive della cute" (R.C.2019 – 280/02 – Borsa di Studio sul tema n. 27) funded by U.O.C. Dermatologia - Fondazione IRCCS Ca' Granda – Ospedale Maggiore Policlinico (Milan, Italy).
2020	Scholarship on the project "Studio genomico mediante Next Generation Sequencing (NGS) delle patologie proliferative emopoietiche primitive della cute" (R.C. 2020 – 280/02 – Borsa di studio sul Tema n. 51) funded by U.O.C. Dermatologia - Fondazione IRCCS Ca' Granda – Ospedale Maggiore Policlinico (Milan, Italy).
2020	Doctoral scholarship funded by Università degli Studi di Milano and Joint Research Centre (JRC-Ispra) of the European Commission.

TRAINING OR RESEARCH ACTIVITY

Jessica Gliozzo is a research fellow at the Department of Computer Science, Università degli Studi di Milano. She received her bachelor's and master's degrees, respectively in Medical Biotechnology (year 2014, final grade: 104/110) and Molecular Biotechnology and Bioinformatics (year 2016, final grade: 110/110 cum laude), in the same university. During her master's internship at the Department of Computer Science (AnacletoLab, Computational Biology and Bioinformatics Lab), she was a visiting researcher at Royal Holloway, University of London (PACCANAROLAB, CENTRE FOR SYSTEMS BIOLOGY, Department of

Computer Science) where she worked on her master's thesis regarding the development of a semi-supervised network-based method for the prediction of patient's clinical outcomes from genomic data, which was later published on Nature Scientific Reports [10].

She was a research fellow at the hospital "U.O.C. Dermatologia, Fondazione IRCCS Ca' Granda – Ospedale Maggiore Policlinico" working on the bioinformatic analysis of whole genome and RNA sequencing data from blastic plasmacytoid dendritic cell neoplasm and primary cutaneous aggressive epidermotropic cytotoxic T-cell lymphoma samples to detect diagnostic, prognostic and therapeutic markers. Later, she worked on the analysis on Magnetic Resonance Imaging (MRI) at the "Neuroradiology Unit, IRCCS Ospedale San Raffaele". In particular, she collaborated in the application of statistical methods to decompose the multi-exponential T2 signal coming from brain MRI to obtain myelin water fraction maps and study the development of white matter in normal paediatric subjects and children affected by metachromatic leukodystrophy.

She recently earned a PhD in Computer Science at the University of Milan (year 2024, cum laude) which results are presented in her PhD thesis [39] entitled "Patient similarity networks-based methods for multimodal data integration and clinical outcome prediction". The PhD was part of the Collaborative Doctoral Partnership (CDP) programme between Università degli Studi di Milano and Joint Research Centre of the European Commission.

During these years, she worked on various research lines:

1. Analysis of unimodal and integration of multi-modal data through patient similarity networks [5,10,22,39]
2. Effective dimensionality reduction guided by intrinsic dimensionality for multi-modal data fusion [2,23,39]
3. Genome-wide prediction of tissue-specific regulatory regions using deep neural networks [4,27]
4. Prediction of pathogenic variants in non-coding regions of the human genome related to Mendelian diseases [15,25]
5. Methods for the integration, classification and the visual analysis of biomolecular networks [1,7,11,16,17,19,20,21,24,26]
6. Methods to perform cells count in immunohistochemistry images [12,18]
7. Bioinformatics analysis of Next Generation Sequencing data [6]
8. Human Digital Twin to track and prompt suggestions to improve the fitness status of athletes [8]

The third project was a collaboration with the Berlin Institute of Health (Kircher Lab – Computational genome biology group).

PROJECT ACTIVITY

Year	Project
2018-2019	Project "Developing machine learning methods for the prioritization of regulatory variants in human diseases" concerns the development of machine learning methods, mostly based on deep neural networks, to prioritize regulatory variants of human diseases. It was funded by the "MIUR-DAAD Joint Mobility Program".
2017-2019	Project "Analisi genomica alla definizione di una terapia molecolare personalizzata dei linfomi T aggressivi refrattari alla chemioterapia" involving the bioinformatic analysis of DNA and RNA sequencing data from rare lymphomas.
2019-2020	Project "Studio genomico mediante Next Generation Sequencing (NGS) delle patologie proliferative emopoietiche primitive della cute" involving the bioinformatic analysis of DNA and RNA sequencing data from rare lymphomas.
2020	Project "Biomarker Imaging and New Challenging Approaches to assess white matter disorders in developmental age", where I contributed to the analysis of Magnetic Resonance images to compute the so-called myelin water fraction maps necessary to study the

	development of white matter paediatric subjects.
2020	Project “Multicriteria Data Structures and Algorithms: from compressed to learned indexes, and beyond” (PRIN no. 2017WR7SHH), which funded the first year of PhD. In this context, we studied the application of neural network compression approaches on pre-trained networks with a focus on the analysis of immunohistochemical images.
2021-2022	Project “AI-driven data analysis and integration for bio-medical applications” funded by Piano di Sostegno alla Ricerca (PSR2021, PSR2022), where I contributed with the development of (I) data integration methods based on patient similarity networks able to fuse multiple high-dimensional genomic data sources having completely missing samples, (II) multi-modal semi-supervised method based on patient similarity networks able to effectively integrate different data sources (e.g. epigenomic, gene expression and clinical data) to predict patients’ outcomes.
2023	Project “MULTI-modal Data IntegratiON: dEvelopment and validation (MULTIONE)” that was funded with HPC hours from CINECA. The project regards the study of effective dimensionality reduction techniques guided by intrinsic dimensionality for the integration of multi-omics data.
2023-Current date	Project “Multi-OneT: MULTI-modal Data IntegratiON for Explainable and Translational results” that was funded with HPC hours from INDACO (Università degli Studi di Milano) regarding (I) the study of methods for multi-modal data integration based on patient similarity networks, (II) the development of a data fusion technique based on patient similarity networks able to integrate datasets having patients with some data sources completely missing.
2022-Current date	Project “Sistema integrato di Ateneo per lo studio, il monitoraggio e il controllo delle infezioni, delle emergenze epidemiche e della resistenza ai farmaci antimicrobici (IDEA)” funded by Grandi Sfide di Ateneo, Università degli Studi di Milano. I contributed to the identification of automatic bioinformatics pipelines for the analysis of sequencing genomic data from SARS-CoV-2, which are necessary to monitor viral lineages through the prompt detection of mutations of concern for public health.

PATENTS

Patent
None

CONGRESSES AND SEMINARS

Date	Title	Place
25-27th October 2018	Poster at “Grand BIMSB Opening Symposium - 11th Berlin (Late) Summer Meeting”	Berlin, Germany
27-29th June 2022	Poster at “BITS 2022 - 18th Annual Meeting of the Bioinformatics Italian Society”	Verona, Italy
16-18th February 2023	Oral presentation at “Bioinformatics 2023 – 14th International Conference on Bioinformatics Models, Methods and Algorithms.	Lisbon, Portugal

PUBLICATIONS

Books

None

Articles in reviews

[1] Emanuele Cavalleri, Alberto Cabri, Mauricio Soto-Gomez, Sara Bonfitto, Paolo Perlasca, Jessica Gliozzo, Tiffany J Callahan, Justin Reese, NR Peter, Elena Casiraghi, Giorgio Valentini and Marco Mesiti. «An ontology-based knowledge graph for representing interactions involving RNA molecules». In: Scientific Data, Nature Publishing (2024). [Second Round of Minor Revisions].

[2] Jessica Gliozzo, Valentina Guarino, Arturo Bonometti, Alberto Cabri, Emanuele Cavalleri, Mauricio Soto-Gomez, Justin Reese, Peter N Robinson, Marco Mesiti, Giorgio Valentini and Elena Casiraghi. «Intrinsic-Dimension analysis for guiding dimensionality reduction and data-fusion in multi-omics data processing». In: Artificial Intelligence In Medicine (2024). [Submitted]. doi: 10.1101/2024.01.23.576822. url: https://www.biorxiv.org/content/early/2024/01/25/2024.01.23.576822.

[3] Giorgio Valentini, Dario Malchiodi, Jessica Gliozzo, Marco Mesiti, Mauricio Soto-Gomez, Alberto Cabri, Justin Reese, Elena Casiraghi and Peter N. Robinson. «The promises of large language models for protein design and modeling». In: Frontiers in Bioinformatics 3 (23 nov. 2023). issn: 2673-7647. doi: 10.3389/fbinf.2023.1304099. url: https://www.frontiersin.org/articles/10.3389/fbinf.2023.1304099

[4] Luca Cappelletti, Alessandro Petrini, Jessica Gliozzo, Elena Casiraghi, Max Schubach, Martin Kircher and Giorgio Valentini. «Boosting tissue-specific prediction of active cis-regulatory regions through deep learning and Bayesian optimization techniques». In: BMC Bioinformatics 23.2 (12 dic. 2022), p. 154. doi: 10.1186/s12859-022-04582-5. url: https://doi.org/10.1186/s12859-022-04582-5.

[5] Jessica Gliozzo, Marco Mesiti, Marco Notaro, Alessandro Petrini, Alex Patak, Antonio Puertas-Gallardo, Alberto Paccanaro, Giorgio Valentini and Elena Casiraghi. «Heterogeneous data integration methods for patient similarity networks». In: Briefings in Bioinformatics 23.4 (13 giu. 2022), bbac207. issn: 1477-4054. doi: 10.1093/bib/bbac207. eprint: https://academic.oup.com/bib/article-pdf/23/4/bbac207/45016588/bbac207.pdf. url: https://doi.org/10.1093/bib/bbac207.

[6] Adriana Cassaro, Giovanni Grillo, Marco Notaro, Jessica Gliozzo, Ilaria Esposito, Gianluigi Reda, Alessandra Trojani, Giorgio Valentini, Barbara Di Camillo, Roberto Cairoli and Alessandro Beghini. «FZD6 triggers Wnt-signalling driven by WNT10BIVS1 expression and highlights new targets in T-cell acute lymphoblastic leukemia». In: Hematological Oncology 39.3 (26 gen. 2021), pp. 364–379. doi: https ://doi.org/10.1002/hon.2840. eprint: https://onlinelibrary.wiley.com/doi/pdf/10.1002/hon.2840. url: https://onlinelibrary.wiley.com/doi/abs/10.1002/hon.2840.

[7] Marco Notaro, Marco Frasca, Alessandro Petrini, Jessica Gliozzo, Elena Casiraghi, Peter N Robinson and Giorgio Valentini. «HEMDAG: a family of modular and scalable hierarchical ensemble methods to improve Gene Ontology term prediction». In: Bioinformatics 37.23 (8 lug. 2021), pp. 4526–4533. issn: 1367-4803. doi: 10.1093/bioinformatics/btab485. eprint: https://academic.oup.com/bioinformatics/article-pdf/37/23/4526/50579686/btab485. pdf. url: https://doi.org/10.1093/bioinformatics/btab485.

[8] Barbara Rita Barricelli, Elena Casiraghi, Jessica Gliozzo, Alessandro Petrini and Stefano Valtolina. «Human Digital Twin for Fitness Management». In: IEEE Access 8 (4 feb. 2020), pp. 26637–26664. doi: 10.1109/ACCESS.2020.2971576.

[9] Arturo Bonometti, Jessica Gliozzo, Chiara Moltrasio, Filippo Bagnoli and Emilio Berti. «Cutaneous-group histiocytoses associated with myeloid malignancies: A systematic review of 102 cases». In: Australasian Journal of Dermatology 62.2 (30 ott. 2020), e162–e169. doi: https://doi.org/10.1111/ajd.13491. eprint: https://onlinelibrary.wiley.com/doi/pdf/10.1111/ajd.13491. url: https://onlinelibrary.wiley.com/doi/abs/10.1111/ajd.13491.

[10] Jessica Gliozzo, Paolo Perlasca, Marco Mesiti, Elena Casiraghi, Viviana Vallacchi, Elisabetta Vergani, Marco Frasca, Giuliano Grossi, Alessandro Petrini, Matteo Re, Alberto Paccanaro and Giorgio Valentini.

«Network modeling of patients' biomolecular profiles for clinical phenotype/outcome prediction». In: Scientific Reports, Nature Publishing 10.1 (27 feb. 2020), p. 3612. issn: 2045-2322. doi: 10.1038/s41598-020-60235-8. url: https://doi.org/10.1038/s41598-020-60235-8.

[11] Paolo Perlasca, Marco Frasca, Cheick Tidiane Ba, Jessica Gliozzo, Marco Notaro, Mario Pennacchioni, Giorgio Valentini and Marco Mesiti. «Multi-resolution visualization and analysis of biomolecular networks through hierarchical community detection and web-based graphical tools». In: PLOS ONE 15.12 (22 dic. 2020), pp. 1–28. doi: 10.1371/journal.pone.0244241. url: https://doi.org/10.1371/journal.pone.0244241.

[12] Barbara Rita Barricelli, Elena Casiraghi, Jessica Gliozzo, Veronica Huber, Biagio Eugenio Leone, Alessandro Rizzi and Barbara Vergani. «ki67 nuclei detection and ki67-index estimation: a novel automatic approach based on human vision modeling». In: BMC Bioinformatics 20.1 (27 dic. 2019), p. 733. doi: 10.1186/s12859-019-3285-4. url: https://doi.org/10.1186/s12859-019-3285-4.

[13] Armando N. Bastidas Torres, Davy Cats, Hailiang Mei, Daniele Fanoni, Jessica Gliozzo, Laura Corti, Marco Paulli, Maarten H. Vermeer, Rein Willemze, Emilio Berti and Cornelis P. Tensen. «Whole-genome analysis uncovers recurrent IKZF1 inactivation and aberrant cell adhesion in blastic plasmacytoid dendritic cell neoplasm». In: Genes, Chromosomes and Cancer 59.5 (17 dic. 2019), pp. 295–308. doi: https://doi.org/10.1002/gcc.22831. eprint: https://onlinelibrary.wiley.com/doi/pdf/10.1002/gcc.22831. url: https://onlinelibrary.wiley.com/doi/abs/10.1002/gcc.22831.

[14] Arturo Bonometti, Jessica Gliozzo, Chiara Moltrasio, Filippo Bagnoli, Luigia Venegoni, Emanuela Passoni, Marco Paulli and Emilio Berti. «Disfiguring Nodular Cephalic Xanthoma Disseminatum: An Exceptional Variant of a Forgotten Entity». In: Acta Dermato-Venereologica 99.4 (4 feb. 2019), pp. 450-451. doi:10.2340/00015555-3111. url: https://medicaljournalssweden.se/actadv/article/view/3161.

[15] Luca Cappelletti, Jessica Gliozzo, Alessandro Petrini and Giorgio Valentini. «Training Neural Networks with Balanced Mini-batch to Improve the Prediction of Pathogenic Genomic Variants in Mendelian Diseases». In: Sensors & Transducers 234.6 (30 giu. 2019), pp. 16–21. issn: 2306-8515. url: https://www.sensorsportal.com/HTML/DIGEST/P_3087.htm.

[16] Paolo Perlasca, Marco Frasca, Cheick Tidiane Ba, Marco Notaro, Alessandro Petrini, Elena Casiraghi, Giuliano Grossi, Jessica Gliozzo, Giorgio Valentini and Marco Mesiti. «UNIPred-Web: a web tool for the integration and visualization of biomolecular networks for protein function prediction». In: BMC Bioinformatics 20.1 (14 ago. 2019), p. 422. issn: 1471-2105. doi: 10.1186/s12859-019-2959-2. url:https://doi.org/10.1186/s12859-019-2959-2.

[17] Marco Frasca, Giuliano Grossi, Jessica Gliozzo, Marco Mesiti, Marco Notaro, Paolo Perlasca, Alessandro Petrini and Giorgio Valentini. «A GPU-based algorithm for fast node label learning in large and unbalanced biomolecular networks». In: BMC Bioinformatics 19.10 (15 ott. 2018), p. 353. issn: 1471-2105. doi:10.1186/s12859-018-2301-4. url: https://doi.org/10.1186/s12859-018-2301-4

Congress proceedings

[18] Jessica Gliozzo, Giosuè Marinò, Arturo Bonometti, Marco Frasca and Dario Malchiodi. «Resource-Limited Automated Ki67 Index Estimation in Breast Cancer». In: Proceedings of the 2023 10th International Conference on Bioinformatics Research and Applications, Barcelona, Spain, September 22-24, 2023. ICBRA '23. New York, NY, USA: Association for Computing Machinery, 27 feb. 2024, pp. 165-172. doi:10.1145/3632047.3632072. url: https://doi.org/10.1145/3632047.3632072.

[19] Francesco Torgano, Emanuele Cavalleri, Jessica Gliozzo, Emanuele Saitto, Marco Mesiti, Elena Casiraghi and Giorgio Valentini. «RNA Knowledge Graph analysis via embedding methods». In: BIOMEDICINE 2024 - 4th International Conference on Biology and Biomedicine, Heraklion, Crete Island, Greece. July 19-22,2024. [Accepted]. Lug. 2024.

[20] Emanuele Cavalleri, Sara Bonfitto, Alberto Cabri, Jessica Gliozzo, Paolo Perlasca, Mauricio Soto-Gomez, Gabriella Trucco, Elena Casiraghi, Giorgio Valentini and Marco Mesiti. «A Meta-Graph for the Construction of an RNA-Centered Knowledge Graph». In: Bioinformatics and Biomedical Engineering, 10th International Work-Conference, IWBBIO 2023, Meloneras, Gran Canaria, Spain, July 12–14, 2023. A cura di Ignacio Rojas, Olga Valenzuela, Fernando Rojas Ruiz, Luis Javier Herrera e Francisco Ortuño. Cham:Springer

Nature Switzerland, 29 giu. 2023, pp. 165–180. isbn: 978-3-031-34953-9. doi: 10.1007/978-3-031-34953-9_13. url: https://doi.org/10.1007/978-3-031-34953-9_13.

[21] Emanuele Cavalleri, Sara Bonfitto, Alberto Cabri, Jessica Gliozzo, Paolo Perlasca, Mauricio Soto-Gomez, Gabriella Trucco, Elena Casiraghi, Giorgio Valentini, Marco Mesiti et al. «Towards the Construction of an RNA-based Knowledge Graph». In: CEUR WORKSHOP PROCEEDINGS, SEBD 2023: 31st Symposium of Advanced Database Systems, 2 July 2023 - 5 July 2023. Vol. 3478. CEUR-Ws. Galzignano Terme, Italy, lug. 2023, pp. 173–180. url: https://ceur-ws.org/Vol-3478/paper30.pdf.

[22] Jessica Gliozzo., Alex Patak., Antonio Puertas-Gallardo., Elena Casiraghi. and Giorgio Valentini. «Patient Similarity Networks Integration for Partial Multimodal Datasets». In: Proceedings of the 16th International Joint Conference on Biomedical Engineering Systems and Technologies (BIOSTEC 2023), Lisbona, Portugal, February 16–18, 2023 - BIOINFORMATICS. INSTICC. SciTePress, 2023, pp. 228–234. isbn: 978-989-758-631-6. doi: 10.5220/0011725500003414.

[23] Valentina Guarino., Jessica Gliozzo., Ferdinando Clarelli., Béatrice Pignolet., Kaalindi Misra., Elisabetta Mascia., Giordano Antonino., Silvia Santoro., Laura Ferré., Miryam Cannizzaro., Melissa Sorosina., Roland Liblau., Massimo Filippi., Ettore Mosca., Federica Esposito., Giorgio Valentini. and Elena Casiraghi. «Intrinsic-Dimension Analysis for Guiding Dimensionality Reduction in Multi-Omics Data». In: Proceedings of the 16th International Joint Conference on Biomedical Engineering Systems and Technologies (BIOSTEC 2023), Lisbona, Portugal, February 16–18, 2023 - BIOINFORMATICS. INSTICC. SciTePress, 2023, pp. 243–251. isbn: 978-989-758-631-6. doi: 10.5220/0011775200003414.

[24] Paolo Perlasca, Marco Frasca, Cheick Tidiane Ba, Jessica Gliozzo, Marco Notaro, Mario Pennacchioni, Giorgio Valentini and Marco Mesiti. «Integration and Visual Analysis of Biomolecular Networks Through UNIPred-Web». In: Current Trends in Web Engineering ICWE 2022. Communications in Computer and Information Science, International Workshops, BECS, SWEET and WALS, Bari, Italy, July 5-8,2022. A cura di Giuseppe Agapito, Anna Bernasconi, Cinzia Cappiello, Hasan Ali Khattak, InYoung Ko, Giuseppe Loseto, Michael Mrissa, Luca Nanni, Pietro Pinoli, Azzurra Ragone, Michele Ruta, Floriano Scioscia e Abhishek Srivastava. Vol. 1668. Cham: Springer Nature Switzerland, 2 feb. 2023, pp. 192–197. isbn: 978-3-031-25380-5. doi: https://doi.org/10.1007/978-3-031-25380-5_15.

[25] Alessandro Petrini, Marco Notaro, Jessica Gliozzo, Tiziana Castrignanò, Peter N. Robinson, Elena Casiraghi and Giorgio Valentini. «ParSMURF-NG: A Machine Learning High Performance Computing System for the Analysis of Imbalanced Big Omics Data». In: Artificial Intelligence Applications and Innovations. AIAI 2022 IFIP WG 12.5 International Workshops. AIAI 2022. IFIP Advances in Information and Communication Technology. Hersonissos, Crete, Greece, June 17–20, 2022. A cura di Ilias Maglogiannis, Lazaros Iliadis, John Macintyre e Paulo Cortez. Vol. 652. Cham: Springer International Publishing, 10 giu. 2022, pp. 424–435. isbn: 978-3-031-08341-9. doi: https://doi.org/10.1007/978-3-031-08341-9_34.

[26] Cheick Tidiane Ba, Elena Casiraghi, Marco Frasca, Jessica Gliozzo, Giuliano Grossi, Marco Mesiti, Marco Notaro, Paolo Perlasca, Alessandro Petrini, Matteo Re and Giorgio Valentini. «A Graphical Tool for the Exploration and Visual Analysis of Biomolecular Networks». In: Computational Intelligence Methods for Bioinformatics and Biostatistics. CIBB 2018. Lecture Notes in Computer Science. 15th International Meeting, CIBB 2018, Caparica, Portugal, September 6-8, 2018. A cura di Maria Raposo, Paulo Ribeiro, Susana Sério, Antonino Staiano e Angelo Ciaramella. Vol. 11925. Cham: Springer International Publishing, 23 gen. 2020, pp. 88–98. isbn: 978-3-030-34585-3. doi: 10.1007/978-3-030-34585-3_8.

[27] Luca Cappelletti, Alessandro Petrini, Jessica Gliozzo, Elena Casiraghi, Max Schubach, Martin Kircher and Giorgio Valentini. «Bayesian Optimization Improves Tissue-Specific Prediction of Active Regulatory Regions with Deep Neural Networks». In: Bioinformatics and Biomedical Engineering, IWBBIO 2020. Lecture Notes in Computer Science, 8th International Work-Conference, IWBBIO 2020, Granada, Spain, May 6–8, 2020. A cura di Ignacio Rojas, Olga Valenzuela, Fernando Rojas, Luis Javier Herrera e Francisco Ortuño. Vol. 12108. Cham: Springer International Publishing, 30 apr. 2020, pp. 600–612. isbn: 978-3-030-45385-5. doi: 10.1007/978-3-030-45385-5_54.14

OTHER INFORMATION

Author of the following abstracts presented as conference posters:

[28] Mirco Gnuva, Jessica Gliozzo, Alberto Paccanaro, Giorgio Valentini and Elena Casiraghi. «Comparison of early integration approaches for cancer survival prediction». In: BITS 2022, 18th Annual Meeting of the Bioinformatics Italian Society, Verona, Italy (giu. 2022).

[29] Silvia Alberti-Violetti, Daniele Fanoni, Chiara Moltrasio, Jessica Gliozzo, Luigia Venegoni, Valentina Merlo, Giorgia Saporiti, Francesco Onida and Emilio Berti. «Blastic Plasmacytoid Dendritic Cell Neoplasm: clinic-pathologic and molecular data from a single medical center». In: 24th World Congress of Dermatology (WCD), 10-15 June 2019, Milan, Italy (giu. 2019). url: https://www.wcd2019milan-dl.org/abstract-book/documents/abstracts/39-skin-cancer/blastic-plasmocytoid-dendritic-cells-neoplasm-4804.pdf.

[30] Arturo Bonometti, Chiara Moltrasio, Jessica Gliozzo, Filippo Bagnoli, Gianluca Nazzaro, Silvia Alberti-Violetti, Emanuela De Juli, Emanuela Passoni, Marco Paulli and Emilio Berti. «Myeloid Leukemia and Cutaneous Histiocytosis: fortuitous encounter?» In: 24th World Congress of Dermatology (WCD), 10-15 June 2019, Milan, Italy (giu. 2019). url: https://www.wcd2019milan-dl.org/abstract-book/documents/abstracts/10-dermatopathology/myeloid-leukemia-and-cutaneous-histiocytosis-3840.pdf.

[31] Arturo Bonometti, Chiara Moltrasio, Jessica Gliozzo, Filippo Bagnoli, Emanuela Passoni, Gianluca Nazzaro, Silvia Alberti-Violetti, Emanuela De Juli, Marco Paulli and Emilio Berti. «Uncommon variants of Non-Langerhans Cell Histiocytosis». In: 24th World Congress of Dermatology (WCD), 10-15 June 2019, Milan, Italy (giu. 2019). url: https://www.wcd2019milan-dl.org/abstract-book/documents/abstracts/10-dermatopathology/uncommon-variants-of-non-langerhans-3772.pdf.

[32] Sebastiano Recalcati, Chiara Moltrasio, Gianluca Nazzaro, Emanuela Passoni, Jessica Gliozzo, Emilio Berti and Simona Muratori. «Effects of Polydeoxyribonucleotide in the treatment of Scleroderma». In: 24th World Congress of Dermatology (WCD), 10-15 June 2019, Milan, Italy (giu. 2019). url: https://www.wcd2019milan-dl.org/abstract-book/documents/abstracts/07-autoimmune-connective-tissue-diseases/effects-of-polydeoxyribonucleotide-in-the-2428.pdf.

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[34] Arturo Bonometti, Jessica Gliozzo, Chiara Moltrasio, Bagnoli Filippo, Emanuela DeJuli, Emanuela Passoni and Emilio Berti. «RETICULOHISTIOCYTOSES, GENERALIZED ERUPTIVE HISTIOCYTOSIS AND MYELOID NEOPLASM: A SYSTEMATIC REVIEW». In: Abstracts from the 34th Annual Meeting of the Histiocyte Society Lisbon, Portugal, October 22–23, 2018, Pediatric Blood & Cancer 66.S1 (13 nov. 2018), e27548. doi: https://doi.org/10.1002/pbc.27548.

[35] Jessica Gliozzo, Paolo Perlasca, Marco Mesiti, Juan Caceres Silva, Alessandro Petrini, Elena Casiraghi, Marco Frasca, Giuliano Grossi, Matteo Re, Alberto Paccanaro and Giorgio Valentini. «Patients' networks for clinical phenotype/outcome prediction». In: Grand BIMSB Opening Symposium - 11th Berlin (Late) Summer Meeting, 25-27 October 2018, Berlin, Germany. Ott. 2018.

[36] Jessica Gliozzo, Marco Notaro, Alessandro Petrini, Paolo Perlasca, Marco Mesiti, Elena Casiraghi, Marco Frasca, Giuliano Grossi, Matteo Re, Alberto Paccanaro and Giorgio Valentini. «Modeling biomolecular profiles in a graph-structured sample space for clinical outcome prediction with melanoma and ovarian cancer patients». In: BITS 2017, Bioinformatics Italian Society Meeting, Cagliari, Italy. 5-7 July 2017 (5 lug. 2017).

[37] Paolo Perlasca, Marco Mesiti, Marco Notaro, Alessandro Petrini, Jessica Gliozzo, Giorgio Valentini and Marco Frasca. «A Web Graphical Tool for the Integration of Unbalanced Biomolecular Networks». In: BITS 2017, Bioinformatics Italian Society Meeting, Cagliari, Italy. 5-7 July 2017 (lug. 2017).

[38] Alessandro Petrini, Marco Notaro, Jessica Gliozzo, Giorgio Valentini, Giuliano Grossi and Marco Frasca. «Speeding up node label learning in unbalanced biomolecular networks through a parallel and sparse GPU – based Hopfield model». In: BITS 2017, Bioinformatics Italian Society Meeting, Cagliari, Italy. 5-7 July 2017

(5 lug. 2017).

PhD thesis:

[39] Jessica Gliozzo. «PATIENT SIMILARITY NETWORKS-BASED METHODS FOR MULTIMODAL DATA INTEGRATION AND CLINICAL OUTCOME PREDICTION». In: Dipartimento di Informatica Giovanni Degli Antoni, Università degli Studi di Milano (17 apr. 2024). A cura di A. Patak; coordinator: R. Sassi. supervisor: G. Valentini; co-supervisor: E. Casiraghi. PhD Thesis. 36. ciclo, Academic Year 2022/2023. url: https://hdl.handle.net/2434/1040030.

Productivity indices:

Productivity indices are showed in the following table which data were extracted in date 12 June 2024 from Scopus and Google Scholar databases.

	h-index	i10-index	Number of citations
Scopus	7	4	207
Google Scholar	7	5	321

I published 15 papers on peer-reviewed international journals and 9 papers in conference proceedings.

Teaching activities:

- Lecturer for one lesson entitled "Kernels on graphs and the P-Net algorithm" for the course "Bioinformatics" (master's degree program in Computer Science [LM-18], Università degli Studi di Milano) in the academic years 2020-2021 and 2021-2022. The same lecture was also provided into the course "Principles and Models of Perception" (bachelor's degree in Computer Science for New Media Communications [L-31], Università degli Studi di Milano) in the academic year 2021-2022.
- Tutor for the practical lessons of the course "Bioinformatics" (master's degree program in Computer Science [LM-18], Università degli Studi di Milano) in the academic years 2022-2023 and 2023-2024.
- Lecturer in the advanced program entitled "FILOGENESI APPLICATA ALLA EPIDEMIOLOGIA E SORVEGLIANZA GENOMICA DEGLI AGENTI INFETTIVI'" at Dipartimento di Scienze Biomediche e Cliniche, Università degli Studi di Milano. I will present my work entitled "Pipelines automatiche per l'analisi di genomi virali SARS-CoV-2" (lecture programmed in date 5 July 2024).

Co-supervisor of the following bachelor's thesis:

- "Classificazione del rischio di pazienti COVID-19 tramite uno score radiologico di esperti e uno score radiologico ottenuto tramite AI" for the degree program in Computer Science for New Media Communications [L-31]
- "Imputazione di dati mancanti in ambito medico: uno studio su dati di pazienti COVID-19" for the degree program in Computer Science for New Media Communications [L-31]
- "Similarity measures for patient-networks based on clinical and genomic data" for the degree program in Computer Science for New Media Communications [L-31]
- "Integrazione di dati multimodali tramite fattorizzazione di matrici" for the degree program in Computer Science [L-31]

Co-supervisor of the following master's thesis:

- "Deep Neural Network Multimodali per la predizione di regioni regolatorie nel genoma umano" for the degree program in Computer Science [LM-18]
- "Sviluppo di una pipeline bioinformatica automatizzata per l'analisi di genomi virali SARS-CoV-2" for the degree program in Computer Science [LM-18]

Reviewer for scientific journals:

- Reviewer of one paper for the journal Nature Scientific Reports (Sci Rep) in November 2022.
- Reviewer of one paper for the journal Nature Communications (Nat. Commun.) in April 2024.

Organization of conferences and workshops:

I am currently in the Program Committee of the workshop “SAI-Care 2024: Integrating Symbiotic AI in Biomedical Informatics, A Workshop on Advanced SAI-based applications in Healthcare'”.

Computational skills:

- Developer of the software library *miss-SNF*
  (R library publicly available on https://github.com/GliozzoJ/missSNF)
- Developer of the software library *P-Net*: *Network-based ranking of patients with respect to a given phenotype/outcome*
  (R library publicly available on https://github.com/GliozzoJ/P-Net)
- Developer of the software library *pathonet_compression: Reducing the Complexity of Deep Learning Models for Medical Applications in Resource-limited Contexts.*
  (Python repository publicly available on https://github.com/GliozzoJ/pathonet_compression)
- Contributor of the library *PathoNet: deep neural network backend for evaluation of Ki-67 and tumor-infiltrating lymphocytes in breast cancer.*
  (Python repository publicly available on https://github.com/SHIDCenter/PathoNet)
- Maintainer of the software library *NetInt: Methods for Unweighted and Weighted Network Integration.*
  (R library available on CRAN https://cran.r-project.org/web/packages/NetInt/index.html)
- Contributor of the R package *mclustcomp: Measures for Comparing Clusters.*
  (R library available on https://github.com/kisungyou/mclustcomp)

Other courses:

- Followed the course “VIII Edition - NGS data analysis and applications in diagnostic (University of Pavia)”, 16-19th July 2018
- Attended the summer school "Jacob T. Schwartz International School for Scientific Research - Lipari School on Computational Life Sciences" entitled Artificial Intelligence in Biomedicine (July 24th - July 30th, 2022), in Lipari Island, Italy

Declarations given in the present curriculum must be considered released according to art. 46 and 47 of DPR n. 445/2000.

The present curriculum does not contain confidential and legal information according to art. 4, paragraph 1, points d) and e) of D.Lgs. 30.06.2003 n. 196.

Please note that CV WILL BE PUBLISHED on the University website and It is recommended that personal and sensitive data should not be included. This template is realized to satisfy the need of publication without personal and sensitive data.

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Place and date: Cesano Boscone (Milan), 19/06/2024