



Simple estimators of false discovery rates given as few as one or two p-values without strong parametric assumptions

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Multiple comparison procedures that control a family-wise error rate or false discovery rate provide an achieved error rate as the adjusted p-value for each hypothesis tested. However, since such p-values are not probabilities that the null hypotheses are true, empirical Bayes methods have been devised to estimate such posterior probabilities, called local false discovery rates (LFDRs) to emphasize the frequency interpretation of their priors. The main approaches to LFDR estimation, relying either on numerical algorithms to maximize likelihood or on the selection of smoothing parameters for nonparametric density estimation, lack the automatic nature of the methods of error rate control. To begin filling the gap, this paper introduces automatic methods of LFDR estimation with proven asymptotic conservatism under the independence of p-values but without strong parametric assumptions. Simulations indicate that they remain conservative even for very small numbers of hypotheses. One of the proposed procedures enables interpreting the original FDR control rule in terms of LFDR estimation, thereby facilitating practical interpretation. The most conservative of the new procedures is applied to measured abundance levels of 20 proteins.

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