Contribution ID : **79** Type : **not specified**

Strain-resolved metagenomics for human and food microbiome studies

The microbiome plays a critical role in human health and has also become a key focus in the development of food products. Our understanding of these complex microbial communities has been improved thanks to recent advances in metagenomics and computational development that has enabled large-scale integrative analyses. In this talk, we will provide an overview of recent and ongoing research that explores different aspects of strain-resolved metagenomics. Our work includes the development of tools to achieve microbial analysis at the strain level, as well as large-scale studies across diverse environments, with a focus on the intersection between human and food sources. We will also introduce machine learning approaches for predicting host phenotypes from metagenomic data, highlighting the growing potential for integrating computational methods into microbiome research.

References:

- Pasolli et al, Bifidobacteriaceae diversity in the human microbiome from a large-scale genome-wide analysis, under review
- Carlino et al, Unexplored microbial diversity from 2,500 food metagenomes and links with the human microbiome, Cell, 2024
- Bazzani et al, Favorable subgingival plaque microbiome shifts are associated with clinical treatment for peri-implant diseases, npj Biofilms and Microbiomes, 2023
- Manara et al, Maternal and food microbial sources shape the infant microbiome of a rural Ethiopian population, Current Biology, 2023
- Giliberti et al, Host phenotype classification from human microbiome data is mainly driven by the presence of microbial taxa, PLOS Computational Biology, 2022
- Tett et al, Prevotella diversity, niches and interactions with the human host, Nature Reviews Microbiology, 2021
- Pasolli et al, Large-scale genome-wide analysis links lactic acid bacteria from food with the gut microbiome, Nature Communications, 2020
- Pasolli et al, Extensive unexplored human microbiome diversity revealed by over 150,000 genomes from metagenomes spanning age, geography, and lifestyle, Cell, 2019
- Pasolli et al, Accessible, curated metagenomic data through ExperimentHub, Nature Methods, 2017

Department

Agricultural Sciences

Primary author(s) : PASOLLI, Edoardo (University of Naples Federico II)

Presenter(s) : PASOLLI, Edoardo (University of Naples Federico II)