Simone Marini

University of Florida
Department of Epidemiology
2004 Mowry Rd,
Gainesville, FL 32603
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	MS, 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	BS, 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

06/01/2020-present	Department of Epidemiology and Emerging Pathogens Institute,University of Florida, Gainesville, FL, USA

Artificial Intelligence Advisor

12/01/2016-present	enGenome srl, Pavia, Italy

Research Assistant Scientist

01/01/2019-05/31/2020	Department of Epidemiology and Emerging Pathogens Institute,University of Florida, Gainesville, FL, USA

Research Investigator

08/01/2017-12/31/2019	Department of Surgery, and Department of Computational Medicine and Bioinformatics, University of Michigan, Ann Arbor, MI, USA

Postdoctoral Fellow

12/01/2016-07/31/2017	Laboratory of Biomedical Informatics, University of Pavia, Italy
26/11/2015-26/11/2016	Laboratory of Mathematical Bioinformatics, University of Kyoto, Japan
01/06/2013-25/11/2016	Laboratory of Biomedical Informatics, University of Pavia, Italy

Publications

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

Journals (peer reviewed)

2020

1. 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*, in press

2. 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*, in press.

3. 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* 204 (8)

4. 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. J*ournal of Clinical Medicine*, in press

5. 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*, in press

7. Endogenous WISP-1 / CCN4 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. J*CI insight*, in press

8. 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. T*he American Journal of Pathology*, in press

9. 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*, in press.

2019

10. MTGO-SC, a tool to explore gene modules in single cell RNA-seq data Nazzicari N, Vella D, Coronnello C, Di Silvestre D, Bellazzi R, **Marini S*§**. *Frontiers in Genetics* 10(953)

11. Protease target prediction via matrix factorization
Marini S*§, Vitali F*, Rampazzi S, Demartini A, Akutsu T. *Bioinformatics* bty746

12. 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* 10

13. 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* 7(1)

2018 14. A comprehensive roadmap of murine spermatogenesis defined by single-cell RNA-seq
Green CD, Ma Q, Manske GL, Shami AN, Zheng X, **Marini S**, Moritiz L, Sultan C, Gurczynski SJ, Moore BB, Tallquist MD, Li JZ, Hammoud SS. *Developmental Cell* 46(5)

15. MTGO: PPI network analysis via topological and functional module identification
Vella D, **Marini S§**, Vitali F, Di Silvestre D, Mauri G, and Bellazzi R. *Nature Scientific Reports* 8(1)

16. 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* 1(1).

17. 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* bby041

18. 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* 1479164118780808.

19. Patient similarity for precision medicine: A systematic review
Parimbelli E, **Marini S**, Sacchi L, Bellazzi R *Journal of Biomedical Informatics* 83

20. 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* 13(12)

2017 21. 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* 10(2)

22. Dscam1 Web Server: online prediction of Dscam1 self- and hetero-affinity
Marini S*§, Nazzicari N*, Biscarini F, Wang GZ. *Bioinformatics* 33(12)

23. Machine learning methods to predict Diabetes complications
Dagliati A*, **Marini S***, Sacchi L, Bellazzi R. *Journal of Diabetes Science and Technology* 1932296817706375

2016

24. 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* 11(12)

25. "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*, 12(36)

26. 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, T**he SUMMIT Consortium**, BioBank Japan Project. *The American Journal of Human Genetics*, 99(3)

2015

27. 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, Malovino A, Manfrini M, Cobelli C, Bellazzi R. *Journal of Biomedical Informatics* 57

28. PaPI: pseudo amino acid composition to score human coding variants
Limongelli I, **Marini S**, Bellazzi R. *BMC Bioinformatics* 16(123)

29. Developing a parsimonius predictor for binary traits in sugar beet (Beta vulgaris)
Biscarini F, **Marini S**, Stevanato P, Broccanello C, Bellazzi R, Nazzicari N. *Molecular Breeding* 35(10)

2014

30. Improvement of Dscam homophilic binding affinity throughout Drosophila evolution
Wang GZ*, **Marini S***, Ma X, Yang Q, Zhang X, Zhu Y. *BMC Evolutionary Biology*, 14:186

2013

31. 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*, 8:12::e85065

2011 32. In silico Protein-Protein Interaction prediction with sequence alignment and classifier stacking
Marini S, Xu Q, Yang Q. *Curr Protein Pept Sci*, 12:7

Conference Papers (peer reviewed)

2019 1. 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. 19TH Conference of Artificial Interlligence in Medicine (AIME 2019)

2016 2. Learning T2D evolving complexity from EMR and administrative data using Continuous Time Bayesian Networks
Marini S, Dagliati A, Sacchi L, Bellazzi R. 9th International Joint Conference on Biomedical Engineering System and Technology (HEALTHINF 2016)

2015 3. A genomic data fusion framework to exploit rare and common variants for association discovery
Marini S, Limongelli I, Rizzo E, Da T, Bellazzi R. 15TH Conference of Artificial Interlligence in Medicine (AIME 2015)

4. Matrix tri-factorization for miRNA-gene association discovery in acute myeloid leukemia
De Martini A, **Marini S**, Vitali F, Bellazzi R. 15th Conference of Artificial Intelligence in Medicine (AIME 2015) [Workshop]

Conference Abstracts (peer reviewed)

2020 1. 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

2. 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.

3. 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

4. Learning antimicrobial resistance through secondary structure of protein variant. **Marini S**, Slizovskiy I, Noyes N, Boucher C, Prosperi M. International Conference on Intelligent Systems for Molecular Biology (ISMB)

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)

2019 6. Estimating cancer stemness with single-cell RNA sequencing
Marini S, Brooks M, Wicha M, Li J. 2019 Keystone Symposia Conference (L1: Single Cell Biology)

7. 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)

2018 8. Gene-gene interaction module identification in single-cell RNA sequencing
Marini S, Vella D, Nazzicari N, Bellazzi R. 7th International Conference on Complex Networks and Their Applications (Complex Networks 2018)

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

2016 10. Data Fusion for cleavage target prediction
Marini S, Demartini A, Vitali F, Bellazzi R, Akutsu T. Bioinformatics Italian Society National Congress (BITS 2106)

11. 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)

12. Predicting Microvascular Complications from Type 2 Diabetes Retrospective Data
Sacchi L, Colombo C, Dagliati D, **Marini S**, Cerra C, Chiovato L, Bellazzi R. 15th Annual Diabetes Technology Meetings (DTM 2016)

2014 13. A multivariate data-driven model to investigate the arising of complications in T2D patients
Marini S, Malavolti M, Dagliati A, Bellazzi R. 14th Annual Diabetes Technology Meeting (DTM 2014)

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

15. A novel algorithm to predict the deleteriousness of genomic coding variants
Limongelli I, **Marini S**, Bellazzi R. NGS-ISCB 2014;34:132

16. 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

17. 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

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

Preprints

1. Regaining perspective on SARS-CoV-2 molecular tracing and its implications. Mavian, **Marini S**, Manes C, Capua I, Prosperi M, Salemi M. *medRxiv*

Awards and Fellowships

02/2018 Elsevier Outstanding contribution in reviewing
11/2015-11/2016 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 HKUST Overseas Research Award for PhD Students

Invited Talks and Lectures (extramural)

07/2020 Multi-sample, multi-condition analysis in scRNAseq data sets. ISMB 2020, BioinfoCore Workshop

06/2019 Enhancing data analysis by leveraging prior biomedical knowledge. Department of Epidemiology, University of Florida, Gainesville, FL, USA.

06/2018 Data exploration of single-cell landscapes. Center for Health Technologies, Pavia, Italy.

10/2017 Joint data integration for precision oncology. UFHCC Topics in Cancer seminar series, University of Florida, Gainsville, FL, USA.

07/2017 miRNA Bioinformatics, sequence analysis and statistical processes. Training school "Omics technologies and bioinformatics application in ME/CFS research", University of Pavia, Pavia, Italy.

01/2017 Investigating epileptogenesis with data fusion. University of Michigan, Ann Arbor, USA

09/2016 Mining heterogeneous data sources to enhance association studies. University of Arizona, Tucson, USA

06/2016 Leveraging on public databases for novel peptidase target discovery, University of Pavia, Pavia, Italy

05/2011 Motif search, sequence alignment and Support Vector Regression for Dscam protein self- and hetero-binding affinity prediction. Institute of Biophysics, the Chinese Academy of Science, Beijing, China

Funding

Ongoing Research Support

12/2018-present University of Michigan, Mcubed Program (mini-cube).
Title: Mapping diabetic foot ulcers at the single-cell level
Role: PI

Completed Research Support

NIH U01DA043098 (contact PI: Akil, MPI: Li)
Title: Genetics of novelty seeking and propensity for drug abuse in outbred rats
Role: Co-I

Kyoto University
Japanese Society for the Promotion of Science funding
Role: Postdoctoral fellow

Teaching and Supervising Experiences

University of Florida, USA

01/2020-present Supervising 1 postdoc and 1 PhD student

06/2020-present Instructor of record: Computational Epidmiology

University of Michigan, USA

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

Kyoto University, Japan

06/2016-09/2016 Supervised 1 undergraduate student

University of Pavia, Italy

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

The Hong Kong University of Technology, China

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

Service to Profession

Journal Reviewer

2018-present Bioinformatics
2018-present Molecules
2018-present Plos one
2014-present Journal of Biomedical Informatics
2016 Computers in Biology and Medicine
2015 Briefings in Bioinformatics

Conference Reviewer

2016-2019 Artificial Intelligence in Medicine (AIME)
2016-2017 AMIA joint Summits on TranslationalScience

2017 IEEE International Conference on Healthcare Informatics (ICHC)

Conference Program Committee Member

2018-2020 IEEE International Symposium on Computer-Based Medical Systems (CBMS)
2019 IEEE ICTS4eHealth 2019

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

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

Introducing machine learning in high school

04/2017, 11/2015, 05/2014, 03/2013 Introduction to data science and artificial intelligence. G. Galilei high school, Voghera, Italy.

01/2013-03/2013 Introduction to data science and artificial intelligence. Settore Istruzione e Politiche Giovanili, Pavia. Italy.

Software developer

06/2014 VSO Poverty Alleviation, remote services. Development of a software to help managing dairy cooperatives. DCPUK, Bangladesh.

Co-founder

06/2007-12/2013 OMP, non-profit publishing house, the first copyleft (Creative Commons) publishing house in Italy.

Editor in Chief

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

Front desk volunteer

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