

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>
Graduate Degrees	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
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 (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.
2003-2011; 2015-2016	Consultant for Informa Pro , LLC (http://www.informapro.it/), Rome, 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.

PERSONAL STATEMENT

My research interests are in the areas of *biomedical modelling* and *big data science* focused on *precision medicine*, *precision public health*, and *translational science*. My approach to data analytics is layered and integrates multiple domains, such as socio-demographic, ecological, clinical, -omics, and sensor technology. 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.

Before moving to US, at University of Manchester, UK, I was Team Leader (2012- 2015) in the £18Million project Health e-Research Centre (HeRC, <http://www.herc.ac.uk/>) funded by the Medical Research Council. HeRC was a nationwide British project combining 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 to more efficiently promote patient-provider relationships. Within HeRC, I helped building a nationwide ‘e-Laboratory’ research network.

I am now one of the PIs of the “Virogenesis” project, an intercontinental €3Million consortium on next-generation modelling of viral metagenomics, funded by the European Commission’s Horizon2020 Programme.

Recently, I have been also awarded a new NSF project as PI, applying artificial intelligence and text mining of social media streams to predict dramatic life events such as job loss.

In my future research I envision pursuing ideas in ‘humanly ethical’ artificial intelligence for health and beyond.

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” (<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 program member of several conferences, including ACM’s Conference on Bioinformatics, Computational Biology, and Health Informatics.

PUBLICATIONS

My total publication record includes **105 works** in peer-reviewed international journals (#citations 2064, **h-index 26**, i10-index 52), with 50+ papers as first/senior author, including pieces with the *Nature* and *PNAS* publishers, and book chapters. My articles cover multiple areas of research, including biomedical and health informatics, computational biology, biomathematics, machine learning, epidemiology, robotics, and algorithms.

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 published papers 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]

Ongoing Research Support

Extramural Funding

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

Role (budget): Co-I (with own subcontract \$130,477, total project costs \$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) 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 natural language processing methods.

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

Role (budget): Co-I (with own subcontract \$37,590, 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.

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

Role (budget): PI of Work Package (core €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 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.

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.

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

UK MRC MR/L011808/1 (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/L012693/1 (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 AI097405-03 (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

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 PHC6937 “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: “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: “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 Reconstruction in Virology” Hospital de Pediatria Garrahan, Buenos Aires, Argentina.
Aug. 2010 (course, 5 hrs)	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, 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.

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

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).

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

EDITORIAL APPOINTMENTS, MEMBERSHIPS, RELEVANT SERVICES

Editorial Appointments

2017	Guest editor of Current Medicinal Chemistry (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

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 Reviews

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.

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 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/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

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

1. 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.
2. 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.

3. 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>.
4. 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>.
5. 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.
6. 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>.
7. 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.
8. 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.
9. 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.
10. 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.
11. 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.
12. **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. 7th ACM-BCB conference 2016 Oct 1-5, Seattle, WA.
13. 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.
14. 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
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