

## Simone Marini

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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](#)**

Senior or principal authorship underlined.

#### **Journals (peer reviewed)**

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

2. Rancati S, Nicora G, Prosperi M, Bellazzi R, Salemi M, **Marini S**. Forecasting dominance of SARS-CoV-2 lineages by anomaly detection using deep AutoEncoders. *Briefings in Bioinformatics*. 2025;25(6):bbae535.
3. Sun, C, Li, Y, **Marini S**, Riva A, Wu DO, Fang R, Marco S, Magalis B. Phylogenetic-informed graph deep learning to classify dynamic transmission clusters in infectious disease epidemics. *Bioinformatics Advances*. 2025;4(1):vbae158.
4. Chi Y, **Marini S**, Wang GZ, BrainCellR: A Precise Cell Type Nomenclature Pipeline for Comparative Analysis Across Brain Single-Cell Datasets. *Computational and Structural Biotechnology Journal*. 2024;23: 4306-14.
5. Serajian M, **Marini S**, Alanko JN, Noyes NR, Prosperi M, Boucher C. Scalable de novo classification of antibiotic resistance of Mycobacterium tuberculosis. *Bioinformatics*. 2024;40(Suppl 1):i39-i47
6. Magalis BR, Riva A, **Marini S**, Salemi M, Prosperi M. Novel insights on unraveling dynamics of transmission clusters in outbreaks using phylogeny-based methods. *Infection, Genetics and Evolution*. 2024;124:105661.
7. 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. DnaK reduces the activity of anti-cancer drugs cisplatin and 5FU. *Journal of Translational Medicine*. 2024;22(1):269.
8. **Marini S**, Huber A, Cash MN, Salemi M, Cook RL, Borsa P, Mavian CN. Oral Cannabidiol Treatment Is Associated with an Anti-Inflammatory Gene Expression Signature in Myeloid Cells of People Living with HIV. *Cannabis and Cannabinoid Research*. 2024;9(4):1028-37.
9. Ramirez-Mata AS, Ostrov D, Salemi M, **Marini S**, Magalis BR. Machine learning prediction and phyloanatomic modeling of viral neuroadaptive signatures in the macaque model of HIV-mediated neuropathology. *Microbiology Spectrum*. 2023;11(2): e03086-22.
10. **Marini S**, Boucher C, Noyes N, Prosperi M. The K-mer antibiotic resistance gene variant analyzer (KARGVA). *Front. Microbiol*. 2023;14:1060891.
11. Bonin N, Doster E, Worley H, Pinnell LJ, Bravo JE, Ferm P, **Marini S**, Prosperi M, Noyes N, Morley PS, Boucher C. MEGARes and AMR++, v3. 0: an updated comprehensive database of antimicrobial resistance determinants and an improved software pipeline for classification using high-throughput sequencing. *Nucleic Acids Research*. 2023;51(D1):D744-57.
12. **Marini S**, Mora R, Boucher C, Noyes N, Prosperi M. Towards routine employment of computational tools for antimicrobial resistance determination via high-throughput sequencing. *Briefings in Bioinformatics*. 2022;23(2):bbac020.
13. Prosperi M, Boucher C, Bian J, **Marini S**. Assessing putative bias in prediction of anti-microbial resistance from real-world genotyping data under explicit causal assumptions. *Artificial Intelligence in Medicine*. 2022;130:120326.
14. Nicora G, Salemi M, **Marini S**, Bellazzi R. Predicting emerging SARS-CoV-2 variants of concern through a One Class dynamic anomaly detection algorithm. *BMJ Health & Care Informatics*. 2022;29(1):e100643.
15. Barquero A, **Marini S**, Boucher C, Ruiz J, Prosperi M. KARGAMobile: Android app for portable, real-time, easily interpretable analysis of antibiotic resistance genes via nanopore sequencing. *Frontiers in Bioengineering and Biotechnology*. 2022;10:1016408.
16. **Marini S**, Oliva M, Slizovskiy I, Das R, Noyes N, Kahveci T, Boucher C, Prosperi M. AMR-meta: a k-mer and metafeature approach to classify antimicrobial resistance from high-throughput short-read metagenomics data. *Gigascience*. 2022;11:giac029.
17. 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. Severe acute respiratory

syndrome coronavirus 2 Delta vaccine breakthrough transmissibility in Alachua County, Florida. *Clin Infect Dis*. 2022;75(9):1618-27.

18. Cella E, Ali S, Schmedes SE, Magalis BR, **Marini S**, Salemi M, Blanton J, Azarian T. Early emergence phase of SARS-CoV-2 Delta variant in Florida, US. *Viruses*. 2022;14(4):766.
19. 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. Low-frequency variants in mildly symptomatic vaccine breakthrough infections present a double-edged sword. *Journal of Medical Virology*. 2022;94(7):3192-202.
20. 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. Macrophage TGF $\beta$  signaling is critical for wound healing with heterotopic ossification after trauma. *JCI Insight*. 2022;7(20):e144925.
21. **Marini S**, Mavian C, Riva A, Salemi M, Magalis BR. Optimizing viral genome subsampling by genetic diversity and temporal distribution (TARDIS) for Phylogenetics. *Bioinformatics*. 2022;38(3):856-60.
22. **Marini S**, Oliva M, Slizovskiy IB, Noyes NR, Boucher C, Prosperi M. Exploring Prediction of Antimicrobial Resistance Based on Protein Solvent Accessibility Variation. *Frontiers in Genetics*. 2021;12:564186.
23. Prosperi M, **Marini S**, Boucher C. Fast and exact quantification of motif occurrences in biological sequences. *BMC bioinformatics*. 2021;22:1-0.
24. Mavian C, Ramirez-Mata AS, Dollar JJ, Nolan DJ, Cash M, White K, Rich SN, Magalis BR, **Marini S**, Prosperi MC, Amador DM. 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. *Journal of neurovirology*. 2021;27:101-15.
25. Lednicky J, Salemi M, Subramaniam K, Waltzek TB, Sabo-Attwood T, Loeb JC, Hentschel S, Tagliamonte MS, **Marini S**, Alam MM, Stephenson CJ. Earliest detection to date of SARS-CoV-2 in Florida: Identification together with influenza virus on the main entry door of a university building. *PloS One*. 2021;16(1): e0245352
26. Pagani CA, Huber AK, Hwang C, **Marini S**, Padmanabhan K, Livingston N, Nunez J, Sun Y, Edwards N, Cheng YH, Visser N. Novel lineage-tracing system to identify site-specific ectopic bone precursor cells. *Stem Cell Reports*. 2021;16(3):626-40
27. Lee S, Hwang C, **Marini S**, Tower RJ, Qin Q, Negri S, Pagani CA, Sun Y, Stepien DM, Sorkin M, Kubiak CA NGF-TrkA signaling dictates neural ingrowth and aberrant osteochondral differentiation after soft tissue trauma. *Nature Communications*. 2021;12(1):4939.
28. Tarchi L, Damiani S, **Marini S**, Cappelli C, Liuzzi G, Minerva M, Politi P. Do local curriculum scores correlate with national residency test results? A pluriannual, nationwide survey of Italian Medical Universities. *Italian Journal of Medicine*. 2021 Feb 12;15(2)
29. Tarchi L, Damiani S, La Torraca Vittori P, **Marini S**, Nazzicari N, Castellini G, Pisano T, Politi P, Ricca V. The colors of our brain: an integrated approach for dimensionality reduction and explainability in fMRI through color coding (i-ECO). *Brain Imaging and Behavior*. 2021;24:1-4.
30. Damiani S, Tarchi L, Scalabrini A, **Marini S**, Provenzano U, Rocchetti M, Oliva F, Politi P. Beneath the surface: Hyper-connectivity between caudate and salience regions in ADHD fMRI at rest. *European Child & Adolescent Psychiatry*. 2021;30:619-31.
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32. Smullin SJ, Tarlow BD, **N95DECON Consortium**. Room temperature wait and reuse for bioburden reduction of SARS-CoV-2 on N95 filtering facepiece respirators. *Applied Biosafety*. 2021;26(2):103-11.
33. Rempel D, Henneman J, Agalloco J, Crittenden J, **N95DECON Consortium**. Hydrogen peroxide methods for decontaminating N95 filtering facepiece respirators. *Applied Biosafety*. 2021;26(2):71-9.
34. Grist SM, Geldert A, Gopal A, Su A, Balch HB, Herr AE, **N95DECON Consortium**. Current understanding of ultraviolet-C decontamination of N95 filtering facepiece respirators. *Applied Biosafety*. 2021;26(2):90-102.
35. Rempel D, **N95DECON Consortium**. Scientific collaboration during the COVID-19 pandemic: N95DECON. org. *Annals of Work Exposures and Health*. 2020;64(8):775-7.
36. **Marini S**, Mavian C, Prosperi M, Salemi M. A snapshot of SARS-CoV-2 genome availability up to April 2020 and its implications. *JMIR Public Health and Surveillance*. 2020;6(2):e19170.
37. 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. Endogenous CCN family member WISP1 inhibits trauma-induced heterotopic ossification. *JCI insight*. 2020;5(13):e135432.
38. 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. 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. *Bone*. 2020;139:115517.
39. Huber AK, Patel N, Pagani CA, **Marini S**, Padmanabhan K, Matera DL, Said M, Hwang C, Hsu GC, Poli AA, Strong AL. Immobilization after injury alters extracellular matrix and stem cell fate. *The Journal of Clinical Investigation*. 2020;130(10):5444-60.
40. 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, Hadeheld 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. Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. *Proceedings of the National Academy of Sciences*. 2020;117(23):12522-3.
41. 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. Tuning Macrophage Phenotype to Mitigate Skeletal Muscle Fibrosis. *The journal of immunology*. 2020;204(8):2203-15.
42. 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. Comparative study of salivary, duodenal and fecal microbiota composition across adult celiac disease *Journal of Clinical Medicine*. 2020;9(4):1109.
43. Sono T, Hsu CY, Wang Y, Xu J, Cherief M, **Marini S**, Huber AK, Miller S, Péault B, Levi B, and James AW. Perivascular fibro-adipogenic progenitor tracing during post-traumatic osteoarthritis *The American Journal of Pathology*. 2020;190(9):1909-20.
44. 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. Activin A does not drive post-traumatic heterotopic ossification. *Bone*. 2020;138:115473.
45. Edwards NJ, Hwang C, **Marini S**, Pagani CA, Spreadborough PJ, Rowe CJ, Yu P, Mei A, Visser N, Li S, Hespe GE. The role of neutrophil extracellular traps and TLR signaling in skeletal muscle ischemia reperfusion injury. *The FASEB Journal*. 2020;34(12):15753-70

46. Nazzicari N, Vella D, Coronello C, Di Silvestre D, Bellazzi R, **Marini S**. MTGO-SC, a tool to explore gene modules in single cell RNA-seq data. *Frontiers in Genetics*. 2019;10:953.
47. **Marini S**, Vitali F, Rampazzi S, Demartini A, Akutsu T. Protease target prediction via matrix factorization. *Bioinformatics*. 2019;35(6):923-9.
48. 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. Disruption of Neutrophil Extracellular Traps (NETs) Links Mechanical Strain to Post-traumatic Inflammation. *Frontiers in Immunology*. 2019;10:2148.
49. 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. Mesenchymal VEGFA induces aberrant differentiation in heterotopic ossification *Nature Bone Research*. 2019;7(1):36.
50. 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. A comprehensive roadmap of murine spermatogenesis defined by single-cell RNA-seq. *Developmental Cell*. 2018;46(5):651-67.
51. Vella D, **Marini S**, Vitali F, Di Silvestre D, Mauri G, and Bellazzi R. MTGO: PPI network analysis via topological and functional module identification *Scientific Reports*. 2018;8(1):5499.
52. **Marini S**, Vitali F, Pala D, Demartini A, Montoli S, Zambelli A, Bellazzi R. Patient similarity by joint matrix tri-factorization to identify subgroups in precision oncology. *Jamia Open*. 2018;1(1):75-86.
53. Bao Y., **Marini S**, Tamura T, Kamada M, Maegawa S, Hosokawa H, Song J Akutsu T. Towards more accurate prediction of caspase cleavage sites: a comprehensive review of current methods, tools and features. *Briefings in Bioinformatics*. 2018;20(5):1669-84.
54. Teliti M, Cogni G, Sacchi L, Dagliati A, **Marini S**, Tibollo V, De Cata P, Bellazzi R, Chiovato L. Risk factors for the development of micro-vascular complications of type 2 diabetes in a single-centre cohort of patients. *Diabetes and Vascular Disease Research*. 2018;15(5):424-32.
55. Parimbelli E, **Marini S**, Sacchi L, Bellazzi R. Patient similarity for precision medicine: A systematic review *Journal of Biomedical Informatics*. 2018;83:87-96.
56. 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, **SUMMIT Consortium**, Groop LC, McCarthy MI, Kadowaki T, Maeda S. A variant within the FTO confers susceptibility to diabetic nephropathy in Japanese patients with type 2 diabetes. *PLoS One*. 2018;13(12):e0208654.
57. Machine learning methods to predict Diabetes complications. **Marini S**, Dagliati A, Sacchi L, Bellazzi R. *Journal of Diabetes Science and Technology*. 2018;12(2):295-302.
58. Vitali F, **Marini S**, Balli M, Grosemans H, Sampaolesi M, Lussier YA, Cusella De Angelis MG, Bellazzi R. Exploring Wound-Healing Genomic Machinery with a Network-Based Approach. *Pharmaceuticals*. 2017;10(22):55.
59. **Marini S**, Nazzicari N, Biscarini F, Wang GZ. Dscam1 Web Server: online prediction of Dscam1 self- and hetero-affinity. *Bioinformatics*. 2017;33(12):1879-80.
60. **Marini S**, Limongelli I, Rizzo E, Errichiello E, Vetro A, Tan D, Zuffardi O, Bellazzi R. A data fusion approach to enhance association study in epilepsy. *Plos One*. 2016;11(12):e0164940.
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BioBank Japan Project. Trans-ethnic fine mapping highlights kidney-function genes linked to salt sensitivity. *The American Journal of Human Genetics*. 2016;99(3):636-46.

63. **Marini S**, Trifoglio E, Barbarini N, Sambo F, Di Camillo B, Malovini A, Manfrini M, Cobelli C, Bellazzi R. Dynamic Bayesian Network model for long-term simulation of clinical complications in type 1 diabetes. *Journal of Biomedical Informatics*. 2015;75:369-76.
64. Limongelli I, **Marini S**, Bellazzi R. PaPI: pseudo amino acid composition to score human coding variants. *BMC Bioinformatics*. 2015;16:1-14.
65. Biscarini F, **Marini S**, Stevanato P, Broccanello C, Bellazzi R, Nazzicari N. Developing a parsimonious predictor for binary traits in sugar beet (*Beta vulgaris*). *Molecular Breeding*. 2015;35:11-2.
66. 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;14:1-10.
67. 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;8(12):e85065.
68. In silico Protein-Protein Interaction prediction with sequence alignment and classifier stacking. **Marini S**, Xu Q, Yang Q. *Current Protein and Peptide Science*. 2011;12(7):614-620.

### Conference Papers (peer reviewed)

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

11. Jun I, Rich SN, **Marini S**, Feng Z, Bian J, Morris JG, Prosperi M. Moving from predicting hospital deaths by antibiotic-resistant bloodstream bacteremia toward actionable risk reduction using machine learning on electronic health records. *AMIA Annual Symposium 2022*
12. Prosperi M, **Marini S**. KARGA: Multi-platform Toolkit for k-mer-based Antibiotic Resistance Gene Analysis of High-throughput Sequencing Data. *IEEE International Conference on Biomedical and Health Informatics (BHI) 2021*
13. Prosperi M, **Marini S**, Boucher C, Bian J. Assessing putative bias in prediction of anti-microbial resistance from real-world genotyping data under explicit causal assumptions. *KDD Health Day and 2021 KDD Workshop on Applied Data Science for Healthcare 2021*
14. Nicora G, **Marini S**, Limongelli I, Rizzo E, Montoli S, Tricomi FF, Bellazzi R. A semi-supervised learning approach for pan-cancer somatic genomic variant classification. *Conference of Artificial Intelligence in Medicine (AIME) 2019*
15. **Marini S**, Dagliati A, Sacchi L, Bellazzi R. Learning T2D evolving complexity from EMR and administrative data using Continuous Time Bayesian Networks. *International Joint Conference on Biomedical Engineering System and Technology (HEALTHINF) 2019A* 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*
16. De Martini A, **Marini S**, Vitali F, Bellazzi R. Matrix tri-factorization for miRNA-gene association discovery in acute myeloid leukemia. *Conference of Artificial Intelligence in Medicine (AIME) 2016*
17. **Marini S**, Dagliati A, Bellazzi R. A continuous time, multivariate model to simulate Type 2 Diabetes patients trajectories. *AMIA 2016*

#### Conference Abstracts (peer reviewed)

1. Rancati S, Nicora G, Bergomi L, Buonocore TM, Czyz D, Parimbelli E, Propseri M, Bellazzi R, **Marini S**, Salemi M. SARITA: A Generative Large Language Model Accurately Predicting The Emergence Of SARS-CoV-2 Critical Mutations. *32nd International Dynamics & Evolution of Human Viruses, Abbaye de Royaumont, France 2025*
2. Sy M, Prosperi M, Serajian M, Boucher C, Benos PT, **Marini S**. Prediction of A. Baumannii Amikacin Resistance in Clinical Metagenomics. *Medical Informatics Europe Conference (MIE) 2024*
3. Tagliamonte M, Hitchings M, **Marini S**, Cash M, Morris JG, Salemi M, Cummings DA, Mavian C. Integrative modeling of phylodynamic, vector, human travel, and epidemiological data to infer arboviral importation and local transmission. *31st International Dynamics & Evolution of Human Viruses 2024*
4. Tagliamonte M, Hitchings M, **Marini S**, Cash M, Morris JG, Salemi M, Cummings DA, Mavian C. Integrative modeling of phylodynamic, vector, human travel, and epidemiological data to infer arboviral importation and local transmission. *Ecology and Evolution of Infectious Diseases (EEID) 2024*
5. Tagliamonte M, Hitchings M, **Marini S**, Cash M, Morris JG, Salemi M, Cummings DA, Mavian C. Integrative modeling of phylodynamic, vector, human travel, and epidemiological data to infer arboviral importation and local transmission. *8th World One Health Congress 2024*
6. Tagliamonte M, Hitchings M, Cash MN, Morris JG, Salemi M, Cummings DA, **Marini S**, Mavian C. A One Health approach: integrative modeling of phylodynamic, vector, human travel, and epidemiological data to infer arboviral importation and local transmission. *8th World One Health Congress Scientific and Science Policy Interface Program (2024)*
7. Rancati S, Nicora G, **Marini S**, Salemi M, Bellazzi R. Identifying Dominant Omicron Lineages Using Embeddings and Anomaly Detection. *EMBC 2024*
8. Hwang C, Caragher SP, Kiwanuka H, Karinja SJ, Endo Y, **Marini S**, Tereshenko V, Raasveld FV, Valerio IL, Eberlin KR, Sinha I. Young Regenerative Muscle Exhibits Upregulation In Peripheral

- Nerve And Extracellular Matrix Transcriptional Programs. *Plastic and Reconstructive Surgery Global Open*. 11(5 Suppl) 2024
9. Rancati S, Nicora G, **Marini S**, Salemi M, Prosperi M, Bellazzi R. Predicting emerging SARS-Cov-2 lineages through an Autoencoder-based anomaly detection algorithm. *CIBB 2023*
  10. **Marini S**, Cash MN, Salemi M, Cook RL, Borsa P, Mavian C. An anti-inflammatory gene expression signature is associated with CBD treatment in people living with HIV. *The Cannabis Clinical Outcomes Research Conference (CCORC) 2023*
  11. Liu Y, Parisi C, Frisk-Hoffman R, Salemi M, Viteri D, Prosperi M, **Marini S**. Behavioral and demographic profiles of HIV contact networks in Florida. *International Conference on Intelligent Biology and Medicine (ICIBM) 2023*
  12. Bonin N, Doster E, Worley H, Pinnell L, Bravo J, Ferm P, **Marini S**, Prosperi M, Noyes N, Morley P, Boucher C. Updates to the MEGARes v3.0 database and its associated AMR++ bioinformatic pipeline for resistome analysis. *CRWAD 2023*
  13. Cohen SA, **Marini S**, Morris JG, Prosperi M. Sequence-based computational algorithm can predict antimicrobial resistance in major human pathogens: A comparative analysis with traditional clinical methods. *NIAMRRE Annual Conference 2023*
  14. **Marini S**, Cook R, Borsa P, Cash M, Prosperi M, Salemi M, Mavian C. Single-cell RNA sequencing reveals CBD genetic signature in monocyte gene expression. HIV *Persistence during therapy – International Workshop 2022*
  15. Prosperi M, Xu J, Guo JS, Bian J, Chen WH, Canidate S, **Marini S**, Wang M. Identification of Social and Racial Disparities in Risk of HIV Infection in Florida using Causal AI Methods. *IEEE International Conference on Bioinformatics and Biomedicine (BIBM) 2022*
  16. Prosperi M, Rife B, **Marini S**, Salemi M. Transmission cluster characteristics of global, regional, and lineage-specific SARS-CoV-2 phylogenies. *IEEE International Conference on Bioinformatics and Biomedicine (BIBM) 2022*
  17. Ugwoaba UA, Brockmann A, Arroyo KM, Swanson TN, Barrett KL, Shankar MN, **Marini S**, Ross KM. Behavioral Weight Loss Success: Android vs. iOS. *SBM 44th Annual Meeting and Scientific Session 2022*
  18. Mora R, Jeong KC, **Marini S**, Prosperi M. Assessing High-Throughput Sequencing Based Algorithms As An Alternative And/or Complement To Phenotypic Antibiotic Susceptibility Testing In Livestock. *ASM Microbe 2022*
  19. Nicora G, **Marini S**, Salemi M, Bellazzi R. Dynamic prediction of Non-neutral SARS-Cov-2 Variants using Incremental Machine Learning. *Medical Informatics Europe 2022*
  20. Tarchi L, Fantoni T, Pisano T, Damiani S, Vittori PL, **Marini S**, Nazzicari N, Castellini G, Politi P, Ricca V. i-ECO: a novel method for the analysis and visualization of fMRI results in Psychiatry. *30th European Congress of Psychiatry 2022*
  21. Chowdary AR, Maertz T, Henn D, Hankenson KD, Pagani CA, **Marini S**, Gallagher K, Aguilar CA, Tower RJ, Levi B. Macrophage-mediated PDGF Activation Correlates with Regenerative Outcomes Following Musculoskeletal Trauma. *Annals of Surgery 2022*
  22. 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. Peripheral Nerves Engage in Reciprocal Neuro-and Angiogenic Crosstalk With SMCs in Extremity Trauma. *Plastic and Reconstructive Surgery–Global Open 2021*
  23. **Marini S**, Slizovskiy I, Noyes N, Boucher C, Prosperi M. Learning antimicrobial resistance through secondary structure of protein variants. *International Conference on Intelligent Systems for Molecular Biology (ISMB) 2020*
  24. **Marini S**, Mavian C, Salemi M, Rife Magalis B. Optimizing viral genome subsampling by genomic diversity and temporal distribution. *COVID-19 Dynamics & Evolution 2020*



25. Rife Magalis B, **Marini S**, Salemi M, Prosperi M. Dynamic identification of viral transmission epicenters. *International Conference on Intelligent Systems for Molecular Biology (ISMB) 2020*
26. Stepien DM, **Marini S**, Hwang C, Pagani CA, Sorkin M, Visser ND, Huber AK, Vasquez K, Li J, Hatsell S, Economides A. Identifying The Myeloid Subpopulation Responsible For Tissue Fibrosis Across Organ Systems Via Machine Learning Parameterization And Predictive Transcriptomics. *Plastic and Reconstructive Surgery–Global Open 2020*
27. Patel N, Huber AK, Pagani C, **Marini S**, Hwang C, Loder S, Visser N, Greenstein JA, Vasquez K, Li J, Mishina Y. Post-Traumatic Limb Immobilization Alters Mesenchymal Stem Cell Fate. *Plastic and Reconstructive Surgery–Global Open 2020*
28. Hwang C, **Marini S**, Huber AK, Lee S, Stepien DM, Kubiak CA, Meyers C, Sorkin M, Pagani CA, Rehse T, Visser ND. Nerve Growth Factor Derives From Pericytes And Smooth Muscle Cells After Extremity Trauma. *Plastic and Reconstructive Surgery–Global Open 2020*
29. Rife Magalis B, **Marini S**, Salemi M, Prosperi M. Differing impacts of global and regional responses on SARS-CoV-2 transmission cluster dynamics. *COVID-19 Dynamics & Evolution 2020*
30. **Marini S**, Brooks M, Wicha M, Li J. Estimating cancer stemness with single-cell RNA sequencing. *Keystone Symposia Conference (L1: Single Cell Biology) 2019*
31. 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. Diverse mesenchymal stem cell populations contribute to VEGFA expression in post-traumatic heterotopic ossification. *American Society for Bone and Mineral Research Annual Meeting (ASMBR) 2019*
32. **Marini S**, Vella D, Nazzicari N, Bellazzi R. Gene-gene interaction module identification in single-cell RNA sequencing. *International Conference on Complex Networks and Their Applications (Complex Networks) 2018*
33. **Marini S**, Vitali F, Demartini A, Bellazzi R. Gene interaction discovery in myelodysplastic syndromes. *European Conference of Human Genetics (ESHG) 2018*
34. **Marini S**, Demartini A, Vitali F, Bellazzi R, Akutsu T. Data Fusion for cleavage target prediction. *Bioinformatics Italian Society National Congress (BITS) 2016*
35. Sacchi L, Colombo C, Dagliati D, **Marini S**, Cerra C, Chiovato L, Bellazzi R. Predicting Microvascular Complications from Type 2 Diabetes Retrospective Data. *Annual Diabetes Technology Meetings (DTM) 2014*
36. **Marini S**, Malavolti M, Dagliati A, Bellazzi R. A multivariate data-driven model to investigate the arising of complications in T2D patients. *Annual Diabetes Technology Meeting (DTM) 2014*
37. **Marini S**, Limongelli I, Bellazzi R. PaPI: the Pseudo Amino acid variant Predictor. *Bioinformatics Italian Society National Congress (BITS) 2014*
38. Limongelli I, **Marini S**, Bellazzi R. A novel algorithm to predict the deleteriousness of genomic coding variants. *NGS-ISCB 2014*
39. Barbarini N, Bellazzi R, Cobelli C, Di Camillo B, Manfrini F, Malovini A, **Marini S**, Sambo F, Trifoglio E. Dynamic Bayesian Networks to simulate type 1 diabetes patients cohorts. *Economics, Modelling and Diabetes: Mount Hood Challenge 2014*
40. Limongelli I, **Marini S**, Bellazzi R. PaPI: using pseudo amino acid composition to predict deleterious coding variants. *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.

05/2011 *University of Pavia, Italy*  
 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

### Current Research Support (PI or MPI)

- NIH NIA 1R21AG088603 (\$405,401) 09/2024 – 08/2026. **Contact PI: Marini.** MPIs: Wang, Sibille. *Medical Marijuana and chronic musculoskeletal pain in older adults: a multi-level, precision medicine analysis*
- MERCK AND COMPANY INC RES LAB (\$350,151) 10/2024 – 10/2026 **Contact PI: Marini.** 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 (\$249,630) [contract under negotiation] **Contact PI: Marini.** 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 **Contact PI: Marini.** *ViraLingo: decoding pan-viral genomics with AI*

### Completed Research Support (PI or MPI)

- PI/PD UFII 2022 (\$40,000) & PI/PD UFBI 2022 (\$25,000) 05/2021 - 05/2022. **Contact PI: Mavian. MPI: Marini.** *Seed grant: Microbiome-based explainable AI for pathogen prediction*
- Medical Marijuana Clinical Outcomes 2021 (\$74,040); 07/2021 - 07/2022. **Contact PI: Marini.** 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); 06/2019 - 01/2020. **Contact PI: Marini.** *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 (postgraduate)
01/2022-2024	Instructor: Topics in Precision Medicine and Public Health Informatics (postgraduate)
05/2021-06/2023	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

### **Service to Profession**

#### Journal Editor

05/2023-present      Nature Scientific Reports

#### 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. 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

12/2020-12/2022	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. <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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