

Simone Marini

University of Florida
Department of Epidemiology
2004 Mowry Rd,
Gainesville, FL 32610
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simone.marini@ufl.edu

Education

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

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

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

Professional Appointments

Research Assistant Professor

06/2020-present 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. AMR-meta: a k-mer and metafeature approach to classify antimicrobial resistance from high-throughput short-read metagenomics data. **Marini S**, Oliva M, Slizovskiy I, Das R, Noyes N, Kahveci T, Boucher C, Prosperi M. *Gigascience*, *in press*
2. Towards routine employment of computational tools for antimicrobial resistance determination via high-throughput sequencing, **Marini S*§**, Mora R*, Boucher C, Noyes N, Prosperi M§. *Briefings in Bioinformatics* 2022, *in press*
3. SARS-CoV-2 Delta vaccine breakthrough transmissibility in Alachua County, Florida. Magalis BR, Rich S, Tagliamonte MS, Mavian C, Cash MN, Riva A, **Marini S**, Moraga Amador DM, Zhang Y, Shapiro J, Horine A, Starostik P, Pieretti M, Vega S, Lacombe AP, Salinas J, Stevenson M, Myers P, Morris JG, Lauzardo M, Prosperi M, Salemi M. *Clin Infect Dis.* 2022, *in press*
4. Low-frequency variants in mildly symptomatic vaccine breakthrough infections presents a doubled-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, *in press*
5. 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
6. 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
7. Fast and exact quantification of motif occurrences in biological sequences. Prosperi M, **Marini S**, Boucher C. *BMC bioinformatics* 2021
8. 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
9. 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
10. 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
11. 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

12. 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
13. 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
14. 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
15. 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
16. 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
17. Hydrogen Peroxide Methods for Decontaminating N95 Filtering Facepiece Respirators. Rempel D, Henneman J, Agalloco J, Crittenden J, **N95DECON Consortium**. *Applied Biosafety* 2021
18. 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
19. 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
20. 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
21. 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
22. Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. Mavian C, Kosakovsky Pond SL, **Marini S**, Magalis BR, Vandamme AM, Dellincour S, Scarpino SV, Houldcroft CJ, Villabona-Arenas J, Paisie TK, Trovão NS, Boucher C, Zhang Y, Scheuermann RH, Gascuel O, Lam TTY, Suchard MA, Abecasis A, Wilkinson E, de Oliverira T, Bento A, Schmidt HA, Martin DP, Hadefield J, Faria N, Grubaugh N, Neher R, Beale G, Lemey P, Stadler T, Albert J, Crandall KA, Leitner T, Stamatakis A, Prosperi M, Salemi M. *PNAS* 2020
23. 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

24. 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
25. Comparative study of salivary, duodenal and fecal microbiota composition across adult celiac disease. Panelli S, Capelli E, Lupo G, Schiepatti E, Betti E, Sauta E, **Marini S**, Bellazzi R, Vanoli A, Pasi A, Cacciatore R, Bacchi S, Balestra S, Pastoris O, Frulloni L, Corazza GR, Biagi F, Ciccocioppo E. *Journal of Clinical Medicine* 2020
26. 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
27. 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
28. Scientific Collaboration During the COVID-19 Pandemic: N95DECON.org. Rempel D, **Members of the N95DECON Consortium**. *Annals of Work Exposures and Health* 2020
29. 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.
30. 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
31. Protease target prediction via matrix factorization. **Marini S**, Vitali F*, Rampazzi S, Demartini A, Akutsu T. *Bioinformatics* 2019
32. 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
33. 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
34. 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
35. 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
36. 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
37. 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
38. 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

39. Patient similarity for precision medicine: A systematic review. Parimbelli E, **Marini S**, Sacchi L, Bellazzi R *Journal of Biomedical Informatics* 2018
40. 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
41. 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
42. Dscam1 Web Server: online prediction of Dscam1 self- and hetero-affinity. **Marini S**, Nazzicari N*, Biscarini F, Wang GZ. *Bioinformatics* 2017
43. Machine learning methods to predict Diabetes complications. **Marini S**, Dagliati A*, Sacchi L, Bellazzi R. *Journal of Diabetes Science and Technology* 2017
44. 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
45. “Noisy bees”: 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
46. 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
47. 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
48. PaPI: pseudo amino acid composition to score human coding variants. Limongelli I, **Marini S**, Bellazzi R. *BMC Bioinformatics* 2015
49. 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
50. 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
51. 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
52. In silico Protein-Protein Interaction prediction with sequence alignment and classifier stacking. **Marini S**, Xu Q, Yang Q. *Current Protein and Peptide Science* 2011

Conference Papers (peer reviewed)

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

Conference Abstracts (peer reviewed)

1. Assessing High-Throughput Sequencing Based Algorithms As An Alternative And/or Complement To Phenotypic Antibiotic Susceptibility Testing In Livestock. Mora R, Jeong KC, **Marini S**, Prosperi M.
2. 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*
3. 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*
4. Optimizing viral genome subsampling by genomic diversity and temporal distribution. **Marini S**, Mavian C, Salemi M, Rife Magalis B. *COVID-19 Dynamics & Evolution 2020*
5. 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*
6. 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*
7. 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*

8. 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
9. 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
10. Estimating cancer stemness with single-cell RNA sequencing. **Marini S**, Brooks M, Wicha M, Li J. *Keystone Symposia Conference (L1: Single Cell Biology)* 2019
11. 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
12. 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
13. Gene interaction discovery in myelodysplastic syndromes. **Marini S**, Vitali F, Demartini A, Bellazzi R. *European Conference of Human Genetics (ESHG)* 2018
14. Data Fusion for cleavage target prediction. **Marini S**, Demartini A, Vitali F, Bellazzi R, Akutsu T. *Bioinformatics Italian Society National Congress (BITS)* 2016
15. 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
16. 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
17. 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
18. PaPI: the Pseudo Amino acid variant Predictor. **Marini S**, Limongelli I, Bellazzi R. *Bioinformatics Italian Society National Congress (BITS)* 2014
19. A novel algorithm to predict the deleteriousness of genomic coding variants Limongelli I, **Marini S**, Bellazzi R. NGS-ISCB 2014
20. 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
21. 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

| | |
|---------|---|
| 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)

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| 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>Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology, 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.
The Chinese Academy of Science, Beijing, China

Funding

Current Research Support

Medical Marijuana Clinical Outcomes 2021 (\$67,309)

Role: **PI**; Effort 10% 06/2021-05/2022

CBD-induced biomarkers of inflammation reduction in people living with HIV at the single cell level

Rockefeller Foundation 2021 HTH 012 (\$200,000); PI: Salemi

Role: **Co-I**; Effort 10% 06/2021-05/2022

Expanding genomic surveillance and epidemiology capacity in Central Florida and Southeastern US

Pending Research Support

NIH R21 2022

Role: **PI**; Effort 20%;

Medical Marijuana and chronic musculoskeletal pain: a multi-level, precision medicine analysis

NIH R01 2022; PI: Mavian

Role: **MPI**; Effort 40%;

Multi-scale spillover risk assessment of coronaviruses in North-American bats

NIH R21 2022; PI: Mavian

Role: **MPI**; Effort 40%;

Microbiome-based explainable AI for coronavirus prediction in Florida bat populations

NIH R01 2022; PI: Salemi

Role: **Co-I**; Effort: 25%; **Ranked in the top 12%**

A Phylodynamic Artificial Intelligence framework to predict evolution of SARS-CoV-2 variants of concern in Immunocompromised persons with HIV (PhAI-CoV): PI: SALEMI

NIH R01 2022; PI: Morris

Role: **Co-I**; Effort 25%

Haiti as a model for endemic SARS-CoV-2 infection in LMIC

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

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|-----------------|---|
| 01/2020-present | Supervising 2 postdocs, 1 PhD student, 2 Research assistants |
| 01/2022-04/2022 | Instructor: Topics in Precision Medicine and Public Health Informatics (postgraduate) |
| 01/2021-04/2021 | Instructor: Topics in Precision Medicine and Public Health Informatics (postgraduate) |
| 05/2020-08/2020 | Instructor of record: Computational Epidemiology (postgraduate) |

University of Michigan, USA

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| 08/2017-12/2019 | Supervised 1 postdoc, 2 postgraduates and 1 undergraduate students |
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Kyoto University, Japan

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| 06/2016-09/2016 | Supervised 1 undergraduate student |
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University of Pavia, Italy

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| 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

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| 01/2010-06/2010 | Teaching assistant: Introduction to Bioengineering |
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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 TranslationalScience, IEEE International Conference on Healthcare Informatics (IHC), 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

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|-----------------|--|
| 12/2020-present | COMINTART, the Italian YouTube channel to discuss and disseminate AI in layman terms. Italian audience. 15,000+ visualizations |
| 06/2007-12/2013 | OMP, non-profit publishing house, the first copyleft (Creative Commons) publishing house in Italy. <i>Pavia, Italy</i> |

Translator

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|---------|---|
| 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

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|-----------------|---|
| 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. *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*