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The contaminated chi-square model and its application to microarray data analysis

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A Contaminated Beta (CB) model may be used to describe the distribution of P values corresponding to a large number of hypothesis tests, such as those assessing differential expression at numerous genes on a microarray. If those P values originate from Z or T statistics, then one may also describe the Z or T statistics themselves using a Contaminated Normal (CN) model. An advantage of the CN model over the CB model is that, under some circumstances, there may be more power to reject an omnibus null hypothesis of no differential expression and more accurate estimation of the proportion of genes differentially expressed. However, comparisons involving three or more groups may give rise to chi-square or F statistics rather than Z or T statistics, so that the CN model is inapplicable in these instances. Therefore, we propose using a Contaminated Chi-Square (CCS) model to describe the distribution of chi-square or F statistics corresponding to a large number of hypothesis tests. Using the CCS model, we present methodology for testing an omnibus null hypothesis of no differential expression and for estimating the proportion of genes differentially expressed. Through simulation studies and real data analyses, we ascertain the circumstances under which using the CCS model for chi-square or F statistics is preferable to using the CB model for P values.

Biography

Richard Charnigo is an Associate Professor of Statistics and Biostatistics at the University of Kentucky in Lexington, KY, USA. He completed his Ph.D. in Statistics at Case Western Reserve University in Cleveland, OH, USA. His research interests in statistics include mixture modeling with applications to genetics and perinatal epidemiology as well as nonparametric regression with applications to nanoparticle characterization and Raman spectroscopy. His applied research interests include psychology, health behavior, organizational behavior, mechanical engineering, and cardiology. He serves on the editorial board of the Journal of Biometrics and Biostatistics

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