

Testing Procedures on Comparisons of Several Treatments with one Control in a Microarray Setting

Ziv Shkedy^a, Dan Lin^a, Tomasz Burzykowski^a, Hinrich W.H. Göhlmann^b, An De Bondt^b, Tim Perera^b, Tamara Geerts^b, Luc Bijnen^b

^a:Hasselt University, Center for Statistics, Agoralaan, Building D, B-3590 Diepenbeek, Belgium. ^b:Johnson & Johnson PRD, Turnhoutseweg 30, 2340 Beerse, Belgium

We discuss a particular situation in a microarray experiment; when two dimensional multiple testing occurs because of comparing several treatments with a control at one hand and testing tens of thousands of genes simultaneously at the other hand. Dunnett's single step procedure (Dunnett 1995) for testing effective treatments can be used to address one dimensional question of primary interest. The Dunnett's procedure is implemented within resampling-based algorithms such as Significance Analysis of Microarray (SAM, Tusher *et al.* 2001) and Benjamini and Hochberg False Discovery Rate (FDR, Benjamini and Hochberg 1995). To combine the two-dimensional testing problem into one testing procedure, we proposed an approach to test for $m \times K$ (number of genes * number of comparisons between several treatments with the control) tests simultaneously. We compare the performance of SAM and the classical BH-FDR. The method was applied to a microarray experiment with four treatment groups (three microarrays in each group) and 16998 genes. Additionally a simulation study was conducted to investigate the power of the methods proposed and to investigate how to choose the fudge factor in SAM to leverage the genes with small variances.

Keywords: Dunnett's single step procedure; microarray; multiple testing; Benjamini and Hochberg false discovery rate (BH-FDR); SAM.