3-14-2016

Biostatistics News

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A diagnostic cut-off point of a biomarker measurement is needed for classifying a random subject to be either diseased or healthy. However, the cut-off point is usually unknown and needs to be estimated by some optimization criteria. One important criterion is the Youden index, which has been widely adopted in practice. The Youden index, which is defined as the maximum of \((\text{sensitivity} + \text{specificity} - 1)\), directly measures the largest total diagnostic accuracy a biomarker can achieve. Therefore, it is desirable to estimate the optimal cut-off point associated with the Youden index. Sometimes, taking the actual measurements of a biomarker is very difficult and expensive, while ranking them without the actual measurement can be relatively easy. In such cases, ranked set sampling can give more precise estimation than simple random sampling, as ranked set samples are more likely to span the full range of the population. In this study, kernel density estimation is utilized to numerically solve for an estimate of the optimal cut-off point.

The asymptotic distributions of the kernel estimators based on two sampling schemes are derived analytically and we prove that the estimators based on ranked set sampling are relatively more efficient than that of simple random sampling and both estimators are asymptotically unbiased. Furthermore, the asymptotic confidence intervals are derived. Intensive simulations are carried out to compare the proposed method using ranked set sampling with simple random sampling, with the proposed method outperforming simple random sampling in all cases. A real data set is analyzed for illustrating the proposed method.

“Improved nonparametric estimation of the optimal diagnostic cut-off point associated with the Youden index under different sampling schemes,” was published in the Biometrical Journal.

Dr. Jingjing Yin, Assistant Professor of Biostatistics at the Jiann-Ping Hsu College of Public Health Georgia Southern University (JPHCOPH) was the lead author. Dr. Hani Samawi, Director of the K.E. Peace Center for Biostatistics, and Dr. Daniel Linder, Assistant Professor of Biostatistics at JPHCOPH were co-authors.
Georgia Southern Examines Correction of Verification Bias

March 14, 2016

In diagnostic medicine, the test that determines the true disease status without an error is referred to as the gold standard. Even when a gold standard exists, it is extremely difficult to verify each patient due to the issues of cost effectiveness and invasive nature of the procedures. In practice some of the patients with test results are not selected for verification of the disease status which results in verification bias for diagnostic tests. The ability of the diagnostic test to correctly identify the patients with and without the disease can be evaluated by measures such as sensitivity, specificity and predictive values. However, these measures can give biased estimates if we only consider the patients with test results who also underwent the gold standard procedure.

The emphasis of this paper is to apply the log-linear model approach to compute the maximum likelihood estimates for sensitivity, specificity and predictive values. We also compare the estimates with Zhou’s results and apply this approach to analyze Hepatic Scintigraph data under the assumption of ignorable as well as non-ignorable missing data mechanisms. We demonstrated the efficiency of the estimators by using simulation studies.


Dr. Haresh Rochani, Assistant Professor of Biostatistics at the Jiann-Ping Hsu College of Public Health Georgia Southern University (JPHCOPH) was the lead author. Dr. Hani Samawi, Director of the K.E. Peace Center for Biostatistics, Dr. Robert Vogel, Dual Department Chair for Biostatistics and Epidemiology, and Dr. Jingjing Yin, Assistant Professor of Biostatistics at JPHCOPH were co-authors.