



Master project 2024-2025

Personal Information

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Project

Computational systems biology

Project Title:

Role of the microbiome in associations between the exposome and child development

Keywords:

exposome; microbiome; metagenomics; epidemiology

Summary:

The gut microbiome is not only a major modulator of human physiology and biochemistry but represents a critical interface between the host and its environment. Trillions of microbial cells are present in the human gut, harbouring vast genetic and, therefore, phenotypic diversity. A substantial part of metabolic activity in humans is accounted for by the gut microbiome. The microbiome also impacts upon the immune system and inflammatory response in a number of ways, changing gut physiology and contributing to the presentation of chronic disease. Significantly for exposome research, the microbiome has a major effect on the metabolic fate of environmental chemicals either directly, for example activating PAHs and deactivating digoxin, or indirectly, via xenobiotic enzyme induction.⁸² Conversely, exposures, particularly dietary and physical activity, can reshape the gut microbiome and modulate health risk in this way.^{83,84} Few metagenomic data are available for adolescent cohorts, although this period is of interest as gut microbiomes during this period are enriched in functions that support ongoing development. We have sequenced the faecal microbiome in adolescents (new HELIX subcohort follow-up), generating a unique resource for exposome research and the wider scientific community. The aim is to develop an approach for integrative analyses of microbiome (shotgun quantitative metagenomics data) with the exposome in adolescents. This project will use a unique dataset available through the European Project ATHLETE (<https://athleteproject.eu/>), led by ISGlobal (campus Mar - PRBB <https://www.isglobal.org/en/child-health?inheritRedirect=true>), pioneers' researchers in the field of exposome research (<https://www.isglobal.org/exposome-hub>). The dataset consists of 800 mother-adolescent pairs with exposomics and metagenomic data. The metagenomics data have already been processed by our collaborators in Nottingham University, UK. They are composed of an average of 127,262 sequences per sample, 179,878,417 genes predicted and a total of 47,132 Metagenome-assembled genomes (MAGs). Project objectives: 1- Identify the main statistical tools present in the literature for integrating metagenomic data in epidemiological studies 2- Develop a bioinformatic pipeline in R to look for association between metagenomic and exposomic data 3- Prepare a scientific manuscript The student will learn: - How to conduct an epidemiological analysis with advanced statistical tools - To work with metagenomic and exposome data, which are highly promising new omics technologies in the post-genomic era in the health sector - Write a scientific manuscript The student will fully integrate the regular team meetings and seminars with opportunities to present their work and get training in epidemiology and statistics.

References:

Maitre, L et al. Nature Communications <https://www.nature.com/articles/s41467-022-34422-2> Clarke, G. et al. Pharmacol. Rev. (2019) Allen, J. M. et al. Med. Sci. Sports Exerc. (2018) Flint, H. J. et al. Nat. Rev. Gastroenterol. Hepatol. (2012) Hoyles, L. et al. Microbiome (2018)

Expected skills:

R programming, Statistics, Biology

Possibility of funding:

To be discussed

Possible continuity with PhD:

To be discussed

Comments:

possibility of remote work