SPEECH INFORMATION (For Conference Program Book)	
Topic	Microbiome analysis for human and planetary health
Abstract (No more than 350 words)	Environmental sequencing, that is metagenomics, has become a major driver for uncovering microbial biodiversity and increasingly also for molecular functionality on our planet. Based on computational methods and resources, often developed in our group, here I (i) introduce into our work on the gut microbiome, arguable the best-studied microbial community, serving as a model for other habitats. Metagenome-wide association studies and systemic approaches enable bioinformatics-driven hypothesis generation, for fundamental understanding and applications, like biomarker-based diagnostics (1). I (ii) further show how to apply the underlying concepts to other habitats, like ocean and soil, to get closer to a much needed understanding of microbial life on earth and its contributions to ecosystems services. For this, we have developed a planetary-scale microbial resource (SPIRE) that we have started to mine, e.g. for gene evolution at global sale or fluxes of molecular functions across habitats, such as antibiotic resistance (2). We complement analysis of public data with an ambitious, integrative, continental-scale international initiative, TREC (Traversing Ecosystems), that includes expeditions with mobile lab to capture life in context. The first expedition has traversed European coastlines in 2023 and 2024. This multidisciplinary, multiscale and open science endeavor brings molecular data to environmental research at an unprecedented scale, with a holistic view of microbial life and its biotic and abiotic interactions across ecosystems. Analysis of environmental microbiomes and contextual data can also inform on critical aspects of human health. In analogy to microbial diagnostics and treatment for human health, we foresee microbiome-informed bioindicator and remediation strategies towards improving planetary health.