

# **Post-doctoral position in data sciences: Innovative multi-omics data integration methods applied to the prediction of food allergy**

## **Context**

Global 'omics' approaches (e.g. metabolomics) are of high interest for the understanding of human metabolism and the prediction of diseases. Analysis of such datasets (which contain a larger amount of – multicollinear - features compared to observations) require dedicated statistical methods for mining and prediction (Thévenot et al., 2015; Rinaudo et al., 2016).

Today, the combination of complementary omics analyses (e.g. metabolomics and lipidomics) emerges as a promising approach to extend the list of biomarkers and increase the prediction performances. New statistical methods are thus needed to model such multi-table datasets.

To understand the impact of maternal environment to early breast milk composition and the development of food allergy, 300 milk samples from the EDEN mother-child cohort have been analyzed by metabolomics, lipidomics, glycomics and immune approaches.

## **Project**

The objective of this project is to develop new biostatistics methods to integrate the five data sets as well as the clinical covariates and build robust and accurate prediction models of food allergy. Linear (multi-block data analysis, partial correlation network) and nonlinear approaches will be used, in addition to network analysis (to include additional biological and chemical information).

Challenges will include the selection of a restricted multi-omics signature, the confounding effects, the distinct collection times of the samples, and the heterogeneity of the 'allergy' class.

The methods will be implemented in R.

## **Profile**

Interested applicants should have PhD in applied statistics (biostatistics, data analysis, machine learning, feature selection, network analysis), and be motivated by multidisciplinary applications (chemistry, biology, clinic).

## **Contact**

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