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Hypothesis testing in normal admixture models to detect heterogeneous genetic signals

In this work author consider a three-component normal mixture model in which one component is known to have mean zero and the other two contaminating components have a non-negative and a non-positive mean respectively, while all three components share a common unknown variance parameter. One potential application of this model may be in prioritizing statistical scores obtained in biological experiments, including genetics data. Such a mixture model may be useful in describing the distribution of numerous Z test statistics corresponding to different genes or SNPs, such that a "significant" Z test statistic for a particular gene suggests its connection to a medical condition. More specifically, the inferences drawn from such a mixture model may be useful in a filtration algorithm to remove large subsets of genes or SNPs from consideration, thereby reducing the need for stringent and power- depleting multiplicity adjustments for controlling type I errors on the remaining genes. The author show how to test whether there is contamination in at least one direction (i.e., the mixture model truly requires at least two components) and, if so, how to test whether there is contamination in both directions (i.e., the mixture model truly requires all three components). The author assess the testing procedures in simulation studies and illustrate them through application to LOD scores in a genome-wide linkage analysis from an autism study.

Biography

Richard Charnigo is a Professor in the Department of Biostatistics (College of Public Health) and Department of Statistics (College of Arts and Sciences) at the University of Kentucky. He received his PhD in Statistics from Case Western Reserve University in 2003. His research interests include mixture modeling, nonparametric smoothing, cardiology, psychology, and public health.

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