

## 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
Qualifications	French Ministry of Superior Education and Research, France	2010	Maître de Conférences	N/A	Computer Science
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 of Preeminence, <b>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

2010-2018 | Malattie Infettive e Salute Internazionale (MISI) foundation, Brescia, ITA.  
2015-2016 | EuResist foundation, Rome, 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 and information science* and *biomedical modelling*. 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.

My **theoretical research** is focused on development of new computational intelligence approaches tailored to the analysis of high-dimensional and heterogeneous data, e.g. unstructured social and behavioral data, electronic medical records, multi-omics sequencing data.

My **applied research** foresees the development of prediction 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 am head of the *Data Intelligence Systems Lab (DISL)*, (<https://epidemiology.php.ufl.edu/people/faculty-staff/faculty/core-faculty/mattia-prosperi/data-intelligence-systems-lab-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*" and editor of "*BMC Medical Informatics and Decision Making*". I am also member of the *Association for Computing Machinery (ACM)* and program member of several international conferences, including ACM's Conference on Bioinformatics, Computational Biology, and Health Informatics.

### PUBLICATIONS

My publication record includes over 110 articles in peer-reviewed international journals and book chapters (**h-index 27**, i10-index 61), with more than 50 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>
- <http://www.ncbi.nlm.nih.gov/sites/myncbi/1NQd-7sVrcEk-/bibliography/47993434/public/?sort=date&direction=descending>

The complete list of publications is appended at the end of this resume. I also presented several dozens of abstracts at international conferences from 2004 to 2018.

### RESEARCH SUPPORT

#### Ongoing Research Support

#### Extramural Funding

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.

Goal: fine-grained geospatial modelling to relate HIV drug resistance with multiple sociodemographic indicators, from individual- (e.g. age, risk behavior) to community-level factors (e.g. deprivation score).

NIH NIAID 1R21AI138815-01 (Prosperi, Salemi) 04/01/2018-03/31/2020 1.44 calendar months

Role (budget): **PI (\$389,333)**

Title: HIV Dynamic Modelling for Identification of Transmission Epicenters (HIV-DYNAMITE).

Goal: develop a novel theoretical and technical framework to model dynamically HIV transmission clusters on large sequence data.

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.

Goal: investigate the role of viral evolution in the development of HIV-associated neurocognitive disorders during antiviral therapy.

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

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

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

Goal: study individual and network determinants of dramatic life events like job loss using social media streams through deep learning and natural language processing methods.

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.

Goal: Sequence and characterize evolutionary history of *C. Botulinum* via next-gen bioinformatics.

NIH NCI R21CA195251-01A1 (Mai, Prosperi) 01/06/2016-12/31/2017 ext. 12/31/18 1.2 calendar months

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

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) 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.

Goal: To develop novel bioinformatics models, methods and tools for virome analysis and epidemic tracing using next-generation sequencing data.

### **Intramural Funding**

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.

Goal: Profiling microbiota in normal breast tissue and link it to genome methylation.

### **Completed Research Support**

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.

Goal: Develop an agent-based simulation model of outcomes and effectiveness of HIV pre-exposure prophylaxis.

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).

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.

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

Goal: To develop and test parallel C++ assembly methods of next-generation sequencing data.

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.

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

University of Florida's Health Quasi Endowment Fund (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

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.

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

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.

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.

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.

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

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

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 (PHERCOI)

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

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.

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.

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)

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.

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

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) 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

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.

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

Role (budget): **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): **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): **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

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.-Mar. 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” 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, 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

*Postdoctoral fellows:* Carla Mavian (2016-2017); Giuseppe Tradigo (2016); Rebecca Rose (2015-) at University of Florida.

*Graduate students:* Jae Min (PhD, 2015-); Zhaoyi Chen (PhD, 2015-); Kai Wang (2017-) at University of Florida; Paolo Fraccaro (PhD, 2013-2017), Rebecca Howard (PhD, 2013-2017) at University of Manchester, UK; Arturo Franchini (MEng, 2017) at University of Brescia, Italy; Hans-Joachim Sonntag (MSc, 2014) at University of York, UK; currently advising MPH students at University of Florida, 2-3 per year (2015-2018).

Certified supervisor for PhD students (May 2014, University of Manchester, UK –it enables to take the role of main PhD supervisor in UK).

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

## EDITORIAL APPOINTMENTS, MEMBERSHIPS, RELEVANT SERVICES

### Editorial Appointments

2017	Guest editor of <i>Current Medicinal Chemistry</i> (IF=3.8).
2011 – current	Associate Editor of <i>BMC Medical Informatics and Decision Making</i> (IF=1.6).

### International Workshops / Conferences

2014 - current	Member of the program committees (PC) of: ISCB/ISMB (2014); IEEE/CBMS (2014); DMMI-AMIA (2014-2015), IEA/AIE (2017), SIMBIG (2018), ACM-BCB (2017-2018). Track chair for ACM-BCB (2017).
2013 - current	Organizer of the International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology ( <a href="http://rega.kuleuven.be/cev/avd/meetings/international-bioinformatics-workshops">http://rega.kuleuven.be/cev/avd/meetings/international-bioinformatics-workshops</a> ).

### Professional / Scientific Memberships

2016 - current	Member of the Association for Computing Machinery (ACM, <a href="https://www.acm.org/">https://www.acm.org/</a> ).
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 ( <a href="http://www.mastercohort.it/">http://www.mastercohort.it/</a> ).
2003 - current	Member of the scientific committee of the Italian Antiretroviral Resistance Cohort Analysis (ARCA) ( <a href="http://www.hivarca.net">www.hivarca.net</a> ).

### Grants Review / Study Sections

2018	US National Science Foundation (NSF): Computer, Information Science and Engineering (CISE).
2018	UK Royal Society.
2018	UK Wellcome Trust.
2017	US National Institutes of Health (NIH): study section ZAI1 JA-M M2 1.
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; PeerJ; PLOS ONE; Scientific Reports (Nature's).
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.
Epidemiology / Infectious Diseases	AIDS Research and Human Retroviruses; Antiviral Therapy; BMC Infectious Diseases; International Journal of STD & AIDS; Journal of AIDS and HIV Research; The Journal of Infectious Diseases; Virology Journal; Virus Research.

### Other Services

2016 - 2017	Ombudsman for University of Florida's Department of Epidemiology.
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### HONORS, SCHOLARSHIPS & AWARDS

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' "EvoBio" 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

- *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

**Note:** Courier font indicates works focused more on methods/algorithms/software rather than data analytics.

### Peer-reviewed conference proceedings

1. 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>.
2. 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>.
3. 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>.
4. 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.
5. 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.
6. 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.
7. **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.

8. 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.
9. 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.
10. 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.
11. 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.
12. 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.
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