Call for PhD student applications: forslund lab @ ECRC

Starting 2018, this new lab at the ECRC (*joint cooperation of Max-Delbrück Center for Molecular Medicine in the Helmholtz Association and Charité Universitätsmedizin Berlin*) conducts **host-microbiome analysis of cardiovascular disease**. Our areas of operation:

- Computational biology/bioinformatics tool development. Improving, deploying and testing algorithms, programs and resources to enable the systems biology we want to carry out. Here functional annotation of microbial genes using evolutionary bioinformatics is especially important.

- High-throughput host- and microbiome data processing. Working with sequencing centers and other core facilities, we transform raw measurements into biologically and clinically relevant quantitative profiles.

- Host-microbiome systems medicine of cardiometabolic disease. Drawing on the above, for existing and novel human and animal cohorts, we model risk, progression and treatment of, in particular, cardiovascular and metabolic disease. Findings can then be followed up together with experimental collaborators.

PhD project: Causality networks of remote microbiome host impact

Many human health states *(including progression and recovery in cardiovascular and metabolic diseases)* have been linked to signatures *(microbiome composition, gene expression, immune state, circulating marker levels)* measurable in high-throughput. Full interpretation and exploitation of such datasets requires us to **distinguish causality from correlation**, and to disentangle treatment effects from pathology *(see our previous work e.g. Forslund et al., Nature 2015 PMID:26633628)*. Moreover, both risk factors and treatment involve **indirect mechanisms of remote action**, including **microbiome mediation** *(see our previous work e.g. Pedersen et al., Nature 2016 PMID:27409811)*. Presently available case-control study designs involving one or two -omics types at once identify associations but cannot reveal mechanisms. **Longitudinal/interventional** data sets therefore herald a **new paradigm for systems medicine**, so long as the computational challenges can be solved.

You will develop, benchmark and deploy tools and algorithms for **inferring causality networks of host-microbiome interactions** from such longitudinal data, especially **metagenomic, metabolomic, immune cell and phenotype** high-throughput measurements. Starting e.g. from **SEM models** or **Bayesian Networks**, you will write and apply software to find the best-supported **mechanism and directionality** of influences, compare and contrast it to previously generated cross-sectional data, and thereby **tease apart pathology, risk factors, treatment effects and noise** driving outcome in novel and pre-existing human patient cohorts, especially subjects treated for **cardiovascular diseases**. Thus you will help identify **new potential treatment avenues**, drug targets, probiotics and/or diagnostic signatures that could enable **personalized healthcare**.

In the main, **your work will be theoretical and computational**, though you may also be asked to help generate some of the datasets you will work on e.g. in the form of **sample preparation for biobanking or sequencing**. You are expected to participate throughout the whole chain from study and algorithm design, throughout **data generation, processing, analysis, and interpretation**, as well as identification of candidate features for **validation in animal models**. On a personal level, you must commit to **clear and open communication**, to ask for clarification wherever needed, and to help create an **inclusive, respectful collegial environment**, where each person is expected to help and to ask for help as needed, working towards our shared goals, certain in the knowledge that this work will be recognized. Initiative, responsibility, conscientiousness and **dedication to stay true to science** all are necessary, as is the willingness to request, receive and learn from feedback.

On a skills level, **ability to communicate clearly** in writing, speech and visual media is crucial, as is the ability to work in **Linux/UNIX** computer environments, to **program and/or script** (preferably a multipurpose scripting language like Perl or Python as well as R). You will be expected to be able to start from a piece of scientific literature, then acquire, install and test the software pipelines described, and to merge these into a whole for our purposes, including applications on our **high-performance computing systems**. You need the ability and interest to **visualize data and to experiment with new solutions** until objectives are reached. You need the ability to work in an organized manner, including to **document, version control and share your code**. You need statistical and mathematical skills, as well as the **willingness to learn biology and medicine as needed** to design tests and interpret their results.

To apply, you need not already possess all these skills, but you do need to want to learn them during your PhD project in the lab. In return, we undertake to provide **an environment at once nurturing and challenging**, regardless of your background. We welcome you to an **internationally competitive** research environment and the chance to grow both individually as a scientist and by taking place in that larger **network of collaborations** and shared projects, against the backdrop of one of Europe's most iconic and vibrant cities.

How to apply?

Send your application to forslund@forslund-lab.net . Include the following PDF files:

- **Cover letter**, specifically including your research interests and outlining which of the skills sought that you currently possess (referring to your CV), and your contact information. Also specifically list if you have published in peer-reviewed journals. **Max 1 page.**

- Full **curriculum vitae** including which courses you have taken.

- **Letters from preferably two references** who have worked with you including their contact details. They may send these directly as well if they prefer.

To improve your chances, clearly spell out your computational skills. Recruitment will stay open until the position is filled by an appropriate candidate, upon which this notice will be taken down. Sufficiently skilled applicants beyond the selected candidate are still welcome to submit their applications, as we can look into other potential funding sources.

MDC MAX DELBRÜCK CENTER FOR MOLECULAR MEDICINE IN THE HELMHOLTZ ASSOCIATION

CHARITÉ UNIVERSITÄTSMEDIZIN BERLIN