Simone Marini

University of Florida
Department of Epidemiology
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Education

09/2008-11/2012   PhD., Bioengineering. Thesis: "Qualitative and quantitative protein interaction prediction with machine learning". Division of Bioengineering, Hong Kong University of Science and Technology, Hong Kong

10/2004-12/2007   MSc, Biomedical Engineering. Thesis: "Design of a classifier by coevolution of genetic algorithms and genetic programming". Electrical, Computer and Biomedical Engineering department, University of Pavia, Italy

10/2000-03/2004   BSc, Biomedical Engineering. Thesis: "Bone tissue engineering, effects of mechanical shear stress on human osteoblast SAOS2". Electrical, Computer and Biomedical Engineering department, University of Pavia, Italy

Professional Appointments

Research Assistant Professor
08/2022-present   Department of Epidemiology, University of Florida, Gainesville, FL, USA

Research Assistant Professor
06/2020-07/2022   Department of Epidemiology, University of Florida, Gainesville, FL, USA

Research Assistant Scientist
01/2020-05/2020   Department of Epidemiology, University of Florida, Gainesville, FL, USA

Research Investigator
08/2017-12/2019   Department of Surgery, and Department of Computational Medicine and Bioinformatics, University of Michigan, Ann Arbor, MI, USA

Postdoctoral Fellow
12/2016-07/2017   Laboratory of Biomedical Informatics, University of Pavia, Italy

12/2015-11/2016   Laboratory of Mathematical Bioinformatics, University of Kyoto, Japan

01/2013-11/2015   Laboratory of Biomedical Informatics, University of Pavia, Italy

Publications

Journals (peer reviewed)

1. AMR-meta: a k-mer and metafeature approach to classify antimicrobial resistance from high-throughput short-read metagenomics data. **Marini S**, Oliva M, Slizovskiy I, Das R, Noyes N, Kahveci T, Boucher C, Prosperi M. *Gigascience*, *in press*

2. Towards routine employment of computational tools for antimicrobial resistance determination via high-throughput sequencing, **Marini S*§**, Mora R*, Boucher C, Noyes N, Prosperi M§. *Briefings in Bioinformatics 2022, in press*

3. Assessing putative bias in prediction of anti-microbial resistance from real-world genotyping data under explicit causal assumptions. Prosperi M, Boucher C, Bian J, **Marini S§**. *Artificial Intelligence in Medicine 2022, in press*

4. SARS-CoV-2 Delta vaccine breakthrough transmissibility in Alachua County, Florida. Magalis BR, Rich S, Tagliamonte MS, Mavian C, Cash MN, Riva A, **Marini S**, Moraga Amador DM, Zhang Y, Shapiro J, Horine A, Starostik P, Pieretti M, Vega S, Lacombe AP, Salinas J, Stevenson M, Myers P, Morris JG, Lauzardo M, Prosperi M, Salemi M. *Clin Infect Dis. 2022*, *in press*

5. Early emergence phase of SARS-CoV-2 Delta variant in Florida, US. Cella E, Ali S, Schmedes SE, Magalis BR, **Marini S**, Salemi M, Blanton J, Azarian T. *Viruses. 2022, in press*

6. Low-frequency variants in mildly symptomatic vaccine breakthrough infections present a double-edged sword. Magalis BR, Mavian C, Tagliamonte M, Rich SN, Cash M, Riva A, Loeb JC, Norris M, Moraga Amador D, Zhang Y, Shapiro J, Starostik P, **Marini S**, Myers P, Ostrov DA, Lednicky JA, Morris JG, Lauzardo M, Salemi M. *Journal of Medical Virology 2022, in press*

7. Optimizing viral genome subsampling by genetic diversity and temporal distribution (TARDiS) for Phylogenetics. **Marini S**, Mavian C, Riva A, Salemi M, Magalis BR. *Bioinformatics 2021*

8. Exploring Prediction of Antimicrobial Resistance Based on Protein Solvent Accessibility Variation. **Marini S**, Oliva M, Slizovskiy IB, Noyes NR, Boucher C, Prosperi M. *Frontiers in Genetics 2021*

9. Fast and exact quantification of motif occurrences in biological sequences. Prosperi M, **Marini S**, Boucher C. *BMC bioinformatics 2021*

10. Brain tissue transcriptomic analysis of SIV-infected macaques identifies several altered metabolic pathways linked to neuropathogenesis and poly (ADP-ribose) polymerases (PARPs) as potential therapeutic targets. Mavian C, Ramirez-Mata AS, Dollar JJ, Nolan DJ, Cash M, White K, Rich SN, Magalis BR, **Marini S**, Prosperi MC, Amador DM. B. *Journal of neurovirology 2021*

11. Earliest detection to date of SARS-CoV-2 in Florida: Identification together with influenza virus on the main entry door of a university building. Lednicky J, Salemi M, Subramaniam K, Waltzek TB, Sabo-Attwood T, Loeb JC, Hentschel S, Tagliamonte MS, **Marini S**, Alam MM, Stephenson CJ. *PloS One 2021*

12. Novel lineage-tracing system to identify site-specific ectopic bone precursor cells. Pagani CA, Huber AK, Hwang C, **Marini S**, Padmanabhan K, Livingston N, Nunez J, Sun Y, Edwards N, Cheng YH, Visser N. *Stem Cell Reports 2021*

13. NGF-TrkA signaling dictates neural ingrowth and aberrant osteochondral differentiation after soft tissue trauma. Lee S, Hwang C, **Marini S**, Tower RJ, Qin Q, Negri S, Pagani CA, Sun Y, Stepien DM, Sorkin M, Kubiak CA. *Nature Communications 2021*

14. Do local curriculum scores correlate with national residency test results? A pluriannual, nationwide survey of Italian Medical Universities. Tarchi L, Damiani S, **Marini S**, Cappelli C, Liuzzi G, Minerva M, Politi P. *Italian Journal of Medicine 2021*

15. The colors of our brain: an integrated approach for dimensionality reduction and explainability in fMRI through color coding (i-ECO). Tarchi L, Damiani S, La Torraca Vittori P, **Marini S**, Nazzicari N, Castellini G, Pisano T, Politi P, Ricca V. *Brain Imaging and Behavior 2021*

16. Current Understanding of Ultraviolet-C Decontamination of N95 Filtering Facepiece Respirators. Grist SM, Geldert A, Gopal A, Su A, Balch HB, Herr AE, **N95DECON Consortium**. *Applied Biosafety 2021*

17. Heat and Humidity for Bioburden Reduction of N95 Filtering Facepiece Respirators. Anderegg L, Doyle J, Gardel ML, Gupta A, Hallas C, Lensky Y, Love NG, Lucas BA, Mazenc E, Meisenhelder C, Pillarisetti A, **Members of the N95DECON Consortium**. *Applied Biosafety 2021*

18. Room Temperature Wait and Reuse for Bioburden Reduction of SARS-CoV-2 on N95 Filtering Facepiece Respirators. Smullin SJ, Branden DT, **N95DECON Consortium**. *Applied Biosafety 2021*

19. Hydrogen Peroxide Methods for Decontaminating N95 Filtering Facepiece Respirators. Rempel D, Henneman J, Agalloco J, Crittenden J, **N95DECON Consortium**. *Applied Biosafety 2021*

20. A snapshot of SARS-CoV-2 genome availability up to April 2020 and its implications. **Marini S***, Mavian C*, Prosperi M, Salemi M, *JMIR Public Health and Surveillance 2020*

21. Endogenous CCN family member WISP1 inhibits trauma-induced heterotopic ossification. Ching-Yun HG, **Marini S**, Negri S, Wang Y, Xu J, Pagani C, Hwang C, Stepien D, Meyers CA, Miller S, McCarthy E, Lyons EK, Levi B, James AW. *JCI insight 2020*

22. Small molecule inhibition of non-canonical (TAK1-mediated) BMP signaling results in reduced chondrogenic ossification and heterotopic ossification in a rat model of blast-associated combat-related lower limb trauma. Strong AL, Spreadborough PJ, Pagani CA, Haskins RM, Dey D, Grimm PD, Kaneko K, **Marini S**, Huber AK, Hwang C, Westover K, Mishina Y, Matthew JB, Levi B, Davis TA. *Bone 2020*

23. Immobilization after injury alters extracellular matrix and stem cell fate. Huber AK, Patel N, Pagani CA, **Marini S**, Padmanabhan K, Matera DL, Said M, Hwang C, Hsu GC, Poli AA, Strong AL. *The Journal of Clinical Investigation 2020*

24. Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. Mavian C, Kosakovsky Pond SL, **Marini S**, Magalis BR, Vandamme AM, Dellincour S, Scarpino SV, Houldcroft CJ, Villabona-Arenas J, Paisie TK, Trovão NS, Boucher C, Zhang Y, Scheuermann RH, Gascuel O, Lam TTY, Suchard

MA, Abecasis A, Wilkinson E, de Oliverira T, Bento A, Schmidt HA, Martin DP, Hadefield J, Faria N, Grubaugh N, Neher R, Beale G, Lemey P, Stadler T, Albert J, Crandall KA, Leitner T, Stamatakis A, Prosperi M, Salemi M. *PNAS 2020*

25. Beneath the surface: Hyper-connectivity between caudate and salience regions in ADHD fMRI at rest. Damiani S, Tarchi L, Scalabrini A, **Marini S**, Provenzani U, Rocchetti M, Oliva F, Politi P. *European Child & Adolescent Psychiatry 2020*

26. Tuning Macrophage Phenotype to Mitigate Skeletal Muscle Fibrosis. Stepien DM, Hwang C, **Marini S**, Pagani CA, Sorkin M, Visser ND, Huber AK, Edwards MJ, Loder SJ, Vasquez K, Aguilar CA, Kumar R, Mascharak S, Longaker MT, Li J, Levi L. *The journal of immunology 2020*

27. Comparative study of salivary, duodenal and fecal microbiota composition across adult celiac disease. Panelli S, Capelli E, Lupo G, Schiepatti E, Betti E, Sauta E, **Marini S**, Bellazzi R, Vanoli A, Pasi A, Cacciatore R, Bacchi S, Balestra S, Pastoris O, Frulloni L, Corazza GR, Biagi F, Ciccocioppo E. *Journal of Clinical Medicine 2020*

28. Perivascular fibro-adipogenic progenitor tracing during post-traumatic osteoarthritis Sono T, Hsu CY, Wang Y, Xu J, Cherief M, **Marini S**, Huber AK, Miller S, Péault B, Levi B, and James AW. *The American Journal of Pathology 2020*

29. Activin A does not drive post-traumatic heterotopic ossification. Hwang C, Das N, **Marini S**, Pagani CA, Huber AK, Xie LQ, Huang L, Wang L, Wen X, Nannuru K, Murphy A, Economides AN, Hatsell SJ, Levi B. *Bone 2020*

30. Scientific Collaboration During the COVID-19 Pandemic: N95DECON.org. Rempel D, **Members of the N95DECON Consortium**. *Annals of Work Exposures and Health 2020*

31. The role of neutrophil extracellular traps and TLR signaling in skeletal muscle ischemia reperfusion injury. Edwards NJ, Hwang C, **Marini S**, Pagani CA, Spreadborough PJ, Rowe CJ, Yu P, Mei A, Visser N, Li S, Hespe GE. *The FASEB Journal 2020.*

32. MTGO-SC, a tool to explore gene modules in single cell RNA-seq data. Nazzicari N, Vella D, Coronnello C, Di Silvestre D, Bellazzi R, **Marini S§**. *Frontiers in Genetics 2019*

33. Protease target prediction via matrix factorization. **Marini S*§**, Vitali F*, Rampazzi S, Demartini A, Akutsu T§. *Bioinformatics 2019*

34. Disruption of Neutrophil Extracellular Traps (NETs) Links Mechanical Strain to Post-traumatic Inflammation. Agarwal S, Shawn LJ, Cholok D, Li J, Bian J, Yalavarthi S, Li S, Carson WF, Hwang C, **Marini S**, Pagani C, Edwards N, Delano MJ, Standiford TJ, Knight JS, Kunkel SL, Mishina Y, Ward PA, Levi B. *Frontiers in Immunology 2019*

35. Mesenchymal VEGFA induces aberrant differentiation in heterotopic ossification Hwang C, **Marini S**, Huber AK, Stepien D, Sorkin M, Loder, S, Pagani C, Li J, Visser ND, Vasquez K, Garada MA, Li S, Xu J, Yu PB, James AW, Mishina Y, Agarwal S, Li J, Levi B. *Nature Bone Research 2019*

36. A comprehensive roadmap of murine spermatogenesis defined by single-cell RNA-seq. Green CD, Ma Q, Manske GL, Shami AN, Zheng X, **Marini S**, Moritiz L, Sultan C, Gurczynski SJ, Moore BB, Tallquist MD, Li JZ, Hammoud SS. *Developmental Cell 2018*

37. MTGO: PPI network analysis via topological and functional module identification Vella D, **Marini S§**, Vitali F, Di Silvestre D, Mauri G, and Bellazzi R. *Scientific Reports 2018*

38. Patient similarity by joint matrix tri-factorization to identify subgroups in precision oncology. **Marini S***, Vitali F*, Pala D, Demartini A, Montoli S, Zambelli A, Bellazzi R. *Jamia Open 2018*

39. Towards more accurate prediction of caspase cleavage sites: a comprehensive review of current methods, tools and features. Bao Y., **Marini S**, Tamura T, Kamada M, Maegawa S, Hosokawa H, Song J Akutsu T. *Briefings in Bioinformatics 2018*

40. Risk factors for the development of micro-vascular complications of type 2 diabetes in a single-centre cohort of patients. Chiovato L, Teliti M, Cogni G, Sacchi L, Dagliati A, **Marini S**, Tibollo V, De Cata P, Bellazzi R. *Diabetes and Vascular Disease Research 2018*

41. Patient similarity for precision medicine: A systematic review. Parimbelli E, **Marini S**, Sacchi L, Bellazzi R *Journal of Biomedical Informatics 2018*

42. A variant within the FTO confers susceptibility to diabetic nephropathy in Japanese patients with type 2 diabetes. Taira M, Imamura M, Takahashi A, Kamatani Y, Yamauchi T, Araki S, Tanaka N, van Zuydam NR, Ahlqvist E, Toyoda M, Umezono T, Kawai K, Imanishi M, Watada H, Suzuki D, Maegawa H, Babazono T, Kaku K, Kawamori R, The SUMMIT Consortium, Groop LC, McCarthy MI, Kadowaki T, Maeda S. *PloS One 2018*

43. Exploring Wound-Healing Genomic Machinery with a Network-Based Approach. Vitali F, **Marini S§**, Balli M, Grosemans H, Sampaolesi M, Lussier YA, Cusella De Angelis MG, Bellazzi R§. *Pharmaceuticals 2017*

44. Dscam1 Web Server: online prediction of Dscam1 self- and hetero-affinity. **Marini S*§**, Nazzicari N*, Biscarini F, Wang GZ§. *Bioinformatics 2017*

45. Machine learning methods to predict Diabetes complications. **Marini S***, Dagliati A*, Sacchi L, Bellazzi R. *Journal of Diabetes Science and Technology 2017*

46. A data fusion approach to enhance association study in epilepsy. **Marini S§**, Limongelli I, Rizzo E, Errichiello E, Vetro A, Tan D, Zuffardi O, Bellazzi R. *Plos One 2016*

47. "Noisy beets": impact of phenotyping errors on genomic predictions for binary traits in Beta vulgaris. Biscarini F, Nazzicari N, Broccanello C; Stevanato P, **Marini S**. Plant Methods 2016

48. Trans-ethnic fine mapping highlights kidney-function genes linked to salt sensitivity. Mahajan A, Rodan AR, Le TH, Gaulton KJ, Haessler J, Stilp AM, Kamatani Y, Zhu G, Sofer T, Puri S, Schellinger JN, Chu PL, Cechova S, van Zuydam N, Arnlov J, Flessner MF, Giedraitis V, Heath AC, Kubo M, Larsson A, Lindgren CM, Madden PAF, Montgomery GW, Papanicolaou GJ, Reiner AP, Sundström J, Thornton TA, Lind L, Ingelsson E, Cai J, Martin NG, Kooperberg C, Matsuda K, Whitfield JB, Okada Y, Laurie CC, Morris AP, Franceschini N, **The SUMMIT Consortium**, BioBank Japan Project. *The American Journal of Human Genetics 2016*

49. Dynamic Bayesian Network model for long-term simulation of clinical complications in type 1 diabetes. **Marini S*§**, Trifoglio E*, Barbarini N, Sambo F, Di Camillo B, Malovini A, Manfrini M, Cobelli C, Bellazzi R. *Journal of Biomedical Informatics 2015*

50. PaPI: pseudo amino acid composition to score human coding variants. Limongelli I, **Marini S**, Bellazzi R. *BMC Bioinformatics 2015*

51. Developing a parsimonious predictor for binary traits in sugar beet (Beta vulgaris) Biscarini F, **Marini S**, Stevanato P, Broccanello C, Bellazzi R, Nazzicari N. *Molecular Breeding 2015*
52. Improvement of Dscam homophilic binding affinity throughout Drosophila evolution. **Marini S***, Wang GZ*, Ma X, Yang Q, Zhang X, Zhu Y. *BMC Evolutionary Biology 2014*
53. The role of SwrA, DegU and P(D3) in fla/che expression in B. subtilis. Mordini S, Osera C, **Marini S**, Scavone F, Bellazzi R, Galizzi A, Calvio C. *PLoS One 2013*
54. In silico Protein-Protein Interaction prediction with sequence alignment and classifier stacking. **Marini S**, Xu Q, Yang Q. *Current Protein and Peptide Science 2011*

Conference Papers (peer reviewed)
1. KARGA: Multi-platform Toolkit for k-mer-based Antibiotic Resistance Gene Analysis of High-throughput Sequencing Data. Prosperi M§*, **Marini S§***. *IEEE International Conference on Biomedical and Health Informatics (BHI) 2021*
2. Assessing putative bias in prediction of anti-microbial resistance from real-world genotyping data under explicit causal assumptions. Prosperi M, **Marini S**, Boucher C, Bian J. *KDD Health Day and 2021 KDD Workshop on Applied Data Science for Healthcare 2021*
3. A semi-supervised learning approach for pan-cancer somatic genomic variant classification. Nicora G, **Marini S**, Limongelli I, Rizzo E, Montoli S, Tricomi FF, Bellazzi R. *Conference of Artificial Intelligence in Medicine (AIME) 2019*
4. Learning T2D evolving complexity from EMR and administrative data using Continuous Time Bayesian Networks. **Marini S**, Dagliati A, Sacchi L, Bellazzi R. *International Joint Conference on Biomedical Engineering System and Technology (HEALTHINF) 2109*
5. A genomic data fusion framework to exploit rare and common variants for association discovery. Marini S, Limongelli I, Rizzo E, Da T, Bellazzi R. *Conference of Artificial Intelligence in Medicine (AIME) 2016*
6. Matrix tri-factorization for miRNA-gene association discovery in acute myeloid leukemia. De Martini A, **Marini S**, Vitali F, Bellazzi R. *Conference of Artificial Intelligence in Medicine (AIME) 2016*

Conference Abstracts (peer reviewed)
1. Assessing High-Throughput Sequencing Based Algorithms As An Alternative And/or Complement To Phenotypic Antibiotic Susceptibility Testing In Livestock. Mora R, Jeong KC, **Marini S**, Prosperi M. *ASM Microbe 2022*
2. Dynamic prediction of Non-neutral SARS-Cov-2 Variants using Incremental Machine Learning. Nicora G, **Marini S**, Salemi M, Bellazzi R. *Medical Informatics Europe 2022*
3. Peripheral Nerves Engage in Reciprocal Neuro-and Angiogenic Crosstalk With SMCs in Extremity Trauma. Hwang CD, Pagani CA, Lee S, Qin Q, **Marini S**, Huber A, Meyers CA, Hespe GE, Strong AL, Stepien DM, Sorkin M, Nunez J, James AW, Levi B. *Plastic and Reconstructive Surgery–Global Open 2021*
4. Learning antimicrobial resistance through secondary structure of protein variants. **Marini S**, Slizovskiy I, Noyes N, Boucher C, Prosperi M. *International Conference on Intelligent Systems for Molecular Biology (ISMB) 2020*

5. Optimizing viral genome subsampling by genomic diversity and temporal distribution. **Marini S**, Mavian C, Salemi M, Rife Magalis B. *COVID-19 Dynamics & Evolution 2020*

6. Dynamic identification of viral transmission epicenters. Rife Magalis B, **Marini S**, Salemi M, Prosperi M. *International Conference on Intelligent Systems for Molecular Biology (ISMB) 2020*

7. Identifying The Myeloid Subpopulation Responsible For Tissue Fibrosis Across Organ Systems Via Machine Learning Parameterization And Predictive Transcriptomics. Stepien DM, **Marini S**, Hwang C, Pagani CA, Sorkin M, Visser ND, Huber AK, Vasquez K, Li J, Hatsell S, Economides A. *Plastic and Reconstructive Surgery–Global Open 2020*

8. Post-Traumatic Limb Immobilization Alters Mesenchymal Stem Cell Fate. Patel N, Huber AK, Pagani C, **Marini S**, Hwang C, Loder S, Visser N, Greenstein JA, Vasquez K, Li J, Mishina Y. *Plastic and Reconstructive Surgery–Global Open 2020*

9. Nerve Growth Factor Derives From Pericytes And Smooth Muscle Cells After Extremity Trauma. Hwang C, **Marini S**, Huber AK, Lee S, Stepien DM, Kubiak CA, Meyers C, Sorkin M, Pagani CA, Rehse T, Visser ND. *Plastic and Reconstructive Surgery–Global Open 2020*

10. Differing impacts of global and regional responses on SARS-CoV-2 transmission cluster dynamics. Rife Magalis B, **Marini S**, Salemi M, Prosperi M. *COVID-19 Dynamics & Evolution 2020*

11. Estimating cancer stemness with single-cell RNA sequencing. **Marini S**, Brooks M, Wicha M, Li J. *Keystone Symposia Conference (L1: Single Cell Biology) 2019*

12. Diverse mesenchymal stem cell populations contribute to VEGFA expression in post-traumatic heterotopic ossification. Pagani C, Hwang C, **Marini S**, Stepien DM, Sorkin M, Loder S, Visser ND, Vasquez K, Garada MA, James AW, Mishina Y, Agarwal S, Li J, Levi B. *American Society for Bone and Mineral Research Annual Meeting (ASMBR) 2019*

13. Gene-gene interaction module identification in single-cell RNA sequencing. **Marini S**, Vella D, Nazzicari N, Bellazzi R. *International Conference on Complex Networks and Their Applications (Complex Networks) 2018*

14. Gene interaction discovery in myelodysplastic syndromes. **Marini S**, Vitali F, Demartini A, Bellazzi R. *European Conference of Human Genetics (ESHG) 2018*

15. Data Fusion for cleavage target prediction. **Marini S**, Demartini A, Vitali F, Bellazzi R, Akutsu T. *Bioinformatics Italian Society National Congress (BITS) 2016*

16. A continuous time, multivariate model to simulate Type 2 Diabetes patients trajectories. **Marini S**, Dagliati A, Bellazzi R. *American Medical Informatics Association joint Summits on Translational Science (AMIA) 2016*

17. Predicting Microvascular Complications from Type 2 Diabetes Retrospective Data. Sacchi L, Colombo C, Dagliati D, **Marini S**, Cerra C, Chiovato L, Bellazzi R. *Annual Diabetes Technology Meetings (DTM) 2014*

18. A multivariate data-driven model to investigate the arising of complications in T2D patients. **Marini S**, Malavolti M, Dagliati A, Bellazzi R. *Annual Diabetes Technology Meeting (DTM) 2014*

19. PaPI: the Pseudo Amino acid variant Predictor. **Marini S**, Limongelli I, Bellazzi R. *Bioinformatics Italian Society National Congress (BITS) 2014*

20. A novel algorithm to predict the deleteriousness of genomic coding variants Limongelli I, **Marini S**, Bellazzi R. NGS-ISCB 2014
21. Dynamic Bayesian Networks to simulate type 1 diabetes patients cohorts. Barbarini N, Bellazzi R, Cobelli C, Di Camillo B, Manfrini F, Malovini A, **Marini S**, Sambo F. Trifoglio E. *Economics, Modelling and Diabetes: Mount Hood Challenge 2014*
22. PaPI: using pseudo amino acid composition to predict deleterious coding variants. Limongelli I, **Marini S**, Bellazzi R. *Italian Bioengineering Group National Congress (GNB) 2014*

Book Chapters
1. Precision oncology: a data similarity challenge. Zambelli A, Demartini A, Pala D, Vitali F, **Marini S**, Bellazzi R. In: E-Health e Medicina Digitale, Quaglini S, Cesarelli M, Giacomini M, Pinciroli F eds, *Patron eds 2017*

Preprints
1. DYNAMITE: a phylogenetic tool for identification of dynamic transmission epicenters. Magalis BR, **Marini S**, Salemi M, Prosperi M. *bioRxiv 2021*
2. Regaining perspective on SARS-CoV-2 molecular tracing and its implications. Mavian C, **Marini S**, Manes C, Capua I, Prosperi M, Salemi M. *medRxiv 2020*

Awards and Fellowships

02/2018	Elsevier Outstanding contribution in reviewing
11/2015	Japanese Society for the Promotion of Science Postdoctoral Fellowship
06/2015	Elsevier Outstanding contribution in reviewing
10/2011	Bioengineering Division Graduate Student Research Award, 1st ranked
03/2010	The Hong University of Science and Technology Overseas Research Award

Invited Talks and Lectures (extramural)

08/2022	Tracking and predicting antimicrobial resistance *International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology (VEME), Panama city, Panama*
12/2021	The role of AI in the battle against antibiotic resistance *University of Pavia, Italy*
08/2021	When and how should I down-sample large viral datasets? A demo of TARDIS *International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology (VEME), virtual meeting*
07/2020	Single-cell transcriptomics: General principles, databases and bioinformatic tools. Transversal Course on Big Data (postgraduate) *University of Pavia, Italy*
07/2020	Multi-sample, multi-condition analysis in scRNAseq data sets *ISMB 2020, BioinfoCore Workshop, virtual meeting*
06/2019	Enhancing data analysis by leveraging prior biomedical knowledge *University of Florida, USA*
06/2018	Data exploration of single-cell landscapes

	University of Pavia, Italy
10/2017	Joint data integration for precision oncology
	University of Florida, USA
07/2017	miRNA Bioinformatics, sequence analysis and statistical processes
	University of Pavia, Italy
01/2017	Investigating epileptogenesis with data fusion.
	University of Michigan, USA
09/2016	Mining heterogeneous data sources to enhance association studies.
	University of Arizona, USA
06/2016	Leveraging on public databases for novel peptidase target discovery.
	University of Pavia, Italy
05/2011	Motif search, sequence alignment and Support Vector Regression for Dscam protein self- and hetero-binding affinity prediction.
	The Chinese Academy of Science, Beijing, China

Funding

<u>Current Research Support</u>

Medical Marijuana Clinical Outcomes 2021 ($74,040)
Role: **PI**; 06/2021-12/2022
CBD-induced biomarkers of inflammation reduction in people living with HIV at the single cell level

PI/PD UFII 2022 ($40,000) & *PI/PD UFBI 2022* ($25,000); PI: Mavian
Seed grant: Microbiome-based explainable AI for pathogen prediction
Role: **MPI**;

Rockefeller Foundation 2021 HTH 012 ($340,000); PI: Salemi
Role: **Co-I**; 06/2021-05/2022
Expanding genomic surveillance and epidemiology capacity in Central Florida and Southeastern US

NIH R01 2022 ($3,556,267); PI: Salemi
Role: **Co-I**; 08/2022-08/2027
A Phylodynamic Artificial Intelligence framework to predict evolution of SARS-CoV-2 variants of concern in Immunocompromised persons with HIV (PhAI-CoV)

<u>Completed Research Support</u>

12/2018-12/2020	University of Michigan, Mcubed Program ($15,000).
	Mapping diabetic foot ulcers at the single-cell level; Role: MPI
11/2015-11/2016	Japanese Society for the Promotion of Science (JPY 4,544,000.00, ~$40,000); Postdoctoral fellowship

Teaching and Supervising Experiences

<u>University of Florida, USA</u>

01/2020-present	Supervising 2 postdocs, 1 PhD student, 2 Research assistants

01/2022-04/2022	Instructor: Topics in Precision Medicine and Public Health Informatics (postgraduate)
01/2021-04/2021	Instructor: Topics in Precision Medicine and Public Health Informatics (postgraduate)
05/2020-08/2020	Instructor of record: Computational Epidemiology (postgraduate)

<u>University of Michigan, USA</u>

08/2017-12/2019	Supervised 1 postdoc, 2 postgraduates and 1 undergraduate students

<u>Kyoto University, Japan</u>

06/2016-09/2016	Supervised 1 undergraduate student

<u>University of Pavia, Italy</u>

12/2018	Instructor: Introduction to Single cell RNA-seq data analysis (postgraduate)
09/2013-09/2015	Instructor of record: Medical Informatics (undergraduate)
09/2013-09/2015	Instructor of record: Automatic Learning in Medicine (postgraduate)
01/2013-11/2015	Supervised 3 postgraduate and 2 undergraduate students
12/2016-07/2017	Supervised 4 postgraduate and 3 undergraduate students

<u>The Hong Kong University of Technology, China</u>

01/2010-06/2010	Teaching assistant: Introduction to Bioengineering

Service to Profession

<u>Artificial Intelligence Advisor</u>

12/2016-present	enGenome srl, Pavia, Italy

<u>National Science Foundation</u>

02/2022	Program reviewer

<u>Journal Reviewer</u>

Bioinformatics, Plos One, Journal of Biomedical Informatics, Computers in Biology and Medicine, Briefings in Bioinformatics, IEEE/ACM Transactions on Computational Biology and Bioinformatics, IEEE Journal of Biomedical and Health Informatics, Complex and intelligent Systems, Algorithms, Nature Scientific Reports, Molecules, Frontiers in Medicine

<u>Conference Reviewer</u>

AMIA joint Summits on TranslationalScience, IEEE International Conference on Healthcare Informatics (ICHC), IEEE MELECON

<u>Conference Program Committee Member</u>

Artificial Intelligence in Medicine (AIME), IEEE International Symposium on Computer-Based Medical Systems (CBMS), IEEE ICTS4eHealth, ACM International Conference on Information

and Knowledge Management (ACM-CIKM), ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB)

Memberships
04/2021-present   National Institute of Antimicrobial Resistance Research and Education
02/2021-present   Miami Scientific Italian Community
09/2020-present   Community Task Force, University of Florida Dept. of Epidemiology
07/2020-present   Models of Infectious Disease Agent Study (MIDAS) research network
06/2020-03/2022   The N95DECON Consortium
05/2020-present   Awards committee, University of Florida Dept. of Epidemiology

Non-Academic Work
09/2013-06/2014   High school math teacher, EU program to fight against school dropout. Centro Servizi Formazione, Pavia, Italy

11/2007-06/2008   University tutor. Private one-to-one tutoring of undergraduate and graduate students. CESD, Pavia, Italy

Languages

	(Reading)	(Speaking)
Italian	Native speaker	Native speaker
English	Fluent	Fluent
Spanish	Fluent	Fluent

Volunteering and community outreach

Co-founder
12/2020-present   COMINTART, the Italian YouTube channel to discuss and disseminate AI in layman terms. Italian audience. 16,500+ visualizations
06/2007-12/2013   OMP, non-profit publishing house, the first copyleft (Creative Commons) publishing house in Italy. *Pavia, Italy*

Translator
06/2020   Revised the Italian translation of the N95decon documents. N95decon is a scientific consortium for data-driven study of N95 filtering facepiece respirator decontamination. *Remote*

Introducing machine learning in high school
03/2013-04/2017   Introduction to data science and artificial intelligence. *Voghera, Italy*
01/2013-03/2013   Introduction to data science and artificial intelligence. *Pavia, Italy*

Software developer
06/2014   VSO Poverty Alleviation, remote services. Development of a software to help manage dairy cooperatives. DCPUK, Bangladesh. *Remote*

<u>Editor in Chief</u>

08/2007-08/2008   Kronstadt, student-based local news magazine. Monthly issued, city audience (2000 copies). *Pavia, Italy*

<u>Front desk volunteer</u>

01/2006-08/2008   City social services.. Helping immigrants to deal with local bureaucracy and CV writing. *Pavia, Italy*