



Introducing the Human Microbiome Action project to ML4Microbiome

ML4Microbiome online meeting – Wed 7, July, 2021

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Who am I?

- 2014 MSc in Computer Science
- 2019 PhD in Computer Science, minor in Computational Biology
- Currently, postdoc in Prof. Nicola Segata laboratory at the CIBIO Dept. (University of Trento, Italy)
- Working on the Human Microbiome Action project



Human Microbiome Action project

keep Europe at the forefront of microbiome research and innovation and maximize its impact by ensuring coherence and harmony in the way microbiome research is and will be performed

- Bring together leading EU and international players (partners and members of its Strategic Steering Committee and Stakeholders' Advisory Board).
- Collectively develop international synergies for research and knowledgetransfer in the microbiome field at EU and international levels
- Provide instruments to support a robust usage of microbiome knowledge to tackle the epidemics of chronic diseases.
- Leaders: Joël Doré (INRAE), Emmanuelle Maguin (INRAE), and Mani Arumugam (UCPH)

Objectives

- To map the state of play in health and clinical contexts with relevance in different countries and outline requirements towards an increase in data comparability
- 2. To reach consensus on references across different populations
- 3. To propose actions addressing gaps, emerging fields and political priorities
- 4. To facilitate cooperation and promote synergistic collaboration across existing international human microbiome initiatives

Core partners





International connections

International Human Microbiome Consortium IHMC

SSC & SAB



Human Microbiome Action approach & key outputs

European and international stakeholders **build consensus in the field of human microbiome** in collaboration with the International Human Microbiome Consortium (IHMC)

- Strategic Research and Innovation Agenda towards microbiomebased research and innovations for diagnosis and personalized prevention and treatment
- **Sustainability**: European Microbiome Centers Consortium (EMCC) & Human Microbiome Action repository

Human Microbiome Action structure



Standardization is fundamental for reproducibility

WP2 and WP3

 focus on data and analysis
 standardization in the context of the human microbiome

 Standardization is crucial to allow researchers to reproduce published results



WP2&3-Members







Prof. Nicola Segata





Prof. Mani Arumugam







Dr. Francesco Asnicar

WP2 & 3 – Objectives

Data and methods cannot exist without each other

- **Context**: Landscape mapping on sustainable aspects of standards to derive minimal microbiome data types and analysis methods standards
- **Challenge**: Lack of standardization of microbial data types and analytical methods makes it difficult to perform re-analysis and meta-analysis
- Rationale: Landscape mapping of microbiome data and analysis methods

Outcomes:

- SOPs for international committee and researchers for data standardization
- Focusing diverse body types (oral, gut, skin, etc)
- Future perspective of evolution of data and methods as a "moving" target

WP2 & 3 – Main Outcomes

- Standardize human microbiome data and analysis methods
- Determine current and foreseeable minimal requirements for data standards in microbiome investigations
- Consensus standards for essential microbiome data analysis methods
- Identify robust statistical and machine learning methods for integrative multi-omic analysis
- Unified repositories for consistently derived metadata to enable consistent re-analysis and meta-analysis

ML & Human Microbiome

Strong oral plaque microbiome signatures for dental implant

Paolo Ghensi 🔞 1.7, Paolo Manghi 1.7, Moreno Zolfo 👩 1, Federica Armanini 1, Edoardo Pasolli 1, Mattia Bolzan 1.6, Alberto Bertelle²,

-ederico Dell'Acqua², Ester Dellasega², Romina Waldner², Francesco Tessarolo³.4, Cristiano Tomasi⁵ and Nicola Segata 👩 🖻

diseases identified by strain-resolution metagenomics

npj Biofilms and Microbiomes

OPEN

ARTICLE

www.nature.com/npjbiofilm

Check for update

• We do use ML in our analysis

- For example
- Finding links with oral diseases
- Linking the microbiome with habitual diet and cardiovascular health
- Identifying microbial signatures for colorectal cancer

medicine

ARTICLES /doi.org/10.1038/s41591-020-01183-8

Check for updates

Microbiome connections with host metabolism and habitual diet from 1,098 deeply phenotyped individuals

Francesco Asnicar ^{© 1,6}, Sarah E. Berry^{2,16} [⊠], Ana M. Valdes ^{© 3,4}, Long H. Nguyen ^{© 5}, Gianmarco Piccinno [©] 1, David A. Drew ^{© 5}, Emily Leeming⁶, Rachel Gibson ^{© 2}, Caroline Le Roy ^{© 6}, Haya Al Khatib⁷, Lucy Francis ^{© 7}, Mohsen Mazidi⁶, Olatz Mompeo⁶, Mireia Valles-Colomer ^{© 1}, Adrian Tett¹, Francesco Beghini ^{© 1}, Léonard Dubois¹, Davide Bazzani¹, Andrew Maltez Thomas¹, Chloe Mirzayi⁸, Asya Khleborodova⁸, Sehyun Oh⁸, Rachel Hine ^{© 7}, Christopher Bonnett ^{© 7}, Joan Capdevila ^{© 7}, Serge Danzanvilliers ^{© 7}, Francesca Giordano⁷, Ludwig Geistlinger⁸, Levi Waldron ^{© 8}, Richard Davies ^{© 7}, George Hadjigeorgiou ^{© 7}, Jonathan Wolf ^{© 7}, José M. Ordovás ^{© 9,10}, Christopher Gardner ^{© 11}, Paul W. Franks^{12,13}, Andrew T. Chan ^{© 5,13,14,17}, Curtis Huttenhower ^{© 13,14,17}, Tim D. Spector ^{© 6,17} and Nicola Segata ^{© 1,15,17} [⊠]

medicine

ARTICLES //doi.org/10.1038/s41591-019-0405-

Corrected: Author Correctio

Metagenomic analysis of colorectal cancer datasets identifies cross-cohort microbial diagnostic signatures and a link with choline degradation

Andrew Maltez Thomas ^{1,2,3,32}, Paolo Manghi^{1,32}, Francesco Asnicar ¹⁰, Edoardo Pasolli¹, Federica Armanini¹, Moreno Zolfo ¹, Francesco Beghini ⁰, Serena Manara¹, Nicolai Karcher¹, Chiara Pozzi⁴, Sara Gandini ^{0,4}, Davide Serrano⁴, Sonia Tarallo ^{0,5}, Antonio Francavilla ^{0,5}, Gaetano Gallo ^{6,67}, Mario Trompetto⁷, Giulio Ferrero ^{0,8}, Sayaka Mizutani²¹⁰, Hirotsugu Shiroma⁹, Satoshi Shiba¹¹, Tatsuhiro Shibata ^{011,12}, Shinichi Yachida^{11,13}, Takuji Yamada^{9,14}, Jakob Wirbel ⁰¹⁵, Petra Schrotz-King ^{0,6}, Cornelia M. Ulrich¹⁷, Hermann Brenner^{16,18,19}, Manimozhiyan Arumugam ^{020,21}, Peer Bork ^{0,15,22,23,24}, Georg Zeller ^{0,15}, Francesca Cordero⁸, Emmanuel Dias-Neto ^{0,3,25}, João Carlos Setubal^{2,26}, Adrian Tett¹, Barbara Pardini ^{0,5,27}, Maria Rescigno²⁸, Levi Waldron ^{0,29,30,33}, Alessio Naccarati ^{0,5,31,33} and Nicola Segata ^{0,133}*



- The Human Microbiome Action project just started and is still a work in progress
- Our goals will be about data and analysis standardization of human microbiome data
- Standardization (both for data and analysis methods) will be fundamental also for ML
- Currently we are open for collaboration and/or discussion





Thank you!



Human Microbiome Action

- Prof. Joël Doré,
- Prof. Emmanuelle Maguin
- Prof. Mani Arumugam

- Prof. Dr. Peer Bork
- Prof. Nicola Segata
- Dr. Anandhi Iyappan



