Differential network analysis with multiply imputed lipidomic data

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The importance of lipids for cell function and health has been widely recognized, *e.g.*, a disorder in the lipid spectrum of cells has been related to atherosclerosis caused cardiovascular disease (CVD). Lipidomics analyses are characterized by large yet not huge number of mutually correlated variables measured and their associations to outcomes are potentially of complex nature. Differential network analysis responds to the need for efficient and interpretable analysis tools in the fields of lipidomics, and provides a formal statistical method capable of inferential analysis to examine differences in network structures of the lipids under two biological conditions. We provide a recipe to conduct permutation test on association scores resulted from partial least square regression on multiple imputed lipidomic data from the LUdwigshafen RIsk and Cardiovascular Health study, particularly paying attention to the left-censored missing values typical to many life science data sets. With accordingly customized network analysis, we take full advantage of the data achieving useful information about the underlying biological process, find lipids that interact with each other, and recognize the most important differentially expressed lipids between two subgroups of coronary artery disease (CAD) patients, the patients that had a fatal CVD event and the ones who remained stable during two year follow-up.

Keywords: Differential network analysis, multiple imputation, left-censoring, lipidomics.