

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>
French Ministry of Superior Education and Research, France	2010	Qualification of Maître de Conférences	N/A	Computer Science
University of Milan, Milan, Italy	2009	Spec. Course	Merit Scholar.	Phylogenetics & 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
University College London, Royal Free Hospital, London, United Kingdom	2007-2008 (6 m.)	Visiting Scholar	N/A	Biostatistics, Epidemiology
Parc de Recerca Biomèdica de Barcelona, Barcelona, Spain	2007 (6 m.)	Visiting Scholar	N/A	Bioinformatics
Max Planck Institute, Saarbrücken, Germany	2006 (6 m.)	Visiting Scholar	N/A	Bioinformatics
University of Bergen, Bergen, Norway	1999 (1 y.)	Visiting Scholar	N/A	Computer Science Engineering

ACADEMIC POSITIONS AND EMPLOYMENT

2015-current	Preeminence Associate Professor at University of Florida , College of Public Health and Health Professions & College of Medicine, Dept. of Epidemiology (http://epidemiology.php.ufl.edu/), Gainesville, FL, USA.
2015	Honorary Lecturer at the Centre for Health Informatics, Institute of Population Health, University of Manchester , Manchester, UK.
2012-2014	Lecturer in Biomedical Modelling at the Centre for Health Informatics (http://www.population-health.manchester.ac.uk/healthinformatics/), Institute of Population Health, University of Manchester , Manchester, UK. Honorary Lecturer at University Hospital of South Manchester, Education and Research Centre, Manchester, UK.
2010-2012	Post-doctoral associate at the dept. of Pathology, Immunology and Laboratory Medicine, college of Medicine, University of Florida , Emerging Pathogens Institute

	(http://www.epi.ufl.edu/), Gainesville, FL, USA.
2009-2010	Post-doctoral associate and adjunct professor at the doctorate school in Biology and Clinic of Tropical and Infectious Diseases, Catholic University of the Sacred Heart (http://roma.unicatt.it/), Rome, ITA.
2008-2009	Post-doctoral associate at the National Institute of Infectious Diseases “L. Spallanzani” (http://www.inmi.it/), Rome, ITA.
2010-2017	Consultant for the Malattie Infettive e Salute Internazionale (MISI) Foundation (http://www.fondazionemisi.it/), Brescia, ITA.
2010-2012	Consultant for Catholic University of the Sacred Heart (http://roma.unicatt.it/), Rome, ITA.
2007-2009	Consultant for the Italian cohort of naïve to antiretrovirals (Icona) Foundation (http://www.fondazioneicona.org/), Milan, ITA.
2003-2011; 2015-2016	Consultant for Informa Pro , LLC (http://www.informapro.it/), Rome, ITA.

PERSONAL STATEMENT

My research interests are in the areas of biomedical modelling and data science focused on precision medicine and translational science. My approach to big data analytics is layered and integrates multi-source data, such as demographic, environmental, clinical, genetic, sensor technology, and beyond. Presently, I lead my research group towards the development of original algorithms and applications, exploiting machine learning from a rigorous statistical point of view and implementing software with optimized usability. In addition to my research, which is funded by federal agencies in US and EU, I foster Master’s and PhD studentships in order 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” (<http://tinyurl.com/nk4to6n>) and editor of “BMC Medical Informatics and Decision Making”. I am also member of the Association for Computing Machinery (ACM) and sit in the program committee of several bioinformatics conferences, including ISCB-ISMB, IEEE-CBMS, ACM-BCB, and AMIA-DMMI.

Currently I am Work Package PI of the “Virogenesis: Virus discovery and epidemic tracing from high throughput metagenomics sequencing” project, an intercontinental (EU, US, and Africa) 3Million Euro project consortium on next-generation sequencing viral metagenomics modelling, funded by the European Commission under the Horizon2020 programme (EC #634650). I am also MPI and PI of subcontract on two R21 NIH projects.

Before moving to US, at University of Manchester, UK, I was Team Leader (2012-2014, and in 2015 continuing via a honorary contract) in the 18Million GBP project Health e-Research Centre (HeRC, <http://www.herc.ac.uk/>) funded by the Medical Research Council. HeRC is a nationwide British project which combines technology with big health data and modern research methods to improve health for patient and public benefit, by harnessing operational and infrastructure capacity. Also, HeRC established a Patient and Public Involvement engagement team to more efficiently promote patient-provider relationships. Within HeRC, I helped building a nationwide asthma research network (STELAR) which successfully integrated regional cohorts in UK into an e-Laboratory.

PUBLICATIONS

My total publication record includes 98 works in peer-reviewed international journals (#citations 1871, h-index 23, i10-index 48), with 45+ papers as first/senior author, including journals in the Nature and PNAS publishing groups, and book chapters. My articles cover multiple areas of research, including computational biology, machine learning, robotics, algorithms, epidemiology and health informatics.

A comprehensive list can be found via my Google scholar profile

- <https://scholar.google.com/citations?user=lymUyDkAAAAJ&hl=en>

and my NCBI for Pubmed-indexed papers

- <http://www.ncbi.nlm.nih.gov/sites/myncbi/1NQd-7sVrcEk-/bibliography/47993434/public/?sort=date&direction=descending>

I published also several dozens of abstracts at international conferences from 2004 to 2017, of which many were selected as oral presentations. The complete list of published papers is appended at the end of this resume.

RESEARCH SUPPORT

Ongoing Research Support

Extramural Funding

- IT CINECA/ISCRA/SCAI (Milicchio, Prosperi) 10/2016-10/2017 N/A
Role (budget allocation): **MPI** (4Million CPU-hours)
Title: Tools for Assembly of Next-Generation Sequencing U-mer Data Objects (TANGSUDO)
Goal: To develop and test parallel C++ assembly methods of next-generation sequencing data.
- US DEPT OF HOMELAND SECURITY (Blackburn) 06/01/2016-05/31/2019 1.2 calendar months
Role (budget allocation): **PI** of subaward (\$18,695 per year / total project costs \$1,527,011)
Title: Bacterial Population Genetics of Select Agent Pathogens.
Goal: Sequence and characterize evolutionary history of C. Botulinum via next-gen bioinformatics.
- NIH R21MH109360 (Marshall) 04/05/2016-03/31/2018 0.9 calendar months
Role (budget allocation): **PI** of subaward (\$18,795 per year / total project costs \$261,525)
Title: Enhancing pre-exposure prophylaxis implementation to optimize individual and community-level impact.
Goal: Develop agent-based simulation model of outcomes and effectiveness of HIV pre-exposure prophylaxis
- NIH/NCI R21CA195251-01A1 (Mai, Prosperi) 01/06/2016-12/31/2018 1.2 calendar months
Role (budget allocation): **MPI** (\$194,521)
Title: Big data approach for correlating gut microbiota with epithelial methylation pattern.
Goal: Investigate multi-domain large scale modelling to associate methylation data and gut microbiota with colorectal cancer.
- EU H2020-PHC-32-2014 #634650 (Vandamme, *et al.*) 06/01/2015-06/01/2018 2.4 calendar months
Role (budget allocation): **PI** of Work Package (€2,995,968)
Title: Virogenesis: Virus discovery and epidemic tracing from high throughput metagenomics sequencing.
Goal: To develop novel bioinformatics models, methods and tools for virome analysis and epidemic tracing using next-generation sequencing data.
- IT MISI Foundation (Prosperi) 03/31/2015-03/31/2018 0.7 calendar months
Role (budget allocation): **PI** (\$24,354)
Title: Management of standardized evaluation of retroviral HIV Infection (MASTER).

Goal: To integrate data from established HIV cohorts in Italy that have been collecting data on participants for up to 15 years and address research questions regarding HIV treatment, outcomes and hepatitis co-infection.

UK BBSRC BB/M001121/1 (Robertson)

9/2014-8/2017 N/A

Role (budget allocation): Co-Applicant; honorary role after leaving UK (£274,155)

Title: Computational methods for microbial next-generation sequencing data

Goal: 1) To address a specific set of unsolved theoretical problems in the fields of metagenomics and microbiology/virology-associated sequencing projects; and 2) to introduce new methods for visualizing next-generation sequencing alignments graphically, for example, in three-dimensional space.

UK MRC MR/L012693/1 (Johnston)

5/2014-5/2019 N/A

Role (budget allocation): Co-Applicant; honorary role 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

Goal: To conduct computational analysis to identify novel mechanisms related to increased susceptibility to asthma, allergies and respiratory diseases, elucidating the development of functional antiviral and anti-bacterial immune responses and of epigenetic marks in relation to genetics from childhood to adulthood.

Intramural Funding

University of Florida's Health Cancer Center & Institute of Aging (Bird, Gerke, Manini, Proserpi) 2016-2017 N/A

Role (budget allocation): **MPI** (\$40,000)

Title: Endotype discovery in prostate cancer and multi-domain analysis of age-related comorbidities.

Goal: Secondary analysis of large genomic and clinical data base to identify endotypes of prostate diseases related to prostate malignancy and age-related comorbidities.

UFHealth Quasi Endowment Fund (Lucero, renewal)

02/2017-02/2018 1.2 calendar months

Role (budget allocation): Co-I (\$50,000)

Title: Strengthening the UFHealth Nursing Academic Partnership Phase III: Generating Practice-based Evidence for Quality Improvement

Goal: To develop an Electronic Hospital-Acquired Condition Data Registry and build a precision medicine model of fall prevention and post-fall recovery outcomes in high-risk populations.

Completed Research Support

UFHealth Quasi Endowment Fund (Lucero)

02/2016-02/2017 1.2 calendar months

Role (budget allocation): Co-I (\$64,358)

Title: Strengthening the UFHealth Nursing Academic Partnership Phase III: Generating Practice-based Evidence for Quality Improvement

Goal: To develop an Electronic Hospital-Acquired Condition Data Registry and build a precision medicine model of fall prevention and post-fall recovery outcomes in high-risk populations.

Florida Academic Cancer Center Alliance (Yaghjian)

2015-2016 N/A

Role (budget allocation): Co-I (\$50,000)

Title: Gut microflora and estrogens: a new paradigm for breast cancer risk reduction

Goal: The study investigates the association of intestinal microbiome with endogenous estrogen metabolism in healthy postmenopausal women undergoing routine mammographic screening.

IT EuResist Foundation (Prosperi)

07/15/2015-07/14/2016 0.72 calendar months

Role : **PI** \$19,600

Title: EuResist Engine retraining and revision

Goal: Inference and implementation of a machine learning model (command-line and web-service) for the optimization of HIV antiretroviral therapy based on patients' characteristics and viral genotype data.

UK MRC MR/L011808/1 (Griffiths)

9/2014-8/2019 N/A

Role (budget allocation): Researcher; *project still ongoing, but role left after leaving UK* (£5,004,540)

Title: Psoriasis Stratification to Optimise Relevant Therapy (PSORT)

Goal: To better understand determinants of response to biologic therapies and deliver, in close collaboration with commercial partners, a PSORT stratified algorithm to guide psoriasis management.

NIH/NIAID R01 AI097405-03 (Morris)

8/01/2014-11/30/2015 0.96 calendar months

Role (budget allocation): Co-I (\$2,724,560)

Title: Cholera Transmission in Gressier Region, Haiti: Refinement of Bioinformatics

Goal: 1) Identification of *V. cholerae* in household members and in the environment; 2) Assessment and comparison of evolutionary changes in clinical and environmental *V. cholerae* isolates, making use of VNTR and whole genome SNP analysis; 3) Further refinement and validation of mathematical models of cholera transmission, including assessments of the impact of immunization and other interventions on transmission.

IT CINECA/ISCRA/SCAI (Milicchio, Prosperi)

9/2014-9/2015 N/A

Role (budget allocation): **MPI** 9200,000 CPU-hours

Title: PHERCoOI – Parallel High-throughput Error Correction via Oligomers

Goal: To develop and test parallel software in C++ for error correction of next-generation sequencing data.

IT Fondazione MISI (Prosperi)

2012-2014 N/A

Role (budget allocation): **PI** (€18,000)

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

Goal: To integrate data from established HIV cohorts in Italy that have been collecting data on participants for up to 15 years to address research questions regarding HIV treatment, outcomes and hepatitis co-infection. Objectives include epidemiological-, clinical-, laboratory-, and health service research, as well as improving service and infrastructure for future projects.

NIH/NCRR UL1 RR029890 (Prosperi)

2011-2012 N/A

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

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

Goal: Develop and implement algorithms and software for viral population assembly using next-generation sequencing data

University of Florida's EPIG (Prosperi)

2011-2012 N/A

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

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

Goal: Study evolutionary dynamics of HIV-1 intra-host in slow-progressors using phylodynamics methods.

TEACHING, SELECTED INVITED TALKS & MENTORING

Mar. 2017 (seminar)	Invited seminar at Brown University, Providence, Rhode Island “Precision Medicine via Multi-Domain Inference, to Say Nothing of Big Data”.
Mar. 2017 (course, 2 days)	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)	University of Florida’s GMS6850 Foundations of Biomedical Informatics: “Multi-domain Inference in Healthcare” lecture (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, 5 days)	Organizer and teacher at the “21th 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” lecture (4.8/5.0 median students’ evaluation score).
Dec. 2015 (seminar)	University of Florida’s GMS6850 Foundations of Biomedical Informatics: “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, 5 days)	Organizer and teacher at the “20th International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology” University of West Indies, Trinidad and Tobago.
Sep. 2014 (course, 5 days)	Organizer and teacher at the “19th 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, Manchester, UK.
Aug. 2013 (course, 5 days)	Organizer and teacher at the “18th 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./Sep. 2012 (course, 5 days)	Teacher at the “17th International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology” University of Belgrade, Serbia.

Oct. 2011 (course, 5 days)	Teacher at the international workshop “Bioinformatics for Phylogenetic Reconstruction in Virology” Hospital de Pediatria Garrahan, Buenos Aires, Argentina.
Aug./Sep. 2010 (course, 5 days)	Teacher at the “16 th 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” ISI Foundation, 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, ITA.
Dec. 2008 (seminar)	Invited seminar “Bioinformatics helps to make sense of HIV drug resistance” Borodino Ht., Moscow, Russia.
2004-2008 (teaching assistant)	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, M.Eng.), “Intelligenza artificiale” (Artificial Intelligence, M.Eng.), “Fondamenti di automatica” (Foundations of Automation, B.Eng.).

Mentoring

Dissertation reviews: Co-reviewer of BEng and MEng dissertations at Roma Tre University (2004-2008); co-supervisor of BEng and MEng dissertations at Roma Tre University (2004-2008). Certified supervisor for PhD students (May 2014, University of Manchester – this enables to take the role of main PhD supervisor in UK).

Postdoctoral fellows: Carla Mavian (2016-); Giuseppe Tradigo (2016); Rebecca Rose (2015-) at UF.

Graduate students: Jae Min (PhD, 2015-); Zhiaoyi Chen (PhD, 2015-); Kai Wang (2017-) at UF; Paolo Fraccaro (PhD, 2013-), Rebecca Howard (PhD, 2013-) at University of Manchester, UK; Arturo Franchini (MEng, 2017) at University of Brescia, Italy; Hans-Joachim Sonntag (MSc, 2014) at University of York, UK; advising 2 MPH students at UF (2015-2017).

Female proportion is 40%, no under-represented minority yet.

Undergraduate students trained or being trained: 6 (3 Females) since 2013.

MEMBERSHIPS, EDITORIAL APPOINTMENTS, RELEVANT SERVICES

Editorial Appointments

2011 – current | Associate Editor of *BMC Medical Informatics and Decision Making*.

International Workshops / Conferences

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

2014 - current | Member of the Program Committees of: ISCB/ISMB (2014); IEEE/CBMS (2014); DMMI-AMIA (2014-2015), IEA/AIE (2017). Track Chair for ACM-BCB (2017).

Professional / Scientific Memberships

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

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

2012 - current	Member of the scientific committee of the Management of Standardized Evaluation of Retroviral HIV Infection (MASTER) cohort (http://www.mastercohort.it/).
2015 - current	Member of University of Florida's: 1) Cancer Center; 2) Genetics Institute; 3) Emerging Pathogens Institute.

Grants Review / Study Sections

2017	US National Institutes of Health (NIH): study section ZA11 JA-M M2 1.
2017	UK Medical Research Council (MRC).
2016	Swiss Institute of Bioinformatics (SIB).
2013-2014	Research Foundation Flanders - Fonds Wetenschappelijk Onderzoek - Vlaanderen, Belgium.
2013	US-Israel Binational Science Foundation.

Journals

Reviewer for several journals (since 2008), including: AIDS Research and Human Retroviruses; Antiviral Therapy; Bioinformatics; BMC Genomics; BMC Infectious Diseases; BMC Medical Informatics and Decision Making; IEEE/ACM Transactions on Computational Biology and Bioinformatics; Infection, Genetics and Evolution; International Journal of STD & AIDS; Journal of AIDS and HIV Research; PeerJ; PLOS Computational Biology; PLOS ONE; The Journal of Infectious Diseases; Virology Journal; Scientific Reports; Virus Research.

Other Services

2016 - current	Ombudsman for University of Florida's Department of Epidemiology.
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HONORS, SCHOLARSHIPS & AWARDS

2016	First Place in the Illumina, Inc. GoMini Scientific Challenge Grant, award comprising a MiniSeq, a Mini Cooper, and reagents for three sequencing runs (cash value ~\$100,000). The project aims at studying genetic diversity and spread of emerging vector-borne pathogens in Florida (http://www.illumina.com/company/news-center/feature-articles/illumina-announces-winners-of-miniseq-scientific-challenge.html).
2012	Runner-up (2 nd place) in the Geneious' "iEvoBio" challenge for the best bioinformatics plugin (http://www.geneious.com).
2009	Computerworld Honors Awards (Washington DC, http://www.cwhonors.org/), given for the EuResist project (www.euresist.org).
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 from the EU.
1996	Stage offered by "Scuola Normale Superiore di Pisa" to the best high-school students in Italy.

SOFTWARE RELEASED

- 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

Journal papers / full-paper conference proceedings (sorted by date)

1. 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.
2. 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.
3. 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.
4. Milicchio F, Tradigo G, Veltri P, **Prosperi M**. High-performance data structures for de novo assembly of genomes: cache oblivious generic programming. 7th ACM-BCB conference 2016 Oct 1-5, Seattle, WA.
5. **Prosperi M**, Pironti A, Incardona F, Tradigo G, Zazzi M. Predicting human-immunodeficiency virus rebound after therapy initiation/switch using genetic, laboratory, and clinical data. 7th ACM-BCB conference 2016 Oct 1-5, Seattle, WA.
6. 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. 7th ACM-BCB conference 2016 Oct 1-5, Seattle, WA.
7. 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
8. 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
9. 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.
10. **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.
11. 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.
12. 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.
13. 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.
14. 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.
15. 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.
16. 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.
17. 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.

18. 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.
19. 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.
20. 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.
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Book chapters

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