

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.	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

POSITIONS AND EMPLOYMENT

Academic Positions

2015-current	Preeminence Associate Professor of Bioinformatics, 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

2015-2018;	Scientific Advisor and Statistical Consultant, Malattie Infettive e Salute Internazionale (MISI) Foundation, Brescia, ITA.
2012-2014;	
2010-2011.	
2015-2016	Scientific Advisor and Model Developer, EuResist foundation, Rome, ITA.
2010-2012	Statistical Consultant, Catholic University of the Sacred Heart , Rome, ITA.
2003-2008;	Scientific Consultant, Informa Pro , LLC, Rome, ITA.
2009-2011.	
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=106, #citations 2106, **h-index 26**, i10-index 52), 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-/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 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 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 (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 (own 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

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 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. 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 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.

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

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	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; 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 - 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", 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 (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 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 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

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. Min J, Osborne V, Kowalski A, **Prosperi M**. Reported Adverse Events with Painkillers: Data Mining of the US Food and Drug Administration Adverse Events Reporting System. *Drug Saf.* 2017 Nov 2. doi: 10.1007/s40264-017-0611-5.
16. 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.
17. 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.
18. 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.
19. 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>.

20. 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.
21. 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.
22. 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
23. 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
24. 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.
25. **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.
26. 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.
27. 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.
28. 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.
29. 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.
30. 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.
31. 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.
32. 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.
33. 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):ofvo43. doi: 10.1093/ofid/ofvo43. eCollection 2015 Apr.
34. 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.
35. Wu J, **Prosperi MC**, Simpson A, Hollams EM, Sly PD, Custovic A, Holt PG. Relationship Between Cytokine Expression Patterns and Clinical Outcomes: Two Population-based Birth Cohorts. *Clin Exp Allergy*. 2015 Jun 8. doi: 10.1111/cea.12579
36. Custovic A, Sonntag HJ, Buchan IE, Belgrave D, Simpson A, **Prosperi MC**. Evolution pathways of IgE responses to grass and mite allergens throughout childhood. *J Allergy Clin Immunol*. 2015 May 8. pii: S0091-6749(15)00495-9. doi: 10.1016/j.jaci.2015.03.041.
37. Fraccaro P, Nicolo M, Bonetto M, Giacomini M, Weller P, Traverso CE, **Prosperi M**, O Sullivan D. Combining macula clinical signs and patient characteristics for age-related macular degeneration diagnosis: a machine learning approach. *BMC Ophthalmol*. 2015 Jan 27;15(1):10.
38. Postorino MC, **Prosperi M**, Quiros-Roldan E, Maggiolo F, Di Giambenedetto S, Saracino A, Costarelli S, Lorenzotti S, Sighinolfi L, Di Pietro M, Torti C; MASTER Study Group. Use of efavirenz or atazanavir/ritonavir is associated with better clinical outcomes of HAART compared to other protease inhibitors: routine evidence from the Italian MASTER Cohort. *Clin Microbiol Infect*. 2014 Nov 11. pii: S1198-743X(14)00088-3. doi: 10.1016/j.cmi.2014.10.022.
39. Azarian T, Ali A, Johnson JA, Mohr D, **Prosperi M**, Veras NM, Jubair M, Strickland SL, Rashid MH, Alam MT, Weppelmann TA, Katz LS, Tarr CL, Colwell RR, Morris JG Jr, Salemi M. Phylodynamic Analysis of Clinical and Environmental *Vibrio cholerae* Isolates from Haiti Reveals Diversification Driven by Positive Selection. *MBio*. 2014 Dec 23;5(6).

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

60. **Prosperi M CF**, Prosperi L, Gray RR, Salemi M. On Counting the Frequency Distribution of String Motifs in Molecular Sequences. *International Journal of Biomathematics*. 2012;5(6):1250055. DOI: 10.1142/S1793524512500556.
61. De Luca A, Marazzi MC, Mancinelli S, Ceffa S, Altan AM, Buonomo E, **Prosperi MC**, Pedruzzi B, Noorjehan AM, Scarcella P, Liotta G, Palombi L. Prognostic value of virological and immunological responses after 6 months of antiretroviral treatment in adults with HIV-1 infection in sub-Saharan Africa. *J Acquir Immune Defic Syndr*. 2012 Mar 1;59(3):236-44.
62. Zazzi M, Incardona F, Rosen-Zvi M, **Prosperi M**, Lengauer T, Altmann A, Sonnerborg A, Lavee T, Schülter E, Kaiser R. Predicting Response to Antiretroviral Treatment by Machine Learning: The EuResist Project. *Intervirology*. 2012;55(2):123-7.
63. **Prosperi MC**, and Salemi, M. QuRe: software for viral quasispecies characterization from next-generation sequencing data. *Bioinformatics*. 2012 Jan 1;28(1):132-3.
64. Cozzi-Lepri A, **Prosperi MC**, Kjær J, Dunn D, Paredes R, Sabin CA, Lundgren JD, Phillips AN, Pillay D; for the EuroSIDA and the United Kingdom CHIC/United Kingdom HDRD Studies. Can Linear Regression Modeling Help Clinicians in the Interpretation of Genotypic Resistance Data? An Application to Derive a Lopinavir-Score. *PLoS One*. 2011;6(11):e25665.
65. Torti C, **Prosperi M**, Motta D, Digiambenedetto S, Maggiolo F, Paraninfo G, Ripamonti D, Cologni G, Fabbiani M, Caputo SL, Sighinolfi L, Ladisa N, El-Hamad I, Quiros-Roldan E, Frank I. Factors influencing the normalization of CD4+ T-cell count, percentage and CD4+/CD8+ T-cell ratio in HIV-infected patients on long-term suppressive antiretroviral therapy. *Clin Microbiol Infect*. 2012 May;18(5):449-58. doi: 10.1111/j.1469-0691.2011.03650.x. Epub 2011 Sep 15.
66. Bruni R, **Prosperi M**, Marcantonio C, Amadori A, Villano U, Tritarelli E, Lo Presti A, Ciccozzi M and Ciccaglione AR. A computational approach to identify point mutations associated with occult hepatitis B: significant mutations affect coding regions but not regulative elements of HBV. *Virology Journal* 2011 Aug 8;8(1):394.
67. De Luca A, Di Giambenedetto S, Maserati R, Gianotti N, Narciso P, Antinori A, Di Perri G, **Prosperi MC**, Baldanti F, Micheli V, Zazzi M, Perno CF, Santoro MM; TMC114-C226 study group; ARCA study group. Interpretation of genotypic HIV-1 resistance to darunavir and virological response: validation of available systems and of a new score. *Antivir Ther*. 2011;16(4):489-97.
68. **Prosperi MC**, Di Giambenedetto S, Fanti I, Meini G, Bruzzone B, Callegaro A, Penco G, Bagnarelli P, Micheli V, Paolini E, Di Biagio A, Ghisetti V, Di Pietro M, Zazzi M, De Luca A, Arca AR. A Prognostic Model for Estimating the Time to Virologic Failure in HIV-1 Infected Patients Undergoing a New Combination Antiretroviral Therapy Regimen. *BMC Med Inform Decis Mak*. 2011 Jun 14;11(1):40.
69. Di Giambenedetto S, **Prosperi M**, Fanti I, Bruzzone B, Paolucci S, Penco G, Meini G, Di Biagio A, Paolini E, Micheli V, Meraviglia P, Castelli P, Corsi P, Gonnelli A, Fabbiani M, Zazzi M, De Luca A; on behalf of the ARCA Collaborative Group. Update on emergence of HIV-1 resistance to antiretroviral drug classes in an Italian national database: 2007-2009. *Clin Microbiol Infect*. 2011 Sep;17(9):1352-5. doi: 10.1111/j.1469-0691.2011.03563.x.
70. **Prosperi MC**, Mackie N, Di Giambenedetto S, Zazzi M, Camacho R, Fanti I, Torti C, Sönnnerborg A, Kaiser R, Codofier FM, Van Laethem K, Bansi L, van de Vijver DA, Geretti AM, De Luca A; on behalf of the SEHERE consortium. Detection of drug resistance mutations at low plasma HIV-1 RNA load in a European multicentre cohort study. *J Antimicrob Chemother*. 2011; 66(8):1886-1896.
71. **Prosperi MC**, Ciccozzi M, Fanti I, Saladini F, Pecorari M, Borghi V, Di Giambenedetto S, Bruzzone B, Capetti A, Vivarelli A, Rusconi S, Re MC, Gismondo MR, Sighinolfi L, Gray RR, Salemi M, Zazzi M, De Luca A; on behalf of the ARCA collaborative group. A novel methodology for large-scale phylogeny partition. *Nat Commun*. 2011;2:321. doi: 10.1038/ncomms1325. Epub 2011 May 24.
72. **Prosperi MC**, Prosperi L, Bruselles A, Abbate I, Rozera G, Vincenti D, Solmone MC, Capobianchi MR, Ulivi G. Combinatorial analysis and algorithms for quasispecies reconstruction using next-generation sequencing. *BMC Bioinformatics*. 2011 Jan 5;12(1):5.
73. Fabbiani M, Di Giambenedetto S, Ragazzoni E, D'Etterre G, Parruti G, **Prosperi M**, Bracciale L, Cauda R, Navarra P, De Luca A. Darunavir/ritonavir and raltegravir coadministered in routine clinical practice: Potential role for an unexpected drug interaction. *Pharmacol Res*. 2011 Mar;63(3):249-53.
74. Di Giambenedetto S, Zileri Dal Verme L, Sali M, Farina S, Di Cristo V, Manzara S, De Luca A, Pignataro G, **Prosperi M**, Di Franco A, Gentiloni Silveri N, Delogu G, Cauda R, Fabbiani M, Fadda G. Clinical presentation, microbiological features and correlates of disease severity of 2009 pandemic influenza A (H1N1) infection. *Eur J Clin Microbiol Infect Dis*. 2011 Apr;30(4):541-9.
75. **Prosperi MC**, Rosen-Zvi M, Altmann A, Zazzi M, Di Giambenedetto S, Kaiser R, Schülter E, Struck D, Sloot P, van de Vijver DA, Vandamme AM, Sönnnerborg A; for the EuResist and Virolab study groups. Antiretroviral Therapy Optimisation without Genotype Resistance Testing: A Perspective on Treatment History Based Models. *PLoS One*. 2010 Oct 29;5(10):e13753.
76. **Prosperi MC**, De Luca A, Di Giambenedetto S, Bracciale L, Fabbiani M, Cauda R, Salemi M. The Threshold Bootstrap Clustering: A New Approach to Find Families or Transmission Clusters within Molecular Quasispecies. *PLoS One*. 2010 Oct 25;5(10):e13619.
77. **Prosperi MC**, Zazzi M, Punzi G, Monno L, Colao G, Corsi P, Di Giambenedetto S, Meini G, Ghisetti V, Bonora S, Pecorari M, Gismondo MR, Bagnarelli P, Carli T, De Luca A; ARCA Collaborative Group. Low rate of virological failure and maintenance of susceptibility to

- HIV-1 protease inhibitors with first-line lopinavir/ritonavir-based antiretroviral treatment in clinical practice. *J Med Virol.* 2010 Dec;82(12):1996-2003.
78. Zazzi M, Kaiser R, Sönnnerborg A, Struck D, Altmann A, **Prosperi M**, Rosen-Zvi M, Petroczi A, Peres Y, Schülter E, Boucher CA, Brun-Vezinet F, Harrigan PR, Morris L, Obermeier M, Perno CF, Phanuphak P, Pillay D, Shafer RW, Vandamme AM, van Laethem K, Wensing AM, Lengauer T, Incardona F. Prediction of response to antiretroviral therapy by human experts and by the EuResist data-driven expert system (the EVE study). *HIV Med.* 2011 Apr;12(4):211-8. doi: 10.1111/j.1468-1293.2010.00871.x. Epub 2010 Aug 19.
 79. **Prosperi MC**, Cozzi-Lepri A, Antinori A, Cassola G, Torti C, Ursitti MA, Pellizzer GP, Giacometti A, d'Arminio Monforte A, De Luca A; for the Icona; Foundation Study Group. Favourable evolution of virological and immunological profiles in treated and untreated patients in Italy in the period 1998-2008. *HIV Med.* 2011 Mar;12(3):174-82. doi: 10.1111/j.1468-1293.2010.00866.x.
 80. Frentz D, Boucher CA, Assel M, De Luca A, Fabbiani M, Incardona F, Libin P, Manca N, Müller V, O Nualláin B, Paredes R, **Prosperi M**, Quiros-Roldan E, Ruiz L, Sloat PM, Torti C, Vandamme AM, Van Laethem K, Zazzi M, van de Vijver DA. Comparison of HIV-1 genotypic resistance test interpretation systems in predicting virological outcomes over time. *PLoS One.* 2010 Jul 9;5(7):e11505.
 81. **Prosperi MC**, Bracciale L, Fabbiani M, Di Giambenedetto S, Razzolini F, Meini G, Colafigli M, Marzocchetti A, Cauda R, Zazzi M, De Luca A. Comparative determination of HIV-1 coreceptor tropism by Enhanced Sensitivity Trofile, gp120 V3-loop RNA and DNA genotyping. *Retrovirology.* 2010 Jun 30;7:56.
 82. **Prosperi MC**, Cozzi-Lepri A, Castagna A, Mussini C, Murri R, Giacometti A, Torti C, Costantini A, Narciso P, Ghinelli F, Antinori A, d'Arminio Monforte A. Incidence of Malignancies in HIV-Infected Patients and Prognostic Role of Current CD4 Cell Count: Evidence from a Large Italian Cohort Study. *Clin Infect Dis.* 2010 May 1;50(9):1316-21.
 83. Fabbiani M, Di Giambenedetto S, Ragazzoni E, Colafigli M, **Prosperi M**, Cauda R, Navarra P, De Luca A. Mid-dosing interval concentration of atazanavir and virological outcome in patients treated for HIV-1 infection. *HIV Med.* 2010 May;11(5):326-33.
 84. De Luca A, **Prosperi M** and Bracciale L. Resistance considerations in sequencing of antiretroviral therapy in low-middle income countries with currently available options. *Curr Opin HIV AIDS.* 2010 Jan;5(1):27-37.
 85. Menzo S, Vincenti D, Solmone M, **Prosperi M**, Bruxelles A, Abbate I, Rozera G, Capobianchi MR. Low-abundance drug resistance mutations: extending the HIV paradigm to hepatitis B virus. *J Infect Dis.* 2009 Dec 1;200(11):1798-9.
 86. Rozera G, Abbate I, Bruxelles A, Vlasi C, D'Offizi G, Narciso P, Chillemi G, **Prosperi M**, Ippolito G, Capobianchi MR. Archived HIV-1 minority variants detected by ultra-deep pyrosequencing in provirus may be fully replication competent. *AIDS.* 2009 Nov 27;23(18):2541-3.
 87. Marzocchetti A, Tompkins T, Clifford DB, Gandhi RT, Kesari S, Berger JR, Simpson DM, **Prosperi M**, De Luca A, Koralnik JJ. Determinants of survival in progressive multifocal leukoencephalopathy. *Neurology.* 2009 Nov 10;73(19):1551-8.
 88. Bruxelles A, Rozera G, Bartolini B, **Prosperi M**, Del Nonno F, Narciso P, Capobianchi MR, Abbate I. Use of massive parallel pyrosequencing for near full-length characterization of a unique HIV Type 1 BF recombinant associated with a fatal primary infection. *AIDS Res Hum Retroviruses.* 2009 Sep;25(9):937-42.
 89. Bracciale L, Fanti I, Di Giambenedetto S, Colafigli M, **Prosperi M**, Bacarelli A, Santangelo R, Cattani P, Cauda R, De Luca A. Predictors of successful genotype-guided antiretroviral therapy in treatment-experienced individuals over calendar years: A cohort study. *J Clin Virol.* 2009 Nov;46(3):290-4.
 90. Di Giambenedetto S, Torti C, **Prosperi M**, Manca N, Lapadula G, Paraninfo G, Ladisa N, Zazzi M, Trezzi M, Cicconi P, Corsi P, Nasta P, Cauda R, De Luca A; for the UCSC cohort, MASTER cohort and ARCA cohort. Effectiveness of Antiretroviral Regimens Containing Abacavir with Tenofovir in Treatment-Experienced Patients: Predictors of Virological Response and Drug Resistance Evolution in a Multi-Cohort Study. *Infection.* 2009 Oct;37(5):438-44.
 91. Zazzi M, **Prosperi M**, Vicenti I, Di Giambenedetto S, Callegaro A, Bruzzone B, Baldanti F, Gonnelli A, Boeri E, Paolini E, Rusconi S, Giacometti A, Maggiolo F, Menzo S, De Luca A; ARCA Collaborative Group. Rules-based HIV-1 genotypic resistance interpretation systems predict 8 week and 24 week virological antiretroviral treatment outcome and benefit from drug potency weighting. *J Antimicrob Chemother.* 2009 Sep;64(3):616-24.
 92. **Prosperi MC**, Altmann A, Rosen-Zvi M, Aharoni E, Borgulya G, Bazso F, Sönnnerborg A, Schülter E, Struck D, Ulivi G, Vandamme AM, Vercauteren J, Zazzi M; EuResist and Virolab study groups. Investigation of expert rule bases, logistic regression, and non-linear machine learning techniques for predicting response to antiretroviral treatment. *Antivir Ther.* 2009;14(3):433-42.
 93. Colafigli M, Di Giambenedetto S, Bracciale L, Fanti I, **Prosperi M**, Cauda R, De Luca A. Long-term follow-up of nevirapine-treated patients in a single-centre cohort. *HIV Med.* 2009 Sep;10(8):461-9.
 94. **Prosperi MC**, Fanti I, Ulivi G, Micarelli A, De Luca A, Zazzi M. Robust supervised and unsupervised statistical learning for HIV type 1 coreceptor usage analysis. *AIDS Res Hum Retroviruses.* 2009 Mar;25(3):305-14.
 95. Bracciale L, Santangelo R, Fanti I, **Prosperi M**, Colafigli M, Di Giambenedetto S, Marchetti S, Di Franco A, Cauda R, De Luca A. Are mutations in HIV type-1 reverse transcriptase 245 codon predictive of abacavir hypersensitivity reaction? *Antivir Ther.* 2009;14(1):99-101.

96. Bracciale L, Di Giambenedetto S, Colafigli M, La Torre G, **Prosperi M**, Santangelo R, Marchetti S, Cauda R, Fadda G, De Luca A. Virological suppression reduces clinical progression in patients with multiclass-resistant HIV type 1. *AIDS Res Hum Retroviruses*. 2009 Mar;25(3):261-7.
97. Rozera G, Abbate I, Bruselles A, Vlassi C, D'Offizi G, Narciso P, Chillemi G, **Prosperi M**, Ippolito G, Capobianchi MR. Massively parallel pyrosequencing highlights minority variants in the HIV-1 env quasiespecies deriving from lymphomonocyte sub-populations. *Retrovirology*. 2009 Feb 12; 6(1):15
98. Solmone M, Vincenti D, **Prosperi MC**, Bruselles A, Ippolito G, Capobianchi MR. Use of massively parallel ultradeep pyrosequencing to characterize the genetic diversity of hepatitis B virus in drug-resistant and drug-naive patients and to detect minor variants in reverse transcriptase and hepatitis B s antigen. *J Virol*. 2009 Feb;83(4):1718-26.
99. **Prosperi MC**, D'Autilia R, Incardona F, De Luca A, Zazzi M, Ulivi G. Stochastic modelling of genotypic drug-resistance for human immunodeficiency virus towards long-term combination therapy optimization. *Bioinformatics*. 2009 Apr 15;25(8):1040-7.
100. Altmann A, Rosen-Zvi M, **Prosperi M**, Aharoni E, Neuvirth H, Schülter E, Büch J, Struck D, Peres Y, Incardona F, Sönnnerborg A, Kaiser R, Zazzi M, Lengauer T. Comparison of classifier fusion methods for predicting response to anti HIV-1 therapy. *PLoS ONE*. 2008;3(10):e3470.
101. Rosen-Zvi M, Altmann A, **Prosperi M**, Aharoni E, Neuvirth H, Sönnnerborg A, Schülter E, Struck D, Peres Y, Incardona F, Kaiser R, Zazzi M, Lengauer T. Selecting anti-HIV therapies based on a variety of genomic and clinical factors. *Bioinformatics*. 2008 Jul 1;24(13):i399-406.
102. Gasparri A, and **Prosperi MCF**. A Bacterial Colony Growth Algorithm for Mobile Robot Localisation. *Autonomous Robot* 2008; 24(4):349-364. DOI: 10.1007/s10514-007-9076-1, ISSN: 0929-5593 (Print), 1573-7527 (Online).
103. De Luca A, Giambenedetto SD, Trotta MP, Colafigli M, **Prosperi M**, Ruiz L, Baxter J, Clevenbergh P, Cauda R, Perno CF, Antinori A. Improved interpretation of genotypic changes in the HIV-1 reverse transcriptase coding region that determine the virological response to didanosine. *J Infect Dis*. 2007 Dec 1;196(11):1645-53.
104. Di Giambenedetto S, Bracciale L, Colafigli M, Cattani P, Pinnetti C, Bacarelli A, **Prosperi M**, Fadda G, Cauda R, De Luca A. Declining prevalence of HIV-1 drug resistance in treatment-failing patients: a clinical cohort study. *Antivir Ther*. 2007;12(5):835-9.
105. Di Giambenedetto S, Bacarelli A, Pinnetti C, Colafigli M, **Prosperi M**, Gatti G, Cauda R, De Luca A. Genotypic resistance to lopinavir and fosamprenavir with or without ritonavir of clinical isolates from patients failing protease inhibitors-containing HAART regimens: prevalence and predictors. *Scand J Infect Dis*. 2007;39(9):813-8.

Book chapters

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