Testing multiple families of hypotheses

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As the size of large testing problems encountered in genomic research keeps increasing, more of these problems have further structure where the set of hypotheses can be further partitioned into families of the hypotheses, and the true state of the tested signals tends to be more similar within these subsets than across the subsets. Moreover, interest may lie with a discovery of a family with some signal in it, on top of the discovery of a signal in each of the many hypotheses on its own.The challenges in the analysis of such multiple testing problems will be discussed. We then present the concept of control on the average over the selected families of the desired error-rate, be it the familywise error rate the False Discovery Rate, or their generalizations. We discuss the various considerations involved using the genomic part of a Norwegian epidemiological and a study involving genomics and brain imaging.