

Simone Marini

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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

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

([Google Scholar profile](#))

[*] denotes equal contribution. [§] denotes corresponding (senior) authorship.

Journals (peer reviewed)

1. MEGARes and AMR++, v3. 0: an updated comprehensive database of antimicrobial resistance determinants and an improved software pipeline for classification using high-throughput sequencing. Bonin N, Doster E, Worley H, Pinnell LJ, Bravo JE, Ferm P, **Marini S**, Prosperi M, Noyes N, Morley PS, Boucher C. *Nucleic Acids Research* 2023
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
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
4. Predicting emerging SARS-CoV-2 variants of concern through a One Class dynamic anomaly detection algorithm. Nicora G, Salemi M, **Marini S§**, Bellazzi R. *BMJ Health & Care Informatics* 2022
5. KARGAMobile: Android app for portable, real-time, easily interpretable analysis of antibiotic resistance genes via nanopore sequencing. Barquero A, **Marini S**, Boucher C, Ruiz J, Prosperi M. *Frontiers in Bioengineering and Biotechnology* 2022
6. 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*, 2022
7. 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
8. 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
9. 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, Lednický JA, Morris JG, Lauzardo M, Salemi M. *Journal of Medical Virology* 2022
10. Macrophage TGF β signaling is critical for wound healing with heterotopic ossification after trauma. Patel NK, Nunez JH, Sorkin M, **Marini S**, Pagani CA, Strong AL, Hwang CD, Li S, Padmanabhan KR, Kumar R, Bancroft AC, Greenstein JA, Nelson R, Rasheed HA, Livingston N, Vasquez K, Huber AK, Levi B. *JCI Insight* 2022
11. 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

12. 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
13. Fast and exact quantification of motif occurrences in biological sequences. Prosperi M, **Marini S**, Boucher C. *BMC bioinformatics* 2021
14. 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
15. Earliest detection to date of SARS-CoV-2 in Florida: Identification together with influenza virus on the main entry door of a university building. Lednický 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
16. 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
17. 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
18. 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
19. 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
20. 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
21. 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
22. 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
23. Hydrogen Peroxide Methods for Decontaminating N95 Filtering Facepiece Respirators. Rempel D, Henneman J, Agalloco J, Crittenden J, **N95DECON Consortium**. *Applied Biosafety* 2021
24. 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
25. 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
26. 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
 27. 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
 28. 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, Hadeffield 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
 29. 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
 30. 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
 31. Comparative study of salivary, duodenal and fecal microbiota composition across adult celiac disease. Panelli S, Capelli E, Lupo G, Schieppatti 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
 32. 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
 33. 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
 34. Scientific Collaboration During the COVID-19 Pandemic: N95DECON.org. Rempel D, **Members of the N95DECON Consortium**. *Annals of Work Exposures and Health* 2020
 35. 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.
 36. MTGO-SC, a tool to explore gene modules in single cell RNA-seq data. Nazzicari N, Vella D, Coronello C, Di Silvestre D, Bellazzi R, **Marini S**. *Frontiers in Genetics* 2019
 37. Protease target prediction via matrix factorization. **Marini S**, Vitali F*, Rampazzi S, Demartini A, Akutsu T. *Bioinformatics* 2019

38. 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
39. 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
40. A comprehensive roadmap of murine spermatogenesis defined by single-cell RNA-seq. Green CD, Ma Q, Manske GL, Shami AN, Zheng X, **Marini S**, Moritz L, Sultan C, Gurczynski SJ, Moore BB, Tallquist MD, Li JZ, Hammoud SS. *Developmental Cell* 2018
41. 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
42. 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
43. 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
44. 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
45. Patient similarity for precision medicine: A systematic review. Parimbelli E, **Marini S**, Sacchi L, Bellazzi R *Journal of Biomedical Informatics* 2018
46. 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
47. 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
48. Dscam1 Web Server: online prediction of Dscam1 self- and hetero-affinity. **Marini S**, Nazzicari N*, Biscarini F, Wang GZ. *Bioinformatics* 2017
49. Machine learning methods to predict Diabetes complications. **Marini S**, Dagliati A*, Sacchi L, Bellazzi R. *Journal of Diabetes Science and Technology* 2017
50. 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
51. "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
52. 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

53. 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
54. PaPI: pseudo amino acid composition to score human coding variants. Limongelli I, **Marini S**, Bellazzi R. *BMC Bioinformatics* 2015
55. 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
56. 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
57. 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
58. 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. Jun I, **Marini S**, Boucher C, Morris JG, Bian J, Prosperi M. Joint Application of the Target Trial Causal Framework and Machine Learning Modeling to Optimize Antibiotic Therapy: Use Case on Acute Bacterial Skin and Skin Structure Infections due to Methicillin-resistant *Staphylococcus aureus*. *KDD Health Day and 2021 KDD Workshop on Applied Data Science for Healthcare* 2022
2. 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
3. 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
4. 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
5. 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
6. 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

7. 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. Identification of Social and Racial Disparities in Risk of HIV Infection in Florida using Causal AI Methods. Prosperi M, Xu J, Guo JS, Bian J, Chen WH, Canidate S, **Marini S**, Wang M. IEEE International Conference on Bioinformatics and Biomedicine (BIBM) 2022
2. Transmission cluster characteristics of global, regional, and lineage-specific SARS-CoV-2 phylogenies. Prosperi M, Rife B, **Marini S**, Salemi M. IEEE International Conference on Bioinformatics and Biomedicine (BIBM) 2022
3. Updates to the MEGARes v3.0 database and its associated AMR++ bioinformatic pipeline for resistome analysis. Bonin N, Doster E, Worley H, Pinnell L, Bravo J, Ferm P, **Marini S**, Prosperi M, Noyes N, Morley P, Boucher C. CRWAD 2023
4. Moving from predicting hospital deaths by antibiotic-resistant bloodstream bacteremia toward actionable risk reduction using machine learning on electronic health records. Jun I, Rich SN, **Marini S**, Feng Z, Bian J, Morris JG, Prosperi M. *AMIA Annual Symposium Proceedings 2022* (Vol. 2022, p. 274)
5. Behavioral Weight Loss Success: Android vs. iOS. Ugwoaba UA, Brockmann A, Arroyo KM, Swanson TN, Barrett KL, Shankar MN, **Marini S**, Ross KM. *SBM 44th Annual Meeting and Scientific Session 2022*
6. 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*
7. 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*
8. 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*
9. 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*
10. Optimizing viral genome subsampling by genomic diversity and temporal distribution. **Marini S**, Mavian C, Salemi M, Rife Magalis B. *COVID-19 Dynamics & Evolution 2020*
11. 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*
12. 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*

13. 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
14. 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
15. 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
16. Estimating cancer stemness with single-cell RNA sequencing. **Marini S**, Brooks M, Wicha M, Li J. *Keystone Symposia Conference (L1: Single Cell Biology)* 2019
17. 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
18. 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
19. Gene interaction discovery in myelodysplastic syndromes. **Marini S**, Vitali F, Demartini A, Bellazzi R. *European Conference of Human Genetics (ESHG)* 2018
20. Data Fusion for cleavage target prediction. **Marini S**, Demartini A, Vitali F, Bellazzi R, Akutsu T. *Bioinformatics Italian Society National Congress (BITS)* 2016
21. 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
22. 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
23. 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
24. PaPI: the Pseudo Amino acid variant Predictor. **Marini S**, Limongelli I, Bellazzi R. *Bioinformatics Italian Society National Congress (BITS)* 2014
25. A novel algorithm to predict the deleteriousness of genomic coding variants Limongelli I, **Marini S**, Bellazzi R. *NGS-ISCB* 2014
26. 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
27. 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, Pincioli 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

09/2022	Dean's Citation Paper Awards, University of Florida, College of Public Health and Health Professions
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 <i>International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology (VEME), Panama city, Panama</i>
12/2021	The role of AI in the battle against antibiotic resistance <i>University of Pavia, Italy</i>
08/2021	When and how should I down-sample large viral datasets? A demo of TARDIS <i>International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology (VEME), virtual meeting</i>
07/2020	Single-cell transcriptomics: General principles, databases and bioinformatic tools. Transversal Course on Big Data (postgraduate) <i>University of Pavia, Italy</i>
07/2020	Multi-sample, multi-condition analysis in scRNAseq data sets <i>ISMB 2020, BioinfoCore Workshop, virtual meeting</i>
06/2019	Enhancing data analysis by leveraging prior biomedical knowledge <i>University of Florida, USA</i>
06/2018	Data exploration of single-cell landscapes <i>University of Pavia, Italy</i>
10/2017	Joint data integration for precision oncology <i>University of Florida, USA</i>
07/2017	miRNA Bioinformatics, sequence analysis and statistical processes <i>University of Pavia, Italy</i>
01/2017	Investigating epileptogenesis with data fusion. <i>University of Michigan, USA</i>
09/2016	Mining heterogeneous data sources to enhance association studies. <i>University of Arizona, USA</i>
06/2016	Leveraging on public databases for novel peptidase target discovery. <i>University of Pavia, Italy</i>
05/2011	Motif search, sequence alignment and Support Vector Regression for Dscam protein self- and hetero-binding affinity prediction. <i>The Chinese Academy of Science, Beijing, China</i>

Funding

Current Research Support

Medical Marijuana Clinical Outcomes 2021 (\$74,040)

Role: **PI**; 06/2021-01/2023

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)

Completed Research Support

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

University of Florida, USA

01/2022-present Instructor: Topics in Precision Medicine and Public Health Informatics (postgraduate)

09/2022 Guest lecturer: AMR UF (Daniel Czyz)

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

05/2020-08/2020 Instructor of record: Computational Epidemiology (postgraduate)

University of Michigan, USA

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

Kyoto University, Japan

06/2016-09/2016 Supervised 1 undergraduate student

University of Pavia, Italy

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

The Hong Kong University of Technology, China

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

Service to Profession

Artificial Intelligence Advisor

12/2016-present enGenome srl, Pavia, Italy

National Science Foundation

02/2022 Program reviewer

Journal Reviewer

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

Conference Reviewer

AMIA joint Summits on Translational Science, IEEE International Conference on Healthcare Informatics (ICHIC), IEEE MELECON

Conference Program Committee Member

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. <i>Pavia, Italy</i>

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. <i>Remote</i>
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Introducing machine learning in high school

03/2013-04/2017	Introduction to data science and artificial intelligence. <i>Voghera, Italy</i>
01/2013-03/2013	Introduction to data science and artificial intelligence. <i>Pavia, Italy</i>

Software developer

06/2014	VSO Poverty Alleviation, remote services. Development of a software to help manage dairy cooperatives. DCPUK, Bangladesh. <i>Remote</i>
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Editor in Chief

08/2007-08/2008	Kronstadt, student-based local news magazine. Monthly issued, city audience (2000 copies). <i>Pavia, Italy</i>
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Front desk volunteer

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