

# Nicola Segata

Ph.D.

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Curriculum Vitae - February 14, 2019

## Personal Information

birth date February 15, 1982.  
nationality Italian.  
research interests I am working in the fields of human microbiome research and computational biology

## Current position

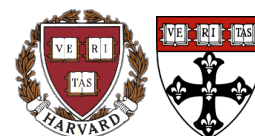
**Associate Professor and Principal Investigator**, *Laboratory of Computational Metagenomics, Centre for Integrative Biology (CIBIO)*, University of Trento, Italy.  
<http://segatalab.cibio.unitn.it>



## 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.

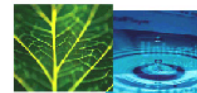
Defence of the thesis "Local approaches for fast, scalable and accurate learning with kernels" under the supervision of prof. Enrico Blanzieri. Committee: prof. Marco Gori (University of Siena), prof. Chih-Jen Lin (National Taiwan University) and prof. Enrico Blanzieri (University of Trento).

2006 **Master Degree in Computer Science**, *University of Trento*, Grade 110/110 cum laude.

Discussion of the thesis "Beta-binders and  $\pi$ -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.



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## Awards

- 2018 **Listed as one of the 98 researchrs in Italy as Highly Cited Researcher in 2018** by Clarivate Analytics and Web of Science.
- 2018 **Co-recipient of the H.G. Goldman Award** by the SIdP for the work by [Ghensi, Manghi, ..., Segata] on the oral microbiome in peri-implantitis.
- 2017 **Co-recipient of the Dr. Darwin award** by the Italian Society for Evolutionary Biology for the paper [Asnicar et al., mSystems 2016].
- 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”.

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## 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.

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## Teaching

- 2016-now “Computational Microbial Genomics”, Master Course, Master in Quantitative and Computational Biology, University of Trento, Trento, Italy
- 2014-now “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

- 2019-2024 **ONCOBIOME**. H2020 Better Health and care, economic growth and sustainable health systems H2020-SC1-BHC-2018-2020 Grant (Work Package Leader) (1,502,618 € to N.S.)
- 2019-2023 **MASTER**. H2020 Sustainable Food Security H2020-SFS-2018-2020 Grant (Work Package Leader) (509,950 € to N.S.)
- 2018-2020 NIH Sub-award from the Forsyth Institute (105,000 € to N.S.)
- 2018-2022 Italian Ministry of Health, “Ricerca Finalizzata” (Local PI) (90,000 € to N.S.)
- 2017-2022 **MetaPG**. H2020 ERC Starting Investigator grant (PI) (1,500,000 € to N.S.)
- 2016-2018 Eklund Foundation (Supervisor) (40,000 € to N.S.)
- 2017-2019 ITI International Team for Implantology Foundation (Supervisor) (40,600 € to N.S.)
- 2013-2016 Futuro in Ricerca 2013 (MIUR) (PI) (348,000 € to N.S.)
- 2015-2017 LEO Pharma Research Foundation Gold Prize 2015 (PI) (134,000 € to N.S.)
- 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 € to N.S.)
- 2016-2018 Lega Italiana per la Lotta contro i Tumori (PI) (72,000 € to N.S.)
- 2015-2016 Italian Cystic Fibrosis foundation (External Collaboration) (24,000 € to N.S.)
- 2013-2017 FP7 Marie Curie Career Integration Grant (PI) (100,000 € to N.S.)
- 2013-2017 CARITRO - Giovani Ricercatori 2013 (PI) (213,000 € to N.S.)
- 2013-2015 Terme di Comano - Skin Microbiome (PI) (78,000 € to N.S.)
- 2014 UNITN award for reaching the final stage of the ERC Starting Grant (PI)(10,000 € to N.S.)
- 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.

## (Co)organization of Conferences, Schools, and Workshops

- Oct 10, 2018 **Microbiota: tra ricerca di base e applicazioni cliniche** Coorganizer
- Sep 16-19, 2018 **EMBO|EMBL Symposium on "The Human Microbiome", Heidelberg, Germany** Coorganizer with Peer Bork and Manimozhayan Arumugam
- Oct 21, 2017 **Microbiota: le nuove frontiere della medicina** Coorganizer
- Sep 24, 2016 **Microbiota nella medicina del futuro** Coorganizer
- Oct 03, 2015 **Microbiota: salute, terme e alimentazione.** Coorganizer
- Sep 08-11, 2014 **Biology Summer School: Systems, Synthetic and Semantic Biology, Trento, Italy** Coorganizer
- Feb 15, 2014 **Il microbiota: interazione tra microrganismi e corpo umano.** Coorganizer

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## Talks, Invited Talks, Tutorials, and Seminars

- Jan 10, 2019 **Shotgun metagenomics for high-resolution microbiome studies.** Invited Talk at the “Host-microbial interactions: at the mucosal surfaces and in systemic organs”, Bern, Switzerland
- Oct 24, 2018 **Uncovering the hidden and strain-level diversity of the human microbiome with large scale shotgun metagenomics.** Invited Talk at the “Symposium: insights into the complexity of host microbiome interactions”, Copenhagen, Denmark
- Oct 23, 2018 **Large-scale strain-level comparative metagenomics.** Keynote Talk at the “Capacity-Building Workshop: Metagenomics in the Diagnostic Laboratory”, Groningen, Netherlands
- Oct 19, 2018 **Toward strain-resolved metagenomics for microbial epidemiology and pathogen monitoring.** Invited Talk at the “13th Annual Workshop of the National Reference Laboratories for E. coli in the EU”, Roma, Italy
- Oct 11, 2018 **The skin microbiota: from health to disease.** Invited Talk at the “2nd European Workshop on Skin immune mediated inflammatory diseases (SIMID)”, Verona, Italy
- Oct 06, 2018 **Vertical mother-to-infant microbiome transmission.** Invited Talk at “Microbiota 5”, Comano, Italy
- Jul 07, 2018 **Are we ready for cultivation-free microbial GWAS?.** Invited Talk at the 7th Sardinian International Summer School, Pula, Italy
- Jun 28, 2018 **Computational metagenomics for large-scale strain-resolved human microbiome studies.** Invited Keynote Talk at the 15th Annual Meeting of the Bioinformatics Italian Society, Turin, Italy
- Jun 27, 2018 **Career paths in computational biology.** Invited Talk at BITS2018-CAREER MORNING, Turin, Italy
- Jun 21, 2018 **Transmission and population biology of members of the human microbiome.** Invited Talk at “The Barcelona Debates on the Human Microbiome: From Microbes to Medicines”, Barcelona, Spain
- Jun 19, 2018 **The human microbiome at the resolution of single microbial strains.** Invited Talk at the Workshop “Metaorganisms, microbial biorefineries and human health”, Bologna, Italy
- Jun 11, 2018 **Shotgun metagenomics for large-scale strain-resolved profiling of the human microbiome.** Invited Seminar at the European Institute of Oncology (IEO), Milan, Italy
- Jun 08, 2018 **Large-scale strain-resolved comparative metagenomics for the human microbiome.** Invited Seminar at the Science for Life Laboratory (SciLifeLab), Stockholm, Sweden
- Apr 26, 2018 **Shotgun metagenomics for high-resolution microbiome studies.** Invited Talk at the International Workshop “The Gut-Brain-Microbiome connection in neuropsychiatric diseases of children and adults”, Genova, Italy
- Feb 26, 2018 **Host-microbiome symbiosis at the resolution of single microbial strains.** Invited Talk at DGMIM 2018, Hamburg, Germany
- Feb 22, 2018 **Strain and gene-level metagenomic profiling to unravel microbial risk factors for colorectal cancer.** Invited Talk at the Gustave Roussy Cancer Center, Paris, France
- Feb 15, 2018 **Biotechnological challenges in the study of the human microbiome.** Invited Talk at BioFacility Day 2018, Trento, Italy
- Dec 06, 2017 **Computational metagenomics for large-scale strain-resolved microbiome profiling.** Invited Seminar EMBL, Heidelberg, Germany
- Dec 01, 2017 **Studying the human microbiome and its connections with human health.** Invited Seminar at the University of Naples, Naples, Italy

- Nov 29, 2017 **Large-Scale Microbiome Meta-Analysis with Strain-Level Resolution.** Invited Talk at the “3rd Annual European Microbiome Conference”, London, United Kingdom
- Nov 14, 2017 **Shotgun metagenomics with strain-level resolution: tools and clinical applications.** Invited Talk at “AMCLI 2017”, Rimini, Italy
- Oct 21, 2017 **Le nuove frontiere nello studio del microbioma cutaneo, orale, e intestinale.** Invited Talk at the “Fourth Microbiota workshop”, Comano, Italy
- Oct 09, 2017 **Computational metagenomics for large-scale strain-resolved microbiome profiling.** Invited Keynote Talk at the “Workshop on Recent Computational Advances in Metagenomics (RCAM’17)”, Institut Pasteur, Paris, France
- Sep 13, 2017 **Shotgun metagenomics with strain-level resolution: tools and clinical applications.** Invited Talk at the “EMBL-EBI Industry Programme Workshop on The Human Microbiome: challenges and opportunities for novel therapeutics”, EMBL-EBI, London, United Kingdom
- Aug 29, 2017 **Microbial population structure and biogeography from metagenomic data.** Invited Keynote Talk at the “Evoluzione 2017” conference, Rome, Italy
- Jul 04, 2017 **Meta’omics for studying the human microbiome.** Invited Talk at the Course “A Field Trip into Metagenomics”, University of Milan-Bicocca, Milan, Italy
- Jun 28, 2017 **Shotgun metagenomics with strain-level resolution.** Invited Talk at the IRSAE Course “Integrating Omics Technologies into Aquatic Ecology: New perspectives in Metagenomic, Metabolomic and Bioinformatic applications in the study of aquatic ecosystems”, San Michele all’Adige, Italy
- Jun 20, 2017 **Large-scale strain-level population genomics from metagenomics.** Invited Talk at the “Workshop on Computational Metagenomics: Methods, Standards and Experimental Procedures”, Bari, Italy
- Jun 05, 2017 **Microbiome meta-analysis and microbial strain profiling using thousands of metagenomic samples.** Invited Plenary Talk at the ASM Microbe 2017, New Orleans, Louisiana, USA
- Jun 02, 2017 **Microbial strain-level population genomics from metagenomes.** Invited Talk at the “Population Genomics” session at ASM Microbe 2017, New Orleans, Louisiana, USA
- May 23, 2017 **High resolution metagenomic analysis to compare the human microbiome across geography and diseases.** Invited Seminar at the Istituto di Tecnologie Biomediche CNR, Segrate Milan, Italy
- May 13, 2017 **The skin microbiome in healthy and disease.** Invited Talk at SIME2017, Rome, Italy
- May 04, 2017 **Large-scale strain-level population genomics of the human microbiome.** Invited Seminar at Institute of Food Research (IFR), Norwich Research Park, Norwich, United Kingdom
- 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

- 2018 **Davide Bazzani.** Meta-analysis of non-human primate gut microbiomes and their overlap with the human microbiome
- 2017 **Stefano Marangoni.**
- 2017 **Giulia Corsi.** Comparative genomics of multiple strains of the pathogenic human parasite *Cryptosporidium parvum*
- 2017 **Francesco Beghini.** Association between tobacco exposure and the oral microbiome in the New York City HANES study
- 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
- 2015 **Francesco Beghini.** A computational meta-analysis of Blastocystis parasites in the human gut microbiome from shotgun metagenomic data
- 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

- 2018-now Member of the “Comitato Tecnico Sanitario” for the Italian Ministry of Health
- 2018-now Associate Editor for *Frontiers in Microbiology*
- 2017-now Associate Editor for *PLOS Computational Biology*
- 2016-now Member of the International Scientific Committee of the Biocodex Microbiota Foundation
- 2015-now Editor for *mSystems* by ASM
- 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: *Nature*, *Briefings in Bioinformatics*, *Nature Microbiology*, *Scientific Data*, *Gut*, *Genome Medicine*, *FEMS Microbiology Reviews*, *Scientific Reports*, *ELife*, *Current Biology*, *Alimentary Pharmacology & Therapeutics*, *Proteomics*, *Nature Methods*, *Nature Communications*, *Nature Biotechnology*, *Nucleic Acid Research*, *PLoS Computational Biology*, *BMC Bioinformatics*, *BMC Microbiology*, *International Journal of Food Microbiology*, *BMC Evolutionary Biology*, *ISME journal*, *PLoS One*, *Genome Research*, *Bioinformatics*, *Genome Biology*

## Publications

H-index 35  
# citations >14,000

### 10 most representative papers as last and corresponding author in the last three years

- [1] Edoardo Pasolli, Francesco Asnicar, Serena Manara, Moreno Zolfo, Nicolai Karcher, Federica Armanini, Francesco Beghini, Paolo Manghi, Adrian Tett, Paolo Ghensi, Maria Carmen Collado, Benjamin L Rice, Casey DuLong, Xochitl C Morgan, Christopher D Golden, Christopher Quince, Curtis Huttenhower, and Nicola Segata. Extensive unexplored human microbiome diversity revealed by over 150,000 genomes from metagenomes spanning age, geography, and lifestyle. **Cell**, [I.F. 31.40], 176(3):649–662, 2019.
- [2] Pamela Ferretti, Edoardo Pasolli, Adrian Tett, Francesco Asnicar, Valentina Gorfer, Sabina Fedi, Federica Armanini, Duy Tin Truong, Serena Manara, Moreno Zolfo, Francesco Beghini, Roberto Bertorelli, Veronica De Sanctis, Ilaria Bariletti, Rosarita Canto, Rosanna Clementi, Marina Cologna, Tiziana Crifò, Giuseppina Cusumano, Stefania Gottardi, Claudia Innamorati, Caterina Masè, Daniela Postai, Daniela Savoi, Sabrina Duranti, Gabriele A Andrea, Leonardo Mancabelli, Francesca Turrone, Chiara Ferrario, Christian Milani, Marta Mangifesta, Rosaria Anzalone, Alice Viappiani, Moran Yassour, Hera Vlamakis, Ramnik Xavier, Maria Carmen Collado, Omry Koren, Saverio Tateo, Massimo Soffiati, Anna Pedrotti, Marco Ventura, Curtis Huttenhower, Peer Bork, and Nicola Segata. Mother-to-infant microbial transmission from different body sites shapes the developing infant gut microbiome. **Cell Host & Microbe**, [I.F. 17.87], 24:133–145, 2018.
- [3] Serena Manara, Edoardo Pasolli, Daniela Dolce, Novella Ravenni, Silvia Campana, Federica Armanini, Francesco Asnicar, Alessio Mengoni, Luisa Galli, Carlotta Montagnani, Elisabetta Venturini, Omar Rota-Stabelli, Guido Grandi, Giovanni Taccetti, and Nicola Segata. Whole-genome epidemiology, characterization, and phylogenetic reconstruction of *Staphylococcus aureus* in a paediatric hospital. **Genome Medicine**, [I.F. 8.90], 10(82), 2018.
- [4] Christopher Quince, Jared T Simpson, Alan W Walker, Nicholas J Loman, and Nicola Segata. Shotgun

- metagenomics, from sampling to analysis. **Nature Biotechnology**, [I.F. 41.67], 35(9):833–844, oct 2017.
- [5] Francesco Beghini, Edoardo Pasolli, Duy Tin Truong, Lorenza Putignani, Simone Caccio, and Nicola Segata. Large-scale comparative metagenomics of Blastocystis, a common member of the human gut microbiome. **ISME Journal**, [I.F. 9.30], 11:2848–2863, sep 2017.
  - [6] 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], 27(4):626–638, jul 2017.
  - [7] Adrian Tett, Edoardo Pasolli, Stefania Farina, Duy Tin Truong, Francesco Asnicar, Moreno Zolfo, Francesco Beghini, Federica Armanini, Olivier Jousson, Veronica De Sanctis, Roberto Bertorelli, Giampiero Girolomoni, Mario Cristofolini, and Nicola Segata. Unexplored diversity and strain-level structure of the skin microbiome associated with psoriasis. **npj Biofilms and Microbiomes**, 3(14):1–23, 2017.
  - [8] 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**, [I.F. 14.17], (16070), 2016.
  - [9] 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.
  - [10] 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.

#### All Journal Papers (titles are web links)

- [1] Francesca De Filippis, Edoardo Pasolli, Adrian Tett, Sonia Tarallo, Alessio Naccarati, Maria De Angelis, Erasmo Neviani, Luca Cocolin, Marco Gobetti, Nicola Segata, and Danilo Ercolini. Distinct genetic and functional strains of human intestinal Prevotella copri are associated with different habitual diets. **Cell Host & Microbe**, [I.F. 17.87], In press, 2019.
- [2] Edoardo Pasolli, Francesco Asnicar, Serena Manara, Moreno Zolfo, Nicolai Karcher, Federica Armanini, Francesco Beghini, Paolo Manghi, Adrian Tett, Paolo Ghensi, Maria Carmen Collado, Benjamin L Rice, Casey DuLong, Xochitl C Morgan, Christopher D Golden, Christopher Quince, Curtis Huttenhower, and Nicola Segata. Extensive unexplored human microbiome diversity revealed by over 150,000 genomes from metagenomes spanning age, geography, and lifestyle. **Cell**, [I.F. 31.40], 176(3):649–662, 2019.
- [3] Renato Pedron, Alfonso Esposito, Irene Bianconi, Edoardo Pasolli, Adrian Tett, Francesco Asnicar, Mario Cristofolini, Nicola Segata, and Olivier Jousson. Microbiome Genomic and metagenomic insights into the microbial community of a thermal spring. **Microbiome**, in press, 2019.
- [4] Evan Bolyen, Jai Ram Rideout, Matthew R Dillon, Nicholas A Bokulich, Christian Abnet, Gabriel A Al-Ghalith, Harriet Alexander, Eric J Alm, Manimozhayan Arumugam, Francesco Asnicar, Yang Bai, Jordan E Bisanz, Kyle Bittinger, Asker Brejnrod, Colin J Brislawn, C Titus Brown, Benjamin J Callahan, Andrés Mauricio Caraballo-Rodríguez, John Chase, Emily Cope, Ricardo Da Silva, Pieter C Dorrestein, Gavin M Douglas, Daniel M Durall, Claire Duvallet, Christian F Edwardson, Madeleine Ernst, Mehrbod Estaki, Jennifer Fouquier, Julia M Gauglitz, Deanna L Gibson, Antonio Gonzalez, Kestrel Gorlick, Jiarong Guo, Benjamin Hillmann, Susan Holmes, Hannes Holste, Curtis Huttenhower, Gavin Huttley, Stefan Janssen, Alan K Jarmusch, Lingjing Jiang, Benjamin Kaehler, Kyo Bin Kang, Christopher R Keefe, Paul Keim, Scott T Kelley, Dan Knights, Irina Koester, Tomasz Kosciolk, Jordan Kreps, Morgan G Langille, Joslynn Lee, Ruth Ley, Yong-Xin Liu, Erikka Loftfield, Catherine Lozupone, Massoud Maher, Clarisse Marotz, Bryan Martin, Daniel McDonald, Lauren J McIver, Alexey V Melnik, Jessica L Metcalf, Sydney C Morgan, Jamie Morton, Ahmad Turan Naimy, Jose A Navas-Molina, Louis Felix Nothias, Stephanie B Orchanian, Talima Pearson, Samuel L Peoples, Daniel Petras, Mary Lai Preuss, Elmar Pruesse, Lasse Buur Rasmussen, Adam Rivers, II Michael S Robeson, Patrick Rosenthal, Nicola Segata, Michael Shaffer, Arron Shiffer, Rashmi Sinha, Se Jin Song, John R Spear, Austin D Swafford, Luke R Thompson, Pedro J Torres, Pauline Trinh, Anupriya Tripathi, Peter J Turnbaugh, Sabah UI-Hasan, Justin JJ van der Hoof, Fernando Vargas, Yoshiki Vázquez-Baeza, Emily Vogtmann, Max von Hippel, William Walters, Yunhu Wan, Mingxun Wang, Jonathan Warren, Kyle C Weber, Chase HD Williamson,

- Amy D Willis, Zhenjiang Zech Xu, Jesse R Zaneveld, Yilong Zhang, Rob Knight, and J Gregory Caporaso. QIIME 2 Reproducible, interactive, scalable, and extensible microbiome data science. **PeerJ Preprints**, 2018.
- [5] Erik Dassi, Pamela Ferretti, Giuseppina Covello, HTM-CMB-2015, Roberto Bertorelli, Michela A Denti, Veronica De Sanctis, Adrian Tett, and Nicola Segata. The short-term impact of probiotic consumption on the oral cavity microbiome. **Scientific Reports**, [I.F. 4.12], 8(10476), 2018.
  - [6] Pamela Ferretti, Edoardo Pasolli, Adrian Tett, Francesco Asnicar, Valentina Gorfer, Sabina Fedi, Federica Armanini, Duy Tin Truong, Serena Manara, Moreno Zolfo, Francesco Beghini, Roberto Bertorelli, Veronica De Sanctis, Iliaria Bariletti, Rosarita Canto, Rosanna Clementi, Marina Cologna, Tiziana Crifò, Giuseppina Cusumano, Stefania Gottardi, Claudia Innamorati, Caterina Masè, Daniela Postai, Daniela Savoi, Sabrina Duranti, Gabriele A Andrea, Leonardo Mancabelli, Francesca Turrone, Chiara Ferrario, Christian Milani, Marta Mangifesta, Rosaria Anzalone, Alice Viappiani, Moran Yassour, Hera Vlamakis, Ramnik Xavier, Maria Carmen Collado, Omry Koren, Saverio Tateo, Massimo Soffiati, Anna Pedrotti, Marco Ventura, Curtis Huttenhower, Peer Bork, and Nicola Segata. Mother-to-infant microbial transmission from different body sites shapes the developing infant gut microbiome. **Cell Host & Microbe**, [I.F. 17.87], 24:133–145, 2018.
  - [7] Eric A Franzosa, Lauren J Mciver, Gholamali Rahnnavard, Luke R Thompson, Melanie Schirmer, George Weingart, Karen Schwarzberg Lipson, Rob Knight, Gregory Caporaso, Nicola Segata, and Curtis Huttenhower. Species-level functional profiling of metagenomes and metatranscriptomes. **Nature Methods**, [I.F. 26.92], 15:962–968, 2018.
  - [8] Daniel Kissling, Jorge Ahumada, Anne Bowser, Miguel Fernandez, Nestor Fernandez, Enrique Alonso Garcia, Robert Guralnick, Nick Isaac, Steve Kelling, Wouter Los, Louise McRae, Jean-Baptiste Mihoub, Matthias Obst, Monica Santamaria, Andrew Skidmore, Kristen Williams, Donat Agosti, Daniel Amariles, Christos Arvanitidis, Lucy Bastin, Francesca De Leo, Willi Egloff, Jane Elith, Donald Hobern, David Martin, Henrique Pereira, Graziano Pesole, Johannes Peterseil, Hannu Saarenmaa, Dmitry Schigel, Dirk Schmeller, Nicola Segata, Eren Turak, Paul Uhlir, Brian Wee, and Alex Hardisty. Building essential biodiversity variables (EBVs) of species distribution and abundance at a global scale. **Biological Reviews**, [I.F. 11.61], 93(1):600–625, 2018.
  - [9] Katri Korpela, Paul Costea, Luis Pedro Coelho, Stefanie Kandels-Lewis, Gonneke Willemsen, Dorret I Boomsma, Nicola Segata, and Peer Bork. Selective maternal seeding and environment shape the human gut microbiome. **Genome Research**, [I.F. 11.28], 28:561–568, 2018.
  - [10] Serena Manara, Edoardo Pasolli, Daniela Dolce, Novella Ravenni, Silvia Campana, Federica Armanini, Francesco Asnicar, Alessio Mengoni, Luisa Galli, Carlotta Montagnani, Elisabetta Venturini, Omar Rota-Stabelli, Guido Grandi, Giovanni Taccetti, and Nicola Segata. Whole-genome epidemiology, characterization, and phylogenetic reconstruction of *Staphylococcus aureus* in a paediatric hospital. **Genome Medicine**, [I.F. 8.90], 10(82), 2018.
  - [11] Federica Pinto, Adrian Tett, Federica Armanini, Francesco Asnicar, Adriano Boscaini, Edoardo Pasolli, Moreno Zolfo, Claudio Donati, Nico Salmaso, and Nicola Segata. Draft genome sequences of novel *Pseudomonas*, *Flavobacterium*, and *Sediminibacterium* strains from a freshwater ecosystem. **Genome Announcements**, pages 2–4, 2018.
  - [12] Nicola Segata. On the road to strain-resolved comparative metagenomics. **mSystems**, [I.F. 5.75], 3(2), 2018.
  - [13] Heba Shaaban, David A. Westfall, Rawhi Mohammad, David Danko, Daniela Bezdán, Ebrahim Afshinnekoo, Nicola Segata, and Christopher E. Mason. The Microbe Directory: An annotated, searchable inventory of microbes' characteristics. **Gates Open Research**, 2018.
  - [14] Angelo Joshua Victoria, Ernelea Cao, Nico Salmaso, Nicola Segata, and Claudio Donati. Draft Genome Sequence of the Cadmium-Resistant Strain JJU2, Belonging to the Family *Hapalosiphonaceae* of the *Cyanobacteria*. **Microbiology Resource Announcements**, 7(8):4–5, 2018.
  - [15] Moran Yassour, Larson Hogstrom, Eeva Jason, Heli Siljander, Jenni Selvenius, Sami Oikarinen, Heikki Hyöty, Jorma Ilonen, Suvi Virtanen, Pamela Ferretti, Edoardo Pasolli, Adrian Tett, Francesco Asnicar, Nicola Segata, Hera Vlamakis, Eric Lander, Curtis Huttenhower, Mikael Knip, and Ramnik Xavier. Strain-level analysis of mother-to-child bacterial transmission during the first few months of life. **Cell Host & Microbe**, [I.F. 17.87], 24:146–154, 2018.

- [16] Moreno Zolfo, Francesco Asnicar, Paolo Manghi, Edoardo Pasolli, Adrian Tett, and Nicola Segata. Profiling microbial strains in urban environments using metagenomic sequencing data. **Biology Direct**, 13(9), 2018.
- [17] Edoardo Pasolli, Lucas Schiffer, Paolo Manghi, Audrey Renson, Valerie Obenchain, Duy Tin Truong, Francesco Beghini, Faizan Malik, Marcel Ramos, Jennifer B Dowd, Curtis Huttenhower, Martin Morgan, Nicola Segata, and Levi Waldron. Accessible, curated metagenomic data through ExperimentHub. **Nature Methods**, [I.F. 25.06], 14:1023–1024, oct 2017.
- [18] Christopher Quince, Jared T Simpson, Alan W Walker, Nicholas J Loman, and Nicola Segata. Shotgun metagenomics, from sampling to analysis. **Nature Biotechnology**, [I.F. 41.67], 35(9):833–844, oct 2017.
- [19] Francesco Beghini, Edoardo Pasolli, Duy Tin Truong, Lorenza Putignani, Simone Caccio, and Nicola Segata. Large-scale comparative metagenomics of Blastocystis, a common member of the human gut microbiome. **ISME Journal**, [I.F. 9.30], 11:2848–2863, sep 2017.
- [20] 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], 27(4):626–638, jul 2017.
- [21] 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**, 2(1), 2017.
- [22] Giovanni Bacci, Alessio Mengoni, Ersilia Fiscarelli, Nicola Segata, Giovanni Taccetti, Daniela Dolce, Patrizia Paganin, Patrizia Morelli, Vanessa Tuccio, Alessandra De Alessandri, Vincenzina Lucidi, and Annamaria Bevivino. A Different Microbiome Gene Repertoire in the Airways of Cystic Fibrosis Patients with Severe Lung Disease. **International Journal of Molecular Sciences**, 18(8):1654, 2017.
- [23] Sabrina Duranti, Gabriele Andrea Lugli, Leonardo Mancabelli, Federica Armanini, Francesca Turroni, Kieran James, Pamela Ferretti, Valentina Gorfer, Chiara Ferrario, Christian Milani, Marta Mangifesta, Rosaria Anzalone, Moreno Zolfo, Alice Viappiani, Edoardo Pasolli, Ilaria Bariletti, Rosarita Canto, Rosanna Clementi, Marina Cologna, Tiziana Crifò, Giuseppina Cusumano, Sabina Fedi, Stefania Gottardi, Claudia Innamorati, Caterina Masè, Daniela Postai, Daniela Savoi, Massimo Soffiati, Saverio Tateo, Anna Pedrotti, Nicola Segata, Douwe van Sinderen, and Marco Ventura. Maternal inheritance of bifidobacterial communities and bifidophages in infants through vertical transmission. **Microbiome**, [I.F. 8.50], 5(1):66, 2017.
- [24] Tarcisio Fedrizzi, Conor J Meehan, Antonella Grottola, Elisabetta Giacobazzi, Fregni Serpini, Sara Tagliazucchi, Anna Fabio, Clotilde Bettua, Roberto Bertorelli, Veronica De Sanctis, Fabio Rumpianesi, Monica Pecorari, Olivier Jousson, Enrico Tortoli, and Nicola Segata. Genomic characterization of Nontuberculous Mycobacteria. **Scientific Reports**, [I.F. 5.23], 7(45254):1–19, 2017.
- [25] Pamela Ferretti, Stefania Farina, Mario Cristofolini, Giampiero Girolomoni, Adrian Tett, and Nicola Segata. Experimental metagenomics and ribosomal profiling of the human skin microbiome. **Experimental Dermatology**, [I.F. 2.67], 26(3):211–219, 2017.
- [26] Lauren J Mciver, Galeb Abu-ali, Eric A Franzosa, Randall Schwager, Xochitl C. Morgan, Levi Waldron, Nicola Segata, and Curtis Huttenhower. bioBakery: A meta'omic analysis environment. **Bioinformatics**, [I.F. 7.30], btx754, 2017.
- [27] Federica Pinto, Adrian Tett, Federica Armanini, Francesco Asnicar, Adriano Boscaini, Edoardo Pasolli, Moreno Zolfo, Claudio Donati, Nico Salmaso, and Nicola Segata. Draft Genome Sequence of the Planktic Cyanobacterium *Tychonema bourrellyi*, Isolated from Alpine Lentic Freshwater. **Genome Announcements**, 5(47):49–50, 2017.
- [28] Adrian Tett, Edoardo Pasolli, Stefania Farina, Duy Tin Truong, Francesco Asnicar, Moreno Zolfo, Francesco Beghini, Federica Armanini, Olivier Jousson, Veronica De Sanctis, Roberto Bertorelli, Giampiero Girolomoni, Mario Cristofolini, and Nicola Segata. Unexplored diversity and strain-level structure of the skin microbiome associated with psoriasis. **npj Biofilms and Microbiomes**, 3(14):1–23, 2017.
- [29] Enrico Tortoli, Tarcisio Fedrizzi, Conor J Meehan, Antonella Grottola, Elisabetta Giacobazzi, Giulia Fregni, Sara Tagliazucchi, Anna Fabio, Clotilde Bettua, Francesca Frascaro, Veronica De Sanctis, Olivier Jousson, Nicola Segata, Daniela M Cirillo, Anna Fabio, Clotilde Bettua, Roberto Bertorelli, Francesca

- Frascaro, Veronica De Sanctis, Monica Pecorari, Olivier Jousson, [Nicola Segata\\*](#), and Daniela M Cirillo\*. The new phylogeny of the genus *Mycobacterium*: The old and the news *Enrico*. **Infection, Genetics and Evolution**, 56(October):19–25, 2017.
- [30] Lorenzo Tosi, Viswanadham Sridhara, Yunlong Yang, Dongli Gua, Polina Shpilker, [Nicola Segata](#), Harry Larman, and Biju Parekkadan. Long-adaptor single-stranded oligonucleotide probes for the massively multiplexed cloning of kilobase genome regions. **Nature Biomedical Engineering**, 1(0092), 2017.
- [31] Sander Wuyts, Stijn Wittouck, Ilke De Boeck, Camille Allonsius, Pasolli Edoardo, [Nicola Segata](#), and Sarah Lebeer. Large-scale phylogenomics of the *Lactobacillus casei* group highlights taxonomic inconsistencies and reveals novel clade-associated features. **mSystems**, 2(4), 2017.
- [32] Moreno Zolfo, Adrian Tett, Olivier Jousson, Claudio Donati, and [Nicola Segata](#). MetaMLST: multi-locus strain-level bacterial typing from metagenomic samples. **Nucleic Acid Research**, [I.F. 10.16], 45(2):e7, 2017.
- [33] 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**, [I.F. 14.17], (16070), 2016.
- [34] 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.
- [35] 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.
- [36] [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.
- [37] 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.
- [38] 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.
- [39] Christian Milani, Gabriele Andrea Lugli, Sabrina Duranti, Francesca Turrone, 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.
- [40] [Nicola Segata](#). Gut Microbiome: Westernization and the Disappearance of Intestinal Diversity. **Current Biology**, [I.F. 9.57], 25(14):R611–R613, aug 2015.
- [41] 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], 11(12):e1004557, jun 2015.
- [42] 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.
- [43] 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.



- [44] Christian Milani, Leonardo Mancabelli, Gabriele Andrea Lugli, Sabrina Duranti, Francesca Turrone, 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], 81(20):02037–15, 2015.
- [45] Francesco Baldini\*, Nicola Segata\*, Julien Pompon\*, Roch Dabiré, Abdoulaye Diabaté, Elena Levashina<sup>^</sup>, and Flaminia Catteruccia<sup>^</sup>. Evidence of natural Wolbachia infections in field populations of *Anopheles gambiae*. **Nature Communications**, [I.F. 10.74], 5, jun 2014.
- [46] 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.
- [47] 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.
- [48] 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], 42(D1):D617–D624, jan 2014.
- [49] 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.
- [50] Christian Milani, Gabriele Lugli, Francesca Turrone, 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.
- [51] 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.
- [52] 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.
- [53] 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.
- [54] 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.
- [55] 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.
- [56] 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.
- [57] 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.
- [58] Annalisa Ballarini\*, Nicola Segata\*, Curtis Huttenhower<sup>^</sup>, and Olivier Jousson<sup>^</sup>. 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.

- [59] [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.
- [60] [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.
- [61] The Human Microbiome Consortium (including [Nicola Segata](#)). [A Framework for Human Microbiome Research.](#) **Nature**, [I.F. 36.28], 486(7402):215–221, jul 2012.
- [62] 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.
- [63] 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.
- [64] Sahar Abubucker, [Nicola Segata](#), Johannes Goll, Alyxandria Schubert, Jacques Izard, Brandi L. Cantarel, Beltran Rodriguez-Mueller, Jeremy Zucker, Mathangi Thiagarajan, Bernard Henrissat, Owen White, Scott T Kelley, Barbara Methe, Patrick D Schloss, Dirk Gevers, Makedonka Mitreva, and Curtis Huttenhower. [Metabolic Reconstruction for Metagenomic Data and Its Application to the Human Microbiome.](#) **PLoS Computational Biology**, [I.F. 5.22], 8(6):e1002358, jun 2012.
- [65] Karoline Faust\*, Fah J Sathirapongsasuti\*, Jacques Izard, [Nicola Segata](#), Dirk Gevers, Jeroen Raes\*, and Curtis Huttenhower\*. [Microbial co-occurrence relationships in the human microbiome.](#) **PLoS Computational Biology**, [I.F. 5.22], 8(7):e1002606, jun 2012.
- [66] Janjua Hussnain, [Nicola Segata](#), Paola Bernabò, Sabrina Tamburini, Albert Ellen, and Olivier Jousson. [Clinical populations of Pseudomonas aeruginosa isolated from acute infections show a high virulence range partially correlated with population structure and virulence gene expression.](#) **Microbiology**, [I.F. 3.06], 158(Pt 8):2089–2098, may 2012.
- [67] Sarah Jane Delany, [Nicola Segata](#), and Brian Mac Namee. [Profiling Instances in Noise Reduction.](#) **Knowledge-Based Systems**, [I.F. 2.42], 31:28–40, 2012.
- [68] [Nicola Segata](#)\*, Edoardo Pasolli\*, Farid Melgani, and Enrico Blanzieri. [Local SVM Approaches for Fast and Accurate Classification of Remote Sensing Images.](#) **International Journal of Remote Sensing**, [I.F. 1.12], 33(19):6186–6201, 2012.
- [69] Levi Waldron, Shuji Ogino, Yujin Hoshida, Kaori Shima, Amy McCart Reed, Peter Simpson, Yoshifumi Baba, Katsuhiko Noshu, [Nicola Segata](#), Gregory J. Kirkner, Edward Giovannucci, John Quackenbus, Georgia Chenevix-Trench, Todd R. Golub, Charles S. Fuchs, Giovanni Parmigiani, and Curtis Huttenhower. [Expression profiling of archival tissues for long-term health studies.](#) **Clinical Cancer Research**, [I.F. 7.74], 18(22):6136–46, 2012.
- [70] Andrew Sczesnak, [Nicola Segata](#), Xiang Qin, Dirk Gevers, Joseph F Petrosino, Curtis Huttenhower, Dan Littman, and Ivaylo Ivanov. [The genome of Th17 cell-inducing segmented filamentous bacteria reveals extensive auxotrophy and adaptations to the intestinal environment.](#) **Cell Host & Microbe**, [I.F. 13.73], 10:260–272, sep 2011.
- [71] [Nicola Segata](#) and Curtis Huttenhower. [Toward an efficient method of identifying core genes for evolutionary and functional microbial phylogenies.](#) **PLoS ONE**, [I.F. 4.41], 6(9):e24704, sep 2011.
- [72] [Nicola Segata](#), Jacques Izard, Levi Waldron, Dirk Gevers, Larisa Miropolsky, Wendy S Garrett, and Curtis Huttenhower. [Metagenomic Biomarker Discovery and Explanation.](#) **Genome Biology**, [article flagged as "Highly accessed" and selected for journal cover, I.F. 6.89], 12:R60, jun 2011.
- [73] Sonia A Ballal, Carey Ann Gallini, [Nicola Segata](#), Curtis Huttenhower, and Wendy S Garrett. [Host and gut microbiota symbiotic factors: lessons from inflammatory bowel disease and successful symbionts.](#) **Cellular microbiology**, [I.F. 5.63], 13(4):508–517, apr 2011.
- [74] [Nicola Segata](#) and Enrico Blanzieri. [Operators for transforming kernels into quasi-local kernels that improve SVM accuracy.](#) **Journal of Intelligent Information Systems**, [I.F. 1.08], 37(2):155–186, 2011.

- [75] Nicola Segata and Enrico Blanzieri. Fast and Scalable Local Kernel Machines. **Journal of Machine Learning Research**, [I.F. 3.12], 11:1883–1926, 2010.
- [76] Nicola Segata, Enrico Blanzieri, Sarah Jane Delany, and Pádraig Cunningham. Noise Reduction for Instance-Based Learning with a Local Maximal Margin Approach. **Journal of Intelligent Information Systems**, [I.F. 1.08], 35:301–331, 2010.
- [77] Nicola Segata and Enrico Blanzieri. Stochastic TT-Calculus Modelling of Multisite Phosphorylation Based Signaling: The PHO Pathway in *Saccharomyces Cerevisiae*. **Transactions on Computational Systems Biology**, X:163–196, 2008.
- [78] Nicola Segata, Enrico Blanzieri, and Corrado Priami. Towards the integration of computational systems biology and high-throughput data: supporting differential analysis of microarray gene expression data. **Journal of Integrative Bioinformatics**, 5(1), 2008.