

Cologne Evolution Colloquium

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CRC 1310 Predictability in Evolution Metabolic interactions and ecological networks of the gut microbiome in healthy versus disease states

AS gut microbiota are now known to impart functional influence in the host-microbe interplay via biological, chemical or physical interactions, much interest is presently garnered in discovering new genes and enzymatic function involved in microbial metabolism and associated metabolites, to newly address fundamental questions about the distribution of microbes and their influence in human health. Little is known however about the temporal dynamics modulating microbial perturbation and adaptation, recently shown to be critical in early-life colonisation, and presentation of antibiotic or dietary selective pressures. Due to the significant computational challenges and data deluge posed in metagenomics, much of the progress has only recently commenced, leaving substantial room in developing *in silico* approaches to expand our spectrum in biomedical inquiry of commensal microbiota. To address this, I present a three-part methodology. First, a gene-targeted approach to study microbial-mediated metabolites is presented for learning key metagenomic features to characterise various perturbations incurring host-phenotypic changes using a range of resolutions (species, strain, orthology, genomic). Next, a species interaction network is employed to examine combinatorial relationships, perturbation patterns, and topology signatures intrinsic in the underlying ecology. Lastly, I expand this paradigm as a hybrid network integrating metabolic data, to curate biochemical exchanges and detect functional triggers in healthy versus diseased states.

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Institute for Biological and Theoretical Physics

Zülpicher Str. 77

Conference Room, Old Building

Hosted by Andreas Beyer and Michael Lässig