

Mapping host-microbe interactions in health and disease with network biology tools.

## Tamás Korcsmáros Imperial College London

Analyzing interspecies interactions between hosts and microbes is crucial for understanding how microbiota changes can disrupt host homeostasis and lead to disease. High-throughput sequencing and omics approaches have advanced our understanding of these interactions in the gastrointestinal tract. We developed MicrobioLink, a computational pipeline that predicts host-microbe protein interactions, integrating multi-omic data with network biology to enhance insights into these complex interactions, especially in inflammatory and infectious diseases. Our research focuses on autophagy, often targeted by microbes. We mapped interactions between human autophagy proteins and 56 pathogenic bacterial species, identifying bacterial proteins that modify autophagy components. We are now using organoid and gut-on-chip systems to validate our computational predictions, moving beyond traditional cell-line infection assays.

Wednesday, 13.11.2024, 17:00
University of Cologne
Institute for Biological Physics
Seminar Room S0.02, Zülpicher Str. 77a