

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, Department of Epidemiology, College of Public Health and Health Professions & College of Medicine, University of Florida , Gainesville, FL, USA.
2012-2015	Assistant Professor [Lecturer as per the British academic nomenclature] in Biomedical Modelling, Centre for Health Informatics, University of Manchester , 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	Scientific Advisor and Statistical Consultant, Malattie Infettive e Salute Internazionale (MISI) Foundation, Brescia, ITA.
2015-2016	Scientific Advisor and Model Developer, EuResist foundation, Rome, ITA.
2010-2012	Statistical Consultant, Catholic University of the Sacred Heart , Rome, ITA.
2003-2011	Scientific Consultant, Informa Pro , LLC, Rome, ITA.
2007-2009	Statistical Consultant, Italian cohort of naïve to antiretrovirals (Icona) Foundation, Milan, ITA.

PERSONAL STATEMENT

My research interests are in the areas of **big data science** and *biomedical process modelling* currently focused on *precision medicine* and *precision public health*. 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. multi-omics datasets.

My applied research focuses on the development of prediction models. My approach to study design and model development is heavily influenced by my epidemiology experience, yet I capitalize on my engineering background 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.

In addition to research, 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 book chapters and articles in peer-reviewed international journals (n=108, #citations 2229, **h-index 26**, i10-index 57), with more than 50 as first/senior author, including pieces with the *Nature* and *PNAS* publishers. My publications cover multiple areas of methodological 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-/bibliograph/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 2017.

RESEARCH SUPPORT

[ordered by end date]

Award Pending

FL DEPT OF HEALTH (Prosperi) [negotiating contract dates] 2.0 calendar months

Role (budget): **PI (\$116,546)**

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).

Ongoing Research Support

Extramural Funding

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): **Primary 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.

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

Role (budget): **Primary 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.

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.

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.

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.

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.

Intramural Funding

University of Florida's Health Cancer Center (Asirvatham, Chim, Mai, Prosperi, Yaghjian) 10/2017-09/2018 N/A

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

Title: Correlations between breast microbiota and tissue methylation pattern.

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

University of Florida's Health Cancer Center & Institute on Aging (Bird, Gerke, Manini, Prosperi) 02/2016-02/2018 N/A

Role (budget): **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 - 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

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

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

Role (budget): **MPI (\$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.

IT CINECA ISCRA SCAI HP10CD4PA7 (Milicchio, Prosperi) 10/2016-10/2017 N/A

Role (budget): **MPI (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.

UK MRC MR/Lo11808/1 (Griffiths) 09/2014-08/2019 N/A
 Role (budget): 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.

UK MRC MR/Lo12693/1 (Johnston) 05/2014-05/2019 N/A
 Role (budget): Co-I; *project still ongoing, but role left 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.

UK BBSRC BB/M001121/1 (Robertson) 09/2014-08/2017 N/A
 Role (budget): Co-I; *role left 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-generations sequencing alignments graphically, for example, in three-dimensional space.

UFHealth 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.

NIH NIAID R01 A1097405-03 (Morris) 8/01/2014-11/30/2015 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.

IT CINECA ISCRA SCAI HP10CU1H2A (Milicchio, Prosperi)

09/2014-09/2015 N/A

Role (budget): **MPI** (200,000 CPU-hours)

Title: Distributed Processing of High-Throughput Sequencing Data via De Bruijn Graphs (PHERCoOI)

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): **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

Jan. 2018 (seminar)	Invited 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 nd 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)	Invited 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 st 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 th 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 th 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 th 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 th 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

Aug. 2010 (course, 5 hrs)	Reconstruction in Virology” Hospital de Pediatria Garrahan, Buenos Aires, Argentina.
June 2010 (seminar)	Teacher at the “16 th International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology” Johns Hopkins University, Rockville, MD, USA.
Jan.-Mar. 2010 (course, 15 hrs)	Invited seminar “Mathematical Models for HIV-1 Therapy Optimisation” ISI Foundation, Turin, Italy.
Dec. 2008 (seminar)	“Biostatistics for physicians” at the doctorate school in Biology and Clinic of Tropical and Infectious Diseases, Catholic University of the Sacred Heart, Rome, Italy.
2004-2008 (teaching assistance, ~10/20 hrs per course)	Invited seminar “Bioinformatics helps to make sense of HIV drug resistance” Borodino Ht., Moscow, Russia.
	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-); Zhiaoyi 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 (2015-2017).

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

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).

Grants Review / Study Sections

2018 | UK The 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 - 2014 | Research Foundation Flanders - Fonds Wetenschappelijk Onderzoek - Vlaanderen, Belgium.
2013 | US-Israel Binational Science Foundation.

Journal Peer Review

Generalist | Interiencia; 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; 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.

HONORS, SCHOLARSHIPS & AWARDS

2017 | Southeastern Conference (SEC) Visiting Faculty Travel Grant (<http://www.theseecu.com/programs/sec-faculty-travel-program/2017-2018-sec-faculty-participants/>).

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 (<http://www.illumina.com/company/news-center/feature-articles/illumina-announces-winners-of-miniseq-scientific-challenge.html>).

2012 | Runner-up (2nd 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 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

- QuRe – Viral quasispecies assembly from next-generation sequencing data (<http://sourceforge.net/projects/qure/>)
- 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 on methods/algorithms/software

Peer-reviewed conference proceedings

1. 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>.
2. 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>.
3. 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.
4. 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.
5. 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.
6. **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.
7. 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.
8. 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.
9. 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.
10. 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.
11. 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.

12. **Prosperi MCF**, Ulivi G, Zazzi M. Statistical Comparison of Machine Learning Techniques for Treatment Optimisation of Drug-Resistant HIV-1. Proceedings of the 20th IEEE International Symposium on Computer-Based Medical Systems (CBMS) 2007: 427-432.
13. Fanti 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 20th IEEE International Symposium on Computer-Based Medical Systems (CBMS) 2007: 465-470. doi: 10.1109/CBMS.2007.55.
14. 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.

Journal papers

15. 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.
16. 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.
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