**MetaHD: an R package for meta-analyzing high-dimensional data**

Modern studies in evidence synthesis, such as those in large-scale biological datasets, have focused on combining results from studies that have measured multiple effect sizes associated with multiple correlated outcomes, necessitating multivariate approaches to meta-analysis. In this context, usually there are many more variables of interest than there are studies, and so the meta-analysis can be considered high-dimensional. As an example of high-dimensional meta-analysis, we consider metabolomics. Since summary measures on the same set of metabolites are often not available, resulting in a reduced number of studies for individual variable inference, multivariate meta-analysis techniques can be all the more useful. Meta-analysis methods currently available for combining such high-dimensional biological data, however, often overlook considerations such as correlation between the metabolites, missing values, and within- and between-study variability. The R package MetaHD performs a multivariate meta-analysis for high-dimensional data, which can be used to integrate and collectively analyze both individual-level data as well summary statistics from multiple studies. This approach accounts for correlation between metabolites, considers variability within and between studies, handles missing values, and uses shrinkage estimation to allow for high dimensionality. MetaHD can be particularly useful in the high-dimensional context in the presence of missing values, as it exploits the borrowing strength between metabolites.

**Availability:** The R package MetaHD can be easily downloaded from CRAN

**Keywords: R package; Metabolomics; High-dimensional data; Meta-analysis**