Use of the Normal Probability Plot to Identify Significant Effects for Microarray Data

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Abstract: Motivated by methodologies for analysis of designed experiments, we propose a novel technique to identify significant effects in replicated microarray experiments. Given a robust measure of location and scale for each gene, a normal or half-normal probability plot of a comparative test statistic is constructed. We then fit robust regression lines to sections of the plot to determine the location of the "change-points." This procedure only requires a small number of comparisons in order to declare a larger subset of genes to be significant. Additionally, it is flexible in that it can incorporate input from the scientist on the number of genes to be declared significant. Illustration of this methodology, as well as extensions to other types of gene expression data, will be given. Joint work with Greg Dyson.