



MASTER'S THESIS PRESENTATION

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Multi-Layer FDR Control for Grouped Hypotheses using E-Values

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ABSTRACT

In many practical applications of multiple testing, there are natural ways to partition the hypotheses into groups using the structural, spatial or temporal relatedness of the hypotheses, and there may be more than one way to partition, not necessarily in hierarchical order. The p-filter procedure is a method that enables researchers to control the $\textit{False Discovery Rate}$ (FDR) simultaneously for all partitions.

In some natural settings, it is possible that the p-values in the hypotheses are arbitrarily correlated. In particular, some p-values may be negatively correlated with the other. On the other hand, the p-filter works the best if the p-values are assumed to be independent, or at least PRDS (Positive Regression Dependence on a Subset), a form of positive dependence. With no assumption on dependence, the FDR of p-filter will be inflated by a factor of $\sum_{i=1}^n \frac{1}{i} \approx \log\{n\}$, where n is the number of hypotheses. Therefore, if we correct for this factor to keep FDR the same, the p-filter may be too conservative to efficiently detect any false hypotheses for large n .

In this paper, we introduce the $\textit{e-filter}$, which is a natural analog of the p-filter that utilizes e-values. By resorting to e-values, the e-filter controls the FDR at the desired level for any dependence structure between the e-values without any correction. If there is only one partition and it is on individual level, i.e., each group contains only one hypothesis, then e-filter recovers the well-known e-BH procedure. Moreover, we could recognize e-filter as a generalization of p-filter through calibration between p-values and e-values. We will justify our findings with simulations where the number of hypotheses is large, but the dependence structure of data is complicated. Overall, the e-filter procedure gives us an alternative to p-filter that could be useful in some natural settings.