

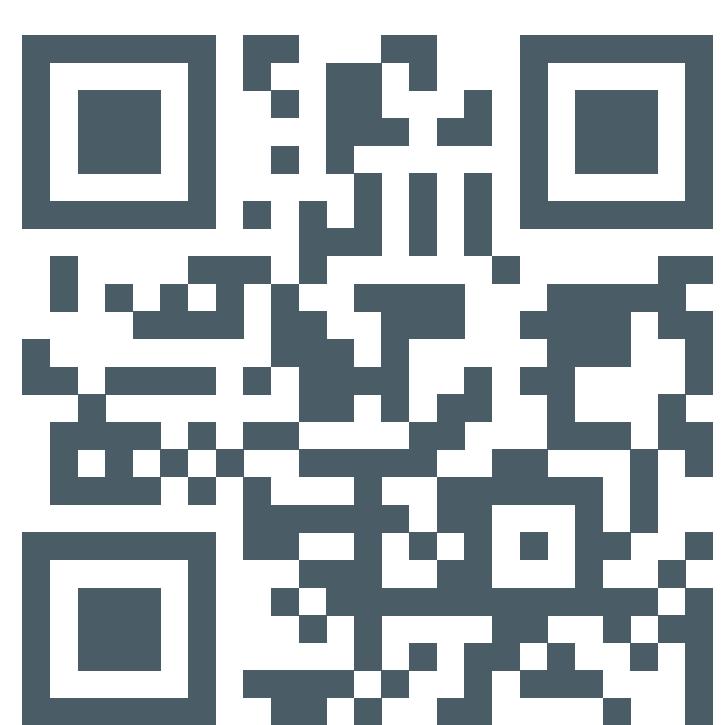
KoBIS

Gäste und Themen:

Quantifying Microbiome Differences

Stefan Janssen

Sequencing-based analysis of microbiota is a crucial tool for many biological and medical disciplines to investigate microbial diversity that would otherwise be missed by culture-based approaches. Shifts in microbial composition can lead to phenotypic changes of the host, like obesity in mice, Clostridium difficile infection in human or the development of Parkinson's disease. Shifts can be induced via dietary changes or addition of (anti-), pre- or probiotics, which might open up routes for beneficial host modulations in e.g. human health. Unfortunately, microbiome data is typically very noisy - not only due to technical biases ranging from sample handling to sequencing platform of choice, but also due to many biological confounding factors like diet, age, ethnicity, hygiene or country. My talk will cover statistical concepts of state of the art tools to disentangle different effects and to quantify microbial ecology sequencing data applied to an ongoing microbiome project investigating the role of the gut microbiome in childhood leukemia development.



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Was ist KoBIS?

Das Kolloquium für Bioinformatik und Systembiologie Mittelhessen (KoBIS) ist eine gemeinsame Initiative der Technischen Hochschule Mittelhessen und der Justus-Liebig-Universität Gießen zum wissenschaftlichen Austausch zwischen Arbeitsgruppen und Hochschulen, die sich mit dem Thema Bioinformatik und Systembiologie beschäftigen.

Präsentiert werden Projekt- und Abschlussarbeiten sowie aktuelle Forschungsthemen von Mitarbeitern und externen Gästen.

Interessierte sind herzlich willkommen!