The project

Extended microbiome characterization by the exploitation of the microbial intra-community synergies — towards better understanding of the Exposome

In recent years the more focus has been placed on human exposome and how it affects human health and well-being. Exposome understood as the set of human environmental exposures (complementing the genome) from conception onward includes: a general external environment, a specific external environment, and internal environment factors. In all three categories, an alive part of the exposome are different microbiomes, e.g. urban microbiome, skin microbiome, gut microbiome.

There are many efforts around the world to pursue the knowledge behind many different types of microbiomes and to extract the information directly from metagenomes. Projects such as MetaHIT, Human Microbiome Project or American Gut Project/Microsetta Initiative had led to the growth of information about plenty of gut connected diseases such as obesity, inflammatory bowel syndrome or ulcerative colitis. Similar insight has been gained by projects focused on skin microbiota (The Human Skin Microbiome Project), environmental microbiome (Earth Microbiome Project), urban and subway microbiomes (MetaSUB International Consortium), and many more. However, only a few of them had also considered establishing interactions between microorganisms among themselves, with the environment, and with human beings as one of the main goals.

Microbiomes are diverse, dynamic, and complex parts of exposomes that are crucial for determining health. The composition of these biomes by nature is strongly related to the ecological niche they occupy and thus synergies and anergies are here dominant factors. Thus, the goal of the project is to extend our knowledge about interactions within and between features that arise in three complementary views on the microbiome: view through the lenses of compositional/taxonomical profile (i.e., abundance of microbial species), view through the lenses of functionalities related to the phenomena under scrutiny and view using variables derived directly from the samples (i.e., sequences obtained from a sample). Where in the last view no prior knowledge of microbial genomes and sequences of functional proteins are used.

In particular, we want to explore synergistic interactions between features and by this go beyond currently available approaches that are ill-fitted to analyse metagenomic data as they are not exploiting the existence of these relations.

Specifically, we will investigate synergies in three exposome related use-cases:

- Anomaly detection in microbiomes - identification of resistomes for AMR studies,
- Patient stratification - usage of microbiota profiles for establishing health status of the patient,
- Calculation of distances between microbiomes - prediction of the geographical origin of the sample.

The proposed type of analysis in the context of selected use-cases can lead to the discovery of new functionalities or new species that are relevant for the interesting phenomena.

The role

The tools we are going to use in the search of synergies are based on Multi Dimensional Feature Selection (MDFS) framework, developed by our team at the University of Białystok. MDFS is currently a statistical filter, aimed on identification of all the relevant features, that influence the response variable via multivariate interactions. It uses information measure of interactions to compute the test statistic. The computations are performed exhaustively for all the k-tuples of features, using GPU for better performance.

The first task for our team is adaptation of the MDFS software to microbiome analysis. This involves both programmer's work, like handling the bigger amount of data, as well as pure statistical problems, like defining a significance criterion for synergistic interactions. New tools for exploration of the cluster structure of the data with respect to particular response variables will also be needed for our analyses. The developed tools will be used to analyse data sets, coming from our partners at Jagiellonian University. Our task will involve identification of relevant features at three levels: taxonomical profiles, functionalities and genetic sequences, then finding all the interesting synergistic interactions between the variables. We will also explore the network or cluster structure of the data to obtain a deeper view into the human microbiome.

Skills/Qualifications

Requirements:

- PhD degree, preferably in computer science/mathematics/natural sciences/engineering;

- good practical programming skills, preferably in C/C++ and R;

- relevant knowledge in statistics;

- ability to understand scientific papers and to communicate scientific results in English.

Desirable qualifications:

- experience in machine learning techniques,

- experience in CUDA technology,

- experience in big data handling,

- experience in bioinformatics,

- knowledge about metagenomics.

PLEASE NOTE:

Due to NCN regulations we are not allowed to hire postdocs who obtained their PhDs at the University of Białystok, nor earlier than 7 years ago. More formal details can be found at

https://www2.ncn.gov.pl/sites/default/files/pliki/uchwaly-rady/2020/uchwala61_2020-zal1.pdf, pages 35-36. For more information or to share your opinion, please contact the agency via e-mail:

kancelaria@ncn.gov.pl.

We offer

- full-time employment from 01.02.2023 to 30.11.2023, with possibility of extension

- remuneration at the rates applicable to projects financed by the NCN for post-doc (i.e. 120 000 PLN per annum, total employment costs)

- opportunity to collaborate with world-class researchers from Jagiellonian University and University of Białystok, as well as institutions such as Weill Cornell Medicine, ETH Zurich, Acibadem University, East China Normal University

- scientific and professional mentorship,

- position 100% focused on research and development (no compulsory teaching),

- opportunity to work on an ambitious and important scientific problem with interdisciplinary applications,

- opportunity and support to participate scientific meetings across the globe,

- flexible working time,

- opportunity to work (partly) remotely.

How to inquire

Please send an email to k.mnich@uwb.edu.pl (in email title please include "SONATA BIS Research Associate 2" and your first and last names) with documents as specified below before 24th of December 2022.

List of documents:

1. application form;
2. CV including information on the candidate's scientific, teaching and organisational achievements, list of publications etc.;
3. copy of the doctoral diploma;
4. information regarding processing of personal data.