Degree project/research practice in CARAMBA (Clinical Analysis & Research Applying Mass spectrometry & Bioinformatics)

We are looking for an ambitious student with an interest in either analytical chemistry and mass spectrometry or multivariate statistics, or preferably a combination of both, for a project in the molecular effects of hematopoietic stem cell transplantation (HSCT) treatment for multiple sclerosis.

Multiple sclerosis is a chronic immune-mediated disease in which the immune system attacks the protective myelin sheaths on the neurons. The exposed axons cause the nerve impulses traveling to and from the brain and spinal cord to be distorted or interrupted, giving rise to a variety of symptoms depending on the afflicted area. By far the most common phenotype is relapsing-remitting multiple sclerosis (RRMS) in which focal inflammation appears over time, initializing clinical relapses that are followed by a partial or complete recovery.

HSCT is a relatively new treatment for RRMS, which is designed to eliminate autoreactive immune cells to enable restoration of a healthy immune system (Burt RK *et al.* 2019, PMID: 30644983). While the removal of autoreactive cells is thought to be key in HSCT, less is known about the molecular mechanisms and events over the time of ongoing treatment.

Mass spectrometry-based untargeted metabolomics is the comprehensive profiling of low-weight molecules or metabolites comprising the dynamic molecular network called the metabolome. As metabolites constitute all intermediate- or end products of all chemical pathways, changes caused by various pathophysiological processes will immediately leave traces in the metabolome. We have previously investigated the chemical pathways and pathological processes occurring in multiple sclerosis (Herman S *et al.* 2019, PMID: 30678351) and integrated these with proteomic, radiological and clinical data (Herman S *et al.* 2018, PMID: 30214633).

In this project, we have access to longitudinal blood samples from RRMS patients who have undergone HSCT. The samples were collected (1) before starting the treatment, (2) while undergoing the treatment and (3) three months after the treatment. The proteome of these patients have been investigated using proximity extension assay (PEA) (www.olink.com). The question of interest is hence, to explore the molecular events occurring when undergoing HSCT using metabolomics technologies and integrate these findings with alterations occurring on a protein level.

If you find this project of interest, please contact the PI:

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