Matteo Bulloni

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📍 Milan, Italy

Languages

English ●●●●●
(in 2015: TOEFL iBT 111/120 - C1)

Italian ●●●●●

Spanish ●●●○○

Mandarin ●●○○○

education

2018-	Ph.D. & (now) postdoc in Bioengineering Polytechnic University of Milan	
2015-2018	M.Sc. Computer Science and Engineering Polytechnic University of Milan	Final grade 110/110, cum laude
2013-2014	B.Sc. Computer Science and Technology Tongji University 同济大学, Shanghai, China	
2012-2015	B.Sc. Computer Science and Engineering Polytechnic University of Milan	Final grade 110/110, cum laude

research

In each study here, I am either first or co-first author - no marginal/inflated contributions.

Links:

❖ **Computational pathology:**
- Within a collaboration between seven European hospitals, I developed a **predictor of cancer outcome according to a description of the 2D spatial organization of proliferating tumor cells,** based on mathematical models from graph theory, stochastic geometry, fractal analysis and information theory fields.

  Ph.D. thesis

- I single-handedly designed and wrote the chapter **"AI in Digital Pathology"** of the university textbook "Manual of Functional Pathological Anatomy" (2022), an analysis of the role of AI in the field accompanied by a gentle introduction to machine and deep learning from scratch for future physicians.

  chapter book

❖ **Bioinformatics:**
- I co-conducted a thorough multi-omics study of the **interplay between the master regulator genes p40 and TTF1 in non-small cell lung cancer,** through statistical and systems biology approaches applied to NGS and microarray data.

  paper 1
  paper 2

- I co-conducted a functional genomics investigation of **human matches for chronic lymphocytic leukemia presentations in mice models** (paper is a rare conference contribution, presenting a small glimpse of the entire work; full paper ahead).

  paper

- (ongoing) I am investigating the **link between Duchenne muscular dystrophy and rhadomyosarcoma** in mice and men through pseudotime trajectory inference and functional genomics approaches, in microarray and NGS (bulk & single-cell) data, in collaboration with the Policlinico of Milan.

- (ongoing) Validating a model I developed for **estimating the loss of Y chromosome from unrelated NGS targeted sequencing data**, i.e., containing few to none targeted regions within the chromosome itself, in collaboration with Humanitas university.

- (ongoing) I developed a model and (to be) Matlab package for **quantification of mitochondrial flickering events in fluorescence microscopy** image sequences during neuronal transmission in hereditary spastic paraplegia, which I am employing in a large drug screening together with genomic data to assess drug efficacy, in collaboration with San Raffaele University.

- (paused) Supervising a project in collaboration with Monzino Cardiologic Center, a European excellence in cardiology research, on predicting deaths in cardiac intensive care unit harnessing topological data analysis.

- (paused) I extended the software Isomut for calling mutations comparing multiple samples to a reference one in absence of the organism's reference genome.

❖ **Radiomics:**
- I demonstrated that high-recall prediction of prosthetic hip implant failure is possible through only four parameters, thanks to a hybrid model combining standard radiological indices and derivative features describing the evolution of the implant's state through time.

  paper

- (paused) Tackling automated segmentation of Gruen zone #1 and radiolucency detection through deep CNNs in hip implant radiographs, an extremely challenging problem with no published attempted solution.

❖ **Anomaly detection:**
- Master's thesis on unsupervised money laundering detection: I devised an ensemble of LSTM autoencoders, a mathematical model based on copula distribution functions and a third element for Napier AI (London, UK).

teaching

❖ University Vita-Salute San Raffaele, Milan:

2021 - 2023 *Bioinformatics* (B. Sc. Biotechnological Research in Medicine)

❖ Polytechnic University of Milan:

2020 - *Systems Biology and Network Analysis* (M. Sc. Bioinformatics for Computational Genomics)

2018 - *Bioinformatics and Functional Genomics* (M. Sc. Biomedical & Computer Science Engineering)

2018 - *Elements of Medical Informatics* (B. Sc. Biomedical Engineering)

publications & scientific activity

❖ **Journal**   (*) = co-first authorship

1. ***Lack of imbalance between the master regulators TTF1/NKX2-1 and ΔNp63/p40 implies adverse prognosis in non-small cell lung cancer***
Vescio M*, Bulloni M*, Pelosi G, Pattini L
Sci Rep 2024;14, 2467, https://doi.org/10.1038/s41598-024-52776-z

2. ***AI-based hip prosthesis failure prediction through evolutional radiological indices***
Bulloni M, Gambaro FM, Chiappetta K, Corino V, Loppini M
Arch Orthop Trauma Surg 2024; 144, 895–907. https://doi.org/10.1007/s00402-023-05069-5

3. ***Automated analysis of proliferating cells spatial organization predicts prognosis in lung neuroendocrine neoplasms***
Bulloni M, Sandrini G, Stacchiotti I, Barberis M, Calabrese F, Carvalho L, Fontanini G, Alì G, Fortarezza F, Hofman P, Hofman V, Kern I, Maiorano E, Maragliano R, Marchiori D, Metovic J, Papotti M, Pezzuto F, Pisa E, Remmelink M, Serio G, Marzullo A, Trabucco SMR, Pennella A, De Palma A, Marulli G, Fassina A, Maffeis V, Nesi G, Naheed S, Rea F, Ottensmeier CH, Sessa F, Uccella S, Pelosi G, Pattini L
Cancers 2021; 13(19), 4875, https://doi.org/10.3390/cancers13194875

4. ***Coexpression of ΔNp63/p40 and thyroid transcription factor-1 within most of the same individual cells identifies life-threatening NSCLC featuring squamous and glandular biphenotypic differentiation: Clinicopathologic correlations***
Pelosi G*, Bulloni M*, Vescio M*, Uccella S, Forest F, Leone G, Barberis M, Rahal D, Bossi P, Finzi G, Marchiori D, De Luca M, Sessa F, Harari S, Spinelli M, Viola P, Macri P, Maria S, Rizzo A, Picone A, Pattini L
*JTO Clin Res Rep. 2021;*2:100222, https://doi.org/10.1016/j.jtocrr.2021.100222

5. ***Intratumor distribution of Ki-67 antigen beyond labelling index for clinical decision-making: A new way of counting***
Bulloni M, Pattini L, Pelosi G
JTO Clin Res Rep. 2021;2:100207, https://doi.org/10.1016/j.jtocrr.2021.100207

❖ **Conference papers & posters**

1. ***Exploring heterogeneity in lymphoid malignancies from mouse to human gene expression profiles***
Vescio M*, Bulloni M*, Brendolan A, Pattini L
GNB 2023, June 21st - 23rd 2023, Padova, Italy

2. ***Predicting Prognosis in Lung Neuroendocrine Neoplasms: An Automated Approach Based on the Analysis of Proliferating Cells Spatial Distribution***
Bulloni M, Sandrini G, Stacchiotti I, Barberis M, Calabrese F, Carvalho L, Fontanini G, Fortarezza F, Hofman P, Hofman V, Kern I, Maiorano E, Maragliano R, Marchiori D, Metovic J, Papotti M, Pezzuto F, Pisa E, Remmelink M, Serio G, Marzullo A, Trabucco SMR, Pennella A, De Palma A, Marulli G, Fassina A, Maffeis V, Nesi G, Naheed S, Rea F, Ottensmeier CH, Sessa F, Uccella S, Pelosi G, Pattini L
8th Digital Pathology & AI Congress: Europe, 2022

3. ***Intratumor Heterogeneity of Ki-67 is a Powerful and Histology-Independent Resource to Dissect Clinical Outcome of Lung Neuroendocrine Neoplasms by Means of Artificial Intelligence Tools***
Pelosi G, Bulloni M, Papotti M, Metovic J, Fontanini G, Pattini L
109th Annual Meeting of the United-States-and-Canadian-Academy-of-Pathology (USCAP) -
Modern Pathology, 2020, Volume: 33, Issue: Suppl. 2, Pages: 1811-1812

❖ **Book chapters**

1. *Intelligenza artificiale in patologia computazionale*
   Bulloni M, Pattini L
   Manuale di Anatomia Patologica Funzionale, Minerva Medica, 2022

❖ **Other attended conferences**

1. *Transcription and Chromatin (14th conference)*
   Virtual (EMBL Advanced Training Center, Heidelberg, Germany), 27-29 August 2020

2. *Multiomics to Mechanisms – Challenges in Data Integration*
   EMBL Advanced Training Center, Heidelberg, Germany, 11-13 September 2019

technical skills

Bioinformatics & comput. pathology	Microarray, NGS (bulk & single-cell) genomic and transcriptomic data analysis and manipulation; GWAS; functional genomics & systems biology tools (GSEA, ARACNe, VIPER, Phenopath, Slingshot, Cytoscape, ...); topological analysis of gene and protein interaction networks, application of graph & point process modeling techniques; analysis of dynamical networks behavior; statistical, enrichment and survival analyses; proportional hazards models; histopathology, radiology and fluorescence microscopy image processing and analysis.
Programming languages	Proficient in Python, Matlab. Solid but rusty knowledge of R. Formerly proficient in C, Java.
Platforms, tools, etc.	Familiar with Jupyter Notebook, Eclipse IDE, Git, Conda. Moderate experience (growing) with Tensorflow, OpenCV. Extensive experience with Pandas, Numpy, Imblearn, Sklearn.
OSs	Linux user since 2012, more or less familiar with everything concerning the Linux environment. Moderate experience in setup of Linux-based environments for distributed computing. Familiar with Windows.
Machine learning	Extensive experience with traditional ML. Moderate (growing) experience with DL for image classification (most recent net handled: CoAtNet-7). Formerly familiar with reinforcement learning algorithms (SARSA, Q-learning, ...). Limited experience with recommender systems design & algorithms.
Others	Familiar with LaTeX. Formerly familiar with propositional & fuzzy logic; linear programming; extending compilers (with related grammars & formal languages); OpenGL, WebGL; SQL; HTML; SROIQ(D).

academic transcript

I am proud of my academic record, with a GPA of 3.97 (4.0 scale, not counting "cum laude" - Italian scale: 29.8/30) in my Master's and 4.0 in my PhD. Polytechnic University of Milan is the highest-ranked university in Italy (according to QS Rankings 2023, 2022, 2021, ...).

academic transcript

Autorizzazioni:

Autorizzo al trattamento dati ai sensi del GDPR 2016/679 del 27 aprile 2016 (Regola-mento Europeo relativo alla protezione delle persone fisiche per quanto riguarda il trat-tamento dei dati personali).
Autorizzo la pubblicazione sul sito istituzione del Politecnico di Milano (sez. Amminis-trazione Trasparente) in ottemperanza al D. Lgs n. 33 del 14 marzo 2013 (e s.m.i.).