

Title	Analysis of the human microbiome using network approaches
Group	Systems and Synthetic Biology
Project type	thesis
Credits	36
Supervisor(s)	Dr. Edoardo Saccenti (SSB), Dr Annelies Kers (MIB)
Examiner(s)	Dr. Edoardo Saccenti, Dr Annelies Kers
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Begin date	

Used skills: Network inference and analysis, multivariate statistics, and programming; Relating results to existing or novel microbiology knowledge

Requirements: Ability to program in R, MATLAB, or Python and (basic) statistics and microbiology knowledge as well are desired skills.

Description: Studies of the human microbiome have revealed that even healthy individuals differ remarkably in the microbes that occupy habitats such as the gut, skin and vagina. Much of this diversity remains unexplained, although diet, environment, host genetics and early microbial exposure have all been implicated. Using data from the Human Microbiome (4,788 specimens from 242 screened and phenotyped adults, this project focuses on the analysis of the composition of microbial communities and on the characterization of subject specific interplay among different bacteria. You will do this applying existing networks and network analysis tools and helping in developing new approach to analyse microbiome data. This project is collaboration between the System and Synthetic and Biology and the Microbiology groups

References

Huttenhower, C., D. Gevers, R. Knight, S. Abubucker, J. H. Badger, et al The Human Microbiome Project (2012). "Structure, function and diversity of the healthy human microbiome." Nature **486**(7402): 207-214.

Altenbuchinger, M., A. Weihs, J. Quackenbush, H. J. Grabe and H. U. Zacharias (2020). "Gaussian and Mixed Graphical Models as (multi-)omics data analysis tools." Biochim Biophys Acta Gene Regul Mech **1863**(6): 194418.

Jahagirdar, S. and E. Saccenti (2021). "Evaluation of Single Sample Network Inference Methods for Metabolomics-Based Systems Medicine." Journal of Proteome Research **20**(1): 932-949.