UNIVERSITÀ DEGLI STUDI DI MILANO

TO MAGNIFICO RETTORE OF UNIVERSITA' DEGLI STUDI DI MILANO   **ID CODE 5810**

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. Marco Mesiti**

Jessica Gliozzo

CURRICULUM VITAE

PERSONAL INFORMATION

Surname	Gliozzo
Name	Jessica

PRESENT OCCUPATION

Appointment	Structure
PhD Student	Collaborative Doctoral Partnership programme between Università degli Studi di Milano and Joint Research Centre (JRC-Ispra) of the European Commission. Currently hosted by Joint Research Centre (JRC-Ispra).

EDUCATION AND TRAINING

Degree	Course of studies	University	year of achievement of the degree
Degree	Biotecnologie Molecolari e Bioinformatica	Università degli Studi di Milano	2016
Specialization			
PhD	Informatica	Università degli Studi di Milano	2024 (Expected date)
Master			
Degree of medical specialization			
Degree of European specialization			
Other			

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Università degli Studi di Milano – Direzione Trattamenti Economici e Lavoro Autonomo
Ufficio Contratti di formazione e Ricerca
Via Sant'Antonio 12 - 20122 Milano, Italia
assegni.ricerca@unimi.it DTELA_M_CVAssegniENG_rev. 00 del 02/09/2021

UNIVERSITÀ DEGLI STUDI DI MILANO

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 PhD student in Computer Science enrolled in the Collaborative Doctoral Partnership (CDP) programme between Università degli Studi di Milano and Joint Research Centre of the European Commission. 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 [7]. 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 pediatric subjects and children affected by metachromatic leukodystrophy. During these years, she continued to collaborate with the Department of Computer Science of Università degli Studi di Milano on various research lines, such:

1. Genome-wide prediction of tissue-specific regulatory regions using deep neural networks
2. Methods for the integration and the visual analysis of biomolecular networks
3. Bioinformatics analysis of Next Generation Sequencing data

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

Currently, she is working on the development of a multi-modal integration approach based on patient similarity networks able to integrate different genomic data sources where one of more data sources can be completely missing for a considered patient.

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 pediatric 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 though patient-similarity networks. |

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] 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 (July 2022).
[2] 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 (May 2021), e162–e169.
[3] 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." BMC bioinformatics 23.2 (2022): 1-32.
[4] Adriana Cassaro, Giovanni Grillo, Marco Notaro, Jessica Gliozzo, Ilaria Esposito, Gianluigi Reda, Alessandra Trojani, Giorgio Valentini, Barbara Di Camillo, Roberto Cairoli, et al. "FZD6 triggers Wnt–signalling driven by WNT10BIVS1 expression and highlights new targets in T-cell acute lymphoblastic leukemia". In: Hematological oncology (2021).
[5] 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 (July 2021). btab485. ISSN: 1367-4803. DOI: 10.1093/bioinformatics/btab485 URL: https://doi.org/10.1093/bioinformatics/btab485.
[6] Barbara Rita Barricelli, Elena Casiraghi, Jessica Gliozzo, Alessandro Petrini, and Stefano Valtolina. "Human Digital Twin for Fitness Management". In: IEEE Access 8 (2020), pp. 26637–26664. ISSN: 2169-3536. DOI: 10.1109/ACCESS.2020.2971576

[7] Jessica Gliozzo, Paolo Perlasca, Marco Mesiti, Elena Casiraghi, Viviana Vallacchi, Elisabetta Vergani, Marco Frasca, Giuliano Grossi, Alessandro Petrini, Matteo Re, et al. "Network modeling of patients' biomolecular profiles for clinical phenotype/outcome prediction". In: Scientific reports 10.1 (2020), pp. 1–15.

[8] 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 (2020), e0244241.

[9] 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 (2019), p. 733.

[10] Armando N Bastidas Torres, Davy Cats, Hailiang Mei, Daniele Fanoni, Jessica Gliozzo, Laura Corti, Marco Paulli, Maarten H Vermeer, Rein Willemze, Emilio Berti, and CP Tensen. "Whole-genome analysis uncovers recurrent IKZF1 inactivation and aberrant cell adhesion in blastic plasmacytoid dendritic cell neoplasm". In: Genes, Chromosomes and Cancer (2019).

[11] 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 99.3 (2019), pp. 450–451.

[12] 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 (2019), pp. 16–21.

[13] 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 (2019), pp. 1–19.

[14] 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 (2018), p. 353.

Congress proceedings

[15] Jessica Gliozzo, Giosuè Marinò, Arturo Bonometti, Marco Frasca, and Dario Malchiodi. "Resource-Limited Automated Ki67 Index Estimation in Breast Cancer". In: ICBRA 2023, 10th International Conference on Bioinformatics Research and Applications, Barcelona, Spain, September 22-24, 2023. [Accepted]

[16] Gliozzo, Jessica, et al. "Patient Similarity Networks Integration for Partial Multimodal Datasets." Proceedings of the 16th International Joint Conference on Biomedical Engineering Systems and Technologies. 3: Bioinformatics. Scitepress, 2023.

[17] Emanuele Cavalleri, Sara Bonfitto, Alberto Cabri, Jessica Gliozzo, Paolo Perlasca, Mauricio Soto-Gomez, Gabriella Trucco, Elena Casiraghi, Giorgio Valentini and Marco Mesiti. "Towards the Construction of an RNA-centered Knowledge Graph". In: SEBD 2023, 31st Symposium on Advanced Database System, 2-5 July 2023, Galzignano Terme, Italy [Accepted]

[18] Emanuele Cavalleri, Sara Bonfitto, Alberto Cabri, Jessica Gliozzo, Paolo Perlasca, Mauricio Soto-Gomez, Gabriella Trucco, Elena Casiraghi, Giorgio Valentini, Marco Mesiti. "A Meta-Graph for the Construction of an RNA-centered Knowledge Graph". In: IWBBIO 2023, 10th International Work-Conference on Bioinformatics and Biomedical Engineering, July 12th-14th, 2023, Gran Canaria, Spain [Accepted]

[19] Valentina Guarino, Jessica Gliozzo, Ferdinando Clarelli et al. "Intrinsic-Dimension Analysis for Guiding Dimensionality Reduction in Multi-Omics Data." Proceedings of the 16th International Joint Conference on Biomedical Engineering Systems and Technologies. 3: Bioinformatics. Scitepress, 2023.

[20] Paolo Perlasca, Marco Frasca, Cheick Tidiane Ba, Jessica Gliozzo, Marco Notaro, Mario Pennacchioni,

Giorgio Valentini and Marco Mesiti (2023). "Integration and Visual Analysis of Biomolecular Networks Through UNIPred-Web". In: Current Trends in Web Engineering. ICWE 2022. Communications in Computer and Information Science, vol 1668. Springer, Cham. https://doi.org/10.1007/978-3-031-25380-5_15

[21] 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: Maglogiannis, I., Iliadis, L., Macintyre, J., Cortez, P. (eds) Artificial Intelligence Applications and Innovations. AIAI 2022 IFIP WG 12.5 International Workshops. AIAI 2022. IFIP Advances in Information and Communication Technology, vol 652. Springer, Cham. https://doi.org/10.1007/978-3-031-08341-9_34

[22] Cheick Tidiane Ba, Elena Casiraghi, Marco Frasca, Jessica Gliozzo, Giuliano Grossi, Marco Mesiti, Marco Notaro, Paolo Perlasca, Petrini Alessandro, Matteo Re, and Giorgio Valentini. Ba, C.T. et al. (2020). "A Graphical Tool for the Exploration and Visual Analysis of Biomolecular Networks". In: Raposo, M., Ribeiro, P., Sério, S., Staiano, A., Ciaramella, A. (eds) Computational Intelligence Methods for Bioinformatics and Biostatistics. CIBB 2018. Lecture Notes in Computer Science(), vol 11925. Springer, Cham. https://doi.org/10.1007/978-3-030-34585-3_8

[23] 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: Rojas, I., Valenzuela, O., Rojas, F., Herrera, L., Ortuño, F. (eds) Bioinformatics and Biomedical Engineering. IWBBIO 2020. Lecture Notes in Computer Science, vol 12108. Springer, Cham. https://doi.org/10.1007/978-3-030-45385-5_54

[24] 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 (2019), e27548. DOI: 10.1002/pbc.27548.

[25] Silvia Alberti-Violetti, Mirco Virgilio Pozzi, Daniele Fanoni, Chiara Moltrasio, Jessica Gliozzo, Luigia Venegoni, Valentina Merlo, and Emilio Berti. "Indolent cytotoxic cutaneous lymphomas with clinical and histological features of atypical lymphoid proliferation not otherwise specified." In: European Journal of Cancer 101 (2018), S22–S23.

OTHER INFORMATION

Author of the following abstracts presented as conference posters:

[26] 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 (2022).

[27] 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) (2019).

[28] Arturo Bonometti, Chiara Moltrasio, Jessica Gliozzo, Filippo Bagnoli, Emanuela Passoni, Gianluca Nazzaro, Silvia Alberti-Violetti, Emanuela De Juli, Marco Paulli, and Emilio Berti. "Myeloid Leukemia and Cutaneous Histiocytosis: fortuitous encounter?" In: 24th World Congress of Dermatology (WCD) (2019).

[29] 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) (2019).

[30] Sebastiano Recalcati, Chiara Moltrasio, Gianluca Nazzaro, Emanuela Passoni, Jessica Gliozzo, Simona Muratori, and Emilio Berti. "Effects of Polydeoxyribonucleotide in the treatment of Scleroderma". In: 24th World Congress of Dermatology (WCD) (2019).

[31] 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, Berlin, Germany. Oct. 2018.

[32] J. Gliozzo, M. Notaro, A. Petrini, P. Perlasca, M. Mesiti, E. Casiraghi, M. Frasca, G. Grossi, M. Re, A. Paccanaro, and G. 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 (2017).

[33] P. Perlasca, M. Mesiti, M. Notaro, A. Petrini, J. Gliozzo, G. Valentini, and M. Frasca. "A Web Graphical Tool for the Integration of Unbalanced Biomolecular Networks". In: BITS 2017, Bioinformatics Italian Society Meeting, Cagliari, Italy (2017).

[34] A. Petrini, M. Notaro, J. Gliozzo, G. Valentini, G. Grossi, and M. 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 (2017).

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 year 2022-2023.

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.

Computational skills:

- Developer of the software library *P-Net*
  (R library publicly available on https://github.com/GliozzoJ/P-Net)
- Developer of the software library *pathonet_compression*
  (Python repository publicly available on https://github.com/GliozzoJ/pathonet_compression)
- Contributor of the library *PathoNet*
  (Python repository publicly available on https://github.com/SHIDCenter/PathoNet)
- Maintainer of the software library *NetInt*

	(R library available on CRAN https://cran.r-project.org/web/packages/NetInt/index.html)
•	Contributor of the R package *mclustcomp* (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.

Please DO NOT SIGN this form.

Place and date: Ispra (Varese), 20/06/2023