



Introduction to metaproteomics

Jean Armengaud

► To cite this version:

Jean Armengaud. Introduction to metaproteomics. HUPO ReConnect 2021 - preconference webinar on Metaproteomics, The Human Proteome Organization (HUPO), Aug 2021, New Mexico, United States. hal-04476615

HAL Id: hal-04476615

<https://hal.inrae.fr/hal-04476615>

Submitted on 25 Feb 2024

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

HUPO ReConnect 2021



November 15 - 19, 2021

www.hupo2021.org

[f](#)
[in](#)
[t](#)
[v](#)
[y](#)
[u](#)

#HUPOreconnect @humanproteomeorg @hupo_org

HUPO ReConnect 2021 Pre Congress Webinar

Coming off the success of the virtual 2020 Congress, HUPO ReCONNECT 2021 builds on that momentum to bring you a highly innovative program that showcases the latest in Proteomics research and application. The program will take a deep dive into the latest in proteomics research and application. #HUPOreconnect is accessible virtually to attendees from anywhere in the world. Scientific sessions, mentoring sessions, breakout discussions, and much more. See the [full congress program](#) and meet the 2021 [congress speakers](#).

Register for the August Pre Congress Webinar!

August 16, 2021, 05:00 PDT - Metaproteomics

Metaproteomics is a key methodology for understanding the function of microbiomes by efficiently connecting genomic and metabolic information. Through the large-scale characterization of the entire protein complement of microbiota and the functional dynamics of the microbiome, metaproteomics has the potential to unravel the mechanistic details of microbial interactions with the host/environment. Functional characterization offers numerous advantages over nucleic acid-based methods that primarily measure taxonomic composition. However, while the techniques in current use for metaproteomics are fundamentally the same as those used for single-organism proteomics, there are a number of key differences in terms of sample preparation, analysis and data processing/interpretation that require specialized expertise for success in metaproteomics experiments.

Metaproteomics from Bench to The Clinic. The first speaker, Dr. Daniel Figeys, will introduce the human gut microbiome and discuss the advantages of using metaproteomics to better understand the biological processes ongoing in this dynamic microbiome environment. He will use a study of pediatric inflammatory bowel disease as an example.

Analysis of Functions Expressed by Microbiomes Using Metaproteomics. Data analysis of metaproteomics experiments presents unique challenges and requires novel software tools. The second speaker, Dr. Pratik Jagtap, will highlight efforts on the implementation of metaproteomics workflows and their use within the Galaxy bioinformatics platform (<https://usegalaxy.org>). These workflows analyze both the taxonomic and functional state of microbiomes and generate outputs for biological interpretation.

Dr. Daniel Figeys is a Professor in the Department of Biochemistry, Microbiology and Immunology and a member of the Ottawa Institute of Systems Biology. Daniel obtained a B.Sc. and a M.Sc. in chemistry from the Université de Montréal, Canada. He obtained a Ph.D. in Chemistry from the University of Alberta and did his postdoctoral studies at the University of Washington. Prior to his current position, Dr. Figeys was Senior VP of System Biology and Lead Profiling with MDS-Proteomics (2000-2004). He was responsible for all the analytical functions of MDS-Proteomics. Dr. Figeys' research focuses on the development and applications of technologies and bioinformatic tools to study the human gut microbiome and drug-microbiome interactions. His laboratory has published over 200 papers and has been cited over 17,000 times.

Pratik Jagtap is a Research Assistant Professor at the Department of Biochemistry, Molecular Biology and Biophysics at the University of Minnesota in Minneapolis, Minnesota. He received his Ph.D. degree from the Center for Cellular and Molecular Biology, Hyderabad, India. During his post-doctoral research work at the Max-Planck Institute in Tuebingen, Germany and later at the University of Michigan in Ann Arbor, he worked on genomic and proteomic analysis of bacteria. Since 2016, he has served as a Galaxy-P project co-lead and has worked with the team to utilize and publish various workflows for multi-omic data analysis. His current research interests include developing workflows for the analysis of complex data, with particular emphasis on mass spectrometry-based proteomics applications in metaproteomics, proteogenomics and data-independent acquisition (DIA).

Jean Armengaud (session chair) is Chief Deputy of the Laboratory of Innovative Technologies for Detection and Diagnostics located near Avignon in France. He is also Director of the ProGénoMIX platform, specialized in proteogenomics and metaproteomics. His goal is to contribute to a better understanding of the functioning of complex biological systems and exploit this knowledge for medical and environmental purposes. He received his Ph.D. in biochemistry in 1994 at the University of Grenoble.

Tim Van Den Bossche (session co-chair) is a Ph.D. student researcher in the CompOmics lab of Prof. Lennart Martens. His focus is the field of microbial community proteomics, commonly known as metaproteomics. He led the first-ever, community-driven, multi-site benchmark study that compared a wide variety of state-of-the-art metaproteomics analysis pipelines (wet-lab and computational). Tim is currently applying machine learning algorithms to improve peptide identifications, and downstream taxonomical and functional annotation of metaproteomics datasets. In addition to playing an active role in several scientific communities such as EuBIC-MS and HUPO-PSI, Tim is a co-founder of the Metaproteomics Initiative (<https://metaproteomics.org/>).