

## CURRICULUM VITAE

**Mattia Prosperi, MEng, PhD**

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### PERSONAL INFORMATION

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### EDUCATION, QUALIFICATIONS AND TRAINING

	<i>Institution and location</i>	<i>Year(s)</i>	<i>Degree/Role</i>	<i>Mark/Merits</i>	<i>Major</i>
Education (Graduate Degrees)	University of Milan, Milan, Italy	2009	Spec. Course	Merit Scholar.	Bioinformatics
	Roma Tre University, Rome, Italy	2004-2008	Ph.D.	Merit Scholar.	Computer Science & Automation
	Roma Tre University, Rome, Italy	1997-2003	M.Eng.	109/110	Computer Science Engineering
Academic Qualifications	French Ministry of Superior Education and Research, France	2010	Maître de Conférences	N/A	Computer Science
	Italian Ministry of Education, University and Research, Italy	2018	Habilitation to University Professorship (Level II)	N/A	Computer Science Engineering, Molecular Biology
Training	University College London, London, United Kingdom	2007-2008	Visiting Scholar	N/A	Biostatistics, Epidemiology
	Parc de Recerca Biomèdica de Barcelona, Barcelona, Spain	2007	Visiting Scholar	N/A	Bioinformatics
	Max Planck Institute, Saarbrücken, Germany	2006	Visiting Scholar	N/A	Bioinformatics
	University of Bergen, Bergen, Norway	1999-2000	Visiting Scholar	N/A	Computer Science Engineering

### POSITIONS AND EMPLOYMENT

#### Academic Positions

2015-current	Associate Professor (Preeminence), tenured in 2019, head of the <b>Data Intelligence Systems Lab, Department of Epidemiology, College of Public Health and Health Professions &amp; College of Medicine, University of Florida</b> , Gainesville, FL, USA.
2012-2015	Assistant Professor [Lecturer as per the British academic nomenclature] in Biomedical Modelling, <b>Centre for Health Informatics, Division of Informatics, Imaging &amp; Data Sciences, University of Manchester</b> , Manchester, UK.  Honorary Lecturer, Education and Research Centre, University Hospital of South Manchester, Manchester, UK.

2010-2012	Post-doctoral associate, Emerging Pathogens Institute, University of Florida, Gainesville, FL, USA.
2009-2010	Post-doctoral associate and adjunct professor, Catholic University of the Sacred Heart, Rome, ITA.
2008-2009	Post-doctoral associate, National Institute of Infectious Diseases, Rome, ITA.

### Professional Consultancies

2010-2012	Malattie Infettive e Salute Internazionale (MISI) foundation, Brescia, ITA.
2010-2012	Catholic University of the Sacred Heart, Rome, ITA.
2003-2011	Informa Pro, LLC, Rome, ITA.
2007-2009	Italian cohort of naïve to antiretrovirals (Icona) foundation, Milan, ITA.

### PERSONAL STATEMENT

My research interests are in the areas of *data science* and *biomedical modelling*. I lead my research group towards the development of original algorithms and applications, exploiting machine learning with a critical eye on causality, and designing usable tools.

My **theoretical research** is focused on development of new computational intelligence approaches tailored to the analysis of high-dimensional and heterogeneous data, e.g. electronic medical records, ecological data bases, social media data.

My **applied research** foresees the development of prediction and intervention (i.e. counterfactual) models of future life statuses, with focus on precision medicine and public health. I capitalize on my engineering background together with epidemiology experience to exploit successfully a layered big data analytics paradigm, which integrates multiple domains, such as socio-demographic, ecological, clinical, -omics, and sensor technology. In such multi-level integration of individual and social-ecological determinants, I hybridize traditional theory-based models with bottom-up data mining.

I lead the **Data Intelligence Systems Lab** (DISL, <https://epidemiology.phhp.ufl.edu/research/disl/>) at University of Florida, promoting interdisciplinary team science, education, and scholarly activities.

I foster Master's and PhD students to create a specialized workforce that will enable the University to excel in the next-generation data science. I am organizer of the "*International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology*", editor of "*BMC Medical Informatics and Decision Making*" and "*Global Health Research and Policy*". I am also member of the *Association for Computing Machinery (ACM)*, the *American Medical Informatics Association (AMIA)* and program member of several international conferences, including ACM's Conference on Bioinformatics, Computational Biology, and Health Informatics.

### PUBLICATIONS

My publication record includes over 150 works in peer-reviewed international journals/books (**h-index 34**, i10-index 85), of which about half authored as first/senior author, including pieces with the *Nature* and *PNAS* publishers. My publications cover multiple areas of basic and applied research, including biomedical and health informatics, machine learning, biomathematics, computational biology, computational epidemiology, and bio-inspired robotics.

A comprehensive list can be found via my Google scholar profile and via my NCBI for PubMed-indexed papers

- <https://scholar.google.com/citations?user=lymUyDkAAAAJ&hl=en>
- <https://www.ncbi.nlm.nih.gov/myncbi/tNQd-7sVrcEk-/bibliography/public/>

The complete list of publications is appended at the end of this resume. I also presented regularly abstracts/posters at international conferences from 2004 to current date.

### RESEARCH SUPPORT

#### Ongoing Research Support

#### **Extramural Funding**

NSF 2013998 (Boucher, Jeong, Prosperi, Ruiz) 1/1/2021-12/31/2024 0.75 calendar months  
 Role (budget): **Co-PI (\$1,187,778)**  
 Title: SCH: INT: Enabling real-time surveillance of antimicrobial resistance

NIH NCI R21CA245858 (Guo) 08/01/2020-07/31/2022 1.2 calendar months  
 Role (budget): Co-I (\$392,115)  
 Title: Using Electronic Health Records from a Large Clinical Data Research Network to Understand Cancer Burden and Cancer Risks among Transgender and Gender Nonconforming (TGNC) Individuals.

NIH NIAID R01AI145552 (Salemi, Prosperi) 05/01/2020-04/30/2024 1.8 calendar months  
 Role (budget): **MPI (\$2,809,658)**  
 Title: Forecasting trajectories of HIV transmission networks with a novel phylodynamic and deep learning framework

FL DEPT OF HEALTH (Prosperi) 05/01/2020-04/30/2021 1.68 calendar months  
 Role (budget): **PI (\$248,068)**  
 Title: HIV outcomes and stigma.

NSF DEB 2028221 (Prosperi, Dean, Salemi) 04/15/2020-03/31/2020 1.0 calendar months  
 Role: **PI (\$166,530)**  
 Title: RAPID: Dynamic Identification of SARS-COV-2 Transmission Epicenters in Presence of Spatial Heterogeneity (COV-DYNAMITE)

AHA 19GPSGC35180031 (Bian UF site PI) 12/01/2019 - 11/30/2023 0.36 calendar months  
 Role: Co-I (\$199,131)  
 Title: Artificial Intelligence-Aided Personalization on Dual Antiplatelet Therapy for Patients Underwent Coronary Stent Implantation

NIH NCATS 5UL1TR001427-04 (Nelson) 04/01/2019 - 03/31/2024 1.0 calendar months  
 Role (budget): Co-I (\$3,418,250 first year)  
 Title: Together: transforming and translating discovery to improve health.

NIH NIA R21AG062884 (Ingibjargardottir-Bjarnadottir, Lucero) 04/01/2019-03/31/2021 1.2 calendar months  
 Role (budget): Co-I (\$415,343)  
 Title: Advancing Interdisciplinary Science of Aging through Identification of Iatrogenic Complications: The UF EHR Clinical Data Infrastructure for Enhanced Patient Safety among the Elderly (UF-ECLIPSE).

IT MISI Foundation (Prosperi) 01/15/2019- 12/31/2021 0.18 calendar months  
 Role (budget): **PI (\$20,400)**  
 Title: Management of standardized evaluation of retroviral HIV Infection (MASTER).

NIH NIAID 1R01AI141810-01 (Boucher, Prosperi) 11/26/2018 - 10/31/2023 2.4 calendar months  
 Role (budget): **MPI (\$2,139,795)**  
 Title: Developing Computational Methods for Surveillance of Antimicrobial Resistant Agents.

NIH NIAID 1R21AI138815-01 (Prosperi, Salemi) 04/01/2018 - 03/31/2020 ext. 2021 1.44 calendar months  
 Role (budget): **PI (\$419,375)**  
 Title: HIV Dynamic Modelling for Identification of Transmission Epicenters (HIV-DYNAMITE).

NIH NINDS R01NS063897 (Salemi) 09/30/2017 - 06/30/2022 1.2 calendar months

Role (budget): Co-I (\$3,623,736)

Title: Viral evolution in peripheral macrophages and brain during progression to AIDS.

NSF SES 1734134 (Prosperi, Bian, Zhou) 09/01/2017 - 08/31/2020 ext. 2021 0.8 calendar months

Role (budget): **PI (\$392,840)**

Title: A Person-Centric Prediction Model of Job Loss based on Social Media.

### ***Intramural Funding***

UNIVERSITY OF FLORIDA's "Creating the Healthiest Generation" Moonshot (Morris) 01/01/2019-12/31/2020 N/A

Role (budget): Co-I (\$265,332 direct only)

Title: Confronting the Threat of Emerging Pathogens and Eliminating Hospital-Acquired Drug Resistant Infections

UNIVERSITY OF FLORIDA's "Creating the Healthiest Generation" Moonshot (Shenkman, Hogan) 01/01/2019-12/31/2020 N/A

Role (budget): Co-I (\$501,150 direct only)

Title: Advance Data Capabilities: Integrating Precision Public Health and Precision Medicine

### **Completed Research Support**

NIH NIAID 5P30A1073961-13 (Pahwa) UM CFAR supplement 10/01/2019 - 05/31/2020 0.12 calendar months

Role: **PI of subaward (\$15,030)**

Title: Preparing to Implement Novel "Data to PrEP" Initiatives to Eliminate HIV Transmission in Florida

FL DEPT OF HEALTH (Prosperi) RENEWAL 04/01/2019 - 03/31/2020 1.2 calendar months

Role (budget): **PI (\$115,704)**

Title: Spatiotemporal analysis of HIV drug resistance in Florida.

FL DEPT OF HEALTH (Prosperi) 05/01/2018 - 03/31/2019 2.0 calendar months

Role (budget): **PI (\$115,704)**

Title: Spatiotemporal analysis of HIV drug resistance in Florida.

NIH NCI R21CA195251-01A1 (Mai, Prosperi) 01/06/2016 - 12/31/2017 ext. 12/31/2018 1.2 calendar months

Role (budget): **PI (\$258,542)**

Title: Big data approach for correlating gut microbiota with epithelial methylation pattern.

US DEPT OF HOMELAND SECURITY (Blackburn) 06/01/2016-05/31/2019 1.2 calendar months

Role (budget): Co-I (\$1,527,011)

Title: Bacterial Population Genetics of Select Agent Pathogens.

ARBOR PHARMACEUTICALS (Cottler) 09/01/2018 - 11/30/2018 0.6 calendar months

Role (budget): Co-I (\$377,539)

Title: Study of Non-Oral Administration of Prescription Stimulants (SNAPS).

UNIVERSITY OF FLORIDA's Health Cancer Center (Asirvatham, Chim, Mai, Prosperi, Yaghjian) 10/2017-09/2018 N/A

Role (budget): **PI (\$42,200)**

Title: Correlations between breast microbiota and tissue methylation pattern.

EU H2020-PHC-32-2014 #634650 (Vandamme) 06/01/2015-05/31/2018 2.4 calendar months

Role (budget): **PI of work package (€437,560 / total project costs €2,995,968)**

Title: Virogenesis: Virus discovery and epidemic tracing from high throughput metagenomics sequencing.

NIH NIMH 1R21MH109360/01-02 (Marshall) 04/05/2016-03/31/2018 0.9 calendar months

Role (budget): **PI** of subaward (**\$37,590** / total project costs \$261,525)  
 Title: Enhancing pre-exposure prophylaxis implementation to optimize individual and community-level impact.  
 IT MISI Foundation (Prosperi) 03/31/2015-03/31/2018 0.7 calendar months  
 Role (budget): **PI (\$24,354)**  
 Title: Management of standardized evaluation of retroviral HIV Infection (MASTER).

IT CINECA ISCRA SCAI HP10CD4PA7 (Milicchio, Prosperi) 10/2016-10/2017 N/A  
 Role (budget): **PI (4Million CPU-hours)**  
 Title: Tools for Assembly of Next-Generation Sequencing U-mer Data Objects (TANGSUDO).

University of Florida's Health Cancer Center & Institute on Aging (Bird, Gerke, Manini, Prosperi) 02/2016-02/2018 N/A  
 Role (budget): **PI (\$40,000)**  
 Title: Endotype discovery in prostate cancer and multi-domain analysis of age-related comorbidities.

UNIVERSITY OF FLORIDA's Health Quasi Endowment Fund – Renewal (Lucero) 02/2017-02/2018 1.2 calendar months  
 Role (budget): Co-I (\$50,000)  
 Title: Strengthening the UFHealth Nursing Academic Partnership Phase III: Generating Practice-based Evidence for Quality Improvement

UNIVERSITY OF FLORIDA's Health Quasi Endowment Fund (Lucero) 02/2016-02/2017 1.2 calendar months  
 Role (budget): Co-I (\$64,358)  
 Title: Strengthening the UFHealth Nursing Academic Partnership Phase III: Generating Practice-based Evidence for Quality Improvement

IT EURESIST FOUNDATION (Prosperi) 07/15/2015-07/14/2016 0.72 calendar months  
 Role (budget): **PI (\$19,600)**  
 Title: EuResist Engine retraining and revision.

FLORIDA ACADEMIC CANCER CENTER ALLIANCE (Yaghjian) 2015-2016 N/A  
 Role (budget): Co-I (\$50,000)  
 Title: Gut microflora and estrogens: a new paradigm for breast cancer risk reduction

IT CINECA ISCRA SCAI HP10CU1H2A (Milicchio, Prosperi) 09/2014-09/2015 N/A  
 Role (budget): **PI (200,000 CPU-hours)**  
 Title: Distributed Processing of High-Throughput Sequencing Data via De Bruijn Graphs (PHERCoOI)

NIH NIAID R01 A1097405-03 (Morris) 08/01/2014-11/30/2015 0.96 calendar months  
 Role (budget): Co-I (\$2,724,560)  
 Title: Cholera Transmission in Gressier Region, Haiti: Refinement of Bioinformatics.

UK MRC MR/L011808/1 (Griffiths) 09/2014-08/2019 N/A  
 Role (budget): Researcher (£5,004,540)  
 Title: Psoriasis Stratification to Optimise Relevant Therapy (PSORT)

UK BBSRC BB/M001121/1 (Robertson) 09/2014-08/2017 N/A  
 Role (budget): Co-I (£274,155)  
 Title: Computational methods for microbial next-generation sequencing data

UK MRC MR/L012693/1 (Johnston) 05/2014-05/2019 N/A

Role (budget): Co-I; role ended after leaving UK (£2,200,000)

Title: Phenotyping immune responses in asthma and respiratory infections - a systems approach to understanding changes from childhood to adulthood

IT FONDAZIONE MISI (Prosperi) 2012-2014 N/A

Role (budget): **PI (€18,000)**

Title: Management of standardized evaluation of retroviral HIV Infection” (MASTER).

UNIVERSITY OF FLORIDA’s NIH NCRR UL1 RR029890 (Prosperi) 2011-2012 N/A

Role (budget): **PI (\$25,000)**

Title: Solving the puzzle of quasispecies reconstruction using next-generation sequencing technologies.

UNIVERSITY OF FLORIDA’s EPIG (Prosperi) 2011-2012 N/A

Role (budget): **PI (\$5,000)**

Title: HIV-1 intra-host evolution in HLA-B\*5701 patients with slow disease progression.

## TEACHING, SELECTED INVITED TALKS & MENTORING

May-June 2020 (course, 28 hrs)	University of Florida’s PHC7083: Computational Epidemiology in Population Science.
Mar. 2020	Invited talk “Dynamic Identification of Transmission Epicenters: Application to HIV Epidemic in FL (HIV-DYNAMITE)” at the NIH-NIAID workshop “Phylogenetic Monitoring of HIV Transmission Hotspots to End the HIV Epidemic.”
Jan.-Apr. 2020 (course, 14 hrs)	University of Florida’s PHC7199: Topics in Precision Medicine and Public Health Informatics.
Nov. 2019 (seminar)	Guest lecture for University of Florida’s GMS6847 (Section 28C7) Translational Research and Therapeutics: Bench, Bedside, Community, & Policy. Title: “Precision Public Health.”
Sep. 2019 (seminar)	Guest seminar “Big data hurdles in precision medicine and public health” at Northeastern University, Boston, MA.
Aug. 2019 (course, 15 hrs)	Organizer of the “24 <sup>th</sup> International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology” University of Hong Kong, Hong Kong.
June 2019 (seminar)	Invited talk “Big data hurdles in precision medicine and public health” at the Digital Health Summit in Grasmere, UK, organized by Lancaster University.
Mar. 2019 (seminar)	Invited seminar “Dynamic Modelling of Phylogenies for Identification of Transmission Epicenters in the HIV Epidemic, HIV-DYNAMITE” at the Center for Statistics and Quantitative Infectious Diseases (CSQUID) working group, University of Florida.
Jan.-Apr. 2019 (course, 14 hrs)	University of Florida’s PHC6937: Topics in Precision Medicine and Public Health Informatics.
Nov. 2018 (seminar)	Guest lecture for University of Florida’s GMS6803: Data Science in Clinical Research. Title: “Eagle’s view on machine learning”.
Oct. 2018 (seminar)	Invited seminar “Predicting human-immunodeficiency virus rebound after therapy initiation/switch using genetic, laboratory, and clinical data” for University of Florida’s HSC6935: Core Seminar in the Translational Science of Alcohol and HIV Infection.
Aug. 2018 (course, 15 hrs)	Organizer and teacher at the “23 <sup>rd</sup> International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology” Robert Koch Institute, Berlin, Germany.
June 2018 (seminar)	Invited seminar “A Combined Man-Machine Modelling Pipeline for Characterizing Life Events from Twitter” School of Business and Administration, Zhejiang GongShang

	University, Hangzhou, China.
May-June 2018 (course, 14 hrs)	University of Florida's PHC7083: Computational Epidemiology in Population Science.
Jan. 2018 (seminar)	Guest seminar (CME-accruing) at Vanderbilt University, Nashville, TN. Title: "Challenges in Next-Generation Metagenomics: Rethinking the Microbiome/Virome Characterization for Known Species, and Chasing the Unknown."
Jan.-Apr. 2018 (course, 14 hrs)	University of Florida's PHC6937: Topics in Precision Medicine and Public Health Informatics.
Nov. 2017 (seminar)	Guest lecture for University of Florida's GMS 6803: Data Science in Clinical Research. Title: "Big Data Schmucks in Precision Medicine and Precision Public Health".
Sep. 2017 (seminar)	Invited seminar at the University of Florida's "College of Medicine Alumni Weekend". Title: "Big Data Science for Precision Medicine and Precision Public Health".
Aug. 2017 (course, 15 hrs)	Organizer and teacher at the "22 <sup>nd</sup> International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology" Nova University, Lisbon, Portugal.
July 2017 (seminar)	Guest lecture for University of Florida's PHC4101: Public Health Concepts. Title: "Big Data Science for Precision Medicine and Precision Public Health".
May-June 2017 (course, 14 hrs)	University of Florida's PHC7083: Computational Epidemiology in Population Science (4.7/5.0 students' evaluation score).
Mar. 2017 (seminar)	Guest lecture for University of Florida's PHC7000: Epidemiology Seminar Series II. Title: "Overview of Genome-Wide Analyses".
Mar. 2017 (seminar)	Guest seminar at Brown University, Providence, Rhode Island "Precision Medicine via Multi-Domain Inference, to Say Nothing of Big Data".
Mar. 2017 (course, 10 hrs)	Co-organizer and teacher for the "Genomic Virology Workshop" held in Montreal, Canada, with McGill University and Genome Quebec, funded by the Canadian Food Inspection Agency.
Feb. 2017 (seminar)	Invited seminar at University of Texas Medical Branch, Galveston, Texas "Challenges in Next-Generation Metagenomics - Refining the Microbiome / Virome Characterization for Known Species, and Chasing the Unknown".
Nov. 2016 (seminar)	Guest lecture for University of Florida's GMS6850: Foundations of Biomedical Informatics. Title: "Multi-domain Inference in Healthcare" (4.3/5.0 students' evaluation score).
Sep. 2016 (keynote)	Invited keynote at the 2016 Annual Meeting of the American College of Clinical Pharmacology, Bethesda, MD. Title: "Multi-domain inference in healthcare".
Aug. 2016 (course, 15 hrs)	Organizer and teacher at the "21 <sup>st</sup> International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology" Korea University, Seoul, South Korea.
May-June 2016 (course, 14 hrs)	University of Florida's PHC6937: Computational Epidemiology in Population Science (4.8/5.0 median students' evaluation score).
Dec. 2015 (seminar)	Guest lecture for University of Florida's GMS6850: Foundations of Biomedical Informatics. Title: "Precision Genomic/Molecular Medicine" (4.7/5.0 students' evaluation score).
Aug. 2015 (keynote)	Invited keynote "Multi-Domain Inference in Healthcare: Building the Big Data Community" at the "Phenotypic Prediction Workshop" University of Florida, FL, USA.
Aug. 2015 (course, 15 hrs)	Organizer and teacher at the "20 <sup>th</sup> International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology" University of West Indies, Trinidad and Tobago.
Sep. 2014 (course, 15 hrs)	Organizer and teacher at the "19 <sup>th</sup> International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology" National Institute of Infectious Diseases, Rome, Italy.

2013-2014 (tutoring, 70 hrs)	Tutor for Professional and Personal Development, University of Manchester, UK.
Dec. 2013 (seminar)	Invited seminar “Big Data Inference in Healthcare” University of Manchester, UK.
Aug. 2013 (course, 20 hrs)	Organizer and teacher at the “18 <sup>th</sup> International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology” University of Florida, FL, USA.
May. 2013 (seminar)	Invited seminar “Bayesian network inference for large-scale data (to say nothing of the other methods)” University of Sheffield, UK.
Mar. 2013 (seminar)	Invited seminar “Bayesian Networks and Large Scale Data Mining” Catholic University of Leuven, Leuven, Belgium.
Aug. 2012 (course, 5 hrs)	Teacher at the “17 <sup>th</sup> International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology” University of Belgrade, Serbia.
Oct. 2011 (course, 15 hrs)	Teacher at the international workshop “Bioinformatics for Phylogenetic Reconstruction in Virology” Hospital de Pediatria Garrahan, Buenos Aires, Argentina.
Aug. 2010 (course, 5 hrs)	Teacher at the “16 <sup>th</sup> International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology” Johns Hopkins University, Rockville, MD, USA.
June 2010 (seminar)	Invited seminar “Mathematical Models for HIV-1 Therapy Optimisation” Institute for Scientific Interchange (ISI), Turin, Italy.
Jan.-Mar. 2010 (course, 15 hrs)	“Biostatistics for physicians” at the doctorate school in Biology and Clinic of Tropical and Infectious Diseases, Catholic University of the Sacred Heart, Rome, Italy.
Dec. 2008 (seminar)	Invited seminar “Bioinformatics helps to make sense of HIV drug resistance” Borodino Ht., Moscow, Russia.
2004-2008 (teaching assistance, ~10/20 hrs per course)	Teaching assistant at the faculty of Computer Science Engineering of the Roma Tre University, Rome, Italy, for the courses of: “Misure e strumentazione per l’automazione” [Measures and Instruments for Automation] (Master’s level), “Intelligenza artificiale” [Artificial Intelligence] (Master’s level), “Fondamenti di automatica” [Foundations of Automation] (Bachelor’s level).

## Mentoring

*Faculty:* Simone Marini (2020-) Res Ast Sci at University of Florida.

*Postdocs/fellows:* Carla Mavian, PhD (2016-2017), Giuseppe Tradigo, PhD (2016), Rebecca Rose, PhD (2015-2018) at University of Florida.

*Graduate assistants:* Kaden King, BSc (2020) at University of Florida.

*PhD students:* Kai Wang (2018), Zhaoyi Chen (2019), Jae Min (2019), Shannan Rich (PhD expected 2021), Inyoung Jun (PhD expected 2022) at University of Florida; Paolo Fraccaro (2017), Rebecca Howard (2018) at University of Manchester, UK. Certified supervisor for PhD students (May 2014, University of Manchester, UK –it enables to take the role of main PhD supervisor in UK).

*Master’s students:* Rebecca Hunter Smith, MSc (2018) at University of Florida; Arturo Franchini, MEng (2017) at University of Brescia, Italy; Hans-Joachim Sonntag, MSc (2014) at University of York, UK.

*Undergraduate students:* 6 at University of Manchester (2013-2014).

*Visiting professors:* SungYoon Jung, PhD from Yeungnam University, South Korea (2019-2020).

## EDITORIAL APPOINTMENTS, MEMBERSHIPS, RELEVANT SERVICES

### Editorial Appointments

2019 – current	Associate Editor of <i>Global Health Research and Policy</i> (IF=TBA).
2017	Guest editor of <i>Current Medicinal Chemistry</i> (IF=3.8).



2011 – current | Associate Editor of *BMC Medical Informatics and Decision Making* (IF=2.6).

### International Workshops / Conferences

2020 | Organizer of the Data Intelligence Symposium (DAISY) – a workshop on transdisciplinary data science (<https://epidemiology.phhp.ufl.edu/daisy2020>)

2014 - current | Member of the program committees of: ISCB-ISMB (2014); IEEE-CBMS (2014); AMIA-DMMI (2014-2015, 2018); IEA/AIE (2017); ACM-BCB (2017-2020, including track and publicity chair); SIMBIG (2018-2019); IEEE-BIBM (2018); DSHealth / KDD Workshop on Applied Data Science for Healthcare: Trustable and Actionable AI for Healthcare (2020); ACM-CIKM (2020); AMIA-KDDM (2020).

2013 - current | Organizer of the International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology (<http://rega.kuleuven.be/cev/avd/meetings/international-bioinformatics-workshops>).

### Professional / Scientific Memberships

2018 - current | Member of the American Medical Informatics Association (AMIA, <https://www.amia.org/>)

2016 - current | Member of the Association for Computing Machinery (ACM, <https://www.acm.org/>).

2015 - current | Member of University of Florida's: 1) Cancer Center; 2) Genetics Institute; 3) Emerging Pathogens Institute.

2012 - current | Member of the scientific committee of the Management of Standardized Evaluation of Retroviral HIV Infection (MASTER) cohort (<http://www.mastercohort.it/>).

2003 - current | Member of the scientific committee of the Italian Antiretroviral Resistance Cohort Analysis (ARCA) ([www.hivarca.net](http://www.hivarca.net)).

### Grants Review / Study Sections

2019; 2017 | US National Institutes of Health (NIH): ZRG1 AARR-N (51) R; ZAI1 JA-M M2 1.

2018; 2020 | US National Science Foundation (NSF): Computer, Information Science and Engineering (CISE).

2018 | UK Royal Society.

2018 | UK Wellcome Trust.

2017 | UK Medical Research Council (MRC).

2016 | Swiss Institute of Bioinformatics (SIB).

2013 - 2018 | Research Foundation Flanders - Fonds Wetenschappelijk Onderzoek - Vlaanderen, Belgium.

2013 | US-Israel Binational Science Foundation.

### Journal Peer Review

Generalist | *Interciencia*; *Nature Machine Intelligence*; *PeerJ*; *PLOS ONE*; *Scientific Reports*.

Bioinformatics / Health Informatics | *Bioinformatics*; *BMC Genomics*; *BMC Medical Informatics and Decision Making*; *IEEE/ACM Transactions on Computational Biology and Bioinformatics*; *IEEE Journal of Biomedical and Health Informatics*; *Journal of Biomedical and Health Informatics*; *Mathematical Problems in Engineering*; *PLOS Computational Biology*.

Molecular Evolution | *Infection, Genetics and Evolution*; *Molecular Biology and Evolution*.

Epidemiology / Infectious Diseases | *AIDS Research and Human Retroviruses*; *Antiviral Therapy*; *BMC Infectious Diseases*; *Emerging Infectious Diseases*; *International Journal of STD & AIDS*; *Journal of AIDS and HIV Research*; *Lancet HIV*; *The Journal of Infectious Diseases*; *Virology Journal*; *Virus Research*.

### Other Services

2016 - 2017 | Ombudsman for University of Florida's Department of Epidemiology.

## HONORS, SCHOLARSHIPS & AWARDS

2018	University of Florida's Faculty Enhancement Opportunity ( <a href="http://aa.ufl.edu/resources/resources-for-faculty/programs-for-faculty/faculty-enhancement-opportunity-feo/">http://aa.ufl.edu/resources/resources-for-faculty/programs-for-faculty/faculty-enhancement-opportunity-feo/</a> ).
2017	Southeastern Conference (SEC) Visiting Faculty Travel Grant ( <a href="http://www.theseecu.com/programs/sec-faculty-travel-program/2017-2018-sec-faculty-participants/">http://www.theseecu.com/programs/sec-faculty-travel-program/2017-2018-sec-faculty-participants/</a> ).
2016	First place in the Illumina, Inc., "GoMini Scientific Challenge", with award comprising a MiniSeq, a Mini Cooper, and reagents for three sequencing runs, for a cash value ~\$100,000 ( <a href="http://www.illumina.com/company/news-center/feature-articles/illumina-announces-winners-of-miniseq-scientific-challenge.html">http://www.illumina.com/company/news-center/feature-articles/illumina-announces-winners-of-miniseq-scientific-challenge.html</a> ).
2012	Runner-up (2 <sup>nd</sup> place) in the Geneious' "iEvoBio" challenge for the best bioinformatics plugin ( <a href="http://www.geneious.com">http://www.geneious.com</a> ).
2009	ComputerWorld Honors Awards (Washington DC, <a href="http://www.cwhonors.org/">http://www.cwhonors.org/</a> ), given to the EuResist project.
2009	Merit scholarship, Specialty Course in Phylogenetics and Bioinformatics, University of Milan.
2005 - 2008	Merit scholarship, Ph.D., Roma Tre University.
1999	"Erasmus" University scholarship (one year) from the EU.
1996	Stage offered by "Scuola Normale Superiore di Pisa" to the best high-school students in Italy.

## SOFTWARE RELEASED

- *HIV-DYNAMITE* – Dynamic identification of transmission clusters using phylogenetic methods (<https://github.com/ProsperiLab/HIVdynamite>)
- *LibSeq* and *NanoPAL* – Generic programming library in C++ for next-generation sequencing data analytics, with focus on portable mobile computing of Oxford's Nanopore data (<https://fmilicchio.bitbucket.io/nanopal.html>).
- *QuRe* – Viral quasispecies assembly from next-generation sequencing data (<http://sourceforge.net/projects/quire/>)
- *HErCoOl* - Error correction software for next-generation sequencing data based on *k*-mer spectrum and de Bruijn graph (<http://sourceforge.net/projects/hercool/>)
- *PhyloPart* – Large-scale phylogeny partition (<http://sourceforge.net/projects/phylopart/>)
- *PhyloTempo* – Assessing/Visualizing Temporal Clustering in Genealogies (<http://sourceforge.net/projects/phylotempo/>)
- *The Threshold Bootstrap Clustering (TBC)* – Bootstrapped partition of molecular sequence alignment via leader clustering (<http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0013619>)
- *Trophix* – Prediction of co-receptor tropism for human immunodeficiency virus (<http://sourceforge.net/projects/trophix/>)

## FULL LIST OF PUBLICATIONS

### Letters and editorials

1. Mavian C, Pond SK, Marini S, Magalis BR, Vandamme AM, Dellicour S, Scarpino SV, Houldcroft C, Villabona-Arenas J, Paisie TK, Trovão NS, Boucher C, Zhang Y, Scheuermann RH, Gascuel O, Lam TT, Suchard MA, Abecasis A, Wilkinson E, de Oliveira T, Bento AI, Schmidt HA, Martin D, Hadfield J, Faria N, Grubaugh ND, Neher RA, Baele 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. *Proc Natl Acad Sci U S A*. 2020 May 7:202007295. doi: 10.1073/pnas.2007295117.
2. Bian J, Min JS, **Prosperi M**, Wang M. Are preregistration and registered reports vulnerable to hacking? *Epidemiology*. 2020 Jan 22. doi: 10.1097/EDE.0000000000001162.
3. Bian J, Min J, **Prosperi M**, Wang M. Re: A Call for Deep Learning Healthcare. *Epidemiology*. 2019 Dec 16. doi: 10.1097/EDE.0000000000001155.

4. **Prosperi M.** G-quadruplex - Characterization of Functions and Potential Therapeutic Uses of Non-canonical DNA Structures. *Curr Med Chem.* 2019;26(16):2879-2880. doi: 10.2174/092986732616190820105842.
5. Bian J, Buchan I, Guo Y, **Prosperi M.** Statistical thinking, machine learning. *J Clin Epidemiol.* 2019 Aug 16. pii: S0895-4356(19)30495-0. doi: 10.1016/j.jclinepi.2019.08.003.
6. **Prosperi M,** Bian J. Is it time to rethink institutional review boards for the era of big data? *Nature Machine Intelligence* 2019; 1. doi: 10.1038/s42256-019-0059-7.
7. Min J, **Prosperi M.** Psychiatric disorders' paradoxical protective effect on cardiovascular procedures and mortality. *Psychiatry Res.* 2019 Jan 11. pii: S0165-1781(18)30888-6. doi: 10.1016/j.psychres.2018.06.030.
8. Wang K, Varma DS, **Prosperi M.** Response to letter. *J Psychiatr Res.* 2019 Sep;116:195. doi: 10.1016/j.jpsychires.2018.12.011. Epub 2018 Dec 10.

#### Journal papers

1. Rich SN, Richards VL, Mavian CN, Switzer WM, Rife Magalis B, Poschman K, Geary S, Broadway SE, Bennett SB, Blanton J, Leitner T, Boatwright JL, Stetten NE, Cook RL, Spencer EC, Salemi M, **Prosperi M.** Employing Molecular Phylogenetic Methods to Identify and Forecast HIV Transmission Clusters in Public Health Settings: A Qualitative Study. *Viruses.* 2020; 12(9):921.
2. Pearson TA, Califf RM, Roper R, Engelgau MM, Khoury MJ, Alcantara C, Blakely C, Boyce CA, Brown M, Croxton TL, Fenton K, Green Parker MC, Hamilton A, Helmchen L, Hsu LL, Kent DM, Kind A, Kravitz J, Papanicolaou GJ, Prospero M, Quinn M, Price LN, Shireman PK, Smith SM, Szczesniak R, Goff DC Jr, Mensah GA. Precision Health Analytics With Predictive Analytics and Implementation Research: JACC State-of-the-Art Review. *J Am Coll Cardiol.* 2020 Jul 21;76(3):306-320. doi: 10.1016/j.jacc.2020.05.043.
3. Rich SN, Poschman K, Hu H, Mavian C, Cook RL, Salemi M, Spencer EC, **Prosperi M.** Sociodemographic, ecological, and spatiotemporal factors associated with HIV drug resistance in Florida: a retrospective analysis, *The Journal of Infectious Diseases,* jiaa413, <https://doi.org/10.1093/infdis/jiaa413>
4. **Prosperi M,** Guo Y, Sperrin M, Buchan I, Koopman J, Rich S, Min J, He X, Wang M, Bian J. Causal inference and counterfactual prediction in machine learning for actionable healthcare. *Nature Machine Intelligence* 2020; 2 (7), 369-375. <https://doi.org/10.1038/s42256-020-0197-y>
5. Hu H, Zhao J, Savitz DA, **Prosperi M,** Zheng Y, Pearson TA. An external exposome-wide association study of hypertensive disorders of pregnancy. *Environ Int.* 2020 May 12;141:105797. doi: 10.1016/j.envint.2020.105797.
6. Mavian C, Marini S, **Prosperi M,** Salemi M. A Snapshot of SARS-CoV-2 Genome Availability up to April 2020 and its Implications: Data Analysis. *JMIR Public Health Surveill.* 2020 Jun 1;6(2):e19170. doi: 10.2196/19170.
7. Boyles SM, Mavian CN, Finol E, Ukhanova M, Stephenson CJ, Hamerlinck G, Kang S, Baumgartner C, Geesey M, Stinton I, Williams K, Mathias DK, **Prosperi M,** Mai V, Salemi M, Buckner EA, Lednický JA, Rivers AR, Dinglasan RR. Under-the-Radar Dengue Virus Infections in Natural Populations of *Aedes aegypti* Mosquitoes. *mSphere.* 2020 Apr 29;5(2):e00316-20. doi: 10.1128/mSphere.00316-20.
8. Oliva M, Milicchio F, King K, Benson G, Boucher C, **Prosperi M.** Portable Nanopore Analytics: Are We There Yet? *Bioinformatics.* 2020 Apr 11:btaa237. doi: 10.1093/bioinformatics/btaa237. Online ahead of print.
9. Zheng Y, Chen Z, Pearson T, Zhao J, Hu H, **Prosperi M.** Design and methodology challenges of environment-wide association studies: A systematic review. *Environmental Research.* 2020. 183:109275. <https://doi.org/10.1016/j.envres.2020.109275>
10. Benvenuto D, Giovanetti M, Salemi M, **Prosperi M,** De Flora C, Junior Alcantara LC, Angeletti S, Ciccozzi M. The global spread of 2019-nCoV: a molecular evolutionary analysis. *Pathog Glob Health.* 2020 Feb 12:1-4. doi: 10.1080/20477724.2020.1725339. [Epub ahead of print]
11. Bailey HM, Zuo Y, Li F, Min J, Vaddiparti K, **Prosperi M,** Fagan J, Galea S, Kalesan B. Changes in patterns of mortality rates and years of life lost due to firearms in the United States, 1999 to 2016: A joinpoint analysis. *PLoS One.* 2019 Nov 22;14(11):e0225223. doi: 10.1371/journal.pone.0225223.
12. Zhang H, Wheldon C, Dunn AG, Tao C, Huo J, Zhang R, **Prosperi M,** Guo Y, Bian J. Mining Twitter to Assess the Determinants of Health Behavior towards Human Papillomavirus Vaccination in the United States. *J Am Med Inform Assoc.* 2019 Nov 11. pii: oc2191. doi: 10.1093/jamia/oc2191.
13. **Prosperi M,** Bian J, Buchan IE, Koopman JS, Sperrin M, Wang M. Raiders of the lost HARK: a reproducible inference framework for big data science. *Palgrave Commun.* 2019; 5:125. doi:10.1057/s41599-019-0340-8
14. Goedel WC, Chan PA, King MRF, **Prosperi MCF,** Marshall BDL, Galárraga O. Cost-effectiveness of a statewide pre-exposure prophylaxis program for gay, bisexual, and other men who have sex with men. *R I Med J* (2013). 2019; 102(9): 36–39.
15. Min J, Gurka KK, Kalesan B, Bian J, **Prosperi M.** Injury Burden in the United States: Accurate, Reliable, and Timely Surveillance Using Electronic Health Care Data. *Am J Public Health.* 2019 Oct 17:e1-e5. doi: 10.2105/AJPH.2019.305306.
16. Wang K, Chen X, Cheng TD, Qiu P, Bird VY, **Prosperi M.** Association of Long-Term Dynamics in Circulating Testosterone with Serum PSA in Prostate Cancer-Free Men with Initial-PSA < 4 ng/mL. *Horm Cancer.* 2019 Oct 16. doi: 10.1007/s12672-019-00369-y. [Epub ahead of print]
17. Wang K, Gerke TA, Chen X, **Prosperi M.** Association of statin use with risk of Gleason score-specific prostate cancer: A hospital-based cohort study. *Cancer Med.* 2019 Oct 8. doi: 10.1002/cam4.2500. [Epub ahead of print]
18. Chan PA, Goedel WC, Nunn AS, Sowemimo-Coker G, Galárraga O, **Prosperi M,** Patel R, Mena L, Montgomery MC, Marshall BDL. Potential Impact of Interventions to Enhance Retention in Care During Real-World HIV Pre-Exposure Prophylaxis Implementation. *AIDS Patient Care STDS.* 2019 Oct;33(10):434-439. doi: 10.1089/apc.2019.0064.
19. Chen Z, **Prosperi M,** Bian J, Min J, Wang M, Li C. Clinical correlates of workplace injury occurrence and recurrence in adults. *PLoS One.* 2019 Sep 12;14(9):e0222603. doi: 10.1371/journal.pone.0222603.

20. Zhao Y, Huo J, **Prosperi M**, Guo Y, Li Y, Bian J. Exploring Lung Cancer Screening Discussions on Twitter. *Stud Health Technol Inform.* 2019 Aug 21;264:2011-2012. doi: 10.3233/SHT190760.
21. Modave F, Zhao Y, Krieger J, He Z, Guo Y, Huo J, **Prosperi M**, Bian J. Understanding Perceptions and Attitudes in Breast Cancer Discussions on Twitter. *Stud Health Technol Inform.* 2019 Aug 21;264:1293-1297. doi: 10.3233/SHT190435.
22. Lakin SM, Kuhnle A, Alipanahi B, Noyes NR, Dean C, Muggli M, Raymond R, Abdo Z, **Prosperi M**, Belk KE, Morley PS, Boucher C. Hierarchical Hidden Markov models enable accurate and diverse detection of antimicrobial resistance sequences. *Commun Biol.* 2019 Aug 6;2:294. doi: 10.1038/s42003-019-0545-9.
23. He X, Zhang R, Rizvi R, Vasilakes J, Yang X, Guo Y, He Z, **Prosperi M**, Huo J, Alpert J, Bian J. ALOHA: developing an interactive graph-based visualization for dietary supplement knowledge graph through user-centered design. *BMC Med Inform Decis Mak.* 2019 Aug 8;19(Suppl 4):150. doi: 10.1186/s12911-019-0857-1.
24. Fische JN, Bian J, Chen Z, Hu H, Min J, Modave F, **Prosperi M**. Prodromal clinical, demographic, and socio-ecological correlates of asthma in adults: a 10-year statewide big data multi-domain analysis. *J Asthma.* 2019 Jul 26:1-13. doi: 10.1080/02770903.2019.1642352.
25. Chen Z, **Prosperi M**, Bird VG, Bird VY. Analysis of Factors Associated with Large Kidney Stones: Stone Composition, Comorbid Conditions, and 24-H Urine Parameters—a Machine Learning-Aided Approach. *SN Compr. Clin. Med.* 2019. <https://doi.org/10.1007/s42399-019-00087-0>.
26. Teng L, Lee S, Ginn A, Markland SM, Mir R, DiLorenzo N, Boucher C, **Prosperi M**, Johnson J, Morris JG Jr, Jeong KC. Genomic Comparison Reveals Natural Occurrence of Clinically Relevant Multi-Drug Resistant Extended-Spectrum  $\beta$ -lactamase producing *Escherichia coli*. *Appl Environ Microbiol.* 2019 May 3. pii: AEM.03030-18. doi: 10.1128/AEM.03030-18.
27. Brown EE, Ball JD, Chen Z, Khurshid GS, **Prosperi M**, Ash JD. The Common Antidiabetic Drug Metformin Reduces Odds of Developing Age-Related Macular Degeneration. *Invest Ophthalmol Vis Sci.* 2019 Apr 1;60(5):1470-1477. doi: 10.1167/iovs.18-26422.
28. Zhao Y, Guo Y, He X, Wu Y, Yang X, **Prosperi M**, Jin Y, Bian J. Assessing mental health signals among sexual and gender minorities using Twitter data. *Health Informatics J.* 2019 Apr 10:1460458219839621. doi: 10.1177/1460458219839621.
29. Guo Y, Bian J, Modave F, Li Q, George TJ, **Prosperi M**, Shenkman E. Assessing the effect of data integration on predictive ability of cancer survival models. *Health Informatics J.* 2019 Jan 23:1460458218824692. doi: 10.1177/1460458218824692.
30. **Prosperi M**, Min JS, Bian J, Modave F. Big data hurdles in precision medicine and precision public health. *BMC Med Inform Decis Mak.* 2018 Dec 29;18(1):139. doi: 10.1186/s12911-018-0719-2.
31. Lucero RJ, Lindberg DS, Fehlberg EA, Bjarnadottir RI, Li Y, Cimiotti JP, Crane M, **Prosperi M**. A data-driven and practice-based approach to identify risk factors associated with hospital-acquired falls: Applying manual and semi- and fully-automated methods. *International Journal of Medical Informatics* 2018; 122:63-69. <https://doi.org/10.1016/j.ijmedinf.2018.11.006>
32. Chen Z, **Prosperi M**, Bird VY. Prevalence of kidney stones in the USA: The National Health and Nutrition Evaluation Survey. *Journal of Clinical Urology.* 2018. <https://doi.org/10.1177/2051415818813820>
33. Rose R, Golosova O, Sukhomlinov D, Tiunov A, **Prosperi M**. Flexible design of multiple metagenomics classification pipelines with UGENE. *Bioinformatics*, bty901, 2018/10/25. doi:10.1093/bioinformatics/bty901.
34. Wang K, Varma DS, **Prosperi M**. A systematic review of the effectiveness of mobile apps for monitoring and management of mental health symptoms or disorders. *J Psychiatr Res.* 2018 Oct 5;107:73-78. doi: 10.1016/j.jpsychires.2018.10.006.
35. Wang K, Chen X, Gerke TA, Bird VY, Ghayee HK, **Prosperi M**. BMI trajectories and risk of overall and grade-specific prostate cancer: An observational cohort study among men seen for prostatic conditions. *Cancer Med.* 2018 Oct;7(10):5272-5280. doi: 10.1002/cam4.1747.
36. Ball JD, Elbadry MA, Telisma T, White SK, Chavannes S, Anilis MG, **Prosperi M**, Cummings DAT, Lednicky JA, Morris JG Jr, Beau de Rochars M. Clinical and Epidemiologic Patterns of Chikungunya Virus Infection and Coincident Arboviral Disease in a School Cohort in Haiti, 2014-2015. *Clin Infect Dis.* 2018 Aug 31. doi: 10.1093/cid/ciy582.
37. Chen Z, Min J, Bian J, Wang M, Zhou L, **Prosperi M**. Risk of health morbidity for the uninsured: 10-year evidence from a large hospital center in Boston, Massachusetts. *Int J Qual Health Care.* 2018 Aug 18. doi: 10.1093/intqhc/mzy175.
38. Chen Z, Bird VY, Ruchi R, Segal MS, Bian J, Khan SR, Elie MC, **Prosperi M**. Development of a personalized diagnostic model for kidney stone disease tailored to acute care by integrating large clinical, demographics and laboratory data: the diagnostic acute care algorithm - kidney stones (DACA-KS). *BMC Med Inform Decis Mak.* 2018 Aug 17;18(1):72. doi: 10.1186/s12911-018-0652-4.
39. Angeletti S, Cella E, **Prosperi M**, Spoto S, Fogolari M, De Florio L, Antonelli F, Dedej E, De Flora C, Ferraro E, Incalzi RA, Coppola R, Dicuonzo G, Francescato F, Pascarella S, Ciccozzi M. Multi-drug resistant *Pseudomonas aeruginosa* nosocomial strains: Molecular epidemiology and evolution. *Microb Pathog.* 2018 Jul 19;123:233-241. doi: 10.1016/j.micpath.2018.07.020.
40. Ball JD, **Prosperi M**, Brown A, Chen X, Kenah E, Yang Y, Cummings DAT, Rivers CM. The role of benzathine penicillin G in predicting and preventing all-cause acute respiratory disease in military recruits: 1991-2017. *Epidemiol Infect.* 2018 Jul 5:1-7. doi: 10.1017/S0950268818001838.
41. Gantenberg JR, King M, Montgomery MC, Galárraga O, **Prosperi M**, Chan PA, Marshall BDL. Improving the population-level impact of pre-exposure prophylaxis implementation among men who have sex with men: An agent-based modelling study. *PLoS ONE.* 2018;13(7):e0199915.
42. Zazzi M, Hu H, **Prosperi M**. The global burden of HIV-1 drug resistance in the past 20 years. *PeerJ.* 2018; 6: e4848. Published online 2018 May 25. doi: 10.7717/peerj.4848.
43. Bian J, Zhao Y, Salloum RG, Guo Y, Wang M, **Prosperi M**, Zhang H, Du X, Ramirez-Diaz LJ, He Z, Sun Y. Using Social Media Data to Understand the Impact of Promotional Information on Laypeople's Discussions: A Case Study of Lynch Syndrome. *J Med Internet Res.* 2017 Dec 13;19(12):e414. doi: 10.2196/jmir.9266.

44. Huo T, George TJ Jr, Guo Y, He Z, **Prosperi M**, Modave F, Bian J. Explore Care Pathways of Colorectal Cancer Patients with Social Network Analysis. *Stud Health Technol Inform.* 2017;245:1270.
45. Min J, Osborne V, Kowalski A, **Prosperi M**. Reported Adverse Events with Painkillers: Data Mining of the US Food and Drug Administration Adverse Events Reporting System. *Drug Saf.* 2017 Nov 2. doi: 10.1007/s40264-017-0611-5.
46. Mavian C, Rife BD, Dollar JJ, Cella E, Ciccozzi M, **Prosperi M**, Lednicky J, Morris JG, Capua I, Salemi M. Emergence of recombinant Mayaro virus strains from the Amazon basin. *Scientific reports* 2017; 7:8718. doi:10.1038/s41598-017-07152-5.
47. Wang K, Chen X, Bird VY, Gerke TA, Manini TM, **Prosperi M**. Association between age-related reductions in testosterone and risk of prostate cancer-An analysis of patients' data with prostatic diseases. *Int J Cancer.* 2017 Jul 12. doi: 10.1002/ijc.30882.
48. Cella E, Ciccozzi M, Presti AL, Fogolari M, Azarian T, **Prosperi M**, et al. Multi-drug resistant *Klebsiella pneumoniae* strains circulating in hospital setting: whole-genome sequencing and Bayesian phylogenetic analysis for outbreak investigations. *Scientific reports* 2017;7(1):3534. doi: 10.1038/s41598-017-03581-4.
49. Chen Z, Gerke T, Bird V, **Prosperi M**. Trends in Gene Expression Profiling for Prostate Cancer Risk Assessment: A Systematic Review. *Biomed Hub* 2017;2:472146. <https://doi.org/10.1159/000472146>.
50. Rife BD, Mavian C, Chen X, Ciccozzi M, Salemi M, Min J, **Prosperi M**. Phylodynamic applications in 21 st century global infectious disease research. *Global Health Research and Policy* 2017; 2:13. DOI: 10.1186/s41256-017-0034-y.
51. Postorino MC, **Prosperi M**, Foca E, Quiros-Rolda E, Di Filippo E, Maggiolo F, Borghetti A, Ladisa N, Di Pietro M, Gori A, Sighinolfi L, Pan A, Mazzini N, Torti C. Role of systemic inflammation scores for prediction of clinical outcomes in patients treated with atazanavir not boosted by ritonavir in the Italian MASTER cohort. *BMC Infect Dis.* 2017 Mar 15;17(1):212.
52. Min J, Cella E, Ciccozzi M, Pelosi A, Salemi M, **Prosperi M**. The global spread of Middle East respiratory syndrome: an analysis fusing traditional epidemiological tracing and molecular phylodynamics. *Global Health Research and Policy* 2016; 1:14. DOI: 10.1186/s41256-016-0014-7
53. Rose R, Constantinides B, Tapinos A, Robertson DL, **Prosperi M**. Challenges in the analysis of viral metagenomes. *Virus Evolution* Jul 2016, 2 (2) vew022; DOI: 10.1093/ve/vew022.
54. Focà E, Fabbiani M, **Prosperi M**, Quiros Roldan E, Castelli F, Maggiolo F, Di Filippo E, Di Giambenedetto S, Gagliardini R, Saracino A, Di Pietro M, Gori A, Sighinolfi L, Pan A, Postorino MC, Torti C; Italian MASTER Cohort. Liver fibrosis progression and clinical outcomes are intertwined: role of CD4+ T-cell count and NRTI exposure from a large cohort of HIV/HCV-coinfected patients with detectable HCV-RNA: A MASTER cohort study. *Medicine (Baltimore).* 2016 Jul;95(29):e4091. doi: 10.1097/MD.0000000000004091.
55. **Prosperi M**, Buchan I, Fanti I, Meloni S, Palladino P, Torvik VI. Kin of coauthorship in five decades of health science literature. *Proc Natl Acad Sci U S A.* 2016 Aug 9;113(32):8957-62. doi: 10.1073/pnas.1517745113. Epub 2016 Jul 25.
56. Fraccaro P, van der Veer S, Brown B, **Prosperi M**, O'Donoghue D, Collins GS, Buchan I, Peek N. An external validation of models to predict the onset of chronic kidney disease using population-based electronic health records from Salford, UK. *BMC Med.* 2016 Jul 12;14(1):104. doi: 10.1186/s12916-016-0650-2.
57. Bian J, Yoshigoe K, Hicks A, Yuan J, He Z, Xie M, Guo Y, **Prosperi M**, Salloum R, Modave F. Mining Twitter to Assess the Public Perception of the "Internet of Things". *PLoS One.* 2016 Jul 8;11(7):e0158450. doi: 10.1371/journal.pone.0158450. eCollection 2016.
58. Leone S, **Prosperi M**, Costarelli S, Nasta P, Maggiolo F, Di Giambenedetto S, Saracino A, Di Pietro M, Gori A. Incidence and predictors of cardiovascular disease, chronic kidney disease, and diabetes in HIV/HCV-coinfected patients who achieved sustained virological response. *Eur J Clin Microbiol Infect Dis.* 2016; 35(9):1511-20.
59. Milicchio F, Rose R, Bian J, Min J, **Prosperi M**. Visual programming for next-generation sequencing data analytics. *BioData Min.* 2016 Apr 27;9:16.
60. Mai V, **Prosperi M**, Yaghjian L. Moving microbiota research toward establishing causal associations that represent viable targets for effective public health interventions. *Ann Epidemiol.* 2016 May;26(5):306-10. doi: 10.1016/j.annepidem.2016.03.011. Epub 2016 Apr 8.
61. Zazzi M, Cozzi-Lepri A, **Prosperi MC**. Computer-Aided Optimization of Combined Anti-Retroviral Therapy for HIV: New Drugs, New Drug Targets and Drug Resistance. *Curr HIV Res.* 2016;14(2):101-9.
62. Fraccaro P, Brown B, **Prosperi M**, Sperrin M, Buchan I, Peek N. Development and preliminary validation of a dynamic, patient-tailored method to detect abnormal laboratory test results. *Stud Health Technol Inform.* 2015;216:701-5.
63. De Luca A, Di Giambenedetto S, Lo Presti A, Sierra S, **Prosperi M**, Cella E, Giovanetti M, Torti C, Caudai C, Vicenti I, Saladini F, Almi P, Grima P, Blanc P, Fabbiani M, Rossetti B, Gagliardini R, Kaiser R, Ciccozzi M, Zazzi M. Two Distinct Hepatitis C Virus Genotype 1a Clades Have Different Geographical Distribution and Association With Natural Resistance to NS3 Protease Inhibitors. *Open Forum Infect Dis.* 2015 Mar 31;2(2):ofv043. doi: 10.1093/ofid/ofv043. eCollection 2015 Apr.
64. Howard R, Rattray M, **Prosperi M**, Custovic A. Distinguishing Asthma Phenotypes Using Machine Learning Approaches. *Curr Allergy Asthma Rep.* 2015 Jul;15(7):542. doi: 10.1007/s11882-015-0542-0.
65. Wu J, **Prosperi MC**, Simpson A, Hollams EM, Sly PD, Custovic A, Holt PG. Relationship Between Cytokine Expression Patterns and Clinical Outcomes: Two Population-based Birth Cohorts. *Clin Exp Allergy.* 2015 Jun 8. doi: 10.1111/cea.12579
66. Custovic A, Sonntag HJ, Buchan IE, Belgrave D, Simpson A, **Prosperi MC**. Evolution pathways of IgE responses to grass and mite allergens throughout childhood. *J Allergy Clin Immunol.* 2015 May 8. pii: S0091-6749(15)00495-9. doi: 10.1016/j.jaci.2015.03.041.
67. Fraccaro P, Nicolo M, Bonetto M, Giacomini M, Weller P, Traverso CE, **Prosperi M**, O Sullivan D. Combining macula clinical signs and patient characteristics for age-related macular degeneration diagnosis: a machine learning approach. *BMC Ophthalmol.* 2015 Jan 27;15(1):10.

68. Postorino MC, **Prosperi M**, Quiros-Roldan E, Maggiolo F, Di Giambenedetto S, Saracino A, Costarelli S, Lorenzotti S, Sighinolfi L, Di Pietro M, Torti C; MASTER Study Group. Use of efavirenz or atazanavir/ritonavir is associated with better clinical outcomes of HAART compared to other protease inhibitors: routine evidence from the Italian MASTER Cohort. *Clin Microbiol Infect.* 2014 Nov 11. pii: S1198-743X(14)00088-3. doi: 10.1016/j.cmi.2014.10.022.
69. Azarian T, Ali A, Johnson JA, Mohr D, **Prosperi M**, Veras NM, Jubair M, Strickland SL, Rashid MH, Alam MT, Weppelmann TA, Katz LS, Tarr CL, Colwell RR, Morris JG Jr, Salemi M. Phylodynamic Analysis of Clinical and Environmental *Vibrio cholerae* Isolates from Haiti Reveals Diversification Driven by Positive Selection. *MBio.* 2014 Dec 23;5(6).
70. Sangeda RZ, Moshia F, **Prosperi M**, Aboud S, Vercauteren J, Camacho RJ, Lyamuya EF, Van Wijngaerden E, Vandamme AM. Pharmacy refill adherence outperforms self-reported methods in predicting HIV therapy outcome in resource-limited settings. *BMC Public Health.* 2014 Oct 4;14(1):1035.
71. **Prosperi MC**, Ingham SL, Howell A, Lalloo F, Buchan IE, Evans DG. Can multiple SNP testing in BRCA2 and BRCA1 female carriers be used to improve risk prediction models in conjunction with clinical assessment? *BMC Med Inform Decis Mak.* 2014 Oct 1;14(1):87.
72. Strickland SL, Rife BD, Lamers SL, Nolan DJ, Veras NM, **Prosperi MC**, Burdo TH, Autissier P, Nowlin B, Goodenow MM, Suchard MA, Williams KC, Salemi M. Spatiotemporal Dynamics of SIV Brain Infection in CD8+ Lymphocyte-Depleted Rhesus Macaques with NeuroAIDS. *J Gen Virol.* 2014 Sep 9. pii: vir.o.070318-0. doi: 10.1099/vir.o.070318-0.
73. **Prosperi MCF**, Marinho S, Simpson A, Custovic A, Buchan IE. Predicting phenotypes of asthma and eczema with machine learning. *BMC Med Genomics.* 2014;7 Suppl 1:S7. doi: 10.1186/1755-8794-7-S1-S7. Epub 2014 May 8.
74. Fabbiani M, Zaccarelli M, Grima P, **Prosperi M**, Fanti I, Colafigli M, D'Avino A, Mondì A, Borghetti A, Fantoni M, Cauda R, Di Giambenedetto S. Single tablet regimens are associated with reduced Efavirenz withdrawal in antiretroviral therapy naïve or switching for simplification HIV-infected patients. *BMC Infect Dis.* 2014 Jan 13;14(1):26. doi: 10.1186/1471-2334-14-26.
75. **Prosperi MC**, Sahiner UM, Belgrave D, Sackesen C, Buchan IE, Simpson A, Yavuz TS, Kalayci O, Custovic A. Challenges in Identifying Asthma Subgroups Using Unsupervised Statistical Learning Techniques. *Am J Respir Crit Care Med.* 2013 Dec 1;188(11):1303-12. doi: 10.1164/rccm.201304-0694OC.
76. **Prosperi MC**, Belgrave D, Buchan I, Simpson A, Custovic A. Challenges in interpreting allergen microarrays in relation to clinical symptoms: A machine learning approach. *Pediatr Allergy Immunol.* 2014 Feb;25(1):71-9. doi: 10.1111/pai.12139. Epub 2013 Oct 16.
77. **Prosperi MC**, Yin L, Nolan DJ, Lowe AD, Goodenow MM, Salemi M. Empirical validation of viral quasispecies assembly algorithms: state-of-the-art and challenges. *Sci Rep.* 2013 Oct 3;3:2837. doi: 10.1038/srep02837.
78. van de Vijver DAMC, **Prosperi M CF**, Ramasco JJ. Transmission of HIV in sexual networks in sub-Saharan Africa and Europe. *Eur. Phys. J. Special Topics*, 222 6 (2013) 1403-1411. DOI: 10.1140/epjst/e2013-01934-8.
79. Zarrabi N, **Prosperi M CF**, Belleman RG, Di Giambenedetto S, Fabbiani M, De Luca A, Sloot PMA. Combining social and genetic networks to study HIV transmission in mixing risk groups. *Eur. Phys. J. Special Topics*, 222 6 (2013) 1377-1387. DOI: 10.1140/epjst/e2013-01932-x.
80. **Prosperi M**, Veras N, Azarian T, Rathore M, Nolan D, Rand K, Cook RL, Johnson J, Morris JG Jr, Salemi M. Molecular Epidemiology of Community-Associated Methicillin-resistant *Staphylococcus aureus* in the genomic era: a Cross-Sectional Study. *Sci Rep.* 2013 May 28;3:1902. doi: 10.1038/srep01902.
81. Murillo W, Veras N, **Prosperi M**, de Rivera IL, Paz-Bailey G, Morales-Miranda S, Juarez SI, Yang C, Devos J, Marín JP, Mild M, Albert J, Salemi M. A single early introduction of HIV-1 subtype B into Central America accounts for most current cases. *J Virol.* 2013 Jul;87(13):7463-70. doi: 10.1128/JVI.01602-12. Epub 2013 Apr 24.
82. Vercauteren J, Beheydt G, **Prosperi M**, Libin P, Imbrechts S, Camacho R, Clotet B, De Luca A, Grossman Z, Kaiser R, Sönnnerborg A, Torti C, Van Wijngaerden E, Schmit JC, Zazzi M, Geretti AM, Vandamme AM, Van Laethem K. Clinical Evaluation of Rega 8: An Updated Genotypic Interpretation System That Significantly Predicts HIV-Therapy Response. *PLoS One.* 2013 Apr 17;8(4):e61436.
83. De Luca A, Dunn D, Zazzi M, Camacho R, Torti C, Fanti I, Kaiser R, Sönnnerborg A, Codoñer FM, Van Laethem K, Vandamme AM, Bansi L, Ghisetti V, van de Vijver DA, Asboe D, **Prosperi MC**, Di Giambenedetto S; SEHERE collaboration in Chain. Declining prevalence of HIV-1 drug resistance in antiretroviral treatment-exposed individuals in Western Europe. *J Infect Dis.* 2013 Apr 15;207(8):1216-20.
84. **Prosperi MC**, Fabbiani M, Fanti I, Zaccarelli M, Colafigli M, Mondì A, D'Avino A, Borghetti A, Cauda R, Di Giambenedetto S. Predictors of first-line antiretroviral therapy discontinuation due to drug-related adverse events in HIV-infected patients: a retrospective cohort study. *BMC Infect Dis.* 2012 Nov 12;12(1):296.
85. Zarrabi N, **Prosperi M**, Belleman RG, Colafigli M, De Luca A, Sloot PM. Combining Epidemiological and Genetic Networks Signifies the Importance of Early Treatment in HIV-1 Transmission. *PLoS One.* 2012;7(9):e46156.
86. **Prosperi MCF**, Meloni S, Fanti I, Panziera S, Ulivi G, Salemi M. Characterization of de novo assemblies of quasispecies from next-generation sequencing via complex network modeling. *Scientific Research and Essays* 2012; 7(33): 2997-3009. DOI: 10.5897/SRE12.242.
87. Norström MM, Buggert M, Tauriainen J, Hartogensis W, **Prosperi MC**, Wallet MA, Hecht FM, Salemi M, Karlsson AC. Combination of immune and viral factors distinguish low-risk versus high-risk HIV-1 disease progression in HLA-B\*5701 subjects. *J Virol.* 2012;86(18):9802-16.
88. Norström MM, **Prosperi MC**, Gray RR, Karlsson AC, Salemi M. PhyloTempo: A Set of R Scripts for Assessing and Visualizing Temporal Clustering in Genealogies Inferred from Serially Sampled Viral Sequences. *Evol Bioinform Online.* 2012;8:261-269.
89. **Prosperi MC**, De Luca A. Computational models for prediction of response to antiretroviral therapies. *AIDS Rev.* 2012 Apr;14(2):145-53.
90. **Prosperi M CF**, Prospero L, Gray RR, Salemi M. On Counting the Frequency Distribution of String Motifs in Molecular Sequences. *International Journal of Biomathematics.* 2012;5(6):1250055. DOI: 10.1142/S1793524512500556.

91. De Luca A, Marazzi MC, Mancinelli S, Ceffa S, Altan AM, Buonomo E, **Prosperi MC**, Pedruzzi B, Noorjehan AM, Scarcella P, Liotta G, Palombi L. Prognostic value of virological and immunological responses after 6 months of antiretroviral treatment in adults with HIV-1 infection in sub-Saharan Africa. *J Acquir Immune Defic Syndr*. 2012 Mar 1;59(3):236-44.
92. Zazzi M, Incardona F, Rosen-Zvi M, **Prosperi M**, Lengauer T, Altmann A, Sonnerborg A, Lavee T, Schülter E, Kaiser R. Predicting Response to Antiretroviral Treatment by Machine Learning: The EuResist Project. *Intervirology*. 2012;55(2):123-7.
93. **Prosperi MC**, and Salemi, M. QuRe: software for viral quasispecies characterization from next-generation sequencing data. *Bioinformatics*. 2012 Jan 1;28(1):132-3.
94. Cozzi-Lepri A, **Prosperi MC**, Kjær J, Dunn D, Paredes R, Sabin CA, Lundgren JD, Phillips AN, Pillay D; for the EuroSIDA and the United Kingdom CHIC/United Kingdom HDRD Studies. Can Linear Regression Modeling Help Clinicians in the Interpretation of Genotypic Resistance Data? An Application to Derive a Lopinavir-Score. *PLoS One*. 2011;6(11):e25665.
95. Torti C, **Prosperi M**, Motta D, Digiambenedetto S, Maggiolo F, Paraninfo G, Ripamonti D, Cologni G, Fabbiani M, Caputo SL, Sighinolfi L, Ladisa N, El-Hamad I, Quiros-Roldan E, Frank I. Factors influencing the normalization of CD4+ T-cell count, percentage and CD4+/CD8+ T-cell ratio in HIV-infected patients on long-term suppressive antiretroviral therapy. *Clin Microbiol Infect*. 2012 May;18(5):449-58. doi: 10.1111/j.1469-0691.2011.03650.x. Epub 2011 Sep 15.
96. Bruni R, **Prosperi M**, Marcantonio C, Amadori A, Villano U, Tritarelli E, Lo Presti A, Ciccozzi M and Ciccaglione AR. A computational approach to identify point mutations associated with occult hepatitis B: significant mutations affect coding regions but not regulative elements of HBV. *Virology Journal* 2011 Aug 8;8(1):394.
97. De Luca A, Di Giambenedetto S, Maserati R, Gianotti N, Narciso P, Antinori A, Di Perri G, **Prosperi MC**, Baldanti F, Micheli V, Zazzi M, Perno CF, Santoro MM; TMC114-C226 study group; ARCA study group. Interpretation of genotypic HIV-1 resistance to darunavir and virological response: validation of available systems and of a new score. *Antivir Ther*. 2011;16(4):489-97.
98. **Prosperi MC**, Di Giambenedetto S, Fanti I, Meini G, Bruzzone B, Callegaro A, Penco G, Bagnarelli P, Micheli V, Paolini E, Di Biagio A, Ghisetti V, Di Pietro M, Zazzi M, De Luca A, Arca AR. A Prognostic Model for Estimating the Time to Virologic Failure in HIV-1 Infected Patients Undergoing a New Combination Antiretroviral Therapy Regimen. *BMC Med Inform Decis Mak*. 2011 Jun 14;11(1):40.
99. Di Giambenedetto S, **Prosperi M**, Fanti I, Bruzzone B, Paolucci S, Penco G, Meini G, Di Biagio A, Paolini E, Micheli V, Meraviglia P, Castelli P, Corsi P, Gonnelli A, Fabbiani M, Zazzi M, De Luca A; on behalf of the ARCA Collaborative Group. Update on emergence of HIV-1 resistance to antiretroviral drug classes in an Italian national database: 2007-2009. *Clin Microbiol Infect*. 2011 Sep;17(9):1352-5. doi: 10.1111/j.1469-0691.2011.03563.x.
100. **Prosperi MC**, Mackie N, Di Giambenedetto S, Zazzi M, Camacho R, Fanti I, Torti C, Sönnnerborg A, Kaiser R, Codoñer FM, Van Laethem K, Bansi L, van de Vijver DA, Geretti AM, De Luca A; on behalf of the SEHERE consortium. Detection of drug resistance mutations at low plasma HIV-1 RNA load in a European multicentre cohort study. *J Antimicrob Chemother*. 2011; 66(8):1886-1896.
101. **Prosperi MC**, Ciccozzi M, Fanti I, Saladini F, Pecorari M, Borghi V, Di Giambenedetto S, Bruzzone B, Capetti A, Vivarelli A, Rusconi S, Re MC, Gismondo MR, Sighinolfi L, Gray RR, Salemi M, Zazzi M, De Luca A; on behalf of the ARCA collaborative group. A novel methodology for large-scale phylogeny partition. *Nat Commun*. 2011;2:321. doi: 10.1038/ncomms1325. Epub 2011 May 24.
102. **Prosperi MC**, Proserpi L, Bruselles A, Abbate I, Rozera G, Vincenti D, Solmone MC, Capobianchi MR, Ulivi G. Combinatorial analysis and algorithms for quasispecies reconstruction using next-generation sequencing. *BMC Bioinformatics*. 2011 Jan 5;12(1):5.
103. Fabbiani M, Di Giambenedetto S, Ragazzoni E, D'Ettore G, Parruti G, **Prosperi M**, Bracciale L, Cauda R, Navarra P, De Luca A. Darunavir/ritonavir and raltegravir coadministered in routine clinical practice: Potential role for an unexpected drug interaction. *Pharmacol Res*. 2011 Mar;63(3):249-53.
104. Di Giambenedetto S, Zileri Dal Verme L, Sali M, Farina S, Di Cristo V, Manzara S, De Luca A, Pignataro G, **Prosperi M**, Di Franco A, Gentiloni Silveri N, Delogu G, Cauda R, Fabbiani M, Fadda G. Clinical presentation, microbiological features and correlates of disease severity of 2009 pandemic influenza A (H1N1) infection. *Eur J Clin Microbiol Infect Dis*. 2011 Apr;30(4):541-9.
105. **Prosperi MC**, Rosen-Zvi M, Altmann A, Zazzi M, Di Giambenedetto S, Kaiser R, Schülter E, Struck D, Sloot P, van de Vijver DA, Vandamme AM, Sönnnerborg A; for the EuResist and Virolab study groups. Antiretroviral Therapy Optimisation without Genotype Resistance Testing: A Perspective on Treatment History Based Models. *PLoS One*. 2010 Oct 29;5(10):e13753.
106. **Prosperi MC**, De Luca A, Di Giambenedetto S, Bracciale L, Fabbiani M, Cauda R, Salemi M. The Threshold Bootstrap Clustering: A New Approach to Find Families or Transmission Clusters within Molecular Quasispecies. *PLoS One*. 2010 Oct 25;5(10):e13619.
107. **Prosperi MC**, Zazzi M, Punzi G, Monno L, Colao G, Corsi P, Di Giambenedetto S, Meini G, Ghisetti V, Bonora S, Pecorari M, Gismondo MR, Bagnarelli P, Carli T, De Luca A; ARCA Collaborative Group. Low rate of virological failure and maintenance of susceptibility to HIV-1 protease inhibitors with first-line lopinavir/ritonavir-based antiretroviral treatment in clinical practice. *J Med Virol*. 2010 Dec;82(12):1996-2003.
108. Zazzi M, Kaiser R, Sönnnerborg A, Struck D, Altmann A, **Prosperi M**, Rosen-Zvi M, Petroczi A, Peres Y, Schülter E, Boucher CA, Brun-Vezinet F, Harrigan PR, Morris L, Obermeier M, Perno CF, Phanuphak P, Pillay D, Shafer RW, Vandamme AM, van Laethem K, Wensing AM, Lengauer T, Incardona F. Prediction of response to antiretroviral therapy by human experts and by the EuResist data-driven expert system (the EVE study). *HIV Med*. 2011 Apr;12(4):211-8. doi: 10.1111/j.1468-1293.2010.00871.x. Epub 2010 Aug 19.
109. **Prosperi MC**, Cozzi-Lepri A, Antinori A, Cassola G, Torti C, Ursitti MA, Pellizzer GP, Giacometti A, d'Arminio Monforte A, De Luca A; for the Icona; Foundation Study Group. Favourable evolution of virological and immunological profiles in treated and untreated patients in Italy in the period 1998-2008. *HIV Med*. 2011 Mar;12(3):174-82. doi: 10.1111/j.1468-1293.2010.00866.x.
110. Frentz D, Boucher CA, Assel M, De Luca A, Fabbiani M, Incardona F, Libin P, Manca N, Müller V, O Nualláin B, Paredes R, **Prosperi M**, Quiros-Roldan E, Ruiz L, Sloot PM, Torti C, Vandamme AM, Van Laethem K, Zazzi M, van de Vijver DA. Comparison of HIV-1 genotypic resistance test interpretation systems in predicting virological outcomes over time. *PLoS One*. 2010 Jul 9;5(7):e11505.



111. **Prosperi MC**, Bracciale L, Fabbiani M, Di Giambenedetto S, Razzolini F, Meini G, Colafigli M, Marzocchetti A, Cauda R, Zazzi M, De Luca A. Comparative determination of HIV-1 coreceptor tropism by Enhanced Sensitivity Trofile, gp120 V3-loop RNA and DNA genotyping. *Retrovirology*. 2010 Jun 30;7:56.
112. **Prosperi MC**, Cozzi-Lepri A, Castagna A, Mussini C, Murri R, Giacometti A, Torti C, Costantini A, Narciso P, Ghinelli F, Antinori A, d'Arminio Monforte A. Incidence of Malignancies in HIV-Infected Patients and Prognostic Role of Current CD4 Cell Count: Evidence from a Large Italian Cohort Study. *Clin Infect Dis*. 2010 May 1;50(9):1316-21.
113. Fabbiani M, Di Giambenedetto S, Ragazzoni E, Colafigli M, **Prosperi M**, Cauda R, Navarra P, De Luca A. Mid-dosing interval concentration of atazanavir and virological outcome in patients treated for HIV-1 infection. *HIV Med*. 2010 May;11(5):326-33.
114. De Luca A, **Prosperi M** and Bracciale L. Resistance considerations in sequencing of antiretroviral therapy in low-middle income countries with currently available options. *Curr Opin HIV AIDS*. 2010 Jan;5(1):27-37.
115. Menzo S, Vincenti D, Solmone M, **Prosperi M**, Bruselles A, Abbate I, Rozera G, Capobianchi MR. Low-abundance drug resistance mutations: extending the HIV paradigm to hepatitis B virus. *J Infect Dis*. 2009 Dec 1;200(11):1798-9.
116. Rozera G, Abbate I, Bruselles A, Vlassi C, D'Offizi G, Narciso P, Chillemi G, **Prosperi M**, Ippolito G, Capobianchi MR. Archived HIV-1 minority variants detected by ultra-deep pyrosequencing in provirus may be fully replication competent. *AIDS*. 2009 Nov 27;23(18):2541-3.
117. Marzocchetti A, Tompkins T, Clifford DB, Gandhi RT, Kesari S, Berger JR, Simpson DM, **Prosperi M**, De Luca A, Korolnik IJ. Determinants of survival in progressive multifocal leukoencephalopathy. *Neurology*. 2009 Nov 10;73(19):1551-8.
118. Bruselles A, Rozera G, Bartolini B, **Prosperi M**, Del Nonno F, Narciso P, Capobianchi MR, Abbate I. Use of massive parallel pyrosequencing for near full-length characterization of a unique HIV Type 1 BF recombinant associated with a fatal primary infection. *AIDS Res Hum Retroviruses*. 2009 Sep;25(9):937-42.
119. Bracciale L, Fanti I, Di Giambenedetto S, Colafigli M, **Prosperi M**, Bacarelli A, Santangelo R, Cattani P, Cauda R, De Luca A. Predictors of successful genotype-guided antiretroviral therapy in treatment-experienced individuals over calendar years: A cohort study. *J Clin Virol*. 2009 Nov;46(3):290-4.
120. Di Giambenedetto S, Torti C, **Prosperi M**, Manca N, Lapadula G, Parainfo G, Ladisa N, Zazzi M, Trezzi M, Cicconi P, Corsi P, Nasta P, Cauda R, De Luca A; for the UCSC cohort, MASTER cohort and ARCA cohort. Effectiveness of Antiretroviral Regimens Containing Abacavir with Tenofovir in Treatment-Experienced Patients: Predictors of Virological Response and Drug Resistance Evolution in a Multi-Cohort Study. *Infection*. 2009 Oct;37(5):438-44.
121. Zazzi M, **Prosperi M**, Vicenti I, Di Giambenedetto S, Callegaro A, Bruzzone B, Baldanti F, Gonnelli A, Boeri E, Paolini E, Rusconi S, Giacometti A, Maggiolo F, Menzo S, De Luca A; ARCA Collaborative Group. Rules-based HIV-1 genotypic resistance interpretation systems predict 8 week and 24 week virological antiretroviral treatment outcome and benefit from drug potency weighting. *J Antimicrob Chemother*. 2009 Sep;64(3):616-24.
122. **Prosperi MC**, Altmann A, Rosen-Zvi M, Aharoni E, Borgulya G, Bazso F, Sannerborg A, Schülter E, Struck D, Ulivi G, Vandamme AM, Vercauteren J, Zazzi M; EuResist and Virolab study groups. Investigation of expert rule bases, logistic regression, and non-linear machine learning techniques for predicting response to antiretroviral treatment. *Antivir Ther*. 2009;14(3):433-42.
123. Colafigli M, Di Giambenedetto S, Bracciale L, Fanti I, **Prosperi M**, Cauda R, De Luca A. Long-term follow-up of nevirapine-treated patients in a single-centre cohort. *HIV Med*. 2009 Sep;10(8):461-9.
124. **Prosperi MC**, Fanti I, Ulivi G, Micarelli A, De Luca A, Zazzi M. Robust supervised and unsupervised statistical learning for HIV type 1 coreceptor usage analysis. *AIDS Res Hum Retroviruses*. 2009 Mar;25(3):305-14.
125. Bracciale L, Santangelo R, Fanti I, **Prosperi M**, Colafigli M, Di Giambenedetto S, Marchetti S, Di Franco A, Cauda R, De Luca A. Are mutations in HIV type-1 reverse transcriptase 245 codon predictive of abacavir hypersensitivity reaction? *Antivir Ther*. 2009;14(1):99-101.
126. Bracciale L, Di Giambenedetto S, Colafigli M, La Torre G, **Prosperi M**, Santangelo R, Marchetti S, Cauda R, Fadda G, De Luca A. Virological suppression reduces clinical progression in patients with multiclass-resistant HIV type 1. *AIDS Res Hum Retroviruses*. 2009 Mar;25(3):261-7.
127. Rozera G, Abbate I, Bruselles A, Vlassi C, D'Offizi G, Narciso P, Chillemi G, **Prosperi M**, Ippolito G, Capobianchi MR. Massively parallel pyrosequencing highlights minority variants in the HIV-1 env quasispecies deriving from lymphomonocyte sub-populations. *Retrovirology*. 2009 Feb 12; 6(1):15
128. Solmone M, Vincenti D, **Prosperi MC**, Bruselles A, Ippolito G, Capobianchi MR. Use of massively parallel ultradeep pyrosequencing to characterize the genetic diversity of hepatitis B virus in drug-resistant and drug-naive patients and to detect minor variants in reverse transcriptase and hepatitis B s antigen. *J Virol*. 2009 Feb;83(4):1718-26.
129. **Prosperi MC**, D'Autilia R, Incardona F, De Luca A, Zazzi M, Ulivi G. Stochastic modelling of genotypic drug-resistance for human immunodeficiency virus towards long-term combination therapy optimization. *Bioinformatics*. 2009 Apr 15;25(8):1040-7.
130. Altmann A, Rosen-Zvi M, **Prosperi M**, Aharoni E, Neuvirth H, Schülter E, Büch J, Struck D, Peres Y, Incardona F, Sönnnerborg A, Kaiser R, Zazzi M, Lengauer T. Comparison of classifier fusion methods for predicting response to anti HIV-1 therapy. *PLoS ONE*. 2008;3(10):e3470.
131. Rosen-Zvi M, Altmann A, **Prosperi M**, Aharoni E, Neuvirth H, Sönnnerborg A, Schülter E, Struck D, Peres Y, Incardona F, Kaiser R, Zazzi M, Lengauer T. Selecting anti-HIV therapies based on a variety of genomic and clinical factors. *Bioinformatics*. 2008 Jul 1;24(13):1399-406.
132. Gasparri A, and **Prosperi MCF**. A Bacterial Colony Growth Algorithm for Mobile Robot Localisation. *Autonomous Robot* 2008; 24(4):349-364. DOI: 10.1007/s10514-007-9076-1, ISSN: 0929-5593 (Print), 1573-7527 (Online).
133. De Luca A, Giambenedetto SD, Trotta MP, Colafigli M, **Prosperi M**, Ruiz L, Baxter J, Clevenbergh P, Cauda R, Perno CF, Antinori A. Improved interpretation of genotypic changes in the HIV-1 reverse transcriptase coding region that determine the virological response to didanosine. *J Infect Dis*. 2007 Dec 1;196(11):1645-53.



134. Di Giambenedetto S, Bracciale L, Colafigli M, Cattani P, Pinnetti C, Bacarelli A, **Prosperi M**, Fadda G, Cauda R, De Luca A. Declining prevalence of HIV-1 drug resistance in treatment-failing patients: a clinical cohort study. *Antivir Ther.* 2007;12(5):835-9.
135. Di Giambenedetto S, Bacarelli A, Pinnetti C, Colafigli M, **Prosperi M**, Gatti G, Cauda R, De Luca A. Genotypic resistance to lopinavir and fosamprenavir with or without ritonavir of clinical isolates from patients failing protease inhibitors-containing HAART regimens: prevalence and predictors. *Scand J Infect Dis.* 2007;39(9):813-8.

#### Peer-reviewed conference proceedings (full papers)

136. Jun I, Zhao Y, He XY, Gollakner R, Court CD, Muñoz OL, Bian J, Capua I, **Prosperi M**. Understanding Perceptions and Attitudes toward Genetically Modified Organisms on Twitter. In *International Conference on Social Media and Society 2020 (SMSociety'20)*. Association for Computing Machinery, New York, NY, USA, 291-298. DOI:<https://doi.org/10.1145/3400806.3400839>.
137. Zhao Y, Zhang H, Huo J, Guo Y, Wu Y, **Prosperi M**, Bian J. Mining Twitter to Assess the Determinants of Health Behavior towards Palliative Care in the United States. *AMIA Jt Summits Transl Sci Proc.* 2020 May 30;2020:730-739. eCollection 2020.
138. **Prosperi M**, Azarian T, Johnson JA, Salemi M, Milicchio F, Oliva M. Unexpected Predictors of Antibiotic Resistance in Housekeeping Genes of *Staphylococcus Aureus*. In *Proceedings of the 10th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics 2019 (BCB '19)*. ACM, New York, NY, USA, 259-268. DOI: <https://doi.org/10.1145/3307339.3342138>.
139. Tagliamonte MS, Waugh SG, **Prosperi M**, Mai V. An Integrated Approach for Efficient Multi-Omics Joint Analysis. In *Proceedings of the 10th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics 2019 (BCB '19)*. ACM, New York, NY, USA, 619-625. DOI: <https://doi.org/10.1145/3307339.3343476>.
140. Zhang H, He Z, He X, Guo Y, Nelson DR, Modave F, Wu Y, Hogan W, **Prosperi M**, Bian J. Computable Eligibility Criteria through Ontology-driven Data Access: A Case Study of Hepatitis C Virus Trials. *AMIA Annu Symp Proc.* 2018 Dec 5;2018:1601-1610.
141. He X, Zhang R, Rizvi R, Vasilakes J, Yang X, Guo Y, He Z, **Prosperi MCF**, Bian J. Prototyping an Interactive Visualization of Dietary Supplement Knowledge Graph. In: Zheng HJ, Callejas Z, Griol D, Wang H, Hu X, Schmidt H, Baumbach J, Dickerson J, Zhang L, editors. *BIBM [Internet]*, IEEE Computer Society, 2018, pp. 1649-1652. Available from: <http://dblp.uni-trier.de/db/conf/bibm/bibm2018.html#HeZRVYGHPB18>.
142. Du X, Bian J, **Prosperi M**. An Operational Deep Learning Pipeline for Classifying Life Events from Individual Tweets. In: Lossio-Ventura J., Muñante D., Alatrística-Salas H. (eds) *Information Management and Big Data. SIMBig 2018*. Communications in Computer and Information Science 2019, vol 898. Springer, Cham.
143. Milicchio F, Oliva M, Boucher C, **Prosperi M**. Third-generation sequencing data analytics on mobile devices: cache oblivious and out-of-core approaches as a proof-of-concept. *Procedia Computer Science* 2018; 134:219-226. <https://doi.org/10.1016/j.procs.2018.07.164>.
144. Tradigo G, Vacca R, Manini T, Bird V, Gerke T, Veltri P, **Prosperi M**. A new approach to disentangle genetic and epigenetic components on disease comorbidities: studying correlation between genotypic and phenotypic disease networks. *Procedia Computer Science* 2017; 110:453-458. <https://doi.org/10.1016/j.procs.2017.06.119>.
145. Milicchio F, **Prosperi M**. Efficient data structures for mobile de novo genome assembly by third-generation sequencing. *Procedia Computer Science* 2017; 110:440-447. <https://doi.org/10.1016/j.procs.2017.06.115>.
146. Cristiano F, Veltri P, **Prosperi M**, Tradigo G. On the identification of long non-coding RNAs from RNA-seq. *IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, Shenzhen, China, Dec 15-18, 2016; pp: 1103-1106.
147. Milicchio F, Buchan IE, and **Prosperi M**. A\* fast and scalable high-throughput sequencing data error correction via oligomers. *IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB)* 2016 Oct 5-7, Chiang Mai, Thailand.
148. Milicchio F, Tradigo G, Veltri P, **Prosperi M**. High-performance data structures for de novo assembly of genomes: cache oblivious generic programming. *7<sup>th</sup> ACM-BCB conference 2016 Oct 1-5, Seattle, WA*.
149. **Prosperi M**, Pironi A, Incardona F, Tradigo G, Zazzi M. Predicting human-immunodeficiency virus rebound after therapy initiation/switch using genetic, laboratory, and clinical data. *7<sup>th</sup> ACM-BCB conference 2016 Oct 1-5, Seattle, WA*.
150. Tradigo G, Cristiano F, Alcaro S, Greco S, Pollastri G, Veltri P, **Prosperi M**. G-quadruplex Structure Prediction and integration in the GenData2020 data model. *7<sup>th</sup> ACM-BCB conference 2016 Oct 1-5, Seattle, WA*.
151. Milicchio F, and **Prosperi MCF**. Accessible Tourism for the Deaf via Mobile Apps. In: *8th ACM International Conference on Pervasive Technologies Related to Assistive Environments (PETRA)*, June 29-July 01, 2016, Corfu Island, Greece.
152. Williams R, Buchan IE, **Prosperi M**, Ainsworth J. Using String Metrics to Identify Patient Journeys through Care Pathways. *Proceedings of the AMIA 2014 Annual Symposium*; November 15-19 2014, Washington DC, USA.
153. Milicchio F and **Prosperi MCF**. HErCoOl: High-throughput Error Correction by Oligomers. *Proceedings of the 27th IEEE Symposium on Computer-Based Medical Systems (CBMS) 2014, New York, USA*.
154. Gasparri A, and **Prosperi M**. A Bacterial Colony Growth Framework for Collaborative Multi-Robot Localization. *IEEE Int. Conference on Robotics and Automation (ICRA)* 2008, pp. 2806-2811.
155. **Prosperi MCF**, Ulivi G, Zazzi M. Statistical Comparison of Machine Learning Techniques for Treatment Optimisation of Drug-Resistant HIV-1. *Proceedings of the 20<sup>th</sup> IEEE International Symposium on Computer-Based Medical Systems (CBMS) 2007: 427-432*.
156. Fantì I, **Prosperi MCF**, Ulivi G, Micarelli A. HIV-1 Coreceptor Usage Prediction via Indexed Local Kernel Smoothing Methods and Grid-Based Multiple Statistical Validation. *Proceedings of the 20<sup>th</sup> IEEE International Symposium on Computer-Based Medical Systems (CBMS) 2007: 465-470*. doi: 10.1109/CBMS.2007.55.

157. Aharoni E, Altmann A, Borgulya G, D'Autilia R, Incardona F, Kaiser R, Kent C, Lengauer T, Neuvirth H, Peres Y, Petroczi A, **Prosperi M**, Rosen-Zvi M, Schuelter E, Sing T, Sonnerborg A, Thompson R, Zazzi M. Integration of viral genomics with clinical data to predict response to anti-HIV treatment. IST Africa Conference Proceedings, Paul Cunningham and Miriam Cunningham (Eds), IIMC International Information Management Corporation, 2007, ISBN: 1-905824-04-1.

**Book chapters**

158. **Prosperi M**, and Ulivi G. Evolutionary Fuzzy Modelling for Drug Resistant HIV-1 Treatment Optimisation. In Engineering Evolutionary Intelligent Systems, Studies in Computational Intelligence 82/2008: 251-287; Springer Berlin Heidelberg; ISSN 1860-949X (Print) 1860-9503 (Online); ISBN 978-3-540-75395-7; DOI 10.1007/978-3-540-75396-4\_9.