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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. Behavioral and Demographic Profiles of HIV Transmission and Exposure Networks in Florida: Network Analysis of HIV Contact Tracing Data. Liu Y, Parisi C, Sun C, Fisk-Hoffman R, Salemi M, Viteri D, Danforth B, Prosperi M, **Marini S§**. *JMIR Public Health and Surveillance* 2025 [in press]

2. BrainCellR: A Precise Cell Type Nomenclature Pipeline for Comparative Analysis Across Brain Single-Cell Datasets. Chi Y, **Marini S**, Wang GZ. *Computational and Structural Biotechnology Journal* 2024
3. Forecasting dominance of SARS-CoV-2 lineages by anomaly detection using deep AutoEncoders. Rancati S, Nicora G, Prosperi M, Bellazzi R\$, Salemi M\$, **Marini S\$**. *Briefings in Bioinformatics* 2025
4. Novel insights on unraveling dynamics of transmission clusters in outbreaks using phylogeny-based methods. Magalis BR, Riva A, **Marini S**, Salemi M, Prosperi M. *Infection, Genetics and Evolution* 2024
5. DnaK reduces the activity of anti-cancer drugs cisplatin and 5FU. Benedetti F, Mongodin EF, Badger JH, Munawwar A, Cellini A, Yuan W, Silvestri G, Kraus CN, **Marini S** Rathinam CV, Salemi M, Tettelin H, Gallo RC, Zella D. *Journal of Translational Medicine* 2024
6. Oral Cannabidiol Treatment Is Associated with an Anti-Inflammatory Gene Expression Signature in Myeloid Cells of People Living with HIV. **Marini S\$** Huber A, Cash MN, Salemi M, Cook RL, Borsa P, Mavian C\$. *Cannabis and Cannabinoid Research* 2024
7. Machine learning prediction and phyloanatomic modeling of viral neuroadaptive signatures in the macaque model of HIV-mediated neuropathology. Ramirez-Mata AS, Ostrov D, Salemi M, **Marini S\$**, Magalis BR\$. *Microbiology Spectrum* 2023
8. The K-mer antibiotic resistance gene variant analyzer (KARGVA). **Marini S**, Boucher C, Noyes N and Prosperi M (2023). *Front. Microbiol.* 2023
9. 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
10. 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
11. 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
12. 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
13. 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
14. 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
15. 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
16. 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
17. 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

18. 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
19. Severe Acute Respiratory Syndrome Coronavirus 2 Delta Vaccine Breakthrough Transmissibility in Alachua County, Florida. Rife Magalis B, Rich S, Tagliamonte MS, Mavian C, Cash MN, Riva A, **Marini S**, Amador DM, Zhang Y, Shapiro J, Horine A. *Clinical Infectious Diseases* 2022
20. 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
21. 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
22. Fast and exact quantification of motif occurrences in biological sequences. Prosperi M, **Marini S**, Boucher C. *BMC bioinformatics* 2021
23. 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. *Journal of neurovirology* 2021
24. 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
25. 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
26. 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
27. 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
28. 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
29. 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
30. 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, Meisenholder C, Pillarisetti A, **Members of the N95DECON Consortium**. *Applied Biosafety* 2021
31. 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
32. Hydrogen Peroxide Methods for Decontaminating N95 Filtering Facepiece Respirators. Rempel D, Henneman J, Agalloco J, Crittenden J, **N95DECON Consortium**. *Applied Biosafety* 2021
33. 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
34. 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

35. 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
36. 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
37. 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, Hadeffeld 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
38. Beneath the surface: Hyper-connectivity between caudate and salience regions in ADHD fMRI at rest. Damiani S, Tarchi L, Scalabrini A, **Marini S**, Provenzano U, Rocchetti M, Oliva F, Politi P. *European Child & Adolescent Psychiatry* 2020
39. 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
40. Comparative study of salivary, duodenal and fecal microbiota composition across adult celiac disease. Panelli S, Capelli E, Lupo G, Schieppati 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
41. 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
42. 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
43. Scientific Collaboration During the COVID-19 Pandemic: N95DECON.org. Rempel D, **Members of the N95DECON Consortium**. *Annals of Work Exposures and Health* 2020
44. 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.
45. 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
46. Protease target prediction via matrix factorization. **Marini S**, Vitali F*, Rampazzi S, Demartini A, Akutsu T. *Bioinformatics* 2019
47. 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
48. 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

49. 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
50. 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
51. 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
52. 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
53. 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
54. Patient similarity for precision medicine: A systematic review. Parimbelli E, **Marini S**, Sacchi L, Bellazzi R *Journal of Biomedical Informatics* 2018
55. 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
56. 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
57. Dscam1 Web Server: online prediction of Dscam1 self- and hetero-affinity. **Marini S***, Nazzicari N*, Biscarini F, Wang GZ. *Bioinformatics* 2017
58. Machine learning methods to predict Diabetes complications. **Marini S***, Dagliati A*, Sacchi L, Bellazzi R. *Journal of Diabetes Science and Technology* 2017
59. A data fusion approach to enhance association simostudy in epilepsy. **Marini S**, Limongelli I, Rizzo E, Errichiello E, Vetro A, Tan D, Zuffardi O, Bellazzi R. *Plos One* 2016
60. “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
61. 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, Arnlöv 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
62. 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
63. PaPI: pseudo amino acid composition to score human coding variants. Limongelli I, **Marini S**, Bellazzi R. *BMC Bioinformatics* 2015
64. 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
65. 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
66. 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

67. *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. OCTOPUS: Disk-based, Multiplatform, Mobile-friendly Metagenomics Classifier. **Marini S**, Barquero A, Wadhwani AA, Bian J, Ruiz J, Boucher C, Prosperi M. *AMIA Annual Symposium* 2024
2. Emulation of a Target Trial to Estimate the Effect of Selective Serotonin Reuptake Inhibitors on the Development of Antimicrobial-Resistant Infections using Electronic Health Record Data and Causal Machine Learning. Ser SE, Snigurska UA, Cohen SA, Jun I, Bjarnadottir IA, Lucero RJ, **Marini S**, Bian J, Prosperi M. *AMIA Informatics Summit* 2024
3. Scalable de novo Classification of Antimicrobial Resistance of Mycobacterium Tuberculosis. Serajian M, Marini S, Alanko JN, Noyes NR, Prosperi M, Boucher C. *ISMB* 2024
4. Benchmarking embeddings and anomaly detection to identify Sars-Cov-2 Omicron Dominant Lineages. Rancati S, Nicora G, Prosperi M, Bellazzi R, **Marini S**, Salemi M. *AIME* 2024
5. An average-case efficient two-stage algorithm for enumerating all longest common substrings of minimum length k between genome pairs. Prosperi M, **Marini S**, Boucher C. *The 12th IEEE International Conference on Healthcare Informatics (IEEE ICHI)* 2024
6. Learning on forecasting HIV epidemic based on individuals' contact networks. Sun C, Liu Y, Parisi C, Frisk-Hoffman R, Salemi M, Fang R, Danforth B, Prosperi M, **Marini S**. *International Joint Conference on Biomedical Engineering System and Technology (HEALTHINF)* 2024
7. Sequencing Efforts and Epidemiological Trends: Analyzing SARS-CoV-2 Dynamics Across European Nations. Rancati S, Pala D, **Marini S**, Salemi R, Bellazzi R, Nicora G. *IEEE International Conference on Bioinformatics and Biomedicine (BIBM)* 2024
8. Optimizing Dynamic Antibiotic Treatment Strategies against Invasive Methicillin-Resistant Staphylococcus Aureus Infections using Causal Survival Forests and G-Formula. Jun I, Cohen SA, Ser SE, **Marini S**, Lucero RJ, Bian J, Prosperi M. *KDD Workshop on Causal Discovery, Prediction and Decision* 2023
9. Predicting emerging SARS-Cov-2 Variants of Concern through a One-Class dynamic anomaly detection algorithm. Nicora G, **Marini S**, Salemi M, Bellazzi R. *AMIA Informatics Summit* 2023
10. 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. Jun I, **Marini S**, Boucher C, Morris JG, Bian J, Prosperi M. *KDD Health Day and 2021 KDD Workshop on Applied Data Science for Healthcare* 2022
11. 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* 2022
12. 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
13. 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
14. 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

15. 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) 2019*
16. 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*
17. 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*
18. A continuous time, multivariate model to simulate Type 2 Diabetes patients trajectories. **Marini S**, Dagliati A, Bellazzi R. *AMIA 2016*

Conference Abstracts (peer reviewed)

1. SARITA: A Generative Large Language Model Accurately Predicting The Emergence Of SARS-CoV-2 Critical Mutations. Rancati S, Nicora G, Bergomi L, Buonocore TM, Czyz D, Parimbelli E, Propseri M, Bellazzi R, **Marini S**, Salemi M. *32nd International Dynamics & Evolution of Human Viruses, Abbaye de Royaumont, France 2025*
2. Prediction of A. Baumannii Amikacin Resistance in Clinical Metagenomics. Sy M, Prosperi M, Serajian M, Boucher C, Benos PT, **Marini S**. *Medical Informatics Europe Conference (MIE) 2024*
3. Integrative modeling of phylodynamic, vector, human travel, and epidemiological data to infer arboviral importation and local transmission. Tagliamonte M, Hitchings M, **Marini S**, Cash M, Morris JG, Salemi M, Cummings DA, Mavian C. *31st International Dynamics & Evolution of Human Viruses 2024*
4. Integrative modeling of phylodynamic, vector, human travel, and epidemiological data to infer arboviral importation and local transmission. Tagliamonte M, Hitchings M, **Marini S**, Cash M, Morris JG, Salemi M, Cummings DA, Mavian C. *Ecology and Evolution of Infectious Diseases (EEID) 2024*
5. Integrative modeling of phylodynamic, vector, human travel, and epidemiological data to infer arboviral importation and local transmission. Tagliamonte M, Hitchings M, **Marini S**, Cash M, Morris JG, Salemi M, Cummings DA, Mavian C. *8th World One Health Congress 2024*
6. Predicting emerging SARS-Cov-2 lineages through an Autoencoder-based anomaly detection algorithm. Rancati S, Nicora G, **Marini S**, Salemi M, Prosperi M, Bellazzi R. *CIBB 2023*
7. A One Health approach: integrative modeling of phylodynamic, vector, human travel, and epidemiological data to infer arboviral importation and local transmission. Tagliamonte M, Hitchings M, Cash MN, Morris JG, Salemi M, Cummings DA, **Marini S**, Mavian C. *8th World One Health Congress Scientific and Science Policy Interface Program (2024)*
8. Identifying Dominant Omicron Lineages Using Embeddings and Anomaly Detection. Rancati S, Nicora G, **Marini S**, Salemi M, Bellazzi R. *EMBC 2024*
9. Young Regenerative Muscle Exhibits Upregulation In Peripheral Nerve And Extracellular Matrix Transcriptional Programs. Hwang C, Caragher SP, Kiwanuka H, Karinja SJ, Endo Y, **Marini S**, Tereshenko V, Raasveld FV, Valerio IL, Eberlin KR, Sinha I. *Plastic and Reconstructive Surgery Global Open. 11(5 Suppl) 2024*
10. An anti-inflammatory gene expression signature is associated with CBD treatment in people living with HIV. **Marini S**, Cash MN, Salemi M, Cook RL, Borsa P, Mavian C. *The Cannabis Clinical Outcomes Research Conference (CCORC) 2023*
11. Behavioral and demographic profiles of HIV contact networks in Florida. Liu Y, Parisi C, Frisk-Hoffman R, Salemi M, Viteri D, Prosperi M, **Marini S**. *International Conference on Intelligent Biology and Medicine (ICIBM) 2023*

12. Sequence-based computational algorithm can predict antimicrobial resistance in major human pathogens: A comparative analysis with traditional clinical methods. Cohen SA, **Marini S**, Morris JG, Prosperi M. *NIAMRRE Annual Conference 2023*
13. Single-cell RNA sequencing reveals CBD genetic signature in monocyte gene expression. **Marini S**, Cook R, Borsa P, Cash M, Prosperi M, Salemi M, Mavian C. *HIV Persistence during therapy – International Workshop 2022*
14. 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*
15. 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*
16. 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*
17. 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*
18. 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*
19. 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*
20. i-ECO: a novel method for the analysis and visualization of fMRI results in Psychiatry. Tarchi L, Fantoni T, Pisano T, Damiani S, Vittori PL, **Marini S**, Nazzicari N, Castellini G, Politi P, Ricca V. *30th European Congress of Psychiatry 2022*
21. Macrophage-mediated PDGF Activation Correlates with Regenerative Outcomes Following Musculoskeletal Trauma. Chowdary AR, Maertz T, Henn D, Hankenson KD, Pagani CA, **Marini S**, Gallagher K, Aguilar CA, Tower RJ, Levi B. *Annals of Surgery 2022*
22. 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*
23. 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*
24. Optimizing viral genome subsampling by genomic diversity and temporal distribution. **Marini S**, Mavian C, Salemi M, Rife Magalis B. *COVID-19 Dynamics & Evolution 2020*
25. 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*
26. 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*
27. 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*

28. 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
29. 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
30. Estimating cancer stemness with single-cell RNA sequencing. **Marini S**, Brooks M, Wicha M, Li J. *Keystone Symposia Conference (L1: Single Cell Biology)* 2019
31. 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
32. 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
33. Gene interaction discovery in myelodysplastic syndromes. **Marini S**, Vitali F, Demartini A, Bellazzi R. *European Conference of Human Genetics (ESHG)* 2018
34. Data Fusion for cleavage target prediction. **Marini S**, Demartini A, Vitali F, Bellazzi R, Akutsu T. *Bioinformatics Italian Society National Congress (BITS)* 2016
35. 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
36. 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
37. PaPI: the Pseudo Amino acid variant Predictor. **Marini S**, Limongelli I, Bellazzi R. *Bioinformatics Italian Society National Congress (BITS)* 2014
38. A novel algorithm to predict the deleteriousness of genomic coding variants Limongelli I, **Marini S**, Bellazzi R. *NGS-ISCIB* 2014
39. 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
40. 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, Pincirolì F eds, *Patron eds* 2017

Awards and Fellowships

07/2024	Best Poster Award, AIME 2024, Salt Lake City, USA
02/2024	Best Paper Award, HEALTHINF 2024, Rome, Italy
05/2023	Best Abstract, The Cannabis Clinical Outcomes Research Conference (CCORC) 2023, Orlando, FL, USA
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)

12/2024	Can AI speak the language of viruses? <i>Human Technopole, Milan, Italy</i>
06/2024	Supervised and Unsupervised learning: Theory and Practice. <i>Analytics Methods Seminar Series (Merck) 2024, NJ, USA</i>
03/2023	Trustworthy AI for Healthcare: What does it mean and where are we at? <i>AMIA Informatics Summit 2023, Seattle, USA</i>
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

- NIH NIA 1R21AG088603 (\$409,574) 09/2024 – 08/2026. Role: **Contact PI**. MPIs: Wang, Sibille. *Medical Marijuana and chronic musculoskeletal pain in older adults: a multi-level, precision medicine analysis*
- MERCK AND COMPANY INC RES LAB (\$350,150) 10/2024 – 10/2026 Role: **Contact PI**. MPIs: Czyz, Cherabuddi. *Genomic characterization of antimicrobial resistance and viral co-infection patterns of Streptococcus pneumoniae by next-generation sequencing and artificial intelligence*.
- MERCK AND COMPANY INC RES LAB (\$249,629.85) [Grant accepted; contract under negotiation] Role: **Contact PI**. MPIs: Mavia, Hitchings. *Causal AI for Predictive Modeling of Dengue Trajectories: A Comprehensive Approach Considering Climate Variability and Intervention Strategies*
- AI and Complex Computational Research Award, NVIDIA UF (\$61,652) 09/2024 - 03/2025 Role: **Contact PI**. *ViraLingo: decoding pan-viral genomics with AI*

Completed Research Support

- PI/PD UFII 2022 (\$40,000) & PI/PD UFBI 2022 (\$25,000); Role: **MPI**, contact PI: Mavian. *Seed grant: Microbiome-based explainable AI for pathogen prediction*
- Medical Marijuana Clinical Outcomes 2021 (\$74,040); Role: **contact PI**. MPI: Mavian *CBD-induced biomarkers of inflammation reduction in people living with HIV at the single cell level*.
- University of Michigan, Mcubed Program (\$15,000); Role: **contact PI**. *Mapping diabetic foot ulcers at the single-cell level*

Teaching

University of Florida, USA

05/2024-present	Instructor: Artificial Intelligence and Data Science for Epidemiology and Population Health
01/2022-2024	Instructor: Topics in Precision Medicine and Public Health Informatics (postgraduate)
05/2021-05/2024	Instructor: Computational Data Science for Epidemiology (postgraduate)
05/2020-08/2020	Instructor of record: Computational Epidemiology (postgraduate)

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)

The Hong Kong University of Technology, China

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

Journal Editor

05/2023-present	Nature Scientific Reports
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Artificial Intelligence Advisor

12/2016-present enGenome srl, Pavia, Italy

National Science Foundation

02/2025 Ad-hoc reviewer

08/2023 Ad-hoc reviewer

02/2022 Program reviewer

National Institute of Health

02/2025 Panel reviewer, NIH Extramural Loan Repayment Program for Clinical Research, ZAG1 ZIJ-R (C1) 1

10/2024 Panel reviewer. Study Section: Population and Public Health Approaches to HIV/AIDS

03/2022 Panel reviewer. Study Section: Mobile Health Technology and Outcomes in Low and Middle Income Countries

Journal Reviewer

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

Conference Program Committee Member

American Medical Informatics Association (AMIA), 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)

Conference Reviewer

American Medical Informatics Association (AMIA) Annual Symposium and Summits on Translational Science, IEEE International Conference on Healthcare Informatics (IHC), IEEE MELECON

Memberships

06/2024-present IEEE Engineering in Medicine and Biology Society (EMBS)

02/2024-present Admissions committee, University of Florida, Dept. of Epidemiology

05/2023-present Seminar committee, University of Florida, Dept. of Epidemiology

01/2023-present American Medical Informatics Association (AMIA)

04/2021-present National Institute of Antimicrobial Resistance Research and Education (NIAMRRE)

02/2021-present Miami Scientific Italian Community

09/2020-09/201 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.

11/2007-06/2008 Centro Servizi Formazione, Pavia, Italy
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

12/2020-12/2022 COMINTART, the Italian YouTube channel to discuss and disseminate AI in layman terms. Italian audience.

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*

Editor in Chief

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

Front desk volunteer

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