The cardiometabolic diseases (CMD) are progressive metabolic disorders leading to chronic stages of cardiovascular diseases and heart insufficiency. For a long time the genetic diversity has been ignored and the same treatment has been applied to all patients with a similar diagnosis. However, it was not clear how individual patients respond to it. Advances in data processing from large epidemiological and genome-wide studies are expected to contribute to the resolution of the worldwide cardiometabolic epidemics. The identification of responders to therapies is crucial to provide the most appropriate treatment and avoid unnecessary medications. Machine learning possesses powerful frameworks to integrate a vast amount of data from heterogeneous sources, design new models, and test multiple hypotheses and therapeutic products. Probabilistic graphical models (PGM), such as Bayesian networks, are widely used to model structures in various applications, and in particular, in bioinformatics. The PGM techniques have been applied to data with arbitrary structure. The PhD candidate will develop methods of data integration of bioclinical and environmental phenotyping together with personalized omics (metagenomics, metabolomics, transcriptomics) with the objective of developing new strategies for personalized medicine. It is expected that the candidate implements the proposed approaches in R/Matlab/C/C++. 