ABSTRACT

Hierarchical modeling allows for two appealing characteristics in shrinkage estimation. First, it leads to a more natural way of taking into account the uncertainty in the estimates than simply summarizing the result of each test in a $p$-value. Second, as the data are treated as exchangeable rather than independent, this allows for feedback as each data point informs the distributions of the rest. Given the estimates of multiple mean parameters, this model gives rise to a natural shrinkage estimator, dubbed Adaptive SHrinkage (ASH). In this talk, I propose an extension of ASH to allow covariates associated with each estimate. Examples of applicable covariates include, but are not limited to, indicators of set membership. The model has applications in meta-analysis but also genomic studies, in which each gene may have a corresponding estimate of some mean effect, and the problem of interest is identifying which of the mean effects are nonzero.