Can chatty bacteria resolve Urinary Tract Infections?
Theoretical MSc project
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Microbes also live in our urinary tract and are sometimes responsible for serious infections. Urinary tract infections (UTI) may range from uncomplicated to severe illness. The most recent research links the imbalance of the whole microbial community that colonizes the urinary tract as an important factor in the development of such infections. The role of interactions between the members of a UTI community is a hallmark to understand and possibly prevent the associated illness, however, such interactions remain largely elusive.

Aim
In this project, we investigate the role of the interactions between members of a UTI community using newly available genomes. By mining the genomic information, we investigate the potential function of each community member from the structural components, such as motility and biosynthesis of secondary metabolites. Furthermore, we reconstruct genome-scale metabolic models to investigate putative interactions between the members of the community. We use metabolomics data to understand the microbial activity in the harsh environment of artificial urine. By combining the data mentioned above with already published data of microbial composition (16s metabarcoding) and pairwise growth data we study the system of UTI community with top-down and bottom-up approaches.

Planned activities (and methods)
This computational project consists of analyzing multiple levels of biological information using various bioinformatics, data science and statistical methods and tools. With this analysis, you will investigate the interactions between bacteria involved in UTIs. We would like to answer questions such as, to what extent do the bacterial interactions enhance the growth of pathogens, as well as, what is their effect on the tolerance of antimicrobial resistance in these communities. By utilizing literature of available studies, we can extend our research questions to the ecological sphere. For example, what environmental factors differentiate an UTI community from their healthy counterpart and how similar are urinary tract communities when compared to other host related biomes.

With this internship, you will learn how to perform research on individual genomes, microbial communities and metabolomics data with the aim to improve human health. You will sharpen your bioinformatics, statistics and modeling skills alongside with biology and ecology knowledge. You will participate in our group meetings and Journal club. Previous experience with coding is a requirement (R, Python, Linux). For this position we look for highly motivated and curious students to whom future academic careers are a potential perspective.

Duration
6 or 9 Months (Available from January 2022)

Important publications to read:

1. Ecological interactions in polymicrobial infection
   Marjon G. J. de Vos, Marcin Zagorski, Alan McNally, Tobias Bollenbach
   Proceedings of the National Academy of Sciences Oct 2017, 114 (40) 10666-10671; DOI: 10.1073/pnas.1713372114

2. Lara, E.G.; van der Windt, I.; Molenaar, D.; de Vos, M.G.J.; Melkonian, C. Using Functional Annotations to Study Pairwise Interactions in Urinary Tract Infection Communities. *Genes* **2021**, *12*, 1221. https://doi.org/10.3390/genes12081221