

Nicola Segata

Ph.D.

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Curriculum Vitae - January 21, 2017

Personal Information

birth date February 15, 1982.
nationality Italian.
research interests My research interests are in the field of computational biology and experimental meta'omics and include microbial and comparative genomics, computational meta'omics, human microbiome studies, host-microbe interaction, and pathogen-microbiome interaction.

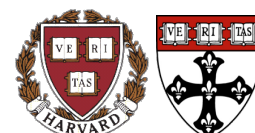
Current position

Assistant Professor and Principal Investigator, *Laboratory of Computational Metagenomics, Centre for Integrative Biology (CIBIO)*, University of Trento, Italy.
<http://segatalab.cibio.unitn.it>



Past research positions

Jul 2010-
Oct 2012 **Postdoctoral fellow**, *Harvard School of Public Health (HSPH)*, Biostatistics department, Harvard University, Boston, MA, USA.
mentor prof. Curtis Huttenhower.

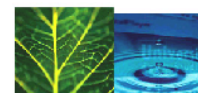


Jan 2010-
Jun 2010 **Postdoctoral fellow**, *Laboratory of Microbial Genomics, Centre for Integrative Biology (CIBIO)*, University of Trento, Italy.
mentor prof. Olivier Jousson.



Education

- 2009 **PhD Dissertation**, *Department of Information Engineering and Computer Science*, University of Trento, Italy.
Defence of the thesis "Local approaches for fast, scalable and accurate learning with kernels" under the supervision of prof. Enrico Blanzieri. Committee: prof. Marco Gori (University of Siena), prof. Chih-Jen Lin (National Taiwan University) and prof. Enrico Blanzieri (University of Trento).
- 2006 **Master Degree in Computer Science**, *University of Trento*, Grade 110/110 cum laude.
Discussion of the thesis "Beta-binders and π -calculus approaches for quantitative modelling of biological pathways", under the supervision of prof. C. Priami and prof. E. Blanzieri.



- 2004 **Bachelor Degree in Computer Science**, *University of Trento*, Grade 110/110 cum laude.
Discussion of the thesis “Sistemi di monitoraggio video: il problema dello sfondo in presenza di variazioni globali di illuminazione”, under the supervision of prof. C. Priami and dott. S. Messelodi.

Awards

- 2015 **LEO Pharma Research Foundation Gold Award 2015 (1M DKK, 134k EUR)** awarded by LEO Pharma in association with the European Society for Dermatology. The award is “given to talented and committed young researchers in recognition of their exceptional contribution to science”.
- 2012 **Travel fellowship** awarded by ISCB with grant funds obtained from the NSF-National Science Foundation Bio-Directorate.
- 2012 **IHMC-2012 travel award** from the National Institutes of Health (NIH).
- 2011 **PQG travel fellowship award** from the Program in Quantitative Genomics at the Harvard School of Public Health.
- 2011 **Travel fellowship award** from the International Society for Computational Biology (ISCB) funded by DOE-Department of Energy Office of Science, NSF-National Science Foundation Bio-Directorate, and NIH NIMGS-National Institute of General Medical Sciences.
- 2009 **Best Paper Award** at the 6th International Conference on Machine Learning and Data Mining, for the paper: Nicola Segata, Enrico Blanzieri: “Fast local support vector machines for large datasets”.

Research visits

- 2008 **University College Dublin, Dublin (Ireland)**, three months research visit.
Case-Based Reasoning and Bioinformatics research under the supervision of prof. P. Cunningham.
- 2004 **ITC-irst, TeV (Tecnologie della Visione) division, Trento (Italy)**, stage period.
Research in computer vision for video-surveillance under the supervision of dott. S. Messelodi.
- 2003 **Technical University of Denmark, Lyngby, Copenhagen (Denmark)**, Erasmus student.

Teaching

- 2014-2015 “Introduction to Metagenomics”, PhD Course, International PhD Program in Biomolecular Sciences, University of Trento, Trento, Italy
- 2013-2015 “High-throughput methodologies 2: data analysis”, Master Degree in Cellular and Molecular Biotechnology, University of Trento, Trento, Italy
- Spring 2010 Assistant teacher for the course “Informatica e Principi di Programmazione”, Bachelor Degree in Cognitive Science, University of Trento, Rovereto, Italy.
- Fall 2009 Assistant teacher for the course “Data Mining for Biological Data” (teaching language English), Master Degree in Computer Science - Bioinformatics specialization, University of Trento, Trento, Italy
- Fall 2009 Teacher for the additional course “Informatica e Principi di Programmazione”, Bachelor Degree in Cognitive Science, University of Trento, Rovereto, Italy.

Grants

- 2017-2022 H2020 ERC Starting Investigator grant (PI) (1,500,000 €)
- 2016-2018 Eklund Foundation (Supervisor) (40,000 €)
- 2017-2019 ITI International Team for Implantology Foundation (Supervisor) (40,600 €)

- 2013-2016 Futuro in Ricerca 2013 (MIUR) (PI) (348,000 €)
- 2015-2017 LEO Pharma Research Foundation Gold Prize 2015 (PI) (134,000 €)
- 2016-2018 Marie Skłodowska-Curie Individual Fellowships (Scientific Coordinator for the Fellowship to Edoardo Pasolli) (180,277 €)
- 2016-2018 Marie Skłodowska-Curie Individual Fellowships (Scientific Coordinator for the Fellowship to Federica Pinto) (180,277 €)
- 2016-2018 SIdP (PI) (30,000 €)
- 2016-2018 Lega Italiana per la Lotta contro i Tumori (PI) (72,000 €)
- 2015-2016 Italian Cystic Fibrosis foundation (External Collaboration) (24,000 €)
- 2013-2017 FP7 Marie Curie Career Integration Grant (PI) (100,000 €)
- 2013-2017 CARITRO - Giovani Ricercatori 2013 (PI) (213,000 €)
- 2013-2015 Terme di Comano - Skin Microbiome (PI) (78,000 €)
- 2014 UNITN award for reaching the final stage of the ERC Starting Grant (PI)(10,000 €)
- 2010-2012 Postdoctoral fellowship at the Harvard School of Public Health, Biostatistics Department, Huttenhower lab, Harvard University, Boston.
- 2010 Postdoctoral research grant at the Laboratory of Microbial Genomics, Centre for Integrative Biology (CIBIO), University of Trento, Italy.
- 2006–2009 PhD research grant at the Department of Information Engineering and Computer Science (XXII cycle), University of Trento, Italy.

Talks, Invited Talks, Tutorials, and Seminars

- Dec 03, 2016 **The skin microbiome** Invited Seminar at “The second school of Psoriasis”, Naples, Italy
- Dec 02, 2016 **Strain-level metagenomics for pathogen detection and profiling** Invited Keynote Speaker at “One Health Symposium: Focus on Genomics of Pathogenic *Escherichia coli*”, Utrecht, The Netherlands
- Nov 17, 2016 **The skin microbiome in psoriasis** Invited Speaker at SIDAPA, Verona, Italy
- Oct 20, 2016 **Studying MRSA in cystic fibrosis patients with an integrated metagenomic approach** Invited Seminar at the Meyer Hospital, Florence, Italy
- Oct 18, 2016 **Strain-level population structure and genetic diversity of the human microbiome** Invited Plenary Seminar at the San Raffaele Scientific Institute, Milan, Italy
- Oct 05, 2016 **Computational challenges in large-scale metagenomics** Invited Keynote talk at the WIVACE 2016 Conference, Salerno, Italy
- Sep 30, 2016 **Perspectives for studying the oral microbiome with strain-level resolution** Invited Seminar at the Institute of Odontology of the University of Gothenburg, Gothenburg, Sweden
- Sep 24, 2016 **Our research on the human microbiome** Invited Talk at the “Third Microbiota workshop”, Comano, Italy
- Sep 09, 2016 **The skin microbiome: a potential target for cosmeceutical approaches?** Invited Talk at the “Prime Giornate di Medicina Estetica in Trentino Alto Adige”, Trento, Italy
- Sep 07, 2016 **Strain-level population metagenomics: personalization, transmission and biogeography of the human microbiome.** Invited Talk at the “Second European Summer school on Nutrigenomics”, Camerino, Italy
- Jul 06, 2016 **Uncovering the diversity of NTM: the computational (meta)genomic approach.** Invited Keynote Talk at “The 37th Annual Congress of the European Society of Mycobacteriology”, Catania, Italy

- Jul 01, 2016 **Strain-level microbial epidemiology and population genomics from shotgun metagenomics.** Invited Talk at “The Barcelona Debates on the Human Microbiome: From Microbes to Medicines”, Barcelona, Spain
- Jun 23, 2016 **Metagenomic analysis of the human microbiome with strain-level resolution.** Invited Keynote talk at the Joint UniMIB-UniSR PhD Course on “The Gut Microbiota Impact on the Immune System: Implications for Autoimmunity and Cancer”, Milan, Italy
- Jun 17, 2016 **Strain-level microbiome profiling and “personalized” intestinal microbes.** Invited Keynote talk at the Third Paris Metagenomic Analysis Group, Paris, France
- Mar 24, 2016 **Shotgun metagenomics for studying oral and intestinal microbiomes at the strain-level.** Invited Seminar at the Center for Biomedicine, EURAC, Bolzano, Italy
- Feb 23, 2016 **The skin microbiome.** Invited Seminar at “LEO Pharma Italy”, Rome, Italy
- Nov 20, 2015 **The human microbiome seen through shotgun metagenomics.** Invited Keynote Seminar at “Science Day 2015”, University of Sassari, Sassari, Italy
- Nov 06, 2015 **Dieta, salute e microorganismi intestinali.** Invited talk at “Pensa Trasversale”, Rovereto, Italy
- Oct 19, 2015 **Strain-level microbiome profiling for comparative (meta)genomics.** Invited Keynote talk at the “2nd Theodor Escherich Symposium on Medical Microbiome Research”, Graz, Austria
- Oct 08, 2015 **Strain-level microbial comparative genomics using shotgun metagenomics.** Invited Keynote talk at “RECOMB Comparative Genomics 2015”, Frankfurt, Germany
- Oct 03, 2015 **Trasmissione, personalizzazione, e modulazione del microbiota umano.** Invited talk at the “Second Microbiota workshop”, Comano Terme, Italy
- Sep 10, 2015 **Metagenomics of the Skin: Results and Perspectives on our Microbial Interface.** Gold Prize Winner talk at the “45th Annual Meeting of the European Society for Dermatological Research”, Rotterdam, The Netherlands
- Jun 06, 2015 **Strain-level population genomics of microbial organisms from shotgun metagenomics.** Invited talk at the “Symbiomes: Systems Biology of Host-Microbiome Interactions” conference, Pulstuk, Poland
- May 12, 2015 **Gut microbiota: The new world inside the human body.** Invited talk at the “Neurogenetics and genetics of the enteric nervous system” conference, Bologna, Italy
- Apr 16, 2015 **Metagenomic approaches for microbial epidemiology with strain-level resolution.** Invited talk at the “Parassitome workshop”, Rome, Italy
- Apr 01, 2015 **Pangenome-based, meta’omic analysis highlights association of E. coli accessory gene content with risk of necrotizing enterocolitis in a cohort of pre-term infants.** Talk at the 5th International Human Microbiome Congress - IHMC Congress, Luxembourg City, Luxembourg
- Mar 19, 2015 **Next generation human microbiome research with computational shotgun metagenomics.** Invited seminar at the Institute of Biomembranes and Bioenergetics of the National Research Council, Bari, Italy
- Mar 05, 2015 **Computational shotgun metagenomics for high precision microbiome research.** Invited seminar at “New frontiers in Systems Biology” day for the PhD School in “Complex Systems for Life Sciences”, Turin, Italy
- Sep 06, 2014 **Machine learning challenges in computational meta’omics.** Invited keynote talk at “Eighth International Workshop on Machine Learning in Systems Biology”, Strasbourg, France
- Jun 27, 2014 **Theory and practical tutorial on shotgun metagenomic sequencing.** Invited session at “WebValley 2014”, San Lorenzo in Banale, Italy
- Jun 26, 2014 **Theory and practical tutorial on 16S sequencing.** Invited session at “WebValley 2014”, San Lorenzo in Banale, Italy

- Jun 24, 2014 **Approcci metagenomici per lo studio del microbiota umano.** Invited Talk at “Microbiota come genotipo esteso”, Cortona, Italy
- Jun 11, 2014 **Strain-level microbiome characterization with shotgun metagenomics.** Invited Talk at “SocBiN Bioinformatics 2014”, Oslo, Norway
- Mar 17, 2014 **Metagenomic Sequencing and Data Analysis in Class: The experience in the Master of Biotechnology at the University of Trento.** Invited Talk at “Assessment of training methods in NGS data analysis” COST Action BM1006 (SeqAhead), Instituto Gulbenkian de Ciência, Oeiras, Portugal
- Feb 15, 2014 **The human microbiome in health and disease.** Invited Talk at the “Microbiota”, Trento, IT
- Oct 28, 2013 **Computational shotgun metagenomics for microbiome studies.** Invited Talk at the “8th CeBiTec Symposium: The Genomics Revolution and its Impact on Future Biotechnology”, Bielefeld University, Bielefeld, DE
- Jul 04, 2013 **Computational shotgun metagenomics for human microbiome studies.** Seminar at University of Parma, Parma, Italy
- Jun 17, 2013 **Computational Marker-based Shotgun Metagenomics for Accurate Microbiome Studies.** “Next Generation Sequencing Data Congress”, CBI Conference Centre, London, UK
- May 12, 2013 **Automating and improving taxonomic assignment with a high-resolution microbial phylogeny for microbiome studies.** Cell Symposia: Microbiome and Host Health, Lisbon, Portugal
- Mar 13, 2013 **Biogeography and diversity of the human microbiome characterized by shotgun metagenomics.** “Symbiomes: systems metagenomics of host microbe interactions”, Fondazione Edmund Mach, San Michele, IT
- Nov 23, 2012 **Integrative computational methods for shotgun metagenomics.** “With a little help from your friends: tools and strategies for analysing microbiome sequence data”, Glasgow Polyomics and University of Glasgow, Glasgow, UK
- Oct 26, 2012 **Computational shotgun metagenomics and the healthy human microbiome.** CIBIO seminar, Trento, Italy
- Oct 08, 2012 **Computational methods for shotgun metagenomics.** Bertinoro Computational Biology 2012, Bertinoro, Italy
- Jul 16, 2012 **Fast and accurate metagenomic profiling of microbial community composition using unique clade-specific marker genes.** 20th Annual International Conference on Intelligent Systems for Molecular Biology, Long Beach, CA, USA
- Sep 22, 2011 **Microbial community function and biomarker discovery in the human microbiome.** Beyond the Genome 2011, Washington DC, USA
- Jul 17, 2011 **Metagenomic biomarker discovery and the human microbiome.** 19th Annual International Conference on Intelligent Systems for Molecular Biology, Vienna, Austria
- Apr 15, 2011 **Metagenomic biomarker discovery and the human microbiome.** First Annual PQG/Interdisciplinary Training Grant Retreat. Harvard School of Public Health, Boston, MA, USA
- Mar 11, 2011 **Tutorial on LEfSe and HUMAnN.** DPWG Bioinformatics Tutorials Sessions, International Human Microbiome Congress, Vancouver, BC, Canada
- Mar 01, 2011 **Metagenomic biomarker discovery and the human microbiome.** Program in Quantitative Genomics (PQG): Working Group Series. Harvard School of Public Health, Boston, MA, USA
- Feb 23, 2011 **Metagenomic biomarker discovery and the human microbiome.** Seminar Series: The Microbial Systems (and Beyond) Seminar. Department of Civil & Environmental Engineering, Massachusetts Institute of Technology (MIT), Boston, MA, USA
- Dec 15, 2010 **Metagenomic biomarker discovery.** Department of Information Engineering and Computer Science, University of Trento, Italy.

- Feb 19, 2010 **Local machine learning approaches and process algebras for computational systems biology.** Department of Biostatistics, Harvard School of Public Health, Boston, MA, USA.
- Jul 23, 2009 **A scalable noise reduction technique for large case-based systems.** 8th International Conference on Case-Based Reasoning, Seattle, USA.
- Jun 11, 2009 **Local kernel machines.** Invited Seminar at the "Instance-Based Learning" doctoral course at DISI, Trento, Italy.
- May 19, 2009 **Empirical assessment of classification accuracy of Local SVM.** 19th Annual Belgian-Dutch Conference on Machine Learning, Tilburg, Belgium.
- Sep 06, 2005 **A Kalman filter based background updating algorithm robust to sharp illumination changes.** 13th International Conference on Image Analysis and Processing, Cagliari, Italy

Thesis supervisor

- 2016 **Moreno Zolfo.** Identification, Discovery and Characterisation of Viruses in the Human Microbiome
- 2016 **Pamela Ferretti.** Improving the reconstruction of bacterial genomes and metagenomes by combining short- and long-read sequencing technologies
- 2016 **Federico Taverna.** Overcoming the curse of compositionality with a novel approach for biomarker discovery in Metagenomics
- 2015 **Serena Manara.** Design and validation of a metatranscriptomic protocol for in-vivo gene expression profiling of lower airways and intestinal bacterial strains
- 2015 **Calogero Zarbo.** A Deep Learning predictive framework for Metagenomics based on microbiome functional potential profiles
A computational meta-analysis of Blastocystis parasites in the human gut microbiome from shotgun metagenomic data
PanPhlAn: Strain-level Characterization of Microbes from Complex Metagenomic Samples
- 2015 **Francesco Beghini.** A computational meta-analysis of Blastocystis parasites in the human gut microbiome from shotgun metagenomic data
PanPhlAn: Strain-level Characterization of Microbes from Complex Metagenomic Samples
- 2015 **Thomas Tolio.** PanPhlAn: Strain-level Characterization of Microbes from Complex Metagenomic Samples
- 2014 **Francesco Asnicar.** PhyloPhlAn2 and GraPhlAn: novel reconstruction and visualization tools for large-scale whole-genome phylogenomics
- 2014 **Moreno Zolfo.** A computational metagenomic pipeline for cultivation-free microbial strain typing
- 2014 **Pamela Ferretti.** Empirical evaluation of DNA sequence assemblers and genome reconstruction of novel clinically relevant pathogen strains
- 2014 **Tiziana Gasperetti.** Bioinformatic approaches to study the evolution of visual opsin genes on the Drosophila phylogeny
- 2013 **Temesgen Dadi.** An integrative kernel-based machine learning framework for accurate microbiome studies

Editorial, Reviewer, and Scientific Committee Activity

- 2016-now Member of the International Scientific Committee of the Biocodex Microbiota Foundation
- 2015-now Editor for mSystems by ASM
- 2015-now Editor for Frontiers in Marine Science and Microbiology (Microbial Symbioses)
- 2014-now Associate Editor for BMC Nutrition

2014-now Invited Editor for mBio
2011-now Reviewer for the following journals in the last 5 years: Briefings in Bioinformatics, Nature Microbiology, Scientific Data, Gut, Genome Medicine, FEMS Microbiology Reviews, Scientific Reports, Genome Biology, Current Biology, Alimentary Pharmacology & Therapeutics, Proteomics, Reviewer for Nature Methods, Nature Communications, Nucleic Acid Research, PLoS Computational Biology, BMC Bioinformatics, BMC Microbiology, International Journal of Food Microbiology, BMC Evolutionary Biology, for ISME journal, PLoS One, Genome Research, Bioinformatics, Genome Biology

Publications

H-index 23

citations >6500

International Journal Papers (titles are web links)

- [1] Francesco Asnicar, Serena Manara, Moreno Zolfo, Duy Tin Truong, Matthias Scholz, Federica Armanini, Pamela Ferretti, Valentina Gorfer, Anna Pedrotti, Adrian Tett, and Nicola Segata. Studying vertical microbiome transmission from mothers to infants by strain-level metagenomic profiling. **mSystems**, in press, 2017.
- [2] Duy Tin Truong, Adrian Tett, Edoardo Pasolli, Curtis Huttenhower, and Nicola Segata. Microbial strain-level population structure and genetic diversity from metagenomes. **Genome Research**, [I.F. 11.28], accepted, 2017.
- [3] Claudio Donati, Moreno Zolfo, Davide Albanese, Duy Tin Truong, Francesco Asnicar, Valerio Iebba, Duccio Cavalieri, Olivier Jousson, Carlotta De Filippo, Curtis Huttenhower, and Nicola Segata. Uncovering oral Neisseria tropism and persistence using metagenomic sequencing. **Nature Microbiology**, (16070), 2016.
- [4] Pamela Ferretti, Stefania Farina, Mario Cristofoloni, Giampiero Girolomoni, Adrian Tett, and Nicola Segata. Experimental metagenomics and ribosomal profiling of the human skin microbiome. **Experimental Dermatology**, [I.F. 2.67], in press, 2016.
- [5] Edoardo Pasolli, Tin Truong, Faizan Malik, Levi Waldron, and Nicola Segata. Machine learning meta-analysis of large metagenomic datasets : tools and biological insights. **PLoS Computational Biology**, [I.F. 4.62], 12(7):e1004977, 2016.
- [6] Matthias Scholz*, Doyle Ward*, Thomas Tolio, Moreno Zolfo, Francesco Asnicar, Duy Tin Truong, Edoardo Pasolli, Adrian Tett, Ardythe Morrow, and Nicola Segata. Strain-level microbial epidemiology and population genomics from shotgun metagenomics. **Nature Methods**, [I.F. 32.1], 13(5):435–438, 2016.
- [7] Nicola Segata, Francesco Baldini, Julien Pompon, Wendy S Garrett, Duy Tin Truong, Rock K Dabiré, Abdoulaye Diabaté, Elena A Levashina, and Flaminia Catteruccia. The reproductive tracts of two malaria vectors are populated by a core microbiome and by gender- and swarm-enriched microbial biomarkers. **Scientific Reports**, [I.F. 5.6], 6(24207):1–10, 2016.
- [8] Doyle Ward, Matthias Scholz, Moreno Zolfo, Diana H Taft, Kurt R Schibler, Adrian Tett, Nicola Segata*, and Ardythe L Morrow*. Metagenomic sequencing with strain-level resolution implicates uropathogenic *E. coli* in necrotizing enterocolitis and death in preterm infants. **Cell Reports**, [I.F. 8.4], 14:1–13, 2016.
- [9] Moreno Zolfo, Adrian Tett, Olivier Jousson, Claudio Donati, and Nicola Segata. MetaMLST: multi-locus strain-level bacterial typing from metagenomic samples. **Nucleic Acid Research**, (in press), 2016.
- [10] Duy Tin Truong, Eric Franzosa, Timothy Tickle, Matthias Scholz, George Weingart, Edoardo Pasolli, Adrian Tett, Curtis Huttenhower, and Nicola Segata. MetaPhlan2 for enhanced metagenomic taxonomic profiling. **Nature Methods**, [I.F. 32.07], 12(10):902–903, oct 2015.
- [11] Christian Milani, Gabriele Andrea Lugli, Sabrina Duranti, Francesca Turroni, Leonardo Mancabelli, Chiara Ferrario, Marta Mangifesta, Arancha González, Alice Viappiani, Matthias Scholz, Stefania Arioli, Borja Sanchez, Jonathan Lane, Doyle V Ward, Rita Hickey, Diego Mora, Nicola Segata, Abelardo Margolles,

- Douwe Van Sinderen, and Marco Ventura. Bifidobacteria exhibit social behavior through carbohydrate resource sharing in the gut. **Scientific Reports**, 5(15782), sep 2015.
- [12] Nicola Segata. Gut Microbiome: Westernization and the Disappearance of Intestinal Diversity. **Current Biology**, [I.F. 9.57], 25(14):R611–R613, aug 2015.
- [13] James Kaminski, Molly K Gibson, Eric A Franzosa, Nicola Segata, Gautam Dantas, and Curtis Huttenhower. High-specificity targeted functional profiling in microbial communities with ShortBRED. **PLoS computational biology**, [I.F. 4.62], accepted, jun 2015.
- [14] Francesco Asnicar, George Weingart, Timothy L. Tickle, Curtis Huttenhower, and Nicola Segata. Compact graphical representation of phylogenetic data and metadata with GraPhlAn. **PeerJ**, 3:e1029, 2015.
- [15] Ana R. Fusco da Costa, Tarcisio Fedrizzi, Maria L Lopes, Monica Pecorari, Wana L Oliveira da Costa, Elisabetta Giacobazzi, Jeann R da Costa Bahia, Veronica De Sanctis, Karla V Batista Lima, Roberto Bertorelli, Antonella Grottola, Anna Fabio, Pamela Ferretti, Francesca Di Leva, Giulia Fregni Serpini, Sara Tagliazucchi, Fabio Rumpianesi, Olivier Jousson, Nicola Segata, and Enrico Tortoli. Characterization of 17 strains belonging to the *Mycobacterium simiae* complex and description of *Mycobacterium paraense* sp. nov. **International Journal of Systematic and Evolutionary Microbiology**, 2015.
- [16] Christian Milani, Leonardo Mancabelli, Gabriele Andrea Lugli, Sabrina Duranti, Francesca Turroni, Chiara Ferrario, Marta Mangifesta, Alice Viappiani, Pamela Ferretti, Valentina Gorfer, Adrian Tett, Nicola Segata, Sinderen van Douwe, and Marco Ventura. Exploring vertical transmission of bifidobacteria from mother to child. **Applied and environmental microbiology**, [I.F. 3.67], pages 02037–15, 2015.
- [17] Francesco Baldini*, Nicola Segata*, Julien Pompon*, Roch Dabiré, Abdoulaye Diabaté, Elena Levashina[^], and Flaminia Catteruccia[^]. Evidence of natural *Wolbachia* infections in field populations of *Anopheles gambiae*. **Nature Communications**, [I.F. 10.74], 5, jun 2014.
- [18] Eric A Franzosa, Xochitl C Morgan, Nicola Segata, Levi Waldron, Joshua Reyes, Ashlee M Earl, Georgia Giannoukos, Matthew Boylan, Dawn M Ciulla, Dirk Gevers, Jacques Izard, Wendy S Garrett, Andrew T Chan, and Curtis Huttenhower. Relating the metatranscriptome and metagenome of the human gut. **Proceedings of the National Academy of Sciences of the United States of America**, [I.F. 9.81], 111(22), jun 2014.
- [19] Michelle G Rooks, Patrick Veiga, LH Wardwell-Scott, Timothy L Tickle, Nicola Segata, Carey A Gallini, Chloé Beal, Monia Michaud, Johan ET Van Hylckama-Vlieg, Sonia A Ballal, Xochitl C Morgan, Jonathan N Glickman, Dirk Gevers, Curtis Huttenhower, and Wendy S Garrett. Gut microbiome composition and function in experimental colitis during active disease and treatment-induced remission. **The ISME journal**, [I.F. 8.95], pages 1–15, feb 2014.
- [20] Katherine Huang, Arthur Brady, Anup Mahurkar, Owen White, Dirk Gevers, Curtis Huttenhower, and Nicola Segata. MetaRef: a pan-genomic database for comparative and community microbial genomics. **Nucleic Acid Research**, [I.F. 8.80], jan 2014.
- [21] Erik Dassi, Annalisa Ballarini, Giuseppina Covello, HTM CMB2013, Alessandro Quattrone, Olivier Jousson, Veronica De Sanctis, Roberto Bertorelli, Michela A Denti, and Nicola Segata. Enhanced microbial diversity in the saliva microbiome induced by short-term probiotic intake revealed by 16S rRNA sequencing on the IonTorrent PGM platform. **Journal of Biotechnology**, [I.F. 3.18], 190:30 – 39, 2014.
- [22] Christian Milani, Gabriele Lugli, Francesca Turroni, Leonardo Mancabelli, Sabrina Duranti, Alice Viappiani, Marta Mangifesta, Nicola Segata, Douwe van Sinderen, and Marco Ventura. Evaluation of bifidobacterial community composition in the human gut by means of an ITS-metagenomics protocol. **FEMS Microbiology Ecology**, [I.F. 3.88], 90(2), 2014.
- [23] Jose U Scher, Andrew Sczesnak, Randy S Longman, Nicola Segata, Carles Ubeda, Craig Bielski, Eric G Pamer, Steven Abramson, Curtis Huttenhower, and Dan Littman. Expansion of intestinal *Prevotella copri* correlates with enhanced susceptibility to arthritis. **eLIFE**, [I.F. 8,52], 2:e01202, oct 2013.
- [24] Nicola Segata, Daniela Börnigen, Xochitl Morgan, and Curtis Huttenhower. PhyloPhlAn is a new method for improved phylogenetic and taxonomic placement of microbes. **Nature Communications**, [I.F. 10.01], 4:2304, jul 2013.
- [25] Timothy L. Tickle, Nicola Segata, Levi Waldron, and Curtis Huttenhower. Two-stage microbial community experimental design. **The ISME Journal**, [I.F. 8.95], pages 1–10, jun 2013.

- [26] [Nicola Segata](#), Daniela Boernigen, Timothy L Tickle, Xochitl Morgan, Wendy S Garrett, and Curtis Huttenhower. Computational meta'omics for microbial community studies. **Molecular Systems Biology**, [Recommended as being of special significance in its field by Jack Gilbert from the F1000 Faculty I.F. 11.34], 9(666):1–15, may 2013.
- [27] [Nicola Segata](#), Annalisa Ballarini, and Olivier Jousson. Genome sequence of *Pseudomonas aeruginosa* PA45, a highly virulent strain isolated from a patient with bloodstream infection. **Genome Announcements**, 1(3), mar 2013.
- [28] Omry Koren, Dan Knights, Antonio Gonzales, Levi Waldron, [Nicola Segata](#), Rob Knight, Curtis Huttenhower, and Ruth E. Ley. A Guide to Enterotypes across the Human Body: Meta- Analysis of Microbial Community Structures in Human Microbiome Datasets. **PLoS computational biology**, [I.F. 5.22], 9(1):e1002863, jan 2013.
- [29] Xochitl Morgan, [Nicola Segata](#), and Curtis Huttenhower. Biodiversity and Functional Genomics in the Human Microbiome. **Trends in Genetics**, [I.F. 9.77], 20(1):51–58, jan 2013.
- [30] Annalisa Ballarini*, [Nicola Segata](#)*, Curtis Huttenhower[^], and Olivier Jousson[^]. Simultaneous quantification of multiple bacteria by the BactoChip microarray designed to target species-specific marker genes. **Plos One**, [I.F. 4.09], 8(2):e55763, 2013.
- [31] [Nicola Segata](#), Levi Waldron, Annalisa Ballarini, Vagheesh Narasimhan, Olivier Jousson, and Curtis Huttenhower. Metagenomic microbial community profiling using unique clade-specific marker genes. **Nature Methods**, [I.F. 19.27], 9:811–814, aug 2012.
- [32] [Nicola Segata](#), Susan Kinder Haake, Peter Mannon, Katherine P Lemon, Levi Waldron, Dirk Gevers, Curtis Huttenhower, and Jacques Izard. Composition of the Adult Digestive Tract Microbiome Based on Seven Mouth Surfaces, Tonsils, Throat and Stool Samples. **Genome Biology**, [article flagged as "Highly accessed", I.F. 6.89], 13(6):R42, jul 2012.
- [33] The Human Microbiome Consortium (including [Nicola Segata](#)). A Framework for Human Microbiome Research. **Nature**, [I.F. 36.28], 486(7402):215–221, jul 2012.
- [34] The Human Microbiome Consortium (including [Nicola Segata](#)). Structure, function and diversity of the healthy human microbiome. **Nature**, [I.F. 36.28], 486(7402):207–214, jul 2012.
- [35] Kjersti Aagaard, Kevin Riehle, Jun Ma, [Nicola Segata](#), Toni-Ann Mistretta, Cristian Coarfa, Sabeen Raza, Sean Rosenbaum, Ignatia Van Den Veyver, Aleksandar Milosavljevic, Dirk Gevers, Curtis Huttenhower, Joseph Petrosino, and James Versalovic. A Metagenomic Approach To Characterization Of The Vaginal Microbiome Signature In Pregnancy. **PLoS ONE**, [I.F. 4.09], 7(6):e36466, jun 2012.
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